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Neerav D. Padliya, Wesley M. Garrett, Kimberly B. Campbell,
David L. Tabb and Bret Cooper

Tandem mass spectrometry for the detection of plant pathogenic fungi and the effects of database composition on protein inferences

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S1. Protein assembly of peptide sequence matches made to tag-filtered U. maydis tandem mass spectra. The NCBI NR database was searched. Protein List with probabilities. The columns are arranged as follows: peptide sequence, Mascot Ions score, Mascot Identity score, computed peptide mass, observed precursor mass, number of tandem mass spectra assigned to same peptide sequence, the charge states observed for the peptide, whether the peptide is shared between protein groups with different probabilities (number in parentheses is number of other groups peptides are shared with) or is distinct (considered a unique identifier for proteins grouped with the same probability), the number of missed tryptic cleavages in this sequence, and the probability for a particular peptide sequence.

1. Group probability: 1.0000. Peptides of the group

AFSMHHVDK	56.37	55.9665	1070.497	1071.193	1	2	distinct	0	0.9442
ADSLVYIGLR	71.52	55.5765	1105.613	1106.248	1	2	distinct	0	0.9857
EVAEVVESHAK	66.21	55.334	1196.604	1196.884	2	2	distinct	0	0.9782
VVEMALDHVNGAPGKR	89.66	54.5603	1691.878	1693.255	11	+2,+3	distinct	1	0.9999
LPLTLGGDHSLALGTVSGSLR	136.53	53.5765	2063.137	2064.343	16	+2,+3	distinct	0	1
KGVDTGPVSLVQAGICQQLESLGWK	103	52.0879	2669.385	2669.743	14	+2,+3	distinct	1	1
DRPIHLSFDVDALDPSVAPSTGTPVR	72.17	51.8967	2761.403	2762.436	5	3	distinct	0	0.9913
VDFTDHHSFDHINQGIDSDTDIGNMK (0000000000000000000000000100)	56.72	51.3531	2957.289	2958.684	5	+2,+3	distinct	0	0.9972

The equivalent proteins include

gi|71021711|ref|XP_761086.1|	35056.82	hypothetical protein UM04939.1 [Ustilago maydis 521]

2. Group probability: 1.0000. Peptides of the group

INVEIVEER	64.36	55.7416	1099.587	1099.67	1	2	distinct	0	0.9724
GTTWELVYR	52.99	55.2238	1123.566	1123.811	1	2	distinct	0	0.9261
MLEQIISGELK	52.29	55.6374	1259.679	1260.552	1	2	distinct	0	0.9256
KMLEQIISGELK	71.71	55.3867	1387.774	1388.375	1	2	distinct	1	0.966
DKEDNDLATYCR	83.55	54.7169	1498.636	1499.036	1	2	distinct	1	0.9955
DVTLDPGFKEFYAFAK	79.51	54.0396	1846.914	1847.497	3	2	distinct	1	0.9945
ANNIPVIIVSSGMTPIIR	81.76	53.8979	1894.071	1894.962	1	2	distinct	0	0.9958
NRPTLFFAGDGISDMSAAR (000000000000000100000)	76.56	53.5175	2024.974	2041.889	10	+2,+3	distinct	0	0.9999
SILSNLIGEKDANEIDVISNEVK	44.38	52.6236	2499.307	2499.949	1	2	distinct	1	0.9086

The equivalent proteins include

gi|71017999|ref|XP_759230.1|	29676.87	hypothetical protein UM03083.1 [Ustilago maydis 521]

3. Group probability: 1.0000. Peptides of the group

KANITITNSVGR	66.22	55.4985	1272.715	1273.207	1	2	distinct	1	0.9789
IQSLISEFFGGR	69.91	55.0668	1352.709	1353.924	2	2	distinct	0	0.9849
ARFEEINAAAFK	75.7	54.986	1365.704	1366.683	2	2	distinct	1	0.9909
IPADKVDDIVLVGGSTR	96.66	54.1099	1753.957	1754.383	3	2	distinct	1	0.9988
ALELLEVQDASADEYR	57.75	54.2002	1820.879	1821.683	1	2	distinct	0	0.9625
ALELLEVQDASADEYRR	72.46	53.7058	1976.98	1977.303	2	2	distinct	1	0.9901
NDLEAYVHSVEETISSPAANLK	71.05	52.8099	2386.165	2386.383	1	2	distinct	0	0.9908
ATAGDTHLGGEDFDNALLDHFKK	61.33	52.8707	2471.172	2472.279	5	+2,+3	distinct	1	0.9992
HDAKNDLEAYVHSVEETISSPAANLK	47.37	51.7535	2837.383	2838.651	1	3	distinct	1	0.9236
TLSSVTQTTVEVDSLFQGVDFQANITR	68.95	51.433	2955.482	2956.662	2	3	distinct	0	0.989

The equivalent proteins include

gi|71020701|ref|XP_760581.1|	45677.76	hypothetical protein UM04434.1 [Ustilago maydis 521]

4. Group probability: 1.0000. Peptides of the group

LGITDVDLK	48.55	56.4518	972.549	973.897	1	2	distinct	0	0.8881
YSLKPVAAEVSK	62.49	55.3784	1290.718	1291.049	3	+1,+2,+3	distinct	0	0.9998
IGTSLFDEAGSHK	78.23	55.2404	1360.662	1361.763	3	+2,+3	distinct	0	0.999
AHSSMVGVQLPKR (000001000000000)	88.96	54.791	1408.761	1409.211	34	+1,+2,+3	distinct	1	1
LGDVYINDAFGTAHR	67.38	54.5936	1647.8	1647.988	1	2	distinct	0	0.9832
ALESPERPFLAILGGAK	74.67	54.1554	1767.988	1768.816	12	+2,+3	distinct	0	0.999
YHVEEEGKGTNEAGEK	89.69	54.1162	1775.796	1776.493	2	2	distinct	1	0.9977
VDFNVPMDGDKITNNQR	60.93	53.8149	1961.926	1962.281	1	2	distinct	1	0.9728
TILWNGPAGVFEFDNFAGGSK	103.11	53.0929	2226.074	2226.793	4	2	distinct	0	0.9994
TGSATDADGIPDEWMGLDAGEESRK	82.93	52.3547	2607.139	2607.721	1	3	distinct	1	0.9965

The equivalent proteins include

gi|71021575|ref|XP_761018.1|	44933.25	hypothetical protein UM04871.1 [Ustilago maydis 521]

5. Group probability: 1.0000. Peptides of the group

EAFTDLGSTGKL	46.39	55.0639	1237.619	1238.121	1	2	distinct	1	0.8809
GVLDIVPAGVVSGK	70.41	55.2862	1309.76	1309.598	2	1	distinct	0	0.9864
HEISTAVSHGVVK	76.06	55.0978	1362.725	1363.347	11	+1,+2,+3	distinct	0	1
GLSNSNQEASIIGAK	85.93	54.8619	1487.758	1488.676	1	2	distinct	0	0.99
MNVDTDTQWAYLLGIR	107.55	53.9001	1894.925	1895.324	8	2	distinct	0	0.9995

DYLMSQVGNPDGADKPNK	73.33	53.934	1947.9	1948.423	1	2	distinct	0	0.9911
AVAPSYGVPVIMHSDHCAK (00000000000100000000)	93.56	53.5911	2037.976	2038.413	8	2	distinct	0	0.9986
SDKENPVFFVFHGGSGSEK	82.63	53.544	2066.97	2067.355	5	+2,+3	distinct	1	0.9995
DYLMSQVGNPDGADKPNKK	87.3	53.4504	2075.995	2076.283	6	+2,+3	distinct	1	0.9999
KLLPWFDGMLAADEEYYK	78.61	53.2812	2188.055	2188.424	5	2	distinct	1	0.9945
FAIPAFNVTSSSVAISALEAAR	125.84	53.1288	2221.174	2221.343	27	+2,+3	distinct	0	1

The equivalent proteins include

gi|71004310|ref|XP_756821.1|	39444.72	hypothetical protein UM00674.1 [Ustilago maydis 521]

6. Group probability: 1.0000. Peptides of the group

VVPGYGHAVLR	61.97	55.5418	1166.656	1167.723	5	2	distinct	0	0.9682
VSQVAPGVLKEHGK	50.12	54.9502	1447.815	1448.463	1	2	distinct	1	0.9202
SMSMDSLEAFLKK	73.93	54.9389	1485.721	1486.16	1	2	distinct	1	0.9898
LGEIQLQHLLGGMR (0000000000000100)	69.53	54.6551	1563.855	1564.485	13	+1,+2,+3	distinct	0	0.9999
DAVAEIIPAKQEQLK	57.41	54.5723	1651.914	1653.047	2	2	distinct	1	0.8911
KTEYWAPVLEDSIDLIAK	99.31	53.358	2090.094	2090.49	15	2	distinct	1	0.9991
VMLWEGSVLDSETGITFHGK	82.05	53.2762	2205.078	2205.895	2	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71006216|ref|XP_757774.1|	51130.68	hypothetical protein UM01627.1 [Ustilago maydis 521]

7. Group probability: 1.0000. Peptides of the group

SGEHLLGAFK	52.49	56.0184	1057.556	1057.815	1	2	distinct	0	0.9237
HVVSLGLVSGR	55.52	55.2768	1122.651	1122.483	3	+1,+2	distinct	0	0.9964
SGEHLLGAFKK	57.33	56.0058	1185.651	1185.413	2	1	distinct	1	0.9518
VANIKEEDLAR	60.36	55.7236	1256.672	1256.855	1	2	distinct	1	0.9633
TLPVAGLHIDLDR	48.66	54.8982	1418.788	1419.676	1	2	distinct	0	0.9062
INNTKPIDDFVEAK	59.54	54.6487	1602.825	1603.848	1	2	distinct	0	0.9653
APEQLDEVLAAFVNTK	71.94	54.2527	1743.904	1743.659	3	2	distinct	0	0.9892
LSAEVLDWFSFANEK	44	54.1691	1754.851	1754.708	1	2	distinct	0	0.8704
GMLTGPVTILNWSFPR (0010000000000000000)	100.71	54.2225	1787.939	1789.194	20	2	distinct	0	0.9964
VQIASSSSLLHTPITIANEK	107.22	53.2555	2108.148	2109.14	2	2	distinct	0	0.9996
IMIATYFNKLESNLEIVK	60.32	53.2959	2125.149	2125.7	1	2	distinct	1	0.9726
EHLALPIFPTTTIGSFPQTK	85.31	53.2272	2197.178	2198.081	8	+2,+3	distinct	0	0.9998
LGEAGAEWVQIDEPVLVLDR	97.73	53.1393	2208.143	2209.533	3	2	distinct	0	0.999
VQIASSSSLLHTPITIANEKK	75.8	53.0751	2236.243	2237.513	4	+2,+3	distinct	1	0.9996
WFDSNYHYLVPELSESTEFK	101.27	52.4395	2490.138	2490.443	6	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71004830|ref|XP_757081.1|	85459.12	hypothetical protein UM00934.1 [Ustilago maydis 521]

8. Group probability: 1.0000. Peptides of the group

WHMYDTVK	45.79	55.8802	1078.491	1078.295	2	1	shared(2)	0	0.8591
LGANSLLDIVVFGR	117.51	54.9405	1472.835	1473.482	43	+1,+2	shared(3)	0	1
HTLSWQHEGTGDK	75.64	54.5851	1494.685	1495.035	8	+1,+2,+3	distinct	0	1
TVIELEHFGLPFSR	69.56	54.571	1643.867	1644.351	11	+2,+3	distinct	0	0.9992
NLLTCATQTMHSAAAR	72.26	54.2773	1744.835	1745.752	1	2	distinct	0	0.9895
IDKVYSTFPDVSIQDR	78.67	54.0036	1881.947	1882.361	2	+2,+3	distinct	1	0.9993
GSDWLGDQDAIHYMCR	69.66	54.0504	1922.804	1923.836	2	2	distinct	0	0.9869
EPIPVLPTVHYNMGGIPTK	51.65	53.4026	2062.092	2062.594	1	2	distinct	0	0.8007
GVISTTLDEAECKPVPPFK	101.11	53.3455	2087.061	2087.372	2	2	distinct	0	0.9993
IVPGLYAAGETACVSVHGANR	99.8	53.2124	2141.069	2141.516	2	2	distinct	0	0.9992
AYFSATSAHTCTGDGMAMVSR	77.68	53.1291	2219.94	2220.956	1	2	distinct	0	0.9947
GVISTTLDEAECKPVPPFKR	94.16	53.2242	2243.162	2243.763	3	2	distinct	1	0.9987
GYPVIDHEYDAIVVGAGGSGLR	97.82	53.2335	2244.117	2244.363	3	+2,+3	distinct	0	1
AGLPLQDLEFVQFHPTGIYGAGCLITEGSR	70.18	50.9484	3245.618	3246.573	5	3	distinct	0	0.9353

The equivalent proteins include

gi|71005306|ref|XP_757319.1|	71954.79	hypothetical protein UM01172.1 [Ustilago maydis 521]

9. Group probability: 1.0000. Peptides of the group

HVAAQGYGYLEDR	83.29	54.7841	1477.695	1477.829	3	2	distinct	0	0.9955
HNEHIAVYGADNDK	83.06	54.4752	1581.717	1582.278	2	2	distinct	0	0.9956
HETGHIGDFSSGVANR	94.28	54.2981	1682.776	1682.85	8	+2,+3	distinct	0	1
HNEHIAVYGADNDKR	92.7	54.1341	1737.818	1737.983	4	+2,+3	distinct	1	1
GGFPGPQGPYYCGAGAGK	76.09	54.1597	1739.772	1739.76	4	2	distinct	0	0.993
VQAEYIWIDGDGEIR	89.49	54.1402	1762.853	1763.015	1	2	distinct	0	0.9934
RGDNVIVLAECYNNDGTPNK	90.11	53.1912	2248.054	2248.473	4	2	distinct	1	0.9981
AVPGDWNGAGCHTNYSTASMR	45.9	53.5067	2250.953	2250.903	2	2	distinct	0	0.9125

The equivalent proteins include

gi|71018887|ref|XP_759674.1|	44352.96	hypothetical protein UM03527.1 [Ustilago maydis 521]

10. Group probability: 1.0000. Peptides of the group

INDNLLISR	68.29	56.0673	1056.593	1057.139	1	2	distinct	0	0.8889
NQKLDHAVELK	67.92	55.1301	1293.704	1294.413	2	2	distinct	1	0.9813
DSPFPAPSEGEIKK	49.78	55.0311	1500.746	1500.944	1	2	distinct	1	0.9177
ASSTISSITGSTPSGVR	52.45	54.5787	1606.816	1607.951	1	2	distinct	0	0.942
KQGIWAPVDASQSPK	83.15	54.4647	1610.842	1611.703	3	2	distinct	1	0.9958
FNNCVCHLATGDMLR (00000000000001000)	84.3	54.1505	1806.796	1806.736	8	2	distinct	0	0.9961
LATYHAQTAAVTDYYR	87.09	54.1198	1842.89	1843.489	3	2	distinct	0	0.9971
LATYHAQTAAVTDYYRK	76.03	53.6745	1970.985	1971.613	2	2	distinct	1	0.9928
EFSPPKKPMTDDVTGEPLIQR	70.76	52.8475	2384.205	2385.562	3	+2,+3	distinct	1	0.9998

The equivalent proteins include

gi|71008792|ref|XP_758235.1|	32732.76	hypothetical protein UM02088.1 [Ustilago maydis 521]

11. Group probability: 1.0000. Peptides of the group

LNRPLSLAEK	50.43	55.128	1139.666	1140.098	2	2	distinct	0	0.9102
SKFTITPGSEQIR	47.97	55.0353	1462.778	1463.466	1	2	shared(3)	1	0.9
CTTDHISAGGPWLK	60.06	54.7314	1541.73	1542.693	3	+2,+3	distinct	0	0.9962
IVYGHLDNPHEQEISR	86	53.9622	1905.933	1906.393	9	+2,+3	distinct	0	0.9996
KQGMLAFEFADPADYDK	90.48	53.8028	1944.893	1945.425	1	2	distinct	1	0.998
AIEINKEVYDFLATATAK	106.47	53.6194	1996.052	1996.545	8	2	distinct	1	0.9929
AGGMVLANACGPCIGQWDR (00001000000000000000)	78.71	53.6317	2031.908	2032.389	5	2	distinct	0	0.9947
VRPDDLVDILGVTELAPGSK	103.95	53.3886	2093.137	2093.203	6	2	distinct	0	0.9994
EAGKPWVVIGDENYGEGSSR	67.25	53.298	2149.007	2149.39	2	+2,+3	distinct	0	0.9989
AGGMVLANACGPCIGQWDRK	98.18	53.2224	2160.003	2161.283	3	+2,+3	distinct	1	1
GHLENISNNCLIGAINAANGK	95.92	53.2287	2179.08	2179.573	2	2	distinct	0	0.9989
DELPLTHTMNDNQISWFK	63.13	53.2498	2188.026	2188.928	2	+2,+3	distinct	0	0.9986
NDANPATHAFVASPDLVTAMAFAGR	81.98	52.4786	2543.223	2543.943	7	+2,+3	distinct	0	1
DGSKDELPLTHTMNDNQISWFK	62.93	52.3488	2575.201	2576.273	1	2	distinct	1	0.9815

The equivalent proteins include

gi|71017631|ref|XP_759046.1|	86741.76	hypothetical protein UM02899.1 [Ustilago maydis 521]

12. Group probability: 1.0000. Peptides of the group

IQFGGDEVVK	46.31	55.9513	1090.566	1090.78	1	2	shared(4)	0	0.638
AVVDLNGNISK	45.59	55.9833	1128.614	1130.11	1	2	distinct	0	0.8652
FAIAVLEAASGK	94.07	55.6228	1175.655	1176.413	7	+1,+2	distinct	0	0.9999
DIAVGIAEHSPK	65.58	55.227	1235.651	1237.08	5	2	distinct	0	0.9778
GADIVVIPAGVPR	60.63	55.6582	1262.735	1262.577	1	1	distinct	0	0.9666
LNDYESELIKK	56.86	55.1051	1350.703	1351.294	1	2	distinct	1	0.9507
RIFGVTTLDVVR	59.96	55.1574	1374.798	1375.13	13	2	distinct	1	0.9637
ATVIGAAGGIGQPLSLLLK	90.05	54.1041	1778.066	1778.573	2	2	distinct	0	0.998
SLAHPEMGYVDLTSDAAGAK (00000000100000000000000)	118.47	53.642	2031.957	2032.61	3	2	distinct	0	0.9998
ASTFISEAAGKPTESLNYR	65.74	53.5205	2041.012	2041.52	2	+2,+3	distinct	0	0.9993
AFVLVISNPVNSTVPIVAEVLK	76.65	52.9707	2308.34	2308.873	15	+2,+3	distinct	0	0.9994
IPVVGGHSGVTIVPLISQSQPPISVDQAK	89.8	51.5404	2922.618	2922.839	12	+2,+3	distinct	0	1

The equivalent proteins include

gi|71021671|ref|XP_761066.1|	48366.87	hypothetical protein UM04919.1 [Ustilago maydis 521]

13. Group probability: 1.0000. Peptides of the group

TILNMIVEIPR	80.29	55.262	1297.743	1298.247	6	2	distinct	0	0.9595
VIVIDINDPLASK	77.75	54.9399	1395.797	1397.003	1	2	distinct	0	0.9927
VLGVMALLDEGETDWK	105.01	54.1671	1774.881	1775.912	6	2	distinct	0	0.9926
IPDGKPENQFAFSGEAK	90.8	54.0647	1833.89	1834.394	2	2	shared(2)	0	0.998
KYATEIVHECNEAWK	71.44	54.1786	1876.878	1877.823	5	2	distinct	1	0.9883
YATEIVHECNEAWKR	51.71	53.9491	1904.884	1905.929	3	+2,+3	distinct	1	0.9894
TGVPASPFHDVPLFADESK	71.21	53.5143	2012.984	2013.404	5	2	distinct	0	0.9898
IYKIPDGKPENQFAFSGEAK	58.75	53.1024	2238.132	2238.973	2	2	shared(2)	1	0.9709
VIVIDINDPLASKLNDIEDVER	59.06	52.5456	2479.317	2479.813	2	+2,+3	distinct	1	0.9982
AKGDNDPLDVCEIGEQVGYTGQIK	43.16	52.3315	2605.233	2606.16	2	+2,+3	distinct	1	0.9877

The equivalent proteins include

gi|71023975|ref|XP_762217.1|	36664.49	hypothetical protein UM06070.1 [Ustilago maydis 521]

14. Group probability: 1.0000. Peptides of the group

KAVIEEANR	52.21	56.2725	1028.561	1028.941	1	2	distinct	1	0.9191
AHSVCSETTK	49.94	55.8111	1118.503	1118.774	1	2	distinct	0	0.9049
DAGAIAGLDVLR	60.42	55.74	1169.64	1169.723	1	1	shared(2)	0	0.9647
LLGNFQLTGIPPAPK	92.15	54.6564	1564.898	1565.076	75	2	distinct	0	0.9821

IVPHSNGDAWLEVR	72.84	54.6123	1591.811	1593.053	4	2	distinct	0	0.9892
HAVITVPAYFNDSQR	78.66	54.337	1716.858	1717.543	9	+2,+3	shared(3)	0	0.9998
EKIDATQQASLQLFK	101.35	54.3581	1718.92	1719.503	1	2	distinct	1	0.9991
AMQEFSEQLPAEEKEK	60.51	54.3667	1892.883	1894.308	2	+2,+3	distinct	1	0.9966
ATNKDQSMTISAGSGLSDNEIEK (00000000100000000000000)	74.15	52.7504	2395.117	2411.836	2	3	distinct	1	0.9917
ALADAGCKPSDIQEVIMVGGMSR	59.56	52.6763	2404.155	2405.473	4	+2,+3	distinct	0	0.9987

The equivalent proteins include

gi|71005380|ref|XP_757356.1|	72320.52	hypothetical protein UM01209.1 [Ustilago maydis 521]

15. Group probability: 1.0000. Peptides of the group

LAEGIAGFAK	57.91	56.374	975.539	975.327	3	2	distinct	0	0.9522
HLIALYESLGVK	78.68	55.2082	1341.766	1341.493	9	+1,+2	distinct	0	0.9999
EYASHEDPGVLSVQR	73.66	54.3349	1685.801	1685.971	2	2	distinct	0	0.9904
VSYINDQAAFLLDLAK	117.07	54.1319	1779.941	1779.967	5	2	distinct	0	0.9998
NIGEILELAGCDFLTISPK	97.99	53.36	2089.076	2089.82	16	2	distinct	0	0.9977
VSYINDQAAFLLDLAKDPMANTK	97.52	52.3789	2537.284	2538.323	5	+2,+3	distinct	1	1

The equivalent proteins include

gi|71020109|ref|XP_760285.1|	35693.66	hypothetical protein UM04138.1 [Ustilago maydis 521]

16. Group probability: 1.0000. Peptides of the group

AISLAAQNIALGQR	50.5	54.8564	1424.81	1425.18	1	2	distinct	0	0.923
VNVLGGGVSLGHPIGSSGAR	93.65	54.0589	1832.986	1834.253	13	+2,+3	distinct	0	1
SIMVAGGMESMSNAPYYLPR	97.31	53.2094	2173.001	2173.814	2	2	distinct	0	0.999
DGLHDVYNQVAMGNCAENTAK (000000000000100000000)	75.7	53.0241	2306.006	2322.665	3	+2,+3	distinct	0	0.9999
AGLKPDQIEEVYMGNVLQGNVGQAPAR (000000000000010000000000000)	102.41	51.8364	2853.444	2853.789	7	+2,+3	distinct	0	1

The equivalent proteins include

gi|71018975|ref|XP_759718.1|	42870.18	hypothetical protein UM03571.1 [Ustilago maydis 521]

17. Group probability: 1.0000. Peptides of the group

AEADKLAQR	59.56	56.1347	1000.53	1000.74	1	2	distinct	1	0.9577
RVEDSLAAQAK	57.03	55.8126	1186.631	1186.848	1	2	distinct	1	0.9507
QSQEAADKLSSR	59.85	55.3454	1318.648	1318.57	1	2	distinct	1	0.9632
AVQHALDDASATK	59.14	55.2991	1325.658	1325.959	1	2	distinct	0	0.9623
YNHFFVESIPGGER	65.42	54.5862	1650.779	1651.86	5	2	distinct	0	0.9793
IIDYLDTHDVGQEIK	79.42	54.1911	1757.884	1757.802	1	2	distinct	0	0.9942
VAAEKAEHQAESALQAVQDK	46.84	53.3293	2122.065	2122.763	1	2	distinct	1	0.9168
ETYIGELPVNHEAPVGYAAPR	52.76	52.9685	2282.133	2282.393	1	2	distinct	0	0.9526
SLSASEPMIAQLAGTIDELTVFLK (000000001000000000000000)	107.78	52.5077	2533.335	2533.923	6	+2,+3	distinct	0	1
ARDDPVLSAAIEALDASGAADTGVETFTTLK	111.08	51.0936	3104.551	3105.209	3	3	distinct	1	0.9998

The equivalent proteins include

gi|71004232|ref|XP_756782.1|	74090.59	hypothetical protein UM00635.1 [Ustilago maydis 521]

18. Group probability: 1.0000. Peptides of the group

AIDDVHAEGGK	69.74	55.2114	1110.53	1110.91	1	2	distinct	0	0.984
LILEGHPALSK	61.6	55.588	1176.687	1177.775	2	2	distinct	0	0.9671
KVIEDGAPAPGR	63.1	55.1895	1208.651	1208.711	1	2	distinct	1	0.9724
YQGFPEFILALVK	57.35	54.5155	1523.839	1524.322	6	2	distinct	0	0.9565
STVIIGDGFAFLQDPK	53.18	54.5793	1706.888	1707.158	1	2	distinct	0	0.9436
LGFLDEESKPFLAYNTK	87.44	53.6679	1970.999	1971.891	3	+2,+3	distinct	0	0.9997
ILLLGSGYVAGPFAQYVTR	71.15	54.0058	2024.109	2024.198	1	2	distinct	0	0.9896
TLTSTLLDYGIPHGVTSMAK	65.82	53.2985	2104.087	2104.608	2	2	distinct	0	0.9843
FWQDGQELTVSGHELMAAAK	64.86	53.1558	2217.052	2217.62	1	2	distinct	0	0.9829
AGITVMNEIGLDPGIDHLYAVK	71.59	52.9323	2325.204	2326.23	5	+2,+3	distinct	0	0.9989
LTQGLHNASAAAVDVNDAAALSALVK	48.87	52.6031	2519.334	2519.93	1	3	distinct	0	0.9318
DGWFHETNSQWPGQAMSLEVQR	104.98	52.2846	2602.166	2602.203	2	2	distinct	0	0.9995
ATWAEVTANMVGASSTSETDLIAAVK	48.81	52.2351	2622.285	2623.633	1	2	distinct	0	0.9447

The equivalent proteins include

gi|71023471|ref|XP_761965.1|	84543.32	hypothetical protein UM05818.1 [Ustilago maydis 521]

19. Group probability: 1.0000. Peptides of the group

QLDAVADHVK	56.12	55.1702	1094.572	1094.973	1	2	distinct	0	0.9454
EANETVNVVVR	74.09	55.6068	1228.641	1228.388	1	2	distinct	0	0.989
TLFHESDANVAEK	65.36	55.0624	1459.694	1460.096	1	2	distinct	0	0.9782
DAGIPWVILGHSER	53.35	54.6878	1548.805	1550.243	4	2	distinct	0	0.9402
IVVAYEPVWAIGTGK	47.21	54.9599	1601.882	1602.634	1	2	distinct	0	0.9006
VATSEQAQEVHAAIR	81.68	54.5263	1608.822	1609.021	1	2	distinct	0	0.9952

QLDAVADHVKDWSK	73.48	54.4647	1610.805	1611.763	5	2	distinct	1	0.9898
RTLFHESDANVAEK	90.35	54.77	1615.795	1616.303	4	+2,+3	distinct	1	0.9999
VATSEQAQEVHAAIRK	87.24	54.1341	1736.917	1737.993	4	2	distinct	1	0.9972
TAAALAENLSVILCIGETLEQR	71.45	52.8605	2371.242	2371.671	5	+2,+3	distinct	0	0.9999
LDSNVEVVVSPPALHLLAVQEQLK	71.93	52.4271	2597.443	2597.498	10	+2,+3	distinct	0	0.9999
VAVAAQNAYHKPSGAFTGEVSVTMLK (00000000000000000000001000)	74.52	52.0749	2675.374	2676.605	7	+2,+3	distinct	0	0.9998
ELAQRPDIDGFLVGGASLKPEFVDIVNANA	78.26	50.973	3154.63	3155.398	7	+2,+3	distinct	0	0.9997

The equivalent proteins include

gi|71018431|ref|XP_759446.1|	26780.93	hypothetical protein UM03299.1 [Ustilago maydis 521]

20. Group probability: 1.0000. Peptides of the group

IQFGGDEVVK	46.31	55.9513	1090.566	1090.78	1	2	shared(4)	0	0.638
LLEAAIPELAK	49.96	55.1943	1166.691	1166.773	1	1	distinct	0	0.9096
DGVEEIHSVGK	53.44	55.7399	1168.572	1169.573	1	2	distinct	0	0.9326
DVEVIVIPAGVPR	55.76	55.0671	1362.787	1363.279	1	2	distinct	0	0.9495
KLYGVTTLDVTR	65.27	54.961	1364.766	1365.225	4	+2,+3	distinct	1	0.999
DQGATFFASPVTLGK	59.29	54.6164	1537.778	1538.064	2	1	distinct	0	0.9658
AVAVLGASGGIGQPLSLLLK	106.01	54.1121	1863.119	1863.41	5	2	distinct	0	0.9995
VSAEEEKLLEAAIPELAK	81.75	53.7858	1939.051	1939.663	2	+2,+3	distinct	1	0.9997
DGAGSATLSMAYAAAVFSDSLLK (0000000000100000000000000)	124.07	53.185	2245.094	2245.846	30	+2,+3	distinct	0	1
AHLLIISNPVNSTVPIVAEVFK	89.28	52.8426	2360.347	2361.843	2	2	distinct	0	0.9981
DQGATFFASPVTLGKDGVEEIHSVGK	61.15	52.0711	2688.339	2688.863	3	2	distinct	1	0.9813
KPSETIVPVVGGHSGVTIVPLLSQANGGDAVAK	85.23	51.03	3196.745	3198.194	3	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71003768|ref|XP_756550.1|	36065.2	hypothetical protein UM00403.1 [Ustilago maydis 521]

21. Group probability: 1.0000. Peptides of the group

VSLDELKER	52.39	56.1012	1087.587	1088.171	1	2	distinct	1	0.8173
LQCSLVVEDAK	72.72	55.6373	1260.638	1260.91	2	2	distinct	0	0.9876
APEADKYSHVAR	85.07	55.4046	1342.663	1343.283	7	+1,+2,+3	distinct	1	0.9999
AIEMDGLVWGSSK	74.55	55.0217	1391.675	1392.589	1	2	distinct	0	0.9903
WYEHIASYEAEHK	78.27	54.4657	1661.747	1662.423	7	2	distinct	0	0.9931
SLVTLDIKPWDDETDMK (0000000000000000100)	69.25	53.659	2004.971	2005.328	4	2	distinct	0	0.987
SYVDGHSASQADVAVYEAIGK	89.78	53.2691	2166.023	2166.302	1	2	distinct	0	0.9981
WYEHIASYEAEHKDLTGDK	76.41	53.1225	2291.049	2291.52	5	+2,+3	distinct	1	0.9997
SLVTLDIKPWDDETDMKELEASVR	77.31	51.8272	2789.379	2790.676	5	+2,+3	distinct	1	0.9999
LDGFLADKSYVDGHSASQADVAVYEAIGK	55.51	51.2982	3025.467	3025.909	3	+2,+3	distinct	1	0.9986

The equivalent proteins include

gi|71005340|ref|XP_757336.1|	24211.81	hypothetical protein UM01189.1 [Ustilago maydis 521]

22. Group probability: 1.0000. Peptides of the group

TVSTYPDDFTVHR	53.47	54.6342	1536.721	1537.102	1	2	distinct	0	0.9388
SVEHGVDSVTIGMPHR	86.83	54.3052	1719.836	1720.58	4	+2,+3	distinct	0	0.9996
HGHNETDQPSFTQPR	84.47	54.1865	1749.782	1750.237	6	+2,+3	distinct	0	0.9994
NDIVILASRPPSSSVATGSK	71.49	53.7059	1998.074	1998.512	1	2	distinct	0	0.9904
LGPGLLPNFVDSGIHELTIR	91.99	53.2515	2147.174	2147.237	5	+2,+3	distinct	0	0.9998
VALSLVANPSHLEAEDPVVLGK	77.84	53.2806	2257.232	2258.226	1	2	distinct	0	0.9949
TGLVLNLPHGYDGQGPEHSSAR	89.39	53.0214	2304.125	2305.223	8	+2,+3	distinct	0	1
FIPEPHASEGKDELVAPDQIK	52.9	52.9533	2319.175	2319.213	2	2	distinct	1	0.9532
KVALSLVANPSHLEAEDPVVLGK	58.16	52.8096	2385.327	2386.043	1	2	distinct	1	0.9726
APPTLMPLPMEAPPVDVSGFSGSTDAVDDHLK	95.97	50.7264	3290.584	3291.954	4	3	distinct	0	0.9991

The equivalent proteins include

gi|71020737|ref|XP_760599.1|	138459.97	hypothetical protein UM04452.1 [Ustilago maydis 521]

23. Group probability: 1.0000. Peptides of the group

LSALSQHR	55.36	55.0181	910.498	910.983	1	2	distinct	0	0.9402
KLSETVLAK	56.97	56.4887	987.596	987.988	1	2	distinct	1	0.9465
FMNVNPAHSK (001000000000)	55.7	55.7364	1143.549	1159.632	2	2	distinct	0	0.9427
LQGLAATHGAPLK	75.79	55.4724	1275.73	1276.171	1	2	distinct	0	0.9912
SLPTYQPSDAAVASR	49.83	54.8744	1561.774	1562.259	1	2	distinct	0	0.9211
AYGEKYPNEHAEIAR	70.97	54.2362	1746.832	1747.207	7	+2,+3	distinct	1	0.9996
LQGLAATHGAPLKADDIEAVK	76.81	53.4012	2117.148	2118.028	8	+2,+3	distinct	1	0.9999
VVSIPCFSVFDAQPIEYR	59.78	53.2584	2126.051	2127.323	2	2	distinct	0	0.9713
WGNAVDFQHPSTQLGDYSGK	82.05	53.2404	2206.008	2206.588	3	+2,+3	distinct	0	0.9997

LSVLPSGKPILSVEAYSTLGWSK	76.3	52.5763	2431.336	2432.283	2	2	distinct	0	0.9944
AIPNLMFWRPADGNETSGAYLVAIESK (00000010000000000000000000000)	74.35	51.3585	2949.469	2950.663	6	3	distinct	0	0.9931

The equivalent proteins include

gi|71021767|ref|XP_761114.1|	74189.8	hypothetical protein UM04967.1 [Ustilago maydis 521]

24. Group probability: 1.0000. Peptides of the group

DSTIIMQLLR	45.88	55.6848	1188.654	1188.947	1	2	shared(4)	0	0.5759
HLIPSAASGESK	59.2	55.1838	1195.62	1196.088	1	2	shared(3)	0	0.9612
YEEMVENMKR	56.37	55.3118	1327.59	1328.147	1	2	shared(2)	1	0.9465
IVSSIEQKEESK	84.45	55.0951	1375.719	1376.138	1	2	shared(2)	1	0.9958
VASSDQELTVEER	56.14	55.0396	1461.695	1461.405	1	2	shared(2)	0	0.9512
EESKGNETQVSMIK	59.9	54.7727	1578.756	1579.175	1	2	distinct	1	0.9663
RVASSDQELTVEER	66.98	54.6857	1617.796	1618.004	1	2	shared(2)	1	0.9819
AASDVAVTELPPTHPIR	97	54.2622	1772.942	1773.847	8	+2,+3	shared(2)	0	1
LAEQAERYEEMVENMK	62	53.6314	1968.892	1969.482	4	+2,+3	shared(3)	1	0.9973
IEAELAQICEDILDVLDK	117.49	53.3295	2086.05	2086.592	9	2	distinct	0	0.9998
QAFDDAIAELDTLSEESYK	106.92	53.2362	2143.98	2144.531	3	2	shared(2)	0	0.9996
EKIEAELAQICEDILDVLDK	120.42	53.0159	2343.188	2344.143	8	+2,+3	distinct	1	1
IEAELAQICEDILDVLDKHLIPSAASGESK	64.8	50.8517	3263.659	3264.922	4	3	distinct	1	0.9859
QAFDDAIAELDTLSEESYKDSTLIMQLLR (00000000000000000000000100000)	81.98	50.756	3314.623	3331.5	7	3	distinct	1	0.9968

The equivalent proteins include

gi|71005694|ref|XP_757513.1|	29376.58	hypothetical protein UM01366.1 [Ustilago maydis 521]

25. Group probability: 1.0000. Peptides of the group

DRDWAVDLIPK	46.98	55.24	1326.693	1327.19	1	2	distinct	1	0.4501
KHDIYISEVSSAQNIAAR	95.77	53.7295	2001.028	2001.593	2	+2,+3	distinct	1	0.9999
LIMANGELTQMLVHTDVTR	87.65	53.237	2141.097	2141.308	1	2	distinct	0	0.9976
SPYIYPLYGLGELPQAFAR	93.25	53.302	2154.115	2154.834	3	2	distinct	0	0.9985
SYDATSHFETVVEDVHDVWR	83.25	52.7583	2391.077	2392.554	3	3	distinct	0	0.9959
YDAVILGTGVTECVLSALLSVDGK	130.9	52.5461	2479.288	2480.543	2	2	distinct	0	1
HPIPNTDNSDSVQLIIPQNQVGR	60.28	52.4598	2541.294	2541.583	3	2	distinct	0	0.9774

The equivalent proteins include

gi|71004474|ref|XP_756903.1|	50895.96	hypothetical protein UM00756.1 [Ustilago maydis 521]

26. Group probability: 1.0000. Peptides of the group

REDLAEYIK	53.76	55.3014	1135.587	1136.229	6	2	distinct	1	0.9308
MVLVGAGGIEHDSLVK	93.72	54.5109	1623.865	1624.783	2	2	distinct	0	0.9984
LAEQHFGSLPVSSSPLK	78.75	54.1289	1795.947	1796.993	5	2	distinct	0	0.9943
YTPQEIQAAIDSIGVQDIQR	90.69	53.233	2244.139	2245.025	1	2	distinct	0	0.9982
SPDYFPMLVLQSIMGNWDR (0000000000000001000000)	97.49	53.4676	2268.071	2268.456	28	2	distinct	0	0.999
AVDIISDILQNSKLENSAIER	58.11	53.0073	2327.233	2328.189	2	3	distinct	1	0.9635
IRDDTSPTCNFALAVEGVSWK	92.03	52.8945	2365.137	2365.803	6	+2,+3	distinct	1	1
RYTPQEIQAAIDSIGVQDIQR	54.79	52.7495	2400.24	2400.4	3	2	distinct	1	0.9605
SQHSLELEVENLGAHLNAYTSR	80.01	52.6046	2467.209	2467.985	8	+2,+3	distinct	0	1

The equivalent proteins include

gi|71023821|ref|XP_762140.1|	58137.94	hypothetical protein UM05993.1 [Ustilago maydis 521]

27. Group probability: 1.0000. Peptides of the group

HGQSEWNK	47.91	55.9745	984.441	984.577	1	2	distinct	0	0.8828
NVIVAAHGNSLR	58.75	55.4003	1249.689	1250.077	6	2	distinct	0	0.9594
EIGQEDIPIHK	47.76	55.4837	1277.662	1277.89	1	2	distinct	0	0.8897
WGEDQVHIWR	70.83	55.2748	1324.631	1325.042	5	2	distinct	0	0.9304
RSYDIPPPGGESLK	76.68	54.7453	1514.773	1514.944	1	2	distinct	1	0.9923
DYGELSGLNKDDAR	62.29	54.6281	1551.716	1552.163	1	2	distinct	1	0.9727
LNLFTGWKDPALTELGR	83.16	53.8108	1930.031	1931.075	12	+2,+3	distinct	1	0.9999
EIGQEDIPIHKDQALNER	62.79	53.2894	2104.055	2104.16	6	+2,+3	distinct	1	0.9975
DIENISDDDIVGLELATGVPILYK	90.7	52.2434	2601.342	2601.703	2	2	distinct	0	0.9985
AMIKDIENISDDDIVGLELATGVPILYK	96.86	51.2035	3044.599	3045.253	1	2	distinct	1	0.9993
DIENISDDDIVGLELATGVPILYKLDSDGK	107.63	50.868	3216.629	3217.578	6	3	distinct	1	0.9997

The equivalent proteins include

gi|71022513|ref|XP_761486.1|	22908.08	hypothetical protein UM05339.1 [Ustilago maydis 521]

28. Group probability: 1.0000. Peptides of the group

CQNIFINSVK	52.81	55.4056	1221.618	1220.656	1	2	distinct	0	0.9267
TPSFVQITGTGDFTK	87.69	54.6719	1597.799	1598.313	6	+1,+2	distinct	0	0.9999
TNGADTVGDLEAVMVSYCMK	104.88	53.2328	2159.954	2160.611	8	2	distinct	0	0.9995
AYTGNWEQLPEWQNFMSATEYCFR (0000000000000001000000000)	73.02	51.2045	3027.296	3028.48	35	+2,+3	distinct	0	0.9991

IHIQAGDEGGELDPHGATGSGNPVGGQVFTR	81.72		51.1117	3072.465	3073.881	14	+2,+3	distinct	0	1

The equivalent proteins include

gi|71004884|ref|XP_757108.1|	32196.17	hypothetical protein UM00961.1 [Ustilago maydis 521]

29. Group probability: 1.0000. Peptides of the group

QLFIVVSSDK	58.46		55.7655	1134.628	1134.513	3	+1,+2	distinct	0	0.9954
GLCGGIHSSVTK	46.8		55.7212	1214.608	1215.68	1	2	distinct	0	0.8836
FDKVNLIYNK	66.92		55.4231	1252.682	1253.271	2	+1,+2	distinct	1	0.9936
GLCGGIHSSVTKR	51.91		55.2625	1370.709	1371.393	1	2	distinct	1	0.9289
DVPTFADASAIADQIIK	91.41		54.2592	1773.915	1774.223	3	2	distinct	0	0.9981
IGASAGDASSSEGPAVVVLGEK	84.3		53.8554	2000.006	2001.131	1	2	distinct	0	0.9971
YVSALSFESDVMEVYSEDALR	79.46		52.6944	2409.105	2410.273	1	2	distinct	0	0.9955
DLAEFSFANAIYAALVEGHASEINSK	111.32		51.9347	2766.35	2766.993	16	+2,+3	distinct	0	1
NLALSFNQIGKDVPTFADASAIADQIIK	104.21		51.3897	2959.565	2960.343	3	2	distinct	1	0.9996

The equivalent proteins include

gi|71022013|ref|XP_761237.1|	33193.08	hypothetical protein UM05090.1 [Ustilago maydis 521]

30. Group probability: 1.0000. Peptides of the group

CLDLLVFMAQK	93.76		55.2355	1336.688	1337.262	15	+1,+2	distinct	0	0.9996
VPTTNVSVVDLTAR	91.97		54.98	1470.804	1471.759	7	+1,+2	distinct	0	0.9943
YDSTHGVFNGDISTK	86.83		54.4205	1639.748	1640.642	1	2	distinct	0	0.997
IVSWYDNEWGYSNR	96.97		54.223	1787.79	1788.634	13	2	shared(2)	0	0.9749
FGIVEGLMTTVHATTATQK (00000000100000000000)	114.01		53.6319	2004.035	2004.502	13	+2,+3	distinct	0	0.9997
AQVVSNASCTTNCLAPLAK	96.42		53.6564	2003.977	2004.921	1	2	distinct	0	0.9874
KVVISAPSADAPMYVCGVNLDAYDPK	52.22		52.0104	2779.356	2779.613	2	+2,+3	distinct	1	0.9353
NSVVHNTANVVAINDPFIDLEYMVYMLK (00000000000000000000001001000)	78.23		50.982	3240.583	3241.433	3	3	distinct	0	0.9953

The equivalent proteins include

gi|5219|emb|CAA30726.1|	36118.36	gapd [Ustilago maydis]
gi|71013598|ref|XP_758638.1|	36033.3	glyceraldehyde 3-phosphate dehydrogenase [Ustilago maydis 521]

31. Group probability: 1.0000. Peptides of the group

KLVDFMNAAR	55.79		55.3524	1163.612	1164.306	1	2	distinct	1	0.9436
NAVSGDTSALVPGGVR	59.26		54.7117	1498.774	1499.11	1	2	distinct	0	0.9668
VENICDLAHITLNK	84.32		54.4199	1638.84	1639.412	1	2	distinct	0	0.9961
DVEAFATSFPLPGVPDTSIIK	47.49		53.216	2203.141	2203.91	1	2	distinct	0	0.9244
YYGGNEYIDQLEVLCQQR	97.9		53.1877	2247.027	2247.633	8	+2,+3	distinct	0	0.9999
VNAAVFPACQGGPHNNTIAGIAVALK	73.73		52.3317	2589.348	2590.163	6	2	distinct	0	0.9938
LQTDGSENHLILWDLRPLGLTGSK	55.97		52.0433	2662.408	2663.704	1	3	distinct	0	0.9612
VLYQPLAEADPEVQQIIENETYR	77.4		52.0936	2717.355	2718.143	3	2	distinct	0	0.995
KISASSIYFQSFPYNVDPATGYINYDELK	52.9		50.6728	3329.613	3330.293	3	3	distinct	1	0.9586
ISASSIYFQSFPYNVDPATGYINYDELKK	126.04		50.6797	3329.613	3330.431	4	3	distinct	1	0.9999

The equivalent proteins include

gi|71004868|ref|XP_757100.1|	55732.66	hypothetical protein UM00953.1 [Ustilago maydis 521]

32. Group probability: 1.0000. Peptides of the group

GSVGPATTSAHSK	61.04		55.4572	1198.594	1198.731	2	2	distinct	0	0.9679
LAWHASGTYDK	50.51		55.7639	1247.593	1247.417	1	1	distinct	0	0.9128
LPDGDKGPDHLR	55.68		55.2324	1318.663	1319.483	7	2	distinct	1	0.9371
KWNGPPQFEDK	61.3		55.4183	1344.646	1345.273	6	2	distinct	1	0.9458
FAPESEHGANAGLGAAR	87.02		54.3405	1653.786	1654.813	3	2	distinct	0	0.9972
VLLTSVAIAAAAGGAFLAFGR	64.47		53.6505	1975.125	1975.872	2	3	distinct	0	0.9788
MGFNDQEIVALSGAHALGR (01000000000000000000)	107.64		54.0993	1984.979	1986.274	9	+2,+3	distinct	0	1
SLMMLMTDMALVQDPSFK	84.28		53.4975	2056.971	2057.641	1	2	distinct	0	0.9922
SGFDGPWTFAPTSFTNEYFNLLMNEK (00000000000000000000010000)	90.25		51.2477	3012.364	3013.052	15	+2,+3	distinct	0	0.9999
ADYQAVYNAIAEQLEANPDYDDGSYGPVLVR	69.12		50.3541	3415.584	3416.693	3	3	distinct	0	0.9908

The equivalent proteins include

gi|71012754|ref|XP_758524.1|	43249.32	hypothetical protein UM02377.1 [Ustilago maydis 521]

33. Group probability: 1.0000. Peptides of the group

RVPAAGFGTK	65.32		56.2443	1002.561	1003.373	4	2	distinct	1	0.9751
RPTMLTTDLSLR	48.55		55.0875	1402.76	1403.629	2	+2,+3	distinct	0	0.9874
NADAIIPDPFDPSKK	50.63		54.7125	1626.825	1627.801	1	3	distinct	1	0.9099
FLENHDEFADAFAR	61.36		54.2633	1680.753	1681.177	2	2	distinct	0	0.9706
ALGLNYNGSSHGVLTHR	67.33		54.1373	1794.912	1796.002	1	2	distinct	0	0.9844
RFLENHDEFADAFAR	64.67		54.0964	1836.854	1837.158	3	+2,+3	distinct	1	0.9964

KISIADLIVLAGNAALEK	93.53	53.9234	1838.088	1839.225	1	2	distinct	1	0.9985
ANLLTLTPPELTVLIGGLR	55.01	53.6319	1990.183	1990.938	3	2	distinct	0	0.9577
GQLSNDFFVNLLDMSTEWK	110.5	53.2403	2243.057	2243.655	9	2	distinct	0	0.9997
ISWADLLILAGNVALESMGFK (00000000000000000010000)	93.68	53.1924	2247.197	2248.361	5	+2,+3	distinct	0	0.9999
LAPMKDWEVNNPQQLAEVIK	73.51	53.0277	2322.204	2322.753	5	2	distinct	1	0.992
EILIWEDPVPTADYALVDDR	88.7	52.9766	2329.148	2329.343	3	2	distinct	0	0.9979
SDPFNAEFDYAAAFNSLDYDALKK	43.14	51.9662	2711.239	2712.311	2	3	distinct	1	0.8806
TDATQEQTEVDTFEFLKPVADGFR	74.95	52.0439	2743.298	2744.316	1	3	distinct	0	0.9927
AGDAITSGLEVVWTSKPTEWSNLYLK	75.06	51.7466	2864.46	2865.238	5	3	distinct	0	0.9933
THGAGNPDLVGPEPNGAPIEAQGFGWTSK	66.61	51.5188	2903.384	2904.241	8	+2,+3	distinct	0	0.9995

The equivalent proteins include

gi|71018631|ref|XP_759546.1|	77418.5	hypothetical protein UM03399.1 [Ustilago maydis 521]

34. Group probability: 1.0000. Peptides of the group

ASFGLALDTFK	65.23	55.6629	1168.613	1168.403	2	1	distinct	0	0.9761
LSDSNATANAHK	78.94	55.4843	1227.584	1227.446	1	2	distinct	0	0.9931
NHIELENHIAK	72.8	55.4094	1316.684	1317.015	15	+1,+2,+3	distinct	0	1
SPNSNVNLEVGTK	71.18	55.305	1357.684	1358.027	3	2	distinct	0	0.9869
APALVSQPVPPSWK	74.2	54.9054	1475.814	1475.994	31	+1,+2	distinct	0	0.9997
MAPALVSQPVPPSWK	70.16	54.5878	1606.854	1606.997	4	2	distinct	0	0.9868
AAGDLLSKDYPIHGNSLEVK	59.98	53.2446	2126.101	2126.557	3	+2,+3	distinct	1	0.9965
INNAGILCLGYTQALRPGVK	103.85	53.2327	2157.173	2157.242	9	2	distinct	0	0.9994

The equivalent proteins include

gi|71023159|ref|XP_761809.1|	31952.46	hypothetical protein UM05662.1 [Ustilago maydis 521]

35. Group probability: 1.0000. Peptides of the group

KLGATAELKPLGK	87.68	55.2997	1324.808	1325.713	7	+1,+2,+3	distinct	1	1
ATETIYGVKPDLTR	51.56	54.8298	1562.83	1563.246	1	2	distinct	0	0.9299
LVPDMTPEKVNELVTK	49.66	54.1669	1811.97	1812.216	1	2	distinct	1	0.9239
YDVMDFVLSDIEGATGSK	121.15	53.8465	1945.898	1946.533	2	2	distinct	0	0.9999
YPCLSLHGIEGAFSEPGTK	47.75	53.4713	2061.983	2061.182	1	2	distinct	0	0.9202
RYDVMDFVLSDIEGATGSK	125.16	53.3596	2101.999	2103.034	2	2	distinct	1	0.9999
QTLDGQEIELPPVILGDLGKDPK	48.09	52.4154	2474.327	2475.093	1	3	distinct	1	0.9191
DLHSGVFGGVVHEPMTDLFTIMSK (00000000000000000000001000)	58.86	52.279	2616.272	2617.253	9	+2,+3	distinct	0	0.9991
GSTDDKGPILGWLNAIEAHQQAGIDLPVNLK	73.37	51.6732	3269.704	3271.127	2	3	distinct	1	0.9935

The equivalent proteins include

gi|71009686|ref|XP_758305.1|	52202.92	hypothetical protein UM02158.1 [Ustilago maydis 521]

36. Group probability: 1.0000. Peptides of the group

LSLLTNNGRPVK	57.37	55.1634	1310.767	1311.03	1	2	distinct	0	0.9545
SYNAGHNVESVVENK	97.59	54.555	1645.77	1646.184	1	2	distinct	0	0.9963
SYNGGHNVIIDNENK	65.68	54.5226	1672.78	1673.009	1	2	distinct	0	0.9257
KAPEFSYYNPGHNVK	98.61	54.1857	1749.847	1749.959	5	+2,+3	distinct	1	0.9999
VTCGTDEVYVDEGHNVVSK	76.49	53.2885	2106.953	2107.833	1	2	distinct	0	0.9936
TDKFSYYNGGHNVESDTQNK	78.9	52.9763	2303.009	2304.013	2	+2,+3	distinct	1	0.9997
GDKYTYYNGGHNIESTNENK	76.63	52.9764	2303.009	2304.113	3	+2,+3	distinct	1	0.9998
TDKYSYYNGGHNVESTNENK	63.61	52.9671	2319.004	2319.884	1	3	distinct	1	0.9767
TDKYSYYDGGHNIELTNENK	82.7	52.8524	2360.056	2360.493	4	+2,+3	distinct	1	0.9998

The equivalent proteins include

gi|71019681|ref|XP_760071.1|	71843.33	hypothetical protein UM03924.1 [Ustilago maydis 521]

37. Group probability: 1.0000. Peptides of the group

KIAAIHSK	54.67	55.3891	866.534	866.705	1	2	distinct	1	0.7885
RLQPAWATR	47.52	55.2128	1097.609	1098.076	1	2	distinct	1	0.8806
NHGALYIFPR	49.43	55.7845	1186.625	1187.275	3	2	distinct	0	0.9006
FGGFDVLVLDER	95.25	54.9868	1365.693	1366.369	5	2	distinct	0	0.9984
VLLAGDACHTHSPK	116.25	54.7602	1504.746	1505.543	6	+1,+2	distinct	0	1
STPEVATMTDAEKR	59.7	54.6917	1534.73	1534.707	1	2	distinct	1	0.9657
MIHEIQFTAPGGFR (0100000000000000)	66.09	54.9402	1602.798	1603.243	6	2	distinct	0	0.9803
VVEWFTCYPIGQR	49.95	54.3405	1653.797	1654.933	1	2	distinct	0	0.9171
GLADPEILLATYHAER	84.12	54.1554	1767.915	1769.007	3	+2,+3	distinct	0	0.9998
SMLYCDDIEAGHGAFK	103.32	54.1518	1812.781	1813.278	1	2	distinct	0	0.9993
MKPVMESTNEGGAPISIIKPTGETK	78	52.2912	2614.335	2614.873	3	+2,+3	distinct	0	1
VTRPWAYQNFEMTDDPTYPVTVTLEK (0000000000001000000000000000)	71.52	51.1252	3100.485	3101.171	7	3	distinct	0	0.9909
RVQSFPTDMEIQDNCTLGLQQGLIEGGFLR	90.37	50.3089	3421.676	3421.736	6	3	distinct	1	0.9985

The equivalent proteins include

gi|71004242|ref|XP_756787.1|	74404.25	hypothetical protein UM00640.1 [Ustilago maydis 521]

38. Group probability: 1.0000. Peptides of the group

WAFDAGYR	45.11	55.9746	984.445	984.798	1	2	distinct	0	0.8502
AAAAIEDSLKK	48.39	55.9175	1115.619	1115.754	1	2	distinct	1	0.8947
WGLTHGNIILPK	74.36	55.2086	1347.766	1348.793	12	+1,+2,+3	distinct	0	0.9999
LWDADHDKAAAAIEDSLK	117.4	53.7318	1967.959	1969.273	5	+2,+3	distinct	1	1
TIGVSNFDVEELDHLLANCR	105.86	53.1073	2301.106	2301.368	6	+2,+3	distinct	0	1
LNVDYMDMYLMHSPGTMGAEK	94.21	52.8035	2402.041	2403.353	4	2	distinct	0	0.9988
KLNVDYMDMYLMHSPGTMGAEK	65.83	52.5995	2530.136	2531.063	3	+2,+3	distinct	1	0.9997

The equivalent proteins include

gi|71021677|ref|XP_761069.1|	35247.67	hypothetical protein UM04922.1 [Ustilago maydis 521]

39. Group probability: 1.0000. Peptides of the group

ASTELLADKIK	80.43	55.7998	1187.676	1188.072	1	2	distinct	1	0.9754
LNFVWIDGVK	46.28	55.5728	1189.649	1190.653	1	1	distinct	0	0.8696
KLAPTYDTLGEK	53.06	55.3299	1334.708	1334.939	1	2	distinct	1	0.9333
SFNEEAITNFIK	55.93	55.0186	1411.698	1411.423	2	1	distinct	0	0.9485
LVEFYAPWCGHCK	58.5	54.3963	1665.743	1666.005	3	2	distinct	0	0.9523
DNYLFGVVHDAAVAEK	96.6	54.2265	1746.858	1747.825	1	2	distinct	0	0.9988
FQAAGSKDWIEFTGDR	94.31	54.0446	1826.859	1827.075	2	2	distinct	1	0.9985
VTDFVSQYTSGSLKPSVK	111.5	53.6692	1942.005	1942.399	4	+2,+3	distinct	0	1
HKVSVDLDPINVTEQAAPAK	94.22	53.2441	2131.127	2131.933	3	2	distinct	1	0.9987
VDCTEENELCAEHGVEGFPTLK	43.71	52.503	2533.11	2533.853	2	3	distinct	0	0.8767
DQDGPVHVLVADEFDAVIGDDSKDK	55.53	52.0851	2683.261	2684.23	1	3	distinct	1	0.961
VVAIAYLDSSDKAHLDAVNAVANNLR	106.69	52.2814	2738.435	2738.513	12	+2,+3	distinct	1	1
VSVDLDPINVTEQAAPAKEAPHHEEL	103.94	51.833	2808.393	2808.523	1	2	distinct	1	0.9996

The equivalent proteins include

gi|71013434|ref|XP_758590.1|	53861.15	hypothetical protein UM02443.1 [Ustilago maydis 521]

40. Group probability: 1.0000. Peptides of the group

RPGMFDLAGK	57.61	55.9513	1090.559	1090.523	6	2	distinct	0	0.9476
YKWDAWNK	47.77	55.2102	1109.529	1110.323	3	2	distinct	1	0.8832
EDAQQAYVDALLEILK	100.43	54.1897	1817.941	1818.37	24	2	distinct	0	0.9991
EDAQQAYVDALLEILKK	94.36	53.8247	1946.036	1947.413	7	+2,+3	distinct	1	0.9999
KHEDEGDSAQYIEQIQNA	71.4	53.4765	2073.924	2074.873	5	+2,+3	distinct	1	0.9988
DGPVQPTQDDQLTFYGLYK	111.96	53.403	2184.037	2184.653	4	2	distinct	0	0.9997
NQGMSKEDAQQAYVDALLEILK (0000100000000000000000)	100.93	52.6046	2463.231	2464.313	19	+2,+3	distinct	1	1

The equivalent proteins include

gi|71017751|ref|XP_759106.1|	11793.81	hypothetical protein UM02959.1 [Ustilago maydis 521]

41. Group probability: 1.0000. Peptides of the group

IIDSIHDGSLAK	57.05	55.3212	1267.677	1267.918	1	2	distinct	0	0.953
KIIDSIHDGSLAK	81.28	54.9606	1395.772	1396.209	6	+1,+2	distinct	1	0.9999
NASVAQLYEDAIKK	71.34	54.7006	1548.815	1548.76	1	2	distinct	1	0.9877
LFSDAGFDMDKIHLK	88.55	54.1183	1735.86	1736.403	4	2	distinct	1	0.9974
DDIYVFDGFAGWDPK	71.09	54.2521	1743.778	1744.251	1	2	distinct	0	0.8961
CIGLSAAKEPEIYNAIR	55.19	53.9225	1903.982	1904.993	2	2	distinct	1	0.955
LDANQAQYHFISGYTSK	45.9	53.7096	1941.922	1943.399	2	+2,+3	distinct	0	0.9846
NIIFLTCDAYGVLPPVSK	58.44	54.1466	2006.055	2006.965	2	2	distinct	0	0.9672
TPGTEDGIQEPSPTFSTCYGQPFIVLHPR	71.87	50.8706	3230.534	3231.684	5	3	distinct	0	0.9921

The equivalent proteins include

gi|71022093|ref|XP_761277.1|	61995.83	hypothetical protein UM05130.1 [Ustilago maydis 521]

42. Group probability: 1.0000. Peptides of the group

QLEQELLTK	48.67	55.8688	1100.608	1100.81	1	2	distinct	0	0.8906
DQEIASLQHK	45.1	55.5424	1167.588	1167.947	1	2	distinct	0	0.8555
LSLAESDLDKLESK	106.29	55.0782	1546.809	1548.203	4	+2,+3	distinct	1	0.9999
LHTLRVEADAASER	46.65	54.5708	1566.811	1567.753	1	2	distinct	1	0.8927
KVELLEGELDTAEK	97.28	54.8713	1572.825	1573.02	2	+1,+2	distinct	1	0.9999
VEADAASERADELAEK	49.52	54.3524	1702.801	1702.805	1	2	distinct	1	0.9226
EEHESNATNSESLQR	73.73	54.2704	1729.75	1730.639	2	2	distinct	0	0.9904
SAREEHESNATNSESLQR	90.52	53.5182	2043.921	2044.483	9	+2,+3	distinct	1	0.9999
QLEQELLTKDQEIASLQHK	49.87	53.5044	2250.186	2251.554	1	3	distinct	1	0.9184

The equivalent proteins include

gi|71020847|ref|XP_760654.1|	118682.47	hypothetical protein UM04507.1 [Ustilago maydis 521]

43. Group probability: 1.0000. Peptides of the group

EIVHLQTGQCGNQVGTK	82.73		53.9064	1867.921	1868.201	3	+2,+3	distinct	0	0.9972
GHYTEGAELVDSVLDVIR	104.42		53.6785	1971.99	1973.099	4	+2,+3	distinct	0	0.9996
GHYTEGAELVDSVLDVIRK	57.68		53.4582	2100.085	2101.066	1	3	distinct	1	0.8046
SGPIGGIFRPDNFVFGQSGAGNNWAK	43.79		52.0635	2692.314	2693.733	1	2	distinct	0	0.8062
LNAPTYGDLNHLVSLVMSGVTTCLR (000000000000000001000000000)	90.73		51.8814	2730.383	2730.743	12	+2,+3	distinct	0	0.9999
FWEVLSDEHGIDHNGNYIGTSDDQLAR	69.78		51.1729	3087.396	3088.664	2	+2,+3	distinct	0	0.9998
EAENCDMLQGFQITHSLGGGTGAGMGTLLISK	59.36		50.834	3292.553	3293.549	1	3	distinct	0	0.9788
KEAENCDMLQGFQITHSLGGGTGAGMGTLLISK	64.37		50.3066	3420.647	3421.96	1	3	distinct	1	0.9544

The equivalent proteins include

gi|71023491|ref|XP_761975.1|	50585.44	tubulin subunit beta-2 [Ustilago maydis 521]

44. Group probability: 1.0000. Peptides of the group

AIEIYFPR	52.19		55.9505	1007.544	1007.491	1	2	distinct	0	0.9195
SGAANGHSDASSLASIK	75.71		54.8718	1571.754	1573.123	1	2	distinct	0	0.9924
VDDFDYTLFHSPYSK	66.91		54.0267	1832.826	1833.236	3	+2,+3	distinct	0	0.9974
RCISEDELEDFDGVAK	75.58		54.0276	1881.841	1881.858	1	2	distinct	1	0.9922
TVLMDLFAPSGNMNIEGIDSK	82.95		53.5078	2251.086	2251.913	3	2	distinct	0	0.9966
NACYGGTAALFNAINWVESSSWDGR	96.32		52.0141	2745.224	2745.744	11	2	distinct	0	0.9991
YMACTDDREDINSFALSVVSGLLEK (001000000000000000000000000)	61.47		51.7073	2832.331	2832.963	12	+2,+3	distinct	1	0.9991
CGNMYTASLYGGLVSLLSNIPSQEIQGK	57.72		51.2678	2999.473	3000.315	1	3	distinct	0	0.9716

The equivalent proteins include

gi|71022559|ref|XP_761509.1|	51011.4	hypothetical protein UM05362.1 [Ustilago maydis 521]

45. Group probability: 1.0000. Peptides of the group

SPLAHADLK	53.4		55.6916	950.518	951.124	1	2	distinct	0	0.7515
RGGPNYQEGLK	55.01		55.6813	1217.615	1218.161	2	2	distinct	1	0.9413
AIGTVDHNTGER	63.77		55.387	1268.611	1268.984	2	2	distinct	0	0.9241
DLTKEEAYIAK	59.52		55.2333	1279.666	1280.348	1	2	distinct	1	0.9609
EFVLTNFPSHK	66.47		55.4027	1317.672	1317.919	1	2	distinct	0	0.9318
LYRPGSVGYVSK	49.8		55.3004	1324.714	1325.353	4	2	distinct	0	0.9113
GPPMYWPAPFGR (00001000000000)	53.68		55.1643	1374.654	1375.024	2	2	distinct	0	0.937
KPIIAWAIGTCAK	94.95		54.9958	1427.796	1428.553	3	2	distinct	0	0.9984
DLISSLVSGLLTIGDR	62.78		54.9003	1657.925	1659.088	3	2	distinct	0	0.9755
HPADDFHIEMATPAR (00000000001000000)	90.2		54.5649	1706.783	1707.34	9	+2,+3	distinct	0	0.9997
REEWTSTLLGGVPAAK	86.57		54.2569	1713.905	1714.38	4	2	distinct	1	0.997
SVYSSTLEVLDCPQIR	60.2		54.0122	1865.919	1866.14	1	2	distinct	0	0.9699
AAGFIVPDTFEDLPAVIR	80.85		53.8261	1930.02	1930.448	2	2	distinct	0	0.9954
LLIIGGGIANFTNVASTFK	120.95		53.7584	1935.083	1934.61	1	2	distinct	0	0.9999
EGDWILFTHEGGVDVGDVDAK	93.23		53.2811	2258.049	2258.343	2	+2,+3	distinct	0	1
VAQIAWDPVTNSITDASQLPAWVQSSK	54.09		51.5423	2911.472	2912.754	1	2	distinct	0	0.9669

The equivalent proteins include

gi|71004972|ref|XP_757152.1|	125391.49	hypothetical protein UM01005.1 [Ustilago maydis 521]

46. Group probability: 1.0000. Peptides of the group

ANELSSQAQQSGDSLVK	113.21		54.1825	1760.854	1761.698	2	2	distinct	0	0.9997
TTNDVQKDAQSLANDASK	46.73		53.9478	1904.908	1905.668	1	3	distinct	1	0.8877
ATAAHVVDQVAHIIAAGQQK	129.36		53.5066	2027.091	2028.213	11	+2,+3	distinct	0	1
QANQAGSNASQLASDATNAASQK	141.46		53.2463	2232.037	2232.519	2	2	distinct	0	1
QATDLASNTLAYVQQTAGSLLGQGK	116.99		52.5356	2534.298	2535.383	2	2	distinct	0	0.9999
DLASHTLDSANQYIKPAEENASGLVNQAR	95.06		51.1636	3111.522	3112.273	16	+2,+3	distinct	0	1
AGEVVDEASKQANQAGSNASQLASDATNAASQK	91.5		50.8888	3217.508	3218.256	1	3	distinct	1	0.9988

The equivalent proteins include

gi|71004108|ref|XP_756720.1|	25340.36	hypothetical protein UM00573.1 [Ustilago maydis 521]

47. Group probability: 1.0000. Peptides of the group

KAEIVAVK	49.11		56.9041	856.538	857.093	1	2	distinct	1	0.8239
SDIVGVLTPAELK	49.9		55.1741	1340.755	1340.673	1	1	distinct	0	0.9153
SDIVGVLTPAELKK	55.37		54.6376	1468.85	1469.253	2	+2,+3	distinct	1	0.9953
LASPGVLTGLDSDTVNK	99.75		54.3926	1685.884	1686.608	2	2	distinct	0	0.9991
VLGSGGSGSMSDVTGGVLWAVEDAK	106.96		52.7481	2378.142	2379.093	1	2	distinct	0	0.9996
TMPQNDVDEDGNGHGTHCAGTIGSR	79.74		52.268	2625.093	2625.763	4	+2,+3	distinct	0	0.9997
YVYQGDGGEGVTAYVIDTGININHVEFEGR	100.48		51.1462	3271.542	3272.985	4	3	distinct	0	0.9994

The equivalent proteins include

gi|71020633|ref|XP_760547.1|	56717.51	hypothetical protein UM04400.1 [Ustilago maydis 521]

48. Group probability: 1.0000. Peptides of the group

DYQASSIPLGR	79.89	55.6118	1205.604	1205.693	1	2	distinct	0	0.9934
CLAAEWATHGIR	84.74	55.0992	1383.672	1384.283	8	2	distinct	0	0.9959
AAAQLWIESGYKK	61.35	54.925	1463.777	1464.655	1	2	distinct	1	0.9691
AYQCDVGDDALVKK	73.82	54.5008	1580.75	1581.444	1	2	distinct	1	0.9901
YVYDTNVLGVFNTAK	82.12	54.3758	1702.857	1703.502	4	2	distinct	0	0.9954
FSEPHEQAEPCVLLLSDK	88.51	53.401	2098.004	2098.992	4	+2,+3	distinct	0	0.9999
QAQDELGQVTGLVANAGVSVVKPAVELTSDDFR	123.29	50.3883	3412.747	3413.464	7	3	distinct	0	0.9999

The equivalent proteins include

gi|71023267|ref|XP_761863.1|	36363.28	hypothetical protein UM05716.1 [Ustilago maydis 521]

49. Group probability: 1.0000. Peptides of the group

NVIIEQPFGGPK	46.66	55.2201	1297.703	1298.04	1	2	distinct	0	0.8834
VGGSSEVEVGEKK	59.92	55.3897	1303.662	1304.054	1	2	shared(2)	1	0.9647
DRYDDALNATR	73.67	55.3147	1308.606	1309.021	4	2	distinct	1	0.9887
AAVEAGVLPGGGVALLK	55.29	54.7728	1520.893	1520.663	2	1	distinct	0	0.9546
TIEDEIEITEGMR	89.11	54.6776	1534.718	1535.589	4	2	distinct	0	0.9953
VEFEKPLILLSEK	55.23	54.7931	1543.886	1544.171	3	+2,+3	shared(2)	0	0.9947
VEFEKPLILLSEKK	54.37	54.5225	1671.981	1672.783	1	2	shared(2)	1	0.9455
ISALQDILPSLEAAAQLR	79.8	53.9117	1908.068	1908.632	1	2	distinct	0	0.995
KISALQDILPSLEAAAQLR	96.36	53.6897	2036.163	2036.585	13	+2,+3	distinct	1	0.9999
LLEKPGDFTYGYDASVGEYK	98.23	53.5105	2251.068	2251.512	1	2	distinct	0	0.9991
SILGDLGILTGAQVFSDELETK	115.74	53.0012	2305.205	2304.692	5	2	distinct	0	0.9998
SILGDLGILTGAQVFSDELETKLDR	65	52.0535	2689.417	2689.823	6	+2,+3	distinct	1	0.9995
TALQDASGVASLLTTSECCIVEAPEEK	89.53	51.6175	2878.358	2879.602	1	2	distinct	0	0.9985
AVTTSAEIAQVATISANGDQHVGQLIATAMEK	66.54	51.3381	3224.635	3226.005	2	3	distinct	0	0.9886
LLEKPGDFTYGYDASVGEYKDMIAAGILDPLK	58.12	50.1827	3488.742	3489.721	2	3	distinct	1	0.9767

The equivalent proteins include

gi|71023497|ref|XP_761978.1|	61214.91	hypothetical protein UM05831.1 [Ustilago maydis 521]

50. Group probability: 1.0000. Peptides of the group

LMSAAMSHAADLFDQK (000000100000000000)	96.94	54.2832	1734.807	1735.104	2	2	distinct	0	0.9988
NPSLLAGLIGGGNSGGLGALAGMLK (000000000000000000000001000)	168.31	53.07	2237.22	2237.086	66	+2,+3	distinct	0	1
LLQDHDEVNNQPGANSSGQIGNAAALAAIK	84.49	51.266	3015.501	3015.711	1	2	distinct	0	0.9979

The equivalent proteins include

gi|71018441|ref|XP_759451.1|	21211.03	hypothetical protein UM03304.1 [Ustilago maydis 521]

51. Group probability: 1.0000. Peptides of the group

EFIHDFVK	45.26	55.8817	1033.523	1034.052	1	2	distinct	0	0.6158
KYYAYGEQK	50.53	55.6006	1148.55	1148.968	1	2	distinct	1	0.9076
HWQWLGDNAK	48.61	55.4244	1253.594	1253.373	3	+1,+2	distinct	0	0.9884
DVWDHPNCVAWVR	46.82	54.3166	1652.752	1653.703	1	2	distinct	0	0.891
WGFEHFAGVDWDQK	85.86	54.2586	1720.763	1721.36	5	2	distinct	0	0.9966
VNEDGWVEVHCHPR	67.23	54.2989	1732.774	1733.293	6	+2,+3	distinct	0	0.9992
YAGQNFVDVIGWFQGQAK	103.04	53.5063	2026.99	2027.801	12	+2,+3	distinct	0	0.9999
FGDEQFSLFDAPLHYNFK	77.22	53.2425	2174.011	2174.755	7	+2,+3	distinct	0	0.9999
GLEPADESEGPIAFSVGEFWK	115.64	53.04	2264.064	2265.116	2	2	distinct	0	0.9998
GASASSTGYDIYDTWDLGEFAHPR	91.81	52.2885	2615.156	2615.673	3	2	distinct	0	0.9986
GASASSTGYDIYDTWDLGEFAHPRDEK	62.54	51.3275	2987.321	2987.913	1	2	distinct	1	0.9843

The equivalent proteins include

gi|71011023|ref|XP_758447.1|	61249.51	hypothetical protein UM02300.1 [Ustilago maydis 521]

52. Group probability: 1.0000. Peptides of the group

HHSTELQGLK	47.3	55.5197	1148.594	1149.275	1	2	distinct	0	0.8809
RIEEHQISAK	51.19	55.2358	1209.647	1210.332	1	2	distinct	1	0.9158
ASVDSQHGEALSK	50.67	55.3574	1327.637	1327.811	2	2	distinct	0	0.9206
KVVGVVPAAASSTTAAR	61.86	54.5597	1583.899	1584.218	1	2	distinct	1	0.9746
RAAGVASAAPPAASTAPVR	92.9	54.3546	1719.938	1720.046	4	+2,+3	distinct	1	0.9999
RVPAVPSSPAASTTSATGVR	60.14	53.8296	1911.017	1911.953	6	+2,+3	distinct	1	0.9981
HAEELSALATAHETTLSQTR	142.21	53.2693	2165.071	2166.103	5	+2,+3	distinct	0	1
VAMLSNQHHEQLEQILAER	51.2	53.2597	2245.127	2244.597	2	2	distinct	0	0.9413

The equivalent proteins include

gi|71004828|ref|XP_757080.1|	136729.8	hypothetical protein UM00933.1 [Ustilago maydis 521]

53. Group probability: 1.0000. Peptides of the group

LVNHFVQEFK	64.36	55.6038	1259.666	1260.05	9	+1,+2	shared(3)	0	0.992
KFDDAEVQSDMK	63.62	55.0187	1411.629	1411.866	1	2	distinct	1	0.8947
TFTPEEISSMVLIK	69.04	54.5124	1593.832	1594.697	3	2	shared(2)	0	0.9432
ATAGDTHLGGEDFDNR	68.44	54.7902	1674.723	1675.633	4	2	shared(13)	0	0.9851
NQVAMNPHNTVFDAK	91.76	54.3229	1684.799	1685.24	1	2	shared(2)	0	0.998
KTFTPEEISSMVLLK	76.19	54.2106	1721.927	1722.263	1	2	distinct	1	0.9923
IDKGSVHEIVLVGGSTR	84.11	54.1534	1765.969	1766.779	4	2	distinct	1	0.9964
IINEPTAAAIAYGIDKK	71.85	54.6758	1786.983	1788.273	1	2	shared(14)	1	0.9837
QAEQFAEEDKQALER	80.78	54.1773	1790.843	1791.19	1	2	distinct	1	0.9948
NQVAMNPHNTVFDAKR	80.09	54.0539	1840.9	1841.223	1	2	shared(2)	1	0.9947
FEELCGDLFSHTIEPVEK	74.4	53.2991	2149.004	2149.413	1	2	distinct	0	0.992
EGIEWLDSNTTASTDELKDK	89.67	53.5065	2251.049	2251.321	2	+2,+3	distinct	1	0.9998
ARFEELCGDLFSHTIEPVEK	56.44	52.7802	2376.142	2377.269	4	+2,+3	distinct	1	0.9971
GVPQIEVTFDVDANAILNVSAAEK	91.23	52.6387	2499.286	2499.723	4	2	distinct	0	0.9947
SEIFSTYADNQPGVLIQVFEGER	72.99	52.3905	2598.26	2598.243	3	2	distinct	0	0.9404
KSEIFSTYADNQPGVLIQVFEGER	81.73	52.0329	2726.355	2727.613	7	+2,+3	distinct	1	0.9994
TQDLLLLDVAPLSMGIETAGGVFTPLIK	90.67	51.5678	2911.598	2911.753	8	2	distinct	0	0.964
TQDLLLLDVAPLSMGIETAGGVFTPLIKR (0000000000000010000000000000000)	50.27	51.2217	3067.699	3069.083	3	+2,+3	distinct	1	0.955

The equivalent proteins include

gi|71019415|ref|XP_759938.1|	70461.05	hypothetical protein UM03791.1 [Ustilago maydis 521]

54. Group probability: 1.0000. Peptides of the group

DASEAANLAVLR	46.53	55.7028	1228.641	1229.139	1	2	distinct	0	0.8808
QTVDFAHAAFAK	59.48	55.3878	1304.651	1303.694	2	+1,+2	distinct	0	0.9976
EHLLLTAEFLR	52.97	55.1742	1340.745	1340.972	2	2	distinct	0	0.9306
VAFSAPHGAENTR	52.19	55.1334	1355.658	1355.924	1	2	distinct	0	0.9308
NNIAVLGSGIESNK	115.58	55.1054	1414.742	1415.61	1	2	distinct	0	0.9997
NVAGGLKDETIQAAIAK	87.77	54.3115	1697.931	1699.253	2	+2,+3	distinct	1	0.9997
GDEDFFVEVLGDVLSK	106.8	54.1688	1767.857	1768.161	20	2	distinct	0	0.9994
SKPTTVAVGDVHLLPYADEVL	58.68	53.0852	2223.179	2223.063	2	2	distinct	0	0.9717
TASHELVSAQLLDSANVVTLDDTFAALEAVK	93.93	50.946	3227.656	3228.394	10	3	distinct	0	0.9989

The equivalent proteins include

gi|71005918|ref|XP_757625.1|	46578.96	hypothetical protein UM01478.1 [Ustilago maydis 521]

55. Group probability: 1.0000. Peptides of the group

LGQHLVER	60.68	55.8728	950.53	950.927	2	2	distinct	0	0.943
RLQSLQQPTTADGK	75.77	54.7314	1541.816	1542.616	1	2	distinct	1	0.9916
GVAADDPHKLGQHLVER	64.81	54.1056	1840.954	1841.613	1	2	distinct	1	0.9806
LGLYESFVQFADFPSR	82.41	54.0378	1874.92	1876.228	4	2	distinct	0	0.9957
WALHQVVPSLSSYVNGR	46.41	53.7944	1911.995	1913.068	1	2	distinct	0	0.903
LAEPEEQTLLSETICKK	77.6	53.6212	1988.014	1988.724	1	2	distinct	1	0.9937
MTFHDGSTHEADLVIGCDGIHSR	60.73	52.4598	2554.133	2555.274	2	3	distinct	0	0.9733
VIVSGDAAHGGVPHQGAMAGQAIEDALFLSK (000000000000000000100000000000000)	96.75	51.2347	3045.534	3046.334	9	+2,+3	distinct	0	1
FDHIWDYDLDAENDQMNQWIQQNL	55.66	51.3984	3050.314	3050.653	1	2	distinct	0	0.968
KGEPWIQETSQEALLDDFATYSSDLIK	72.19	51.1378	3083.497	3084.303	9	+2,+3	distinct	1	0.9999

The equivalent proteins include

gi|71022295|ref|XP_761377.1|	48769.68	hypothetical protein UM05230.1 [Ustilago maydis 521]

56. Group probability: 1.0000. Peptides of the group

GLDFLDREQAK	52.18	55.3503	1290.657	1291.24	1	2	distinct	1	0.9253
QQAEQLYDQQYAN	47.93	54.5743	1597.701	1597.379	1	1	distinct	0	0.9006
FSHEAVGFGAGFVAMR (000000000000000100)	101.92	54.2376	1681.803	1681.991	96	+2,+3	distinct	0	0.9999
EILAGIAGAEVDKLFETK	127.21	53.9408	1903.03	1903.693	55	+2,+3	distinct	1	1
FGFGNHEEAADFVYNQDPR	75.82	53.235	2211.961	2212.323	5	+2,+3	distinct	0	0.9993
MFGFGNHEEAADFVYNQDPR (0100000000000000000000)	70.09	53.2619	2343.001	2342.943	27	+2,+3	distinct	0	0.9995

The equivalent proteins include

gi|71018401|ref|XP_759431.1|	12180.84	hypothetical protein UM03284.1 [Ustilago maydis 521]

57. Group probability: 1.0000. Peptides of the group

EHIIIAK	49.93	55.5323	822.496	822.391	1	1	distinct	0	0.865
GAEVEILGLGNTFK	79.52	55.0662	1446.772	1446.463	2	+1,+2	distinct	0	0.9999
GQVMVIPGSIKPVK	44.89	54.6998	1451.853	1452.92	1	2	distinct	0	0.8744

FIDYASIDKAPEER	46.6	54.3166	1652.805	1653.989	1	3	distinct	1	0.8681
LMEETDKWLDLPPR	77.18	54.1708	1741.871	1742.093	2	+2,+3	distinct	1	0.9989
GITISTAHVEYETGNR	71.6	54.2265	1746.854	1748.023	1	2	distinct	0	0.9889
TADVTVSLTHPPGTEDADEK	70.04	53.5243	2081.975	2082.494	4	+2,+3	distinct	0	0.9995
DLEKPFLMPVEDVFSIPGR	114.14	53.2498	2188.124	2189.093	5	2	distinct	0	0.9998
VDQIDDPEMLELVEMEMR	80.22	53.737	2190.985	2191.126	1	2	distinct	0	0.9952
MVMPGDNVELDGELVHDIALEEGSR	76.32	52.0467	2724.273	2724.984	2	+2,+3	distinct	0	0.9998

The equivalent proteins include

gi|71003209|ref|XP_756285.1|	51423.64	hypothetical protein UM00138.1 [Ustilago maydis 521]

58. Group probability: 1.0000. Peptides of the group

IYQNQDEVGAALK	99.92	54.9403	1447.731	1448.355	1	2	distinct	0	0.999
IYQNQDEVGAALKK	52.52	54.7184	1575.826	1575.825	2	+2,+3	distinct	1	0.9899
FTALDLETSLVDTWK	115.33	54.176	1737.882	1738.73	5	2	distinct	0	0.9998
KYNADPAQVLIAWGVK	89.1	54.2292	1771.962	1772.922	9	+2,+3	distinct	1	0.9999
NIHLTAYSPLGNNLTGK	78.11	54.2091	1811.953	1812.813	7	+2,+3	distinct	0	0.9996
TEDGKFTALDLETSLVDTWK	87.21	53.0307	2268.116	2269.49	3	2	distinct	1	0.9976
LWNTSHQPDKVEAAYNETLK	55.79	53.0157	2343.149	2344.184	5	+2,+3	distinct	1	0.9979
SNFEQLELKDDDYETVTSLYK	52.92	52.4571	2536.186	2536.967	3	+2,+3	distinct	1	0.9948
FNVPFTYSPQWDINVFGEDAEK	99.67	52.2417	2602.202	2602.803	6	2	distinct	0	0.9993
FNVPFTYSPQWDINVFGEDAEKEAK	68.23	51.4368	2930.376	2931.013	3	2	distinct	1	0.9897

The equivalent proteins include

gi|71019819|ref|XP_760140.1|	137076.61	hypothetical protein UM03993.1 [Ustilago maydis 521]

59. Group probability: 1.0000. Peptides of the group

KAEEIAR	51.09	57.0073	815.45	815.736	1	2	distinct	1	0.8149
EHYDIATGVQK	51.66	55.6047	1259.615	1259.724	1	2	distinct	0	0.9214
AHGGYSVFTGVGER	82.68	54.7451	1435.684	1435.466	20	+1,+2,+3	distinct	0	1
FTQAGSETSALLGR	94.41	54.7526	1436.726	1438.173	2	2	distinct	0	0.9984
VALTGLTIAEYFR	96.01	54.8052	1452.798	1453.379	17	2	shared(8)	0	0.9932
TVLIQELINNVAK	89.24	54.8364	1453.85	1454.973	12	2	shared(2)	0	0.9972
VALVFGQMNEPPGAR	76.13	54.7519	1584.808	1585.022	7	2	shared(6)	0	0.9745
LVLEVAQHLGENTVR	84.18	54.5381	1676.921	1677.711	15	+2,+3	shared(6)	0	0.9996
GIAELGIYPAVDPLDSK	54.06	54.191	1756.925	1757.915	1	2	distinct	0	0.95
LAPIHVEPPAFVDQSTK	68.82	54.0133	1847.978	1848.253	15	+2,+3	distinct	0	0.9997
VVDTGLPIQIPVGPGTLGR	71.34	53.9399	1888.078	1888.45	5	2	distinct	0	0.9898
DEEGQDVLLFIDNIFR	112.41	54.0622	1921.942	1922.963	29	2	shared(3)	0	0.9935
FMSQPFAVAQVFTGIEGK (001000000000000000)	110.53	53.7084	1955.981	1956.568	37	+2,+3	distinct	0	1
IPSAVGYQPTLATDMGVMQER	97.78	53.1308	2263.098	2263.623	6	2	distinct	0	0.9784
GDHDALPESAFYMCGGIDDVKK	72.94	52.5745	2424.073	2424.693	3	2	distinct	1	0.9923
EGNDLYHEMIETGVINLEGDSK (0000000010000000000000)	98.75	52.6157	2462.127	2462.713	5	+2,+3	distinct	0	1
SLQDIIAILGMDELSEEDKLTVER (000000000010000000000000)	100.6	52.0836	2716.384	2716.853	46	+2,+3	distinct	1	1
TREGNDLYHEMIETGVINLEGDSK (000000000010000000000000)	98.14	52.1307	2719.276	2719.994	12	+2,+3	distinct	1	1
LAPIHVEPPAFVDQSTKAEVLETGIK	67.93	51.8489	2788.501	2789.891	11	+2,+3	distinct	1	0.9997
EILRGDHDALPESAFYMCGGIDDVK	68.41	51.8326	2807.289	2808.563	1	3	distinct	1	0.9875
AVIGPVVDVQFDTEDLPSIFNALEVQNVTGGGR	62.42	50.2147	3455.757	3456.964	7	3	distinct	0	0.9846

The equivalent proteins include

gi|71018215|ref|XP_759338.1|	55695.02	hypothetical protein UM03191.1 [Ustilago maydis 521]

60. Group probability: 1.0000. Peptides of the group

GFGFVTFATQAEADAAIAALNEQELDGR	100.58	51.5319	2911.399	2912.123	46	+2,+3	distinct	0	1
GFGFVTFATQAEADAAIAALNEQELDGRR	77.54	51.2157	3067.5	3068.586	27	3	distinct	1	0.9952

The equivalent proteins include

gi|71013156|ref|XP_758559.1|	19886.12	hypothetical protein UM02412.1 [Ustilago maydis 521]

61. Group probability: 1.0000. Peptides of the group

IGTEVYHNLK	51.61	55.7371	1172.619	1172.98	1	2	distinct	0	0.918
ELADVYLGFIK	55.53	55.3174	1266.686	1267.273	2	2	distinct	0	0.9444
IGTEVYHNLKK	50.55	55.4044	1300.714	1301.363	3	2	distinct	1	0.9137
ANAGITIIGDDLTVTNPLR	104.84	53.6982	1953.053	1953.653	5	2	distinct	0	0.9995
SGETEDVTIADLVVGLGVGIIK	118.98	53.392	2184.189	2184.822	46	+2,+3	distinct	0	1
IESLEPSAVYAGIDGFTQGETAPK	67.32	52.5508	2479.212	2479.853	1	2	distinct	0	0.9882
YPITSIEDPFDQDDWEAWSHLR	94.47	52.1636	2719.219	2719.533	11	+2,+3	distinct	0	1
KYPITSIEDPFDQDDWEAWSHLR	83.33	51.7318	2847.314	2848.798	13	+2,+3	distinct	1	1

INQIGTISESIQAAQLSQSDNWSVMVSHR	113.03	50.9483	3198.573	3199.894	7	3	distinct	0	0.9998
YGIDATNVGDEGGFAPNVQSADEALEILTEAIK	83.77	50.3255	3406.641	3406.811	4	3	distinct	0	0.9976

The equivalent proteins include

gi|71018545|ref|XP_759503.1|	47609.67	hypothetical protein UM03356.1 [Ustilago maydis 521]

62. Group probability: 1.0000. Peptides of the group

SIVDELKPEFTGVGK	60.57	54.6802	1617.861	1618.21	2	2	distinct	0	0.9694
FNITDDGHSEWVSCVR	96.67	53.8022	1920.842	1921.319	1	2	distinct	0	0.9988
HLYSLEAGDTVNALVFSPNR	130.4	53.1635	2202.107	2202.663	5	2	distinct	0	0.9999
GWITAIATSQENPDLLLTASR	108.68	53.2052	2256.175	2257.402	4	2	distinct	0	0.9996
TNHYGHTGYINTVTVSPDGSLCASGGK	76.16	51.8611	2792.282	2793.203	5	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71013096|ref|XP_758555.1|	47669.03	hypothetical protein UM02408.1 [Ustilago maydis 521]

63. Group probability: 1.0000. Peptides of the group

LNASHGSHEYFK	75.43	55.4028	1388.647	1389.169	10	+1,+2	distinct	0	0.9993
CSLDYLYIDYK	82.65	54.7	1451.664	1452.634	3	2	distinct	0	0.9949
YGLAEALALGIIEK	88.79	55.0656	1459.829	1459.819	1	2	distinct	0	0.992
YRPSCPILTITR	50.91	54.9054	1475.792	1475.88	4	2	distinct	0	0.9202
VENHQGVQNFDEILK	65.99	54.1554	1768.874	1768.951	1	2	distinct	0	0.9812
TQLEWYASLNPLEHGVDNK	84.21	53.1407	2213.075	2213.313	5	+2,+3	distinct	0	0.9998
VENHQGVQNFDEILKESDGIMVAR	75.91	52.0017	2727.329	2728.347	2	3	distinct	1	0.9933

The equivalent proteins include

gi|71003247|ref|XP_756304.1|	58310.87	hypothetical protein UM00157.1 [Ustilago maydis 521]

64. Group probability: 1.0000. Peptides of the group

GSLHACSTTAAPK	48.24	55.2827	1299.624	1300.054	1	2	distinct	0	0.9019
HAALFTSTIMSK (00000000001000)	76.03	55.3525	1305.675	1306.047	7	+1,+2	distinct	0	0.9996
TGEEPIEDFNGHYR	62.53	54.4986	1662.727	1662.948	3	+2,+3	distinct	0	0.9973
LYDSLEIDDGEVVGLKH	92.14	53.8261	1900.942	1901.403	3	+2,+3	distinct	1	0.9999
MTPPTASFINPATAGPQPGSFK	73.33	53.1092	2216.094	2216.941	12	2	distinct	0	0.9924
EVFPGLIVSGMELSEHDGHPR (00000000000100000000000)	94.2	53.0205	2305.116	2305.381	6	2	distinct	0	0.9987

The equivalent proteins include

gi|71010862|ref|XP_758425.1|	38914.34	hypothetical protein UM02278.1 [Ustilago maydis 521]

65. Group probability: 1.0000. Peptides of the group

NNITPAQVLLAWTLGR	90.18	54.1534	1765.984	1766.981	4	+2,+3	distinct	0	1
GGSYVPPPAHESPAEHR	60.88	54.7762	1786.839	1787.344	5	2	distinct	0	0.9722
TVDPTEGWGVADEIFEDGVDQTR	112.93	52.5199	2535.14	2535.993	1	2	distinct	0	0.9998
DLGTDYLDLYLMHWPVAFLNSK (000000000000100000000000)	72.9	52.3281	2610.283	2627.553	5	+2,+3	distinct	0	0.9998
TSEVVDEASIKPVVNQVEVNLGVHNEELR	84.24	50.8781	3202.647	3204.084	1	3	distinct	0	0.9973

The equivalent proteins include

gi|71016811|ref|XP_758925.1|	76559.05	hypothetical protein UM02778.1 [Ustilago maydis 521]

66. Group probability: 1.0000. Peptides of the group

TRDEIQTMR	52	55.6032	1148.561	1148.979	1	2	distinct	1	0.9187
RMEMAADQLYK	65.14	55.0884	1354.637	1354.865	1	2	distinct	1	0.9762
YGGHSLSDPGTTYR	51.78	54.5783	1509.685	1510.017	1	2	distinct	0	0.9316
AAKEEVDQAVEEAK	97.08	54.8344	1515.742	1516.196	2	2	distinct	1	0.9987
LWNLPCVFVCENNK	50.79	54.3399	1791.844	1792.446	1	2	distinct	0	0.9257
HASGYTLGGNGPLLMELVTYR	77.71	53.1448	2248.131	2249.503	2	2	distinct	0	0.9947
LEWETSKDELVHLYSEMVK	64.11	52.8889	2335.141	2336.344	1	3	distinct	1	0.9769
GFCHLAIGQEAVAVGMEAGMKPSDK	80.95	52.2332	2602.234	2603.243	4	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71019541|ref|XP_760001.1|	45766.55	hypothetical protein UM03854.1 [Ustilago maydis 521]

67. Group probability: 1.0000. Peptides of the group

RVVSQLLTLMDGIK	88.32	54.8838	1571.907	1572.247	3	2	shared(2)	1	0.9943
LGDLVSIHACHDIK	54.94	54.6632	1576.803	1576.954	3	2	distinct	0	0.948
RYELFAQNLQSAR	76.29	54.4517	1594.822	1595.904	9	2	distinct	1	0.9918
HTHGFSGADLAEICQR	90.48	54.2843	1797.822	1798.183	2	2	distinct	0	0.9979
NSPAIIFIDEIDSIAPK	91.29	54.1176	1841.977	1842.723	7	2	distinct	0	0.9837
AAAPCVMFFDELDAIAK	80.2	53.9063	1867.885	1868.093	3	2	distinct	0	0.995
VKQELQETVSYPVEHPEK	61.85	53.3126	2139.085	2139.89	1	3	distinct	1	0.9706
AVANETGAFFFLINGPEIMSK	92.86	52.9905	2255.13	2254.894	1	2	shared(2)	0	0.9986
EKMDLIDLDEDTIDAEVLDSLGVTMENFR	50.45	50.9009	3325.558	3327.048	1	3	distinct	1	0.9485

The equivalent proteins include

gi|71005074|ref|XP_757203.1|	90875.04	hypothetical protein UM01056.1 [Ustilago maydis 521]

68. Group probability: 1.0000. Peptides of the group

EHYIDLAK	51.28	56.5114	987.503	987.993	1	2	distinct	0	0.7666
KPFYGGLVK	45.29	55.7999	1007.58	1008.023	1	2	distinct	0	0.853
EIGLWFHEK	46.19	55.7591	1157.587	1158.409	1	2	distinct	0	0.8643
SYVMIKPDGVSR	44.56	55.1445	1350.697	1350.791	1	2	distinct	0	0.86
NIIHASDSHESATK	74.84	54.5782	1508.722	1509.533	11	+1,+2	distinct	0	0.9998
RLVGATNPLDAAPGSIR	70.45	54.5765	1706.943	1707.261	5	2	distinct	1	0.988
YITSGTPVVAMVWQGK	111.37	54.1317	1735.897	1736.893	3	2	distinct	0	0.9993
ELATEYKPIAWDMIMADN	104.9	53.3604	2109.975	2111.463	3	2	distinct	0	0.9995

The equivalent proteins include

gi|71017767|ref|XP_759114.1|	24003.47	hypothetical protein UM02967.1 [Ustilago maydis 521]

69. Group probability: 1.0000. Peptides of the group

YASSAYVAALSK	74.91	55.6129	1229.629	1230.615	1	2	distinct	0	0.9901
VIEGFQDLMSAYR	78.36	54.6817	1527.739	1528.241	1	2	distinct	0	0.9931
ADPITHNLFTVLAENGR	83.08	53.898	1866.959	1866.74	1	2	distinct	0	0.9961
GKADPITHNLFTVLAENGR	118.78	53.905	2052.075	2052.25	7	+2,+3	distinct	1	1
VNPAIQGGLVVDFAGNTVDLSVASK	118.21	52.9059	2470.307	2470.693	11	2	distinct	0	0.9999

The equivalent proteins include

gi|71024483|ref|XP_762471.1|	22855.19	hypothetical protein UM06324.1 [Ustilago maydis 521]

70. Group probability: 1.0000. Peptides of the group

VLDQPELGLPASR	58.27	55.5508	1393.756	1393.933	1	2	distinct	0	0.9591
WVAPIEDSPKPPAK	62.91	54.795	1533.819	1534.267	1	2	distinct	0	0.9741
VRPSPPGDIYFFTDNAASK	99.14	53.5407	2081.022	2081.753	9	+2,+3	distinct	0	0.9999
SQIHTIDEALLDDPEELSDAYEK	81.11	52.8097	2630.223	2630.553	2	+2,+3	distinct	0	1
RSQIHTIDEALLDDPEELSDAYEK	115.31	51.9459	2786.325	2787.152	1	3	distinct	1	0.9998

The equivalent proteins include

gi|71019455|ref|XP_759958.1|	30515.44	hypothetical protein UM03811.1 [Ustilago maydis 521]

71. Group probability: 1.0000. Peptides of the group

TCHAHPTLSEAFK	53.12	54.7209	1497.703	1497.413	4	+1,+2,+3	distinct	0	0.9996
RGALGGTCLNVGCIPSK	55.53	54.2605	1758.887	1759.161	1	2	distinct	1	0.8111
QIVSSTGALELQKVPEK	105.04	54.0574	1826.015	1826.546	1	2	distinct	1	0.9994
RPVTSGLNLEAVGIEKDER	77.6	53.485	2082.107	2082.903	7	+2,+3	distinct	1	0.9999
NIIIATGSEVTPFPGIEIDEK	112.05	53.2143	2242.173	2242.743	1	2	distinct	0	0.9997

The equivalent proteins include

gi|71013524|ref|XP_758608.1|	53946.24	hypothetical protein UM02461.1 [Ustilago maydis 521]

72. Group probability: 1.0000. Peptides of the group

ALIHDGLAR	52.17	55.7286	964.545	964.822	1	2	distinct	0	0.9197
KALIHDGLAR	54.6	55.3438	1092.64	1093.473	2	2	distinct	1	0.9374
LIEALCNEHK	49.63	55.2055	1225.612	1225.674	2	2	distinct	0	0.9035
KVVGCSCVVVK	52.21	55.5233	1233.657	1233.608	1	2	distinct	1	0.9253
GAMSIEDALQEVLKK	100.48	54.6408	1630.86	1631.348	2	2	distinct	1	0.9991
LIEALCNEHKIDLLK	93.67	54.3047	1807.987	1808.803	5	2	distinct	1	0.9933
DYGEESEGLNVLLEYFK	119.86	53.6292	2003.936	2004.409	32	2	distinct	0	0.9998
QAHLCVLVETCNEPEYLK	56.29	53.1992	2202.045	2202.481	8	2	distinct	0	0.9611

The equivalent proteins include

gi|71005598|ref|XP_757465.1|	16438.33	hypothetical protein UM01318.1 [Ustilago maydis 521]

73. Group probability: 1.0000. Peptides of the group

KQGGVVDPSLR	45.45	55.5354	1154.641	1155.252	1	2	distinct	1	0.8647
LKPGFPTLDSLR	52.1	55.3857	1342.761	1343.631	5	2	distinct	0	0.9274
RWIPALSELGIPK	49.75	54.7913	1478.861	1480.243	1	2	distinct	1	0.9149
VLGGSSALNFLVWDR	86.88	54.5959	1632.862	1633.383	3	2	distinct	0	0.997
GNIHITSNDATKYPSIDAK	73.26	53.5348	2044.022	2044.329	9	+2,+3	distinct	1	0.9991
VLYENANVGENLQDHTYSATVYK	45.64	52.3281	2627.25	2627.327	1	2	distinct	0	0.9186
HEIDAWEQLGNPGWNWNNLYSAMK (000000000000000000000000100)	87.64	51.6625	2872.303	2872.876	8	+2,+3	distinct	0	1

The equivalent proteins include

gi|71019921|ref|XP_760191.1|	68279.83	hypothetical protein UM04044.1 [Ustilago maydis 521]

74. Group probability: 1.0000. Peptides of the group

TISPWSAEDCR	53.7	55.2385	1320.577	1321.335	1	2	distinct	0	0.9348
KEEGVEAEVINLR	54.75	54.9533	1484.783	1485.728	1	3	distinct	1	0.8219
TIAPMDVDTIIDSVK	79.19	54.6826	1616.833	1617.488	1	2	distinct	0	0.994
VTGAAVPTPYAQNLEK	59.2	54.9001	1657.867	1658.784	1	2	distinct	0	0.9665

TIAPMDVDTIIDSVKK	83.45	54.2463	1744.928	1745.238	2	2	distinct	1	0.9961
TYYMSGGNVPCPVVFR	60.99	54.1461	1845.854	1845.93	1	2	distinct	0	0.9718
DALNSAMEEEMLRDDK	77.79	53.8979	1865.813	1866.793	1	2	distinct	1	0.9936
GPNGAAAGVGAQHSQDYAAWYGQIPGLK	62.72	52.0201	2783.341	2783.613	6	+2,+3	distinct	0	0.9989

The equivalent proteins include

gi|71024045|ref|XP_762252.1|	43977.57	hypothetical protein UM06105.1 [Ustilago maydis 521]

75. Group probability: 1.0000. Peptides of the group

VSESSRPDLATAPR	44.58	54.8689	1484.758	1485.255	1	2	distinct	0	0.6494
AAVDAGYADNALQVGQTGK	96.12	54.0126	1847.901	1848.271	1	2	distinct	0	0.9883
HAEFANNLSEPLAPLIK	95.4	54.1447	1862.989	1864.233	6	2	distinct	0	0.9987
IVESNSYTHVCTGHTAVGR	94.21	53.3208	2086.985	2087.523	6	+2,+3	distinct	0	1
DADAPIFQVADLGLVADLYEAVPEMLEK	95.61	51.2674	3031.51	3032.503	9	+2,+3	distinct	0	1

The equivalent proteins include

gi|71023343|ref|XP_761901.1|	36622.2	hypothetical protein UM05754.1 [Ustilago maydis 521]

76. Group probability: 1.0000. Peptides of the group

YALIVDDLK	59.8	55.6506	1048.58	1049.133	5	+1,+2	distinct	0	0.8354
AIGSIADLSAMGFGQR	87.32	54.6126	1592.798	1593	5	+1,+2	distinct	0	1
VVDFSPEPNPGAVEVSGADHVLAK	44.46	52.5271	2433.217	2434.049	1	2	distinct	0	0.9126
VVDFSPEPNPGAVEVSGADHVLAKL	63.59	52.4862	2546.302	2546.925	1	2	distinct	1	0.9842
GVDQVIVLAQNDPFVMSAWGVQNK (00000000000000001000000000)	113.63	52.2915	2614.321	2614.993	12	+2,+3	distinct	0	1
AISKGEQIPNTTFTYVPWAPELADGTACGAPTK	56.87	50.5636	3490.708	3491.574	3	3	distinct	1	0.9747

The equivalent proteins include

gi|71017727|ref|XP_759094.1|	26987.09	hypothetical protein UM02947.1 [Ustilago maydis 521]

77. Group probability: 1.0000. Peptides of the group

MSDGMFLHACR	69.86	55.191	1323.552	1323.855	1	2	distinct	0	0.9842
ANPTALILSSIMMLR	90.86	54.6063	1629.895	1630.117	5	2	distinct	0	0.993
EYPHIAYDEDLLDR	62.47	54.198	1747.805	1748.634	1	2	distinct	0	0.9734
DASIFEAVHGSAPDIAGQDK	76.59	53.4721	2026.96	2027.155	2	+2,+3	distinct	0	1
EIYHAANVPIKWEEVSVAPFIK	81.59	52.4162	2539.347	2539.833	1	2	distinct	1	0.9964
VMVMPNLYGDILSDMCAGLIGGLGLTPSGNIGK	74.15	50.5484	3362.675	3363.392	1	3	distinct	0	0.9944

The equivalent proteins include

gi|71005618|ref|XP_757475.1|	42065.74	hypothetical protein UM01328.1 [Ustilago maydis 521]

78. Group probability: 1.0000. Peptides of the group

HLAESLHK	49.72	56.1945	933.503	934.473	1	2	distinct	0	0.8995
KINLGVGAYR	50.7	56.0437	1089.629	1089.896	1	2	distinct	1	0.9106
ISVAGITDHNVK	73.4	55.3781	1252.677	1253.003	3	2	distinct	0	0.9888
LVNEHHVYLTGDGR	68.02	54.5044	1608.801	1610.243	8	+2,+3	distinct	0	0.9982
AGPPDPILGVTEAFKR	78.72	54.3367	1666.904	1667.355	6	2	distinct	1	0.994
GDKEYLPITGLADFTK	67.31	54.1459	1766.909	1766.378	2	+2,+3	distinct	1	0.9986
IAGTILADQQLYQQWLGEVK	88	53.393	2273.206	2273.617	1	2	distinct	0	0.9977

The equivalent proteins include

gi|71004152|ref|XP_756742.1|	47738.55	hypothetical protein UM00595.1 [Ustilago maydis 521]

79. Group probability: 1.0000. Peptides of the group

EHLDDVENQLNNLDK	107.72	54.1373	1794.838	1795.748	2	2	distinct	0	0.9995
REQAQENQYVQQAEK	72.41	54.0123	1847.876	1848.272	3	+2,+3	distinct	1	0.9992
EHLDDVENQLNNLDKK	77.56	54.0504	1922.933	1923.864	7	2	distinct	1	0.9913
EQAQENQYVQQAEKEK	99.44	53.8013	1948.913	1949.307	2	2	distinct	1	0.999
QREHLDDVENQLNNLDK	60.47	53.775	2078.998	2079.766	3	+2,+3	distinct	1	0.9989

The equivalent proteins include

gi|71012538|ref|XP_758508.1|	10187.24	hypothetical protein UM02361.1 [Ustilago maydis 521]

80. Group probability: 1.0000. Peptides of the group

DINTLIAEGQEK	87.89	55.3198	1329.678	1329.563	2	1	distinct	0	0.9849
ALLETVGIEAESER	73.34	54.8864	1515.778	1516.261	1	2	distinct	0	0.9896
ALLETVGIEAESERLDK	73.26	54.1303	1871.984	1872.158	9	2	distinct	1	0.9907
LASVPAGGAAPAAAAAGGAAPAAAGAAK	109.14	53.2497	2158.149	2159.455	2	2	distinct	0	0.9997
LIEELNGKDINTLIAEGQEK	114.24	53.119	2226.174	2226.504	6	+2,+3	distinct	1	1

The equivalent proteins include

gi|71021097|ref|XP_760779.1|	11344.73	hypothetical protein UM04632.1 [Ustilago maydis 521]

81. Group probability: 1.0000. Peptides of the group

RIDANYLDK	57.44	55.5767	1106.572	1106.655	1	2	distinct	1	0.9496
HISTLLAPQLASAPAAQQ	90.18	54.1233	1815.984	1816.38	2	2	distinct	0	0.998
LVKEEVLDDNQMYDR	70.98	54.0122	1865.883	1865.767	1	2	distinct	1	0.9879
TAATLGGVPHDVWGMTSLSVR	49.69	53.2958	2154.089	2154.633	1	2	distinct	0	0.9375
SGSHTPIDHIIANNAGYTDTVFEGK	78.54	52.8593	2643.256	2643.97	4	+2,+3	distinct	0	1
GGVTSSSLEVLCGLSLEDAEYVESMLFK	74.93	51.4933	3019.44	3020.743	1	3	distinct	0	0.9937

The equivalent proteins include

gi|71023803|ref|XP_762131.1|	118154.63	hypothetical protein UM05984.1 [Ustilago maydis 521]

82. Group probability: 1.0000. Peptides of the group

LISEHLVAVFSK	103.46	55.2898	1341.766	1342.212	4	+1,+2	distinct	0	0.9999
HLGGCSDLLDAQK	73.41	55.0639	1412.672	1413.066	3	+1,+2,+3	distinct	0	0.9997
VGILELDQMGSEGSDIQAYLLDK (00000000010000000000000)	123.85	52.6035	2493.231	2493.503	4	2	distinct	0	0.9999
VGILELDQMGSEGSDIQAYLLDKTSQR	81.34	51.3259	2965.47	2966.536	3	3	distinct	1	0.9963

The equivalent proteins include

gi|71021729|ref|XP_761095.1|	11304.84	hypothetical protein UM04948.1 [Ustilago maydis 521]

83. Group probability: 1.0000. Peptides of the group

KLQVEPVSGVEEVNMFK	89.46	53.814	1932.003	1932.285	1	2	distinct	1	0.9978
VHGLPTSNTFAVYGNGVDK	67.95	53.639	1974.98	1975.219	1	2	distinct	0	0.9864
KLAESYQAMNAQHAASQAAAAGTK	107.15	52.6376	2417.176	2417.533	3	+2,+3	distinct	1	1
ELTELVPGILNQLGPDSLASLRK	80.51	52.6385	2462.374	2462.733	2	2	distinct	1	0.9962
LQVEPVSGVEEVNMFKEDGNVLHFAAPK (0000000000000010000000000000)	52.33	51.2269	3082.543	3083.919	5	3	distinct	1	0.9544

The equivalent proteins include

gi|71017981|ref|XP_759221.1|	17692.05	hypothetical protein UM03074.1 [Ustilago maydis 521]

84. Group probability: 1.0000. Peptides of the group

ILVVFTSHTK	52.12	55.7729	1143.665	1143.533	2	1	distinct	0	0.9215
VLISGQNPASAAAVGR	73.72	54.5666	1509.826	1510.668	1	2	distinct	0	0.9907
KITCFTNQEEEQAGLTK	103.11	53.6194	1995.957	1996.828	1	2	distinct	1	0.9993
APLDQSSVDAFKDDADSVK	99.21	54.2973	2006.943	2007.694	2	+2,+3	distinct	1	1
TFYEAGKPTSAVCHAPAVFADVK	63.88	52.5889	2465.205	2465.563	6	+2,+3	distinct	0	0.9987

The equivalent proteins include

gi|71003121|ref|XP_756241.1|	25532.93	hypothetical protein UM00094.1 [Ustilago maydis 521]

85. Group probability: 1.0000. Peptides of the group

RAEFDDIIK	44.6	55.5541	1105.577	1106.173	1	2	distinct	1	0.187
MPEPLIEAFGVLKK	81.8	54.8976	1570.879	1572.193	5	+2,+3	distinct	1	0.9993
IVRPEFMLGPTEYK	68.02	54.451	1678.875	1678.476	2	2	distinct	0	0.9836
THLQDATPLTLGQEFSGYVK	111.13	53.2166	2204.111	2204.763	3	2	distinct	0	0.9997
DTFGPLQVPADRYWGAQTQR	42.57	52.9884	2305.124	2305.793	1	2	distinct	1	0.8799
ILNESLMLATILNSHLGYDNVAAAAK	73.58	52.0325	2741.442	2741.741	8	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71004536|ref|XP_756934.1|	50926.25	hypothetical protein UM00787.1 [Ustilago maydis 521]

86. Group probability: 1.0000. Peptides of the group

RALEFGNR	49.69	56.2041	961.509	962.453	1	2	distinct	1	0.8993
ALRPENAAK	49.18	55.6015	968.54	969.224	1	2	distinct	0	0.6774
EAIEDGWQPGK	48.1	55.6068	1228.572	1228.561	2	2	distinct	0	0.8926
RGALDWAPEFEK	57.58	54.9812	1417.699	1418.335	4	2	distinct	1	0.9554
EDFDKETDAIAAQEMWK	50.16	53.4721	2025.899	2026.828	2	+2,+3	distinct	1	0.9913
ATIAMLLLSDAACAQVYASVK	56.79	53.1762	2195.133	2196.553	1	2	distinct	0	0.9666
NETFAILGYGSQGHGQGLNLR	128.15	53.2146	2231.108	2231.581	19	+2,+3	distinct	0	1

The equivalent proteins include

gi|71021315|ref|XP_760888.1|	70427.86	hypothetical protein UM04741.1 [Ustilago maydis 521]

87. Group probability: 1.0000. Peptides of the group

KPMIVVGSAVAEHPDGK	102.41	54.3043	1733.913	1734.331	6	+2,+3	distinct	0	1
FIYLLNADDITPETIPR	82.05	53.6319	1990.041	1990.915	1	2	distinct	0	0.9958
FVPASWPEALATIAEGLASSGAK	87.82	53.2346	2272.174	2272.722	1	2	distinct	0	0.9979
LASSSVSGTPLLRPIQNFYQTDPISR	52.96	51.7359	2846.493	2847.441	3	3	distinct	0	0.9532
DAFVVYQGHHGDVGAQFADVCLPGSAYTEK	66.47	51.0331	3237.482	3238.901	7	3	distinct	0	0.9878

The equivalent proteins include

gi|71021477|ref|XP_760969.1|	89475.33	hypothetical protein UM04822.1 [Ustilago maydis 521]

88. Group probability: 1.0000. Peptides of the group

GVHTTNFMFDGAR	62.69	54.91	1451.662	1451.861	1	2	distinct	0	0.9726

VGPGAPSPFVDEKR	65.92	54.8365	1454.752	1454.952	1	2	distinct	1	0.9801
TRLELSNPGTVEHLQR	76.1	53.989	1848.981	1849.783	5	+2,+3	distinct	1	0.9998
LSPAFGLTFAGEIDHLQGAAK	114.96	53.1929	2142.111	2143.053	4	2	distinct	0	0.9998
ALNPSPTDLTGIYIVNYLQSLTR	85.74	52.5155	2548.354	2548.973	18	2	distinct	0	0.9976

The equivalent proteins include

gi|71004190|ref|XP_756761.1|	42026.88	hypothetical protein UM00614.1 [Ustilago maydis 521]

89. Group probability: 1.0000. Peptides of the group

LSLYVAGAGIHPR	60.58	55.0152	1352.756	1353.265	3	2	distinct	0	0.9669
DLGEIIDYVKPTAILGLSTIK	68.81	53.2713	2258.277	2258.544	3	2	distinct	0	0.9883
RPIIFPLSNPTDNSECTFEEAVK	96.05	52.0639	2663.29	2664.047	10	+2,+3	distinct	0	1
VTNEMITESALALSDALTDQERAEGR	83.47	51.6986	2819.361	2820.322	1	3	distinct	1	0.9968
LYYATILANKEEILPLIYTPTVGEACQK	72.85	51.0652	3210.689	3211.828	1	3	distinct	1	0.9925

The equivalent proteins include

gi|71011147|ref|XP_758454.1|	70148.96	hypothetical protein UM02307.1 [Ustilago maydis 521]

90. Group probability: 1.0000. Peptides of the group

RPGDDHEEVVR	45.56	55.3707	1307.622	1308.105	1	2	distinct	0	0.8665
YVMAYEHTNKPDWWDK	76.59	53.5406	2081.931	2082.18	2	2	distinct	0	0.9929
SISCGPIVEQATHFCDLSR	94.15	53.2554	2176.004	2176.597	1	2	distinct	0	0.9986
YQNDDPFFSEVSNLIDNIEK	47.27	52.8435	2386.096	2387.083	1	2	distinct	0	0.9207
LVEAFPDVAIFIEKPVSTGPVSDAFK	86.73	51.8286	2775.473	2775.983	4	+2,+3	distinct	0	0.9999
YFGGEVDLATVSAHSLEWFEPAGQLSK	74.44	51.4418	2937.418	2938.646	4	3	distinct	0	0.9932

The equivalent proteins include

gi|71005500|ref|XP_757416.1|	51228.04	hypothetical protein UM01269.1 [Ustilago maydis 521]

91. Group probability: 1.0000. Peptides of the group

ILGGPQIKPFEGNK	62.08	54.7099	1496.835	1497.385	8	2	distinct	0	0.9722
WNTGVLDSFLIEITR	43.65	54.15	1762.925	1763.749	1	2	distinct	0	0.8664
KNPELENLLFDDFFNK	75.16	53.7399	1981.978	1983.307	2	2	distinct	1	0.9919
WTAINALDLGQPVTLIGEAVFAR	145.42	52.6784	2454.327	2454.943	12	+2,+3	distinct	0	1
TAAQSDGEPCCDWVGQTGAGHYVK	55.7	52.3124	2593.096	2593.991	2	3	distinct	0	0.96
MVHNGIEYGDMQLICEAYDILK	47.13	52.3941	2611.212	2612.002	1	3	distinct	0	0.9089

The equivalent proteins include

gi|71014537|ref|XP_758724.1|	54311.67	hypothetical protein UM02577.1 [Ustilago maydis 521]

92. Group probability: 1.0000. Peptides of the group

DFGSLDNLK	56.89	55.9505	1007.492	1007.594	2	+1,+2	distinct	0	0.9725
NIWSVINFK	51.36	55.6434	1119.608	1120.693	4	+1,+2	distinct	0	0.9872
KQIELQSAIK	47.12	55.6763	1156.682	1156.537	1	1	distinct	1	0.8786
AYNSAISSNDVRK	45.38	54.8543	1423.705	1423.783	1	2	distinct	1	0.875
HHQLYVTNLNNAIK	52.2	54.5063	1663.879	1665.148	2	2	distinct	0	0.9341
NLAPASQGGGQLQDGPFK	102.13	54.2906	1783.885	1784.637	2	2	distinct	0	0.9993
STFNATIATIQGSGWGWLGFNPK	104.56	52.6133	2452.217	2453.553	12	2	distinct	0	0.9995

The equivalent proteins include

gi|71018003|ref|XP_759232.1|	23178.72	hypothetical protein UM03085.1 [Ustilago maydis 521]

93. Group probability: 1.0000. Peptides of the group

KPQTPTHK	47.79	56.0158	935.519	935.465	2	1	distinct	0	0.8814
KHLYANAVTK	50.25	55.7729	1143.64	1143.453	1	1	distinct	1	0.9076
AVEHGGEKEYDSVLAIYR	46.01	54.2916	2035.001	2036.286	1	3	distinct	1	0.8795
FDQYIATGDESQIHPDLLR	48.45	53.1847	2217.07	2218.04	1	3	distinct	0	0.9082
CFPEWESASEFINMHLDR	43.68	53.4702	2266.978	2268.439	1	3	distinct	0	0.8547
RFDQYIATGDESQIHPDLLR	82.51	52.7841	2373.171	2374.152	4	+2,+3	distinct	1	0.9999
FLSTGDPTPEEDETLWHVPLMLK	62.47	52.1824	2654.294	2654.813	1	2	distinct	0	0.9815
SSHPIEVPLQGENVEDAINQVFDAISYSK	75.91	50.8969	3185.552	3186.716	5	3	distinct	0	0.9945

The equivalent proteins include

gi|71004544|ref|XP_756938.1|	111749.03	hypothetical protein UM00791.1 [Ustilago maydis 521]

94. Group probability: 1.0000. Peptides of the group

IGGPIQFR	74.06	56.914	886.502	886.643	2	2	distinct	0	0.9879
ALLLHFAEEFK	52.9	55.4026	1316.713	1317.568	1	2	distinct	0	0.9298
ALGEAAATAQTSNFK	94.26	54.7207	1478.736	1479.029	1	2	distinct	0	0.9984
DFTIHDATPYSIK	73.08	54.7292	1506.735	1507.189	1	2	distinct	0	0.989
REEFEQLISPLLER	47.63	54.1911	1757.931	1757.803	1	2	distinct	1	0.9023
LAGEEHIFSATQLLAMYLAK	74.31	53.2756	2205.15	2205.989	1	2	distinct	0	0.9925
KENFELEAHYATPEQIPEGINPWIGK	64.31	51.3804	3009.487	3010.16	2	3	distinct	1	0.9828

The equivalent proteins include

gi|71023671|ref|XP_762065.1|	104108.79	hypothetical protein UM05918.1 [Ustilago maydis 521]

95. Group probability: 1.0000. Peptides of the group

IFNTNNLWLNLR	69.42	54.8795	1516.815	1516.754	2	2	distinct	0	0.9235
LLEIAQVPSEHVEDFK	72.54	53.975	1852.957	1853.392	1	2	distinct	0	0.9898
KAFDAEMSNFFTLFNR	128.46	53.7449	1936.914	1937.803	1	2	distinct	1	0.9999
SCSDLLLITSDLYSLEHGK	78.51	53.2074	2150.056	2150.842	2	+2,+3	distinct	0	0.9996
NLWYPPGHGDLFDAMNNSGLLDR	42.25	52.2651	2601.207	2601.431	1	3	distinct	0	0.8654
QIEHLNSSHNVNVPFILMNSFNTDDDTAR	42.42	50.7176	3327.558	3328.568	1	3	distinct	0	0.8962

The equivalent proteins include

gi|71023003|ref|XP_761731.1|	56490.35	hypothetical protein UM05584.1 [Ustilago maydis 521]

96. Group probability: 1.0000. Peptides of the group

AAIQEASSTKR	47.79	55.6498	1160.615	1160.929	1	2	distinct	1	0.8896
MMGHVAGVGIDCEK	84.28	55.0513	1502.668	1502.829	1	2	distinct	0	0.996
EVHAPTAPHTEIDAR	66.12	54.4672	1642.806	1643.283	1	2	distinct	0	0.9813
SLPAPGHGVIGSADGMQR	79.38	54.2028	1748.863	1749.214	6	+2,+3	distinct	0	0.9993
ANDKNESHVYQELFTR	44.87	53.7503	1949.923	1950.794	1	3	distinct	1	0.8586
MNFLPVGVPYHSSYLIGATEK	61.39	53.0113	2322.172	2322.673	1	2	distinct	0	0.9777
YYDNDESKVPVADYVSNDPLAIDEADVYAR	59.64	50.325	3405.552	3406.78	1	3	distinct	1	0.978

The equivalent proteins include

gi|71017775|ref|XP_759118.1|	431546.84	hypothetical protein UM02971.1 [Ustilago maydis 521]

97. Group probability: 1.0000. Peptides of the group

AIAAHPMAVFYSNR	62.08	55.081	1546.771	1547.887	2	2	distinct	0	0.972
LPSPTFVTAYLEAFR	105.46	54.2881	1710.898	1711.801	3	2	distinct	0	0.9994
AIEADAEDPDIYYHR	70.62	54.1167	1776.795	1777.123	1	2	distinct	0	0.9875
KKPTGAGAASGSSSTDAPSQR	114.06	53.7731	1959.961	1961.143	2	2	distinct	1	0.9998
SYPHAFTLFSEAIEQGLSNQDLEANAYNMR	67.95	50.3542	3415.578	3416.706	1	3	distinct	0	0.9894

The equivalent proteins include

gi|71023563|ref|XP_762011.1|	77610.35	hypothetical protein UM05864.1 [Ustilago maydis 521]

98. Group probability: 1.0000. Peptides of the group

IMANLTHNLIR	71.98	55.1215	1294.718	1295.983	3	2	distinct	0	0.95
KATESFQVDEHPR	97.09	54.7303	1542.743	1543.041	2	2	distinct	1	0.9987
TNVFGGAIALGHPLGASGAR	91.97	54.0295	1864.991	1865.422	1	2	distinct	0	0.9926
LCGSGFQSIINAVHEIR	102.77	53.8283	1899.962	1900.768	4	+2,+3	distinct	0	0.9999
ELELPNDKTNVFGGAIALGHPLGASGAR	63.07	51.7667	2803.462	2804.524	3	3	distinct	1	0.982

The equivalent proteins include

gi|71018429|ref|XP_759445.1|	41311.46	hypothetical protein UM03298.1 [Ustilago maydis 521]

99. Group probability: 1.0000. Peptides of the group

SIDQAIDVGHK	62.86	55.2586	1181.604	1182.044	1	2	distinct	0	0.9708
QLQAANDKEGLK	56.8	55.3044	1313.694	1313.664	1	2	distinct	1	0.952
SHLETAEAQQAIK	71.65	54.8503	1424.726	1424.769	2	+1,+2	distinct	0	0.9985
LGGMCIGQVGPILK	58.74	54.9089	1441.778	1442.339	1	2	distinct	0	0.9626
RVVIITQGSQPTIVAK	117.18	54.24	1709.02	1709.803	8	2	distinct	1	0.9998
SIYQFSDDQPTGSCAVVITGHNR	55.92	52.7126	2551.176	2552.351	3	3	distinct	0	0.959

The equivalent proteins include

gi|71004556|ref|XP_756944.1|	37029.86	hypothetical protein UM00797.1 [Ustilago maydis 521]

100. Group probability: 1.0000. Peptides of the group

GTDGFSLTEGR	46.17	55.284	1138.525	1139.502	1	2	distinct	0	0.8737
KPEFTALFPYGK	84.16	54.94	1396.739	1397.07	7	+1,+2	distinct	0	0.9997
APIGQIYGFAGHFK	83.04	54.7602	1504.783	1505.533	6	+1,+2	distinct	0	1
MAPIGQIYGFAGHFK	86.57	54.6511	1635.823	1636.677	3	2	distinct	0	0.9969
SVLEVAPDVDSYTISPLDLSKPEDK	42.78	52.089	2716.369	2717.236	1	3	distinct	0	0.8808

The equivalent proteins include

gi|71013430|ref|XP_758589.1|	46281.64	hypothetical protein UM02442.1 [Ustilago maydis 521]

101. Group probability: 1.0000. Peptides of the group

SYAANYNHIPGK	57.93	55.3752	1333.641	1334.12	1	2	distinct	0	0.9564
QGWDYHVTEPK	51.68	55.3549	1358.625	1358.895	1	2	distinct	0	0.922
SKEDAIHFCEK	70.62	55.1012	1362.624	1363.803	4	2	distinct	1	0.9853
HEQAVTADLVSSAPEELHQR	111.2	53.1079	2216.082	2216.913	3	+2,+3	distinct	0	1
RHEQAVTADLVSSAPEELHQR	67.65	52.8331	2372.183	2373.404	1	3	distinct	1	0.9842

The equivalent proteins include

gi|71003986|ref|XP_756659.1|	20806.49	hypothetical protein UM00512.1 [Ustilago maydis 521]

102. Group probability: 1.0000. Peptides of the group

APISSLPVITPQK	48.34	55.1492	1349.792	1350.235	1	2	distinct	0	0.903

LAEYDGFIFGFPTR	94.15	54.6195	1631.798	1632.051	1	2	distinct	0	0.9983
LQGEHFAQIVNTYVK	89.09	54.245	1745.91	1747.353	4	2	distinct	0	0.9975
IHGVSPYGAGTIAAGDGSR	97.36	54.2882	1784.88	1785.256	6	+2,+3	distinct	0	0.9999
APAQVSAFFDQTGGLWASGALIGK	54.13	52.7602	2391.222	2392.533	1	2	distinct	0	0.9624

The equivalent proteins include

gi|71018159|ref|XP_759310.1|	25508.15	hypothetical protein UM03163.1 [Ustilago maydis 521]

103. Group probability: 1.0000. Peptides of the group

IPYRYPAAGADPIADAIR	46.32	53.8251	1929.011	1930.462	1	3	distinct	1	0.8839
ALQNYDLIQDGIVEAFSK	95.99	54.049	2023.026	2023.31	1	2	distinct	0	0.9988
HLLLAGEADGKLPETLQAFTSK	109.15	52.9683	2338.253	2339.253	5	+2,+3	distinct	1	1
GHGSSAIPAEPCTIAQLSDDVAFLLDSLAVK	95.08	51.1298	3181.596	3182.94	1	3	distinct	0	0.999

The equivalent proteins include

gi|71023813|ref|XP_762136.1|	53539.36	hypothetical protein UM05989.1 [Ustilago maydis 521]

104. Group probability: 1.0000. Peptides of the group

VHLVAVDIFTTK	72.38	55.2082	1341.766	1341.478	23	+1,+2	distinct	0	0.9998
YEDISPSTHNMDVPNVR	61.09	53.6191	1972.895	1974.093	1	2	distinct	0	0.9733
KYEDISPSTHNMDVPNVR (000000000000010000000)	98.83	53.4507	2100.99	2101.421	10	+2,+3	distinct	1	0.9999
REEYQLVNIDDGFLNLMTNDGDTK	84.7	51.9714	2799.302	2800.741	2	3	distinct	1	0.9969

The equivalent proteins include

gi|71013478|ref|XP_758597.1|	17885.56	hypothetical protein UM02450.1 [Ustilago maydis 521]

105. Group probability: 1.0000. Peptides of the group

NIVVAAGLHK	50.29	55.9079	1020.608	1021.051	1	2	distinct	0	0.6961
FQQHVAASDR	47.85	55.7675	1157.558	1157.833	1	2	distinct	0	0.8859
GLGCPPGLMVLAASK	50.28	54.8445	1469.773	1470.166	1	2	distinct	0	0.9242
IGHMGITVVNDKER	73.24	54.5267	1567.814	1568.328	7	+2,+3	distinct	1	0.9992
VLTFTHVDTSTGVLSDAK	82.58	53.9138	1889.973	1890.499	1	2	distinct	0	0.9961
VSPETILVLDGVCSVGSEEIR	68.54	53.3899	2258.146	2259.003	1	2	distinct	0	0.988
AYEAGTGAYFATPPTNLIYALHASLTTITK	65.45	50.9406	3155.618	3156.481	6	3	distinct	0	0.9866

The equivalent proteins include

gi|71015054|ref|XP_758768.1|	49481.74	hypothetical protein UM02621.1 [Ustilago maydis 521]

106. Group probability: 1.0000. Peptides of the group

GIVGEIIKR	54.15	55.6534	983.613	983.812	1	2	distinct	1	0.9326
MVHASEEHLEK	66.79	55.3137	1308.613	1308.385	8	+1,+2,+3	distinct	0	0.9998
NVCHGSDSVESAK	59.37	55.3876	1388.599	1388.892	1	2	distinct	0	0.9629
YMASGPVVCIVFEGK	84.55	54.3919	1655.805	1656.207	1	2	distinct	0	0.9963
AEIALWFGEQNPTIQYTR	98.95	53.2262	2136.064	2137.189	4	2	distinct	0	0.9991

The equivalent proteins include

gi|71016794|ref|XP_758923.1|	22837.86	hypothetical protein UM02776.1 [Ustilago maydis 521]

107. Group probability: 1.0000. Peptides of the group

MGHAGAIIAGGK (01000000000000)	66.01	55.1162	1081.57	1081.842	7	+1,+2	distinct	0	0.9988
ANPKPVVAFIAGR	50.2	55.0837	1338.777	1339.447	3	2	distinct	0	0.9177
AGQTHLGLPVFGSVK	70.35	54.5665	1509.83	1510.513	5	2	distinct	0	0.987
TGTFHCQQALEYGTK	80.47	54.1542	1739.794	1740.215	1	2	distinct	0	0.9947
LLLDHDKSEGIVLIGEIGGSMEEDAAEYLAK	107.03	50.8352	3314.659	3315.569	1	3	distinct	1	0.9997

The equivalent proteins include

gi|71006306|ref|XP_757819.1|	34445.08	hypothetical protein UM01672.1 [Ustilago maydis 521]

108. Group probability: 1.0000. Peptides of the group

IKELQEAILYGK	78.91	55.1206	1403.802	1404.087	1	2	distinct	1	0.9931
THGIVQFDPTGDKFDPK	58.06	53.8302	1900.932	1901.298	3	2	distinct	1	0.9651
ASGEAMGATDKDAAAGAGSEALQAQIK (000000100000000000000000000)	83.45	52.5662	2518.197	2518.761	2	+2,+3	distinct	1	0.9997
EHEALYQAPVPGKEPGTVLECSK	78.51	52.4118	2538.242	2539.373	6	+2,+3	distinct	1	1

The equivalent proteins include

gi|71018819|ref|XP_759640.1|	27454.41	hypothetical protein UM03493.1 [Ustilago maydis 521]

109. Group probability: 1.0000. Peptides of the group

IFNGSGAPIDKGPR	58.84	55.0522	1427.752	1427.926	1	2	distinct	1	0.9628
LALTTAEYYAYQLEK	76.62	54.1671	1775.898	1775.751	1	2	distinct	0	0.9926
GYPGYMYTDLSTIYER	64.43	53.8327	1927.866	1929.104	5	2	distinct	0	0.9793
ADHSDVSNQMYAAYATGR	47.1	53.704	1955.843	1956.074	1	3	distinct	0	0.8918
IPIFSAAGLPHNEIAAQICR	109.33	53.2804	2177.141	2177.873	21	+2,+3	distinct	0	1

The equivalent proteins include

gi|71006198|ref|XP_757765.1|	47497.92	hypothetical protein UM01618.1 [Ustilago maydis 521]

110. Group probability: 1.0000. Peptides of the group

KQGFGAAAQYAR	45.56	55.3146	1266.647	1267.112	1	2	distinct	1	0.8713
NLQSTGGEHLAATEK	56.32	54.7177	1554.764	1555.159	1	2	distinct	0	0.9555
GYHEFSFAHETMGK (0000000000001000)	79.97	54.3898	1639.709	1640.293	3	2	distinct	0	0.9942
GKDFMNAPWLFAEAYK	85.74	53.9448	1886.902	1888.133	4	2	distinct	1	0.9968
LRPIIDDGEGDIPLWNK	60.22	53.7338	1950.021	1950.523	1	2	distinct	0	0.9711
YAVVLLSDGLPGKPVSFNQQ	62.2	53.2577	2131.131	2131.546	1	2	distinct	0	0.9784
SDVVVGVPGDVSNKLDSEEPGWR	54.12	52.621	2440.187	2441.016	1	2	distinct	1	0.9611

The equivalent proteins include

gi|71012428|ref|XP_758494.1|	57487.61	hypothetical protein UM02347.1 [Ustilago maydis 521]

111. Group probability: 1.0000. Peptides of the group

GPAPAPTSFPGADKLR	87.2	54.527	1580.831	1581.034	4	+2,+3	distinct	1	0.9996
IGLDTGVPVILGVLTALTEDQALER	93	52.3246	2592.437	2593.763	12	+2,+3	distinct	0	1
AGVKPENIVIESVPGSWELPFGVSR	80.75	52.1722	2666.407	2667.26	12	+2,+3	distinct	0	0.9996

The equivalent proteins include

gi|71017977|ref|XP_759219.1|	20309.38	hypothetical protein UM03072.1 [Ustilago maydis 521]

112. Group probability: 1.0000. Peptides of the group

HGIVTMTYSALAPFYK	117.29	54.2215	1797.912	1799.354	7	+2,+3	distinct	0	1
AKEYLDQLDSNNDAQLK	80.8	53.7669	1963.949	1964.219	2	+2,+3	distinct	1	0.9998
FIDGAEVYANEASMGAGIESFLASSGLK	95.6	51.7175	2833.348	2833.951	1	2	distinct	0	0.9992

The equivalent proteins include

gi|71023939|ref|XP_762199.1|	35315.3	hypothetical protein UM06052.1 [Ustilago maydis 521]

113. Group probability: 1.0000. Peptides of the group

HKGVMVGMGQK (0000010000000)	70.83	55.6094	1170.6	1170.959	31	+1,+2	shared(8)	1	0.9992
AVFPSVVGRPR	52.64	55.9012	1183.682	1184.433	2	2	distinct	0	0.9275
KEYDESGPSIVHR	51.92	54.8172	1515.732	1516.145	1	2	shared(3)	1	0.8424
SYELPDGKVITIGNER	64.43	54.1766	1789.921	1790.679	1	2	shared(14)	1	0.9686
YPIEHGIVTNWDDMEK	86.65	53.8856	1945.888	1946.228	3	+2,+3	shared(6)	0	0.9985
VAPEEHPVLLTEAPINPK	88.95	53.6979	1953.057	1953.863	9	2	shared(9)	0	0.9916
TPEVLFQPAFLGLEAAGIHETTYNSIMK	96.94	51.1644	3076.558	3077.875	18	+2,+3	distinct	0	1
TTGIVLDSGDGVTHTVPIYEGYSLPHSILR	74.6	51.0553	3196.64	3198.047	8	+2,+3	distinct	0	0.9997

The equivalent proteins include

gi|71024269|ref|XP_762364.1|	41674.02	actin [Ustilago maydis 521]

114. Group probability: 1.0000. Peptides of the group

GVQVHPDGNIHYESFVR	76.01	53.698	1952.949	1953.923	4	2	distinct	0	0.9928
ALGQNPTQAEVADLANAAPK	108.18	53.7454	1978.012	1978.986	1	2	distinct	0	0.9996
GFQVFDKDGNGFIGAGELR	98.09	53.5107	2025.991	2026.372	3	+2,+3	distinct	1	1
DIDYASFLNILNRPNGFKPAGTPEEFIR	42.41	51.0539	3193.62	3193.424	1	3	distinct	0	0.8916

The equivalent proteins include

gi|71004914|ref|XP_757123.1|	20178.32	hypothetical protein UM00976.1 [Ustilago maydis 521]

115. Group probability: 1.0000. Peptides of the group

KGLQSLLQK	55.24	56.1474	1013.623	1014.214	1	2	distinct	1	0.9381
GGAIAIGHPLGASGGR	59.84	55.2864	1389.748	1390.087	15	+1,+2	distinct	0	0.9983
ERQDQFAAESHR	69.43	54.92	1472.676	1473.054	2	2	distinct	1	0.9565
MAALHAGMPITSAYK	46.87	54.724	1560.779	1561.069	1	2	distinct	0	0.8981
DAYPEELLAHVLQR	66.96	54.3166	1652.852	1654.029	2	2	distinct	0	0.982
GVKPDVMGIGPAEAVPK	73.32	54.5068	1663.897	1664.883	3	2	distinct	0	0.9907
LISQDEGIRPGTTLESLGK	45.19	53.4946	2013.074	2013.499	1	2	distinct	0	0.9001

The equivalent proteins include

gi|71006648|ref|XP_757990.1|	44805.03	hypothetical protein UM01843.1 [Ustilago maydis 521]

116. Group probability: 1.0000. Peptides of the group

VGPNLHGIFGR	63.43	55.2336	1165.636	1165.277	7	2	shared(3)	0	0.9083
DRNDLITYLR	53.64	55.4837	1277.673	1277.87	2	2	distinct	1	0.9317
NDLITYLREETK	55.33	54.5851	1493.773	1494.714	1	2	distinct	1	0.9462
CAQCHTLGAGEPNK	67.74	54.6721	1541.671	1541.89	1	2	distinct	0	0.9831
GVTWDEETLFEYLENPK	106.38	53.5171	2068.963	2069.011	16	2	distinct	0	0.9991
GVTWDEETLFEYLENPKK	107.05	53.2298	2197.058	2197.703	8	2	distinct	1	0.9995

The equivalent proteins include

gi|71015943|ref|XP_758855.1|	12099.08	cytochrome c [Ustilago maydis 521]

117. Group probability: 1.0000. Peptides of the group

SHLLGWSSGK	77.8	55.7526	1070.551	1070.369	5	1	distinct	0	0.9918

IVTLTASGMHTWTK (0000000001000000)	74.92		54.8798	1544.802	1544.944	4	2	distinct	0	0.9909
ALDISATAPNAPVHFR	71.31		54.2846	1678.879	1679.753	14	+2,+3	distinct	0	0.9991
HAPLGASGYFADVTLTGK	121.35		54.2645	1803.915	1805.314	7	2	distinct	0	0.9999

The equivalent proteins include

gi|71002987|ref|XP_756174.1|	27605.43	hypothetical protein UM00027.1 [Ustilago maydis 521]

118. Group probability: 1.0000. Peptides of the group

GGHMFAPTK	48.39		56.6103	944.454	944.303	2	+1,+2	distinct	0	0.9842
AGHQTSAESWGTGR	74.28		54.9503	1443.649	1444.086	1	2	distinct	0	0.9904
LNLLKLAPGGHIGR	62.77		54.9851	1457.883	1458.891	16	+2,+3	distinct	1	0.9968
GHRVEELEEIPLVVADAAESLTK	91.44		52.5407	2504.312	2505.339	3	+2,+3	distinct	1	1

The equivalent proteins include

gi|71017629|ref|XP_759045.1|	36494.8	hypothetical protein UM02898.1 [Ustilago maydis 521]

119. Group probability: 1.0000. Peptides of the group

VVDALGNPIDGK	87.75		55.4031	1196.64	1197.823	1	2	shared(6)	0	0.9821
TGQIVDVPVGPK	59.36		55.1025	1208.676	1209.174	2	+1,+2	distinct	0	0.9938
TAVAIDTIINQK	45.22		55.3925	1285.724	1285.683	1	1	shared(2)	0	0.8672
HAIIIYDDLSK	80.76		55.5162	1286.687	1287.158	9	+1,+2	shared(5)	0	0.9997
GIRPAINVGLSVSR	71.89		54.778	1437.842	1438.903	22	2	shared(4)	0	0.9882
EAYPGDVFYIHSR	58.88		54.6289	1552.731	1554.178	3	2	shared(8)	0	0.9619
VVDALGNPIDGKGPIEAAER	120		54.0488	2020.059	2020.947	3	+2,+3	distinct	1	0.9992
SVNQPMQTGIKPIDAMVPIGR	77.86		53.509	2251.182	2251.873	12	+2,+3	distinct	0	0.9996

The equivalent proteins include

gi|71022593|ref|XP_761526.1|	47759.01	hypothetical protein UM05379.1 [Ustilago maydis 521]

120. Group probability: 1.0000. Peptides of the group

AIVVFVPMPQLK	64.54		55.2288	1340.789	1341.251	3	2	distinct	0	0.9757
TLTAVHESILEDLVYPSEITGKR	82.72		52.4654	2570.359	2570.923	5	+2,+3	distinct	1	0.9999
TANAPTGPADEVETVVAQALIDLESNVSELK	88.22		51.1949	3180.604	3181.434	15	+2,+3	distinct	0	1

The equivalent proteins include

gi|71021913|ref|XP_761187.1|	22102.74	hypothetical protein UM05040.1 [Ustilago maydis 521]

121. Group probability: 1.0000. Peptides of the group

HVVFGEVVEGLDIVK	119.3		54.4352	1638.898	1640.183	28	+2,+3	distinct	0	0.9999
ELCTGAHGFGYEGSSFHR	84.73		53.5045	2010.864	2012.193	12	+2,+3	distinct	0	1
VIPDFMLQGGDFTAGNGTGGK	103.57		53.7306	2080.989	2081.487	1	2	distinct	0	0.9901

The equivalent proteins include

gi|71019285|ref|XP_759873.1|	17435.85	hypothetical protein UM03726.1 [Ustilago maydis 521]

122. Group probability: 1.0000. Peptides of the group

KYDSSASSSYK	51.36		55.3228	1221.551	1221.24	2	+1,+2	distinct	1	0.992
CSSIACFLHK	47.12		55.1557	1221.563	1222.171	2	2	distinct	0	0.8799
KYYSVYDLGK	54.7		55.3788	1234.623	1234.869	3	+1,+2	distinct	1	0.9942
VKDLPPLTFYIDGQPFK	57.33		53.7048	1977.061	1977.783	1	2	distinct	1	0.9628
DLPPLTFYIDGQPFKLEGK	88.19		53.28	2177.141	2178.323	7	2	distinct	1	0.9977
GHGVPLTDFLNAQYFCDISLGTPAQDFK	54.84		51.264	3110.481	3111.142	4	3	distinct	0	0.9634

The equivalent proteins include

gi|71021685|ref|XP_761073.1|	45013.57	hypothetical protein UM04926.1 [Ustilago maydis 521]

123. Group probability: 1.0000. Peptides of the group

VAIHEIAK	46.85		55.7335	879.518	879.75	1	2	distinct	0	0.872
LLISHNLMGTVIGR (0000000010000000)	92.89		54.6158	1522.865	1523.678	8	+2,+3	distinct	0	0.9998
VLSVTGTLVGISDAFALIAK	108.35		53.6286	1974.14	1974.441	9	2	distinct	0	0.9996
TILENPLNAPVQADGSPAEAAAQTTSVR	82.55		51.7012	2820.425	2820.648	1	2	distinct	0	0.9974

The equivalent proteins include

gi|71019141|ref|XP_759801.1|	45408.13	hypothetical protein UM03654.1 [Ustilago maydis 521]

124. Group probability: 1.0000. Peptides of the group

SNFNLRPGVIVK	44.9		55.3857	1342.772	1343.421	2	2	distinct	0	0.8634
DLGLQKPQYLATAAGGHFGR	91.97		53.3706	2099.091	2099.549	3	+2,+3	distinct	0	1
KVIPANLLDNDTIYHIQPSGR	95.76		52.8379	2363.26	2364.193	7	+2,+3	distinct	1	1

The equivalent proteins include

gi|71021871|ref|XP_761166.1|	42441.63	hypothetical protein UM05019.1 [Ustilago maydis 521]

125. Group probability: 1.0000. Peptides of the group

HLGLDTQANQIAESVYK	106.78		53.8884	1885.953	1886.333	2	2	distinct	0	0.9995
GILFTPIETGSHNSWNVAMR	88.49		53.3033	2229.1	2230.263	4	2	distinct	0	0.9978
DIMGTNAANPAAMILSATMMLR	102.7		53.033	2292.11	2293.134	3	2	distinct	0	0.9994

EIFEVMNVPVEWEQFNVSGETHGSESLFK	50.44	50.5211	3367.571	3367.918	2	3	distinct	0	0.9488

The equivalent proteins include

gi|71005620|ref|XP_757476.1|	42235.68	hypothetical protein UM01329.1 [Ustilago maydis 521]

126. Group probability: 1.0000. Peptides of the group

LDNKFDLLYSK	49.05	54.9769	1354.713	1355.165	1	2	distinct	1	0.9025
IHFPLATYAPILSAAK	69.56	54.278	1711.966	1712.99	4	2	distinct	0	0.9867
IGICNEPPTTVPGGDLAK	52.52	53.9229	1837.924	1838.997	1	2	distinct	0	0.9451
SLFHPETLVTGKEDAANNYAR	105.17	52.8838	2332.145	2333.213	4	+2,+3	distinct	1	1
FDGSLNVDLNEFQVNLVPFPR	69.8	52.6879	2419.217	2420.503	1	2	distinct	0	0.9894

The equivalent proteins include

gi|71005404|ref|XP_757368.1|	49585.45	tubulin subunit alpha-1A [Ustilago maydis 521]

127. Group probability: 1.0000. Peptides of the group

FDALHGVTGPYGR	49.61	55.3876	1388.684	1388.73	1	2	distinct	0	0.9128
YFSKPAIQAIIR	57.73	55.0898	1405.808	1406.043	3	2	distinct	0	0.9559
EKPGTSVSDVLLAFYK	101.71	54.0799	1752.93	1753.398	2	2	distinct	0	0.9992
LIIGQDGILSTPAASHVIR	70.44	53.7732	1960.11	1960.945	9	3	distinct	0	0.9865
GAFVNPSDSVAIIADWAQK	99.75	54.0774	1988	1988.306	2	2	distinct	0	0.9992

The equivalent proteins include

gi|71003934|ref|XP_756633.1|	59720.3	hypothetical protein UM00486.1 [Ustilago maydis 521]

128. Group probability: 1.0000. Peptides of the group

IFDDKEYTEVGCK	87.59	54.9599	1602.724	1602.995	1	2	distinct	1	0.9969
IPPFLDQPTIQAAGPSR	97.9	54.2825	1806.963	1807.478	2	2	distinct	0	0.9989
GNPSLTVISIDHLPTLLPR	106.35	53.5005	2042.152	2042.953	17	+2,+3	distinct	0	1

The equivalent proteins include

gi|71020369|ref|XP_760415.1|	43166.16	hypothetical protein UM04268.1 [Ustilago maydis 521]

129. Group probability: 1.0000. Peptides of the group

RGSPLLIGVK	57.27	55.1119	1038.655	1039.993	1	2	distinct	1	0.6281
ALQSLAHNTLAK	58.02	55.1363	1265.709	1265.405	2	+1,+2	distinct	0	0.9978
VSISQMGMAHTR	63.29	55.4678	1316.633	1317.201	1	2	distinct	0	0.9727
CGIFAYINHLVEK	55.68	54.868	1562.791	1563.61	1	2	distinct	0	0.8537
GYDSAGIAIDGDTEKDTLIFK	49.99	53.2259	2228.085	2228.771	1	3	distinct	1	0.9253
KGQPIVICNDDDQDIKPGMK	69.29	53.0421	2270.103	2271.37	2	+2,+3	distinct	1	0.9998

The equivalent proteins include

gi|71018231|ref|XP_759346.1|	78022.08	hypothetical protein UM03199.1 [Ustilago maydis 521]

130. Group probability: 1.0000. Peptides of the group

LTANNPLLTGQR	57.43	55.1894	1296.715	1297.072	1	2	distinct	0	0.9547
SALGEGDKVTLDVAK	84.29	55.0682	1501.799	1502.181	2	+2,+3	distinct	1	0.9995
VKEHCSDVIYQLTQQK	65.1	53.6387	1974.983	1974.975	1	2	distinct	1	0.9806
NIVDFHNHAQAAIANNPDMTWAK	78.49	52.4074	2577.218	2578.043	4	+2,+3	distinct	0	0.9998

The equivalent proteins include

gi|71004204|ref|XP_756768.1|	47244.53	hypothetical protein UM00621.1 [Ustilago maydis 521]

131. Group probability: 1.0000. Peptides of the group

ANLDVLTGHLVTK	68.78	55.0239	1379.777	1379.889	1	2	distinct	0	0.9839
NTVGTEFHPSSTCSMLPR	45.66	54.0489	2019.914	2021.124	1	2	distinct	0	0.8995
HSSIEQNVWADLIDDTQDWTWDK	83.43	51.8756	2801.257	2801.971	8	+2,+3	distinct	0	1
RVGSTPPLSTFTSSEAAPGSGVASDAQWETWIR	85.41	50.1904	3447.669	3449.044	5	3	distinct	1	0.9979

The equivalent proteins include

gi|71021747|ref|XP_761104.1|	63595.86	hypothetical protein UM04957.1 [Ustilago maydis 521]

132. Group probability: 1.0000. Peptides of the group

DKADSGYESLR	50.48	55.088	1239.573	1240.032	1	2	distinct	1	0.9138
GISGPIARPGVDLK	55.08	55.0309	1378.793	1380.103	3	2	distinct	0	0.9483
NVNDKIGYAEHK	47.67	55.279	1386.689	1387.533	1	2	distinct	1	0.8931
NLKDEANSSLYNLR	80.63	54.6344	1635.822	1635.741	1	2	distinct	1	0.9945
AAEGLDYAGDKLHSGAR	89.94	54.2705	1729.838	1730.244	2	2	distinct	1	0.9978
HNEANQLPGSVPYGTVSK	67.07	53.8286	1896.933	1897.344	2	2	distinct	0	0.9847

The equivalent proteins include

gi|71003201|ref|XP_756281.1|	83044.8	hypothetical protein UM00134.1 [Ustilago maydis 521]

133. Group probability: 1.0000. Peptides of the group

GAAEADKIIELLTK	87.1	54.9799	1470.829	1471.484	1	2	distinct	1	0.9969
HSAGVDFQALMAQAK	111.51	54.724	1572.772	1573.713	1	2	distinct	0	0.9996
ANSDEEPDCHGYVPGR	59.64	54.3036	1801.733	1801.945	1	2	distinct	0	0.9682

SRDDPNTIIVFEQYDNK	88.21	53.8272	2052.975	2053.151	4	2	distinct	1	0.9975

The equivalent proteins include

gi|71023849|ref|XP_762154.1|	14760.15	hypothetical protein UM06007.1 [Ustilago maydis 521]

134. Group probability: 1.0000. Peptides of the group

SALLNTHLTDLK	60.86	55.2751	1324.735	1324.974	1	2	distinct	0	0.9664
KYPWGIVEVDNPK	84.49	54.8787	1543.803	1544.439	3	2	distinct	1	0.9959
EITHDFLYENYR	57.25	54.7506	1598.736	1599.274	1	2	distinct	0	0.9544
IKPVHVELEEDGMR	88.85	54.5734	1650.84	1651.413	5	+2,+3	distinct	0	0.9998
EITHDFLYENYRTEK	45.23	53.6957	1956.922	1957.743	2	2	distinct	1	0.8848

The equivalent proteins include

gi|71018731|ref|XP_759596.1|	41453.18	hypothetical protein UM03449.1 [Ustilago maydis 521]

135. Group probability: 1.0000. Peptides of the group

NYASSHSYTYIEGK	80.21	54.6192	1618.726	1619.17	1	2	distinct	0	0.9943
GAVPHDPHAYYPAENYA	44.06	53.9891	1870.827	1871.452	1	2	distinct	0	0.8804
SATPPSAASDPAGNLYHNR	73.52	53.7368	1924.903	1925.531	2	2	distinct	0	0.9916
ASDASSTGFYSASNLPPRPPFK	81.87	52.9742	2296.112	2296.493	10	+2,+3	distinct	0	1

The equivalent proteins include

gi|71024379|ref|XP_762419.1|	24727.45	hypothetical protein UM06272.1 [Ustilago maydis 521]

136. Group probability: 1.0000. Peptides of the group

KGLLSAFPR	65.98	56.3836	987.586	988.513	5	2	distinct	1	0.9716
SVIVDETWVPTTGGGK	56.67	54.5678	1644.836	1645.423	1	2	distinct	0	0.9585
TKPWVPTDAAAPAHEEL	53.27	54.0257	1831.91	1832.821	2	+2,+3	distinct	0	0.9961
LIHTGQFFFDDELNMMMDK	58.26	52.9264	2331.037	2331.822	1	3	distinct	0	0.9614
NWEDSLQIFQVSHENGYFPTFDVEK	57.9	51.1648	3028.388	3029.563	6	+2,+3	distinct	0	0.9991

The equivalent proteins include

gi|71023811|ref|XP_762135.1|	42755.28	hypothetical protein UM05988.1 [Ustilago maydis 521]

137. Group probability: 1.0000. Peptides of the group

FLEANYKPIK	56.91	55.1929	1221.676	1222.336	1	2	distinct	0	0.9491
KFLEANYKPIK	67.71	55.1641	1349.771	1351.083	12	+1,+2,+3	distinct	1	0.9999
LHLCQTGQASAGAR	81.63	54.6979	1468.72	1469.019	3	2	distinct	0	0.995
HVELDGLSSADVEKK	74.1	54.6433	1625.826	1627.13	2	3	distinct	1	0.9885

The equivalent proteins include

gi|71006086|ref|XP_757709.1|	10610.56	hypothetical protein UM01562.1 [Ustilago maydis 521]

138. Group probability: 1.0000. Peptides of the group

MLMHYIPEVK	64.93	55.6374	1259.641	1260.833	3	2	distinct	0	0.9746
QVMESGTHEFLDTR	67.54	54.5859	1648.751	1649.192	1	2	distinct	0	0.9828
VRPAIQEDGGDLEYR	43.39	54.3406	1716.843	1717.613	1	2	distinct	0	0.8628
GVEQVLDPEEEIALDEFAK	80.71	53.2593	2130.037	2131.499	1	2	distinct	0	0.9956
LFNIPGVVSVFYGPDFVTVSK	99.23	52.9943	2284.214	2285.083	8	2	distinct	0	0.9992

The equivalent proteins include

gi|71021777|ref|XP_761119.1|	32516.43	hypothetical protein UM04972.1 [Ustilago maydis 521]

139. Group probability: 1.0000. Peptides of the group

ELSLDEKK	49.68	56.4064	960.513	960.681	1	2	distinct	1	0.6818
KPLTSPGQGAK	58.94	55.2389	1082.608	1082.985	4	+1,+2	distinct	0	0.9977
QNPITGIASENYK	53.02	54.835	1433.715	1434.459	1	2	distinct	0	0.9361
TLSKEEQYGVFR	74.38	54.8765	1455.736	1456.092	6	2	distinct	1	0.9898
VQLSHVVPNIEASWK	74.09	54.5596	1705.915	1706.386	11	+2,+3	distinct	0	0.9995

The equivalent proteins include

gi|71022765|ref|XP_761612.1|	20483.67	hypothetical protein UM05465.1 [Ustilago maydis 521]

140. Group probability: 1.0000. Peptides of the group

HLIPSAASGESK	59.2	55.1838	1195.62	1196.088	1	2	shared(3)	0	0.9612
YEEMVENMKR	56.37	55.3118	1327.59	1328.147	1	2	shared(2)	1	0.9465
IVSSIEQKEESK	84.45	55.0951	1375.719	1376.138	1	2	shared(2)	1	0.9958
VASSDQELTVEER	56.14	55.0396	1461.695	1461.405	1	2	shared(2)	0	0.9512
RVASSDQELTVEER	66.98	54.6857	1617.796	1618.004	1	2	shared(2)	1	0.9819
AASDVAVTELPPTHPIR	97	54.2622	1772.942	1773.847	8	+2,+3	shared(2)	0	1
LAEQAERYEEMVENMK	62	53.6314	1968.892	1969.482	4	+2,+3	shared(3)	1	0.9973
QAFDDAIAELDTLSEESYK	106.92	53.2362	2143.98	2144.531	3	2	shared(2)	0	0.9996
QAFDDAIAELDTLSEESYKDSTLIMQLPR (0000000000000000000000000100000)	71.86	50.8352	3314.586	3315.709	2	3	distinct	1	0.9113

The equivalent proteins include

gi|62420901|gb|AAX82172.1|	28911.23	14-3-3 1 protein [Phanerochaete chrysosporium]

141. Group probability: 1.0000. Peptides of the group

SAHTGLMK	46.73	56.934	843.427	843.555	2	+1,+2	distinct	0	0.9813
LDTAQAPGSETALKDDSK	75.91	54.0415	1845.896	1847.192	2	2	distinct	1	0.9929
KFTSNVASNVGPQFQNIGK	45.85	54.2912	2035.049	2036.04	1	3	distinct	1	0.8821
FGAVDQEDITELPQEYKDLER	59.62	52.6495	2494.186	2494.929	1	3	distinct	1	0.9683
AQAEYHAAAAELLANVQQELAQLATSVESDYR	100.74	50.1602	3459.691	3460.174	9	3	distinct	0	0.9994

The equivalent proteins include

gi|71018911|ref|XP_759686.1|	36105.36	hypothetical protein UM03539.1 [Ustilago maydis 521]

142. Group probability: 1.0000. Peptides of the group

EGEIPTDEQQATGLER	64.5	54.2143	1771.822	1771.917	1	2	distinct	0	0.9793
CPECGSVYEMDFEGDANAGHH	47.1	52.8482	2380.878	2381.971	1	3	distinct	0	0.9044
IVGCTGYPADSHDTIYLHLNNQLK	77.43	51.9853	2728.328	2728.944	9	+2,+3	distinct	0	0.9995
LQGVDVFDMEPLQMTHLGTTEKPIK (0000000001000000000000000)	63.99	51.9641	2826.43	2826.563	14	+2,+3	distinct	0	0.9996

The equivalent proteins include

gi|71021437|ref|XP_760949.1|	16921.43	hypothetical protein UM04802.1 [Ustilago maydis 521]

143. Group probability: 1.0000. Peptides of the group

VTGNDKTDESLLDK	89.27	54.7392	1533.752	1533.999	2	2	distinct	1	0.9974
SNSQQLGDKVTGNDK	48.07	54.72	1589.764	1589.646	1	2	distinct	1	0.9083
DLSDQASSALKPDSQK	79.77	54.463	1688.822	1688.835	2	2	distinct	0	0.9945
RDLSDQASSALKPDSQK	68.42	54.2143	1844.923	1845.174	3	+2,+3	distinct	1	0.9997

The equivalent proteins include

gi|71003343|ref|XP_756352.1|	8461.16	hypothetical protein UM00205.1 [Ustilago maydis 521]

144. Group probability: 1.0000. Peptides of the group

RFDGDFLTIQSLLTDK	110.3	53.8832	1867.968	1869.423	2	2	distinct	1	0.9996
VSLGATCLSSHIDAEQPR	83.85	53.7332	1939.942	1940.452	1	2	distinct	0	0.9965
LFPDVAILPDFDSVLTNLPK	76.33	53.1409	2213.198	2214.449	2	2	distinct	0	0.9938
LGWTPSSHPEEFGVYSETDSESLR	53.56	52.0706	2709.219	2710.026	1	3	distinct	0	0.952

The equivalent proteins include

gi|71006512|ref|XP_757922.1|	47239.23	hypothetical protein UM01775.1 [Ustilago maydis 521]

145. Group probability: 1.0000. Peptides of the group

SNKPAAAAAAAAAATPSPAPPIAK	142.56	53.3551	2114.148	2114.295	8	+2,+3	distinct	0	1
ESGSHHAASTPYASPAAPSSAAR	75.88	53.1381	2209.015	2209.603	1	2	distinct	0	0.9942
ELFPTWTDEDLLFALQESLGDVENAVVR	47.92	50.9811	3205.582	3206.408	1	3	distinct	0	0.9332

The equivalent proteins include

gi|71011109|ref|XP_758449.1|	99989.76	hypothetical protein UM02302.1 [Ustilago maydis 521]

146. Group probability: 1.0000. Peptides of the group

IDNVVGAVTGDK	68.78	55.7867	1186.619	1187.964	3	+1,+2	distinct	0	0.9971
ETIGNALGSTEWQK	76.53	54.8598	1532.747	1532.933	7	+1,+2	distinct	0	0.9999
AAQAQGYAEGTKDQVSGK	92.84	54.2844	1807.87	1808.465	8	2	distinct	1	0.9984

The equivalent proteins include

gi|71003954|ref|XP_756643.1|	10145.05	hypothetical protein UM00496.1 [Ustilago maydis 521]

147. Group probability: 1.0000. Peptides of the group

VTVHFNTVPIEAK	57.72	54.837	1453.793	1454.336	1	2	distinct	0	0.9577
VVIIGSGPAGHTAAIYLAR	123.66	54.0474	1865.052	1865.15	5	+2,+3	distinct	0	1
DMDANGLFYAIGHLPATSLVK	80.65	53.2378	2232.125	2232.92	1	2	distinct	0	0.9959
LLAEEEVLDPVDAAQANHYTGTDKA	50.24	52.1199	2669.282	2670.309	1	3	distinct	1	0.938

The equivalent proteins include

gi|71019359|ref|XP_759910.1|	37731.21	hypothetical protein UM03763.1 [Ustilago maydis 521]

148. Group probability: 1.0000. Peptides of the group

YLDENINSVHVK	61.33	55.0145	1429.72	1430.067	1	2	distinct	0	0.9679
LGVDQIDLYYAHR	77.49	54.8581	1561.789	1561.793	1	2	distinct	0	0.9925
RLGYNEEQFGAYFK	56.25	54.2248	1720.821	1722.183	4	2	distinct	1	0.9541
LSDADVAEIDDVINSFEVSGTR	129.53	52.9572	2351.113	2350.963	2	2	distinct	0	0.9999

The equivalent proteins include

gi|37596307|gb|AAQ94939.1|	38137.23	oxidoreductase [Ustilago maydis]

149. Group probability: 1.0000. Peptides of the group

FQGEHTVTGR	53.87	55.8086	1130.547	1130.824	1	2	distinct	0	0.9327
NIVLSGGSTMFQHFGQR	98.26	54.1788	1877.921	1878.084	2	2	distinct	0	0.999
TTAAGSSGGGGSRPSVPSKPGGLSSSSSLASK	75.31	51.6988	2818.406	2819.429	4	3	distinct	0	0.9947
TLTGTVIDSGDGVTHVIPVAEGYVIGSAIK	89.4	51.3775	2968.576	2969.407	1	3	distinct	0	0.9983

The equivalent proteins include

gi|71005030|ref|XP_757181.1|	46701.22	hypothetical protein UM01034.1 [Ustilago maydis 521]							
150. Group probability: 1.0000. Peptides of the group									
ESLVDGIKR	59.29	56.394	1015.566	1016.036	1	2	distinct	1	0.9564
SKFDNYYGCR	46.05	55.3135	1308.556	1308.795	1	2	distinct	1	0.8676
ELDEEVALAHLGR	92.98	54.9568	1450.742	1451.059	2	2	distinct	0	0.9937
ANAQSVSNIKPQVDR	51.99	54.6437	1625.848	1626.928	2	+2,+3	distinct	0	0.9941
GVSEETTTGVHILYSAMK	84.49	53.7808	1921.945	1922.336	2	2	distinct	0	0.9967
The equivalent proteins include									
gi|71019301|ref|XP_759881.1|	47518.02	hypothetical protein UM03734.1 [Ustilago maydis 521]							
151. Group probability: 1.0000. Peptides of the group									
VFRPQENWAR	59.03	55.4149	1301.663	1303.083	1	2	distinct	0	0.8432
IATNPSTSVDWDKLGFK	83.94	54.0636	1877.952	1878.507	1	2	distinct	1	0.9964
MASMPELPEELFLEAIK	45.99	53.8657	1946.973	1948.032	1	2	distinct	0	0.8992
DSHLNVHAAAPCLNYGQQAFEGIK	102.82	52.279	2639.255	2640.092	5	+2,+3	distinct	0	1
The equivalent proteins include									
gi|71016847|ref|XP_758930.1|	43547.06	hypothetical protein UM02783.1 [Ustilago maydis 521]							
152. Group probability: 1.0000. Peptides of the group									
HGVQELEIELQSQLSKK	97.18	53.7382	1965.053	1965.703	1	2	distinct	1	0.9989
LASYLDKVQALEEANNDLENK	43.56	52.7796	2376.181	2376.953	1	3	distinct	1	0.8698
EIETYHNLLEGGQEDFESSGAGK	58.9	52.5162	2509.124	2510.04	2	+2,+3	distinct	0	0.9982
NYSPYYNTIDDLKDQIVDLTVGNNK	44.05	51.5455	2901.403	2901.685	1	3	distinct	1	0.8945
DIENQYETQITQIEHEVSSSGQEVQSSAK	55.49	50.8505	3263.506	3264.62	1	3	distinct	0	0.9669
The equivalent proteins include									
gi|435476|emb|CAA82315.1|	62319.99	cytokeratin 9 [Homo sapiens]							
gi|453155|emb|CAA52924.1|	62177.91	keratin 9 [Homo sapiens]							
gi|55956899|ref|NP_000217.2|	62254.9	keratin 9 [Homo sapiens]							
153. Group probability: 1.0000. Peptides of the group									
RDEITLEGIK	56.56	55.7892	1172.64	1173.079	13	2	distinct	1	0.9468
TATFSIAILQR	69.13	55.5607	1219.692	1219.769	1	2	distinct	0	0.907
GHDVIAQAQSGTGK	108.22	55.0013	1367.679	1367.993	3	+2,+3	distinct	0	0.9999
EFTVSAMHGDMEQAQR	64.26	54.1255	1835.793	1836.177	1	2	distinct	0	0.9789
IDCHACIGGTNVREDMAK	45.63	53.4898	2045.908	2046.493	1	2	distinct	1	0.9004
The equivalent proteins include									
gi|71022799|ref|XP_761629.1|	46557.71	hypothetical protein UM05482.1 [Ustilago maydis 521]							
154. Group probability: 1.0000. Peptides of the group									
KLNDEPSLLNK	58.14	55.7945	1269.693	1270.089	1	2	distinct	1	0.8082
LSNPADFETLLTAEAYQK	117.46	53.5835	2009.995	2010.623	7	2	distinct	0	0.9998
LNDEPSLLNKQPESDGWLCQIK	66.72	52.4186	2583.264	2584.003	4	+2,+3	distinct	1	0.9992
FTEEHEWVSFDDATNIGTVGITDYAQK	53.32	51.164	3072.399	3073.266	7	3	distinct	0	0.9568
The equivalent proteins include									
gi|71003466|ref|XP_756407.1|	20580.28	hypothetical protein UM00260.1 [Ustilago maydis 521]							
155. Group probability: 1.0000. Peptides of the group									
STIATALEQHLLSLK	68.81	54.5109	1623.92	1624.655	1	2	distinct	0	0.9852
STIATALEQHLLSLKK	52.39	54.1174	1752.014	1753.274	2	+2,+3	distinct	1	0.994
AELLSQQGLTIWLTGLSASGK	95.73	53.2582	2172.179	2172.791	2	2	distinct	0	0.9989
EFTGISAPYEKPEQPEIHIDADKTSIEDAVR	65.27	50.257	3484.7	3485.724	1	3	distinct	1	0.9871
The equivalent proteins include									
gi|71006414|ref|XP_757873.1|	22766.91	hypothetical protein UM01726.1 [Ustilago maydis 521]							
156. Group probability: 1.0000. Peptides of the group									
HYIPIDLGFK	50.79	55.6694	1201.649	1201.417	2	1	distinct	0	0.912
SSGSAFYGFHR	46.49	55.6696	1214.547	1215.118	1	2	distinct	0	0.8762
VLPAEDVLCPER	45.97	54.9451	1396.702	1397.096	1	2	distinct	0	0.8768
NAEVFLPTAHPSGYIK	66.88	54.2529	1742.899	1743.833	1	2	distinct	0	0.9832
NPSSLPQFCDIHSSVK	86.84	54.0913	1814.862	1815.037	1	2	distinct	0	0.9971
CLLHGESLTPSYTEADNSPVVATDTVK	58.35	51.4973	2903.386	2903.913	1	3	distinct	0	0.972
The equivalent proteins include									
gi|71004306|ref|XP_756819.1|	36074.63	hypothetical protein UM00672.1 [Ustilago maydis 521]							
157. Group probability: 1.0000. Peptides of the group									
WHLGLTK	45.92	55.0468	853.481	853.383	1	1	distinct	0	0.4663
LTGFHTASACSPTR	53.32	54.7604	1504.709	1505.26	1	2	distinct	0	0.94
QAAHPAVEVFDRDPK	46.83	54.4237	1678.843	1679.343	1	2	distinct	1	0.8984
RVPAYQGHEGYEGVLNDR	71	53.4882	2058.987	2060.083	6	+2,+3	distinct	1	0.9996

QLQLSELPKPFYSSDVFASK	90.69		52.9212	2283.179	2283.601	1	2	distinct	0	0.9982

The equivalent proteins include

gi|71021969|ref|XP_761215.1|	61489.82	hypothetical protein UM05068.1 [Ustilago maydis 521]

158. Group probability: 1.0000. Peptides of the group

TQNTVGDEAQVKPAPILAPATIEGK	45.3		52.5067	2547.354	2548.602	1	3	distinct	0	0.9036
GTSDEIIALVHAAEVDPNFLLLGAR	75.7		52.2232	2620.386	2621.663	5	+2,+3	distinct	0	0.9998
VYVHADADAAQQLIQLTNASWSAVAETLAK	118.19		50.9541	3183.62	3183.881	10	3	distinct	0	0.9999

The equivalent proteins include

gi|71021311|ref|XP_760886.1|	35302.4	hypothetical protein UM04739.1 [Ustilago maydis 521]

159. Group probability: 1.0000. Peptides of the group

GHLYVIAQPEVYK	70.59		54.82	1515.808	1515.503	16	+1,+2	distinct	0	0.9998
SSHSDVYIVFGEAK	70.94		54.6165	1537.741	1538.139	3	2	distinct	0	0.9738
LLAESLQNSSASGAEK	105.01		54.5992	1603.805	1604.506	2	2	distinct	0	0.9994

The equivalent proteins include

gi|71022779|ref|XP_761619.1|	20695.2	hypothetical protein UM05472.1 [Ustilago maydis 521]

160. Group probability: 1.0000. Peptides of the group

WFVSGGFATVHPNNK	99.11		54.9806	1659.816	1659.851	11	2	distinct	0	0.999
LVVNAIEAYPLDQFSAEAVR	75.11		53.2139	2204.148	2204.529	5	+2,+3	distinct	0	0.9993
VASSGSSAEAKAEAEIEIEVYTALQAALGR	75.66		51.4568	3020.53	3021.523	1	2	distinct	1	0.9955

The equivalent proteins include

gi|71005168|ref|XP_757250.1|	17671.21	hypothetical protein UM01103.1 [Ustilago maydis 521]

161. Group probability: 1.0000. Peptides of the group

HVNGMLLNDKK	48.02		55.3212	1267.671	1267.929	1	2	distinct	1	0.8925
RQQLEAQIMQR	66.07		55.3098	1399.735	1400.223	3	2	distinct	1	0.9779
MLDNRPLYVALAQR	59.32		54.9795	1658.893	1659.543	1	2	distinct	0	0.9644
LREEFAPFGAITSCK	88.95		54.2346	1724.856	1725.953	3	2	distinct	1	0.9975
ALHDTFAAFGNILSCK	96.45		54.1234	1763.866	1764.492	1	2	distinct	0	0.9835

The equivalent proteins include

gi|71018821|ref|XP_759641.1|	70785.28	hypothetical protein UM03494.1 [Ustilago maydis 521]

162. Group probability: 1.0000. Peptides of the group

LKENNPENADVSLDNLVGK	100.04		53.5311	2068.044	2068.191	2	+2,+3	distinct	1	0.9999
KAFVEDNAPDVTVTSAENVLK	89.94		53.1823	2246.143	2247.613	1	2	distinct	1	0.9982
SIIVGVPGAFTPPCSSQVPGYIQHASEFQSK	57.18		51.0841	3287.628	3288.609	3	3	distinct	0	0.9733

The equivalent proteins include

gi|71018187|ref|XP_759324.1|	18313.43	hypothetical protein UM03177.1 [Ustilago maydis 521]

163. Group probability: 1.0000. Peptides of the group

TDLFIFHR	44.99		55.9021	1047.55	1047.696	1	2	distinct	0	0.6112
TDLFIFHRI	52.47		55.6191	1160.634	1161.996	4	2	distinct	1	0.922
VDGILALIWNLEDR	72.58		54.5973	1625.878	1626.304	4	2	distinct	0	0.9566
WIDKEQGIWEYPYR	71		54.0275	1881.905	1881.693	4	2	distinct	1	0.9875
ARPSYPPAAIAAIVAEATNTSSPSPLR	68.89		52.0544	2707.429	2708.837	2	+2,+3	distinct	0	0.9997

The equivalent proteins include

gi|71010058|ref|XP_758348.1|	39289.86	hypothetical protein UM02201.1 [Ustilago maydis 521]

164. Group probability: 1.0000. Peptides of the group

NDIPYPPHTQDR	50.13		54.91	1451.679	1451.846	1	2	distinct	0	0.9145
NAFEPSEVISEWLQTESGAR	94.34		53.555	2249.06	2250.066	6	2	distinct	0	0.9987
FDWLHDNFCHILTNTTLSK	54.71		52.8584	2361.121	2361.733	1	2	distinct	0	0.9572
LFQAYLIPITTQIEAAAILDHANK	62.52		52.1657	2653.448	2653.709	5	+2,+3	distinct	0	0.9988

The equivalent proteins include

gi|71023297|ref|XP_761878.1|	31953.88	hypothetical protein UM05731.1 [Ustilago maydis 521]

165. Group probability: 1.0000. Peptides of the group

KAGVTLEGHCAQK	56.38		55.1718	1397.708	1398.387	1	2	distinct	1	0.952
KDEAAAGTPHQLER	65.33		54.6057	1521.754	1523.12	2	3	distinct	1	0.9743
KPLNPILGELFLGK	69.01		54.6121	1537.923	1538.73	1	2	distinct	0	0.9849
FVHLDNDQEYSQLAAMFK	111.59		53.2774	2155.004	2155.893	2	2	distinct	0	0.9997

The equivalent proteins include

gi|93204598|sp|P0C199|KES1_USTMA	42451.45	Protein KES1
gi|71018813|ref|XP_759637.1|	314066.94	hypothetical protein UM03490.1 [Ustilago maydis 521]

166. Group probability: 1.0000. Peptides of the group

WASQLGHSNGVLSAR	86.09	54.498	1581.801	1582.242	12	2	distinct	0	0.9967
TKDEIDEANAVDISK	108.7	54.5284	1646.8	1646.947	1	2	distinct	1	0.9996
ATVSDFLSSMGASSDVLALAK	43.65	53.6699	2069.035	2070.074	1	2	distinct	0	0.8931
KGPAPLNLEVPEYDFNDGENK	55.35	52.9036	2345.117	2346.053	2	2	distinct	1	0.9623

The equivalent proteins include

gi|71019483|ref|XP_759972.1|	45110.76	hypothetical protein UM03825.1 [Ustilago maydis 521]

167. Group probability: 1.0000. Peptides of the group

TVGNADLHIVHR	63.94	55.3969	1330.711	1331.186	1	2	distinct	0	0.9199
LLVVVGPCSIHDVDQAK	58.36	53.9881	1848.977	1849.397	1	2	distinct	0	0.8916
VAGFEPLISPSLLLHEIPVPK	75.55	53.013	2255.293	2256.363	8	+2,+3	distinct	0	0.9998
VVDAIVEQLEQGEDAITGVMIESHLNEGK	79.37	51.1383	3122.544	3123.898	4	3	distinct	0	0.9959

The equivalent proteins include

gi|71012850|ref|XP_758532.1|	42423.72	hypothetical protein UM02385.1 [Ustilago maydis 521]

168. Group probability: 1.0000. Peptides of the group

KPCADYISLSHPDGDASR	68.94	53.6221	1987.906	1989.183	2	+2,+3	distinct	0	0.9997
LVHASNLYHNEWSGELADR	97.2	53.2415	2210.05	2210.869	1	2	distinct	0	0.999
NLVAMFPDLLLDDPSAGKPSPR	62.22	52.8995	2352.215	2352.913	1	2	distinct	0	0.9801

The equivalent proteins include

gi|71023177|ref|XP_761818.1|	74781.31	hypothetical protein UM05671.1 [Ustilago maydis 521]

169. Group probability: 1.0000. Peptides of the group

SASFFIGEHCK	45.95	55.1614	1281.581	1281.746	1	2	distinct	0	0.8715
NIPGSPEGQPQIHEK	76.71	54.6058	1629.811	1630.04	2	2	distinct	0	0.9926
EWEAHYQCLEQHNQEFYR	71.19	52.5496	2466.045	2467.073	5	+2,+3	distinct	0	0.9995
LSDSCGKEWEAHYQCLEQHNQEFYR	67.3	50.9956	3213.367	3214.836	1	3	distinct	1	0.9864

The equivalent proteins include

gi|71023031|ref|XP_761745.1|	17647.68	hypothetical protein UM05598.1 [Ustilago maydis 521]

170. Group probability: 1.0000. Peptides of the group

VLQGHIAIDR	53.64	55.6429	1120.635	1120.91	1	2	distinct	0	0.9315
IENLVIVRPAQTPNNFGSK	73.59	53.6704	2096.138	2096.723	2	2	distinct	0	0.9917
DGAALCQYFAWLEEQLHAGNK	43.24	52.7219	2420.122	2421.039	1	3	distinct	0	0.8663
HGVTAYVIPSGDEHASEYPAESDLR	60.36	52.0397	2699.246	2700.518	2	3	distinct	0	0.9745
GYLTFEHLTMCPIQVSLVDPDLLTK	79.65	51.5919	2889.466	2890.153	3	2	distinct	0	0.9962

The equivalent proteins include

gi|71019299|ref|XP_759880.1|	79666.55	hypothetical protein UM03733.1 [Ustilago maydis 521]

171. Group probability: 1.0000. Peptides of the group

LAGGKPDAAANTAELDK	62.79	54.4185	1640.837	1641.172	1	2	distinct	0	0.9766
SELDAIQAEQDKQAGSR	61.92	54.1779	1844.886	1845.486	1	2	distinct	1	0.9749
EHAAQLREEAAMPAFAK	59.7	53.9667	1868.92	1869.973	1	2	distinct	1	0.9697
LAGGKPDAAANTAELDKLAK	78.07	53.698	1953.053	1954.133	4	+2,+3	distinct	1	0.9995

The equivalent proteins include

gi|71004664|ref|XP_756998.1|	54983.67	hypothetical protein UM00851.1 [Ustilago maydis 521]

172. Group probability: 1.0000. Peptides of the group

FFGVIQAFR	61.3	55.4025	1083.586	1083.92	2	2	distinct	0	0.9642
ADAQDTVAHAK	47.79	55.3135	1125.541	1125.566	1	2	distinct	0	0.8903
AEGAAHAQDVTDAVDPNASR	81.34	53.7462	1993.909	1993.829	1	2	distinct	0	0.9959
LAGVDHPAPDNEFHDDIPNALR	69.15	52.83	2412.146	2413.357	4	+2,+3	distinct	0	0.9994

The equivalent proteins include

gi|71022485|ref|XP_761472.1|	103259.05	hypothetical protein UM05325.1 [Ustilago maydis 521]

173. Group probability: 1.0000. Peptides of the group

DAFQTQIGVGR	80.64	55.5728	1190.604	1190.703	3	2	distinct	0	0.9938
VIQGWDQGVPQLSLGER	91.47	54.0274	1880.974	1882.183	11	2	distinct	0	0.9981
TFPKPGDTVTMHYTGTLAK	72.25	53.6058	2064.035	2064.93	28	+2,+3	distinct	0	0.999

The equivalent proteins include

gi|71019879|ref|XP_760170.1|	27171.22	hypothetical protein UM04023.1 [Ustilago maydis 521]

174. Group probability: 1.0000. Peptides of the group

KPGMGVASAVVVK	48.62	55.4597	1241.716	1242.74	2	2	distinct	0	0.9047
FTIIYGLDKLPK	68.74	54.909	1406.817	1407.425	7	2	distinct	1	0.9755
EIKPYNHDSATLIFELPEGK	75.92	53.0554	2300.169	2300.532	4	2	distinct	0	0.9935
DVIRPYTPITSPDTVGHMDFLVK	68.08	52.2458	2600.331	2601.634	5	+2,+3	distinct	0	0.9992

The equivalent proteins include

gi|71019383|ref|XP_759922.1|	37646.67	hypothetical protein UM03775.1 [Ustilago maydis 521]

175. Group probability: 1.0000. Peptides of the group

KPELDAIADELKK	84.1	54.6534	1468.814	1469.23	8	+2,+3	distinct	1	1
FTAVAQVHPAMVDAADAEK	72.6	53.6499	1969.957	1970.379	2	+2,+3	distinct	0	0.9995

The equivalent proteins include

gi|71006386|ref|XP_757859.1|	27215.6	hypothetical protein UM01712.1 [Ustilago maydis 521]

176. Group probability: 1.0000. Peptides of the group

AVGIGHLR	50.93	55.9448	821.487	821.824	1	2	distinct	0	0.9101
VVQGLEGIGVLEKDPK	70.51	54.2649	1679.946	1680.601	1	2	distinct	1	0.9877
DVDASTFIDAYAQHLK	81.78	54.3151	1792.863	1793.233	2	2	distinct	0	0.9954
DVDASTFIDAYAQHLKR	86.61	53.7995	1948.964	1949.477	3	2	distinct	1	0.9971

The equivalent proteins include

gi|71021157|ref|XP_760809.1|	33186.32	hypothetical protein UM04662.1 [Ustilago maydis 521]

177. Group probability: 1.0000. Peptides of the group

IFKAAGFDWR	74.05	55.2091	1209.629	1209.532	1	2	distinct	1	0.9887
AVIAESFGDIFR	61.25	55.265	1323.682	1324.3	1	2	distinct	0	0.9675
EHAAWSLLDFGIR	68.25	54.7922	1513.768	1514.371	2	2	distinct	0	0.9832
RTDCTLATVDHNIPTASR	65.55	53.5069	2026.985	2027.753	5	+2,+3	distinct	1	0.9976

The equivalent proteins include

gi|71023855|ref|XP_762157.1|	83913.38	3-isopropylmalate dehydratase [Ustilago maydis 521]

178. Group probability: 1.0000. Peptides of the group

EATAVFGSDDLAHPAITYLHK	69.27	53.0126	2255.122	2256.003	2	+2,+3	distinct	0	0.9993
TGGAGNFFLIHVATPLEYCEATDR	78.08	52.1358	2638.248	2638.683	4	+2,+3	distinct	0	1

The equivalent proteins include

gi|71022039|ref|XP_761250.1|	63728.85	hypothetical protein UM05103.1 [Ustilago maydis 521]

179. Group probability: 1.0000. Peptides of the group

FHTQSLIDHK	54.46	55.2055	1224.625	1225.473	2	+1,+2	distinct	0	0.9935
LTFSNILIEIPVSLR	75.85	54.2413	1714.003	1713.94	1	2	distinct	0	0.9921
IAPQSAAVAAPAPATTAASAIAK	56.4	53.6848	2048.127	2048.943	1	2	distinct	0	0.9674
IPAEPSRLEATLLLGQIDSSAR	65.23	52.9472	2336.27	2337.052	1	3	distinct	1	0.9812

The equivalent proteins include

gi|71003331|ref|XP_756346.1|	42208.06	hypothetical protein UM00199.1 [Ustilago maydis 521]

180. Group probability: 1.0000. Peptides of the group

YHSLLADAK	52.44	56.2098	1016.529	1016.335	1	1	distinct	0	0.7883
KYHSLLADAK	57.67	55.7666	1144.624	1144.423	8	+1,+2	distinct	1	0.9966
AEGVNHYQVCSDLAK	80.26	54.5607	1689.778	1690.009	7	+2,+3	distinct	0	0.9992
AEGVNHYQVCSDLAKK	51.31	54.1626	1817.873	1817.483	1	2	distinct	1	0.9341

The equivalent proteins include

gi|71021365|ref|XP_760913.1|	13700.04	hypothetical protein UM04766.1 [Ustilago maydis 521]

181. Group probability: 1.0000. Peptides of the group

VNPVGGAIAMGHPLGATGAR	103.18	54.2145	1844.968	1845.148	7	2	distinct	0	0.9994
KGGLSQCAPEEMLGWTLK	98.8	53.6287	2003.981	2004.506	3	2	distinct	1	0.9991
FVTCAVVGVPPNIMGVGPAYAIPR	47.76	52.6636	2484.302	2485.713	1	2	distinct	0	0.9343

The equivalent proteins include

gi|71015996|ref|XP_758862.1|	42138.55	hypothetical protein UM02715.1 [Ustilago maydis 521]

182. Group probability: 1.0000. Peptides of the group

DGRPVPHVDAAK	46.38	55.5986	1260.657	1261.196	2	2	distinct	0	0.8795
HVFDVHPDKGDR	55.38	54.8868	1420.685	1420.751	1	2	distinct	1	0.9461
GRVDDVINVSGHR	57.8	54.8543	1422.733	1423.833	3	2	distinct	1	0.917
VIGSVGEPINPEAWHWYNDNVGR	93.84	52.3004	2608.246	2609.733	3	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71017971|ref|XP_759216.1|	73720.57	hypothetical protein UM03069.1 [Ustilago maydis 521]

183. Group probability: 1.0000. Peptides of the group

LVRPFGILECAR	49.52	54.9908	1429.786	1430.181	2	2	distinct	0	0.9097
HTLNCLVQNEPGVLSR	117.07	54.1332	1835.931	1836.297	6	+2,+3	distinct	0	1
RQLEDLVPVWAVLDYTNTK	53.74	53.3815	2259.19	2259.554	1	2	distinct	1	0.9529

The equivalent proteins include

gi|71021875|ref|XP_761168.1|	45471.48	hypothetical protein UM05021.1 [Ustilago maydis 521]

184. Group probability: 1.0000. Peptides of the group

AGMTHIVR	52.41	55.9364	883.47	884.525	1	2	distinct	0	0.9211
HGSLGFLPR	60.68	55.6723	982.535	983.136	3	2	distinct	0	0.962
KSLQVHTSR	61.61	55.6199	1054.588	1055.219	2	2	distinct	1	0.965
AITPLGGFPHYGLVK	66.51	54.7531	1568.871	1569.653	1	2	distinct	0	0.9818

SLTTVWAEHLSDEVK	64.9	54.2285	1713.857	1714.314	1	2	distinct	0	0.9792

The equivalent proteins include

gi|71019525|ref|XP_759993.1|	53414.33	hypothetical protein UM03846.1 [Ustilago maydis 521]

185. Group probability: 1.0000. Peptides of the group

VIDSLQIGDKYR	60.92	55.105	1405.756	1406.132	1	2	distinct	1	0.9667
IIGLSANDIASHDR	102.99	54.7528	1480.763	1481.024	1	2	distinct	0	0.9992
LFPGYETVKPYLR	51.56	54.4384	1581.855	1582.358	4	2	distinct	0	0.9279
DINEVGNTSVNFPIIGDKDR	61.75	53.2089	2202.092	2202.309	1	2	distinct	1	0.9776

The equivalent proteins include

gi|71024643|ref|XP_762551.1|	24715.72	hypothetical protein UM06404.1 [Ustilago maydis 521]

186. Group probability: 1.0000. Peptides of the group

FAMPAMSPTMTSGGIAAWK (000000000010000000000)	87.44	53.6981	1953.915	1954.173	3	2	distinct	0	0.9975
SVPEPSTQTAASTGSASPSSPNASSSDTHLSFK	74.47	50.9006	3219.48	3220.367	1	3	distinct	0	0.9946
KSVPEPSTQTAASTGSASPSSPNASSSDTHLSFK	79.51	50.6551	3347.575	3348.374	1	3	distinct	1	0.9966

The equivalent proteins include

gi|71003484|ref|XP_756412.1|	35018.69	hypothetical protein UM00265.1 [Ustilago maydis 521]

187. Group probability: 1.0000. Peptides of the group

IGGIGTVPVGR	66.14	55.3583	1024.603	1024.899	11	2	shared(36)	0	0.978
YMVTVIDAPGHR (00100000000000)	71.25	55.3019	1357.681	1357.971	20	+2,+3	shared(4)	0	0.9823
AHVNVVVIGHVDSGK	45.74	55.1391	1529.831	1529.647	1	2	shared(2)	0	0.8865
MIPTKPMCVESFSTYPPLGR (0100000000000000000000)	81.55	52.9449	2310.121	2310.743	13	2	distinct	0	0.9959
SVEMHHETLAEGLPGDNVGFNVK (0000100000000000000000000)	117.24	52.5434	2479.18	2479.493	13	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71004810|ref|XP_757071.1|	50311.08	elongation factor 1-alpha [Ustilago maydis 521]

188. Group probability: 1.0000. Peptides of the group

YVSEPLAAHLGGEDGYVATGK	58.71	53.2713	2133.038	2134.058	1	2	distinct	0	0.9717
LSGFDHIITSSSASHFDYLK	83.3	53.1324	2224.08	2224.633	4	+2,+3	distinct	0	0.9997
IFITEFPAVLGSDAAGEVVAVGSSVK	75.21	52.4706	2562.358	2563.473	1	2	distinct	0	0.9945

The equivalent proteins include

gi|71004362|ref|XP_756847.1|	37055.21	hypothetical protein UM00700.1 [Ustilago maydis 521]

189. Group probability: 1.0000. Peptides of the group

VNQVFHTAIK	53.74	55.5106	1155.64	1155.997	2	2	distinct	0	0.9323
AANIVNHFYTTK	44.33	55.0647	1377.704	1378.034	1	2	distinct	0	0.8574
GHPETVISDLEKR	68.02	54.8584	1479.768	1479.913	1	2	distinct	1	0.9828
YLHAYGVDNCLVK	50.36	54.6313	1550.755	1551.429	1	2	distinct	0	0.9196
FLADDVPAFEPEMAFHIAR	80.98	53.2332	2175.046	2175.374	2	2	distinct	0	0.9957

The equivalent proteins include

gi|71017627|ref|XP_759044.1|	67552.44	hypothetical protein UM02897.1 [Ustilago maydis 521]

190. Group probability: 1.0000. Peptides of the group

TIVTILCDGAYR	66.01	54.9314	1380.707	1381	1	2	distinct	0	0.9788
KLDTAIPEHLQK	62.53	55.0218	1391.777	1392.953	3	2	distinct	1	0.9711
VQCWLADPPGSVLHSYIQTK	50.9	53.0109	2298.147	2298.783	1	2	distinct	0	0.9421
MLGAEVHPVPAVAFDNPDNYNHQAK	60.47	51.9098	2733.297	2733.563	2	+2,+3	distinct	0	0.9982

The equivalent proteins include

gi|71024525|ref|XP_762492.1|	41460.16	hypothetical protein UM06345.1 [Ustilago maydis 521]

191. Group probability: 1.0000. Peptides of the group

WGGYHNAAENSTGFK	81.11	54.4555	1637.722	1637.647	2	2	distinct	0	0.995
VAEHLQSAVDACNPHYQYLLSK	90.54	52.5106	2542.227	2543.623	3	+2,+3	distinct	0	1

The equivalent proteins include

gi|71006552|ref|XP_757942.1|	37183.36	hypothetical protein UM01795.1 [Ustilago maydis 521]

192. Group probability: 1.0000. Peptides of the group

RVNDYSTAVR	44.76	55.324	1179.6	1179.825	1	2	distinct	1	0.8517
YVGFFDAVEDLFELQR	121.79	53.8624	1946.941	1947.637	16	+2,+3	distinct	0	1
GLNNCFAYDLVPSPEVIESALR	42.59	52.6046	2463.21	2464.123	1	2	distinct	0	0.8892

The equivalent proteins include

gi|71013560|ref|XP_758624.1|	16002.16	hypothetical protein UM02477.1 [Ustilago maydis 521]

193. Group probability: 1.0000. Peptides of the group

KNTPFTQAHER	53.53	55.3563	1327.663	1328.263	2	2	distinct	1	0.9336
AGVNISVVHGMLPPAAVR	58.06	54.6763	1786.988	1788.233	2	2	distinct	0	0.9657
GVGGIFFDDLTLPQWASTHSGK	83.68	52.884	2332.149	2332.883	3	+2,+3	distinct	0	0.9997
AFIPLSDGSKPTSSQPLVASISSTK	41.9	52.596	2517.333	2517.535	1	3	distinct	0	0.8699
The equivalent proteins include									
gi|71011468|ref|XP_758464.1|	51560.99	hypothetical protein UM02317.1 [Ustilago maydis 521]							
194. Group probability: 1.0000. Peptides of the group									
LFTPMMLFVCR	74.52	55.1436	1413.697	1414.047	1	2	distinct	0	0.9895
IAHGIEVGDGIPEMR	66.15	54.5858	1592.798	1593.298	1	2	distinct	0	0.9813
LVPQGTHSVGASLVTAADALVDGGR	78.79	52.8046	2390.255	2391.153	4	+2,+3	distinct	0	0.9995
The equivalent proteins include									
gi|71018197|ref|XP_759329.1|	39086.2	hypothetical protein UM03182.1 [Ustilago maydis 521]							
195. Group probability: 1.0000. Peptides of the group									
SSGYVESLPTHVR	79.13	55.0003	1430.715	1430.975	2	2	distinct	0	0.981
NHIALSELITERDEEALR	81.33	53.2558	2108.086	2109.253	1	2	distinct	1	0.9957
NSDAVAPTPQNTPLSNAPLTR	91.47	53.8679	2163.092	2163.797	1	2	distinct	0	0.9984
The equivalent proteins include									
gi|71022119|ref|XP_761290.1|	46401.58	hypothetical protein UM05143.1 [Ustilago maydis 521]							
196. Group probability: 1.0000. Peptides of the group									
DIVPDLTQFYK	44.44	55.2622	1337.687	1337.573	1	1	distinct	0	0.853
SNNTPSEGEHLQSPEER	64.42	53.8015	1909.84	1910.473	1	2	distinct	0	0.9263
LATPTSDNVGSSGKPQHLK	65.17	53.7597	1936.001	1936.233	2	2	distinct	0	0.9826
LQSYTLDLNQTGPMVLDALIK	98.86	52.8836	2332.235	2333.143	2	2	distinct	0	0.9992
The equivalent proteins include									
gi|71004650|ref|XP_756991.1|	34001.74	succinate dehydrogenase [Ustilago maydis 521]							
gi|5217|emb|CAA44612.1|	33977.76	succinate dehydrogenase [Ustilago maydis]							
197. Group probability: 1.0000. Peptides of the group									
EQHLQSLFDAAR	49.11	55.0923	1413.7	1414.194	1	2	distinct	0	0.9062
TTSVTVQEGLDKGSAGGVLLAGHAGK	105.73	52.6198	2452.292	2453.263	7	+2,+3	distinct	1	1
The equivalent proteins include									
gi|71019735|ref|XP_760098.1|	25212.47	hypothetical protein UM03951.1 [Ustilago maydis 521]							
198. Group probability: 1.0000. Peptides of the group									
NLFVIAVHGIGAR	74.8	54.986	1365.788	1366.466	1	2	distinct	0	0.9905
LNRLPAAAAGDMVVASVK	102.89	54.2718	1781.982	1782.359	2	2	distinct	1	0.9993
MTLALPVGAVMNCADNSGAK	83.97	53.6168	2018.959	2019.515	1	2	distinct	0	0.9667
The equivalent proteins include									
gi|71018899|ref|XP_759680.1|	14531.8	60S ribosomal protein L23 [Ustilago maydis 521]							
199. Group probability: 1.0000. Peptides of the group									
TLLANSATSALALPDLVLELQK	86.78	52.9322	2280.294	2280.895	1	2	distinct	0	0.9977
ASLETYPATHPFASSLSGSDNIIAFHTK	60.42	51.3466	2961.451	2962.43	2	3	distinct	0	0.9775
DALPQGYLSVPTHSLTPPPLADVASGEEYVK	78.19	50.8783	3250.64	3251.384	3	3	distinct	0	0.9958
The equivalent proteins include									
gi|71006378|ref|XP_757855.1|	40384.22	hypothetical protein UM01708.1 [Ustilago maydis 521]							
200. Group probability: 1.0000. Peptides of the group									
DMEYIETLLNTPSIKK	73.29	54.3426	1893.976	1894.371	1	2	distinct	1	0.9904
LPFFTASGESYAGTYLPNIASTIYKK	68.92	52.0569	2691.379	2692.344	1	3	distinct	1	0.988
GAGNVAFAQVYAAGHMVPYDQPEVASDMINR	62.37	50.9467	3277.528	3278.464	2	3	distinct	0	0.9831
FPEYSKLPFTASGESYAGTYLPNIASTIYK	40.74	50.8356	3314.639	3315.957	1	3	distinct	1	0.8836
The equivalent proteins include									
gi|71006734|ref|XP_758033.1|	66003.22	hypothetical protein UM01886.1 [Ustilago maydis 521]							
201. Group probability: 1.0000. Peptides of the group									
VVIVVNTASK	51.5	56.392	1028.623	1029.288	1	2	distinct	0	0.9161
FLIDKEGNVIER	53.36	54.9952	1431.772	1432.804	1	2	distinct	1	0.6626
YGSNTKPSAIAPAIEK	83.76	54.5013	1645.867	1646.399	2	2	distinct	0	0.9961
AKKPSQEDYTFDQLK	54.96	54.1288	1796.894	1797.052	2	2	distinct	1	0.9505
SDVNGSNTNEVFQFLKK	55.91	53.8083	1925.948	1927.426	1	2	distinct	1	0.9578
The equivalent proteins include									
gi|71006530|ref|XP_757931.1|	18147.05	hypothetical protein UM01784.1 [Ustilago maydis 521]							

202. Group probability: 1.0000. Peptides of the group

LRDTPGQDEVALER	59.22	54.7669	1597.806	1598.478	2	2	distinct	1	0.9642
GFDANMALFIPNYAEYK	60.4	53.8117	1962.919	1963.364	1	2	distinct	0	0.9716
LAQELSYEQENSNLFIGDSPTSEPGFVSEFK	65.62	50.1401	3461.615	3460.324	1	3	distinct	0	0.9875
ISATITKPAGGAIVMDGFVQDGDLNIDNIAYYK	59.88	50.1606	3469.744	3470.917	4	3	distinct	0	0.9807

The equivalent proteins include

gi|50726904|gb|AAT81148.1|	30591.89	mitochondrial Mrb1 [Ustilago maydis]

203. Group probability: 1.0000. Peptides of the group

AMGGYSTHIR	63.96	55.7695	1091.518	1091.85	1	2	distinct	0	0.9722
HDFCIPGHEIIGIATK	80.12	54.3387	1806.909	1807.342	3	+2,+3	distinct	0	0.9994
KETDDDVDIAITHCGVCGSDVHTISGGWGPLK	62.65	50.2169	3438.582	3439.589	1	3	distinct	1	0.9843

The equivalent proteins include

gi|71006684|ref|XP_758008.1|	39687.76	hypothetical protein UM01861.1 [Ustilago maydis 521]

204. Group probability: 1.0000. Peptides of the group

EFAFQRPAYDDK	69.57	54.9977	1485.689	1486.267	1	2	distinct	0	0.9844
YSELKPETAAPSGEITIIDVR	71.77	53.2308	2288.19	2288.353	3	2	distinct	0	0.991
EPNEVAQGIIPSAVNVPLSQFQK	87.95	52.5949	2464.296	2465.283	1	2	distinct	0	0.998

The equivalent proteins include

gi|71020915|ref|XP_760688.1|	21808.16	hypothetical protein UM04541.1 [Ustilago maydis 521]

205. Group probability: 1.0000. Peptides of the group

IVQLTTAAGAPVEPIWATLLAK	80.5	53.0765	2262.299	2263.454	18	+2,+3	distinct	0	0.9999
ELLTNVGGGGAAIAVAAPAAGAAAGGAAEETKEEK	82.04	51.0785	3121.589	3122.046	4	3	distinct	1	0.9974

The equivalent proteins include

gi|71003425|ref|XP_756393.1|	21941.79	hypothetical protein UM00246.1 [Ustilago maydis 521]

206. Group probability: 1.0000. Peptides of the group

DATEAFWTYHSEK	74.99	54.567	1583.689	1583.88	1	2	distinct	0	0.9907
VYDVTGFLDDHPGGK	69.53	54.6127	1618.763	1618.907	1	2	distinct	0	0.9861
VYDVTGFLDDHPGGKK	89.57	54.2267	1746.858	1748.143	4	2	distinct	1	0.9977

The equivalent proteins include

gi|71006442|ref|XP_757887.1|	55811.65	hypothetical protein UM01740.1 [Ustilago maydis 521]

207. Group probability: 1.0000. Peptides of the group

KVDLSNVEAVR	79.27	55.6442	1228.677	1230.028	3	2	distinct	1	0.993
EFNAYETLRK	49.46	55.824	1269.635	1269.807	1	2	distinct	1	0.9008
VKVWFDQPGAK	59.37	55.4682	1273.682	1273.699	1	2	distinct	1	0.9602
QVQSVLPLPAGTEAEKPR	47.7	53.8424	1919.048	1919.986	2	+2,+3	distinct	0	0.9891

The equivalent proteins include

gi|71017681|ref|XP_759071.1|	23910.35	hypothetical protein UM02924.1 [Ustilago maydis 521]

208. Group probability: 1.0000. Peptides of the group

TLFSEAGTVTHAQVITR	99.7	54.0525	1829.964	1830.577	2	+2,+3	distinct	0	1
EISVESAKPQTSAATNDAKPK	48.33	53.2915	2171.107	2171.343	2	+2,+3	distinct	0	0.9934

The equivalent proteins include

gi|71023135|ref|XP_761797.1|	54458.29	hypothetical protein UM05650.1 [Ustilago maydis 521]

209. Group probability: 1.0000. Peptides of the group

LLGGVTISQGGVLPFIQSELLPAK	95.53	52.6062	2436.399	2437.423	1	2	distinct	0	0.999
VGAGAPVYLAAVLEYLAAEILELAGNAAR	80.64	51.6645	2884.57	2885.939	1	3	distinct	0	0.9883
NDEELNKLLGGVTISQGGVLPFIQSELLPAK	56.59	50.9168	3278.776	3279.953	2	3	distinct	1	0.972

The equivalent proteins include

gi|71005970|ref|XP_757651.1|	14190.76	histone H2A [Ustilago maydis 521]

210. Group probability: 1.0000. Peptides of the group

GVGGAAWGATGAGAAPAPAR	68.13	54.5092	1664.838	1665.29	1	2	distinct	0	0.9868
GVNIPGKEETVHIAGIAAPR	107.29	53.5065	2028.112	2028.17	3	+2,+3	distinct	1	1

The equivalent proteins include

gi|71007524|ref|XP_758121.1|	109504.47	hypothetical protein UM01974.1 [Ustilago maydis 521]

211. Group probability: 1.0000. Peptides of the group

VANYHHVDLVLVGK	73.11	54.868	1562.857	1563.643	4	+1,+2	distinct	0	0.9994
GLTTAGTVSSYLVSHSNAPVLVIK	59.9	52.8255	2413.322	2413.503	1	2	distinct	0	0.9773
TDSHVFLCTVLPANVISTPWVAGPLTIDTER	54.15	50.4323	3408.739	3409.402	2	3	distinct	0	0.9656

The equivalent proteins include

gi|71005336|ref|XP_757334.1|	25374.58	hypothetical protein UM01187.1 [Ustilago maydis 521]

212. Group probability: 1.0000. Peptides of the group

TVVSDGLHAYDR	65.2	55.3394	1331.647	1331.854	1	2	distinct	0	0.977
LGAQPLLDVLDHLR	80.27	54.7815	1558.883	1559.353	5	2	distinct	0	0.9943
SHPIPADAGLFGAGQYVASENAK	80.77	53.0461	2299.123	2299.713	1	2	distinct	0	0.9962

The equivalent proteins include

gi|71015770|ref|XP_758840.1|	99068.96	hypothetical protein UM02693.1 [Ustilago maydis 521]

213. Group probability: 1.0000. Peptides of the group

YISHLSNLSSVAK	48.46	55.0265	1417.756	1418.285	1	2	distinct	0	0.9042
LEPAEQHKNPSVAR	73.89	54.7185	1574.816	1575.696	4	+2,+3	distinct	1	0.9987
MVIGVCNLKPASMR	56.78	54.714	1574.809	1575.271	2	+2,+3	distinct	0	0.9957

The equivalent proteins include

gi|71017621|ref|XP_759041.1|	50012.74	hypothetical protein UM02894.1 [Ustilago maydis 521]

214. Group probability: 1.0000. Peptides of the group

LIHTQVGDGPR	76.16	55.4311	1191.636	1191.914	1	2	distinct	0	0.9909
TVQTSPLLQHR	50.08	55.4562	1278.704	1278.945	1	2	distinct	0	0.91
HYFPNADFDDTFDLLGK	103.36	53.5964	2013.911	2014.753	4	2	distinct	0	0.9993

The equivalent proteins include

gi|71022191|ref|XP_761326.1|	46919.72	hypothetical protein UM05179.1 [Ustilago maydis 521]

215. Group probability: 1.0000. Peptides of the group

SIIAAEGVSSLFK	55.19	55.3188	1320.729	1320.633	1	1	distinct	0	0.9466
KTVSGFATDFLMGGVSAAVSK	66.52	53.6062	2072.061	2072.515	1	2	distinct	1	0.9856
GIAGAGVLSGYDKLQELMFGK	100.26	53.2989	2153.119	2153.873	7	2	distinct	1	0.9993

The equivalent proteins include

gi|71004800|ref|XP_757066.1|	33781.6	hypothetical protein UM00919.1 [Ustilago maydis 521]

216. Group probability: 1.0000. Peptides of the group

DLGLEDQVKPR	55.76	55.3843	1268.672	1268.83	1	2	distinct	0	0.9454
EGGAKVENVDELISK	98.2	54.9201	1586.815	1587.318	1	2	distinct	1	0.9989
FSMNPFDEIAVEEAVR	100.37	54.0941	1852.866	1853.923	3	2	distinct	0	0.9907

The equivalent proteins include

gi|71004000|ref|XP_756666.1|	32238.41	hypothetical protein UM00519.1 [Ustilago maydis 521]

217. Group probability: 1.0000. Peptides of the group

AEAPPNEKPATVK	69.08	55.178	1350.714	1351.099	2	2	distinct	0	0.9843
AKAEAPPNEKPATVK	60.9	54.6689	1549.846	1549.832	2	2	distinct	1	0.9703
DMIVVPEMIGSMIGIYTGR	95.29	53.5405	2081.036	2082.346	4	2	distinct	0	0.9988

The equivalent proteins include

gi|71021099|ref|XP_760780.1|	20195.52	hypothetical protein UM04633.1 [Ustilago maydis 521]

218. Group probability: 1.0000. Peptides of the group

IGGLLMYGIPNMK	51.74	55.0161	1405.746	1406.377	1	2	distinct	0	0.9282
MAQGAKPGEGGELPGHK	58.44	54.4505	1662.815	1663.953	3	2	distinct	0	0.9658
KCHLNTCAAGIATQDPELR	42.41	53.3039	2154.031	2154.705	1	3	distinct	1	0.8438
NSGAHAVVEGVGDHGCEYQTGGR	54.99	53.1302	2356.025	2357.472	1	3	distinct	0	0.9552
VLTLPQAVMMMIPEAWQGSADHMEPEK	55.36	51.2483	3038.437	3039.732	2	3	distinct	0	0.9638

The equivalent proteins include

gi|71019533|ref|XP_759997.1|	239381.88	hypothetical protein UM03850.1 [Ustilago maydis 521]

219. Group probability: 1.0000. Peptides of the group

HKLDITSVDEYR	64.19	54.9358	1474.742	1474.753	1	2	distinct	1	0.9751
ILISPDGDIQVTNDGATIMNNMELDHQIAK	62.47	50.8166	3265.596	3266.464	1	3	distinct	0	0.9827
DCGANLVVCQWGFDDEANHLLLQHQLPAVR	90.47	50.0483	3474.656	3475.217	1	3	distinct	0	0.9985

The equivalent proteins include

gi|71019751|ref|XP_760106.1|	59931.27	hypothetical protein UM03959.1 [Ustilago maydis 521]

220. Group probability: 1.0000. Peptides of the group

LVEDVVYEVDAAK	101.31	55.0343	1448.74	1449.243	2	2	distinct	0	0.9991
LAESNPDRVPAFEK	59.4	54.8713	1571.794	1573.128	3	2	distinct	1	0.9647
IVGSFNDWEFFTGESMDPEGMVALLNYR (000000000000000010000100000000)	62.19	51.5188	3255.453	3256.773	1	3	distinct	0	0.9807

The equivalent proteins include

gi|71005528|ref|XP_757430.1|	17224.5	hypothetical protein UM01283.1 [Ustilago maydis 521]

221. Group probability: 1.0000. Peptides of the group

TGFKPVALEADPNKVR	72.75	54.1718	1740.952	1741.573	5	+2,+3	distinct	1	0.9995
DALLFVICSPVGPYYK	49.8	54.0541	1840.943	1841.261	1	2	distinct	0	0.925
ITDIQLGKVEHEWSVVVDDL	64.91	52.974	2294.179	2294.523	3	2	distinct	1	0.9831

The equivalent proteins include

gi|71022907|ref|XP_761683.1|	64279.39	hypothetical protein UM05536.1 [Ustilago maydis 521]

222. Group probability: 1.0000. Peptides of the group

ADMLQGFQLVHSLGGGTGSGLGTNLLTK	58.08	52.029	2771.428	2772.107	2	+2,+3	distinct	0	0.9993
EKNPAGFVEWIPNNVLTSLCDIAPPQLK	59.1	51.3631	3149.622	3150.048	7	3	distinct	1	0.9748
EAEKADMLQGFQLVHSLGGGTGSGLGTNLLTK	52.73	50.8591	3228.645	3229.945	1	3	distinct	1	0.9621

The equivalent proteins include

gi|71022475|ref|XP_761467.1|	32678.15	hypothetical protein UM05320.1 [Ustilago maydis 521]

223. Group probability: 1.0000. Peptides of the group

REDGAGHMAEGYAR	59.01	54.885	1518.663	1518.988	2	2	distinct	1	0.9635
IATSGRPGPVLVDIPK	46.09	54.6125	1618.941	1619.045	3	2	distinct	0	0.8949
RPIIYAGQGILSSPEGPK	63.92	53.9077	1882.031	1882.873	1	2	distinct	0	0.9798
HVFGYPGGAILPVFDAIYNSK	71.36	53.0364	2264.163	2264.726	1	2	distinct	0	0.9907

The equivalent proteins include

gi|71018311|ref|XP_759386.1|	80334.9	hypothetical protein UM03239.1 [Ustilago maydis 521]

224. Group probability: 1.0000. Peptides of the group

INTLIRPDGK	58.86	55.3133	1125.651	1125.954	1	2	distinct	0	0.957
LTPDQDALDVSNR	76.71	54.8973	1442.7	1442.89	1	2	distinct	0	0.992
KIEENNTLVFIVDR	91.53	54.5607	1688.91	1689.61	1	2	distinct	1	0.9979

The equivalent proteins include

gi|71023831|ref|XP_762145.1|	16363.04	hypothetical protein UM05998.1 [Ustilago maydis 521]

225. Group probability: 1.0000. Peptides of the group

AAHLDLEGLTLDR	76.1	54.8513	1422.747	1423.35	1	2	distinct	0	0.9915
FELAFYGLKPDIK	75.91	54.5739	1539.834	1540.247	5	2	distinct	0	0.9915
EHTDPVDVFLTLNALAR	71.95	53.793	1909.99	1910.586	1	2	distinct	0	0.9897

The equivalent proteins include

gi|71021577|ref|XP_761019.1|	47529.32	hypothetical protein UM04872.1 [Ustilago maydis 521]

226. Group probability: 1.0000. Peptides of the group

KVASNPDVVGGK	61.49	55.608	1169.64	1170.556	1	2	distinct	1	0.968
VLSPSGADAETPVLVDFFATWCQPCK	83.29	51.5548	2894.362	2894.903	17	+2,+3	distinct	0	1

The equivalent proteins include

gi|71005702|ref|XP_757517.1|	19367.9	hypothetical protein UM01370.1 [Ustilago maydis 521]

227. Group probability: 1.0000. Peptides of the group

DGTPQSAIDEHK	49.11	55.1847	1296.595	1296.967	1	2	distinct	0	0.906
DGTPQSAIDEHKTK	61.63	54.5945	1525.737	1526.076	1	2	distinct	1	0.9711
GFAATLPESFAQELTSASVGGK	108.83	53.4384	2167.08	2168.273	1	2	distinct	0	0.9997

The equivalent proteins include

gi|71009459|ref|XP_758276.1|	11684.61	hypothetical protein UM02129.1 [Ustilago maydis 521]

228. Group probability: 1.0000. Peptides of the group

ASNYGISPADKHQTK	52.47	54.7503	1615.795	1615.613	2	2	distinct	1	0.9376
NFPNAIEHTIQWAR	62.2	54.2925	1695.848	1696.733	3	2	distinct	0	0.9674
QLLHSLPADAVTSSGQPFWSGPK	75.34	52.6206	2422.228	2422.663	2	+2,+3	distinct	0	0.9995

The equivalent proteins include

gi|71024211|ref|XP_762335.1|	113707.36	hypothetical protein UM06188.1 [Ustilago maydis 521]

229. Group probability: 1.0000. Peptides of the group

DVELLLMHNGVYAAEIAHNVSSK	98.82	52.5166	2509.263	2510.133	7	+2,+3	distinct	0	1

The equivalent proteins include

gi|71004812|ref|XP_757072.1|	95076.73	hypothetical protein UM00925.1 [Ustilago maydis 521]

230. Group probability: 1.0000. Peptides of the group

HGCIQETHELIEK	83.8	54.6161	1592.762	1593.183	1	2	distinct	0	0.9957
FENALPHDSSSTITQEWLWPR	72.69	52.5111	2513.197	2513.773	2	2	distinct	0	0.9918
LVQLGSQSVQGVPGDFNMGFLDLIEEHPK	56.13	50.9564	3153.58	3154.63	1	3	distinct	0	0.9687

The equivalent proteins include

gi|71019821|ref|XP_760141.1|	64393.82	hypothetical protein UM03994.1 [Ustilago maydis 521]

231. Group probability: 1.0000. Peptides of the group

DRADAAFDPLSMFWYEPTAK	56.45	52.9446	2330.068	2330.463	1	2	distinct	1	0.9645
ASILTGHQTHGDLDAGDFVLDALGTR	80.54	52.1168	2679.325	2679.623	7	+2,+3	distinct	0	1

The equivalent proteins include

gi|71004376|ref|XP_756854.1|	111640.48	hypothetical protein UM00707.1 [Ustilago maydis 521]

232. Group probability: 1.0000. Peptides of the group

VAFDHSEALKK	55.64	55.6292	1243.656	1244.673	1	2	distinct	1	0.9446
IHPQLAYVDSLAVK	63.76	54.5524	1552.861	1553.288	1	2	distinct	0	0.9761
SHSLLATTYGYGENLINSSLK	98.16	53.4581	2267.143	2267.669	1	2	distinct	0	0.9991

The equivalent proteins include

gi|71020213|ref|XP_760337.1|	33900.61	hypothetical protein UM04190.1 [Ustilago maydis 521]

233. Group probability: 1.0000. Peptides of the group

LHDIPDEHLTELLPVAK	81.69	53.8003	1939.041	1939.175	5	+2,+3	distinct	0	0.9995
TYAFLDIGPISEGHALVIPK	86.68	53.3132	2140.157	2140.371	7	2	distinct	0	0.9975

The equivalent proteins include

gi|71023843|ref|XP_762151.1|	15683.19	hypothetical protein UM06004.1 [Ustilago maydis 521]

234. Group probability: 1.0000. Peptides of the group

ILNDIAHHK	49.7	56.0603	1059.582	1060.038	1	2	distinct	0	0.8996
LVALGVTQDHSVFK	66.15	54.647	1512.83	1513.288	1	2	distinct	0	0.9806
LMGYVGFANLPNQVHR	68.95	54.1263	1814.925	1816.163	1	2	distinct	0	0.986
AYPWGVIEVDNEEHCDFVK	53.86	52.9686	2306.031	2306.105	1	2	distinct	0	0.9538

The equivalent proteins include

gi|71019303|ref|XP_759882.1|	51045.48	hypothetical protein UM03735.1 [Ustilago maydis 521]

235. Group probability: 1.0000. Peptides of the group

GIQGGTSHCLGQNFSK	67.77	54.5506	1689.789	1690.302	1	2	distinct	0	0.9843
EKDHIEGFAPEVAWVTK	70.57	53.6913	1954.979	1955.412	1	2	distinct	1	0.9884
TSFSVDGLYGSISTLLDQIHDDMFAK	74.14	51.6895	2859.364	2860.26	2	3	distinct	0	0.9927

The equivalent proteins include

gi|71004672|ref|XP_757002.1|	81592.11	hypothetical protein UM00855.1 [Ustilago maydis 521]

236. Group probability: 1.0000. Peptides of the group

EGAGALLTGLGPTVLGYFLQGGFK	86.26	52.8774	2365.268	2366.233	1	2	distinct	0	0.9977
FFLAGALCCSLTHGAVTPIDVVK	64.7	52.4269	2475.265	2476.464	4	+2,+3	distinct	0	0.9994

The equivalent proteins include

gi|71022043|ref|XP_761252.1|	34520.3	hypothetical protein UM05105.1 [Ustilago maydis 521]

237. Group probability: 1.0000. Peptides of the group

GHVNPDAHAISMIK	77.75	54.855	1488.751	1489.185	4	2	distinct	0	0.9799
AVYSIAYEGIDAHDLTSRL	87.2	53.3819	2093.043	2094.242	2	2	distinct	1	0.9975
YLPGCKLPDNVIANPNPVDAVK	58.26	52.7928	2393.241	2394.023	1	2	distinct	1	0.9719

The equivalent proteins include

gi|71004072|ref|XP_756702.1|	38953.83	hypothetical protein UM00555.1 [Ustilago maydis 521]

238. Group probability: 1.0000. Peptides of the group

IAGFTTHLMK	50.44	55.8304	1117.595	1117.964	2	2	distinct	0	0.909
LSNVDFHQNKR	54.54	55.3289	1356.69	1357.3	4	2	distinct	1	0.9393
SFGFDSLPVTVTAPVTAYQAPERR	41.84	52.2877	2608.328	2609.209	1	3	distinct	1	0.8653
KDQYVPEVSALDTSAPGSLEVDPDTK	53.76	51.9058	2760.334	2760.987	1	3	distinct	1	0.9562
DQYVPEVSALDTSAPGSLEVDPDTKDMLR	52.13	51.2631	3147.492	3147.962	1	3	distinct	1	0.9552

The equivalent proteins include

gi|71004698|ref|XP_757015.1|	45442.05	hypothetical protein UM00868.1 [Ustilago maydis 521]

239. Group probability: 1.0000. Peptides of the group

DSGCIDGNCVNKR	50.15	54.6153	1493.635	1494.131	5	+2,+3	distinct	1	0.9879
KNTGPINSFCTSDDQCATSGYCYR	69.28	51.8759	2801.148	2802.044	7	+2,+3	distinct	1	0.9999

The equivalent proteins include

gi|71022141|ref|XP_761301.1|	38197.38	hypothetical protein UM05154.1 [Ustilago maydis 521]

240. Group probability: 1.0000. Peptides of the group

NKDVVSQAQK	47.88	55.9175	1115.593	1115.733	1	2	distinct	1	0.6622
NTLAQISAFR	64.31	55.788	1119.604	1119.779	1	2	distinct	0	0.9731
QQNTDIDFAHYSNVLR	54.53	53.8366	1919.913	1920.381	1	2	distinct	0	0.9507
ILSEFKPVTYDVQAQLK	55.69	53.7457	1978.077	1978.753	3	+2,+3	distinct	0	0.9966

The equivalent proteins include

gi|71024733|ref|XP_762596.1|	64952	hypothetical protein UM06449.1 [Ustilago maydis 521]

241. Group probability: 1.0000. Peptides of the group

VYSPPVEVDDAASADHAK	60.03	53.9672	1869.874	1870.648	1	3	distinct	0	0.965
LLMSAMPFSIIGSTDDVR	62.77	53.6893	1951.975	1952.402	1	2	distinct	0	0.9337
DSWTPIVDFIDDQHELYMR	102.1	52.7447	2379.084	2380.113	2	2	distinct	0	0.9993

The equivalent proteins include

gi|71019031|ref|XP_759746.1|	43690.64	hypothetical protein UM03599.1 [Ustilago maydis 521]

242. Group probability: 1.0000. Peptides of the group

GQPQSHQSLDSK	52.53	55.0438	1310.621	1311.196	1	2	distinct	0	0.9305
GQPQSHQSLDSKDEK	64.79	54.2982	1682.786	1682.839	4	2	distinct	1	0.979
NAPGPNPDVGMHHDDDR	66.24	54.1179	1842.77	1842.641	3	2	distinct	0	0.9829
NAPGPNPDVGMHHDDDRK	49.69	53.672	1970.865	1971.6	1	2	distinct	1	0.93

The equivalent proteins include

gi|71020983|ref|XP_760722.1|	13132.37	hypothetical protein UM04575.1 [Ustilago maydis 521]

243. Group probability: 1.0000. Peptides of the group

FAIFVVHNK	65.86	56.0578	1073.602	1073.838	1	2	distinct	0	0.9757
AEFDPDLMVAIGGGGFYPAR	53.63	53.4849	2081.988	2083.17	1	2	distinct	0	0.954
YYSTQDIGDVWICYPWEEEDIIEHNR	91.33	50.6786	3329.461	3330.324	2	3	distinct	0	0.9984

The equivalent proteins include

gi|71023089|ref|XP_761774.1|	28206.72	hypothetical protein UM05627.1 [Ustilago maydis 521]

244. Group probability: 1.0000. Peptides of the group

YTALVEVLNDILDGYDQSFR	100.37	52.9045	2330.143	2331.273	2	2	distinct	0	0.9992
ELIETLRNPELPYGQASQILSSLGGR	54.79	51.9348	2840.503	2841.613	2	+2,+3	distinct	1	0.9976

The equivalent proteins include

gi|71021091|ref|XP_760776.1|	240711.92	hypothetical protein UM04629.1 [Ustilago maydis 521]
gi|600098|emb|CAA86983.1|	240679.9	acetyl CoA carboxylase [Ustilago maydis]

245. Group probability: 1.0000. Peptides of the group

ADEPDSLSHDPVYR	66.63	54.7811	1599.716	1599.828	1	2	distinct	0	0.9813
YQEASPLGWHTVPGK	70.78	54.3363	1668.826	1669.37	8	+2,+3	distinct	0	0.9984
TGAAPHDWPMGSWASNR	51.16	53.9898	1839.811	1840.228	2	2	distinct	0	0.9358

The equivalent proteins include

gi|71024031|ref|XP_762245.1|	107011.06	hypothetical protein UM06098.1 [Ustilago maydis 521]

246. Group probability: 1.0000. Peptides of the group

AASDVYDASSSKR	50.95	55.1274	1355.632	1356.063	1	2	distinct	1	0.9229
ISLLNFHAPWAEPCK	81.08	54.2258	1781.892	1782.433	4	2	distinct	0	0.995
VDFGHYDILKDENVR	80.62	54.2288	1818.89	1819.743	1	2	distinct	1	0.9948

The equivalent proteins include

gi|71020279|ref|XP_760370.1|	29454.65	hypothetical protein UM04223.1 [Ustilago maydis 521]

247. Group probability: 1.0000. Peptides of the group

IVTGHDGKPK	51.5	55.2418	1050.582	1051.132	1	2	distinct	0	0.918
KPSSNSSSPAPSATAPAER	64.49	54.055	1840.891	1841.047	1	2	distinct	0	0.9814
SAESAAAAAASSNSSKPNPFGNAKPVDASER	89.81	51.3776	2988.417	2989.46	2	3	distinct	0	0.9985

The equivalent proteins include

gi|71024015|ref|XP_762237.1|	58338.68	hypothetical protein UM06090.1 [Ustilago maydis 521]

248. Group probability: 1.0000. Peptides of the group

VLALSGISLAK	49.13	56.0075	1070.67	1071.153	1	1	distinct	0	0.9011
QASHLSVIHR	61.28	55.7555	1146.626	1147.543	1	2	distinct	0	0.9649
ILKPVANAYANATGHR	69.59	54.2716	1694.922	1696.154	2	2	distinct	0	0.9867
YDDLLIEESDRVQK	54.11	54.2235	1721.847	1722.647	3	2	distinct	1	0.9446

The equivalent proteins include

gi|71020307|ref|XP_760384.1|	14595.62	hypothetical protein UM04237.1 [Ustilago maydis 521]

249. Group probability: 1.0000. Peptides of the group

KALEHASQAR	58.5	55.1693	1109.594	1109.736	1	2	distinct	1	0.9557
HTTNLALALKPSAK	64.76	55.0359	1463.846	1464.099	1	2	distinct	0	0.9779
SAVEDVLGSMADLLHSLLDDR	84.8	53.0124	2255.11	2255.924	1	2	distinct	0	0.9971

The equivalent proteins include

gi|71021525|ref|XP_760993.1|	123420.74	hypothetical protein UM04846.1 [Ustilago maydis 521]

250. Group probability: 1.0000. Peptides of the group

AGNLGDHVQITR	46.54	55.2312	1279.663	1280.989	1	3	distinct	0	0.855
FFIDFSGPANDGILDAAAFEK	141.27	53.231	2244.074	2244.544	16	2	distinct	0	1

The equivalent proteins include

gi|71004334|ref|XP_756833.1|	20629.73	hypothetical protein UM00686.1 [Ustilago maydis 521]

251. Group probability: 1.0000. Peptides of the group

GGFGGGGAYIANLGHGITPGVDPEAVR	54.64	52.4118	2538.261	2539.343	3	+2,+3	distinct	0	0.998
KVVDLASPGKPSYQDASGQNEAGHR	93.14	52.3036	2610.279	2611.054	2	3	distinct	1	0.9986

The equivalent proteins include

gi|71024153|ref|XP_762306.1|	46126.72	hypothetical protein UM06159.1 [Ustilago maydis 521]

252. Group probability: 1.0000. Peptides of the group

VPEDIHTHSK	54.38	55.6417	1161.578	1162.027	1	2	distinct	0	0.9358
SFYHPIAAAQIEK	55.2	54.9407	1473.762	1473.747	1	2	distinct	0	0.9471
VDWDAWLYGEGLELPVK	100.05	53.6164	1988.988	1989.403	1	2	distinct	0	0.9991

The equivalent proteins include

gi|71003273|ref|XP_756317.1|	147091.86	hypothetical protein UM00170.1 [Ustilago maydis 521]

253. Group probability: 1.0000. Peptides of the group

HSQAEHNVADDYSIADAPLTPLGK	102.01	52.5205	2548.219	2549.155	4	+2,+3	distinct	0	1

The equivalent proteins include

gi|71023081|ref|XP_761770.1|	31103.17	hypothetical protein UM05623.1 [Ustilago maydis 521]

254. Group probability: 1.0000. Peptides of the group

HSQTDRVDSQK	47.49	55.348	1299.617	1300.33	2	2	distinct	1	0.8873
HEKEEADYFASTK	81.5	54.7249	1553.7	1554.823	3	2	distinct	1	0.9948
AAAGADAVEGEQQKDAR	51.81	54.3928	1685.797	1686.823	2	+2,+3	distinct	1	0.9949

The equivalent proteins include

gi|71017743|ref|XP_759102.1|	30497.4	hypothetical protein UM02955.1 [Ustilago maydis 521]

255. Group probability: 1.0000. Peptides of the group

TAYPHVAVTAAR	58.01	55.7595	1255.667	1256.194	3	+1,+2	distinct	0	0.9949
AVTAHDSYSVER	46.61	55.3573	1333.626	1333.76	1	2	distinct	0	0.8825
VQAICSYEHAADKQ	51.51	54.6125	1618.741	1619.033	1	2	distinct	1	0.9299
VESVIDVGVPSNADKTAYPHVAVTAAR	44.28	51.9799	2765.435	2765.543	1	2	distinct	1	0.921

The equivalent proteins include

gi|71018039|ref|XP_759250.1|	17327.83	hypothetical protein UM03103.1 [Ustilago maydis 521]

256. Group probability: 1.0000. Peptides of the group

LPGFWEIPMYAIFDER (000000000100000000)	62.16	53.7623	1982.96	1983.713	4	2	distinct	0	0.9748
TRIPNNCDTPFWDPVAAK	65.1	53.3917	2101.005	2102.083	3	2	distinct	1	0.982
DVPQFIVFTADDAVQDYTINSINQFLAQR	72.09	50.6833	3327.641	3328.24	16	3	distinct	0	0.9923

The equivalent proteins include

gi|71012790|ref|XP_758528.1|	59687.46	hypothetical protein UM02381.1 [Ustilago maydis 521]

257. Group probability: 1.0000. Peptides of the group

LAQHGNAGHDGALR	60.03	55.0832	1415.702	1416.285	5	2	distinct	0	0.9665
SPSIGGNAPMPGSAGPR	54.88	54.6306	1551.746	1552.12	1	2	distinct	0	0.9531
NLGNFGGGGLSPGLAGQAGR	88.14	54.2544	1798.907	1799.236	1	2	distinct	0	0.9977

The equivalent proteins include

gi|71018529|ref|XP_759495.1|	76524.31	hypothetical protein UM03348.1 [Ustilago maydis 521]

258. Group probability: 1.0000. Peptides of the group

VLQMGTHPNYLYR	48.26	54.6468	1590.798	1591.278	2	2	distinct	0	0.9033
LLTVQDLIAIAESLNHDESK	80.19	53.1846	2208.164	2206.883	3	+2,+3	distinct	0	0.9993
LSSDDQDSVRLLTVQDLIAIAESLNHDESK	48.35	50.9943	3310.653	3310.324	1	3	distinct	1	0.9401

The equivalent proteins include

gi|71017753|ref|XP_759107.1|	65072.25	hypothetical protein UM02960.1 [Ustilago maydis 521]

259. Group probability: 1.0000. Peptides of the group

AGYGHCSLSQPSK	70.76	55.1213	1390.63	1391.186	1	2	distinct	0	0.9864
NNELLAANFDTILDHK	67.84	54.0163	1826.916	1827.399	1	2	distinct	0	0.9846
THEDEVLGSLLTNPGGPGGSGFEFIAR	63.39	51.9601	2756.34	2757.267	2	3	distinct	0	0.9818

The equivalent proteins include

gi|71007720|ref|XP_758141.1|	72346.69	hypothetical protein UM01994.1 [Ustilago maydis 521]

260. Group probability: 1.0000. Peptides of the group

KVVAAAQTAK	55.12	56.3057	985.592	985.459	1	1	distinct	1	0.939
KDDHAHSAK	56.23	55.9505	1007.478	1007.529	1	2	distinct	1	0.8506
KLSDEHAHEK	68.13	55.3067	1192.584	1192.757	2	2	distinct	1	0.9809
HDAPEGDKHLDSK	64.72	55.0163	1447.669	1447.692	3	2	distinct	1	0.977

The equivalent proteins include

gi|71018217|ref|XP_759339.1|	21237.67	hypothetical protein UM03192.1 [Ustilago maydis 521]

261. Group probability: 1.0000. Peptides of the group

LAHSPSALTAISNLVEVMK (00000000000000000100)	107.57	53.7974	1980.071	1980.232	20	+2,+3	distinct	0	1

The equivalent proteins include

gi|71008186|ref|XP_758192.1|	15856.17	hypothetical protein UM02045.1 [Ustilago maydis 521]

262. Group probability: 1.0000. Peptides of the group

HALENAPEDAGVKR	64.59	54.7557	1505.759	1506.26	2	2	distinct	1	0.9777
RVESVETVASDRPK	56.2	54.8717	1571.827	1572.951	2	+2,+3	distinct	1	0.9972
YLQLHPILPEDTPADLAANYTTLK	49.41	52.052	2696.406	2696.786	1	3	distinct	0	0.931

The equivalent proteins include

gi|71024353|ref|XP_762406.1|	43838.09	hypothetical protein UM06259.1 [Ustilago maydis 521]

263. Group probability: 1.0000. Peptides of the group

TDDLELLQEIISSGAFDANHSDGVGR	89.63	51.9556	2758.304	2759.479	3	3	distinct	0	0.9981
TNADTPLHAAVSVDIPEGAAGKEVEEIR	86.21	51.5925	2888.451	2889.714	1	3	distinct	1	0.9976

The equivalent proteins include

gi|71018561|ref|XP_759511.1|	14904.28	hypothetical protein UM03364.1 [Ustilago maydis 521]

264. Group probability: 1.0000. Peptides of the group

VVVVTDHTDKNGR	75.76	54.778	1438.753	1438.864	2	2	distinct	1	0.9913
VSGVGGAMDLVSNPSNTK	60.96	54.2926	1731.846	1732.772	1	2	distinct	0	0.9736
HPHINDLTVVSNNAGTGELGLGK	62.23	53.2892	2342.198	2342.473	1	2	distinct	0	0.9806

The equivalent proteins include

gi|71015510|ref|XP_758814.1|	56408.33	hypothetical protein UM02667.1 [Ustilago maydis 521]

265. Group probability: 1.0000. Peptides of the group

VSQIAGHLSGPAPLLK	81.17	54.9451	1586.914	1587.241	3	2	distinct	0	0.9951
LFASHGAHVVVSDLDAK	99.3	54.1318	1764.916	1765.34	1	2	distinct	0	0.9991

The equivalent proteins include

gi|71006606|ref|XP_757969.1|	120642	hypothetical protein UM01822.1 [Ustilago maydis 521]

266. Group probability: 1.0000. Peptides of the group

HTGPGIVSMANAGR (0000000001000000)	65.15	54.9155	1366.678	1367.243	9	+2,+3	distinct	0	0.9886
VPTGYGDKPVHDVLVK	70.33	54.1958	1722.93	1723.585	3	2	distinct	0	0.9876
YIEKVPTGYGDKPVHDVLVK	56.7	53.1488	2256.215	2256.596	2	2	distinct	1	0.9651

The equivalent proteins include

gi|71004998|ref|XP_757165.1|	22897.7	hypothetical protein UM01018.1 [Ustilago maydis 521]

267. Group probability: 1.0000. Peptides of the group

KFLDGIYCTGK	67.56	55.4045	1300.648	1301.53	1	2	distinct	1	0.9806
DQVLVEGNDIDLVSQSAALLHGATLVR	64.17	51.7005	2832.498	2833.399	3	3	distinct	0	0.9831
AQKDQVLVEGNDIDLVSQSAALLHGATLVR	62.69	50.9969	3159.689	3161.134	3	3	distinct	1	0.983

The equivalent proteins include

gi|71021511|ref|XP_760986.1|	28146.52	hypothetical protein UM04839.1 [Ustilago maydis 521]

268. Group probability: 1.0000. Peptides of the group

KPSAGGAGGAGAAGGAR	77.36	55.1917	1311.664	1312.219	1	2	distinct	0	0.9934
AIEAADTKPAATEQQPATK	51.59	53.733	1939.985	1941.351	1	2	distinct	0	0.9427
STMVHGIEQEESSPCFGQQQIHDK	66.87	52.088	2771.228	2771.677	2	3	distinct	0	0.9851

The equivalent proteins include

gi|71005790|ref|XP_757561.1|	53276.52	hypothetical protein UM01414.1 [Ustilago maydis 521]

269. Group probability: 1.0000. Peptides of the group

SKDSNHNHDHGSAASSK	55.26	54.1206	1777.773	1778.293	1	2	distinct	1	0.9551
GTPPAPTSDGLKGPTVDDETANAIVGTGK	47.98	51.9837	2765.372	2765.636	1	3	distinct	1	0.9346
KGVLSEILADLESFSGSSGSSSESALSSINK	86.69	51.1926	3085.53	3086.506	1	3	distinct	1	0.998

The equivalent proteins include

gi|71008940|ref|XP_758257.1|	79552.28	hypothetical protein UM02110.1 [Ustilago maydis 521]

270. Group probability: 1.0000. Peptides of the group

FGLSGAHQTSPIR	86.8	55.202	1369.71	1370.252	4	2	distinct	0	0.9967
AGMILHGLGFSPEMMK	92.13	54.4049	1717.835	1719.108	1	2	distinct	0	0.9982

The equivalent proteins include

gi|71005644|ref|XP_757488.1|	69921.89	hypothetical protein UM01341.1 [Ustilago maydis 521]

271. Group probability: 1.0000. Peptides of the group

LATLQPTLHPTSEELAIGQVK	77.82	53.2328	2245.232	2245.301	2	+2,+3	distinct	0	0.9995
DYFPEVDGIVFLVDTQDHER	68.17	52.7776	2393.117	2394.593	2	2	distinct	0	0.9873

The equivalent proteins include

gi|71024587|ref|XP_762523.1|	21461.22	hypothetical protein UM06376.1 [Ustilago maydis 521]

272. Group probability: 1.0000. Peptides of the group

NSGIIPSGIKPK	61.98	55.2091	1209.708	1209.644	2	2	distinct	0	0.8746
GLGLESVLWTDDTDDWK	69.85	53.8031	1948.905	1949.433	1	2	distinct	0	0.9876
ATMFYIGSNVLDWPLEAQR	80.71	53.2106	2210.083	2210.446	8	2	distinct	0	0.9956

The equivalent proteins include

gi|71015736|ref|XP_758836.1|	64931.43	hypothetical protein UM02689.1 [Ustilago maydis 521]

273. Group probability: 1.0000. Peptides of the group

HLAELTSSKHDDSTAAK	95.67	54.0907	1809.886	1810.383	3	2	distinct	1	0.9987
GWIVPNYNLSPDLEHIDILR	77.19	52.8137	2363.227	2363.693	2	2	distinct	0	0.9943

The equivalent proteins include

gi|71023961|ref|XP_762210.1|	65404.79	hypothetical protein UM06063.1 [Ustilago maydis 521]

274. Group probability: 1.0000. Peptides of the group

KQTLYAPWK	57.02	55.7655	1133.623	1134.307	10	+1,+2	distinct	1	0.9951
ADTHTASVQEANAAR	73.05	54.6754	1540.723	1540.908	2	+2,+3	distinct	0	0.9984

The equivalent proteins include

gi|71024175|ref|XP_762317.1|	13695.84	hypothetical protein UM06170.1 [Ustilago maydis 521]

275. Group probability: 1.0000. Peptides of the group

MHLIEASHTGK	60.42	55.1929	1222.613	1222.657	4	+1,+2	distinct	0	0.9987
IVDKLDVDHDGLVPLDDVLELAR	74.2	52.3674	2558.359	2559.023	1	2	distinct	1	0.9933

The equivalent proteins include

gi|71020171|ref|XP_760316.1|	85934.5	hypothetical protein UM04169.1 [Ustilago maydis 521]

276. Group probability: 1.0000. Peptides of the group

IQLEPQEGTTGLR	55.8	54.82	1440.757	1440.459	1	2	distinct	0	0.9499
YQIVVTSLAHPDKYIGYTDTVK	74.83	52.4863	2510.306	2510.963	14	+2,+3	distinct	1	0.9998

The equivalent proteins include

gi|71020123|ref|XP_760292.1|	18981.48	hypothetical protein UM04145.1 [Ustilago maydis 521]

277. Group probability: 1.0000. Peptides of the group

AEAAAQQLQAHHAASSATK	98.08	53.9306	1889.934	1890.373	3	2	distinct	0	0.999
ERAEAAAQQLQAHHAASSATK	73.97	53.2588	2175.078	2175.78	1	3	distinct	1	0.9909

The equivalent proteins include

gi|71003884|ref|XP_756608.1|	107292.86	hypothetical protein UM00461.1 [Ustilago maydis 521]

278. Group probability: 1.0000. Peptides of the group

FNMPAMSPTMTEGGIAAWK	92.07	53.5905	2038.931	2039.29	5	2	distinct	0	0.9984
ADVENYKPEAAVAAPAASSAAPAK	76.22	52.9439	2298.149	2298.447	2	2	distinct	0	0.9946

The equivalent proteins include

gi|71004150|ref|XP_756741.1|	52584.78	hypothetical protein UM00594.1 [Ustilago maydis 521]

279. Group probability: 1.0000. Peptides of the group

FLEQQNKVLQTK	86.32	54.9315	1474.814	1475.173	1	2	shared(2)	1	0.9933
THNLEPYFESFINNLR	77.07	53.7413	1992.969	1994.343	15	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|109096823|ref|XP_001098292.1|	65340.78	PREDICTED: similar to keratin 1 isoform 7 [Macaca mulatta]
gi|109096825|ref|XP_001098082.1|	64503.44	PREDICTED: similar to keratin 1 isoform 5 [Macaca mulatta]
gi|109096827|ref|XP_001097902.1|	63150.85	PREDICTED: similar to keratin 1 isoform 3 [Macaca mulatta]
gi|109096829|ref|XP_001097988.1|	62009.39	PREDICTED: similar to keratin 1 isoform 4 [Macaca mulatta]
gi|109096831|ref|XP_001098182.1|	63139.76	PREDICTED: similar to keratin 1 isoform 6 [Macaca mulatta]
gi|109096833|ref|XP_001097800.1|	61737.33	PREDICTED: similar to keratin 1 isoform 2 [Macaca mulatta]
gi|109096835|ref|XP_001097706.1|	59017.2	PREDICTED: similar to keratin 1 isoform 1 [Macaca mulatta]
gi|55638143|ref|XP_522394.1|	98632.68	PREDICTED: similar to keratin 1B [Pan troglodytes]

gi|7428712|pir||KRHU2	65568.53	keratin 1, type II, cytoskeletal - human
gi|7331218|gb|AAF60327.1|	66149.05	keratin 1 [Homo sapiens]
gi|11935049|gb|AAG41947.1|	66198.07	keratin 1 [Homo sapiens]

280. Group probability: 1.0000. Peptides of the group

APGFAHLAGADFMAR	73.85	55.1779	1530.74	1530.463	9	+1,+2,+3	distinct	0	1

The equivalent proteins include

gi|71021681|ref|XP_761071.1|	56332.48	hypothetical protein UM04924.1 [Ustilago maydis 521]

281. Group probability: 1.0000. Peptides of the group

FFGSSSGCGDTLYIYTFK	90.82	53.6848	2048.919	2048.999	6	2	distinct	0	0.9981
LQFDPAAGTVFGHIYGNIDPEVDFSGPVEVK	75.4	50.7647	3317.624	3318.344	2	3	distinct	0	0.9946

The equivalent proteins include

gi|71003746|ref|XP_756539.1|	14426.1	hypothetical protein UM00392.1 [Ustilago maydis 521]

282. Group probability: 1.0000. Peptides of the group

HGLLVPSTTTDQELQHLR	92.09	53.5329	2044.07	2044.467	5	+2,+3	distinct	0	1

The equivalent proteins include

gi|71024721|ref|XP_762590.1|	26488.42	hypothetical protein UM06443.1 [Ustilago maydis 521]

283. Group probability: 1.0000. Peptides of the group

IREDLILPFLDIELK	90.59	54.0446	1826.055	1827.133	5	2	distinct	1	0.9978
WEVFNYPEGGGSGLAMYNTTESITGFAHSSFK	74.61	50.3861	3483.572	3484.053	1	3	distinct	0	0.9945

The equivalent proteins include

gi|71024057|ref|XP_762258.1|	48323.52	hypothetical protein UM06111.1 [Ustilago maydis 521]

284. Group probability: 1.0000. Peptides of the group

VLEYCSHHR	53.51	55.6138	1199.551	1200.633	1	2	distinct	0	0.9288
KLFNIQNDFSPEEEAQIR	75.79	53.2803	2177.075	2178.063	1	2	distinct	1	0.993
QMLEDIGDTEQPIPLVNVSSNVLKK	61.06	51.9441	2766.447	2767.395	1	3	distinct	1	0.9761

The equivalent proteins include

gi|71021055|ref|XP_760758.1|	18270.08	hypothetical protein UM04611.1 [Ustilago maydis 521]

285. Group probability: 1.0000. Peptides of the group

HNHAAGAGFSSGLDSSR	85.92	54.3724	1669.756	1670.701	2	+2,+3	distinct	0	1

The equivalent proteins include

gi|71024661|ref|XP_762560.1|	32546.16	hypothetical protein UM06413.1 [Ustilago maydis 521]

286. Group probability: 1.0000. Peptides of the group

AAIIAVENEAEEKK	61.38	54.7928	1513.799	1514.318	1	2	distinct	1	0.9704
KVWLDPAEQNDIGNANSR	85.02	53.5119	2025.987	2026.307	2	+2,+3	distinct	1	0.9996

The equivalent proteins include

gi|71006230|ref|XP_757781.1|	22505.34	hypothetical protein UM01634.1 [Ustilago maydis 521]

287. Group probability: 1.0000. Peptides of the group

AFPLADATLTNQILDLIQQASHYK	108.35	52.1713	2670.402	2671.503	4	+2,+3	distinct	0	1

The equivalent proteins include

gi|71024555|ref|XP_762507.1|	13900.42	hypothetical protein UM06360.1 [Ustilago maydis 521]

288. Group probability: 1.0000. Peptides of the group

NLHNTLLSEDKFK	72.22	54.7309	1557.815	1558.402	4	2	distinct	1	0.9882
CVLSQAGNCIEMSNDHKPTLDSER	55.79	51.906	2760.227	2760.995	2	3	distinct	0	0.9607
LVESPHTDAKPASSNQESDKMEVDDDTNTSAK	55.16	50.2152	3445.543	3446.774	1	3	distinct	1	0.9698

The equivalent proteins include

gi|71020473|ref|XP_760467.1|	52578.22	hypothetical protein UM04320.1 [Ustilago maydis 521]

289. Group probability: 1.0000. Peptides of the group

AQAVLHKPEVK	73.73	55.6058	1218.708	1219.001	2	2	distinct	0	0.9887
TVADVHEEAKR	57.29	55.2061	1253.636	1254.452	2	2	distinct	1	0.9524
KQGGHTGTSAPLPSTGAK	61.03	54.2635	1693.875	1694.923	1	2	distinct	1	0.9738

The equivalent proteins include

gi|71023827|ref|XP_762143.1|	97607.33	hypothetical protein UM05996.1 [Ustilago maydis 521]

290. Group probability: 1.0000. Peptides of the group

HNCVSYTQFHCMSEK	81.86	53.7947	1926.781	1927.396	1	2	distinct	0	0.9954
FSDYYAQTHAALAGPVLLR	84.29	53.3887	2092.074	2092.963	2	2	distinct	0	0.9968

The equivalent proteins include

gi|71023765|ref|XP_762112.1|	17120.33	hypothetical protein UM05965.1 [Ustilago maydis 521]

291. Group probability: 1.0000. Peptides of the group

DLGSGPEDKGDVPVQR	86.64		54.3409	1667.811	1667.75	2	+2,+3	distinct	1	0.9998
EINVVPVEGAADEAAKK	48.76		54.1762	1738.91	1739.313	1	2	distinct	1	0.9205

The equivalent proteins include

gi|71018449|ref|XP_759455.1|	57205.09	hypothetical protein UM03308.1 [Ustilago maydis 521]

292. Group probability: 1.0000. Peptides of the group

DGEKEEWVPVTSVGR	43.41		54.3793	1686.821	1687.295	1	3	distinct	1	0.8314
GYWGNALGEPHTVPMK	59.98		54.1943	1755.84	1756.416	1	2	distinct	0	0.9692
EIAPPATPYVEFASHLAR	84.33		53.7373	1968.01	1969.314	4	2	distinct	0	0.9966

The equivalent proteins include

gi|71022111|ref|XP_761286.1|	28293.07	hypothetical protein UM05139.1 [Ustilago maydis 521]

293. Group probability: 1.0000. Peptides of the group

ESAYIHAVPATPVASVAELK	57.72		53.8591	2052.089	2052.526	1	2	distinct	0	0.9676
NAPNVIDNFVNLLGRPFSSLSESEK	57.6		51.9633	2746.392	2747.673	1	3	distinct	0	0.9676
DFLSGVPIAGAVLSVPQWFPEAQIAALKK	63.27		51.3082	3051.68	3053.147	2	3	distinct	1	0.9831

The equivalent proteins include

gi|71022549|ref|XP_761504.1|	59863.96	hypothetical protein UM05357.1 [Ustilago maydis 521]

294. Group probability: 1.0000. Peptides of the group

TAVHHYQGTNVALGTAAGK	102.51		53.9066	1894.965	1895.783	10	+2,+3	distinct	0	1

The equivalent proteins include

gi|71021489|ref|XP_760975.1|	24059.4	hypothetical protein UM04828.1 [Ustilago maydis 521]

295. Group probability: 1.0000. Peptides of the group

VVGTEGHEEKRPDVK	61.22		54.2845	1678.864	1679.683	2	2	distinct	1	0.9713
IIMLHGDIIENHGQEAWK	49.93		53.2886	2103.057	2104.376	1	3	distinct	0	0.9163
SGPSGTEPTKTPVYIQEVTPEITTFDYPFSR	71.01		50.2992	3443.677	3444.444	2	3	distinct	1	0.9922

The equivalent proteins include

gi|71006182|ref|XP_757757.1|	31498.91	hypothetical protein UM01610.1 [Ustilago maydis 521]

296. Group probability: 1.0000. Peptides of the group

HVPYFNAPIYLENK	79.63		54.4282	1703.867	1704.768	6	+2,+3	distinct	0	0.9998
SQIGKVDEILGPINEVFFTVK	69.89		52.834	2332.268	2333.763	2	2	distinct	1	0.8974

The equivalent proteins include

gi|71020979|ref|XP_760720.1|	22476.29	hypothetical protein UM04573.1 [Ustilago maydis 521]

297. Group probability: 1.0000. Peptides of the group

EAPEYGFGDVVNKPK	94.96		54.527	1648.81	1649.35	1	2	distinct	0	0.9985
IVIATGGRPVIPSDDKIPGASLGIDSDGFFELK	64.48		50.4704	3383.798	3384.844	1	3	distinct	1	0.9871

The equivalent proteins include

gi|71005242|ref|XP_757287.1|	131005.94	hypothetical protein UM01140.1 [Ustilago maydis 521]

298. Group probability: 1.0000. Peptides of the group

LPQTAQLDALLTIIR	96.94		54.507	1664.982	1665.108	2	2	distinct	0	0.9987
ILFLNLIASPEGLNNMYSK	65.88		53.2313	2136.129	2136.389	1	2	distinct	0	0.9838

The equivalent proteins include

gi|71019579|ref|XP_760020.1|	25527.32	hypothetical protein UM03873.1 [Ustilago maydis 521]

299. Group probability: 1.0000. Peptides of the group

CFAFWQEFQK	62.76		55.1578	1389.618	1390.478	2	2	distinct	0	0.9695
EDYLECLHHTK	60.91		54.925	1443.645	1444.153	3	2	distinct	0	0.9656
CYASADTPSDCILAK	65.27		54.3724	1670.728	1670.967	1	2	distinct	0	0.9798

The equivalent proteins include

gi|71023937|ref|XP_762198.1|	12172.75	hypothetical protein UM06051.1 [Ustilago maydis 521]

300. Group probability: 1.0000. Peptides of the group

GPQLFHADPSGTFVR	64.2		54.6964	1627.811	1628.254	5	+2,+3	distinct	0	0.9966
FGESTAGDEAMMSRPFGVALLIAGIDEK	74.21		51.5326	2911.409	2912.329	3	3	distinct	0	0.9933

The equivalent proteins include

gi|71023807|ref|XP_762133.1|	27562.97	hypothetical protein UM05986.1 [Ustilago maydis 521]

301. Group probability: 1.0000. Peptides of the group

ILTDDKTVADCK	48.41		55.0644	1377.681	1377.895	1	2	distinct	1	0.9003
IQNEQGHAPELQK	62.78		54.855	1490.748	1491.168	1	2	distinct	0	0.9728
AVEYLMTGIPEHLVNPPAAAAEAAAR	70.19		52.2432	2661.358	2661.533	5	2	distinct	0	0.9915

The equivalent proteins include

gi|71022291|ref|XP_761375.1|	44823.1	hypothetical protein UM05228.1 [Ustilago maydis 521]

302. Group probability: 1.0000. Peptides of the group

GPVKADDILALLESER	126.09	54.2348	1724.931	1725.873	4	+2,+3	distinct	1	1

The equivalent proteins include

gi|71004506|ref|XP_756919.1|	35498.98	hypothetical protein UM00772.1 [Ustilago maydis 521]

303. Group probability: 1.0000. Peptides of the group

EGINCAVLLGWHER	64.25	54.3166	1652.809	1654.043	1	2	distinct	0	0.9772
HVTLQSLLEIVNSTK	98.98	54.2393	1680.941	1681.545	3	2	distinct	0	0.999

The equivalent proteins include

gi|71012871|ref|XP_758535.1|	17346.86	hypothetical protein UM02388.1 [Ustilago maydis 521]

304. Group probability: 1.0000. Peptides of the group

MAANLASHMR	58.68	55.8688	1100.522	1100.824	1	2	distinct	0	0.9558
VYEWLEEFYPAPSALGYGK	76.8	53.1843	2218.062	2218.185	1	2	distinct	0	0.9938
CDLIFTSLSDDDAAEQIYEALLQAEEKR	44.91	51.0344	3242.529	3242.126	1	3	distinct	1	0.913

The equivalent proteins include

gi|71014632|ref|XP_758739.1|	39434.11	hypothetical protein UM02592.1 [Ustilago maydis 521]

305. Group probability: 1.0000. Peptides of the group

ILTDYGFEGHPLR	51.49	54.8581	1516.767	1517.212	1	2	distinct	0	0.9268
TYADEVHPVPSATAVFR	62.96	54.4177	1858.921	1859.245	2	2	distinct	0	0.977
NFEANSPWEQVGEGESYKPNAFK	65.63	52.8738	2627.193	2627.986	2	2	distinct	0	0.9857

The equivalent proteins include

gi|71006324|ref|XP_757828.1|	44332.49	hypothetical protein UM01681.1 [Ustilago maydis 521]

306. Group probability: 1.0000. Peptides of the group

SFALNHGFIPK	45.81	55.6691	1229.656	1230.113	1	2	distinct	0	0.8686
KTNATVSSVPSHK	73.35	55.0763	1354.72	1355.095	4	2	distinct	1	0.9892
IAFQEFHSQLGVR	67.56	55.1768	1530.794	1531.182	4	2	distinct	0	0.982

The equivalent proteins include

gi|71020967|ref|XP_760714.1|	52424.35	hypothetical protein UM04567.1 [Ustilago maydis 521]

307. Group probability: 1.0000. Peptides of the group

MKETAEAYLGHK	60.15	55.0504	1376.676	1376.99	2	+1,+2	distinct	1	0.9957
AKFEELNMDLFR	62.36	54.6765	1511.744	1512.824	2	2	shared(2)	1	0.9709
VTHAVVTVPAYFNDAQR	63.11	53.9084	1886.964	1887.089	2	+2,+3	shared(2)	0	0.9983

The equivalent proteins include

gi|57230826|gb|AAW47135.1|	88461.59	heat shock protein, putative [Cryptococcus neoformans var. neoformans JEC21]
gi|57230825|gb|AAW47134.1|	82198.94	heat shock protein, putative [Cryptococcus neoformans var. neoformans JEC21]

308. Group probability: 1.0000. Peptides of the group

DAAPSGEYRPR	45.95	55.6815	1217.579	1218.001	1	2	distinct	0	0.8702
EFLHLPAEIVPATHK	59.24	54.3418	1700.925	1701.461	2	2	distinct	0	0.9658
NFTVQHPELEIPNLEVVK	76.97	53.3143	2105.116	2105.636	3	2	distinct	0	0.9936

The equivalent proteins include

gi|71008553|ref|XP_758226.1|	17634.06	hypothetical protein UM02079.1 [Ustilago maydis 521]

309. Group probability: 1.0000. Peptides of the group

LPANEFVDLWVR	70.93	54.9614	1457.767	1458.227	1	2	distinct	0	0.9862
FPAAANVCGPVVPGTVVPNGAR	42.87	53.3016	2149.11	2149.098	1	2	distinct	0	0.8903
GEDNVRPPPDQVLQDIADYVHNYK	63.93	52.0077	2781.336	2782.156	4	3	distinct	0	0.9807

The equivalent proteins include

gi|71024523|ref|XP_762491.1|	60476.19	hypothetical protein UM06344.1 [Ustilago maydis 521]

310. Group probability: 1.0000. Peptides of the group

SVIVSLHPHNDR	62.33	55.2908	1372.721	1372.777	1	2	distinct	0	0.9704
NVILHMYNASSPLFR	63.57	54.1824	1760.903	1762.023	3	2	distinct	0	0.9767
HPYAGDLVFTAFSGSHQDAIK	67.89	53.2535	2260.091	2261.113	1	2	distinct	0	0.9574

The equivalent proteins include

gi|71020145|ref|XP_760303.1|	70018.62	hypothetical protein UM04156.1 [Ustilago maydis 521]

311. Group probability: 1.0000. Peptides of the group

AAAFSQIGQHDSAIDDAK	82.86	54.2145	1843.87	1844.774	2	+2,+3	distinct	0	0.9997
TTIGHSSETISLPTTPFPLASLITLIANK	42.54	51.3198	3022.659	3023.529	2	3	distinct	0	0.896

The equivalent proteins include

gi|71022553|ref|XP_761506.1|	79738.85	hypothetical protein UM05359.1 [Ustilago maydis 521]								
312. Group probability: 1.0000. Peptides of the group										
TSTPAAHFPYYAQPPAAR	52.84		53.7888	1944.948	1945.343	1	2	distinct	0	0.9468
NPFGQISASGTFKPAGTPGGGR	102.43		53.3345	2103.05	2103.613	2	2	distinct	0	0.9994
The equivalent proteins include										
gi|71021497|ref|XP_760979.1|	99114.25	hypothetical protein UM04832.1 [Ustilago maydis 521]								
313. Group probability: 1.0000. Peptides of the group										
MIGTNTDYLGIAHAVLR	79.64		54.1902	1843.961	1843.894	1	2	distinct	0	0.9947
GVIAPPHPTPEQIQASAR	77.73		53.8962	1867.99	1868.348	5	2	distinct	0	0.994
The equivalent proteins include										
gi|71022659|ref|XP_761559.1|	47562.12	hypothetical protein UM05412.1 [Ustilago maydis 521]								
314. Group probability: 1.0000. Peptides of the group										
TLVPAVVSLNVAGTTCHLYGK	54.67		53.1803	2199.172	2200.429	1	2	distinct	0	0.9597
SAADFSHPQPLVGIIMGSDSDLPVMMAAAEILK	95.78		50.3596	3410.692	3411.458	1	3	distinct	0	0.9992
The equivalent proteins include										
gi|71004948|ref|XP_757140.1|	80300.92	hypothetical protein UM00993.1 [Ustilago maydis 521]								
315. Group probability: 1.0000. Peptides of the group										
ALHEAAIYAQDRK	68.3		54.9533	1484.774	1485.733	3	2	distinct	1	0.9832
TAMGAFDITRPLVAAGAVGLAQR	61.61		53.024	2285.231	2286.263	4	+2,+3	distinct	0	0.9979
The equivalent proteins include										
gi|71005060|ref|XP_757196.1|	46345.44	hypothetical protein UM01049.1 [Ustilago maydis 521]								
316. Group probability: 1.0000. Peptides of the group										
HHLTASDVAK	56.63		56.0744	1077.557	1077.443	4	+1,+2	distinct	0	0.9942
MVNELLKDEIAQLHAFSQK	78.52		53.1443	2213.151	2213.852	2	3	distinct	1	0.9934
The equivalent proteins include										
gi|71019343|ref|XP_759902.1|	27404.59	hypothetical protein UM03755.1 [Ustilago maydis 521]								
317. Group probability: 1.0000. Peptides of the group										
FELDHAAHH	49.58		56.0024	1075.484	1075.982	1	2	distinct	0	0.8987
IAACDGGGGPLGHPK	81.52		55.0205	1405.677	1406.273	9	+2,+3	distinct	0	0.9996
The equivalent proteins include										
gi|71023385|ref|XP_761922.1|	23303.76	hypothetical protein UM05775.1 [Ustilago maydis 521]								
318. Group probability: 1.0000. Peptides of the group										
HSKDPNTLQR	47.5		55.2611	1194.611	1195.383	1	2	distinct	1	0.8836
VLDKETHSGASVK	71.65		55.1138	1369.72	1369.374	14	+1,+2	distinct	1	0.9997
The equivalent proteins include										
gi|71022569|ref|XP_761514.1|	26404.98	hypothetical protein UM05367.1 [Ustilago maydis 521]								
319. Group probability: 1.0000. Peptides of the group										
SWVYNVAADVADGEATAETLAIR	132.17		52.6565	2421.181	2421.743	3	2	distinct	0	1
The equivalent proteins include										
gi|71014384|ref|XP_758706.1|	22429.97	hypothetical protein UM02559.1 [Ustilago maydis 521]								
320. Group probability: 1.0000. Peptides of the group										
AAGSEPSHILK	47.41		55.0903	1108.588	1109.134	1	2	distinct	0	0.8871
LVEGGIEEQTEQALNNLFAVVK	107.61		52.8056	2400.254	2401.583	4	2	distinct	0	0.9996
The equivalent proteins include										
gi|71003063|ref|XP_756212.1|	26553.65	hypothetical protein UM00065.1 [Ustilago maydis 521]								
321. Group probability: 1.0000. Peptides of the group										
LEATLLQHVLR	79.19		55.3892	1291.761	1292.12	1	2	distinct	0	0.993
FTATNPQPNDIPTVLGQHIVASR	48.3		52.4524	2475.287	2476.683	2	+2,+3	distinct	0	0.994
The equivalent proteins include										
gi|71003221|ref|XP_756291.1|	50132.05	hypothetical protein UM00144.1 [Ustilago maydis 521]								
322. Group probability: 1.0000. Peptides of the group										
SQAGDLLAMHYTGTLADGK	72.04		53.8854	1947.936	1948.505	1	2	distinct	0	0.9904
YRPEVCDDKSQAGDLLAMHYTGTLADGK	78.59		51.2668	3110.444	3111.206	1	3	distinct	1	0.9954
The equivalent proteins include										
gi|71020743|ref|XP_760602.1|	21266.6	hypothetical protein UM04455.1 [Ustilago maydis 521]								
323. Group probability: 1.0000. Peptides of the group										
ALAPLSQGVIEGIHFK	102.15		54.2847	1678.941	1679.863	10	+2,+3	distinct	0	1

The equivalent proteins include

gi|71005006|ref|XP_757169.1|	17433.72	hypothetical protein UM01022.1 [Ustilago maydis 521]

324. Group probability: 1.0000. Peptides of the group

LHDHSLGIVINK	84.28		55.4102	1344.751	1345.296	4	+1,+2	distinct	0	0.9995
LLAIAPGTNERPQR	46.79		54.6917	1534.858	1535.039	1	2	distinct	0	0.8937

The equivalent proteins include

gi|71019553|ref|XP_760007.1|	55814	hypothetical protein UM03860.1 [Ustilago maydis 521]

325. Group probability: 1.0000. Peptides of the group

VRPEQGLLALR	51.62		55.4474	1250.746	1251.379	1	2	distinct	0	0.9214
YSLNQPDLADKVEAAVR	58.8		53.8998	1887.969	1889.269	1	3	distinct	1	0.9597
SYDFGGCAIDSTGKPLPDDTLAACK	66.16		52.3006	2658.194	2659.606	1	3	distinct	0	0.9846

The equivalent proteins include

gi|71005452|ref|XP_757392.1|	40357.99	hypothetical protein UM01245.1 [Ustilago maydis 521]

326. Group probability: 1.0000. Peptides of the group

VLNDWHSYYTK	71.65		54.8502	1424.672	1424.945	1	2	distinct	0	0.9866
QYDGTDESKPVYVAVK	44.16		54.2848	1797.878	1798.039	1	2	distinct	0	0.8764
GLGMSSLKPEDAVADYSTLDDK	57.63		52.9957	2311.089	2311.563	1	2	distinct	0	0.9701

The equivalent proteins include

gi|71017849|ref|XP_759155.1|	13111.45	hypothetical protein UM03008.1 [Ustilago maydis 521]

327. Group probability: 0.9999. Peptides of the group

EGILSHHEVMYR	55.21		54.9545	1469.708	1470.303	1	2	distinct	0	0.9452
GFFLTGDGVDLNQALINYGLDFLR	96.12		52.3355	2657.349	2658.213	3	2	distinct	0	0.9991

The equivalent proteins include

gi|71004692|ref|XP_757012.1|	50095.19	hypothetical protein UM00865.1 [Ustilago maydis 521]

328. Group probability: 0.9999. Peptides of the group

TSAGNHVAFLAR	60.59		55.4597	1242.647	1242.874	1	2	distinct	0	0.9655
DHAILPSNVPNLANIAALK	93.02		53.6647	1970.095	1970.257	1	2	distinct	0	0.9985

The equivalent proteins include

gi|71004102|ref|XP_756717.1|	40892.01	hypothetical protein UM00570.1 [Ustilago maydis 521]

329. Group probability: 0.9999. Peptides of the group

KHSALSPESK	59.58		55.2622	1082.572	1082.553	3	1	distinct	1	0.9596
GFEEVFDADHSTK	77.99		54.7466	1480.647	1481.157	1	2	distinct	0	0.981
LDQGVDAVVDLILSAR	50.93		54.2636	1682.92	1684.343	1	2	distinct	0	0.9318

The equivalent proteins include

gi|71024677|ref|XP_762568.1|	66847.8	hypothetical protein UM06421.1 [Ustilago maydis 521]

330. Group probability: 0.9999. Peptides of the group

NHLSALYDTLLEQNLLR	105.62		53.5076	2012.069	2013.166	4	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71015635|ref|XP_758831.1|	47179.61	hypothetical protein UM02684.1 [Ustilago maydis 521]

331. Group probability: 0.9999. Peptides of the group

VIRPAFLTTQK	54.45		55.451	1272.755	1272.956	2	2	distinct	0	0.9387
TVHQANASTPAAPAETH	99.15		54.3336	1701.807	1702.198	1	2	distinct	0	0.999

The equivalent proteins include

gi|71018871|ref|XP_759666.1|	29177.66	hypothetical protein UM03519.1 [Ustilago maydis 521]

332. Group probability: 0.9999. Peptides of the group

APFFTPAGFFPLWAK	70.98		54.2925	1695.881	1696.903	12	2	distinct	0	0.9878
TFVDKPTSKPESEVVDNFNR	57.74		52.9724	2308.133	2309.027	3	+2,+3	distinct	0	0.9951

The equivalent proteins include

gi|71010210|ref|XP_758359.1|	86613.92	hypothetical protein UM02212.1 [Ustilago maydis 521]

333. Group probability: 0.9999. Peptides of the group

ILSLLSQAGERPVVMGR	77.71		54.0155	1825.024	1825.768	2	+2,+3	distinct	0	0.9991
SGLSLSAPCPWSAEKDGSVPAATLGDALIAPTR	45.47		50.9653	3294.655	3294.724	1	3	distinct	1	0.9307

The equivalent proteins include

gi|71004586|ref|XP_756959.1|	87888.22	hypothetical protein UM00812.1 [Ustilago maydis 521]

334. Group probability: 0.9999. Peptides of the group

LTLLEAADLVSHLK	97.75		54.5752	1521.877	1522.377	7	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71021953|ref|XP_761207.1|	19125.26	hypothetical protein UM05060.1 [Ustilago maydis 521]

335. Group probability: 0.9999. Peptides of the group

EAILAHPAEAR	47.61	55.6231	1176.625	1176.955	1	2	distinct	0	0.8879
YIQSHHPETAK	59.95	55.2862	1309.641	1309.934	6	2	distinct	0	0.9623
KPATTPITTTAAVAK	69.06	54.8467	1469.845	1470.172	1	2	distinct	0	0.9854

The equivalent proteins include

gi|71018797|ref|XP_759629.1|	40311.52	hypothetical protein UM03482.1 [Ustilago maydis 521]

336. Group probability: 0.9999. Peptides of the group

AMPTFVFFK	46.69	56.059	1086.557	1087.506	1	2	distinct	0	0.8693
LGFYKVDVDAQDK	82.69	54.6905	1496.751	1496.98	3	+2,+3	distinct	1	0.9995

The equivalent proteins include

gi|71024859|ref|XP_762659.1|	18123.18	hypothetical protein UM06512.1 [Ustilago maydis 521]

337. Group probability: 0.9999. Peptides of the group

SPYDWQHAAK	60.2	55.6381	1201.552	1202.277	1	2	distinct	0	0.9615
VVSPPSSICDPSVK	62.68	54.9865	1470.739	1471.32	2	2	distinct	0	0.9735
YIPLLANQIVQDNKK	65.3	54.181	1755.988	1756.765	1	2	distinct	1	0.9312

The equivalent proteins include

gi|71019783|ref|XP_760122.1|	60237.46	hypothetical protein UM03975.1 [Ustilago maydis 521]

338. Group probability: 0.9999. Peptides of the group

AIQSEPELLEALYER	76.39	54.2533	1759.899	1760.123	1	2	distinct	0	0.9924
STNITGLNVSGSPLSELESR	71.64	53.4622	2060.038	2060.659	1	2	distinct	0	0.9905

The equivalent proteins include

gi|71019695|ref|XP_760078.1|	15585.2	hypothetical protein UM03931.1 [Ustilago maydis 521]

339. Group probability: 0.9999. Peptides of the group

APPAPSSAVAMAAAPR	94.86	55.0345	1463.755	1464.081	2	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71005066|ref|XP_757199.1|	9420.84	hypothetical protein UM01052.1 [Ustilago maydis 521]

340. Group probability: 0.9999. Peptides of the group

KHIIEAATASLER	73.5	54.778	1437.794	1438.674	1	2	distinct	1	0.9894
SHSYGTTIWSPLASGLLTGK	74.85	53.4502	2075.069	2076.033	1	2	distinct	0	0.9929

The equivalent proteins include

gi|71024437|ref|XP_762448.1|	52194.17	hypothetical protein UM06301.1 [Ustilago maydis 521]

341. Group probability: 0.9999. Peptides of the group

NLTELSTLGHFLK	54.49	54.918	1471.803	1472.446	2	2	distinct	0	0.9437
SIVWNYFDQAITTFK	95	54.0264	1831.914	1832.371	2	2	distinct	0	0.9985

The equivalent proteins include

gi|71023157|ref|XP_761808.1|	22836.82	hypothetical protein UM05661.1 [Ustilago maydis 521]

342. Group probability: 0.9999. Peptides of the group

GLFATHSSAVAQYLR	81.15	54.5268	1619.842	1620.826	1	2	distinct	0	0.995
VSAPAFDSAPAASTPALTPAAPKPPAASASR	62.55	51.5978	2874.487	2875.65	1	3	distinct	0	0.9832

The equivalent proteins include

gi|71022515|ref|XP_761487.1|	65958.63	hypothetical protein UM05340.1 [Ustilago maydis 521]

343. Group probability: 0.9999. Peptides of the group

VPAALNPTEEDISLLLAAQTHIGTK	75.18	52.2853	2601.401	2602.107	10	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71022107|ref|XP_761284.1|	30046.26	hypothetical protein UM05137.1 [Ustilago maydis 521]

344. Group probability: 0.9999. Peptides of the group

LHDWPEQYYGNALAR	62.94	54.0412	1831.864	1831.887	3	+2,+3	distinct	0	0.9958
SLVQPSTCTYDYESALALVTK	62.36	52.9002	2345.146	2344.833	1	2	distinct	0	0.9796

The equivalent proteins include

gi|71023725|ref|XP_762092.1|	65169.45	hypothetical protein UM05945.1 [Ustilago maydis 521]

345. Group probability: 0.9999. Peptides of the group

YSALVGGIGYGILHR	85.12	54.7185	1574.857	1575.629	11	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|71017983|ref|XP_759222.1|	9014.8	hypothetical protein UM03075.1 [Ustilago maydis 521]

346. Group probability: 0.9999. Peptides of the group

ASLPIAISASSLLSADKLGDACGK	59.1	52.9154	2344.231	2345.307	2	+2,+3	distinct	1	0.9969
LANNYENPESIESVTWGFIDGQGL	55.96	52.1809	2652.234	2653.033	1	2	distinct	0	0.9683

The equivalent proteins include

gi|71005388|ref|XP_757360.1|	31400.14	hypothetical protein UM01213.1 [Ustilago maydis 521]							
347. Group probability: 0.9999. Peptides of the group									
GVEIIHHVASPYQLNVQDAER	73.48	52.7827	2374.203	2374.493	3	+2,+3	distinct	0	0.9999
The equivalent proteins include									
gi|71019947|ref|XP_760204.1|	38745.03	hypothetical protein UM04057.1 [Ustilago maydis 521]							
348. Group probability: 0.9999. Peptides of the group									
HGAIPLHLTDDDPVK	82.9	54.7126	1626.837	1627.963	1	2	distinct	0	0.9957
YDFVLGHEFVGEIHEAGEGIK	60.05	52.9111	2345.133	2345.763	1	2	distinct	0	0.975
The equivalent proteins include									
gi|71023123|ref|XP_761791.1|	39194.01	hypothetical protein UM05644.1 [Ustilago maydis 521]							
349. Group probability: 0.9999. Peptides of the group									
VFGADSGLDGHIVLVGERPEWK	74.61	52.8233	2380.217	2381.703	5	+2,+3	distinct	0	0.9999
The equivalent proteins include									
gi|71016739|ref|XP_758915.1|	12378.02	hypothetical protein UM02768.1 [Ustilago maydis 521]							
350. Group probability: 0.9999. Peptides of the group									
GLNERPTATK	46.89	55.8174	1085.583	1085.841	1	2	distinct	0	0.8758
KEIENHFEDFGLER	53.05	54.1824	1761.832	1762.048	1	2	distinct	1	0.9393
FIPALINSLIHPVEEVPK	67.18	53.6103	2015.145	2015.586	6	2	distinct	0	0.9849
The equivalent proteins include									
gi|71020137|ref|XP_760299.1|	117438.26	hypothetical protein UM04152.1 [Ustilago maydis 521]							
351. Group probability: 0.9999. Peptides of the group									
HPVSRPDEDLPVR	46.73	54.8185	1515.779	1516.135	1	2	distinct	0	0.889
NPSVEDFVACTLAAHR	98.88	54.7804	1785.847	1786.302	1	2	distinct	0	0.999
The equivalent proteins include									
gi|71005246|ref|XP_757289.1|	37438.03	hypothetical protein UM01142.1 [Ustilago maydis 521]							
352. Group probability: 0.9999. Peptides of the group									
LAWGYANPSRPK	65.7	55.3479	1358.709	1359.174	1	2	distinct	0	0.978
LVTASEDDSSPVIMLWDLR	78.07	53.2537	2146.062	2147.455	1	2	distinct	0	0.9944
The equivalent proteins include									
gi|71023329|ref|XP_761894.1|	149537	hypothetical protein UM05747.1 [Ustilago maydis 521]							
353. Group probability: 0.9999. Peptides of the group									
SPMALAVFEHTANMAGVR	91.7	53.8291	1900.929	1901.37	5	+2,+3	distinct	0	0.9999
The equivalent proteins include									
gi|71008429|ref|XP_758216.1|	19237.34	hypothetical protein UM02069.1 [Ustilago maydis 521]							
354. Group probability: 0.9999. Peptides of the group									
GPTHFGWDPILEIK	62.64	54.5263	1608.83	1609.046	2	+2,+3	distinct	0	0.9966
ALGGACITEDTALGFHALGGLPGPYIK	52.55	52.0099	2698.379	2698.733	1	2	distinct	0	0.9617
The equivalent proteins include									
gi|71007798|ref|XP_758154.1|	21232.66	hypothetical protein UM02007.1 [Ustilago maydis 521]							
355. Group probability: 0.9999. Peptides of the group									
TAADLGWDAIHFFGDK	96.25	54.1609	1762.831	1763.329	1	2	distinct	0	0.9987
TIGHTVQNPQDTMNQLR	45.7	53.6833	1951.953	1952.55	1	2	distinct	0	0.897
The equivalent proteins include									
gi|71021239|ref|XP_760850.1|	30875.48	hypothetical protein UM04703.1 [Ustilago maydis 521]							
356. Group probability: 0.9999. Peptides of the group									
RNQHYGNEAEAMK	90.09	55.1563	1546.695	1547.096	1	2	distinct	1	0.9975
TPFVHGTSLNPVGDDELFDLDGVAPSASSSGSR	48.36	50.6794	3330.564	3330.995	1	3	distinct	0	0.9465
The equivalent proteins include									
gi|71018753|ref|XP_759607.1|	30106.32	hypothetical protein UM03460.1 [Ustilago maydis 521]							
357. Group probability: 0.9999. Peptides of the group									
KGLTADSTEVPVIDTLAAGYGK	95.86	53.2236	2205.153	2205.552	2	+2,+3	distinct	1	0.9999
The equivalent proteins include									
gi|71018475|ref|XP_759468.1|	20721.02	hypothetical protein UM03321.1 [Ustilago maydis 521]							
358. Group probability: 0.9999. Peptides of the group									
LGEDNINVVEGNEQFISASK	73.48	53.8609	2162.049	2162.613	1	2	shared(2)	0	0.9919
SIVHPSYNSNTLNNDIMLIK (00000000000000000010000)	71.08	53.2362	2272.152	2272.633	13	+2,+3	distinct	0	0.9985
The equivalent proteins include									

gi|1421532|pdb|1TGB|	24658.8	Trypsinogen-Ca From Peg
gi|230765|pdb|2TLD|E	23555.36	Chain E, Bovine Trypsin (E.C.3.4.21.4) Complex With A Modified SSI (Streptomyces Subtilisin Inhibit
gi|2392803|pdb|5PTP|	23998.54	Structure Of Hydrolase (Serine Proteinase)
gi|5542503|pdb|1ZZZ|A	25388.25	Chain A, Trypsin Inhibitors With Rigid Tripeptidyl Aldehydes
gi|13096615|pdb|1G3E|A	24562.78	Chain A, Bovine Beta-Trypsin Bound To Para-Amidino Schiff-Base Copper (Ii) Chelate
gi|34811715|pdb|1HJ9|A	23972.49	Chain A, Atomic Resolution Structures Of Trypsin Provide Insight Into Structural Radiation Damage
gi|34810822|pdb|1OPH|B	26076.68	Chain B, Non-Covalent Complex Between Alpha-1-Pi-Pittsburgh And S195a Trypsin
gi|49259462|pdb|1V2P|T	23979.59	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssyi)bt.A4
gi|49259463|pdb|1V2Q|T	24002.6	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Sswi)bt.B4
gi|49259464|pdb|1V2R|T	23972.63	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssri)bt.B4
gi|49259466|pdb|1V2T|T	24005.6	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssfi.Glu)bt.B4
gi|49259469|pdb|1V2W|T	23887.56	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssai)bt.B4
gi|71042446|pdb|1ZR0|C	23960.59	Chain C, Crystal Structure Of Kunitz Domain 1 Of Tissue Factor Pathway Inhibitor-2 With Bovine Tryp
gi|88193016|pdb|2FI4|E	23971.53	Chain E, Crystal Structure Of A Bpti Variant (Cys14->ser) In Complex With Trypsin
gi|88193018|pdb|2FI5|E	24086.56	Chain E, Crystal Structure Of A Bpti Variant (Cys38->ser) In Complex With Trypsin
gi|2507249|sp|P00760|TRY1_BOVIN	26092.68	Cationic trypsin precursor (Beta-trypsin) [Contains: Alpha-trypsin chain 1; Alpha-trypsin chain 2]
gi|76615876|ref|XP_883769.1|	26246.67	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 2 [Bos taurus]
gi|76615878|ref|XP_883804.1|	26537.88	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 3 [Bos taurus]
gi|76615880|ref|XP_871686.1|	26438.81	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 1 [Bos taurus]
gi|76615882|ref|XP_883865.1|	26551.93	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 2 [Bos taurus]
gi|61873128|ref|XP_584594.1|	26452.86	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 1 [Bos taurus]
gi|67549|pir||TRBOTR	24661.84	trypsin (EC 3.4.21.4) precursor - bovine
gi|90109720|pdb|2FX6|A	23974.57	Chain A, Bovine Trypsin Complexed With 2-Aminobenzamidazole

359. Group probability: 0.9999. Peptides of the group

MTGSHMGTFGSMASGAILAQAGK	118.73	53.2194	2210.028	2210.333	4	2	distinct	0	0.9999

The equivalent proteins include

gi|71016754|ref|XP_758916.1|	22004.71	hypothetical protein UM02769.1 [Ustilago maydis 521]

360. Group probability: 0.9999. Peptides of the group

WHMYDTVK	45.79	55.8802	1078.491	1078.295	2	1	shared(2)	0	0.8591
LGANSLLDIVVFGR	117.51	54.9405	1472.835	1473.482	43	+1,+2	shared(3)	0	1
QPIPVLPTVHYNMGGIPTK	47.61	53.4026	2061.108	2062.594	1	2	distinct	0	0.716
AGLPNQDLEFVQFHPTGIYGAGCLITEGSR	66.79	50.9484	3246.577	3246.573	7	3	distinct	0	0.9451

The equivalent proteins include

gi|83773477|dbj|BAE63604.1|	71678.48	unnamed protein product [Aspergillus oryzae]

361. Group probability: 0.9999. Peptides of the group

SIWVHPDEENKGSSSGGYAPPSGPPTDSR	75.51	51.2879	3010.369	3011.704	6	+2,+3	distinct	1	0.9999

The equivalent proteins include

gi|71019699|ref|XP_760080.1|	26108.8	hypothetical protein UM03933.1 [Ustilago maydis 521]

362. Group probability: 0.9999. Peptides of the group

ILDIQPTSIHQR	52.3	54.9287	1419.783	1420.238	1	2	distinct	0	0.9293
CPVFLGSKDDVEDLMK	90.56	53.9622	1851.875	1852.175	1	2	distinct	1	0.9979

The equivalent proteins include

gi|71015920|ref|XP_758850.1|	38127.22	hypothetical protein UM02703.1 [Ustilago maydis 521]

363. Group probability: 0.9998. Peptides of the group

GKDLENGSDAATAAEK	99.43	54.7181	1575.738	1576.087	1	2	distinct	1	0.999
AETYGLERDEALEWAK	55.32	54.1406	1879.895	1880.378	1	2	distinct	1	0.8359

The equivalent proteins include

gi|71016790|ref|XP_758921.1|	49434.21	hypothetical protein UM02774.1 [Ustilago maydis 521]

364. Group probability: 0.9998. Peptides of the group

IQKEEYEQVLAK	51.94	54.7943	1476.782	1477.21	1	2	distinct	1	0.9272
GCIVGPDIQALHLIVVK	89.43	54.0858	1831.039	1831.452	8	2	distinct	0	0.9978

The equivalent proteins include

gi|71004280|ref|XP_756806.1|	30094.32	hypothetical protein UM00659.1 [Ustilago maydis 521]

365. Group probability: 0.9998. Peptides of the group

LEAQPGHSVSGQGGR	58.38	54.722	1478.723	1479.086	1	2	distinct	0	0.9629
LHYEGPGDNVPGAPGGGYGWEVR	49.19	52.8752	2383.098	2383.673	2	+2,+3	distinct	0	0.9955

The equivalent proteins include

gi|71021599|ref|XP_761030.1|	50585.89	hypothetical protein UM04883.1 [Ustilago maydis 521]

366. Group probability: 0.9998. Peptides of the group

VIPDGTVTGAHFVK	44.02	54.7217	1439.777	1440.22	1	2	distinct	0	0.8644
TPLYVQLMALGDFTK	96.62	54.2634	1695.891	1694.649	1	2	distinct	0	0.9987

The equivalent proteins include

gi|71024159|ref|XP_762309.1|	39109.38	hypothetical protein UM06162.1 [Ustilago maydis 521]

367. Group probability: 0.9998. Peptides of the group

TSQAASSAASKPVGDAK	62.53	54.7115	1574.79	1574.944	1	2	distinct	0	0.976
ILSGQQAADSAVFAPCKPLLWAFQAAEK	73.19	51.2859	3016.548	3017.457	1	3	distinct	0	0.9927

The equivalent proteins include

gi|71024271|ref|XP_762365.1|	39478.98	hypothetical protein UM06218.1 [Ustilago maydis 521]

368. Group probability: 0.9998. Peptides of the group

SPFADGMTAAGASAGAGLFVSAIQNSVQSHNK	113.92	51.0978	3090.483	3091	6	3	distinct	0	0.9998

The equivalent proteins include

gi|71017619|ref|XP_759040.1|	14219.85	hypothetical protein UM02893.1 [Ustilago maydis 521]

369. Group probability: 0.9998. Peptides of the group

LVQDYGFVHLSAGDLLR	66.7	53.8658	1902	1902.093	1	2	distinct	0	0.9259
IVPMEVTVALLSNAIAEALSK (000010000000000000000)	86.25	53.3955	2168.213	2184.723	5	2	distinct	0	0.9975

The equivalent proteins include

gi|71020223|ref|XP_760342.1|	47303.27	hypothetical protein UM04195.1 [Ustilago maydis 521]

370. Group probability: 0.9998. Peptides of the group

FAHTTRPYTAEQVVSK	63.97	54.0699	1833.937	1834.913	1	2	distinct	0	0.9783
DHSFILGTTHTELEPLVDILNR	73.84	52.5955	2519.302	2520.184	1	3	distinct	0	0.9912

The equivalent proteins include

gi|71020403|ref|XP_760432.1|	59271.23	hypothetical protein UM04285.1 [Ustilago maydis 521]

371. Group probability: 0.9998. Peptides of the group

AAANASSTSSNAHQIVLSTAHPAK	66.91	52.8279	2333.172	2333.743	3	+2,+3	distinct	0	0.9998

The equivalent proteins include

gi|71020515|ref|XP_760488.1|	68198.83	hypothetical protein UM04341.1 [Ustilago maydis 521]

372. Group probability: 0.9998. Peptides of the group

FVEITCTNAPSYTVAHGLLSR	114.51	52.8398	2335.163	2335.613	2	2	distinct	0	0.9998

The equivalent proteins include

gi|71015531|ref|XP_758818.1|	127345.06	hypothetical protein UM02671.1 [Ustilago maydis 521]

373. Group probability: 0.9998. Peptides of the group

NAAQQATLEKPSANSHAPR	71.08	53.6319	1989.998	1990.877	3	+2,+3	distinct	0	0.9998

The equivalent proteins include

gi|71006736|ref|XP_758034.1|	15121.81	hypothetical protein UM01887.1 [Ustilago maydis 521]

374. Group probability: 0.9998. Peptides of the group

TFTPEEISSMVLIK	69.04	54.5124	1593.832	1594.697	3	2	shared(2)	0	0.9432
ATAGDTHLGGEDFDNR	68.44	54.7902	1674.723	1675.633	4	2	shared(13)	0	0.9851
IINEPTAAAIAYGIDKK	71.85	54.6758	1786.983	1788.273	1	2	shared(14)	1	0.9837
TQDLLLLDVAPLSMGIETAGGVMTPLIK (0000000000000000000000001000000)	90.67	51.5678	2911.565	2911.753	8	2	distinct	0	0.964
TQDLLLLDVAPLSMGIETAGGVMTPLIKR (0000000000000000000000010000000)	49.2	51.2217	3067.666	3069.083	3	+2,+3	distinct	1	0.9471

The equivalent proteins include

gi|4097891|gb|AAD09565.1|	71474.37	heat shock protein 70 [Pneumocystis carinii]

375. Group probability: 0.9998. Peptides of the group

VQSSIHTFTDR	50.03	55.3777	1289.636	1290.681	1	2	distinct	0	0.9098
FLDTSLFIVNK	90.63	55.1845	1295.712	1296.803	3	2	distinct	0	0.9974

The equivalent proteins include

gi|71004396|ref|XP_756864.1|	21103.53	hypothetical protein UM00717.1 [Ustilago maydis 521]

376. Group probability: 0.9998. Peptides of the group

ATAGDTHLGGEDFDNR	68.44	54.7902	1674.723	1675.633	4	2	shared(13)	0	0.9851
IINEPTAAAIAYGLDSK	115.62	54.2428	1745.92	1746.454	5	2	distinct	0	0.9997

The equivalent proteins include

gi|4098876|gb|AAD00456.1|	22760.93	heat shock protein 70B/SSB1 [Pneumocystis carinii f. sp. carinii]
gi|4098878|gb|AAD00457.1|	22581.75	heat shock protein 70B/SSB1 [Pneumocystis carinii f. sp. ratti]
gi|4098880|gb|AAD00458.1|	22518.64	heat shock protein 70B/SSB1 [Pneumocystis carinii f. sp. hominis]

377. Group probability: 0.9998. Peptides of the group

LGYVPADGSGGLNLHWTLADGFAIK	56.52	52.48	2571.312	2572.193	4	+2,+3	distinct	0	0.9972
SEETSVTLPADLAERDDYIVVVLGDSGNASPK	43.3	50.6002	3346.642	3347.657	1	3	distinct	1	0.9138

The equivalent proteins include

gi|71019679|ref|XP_760070.1|	20701.2	hypothetical protein UM03923.1 [Ustilago maydis 521]

378. Group probability: 0.9998. Peptides of the group

HGYIGEFEEVDDHR	64.73	54.3343	1701.738	1702.087	1	2	distinct	0	0.9781
FNVQLGQIENWVQQLLPAR	70.11	53.0585	2252.206	2253.113	3	2	distinct	0	0.9889

The equivalent proteins include

gi|71004696|ref|XP_757014.1|	14724.9	hypothetical protein UM00867.1 [Ustilago maydis 521]

379. Group probability: 0.9997. Peptides of the group

KPVSISIGGGAKPAATTADK	74.76	53.9024	1868.037	1869.229	2	+2,+3	distinct	0	0.9997

The equivalent proteins include

gi|71023225|ref|XP_761842.1|	80492.98	hypothetical protein UM05695.1 [Ustilago maydis 521]

380. Group probability: 0.9997. Peptides of the group

LVVVTHSSGNHAAALACAAK	112.52	53.7057	1976.026	1976.993	2	2	distinct	0	0.9997

The equivalent proteins include

gi|71023565|ref|XP_762012.1|	40480.85	hypothetical protein UM05865.1 [Ustilago maydis 521]

381. Group probability: 0.9997. Peptides of the group

SDQLDDLSHGSTAK	56.25	54.9409	1472.674	1473.411	1	2	distinct	0	0.9534
ATSADQVNASKDER	80.11	54.8394	1490.696	1491.276	1	2	distinct	1	0.9943

The equivalent proteins include

gi|71021781|ref|XP_761121.1|	12843.44	hypothetical protein UM04974.1 [Ustilago maydis 521]

382. Group probability: 0.9997. Peptides of the group

AKEFANSEQGK	70.53	55.1708	1207.583	1207.718	1	2	distinct	1	0.9503
EFANSEQGKDAINK	80.64	54.6351	1549.737	1550.292	2	2	distinct	1	0.9945

The equivalent proteins include

gi|71004468|ref|XP_756900.1|	25107.79	hypothetical protein UM00753.1 [Ustilago maydis 521]

383. Group probability: 0.9997. Peptides of the group

QLVQAIVDGLSAFGAHTIDAGLK	45.12	52.9498	2323.253	2324.698	1	3	distinct	0	0.8939

LLDGDKIASLAAGYLSELVQAAGIK	54.64	52.6094	2515.39	2516.11	2	+2,+3	distinct	1	0.9974

The equivalent proteins include

gi|71021799|ref|XP_761130.1|	60646.15	hypothetical protein UM04983.1 [Ustilago maydis 521]

384. Group probability: 0.9997. Peptides of the group

KIVDGIHDEVLDVK	65.75	54.7377	1578.862	1579.833	1	2	distinct	1	0.9798
ASIPTPPAPPIVVGTPTIR	67.1	53.8486	1883.088	1883.459	4	2	distinct	0	0.9853

The equivalent proteins include

gi|71010951|ref|XP_758437.1|	21361.36	hypothetical protein UM02290.1 [Ustilago maydis 521]

385. Group probability: 0.9997. Peptides of the group

TSVSDIESCFHHFTNER	61	53.6419	2064.896	2065.833	1	2	distinct	0	0.9731
YTQAFPALLEIPAKDHPYDPAK	46.18	52.6585	2484.269	2484.663	2	+2,+3	distinct	1	0.9887

The equivalent proteins include

gi|71008406|ref|XP_758211.1|	13078.84	hypothetical protein UM02064.1 [Ustilago maydis 521]

386. Group probability: 0.9997. Peptides of the group

HLVTTVNYK	53.77	56.0578	1073.587	1073.806	1	2	distinct	0	0.9298
VVITSSSDDKLQK	51.35	54.9511	1418.762	1418.451	1	2	distinct	1	0.9258
LKEGPIPKPEANEVLIK	52.17	54.3125	1874.088	1874.513	1	2	distinct	1	0.9409

The equivalent proteins include

gi|71006732|ref|XP_758032.1|	37850.73	hypothetical protein UM01885.1 [Ustilago maydis 521]

387. Group probability: 0.9997. Peptides of the group

FTTLEGLLQQVYDELSER	110.86	53.2365	2140.069	2141.333	6	2	distinct	0	0.9997

The equivalent proteins include

gi|71021347|ref|XP_760904.1|	62789.51	hypothetical protein UM04757.1 [Ustilago maydis 521]

388. Group probability: 0.9997. Peptides of the group

IVNEPTAAAIAYGLDKK	100.59	54.2445	1772.967	1773.386	5	+2,+3	distinct	1	0.9997

The equivalent proteins include

gi|1708633|gb|AAB38076.1|	72358.5	PrBiP precursor
gi|1929868|gb|AAB58248.1|	72514.54	endoplasmic reticulum HSP70 homolog [Pneumocystis carinii]
gi|99034528|ref|ZP_01314507.1|	34701.76	hypothetical protein Wendoof_01000686 [Wolbachia endosymbiont of Drosophila willistoni TSC#14030-08
gi|58697214|ref|ZP_00372617.1|	53027.62	dnaK protein [Wolbachia endosymbiont of Drosophila simulans]
gi|58698813|ref|ZP_00373691.1|	67632.59	chaperone protein DnaK [Wolbachia endosymbiont of Drosophila ananassae]
gi|99644386|emb|CAK22359.1|	67088.14	heat shock protein A1 [Mycoplasma suis]
gi|108760919|ref|YP_631393.1|	68470.57	chaperone protein DnaK [Myxococcus xanthus DK 1622]
gi|42410490|gb|AAS14599.1|	69491.53	dnaK protein [Wolbachia endosymbiont of Drosophila melanogaster]
gi|58419068|gb|AAW71083.1|	69009.53	Molecular chaperone, DnaK [Wolbachia endosymbiont strain TRS of Brugia malayi]
gi|86158005|ref|YP_464790.1|	68946.95	Chaperone DnaK [Anaeromyxobacter dehalogenans 2CP-C]
gi|20805915|gb|AAM28893.1|	66771.13	DnaK-like protein [Meiothermus ruber]
gi|1854617|gb|AAB48229.1|	23542.37	70-kDa heat shock protein [unidentified soil organism]
gi|1854603|gb|AAB48222.1|	23208.23	70-kDa heat shock protein [unidentified soil organism]

389. Group probability: 0.9997. Peptides of the group

LSSATLHHSNGSR	61.94	54.9805	1365.675	1366.339	1	2	distinct	0	0.9707
LPPTPLQFLTAQNSVR	71.02	54.1274	1780.984	1781.315	1	2	distinct	0	0.9883

The equivalent proteins include

gi|71018179|ref|XP_759320.1|	51422.36	hypothetical protein UM03173.1 [Ustilago maydis 521]

390. Group probability: 0.9997. Peptides of the group

LGEDNINVVEGNEQFISASK	73.48	53.8609	2162.049	2162.613	1	2	shared(2)	0	0.9919
SIVHPSYDSNTLNNDIMLIK	58.44	53.2362	2273.136	2272.633	11	+2,+3	distinct	0	0.9962

The equivalent proteins include

gi|230196|pdb|1NTP|	23977.52	Modified Beta Trypsin (Monoisopropylphosphoryl Inhibited) (E.C.3.4.21.4) (Neutron Data)

391. Group probability: 0.9996. Peptides of the group

HLPASTGSNVYEIHSK	70.85	54.175	1738.864	1739.154	3	+2,+3	distinct	0	0.9996

The equivalent proteins include

gi|71004266|ref|XP_756799.1|	87666.68	hypothetical protein UM00652.1 [Ustilago maydis 521]

392. Group probability: 0.9996. Peptides of the group

DPTNHPLWNPGQER	48.17		54.9752	1659.775	1660.2	1	2	distinct	0	0.9053
RFDGLDGASASGKPAEANK	59		53.9103	1889.923	1891.015	2	+2,+3	distinct	1	0.9962

The equivalent proteins include

gi|71004292|ref|XP_756812.1|	45706.35	hypothetical protein UM00665.1 [Ustilago maydis 521]

393. Group probability: 0.9996. Peptides of the group

NMSVIAHVDHGK (00100000000000)	87.1		55.3053	1306.645	1307.088	11	+1,+2	distinct	0	0.9996

The equivalent proteins include

gi|39590460|emb|CAE66200.1|	95725.85	Hypothetical protein CBG11440 [Caenorhabditis briggsae]
gi|737058|prf||1921319A	18776.68	elongation factor 2
gi|108879886|gb|EAT44111.1|	95301.25	eukaryotic translation elongation factor [Aedes aegypti]
gi|54644076|gb|EAL32818.1|	192989.47	GA15316-PA [Drosophila pseudoobscura]
gi|67464018|pdb|1ZM9|E	93660.34	Chain E, Structure Of Eef2-Eta In Complex With Pj34
gi|89285379|gb|EAR83394.1|	92833.8	Elongation factor G, domain IV family protein [Tetrahymena thermophila SB210]
gi|89292737|gb|EAR90725.1|	94988.54	Elongation factor G, domain IV family protein [Tetrahymena thermophila SB210]
gi|89301992|gb|EAR99980.1|	94965.56	Elongation factor G, domain IV family protein [Tetrahymena thermophila SB210]
gi|89301994|gb|EAR99982.1|	95961.02	Elongation factor G, domain IV family protein [Tetrahymena thermophila SB210]
gi|89302115|gb|EAS00103.1|	107079.21	Elongation factor G, domain IV family protein [Tetrahymena thermophila SB210]
gi|90304379|gb|EAS34010.1|	93987.84	elongation factor 2 [Coccidioides immitis RS]
gi|706975|gb|AAC46607.1|	93614.8	elongation factor-2 [Cryptosporidium parvum]
gi|8927038|gb|AAF81924.1|	90436.75	elongation factor 2 [Candida albicans]
gi|28564217|gb|AAO32487.1|	93626.11	EFT [Saccharomyces castellii]
gi|28564956|gb|AAO32562.1|	93816.32	EFT2 [Saccharomyces kluyveri]
gi|66508439|ref|XP_392691.2|	95547.34	PREDICTED: similar to translation elongation factor 2 [Apis mellifera]
gi|86161656|gb|ABC86958.1|	95060.91	elongation factor 2 [Leishmania braziliensis]
gi|74353984|gb|AAI03386.1|	96276.32	Unknown (protein for MGC:127305) [Bos taurus]
gi|44984670|gb|AAS53513.1|	93943.5	AFR142Cp [Ashbya gossypii ATCC 10895]
gi|84105365|gb|ABC54654.1|	94686.64	translation elongation factor 2 [Naegleria gruberi]
gi|68361350|ref|XP_697966.1|	96849.6	PREDICTED: wu:fj53d02 [Danio rerio]
gi|74189143|dbj|BAE39328.1|	96123.17	unnamed protein product [Mus musculus]
gi|74197201|dbj|BAE35145.1|	96188.3	unnamed protein product [Mus musculus]
gi|74191026|dbj|BAE39354.1|	96164.24	unnamed protein product [Mus musculus]
gi|74204678|dbj|BAE35408.1|	96138.21	unnamed protein product [Mus musculus]
gi|74151550|dbj|BAE38881.1|	96192.25	unnamed protein product [Mus musculus]
gi|74213791|dbj|BAE29333.1|	96119.24	unnamed protein product [Mus musculus]
gi|74197032|dbj|BAE35069.1|	96194.22	unnamed protein product [Mus musculus]
gi|74201313|dbj|BAE26111.1|	96235.28	unnamed protein product [Mus musculus]
gi|74181334|dbj|BAE29945.1|	96231.21	unnamed protein product [Mus musculus]
gi|74140876|dbj|BAE22047.1|	96221.34	unnamed protein product [Mus musculus]
gi|83769606|dbj|BAE59741.1|	94612.81	unnamed protein product [Aspergillus oryzae]
gi|18447458|gb|AAL68292.1|	95424.48	RE38659p [Drosophila melanogaster]
gi|4585664|emb|CAA70857.2|	93865.45	translation elongation factor 2 [Candida albicans]
gi|45382453|ref|NP_990699.1|	96343.28	eukaryotic translation elongation factor 2 [Gallus gallus]
gi|91087369|ref|XP_975635.1|	95712.64	PREDICTED: similar to Elongation factor 2 (EF-2) [Tribolium castaneum]
gi|72081276|ref|XP_797399.1|	100783.26	PREDICTED: similar to eukaryotic translation elongation factor 2, like [Strongylocentrotus purpurat

gi|92887256|gb|ABE88774.1|	95050.75	Translation factor; Elongation factor G, III and V [Medicago truncatula]
gi|92887257|gb|ABE88775.1|	94978.18	Elongation factor Tu, domain 2; Translation elongation factor G [Medicago truncatula]
gi|71032815|ref|XP_766049.1|	93186.9	elongation factor 2 [Theileria parva strain Muguga]
gi|72256098|gb|AAR01295.2|	82298	elongation factor-2 [Metajapyx subterraneus]
gi|71415412|ref|XP_809774.1|	22678.57	elongation factor 2 [Trypanosoma cruzi strain CL Brener]
gi|71401612|ref|XP_803516.1|	19215.83	elongation factor 2 [Trypanosoma cruzi strain CL Brener]
gi|71415388|ref|XP_809762.1|	95099.12	elongation factor 2 [Trypanosoma cruzi strain CL Brener]
gi|71413833|ref|XP_809041.1|	95098.14	elongation factor 2 [Trypanosoma cruzi strain CL Brener]
gi|50284959|ref|XP_444908.1|	93783.19	hypothetical protein CAGL0A03234g [Candida glabrata CBS138]
gi|46136117|ref|XP_389750.1|	91848.9	EF2_NEUCR Elongation factor 2 (EF-2) (Colonial temperature-sensitive 3) [Gibberella zeae PH-1]
gi|71747298|ref|XP_822704.1|	95300.11	elongation factor 2 [Trypanosoma brucei TREU927]
gi|849206|gb|AAB64821.1|	57232.98	Etf1p: Elongation factor 2 (Swiss Prot. accession number P32324). Note that the entire gene is not
gi|73987435|ref|XP_533949.2|	78574.99	PREDICTED: similar to Elongation factor 2 (EF-2) [Canis familiaris]
gi|28629446|gb|AAO39212.1|	93866.57	elongation factor 2 [Pichia pastoris]
gi|50426399|ref|XP_461796.1|	93705.37	hypothetical protein DEHA0G06380g [Debaryomyces hansenii CBS767]
gi|95103088|gb|ABF51485.1|	95749.55	translation elongation factor 2 [Bombyx mori]
gi|103058022|gb|ABF71565.1|	98231.85	translation elongation factor 2 [Bombyx mori]
gi|50308159|ref|XP_454080.1|	93814.55	unnamed protein product [Kluyveromyces lactis]
gi|109122950|ref|XP_001118006.1|	157373.37	PREDICTED: eukaryotic translation elongation factor 2 [Macaca mulatta]
gi|39580704|emb|CAE70384.1|	95542.73	Hypothetical protein CBG16945 [Caenorhabditis briggsae]
gi|47180786|emb|CAG06203.1|	8000.15	unnamed protein product [Tetraodon nigroviridis]
gi|6324707|ref|NP_014776.1|	93686.4	Elongation factor 2 (EF-2), also encoded by EFT2; catalyzes ribosomal translocation during protein
gi|68060335|ref|XP_672146.1|	7209.73	hypothetical protein PB301482.00.0 [Plasmodium berghei strain ANKA]
gi|82595325|ref|XP_725803.1|	94455.66	elongation factor 2 [Plasmodium yoelii yoelii str. 17XNL]
gi|2641946|dbj|BAA23591.1|	93713.74	elongation factor 2 [Schizosaccharomyces pombe]
gi|119167|sp|P28996|EF2_CHLKE	94853.06	Elongation factor 2 (EF-2)
gi|119169|sp|P15112|EF2_DICDI	92497.58	Elongation factor 2 (EF-2)
gi|70943098|ref|XP_741636.1|	42223.35	elongation factor 2 [Plasmodium chabaudi chabaudi]
gi|8393296|ref|NP_058941.1|	96192.24	eukaryotic translation elongation factor 2 [Rattus norvegicus]
gi|85106981|ref|XP_962286.1|	93556.39	ELONGATION FACTOR 2 (EF-2) [Neurospora crassa OR74A]
gi|71076808|ref|XP_770921.1|	100588.78	elongation factor 2 [Giardia lamblia ATCC 50803]
gi|71002010|ref|XP_755686.1|	93595.53	translation elongation factor EF-2 subunit [Aspergillus fumigatus Af293]
gi|119168|sp|P09445|EF2_CRIGR	96304.27	Elongation factor 2 (EF-2)
gi|119173|sp|P05086|EF2_MESAU	96232.27	Elongation factor 2 (EF-2)
gi|66805999|ref|XP_636721.1|	93511.92	elongation factor 2 [Dictyostelium discoideum AX4]
gi|66806657|ref|XP_637051.1|	95477.41	elongation factor 2 [Dictyostelium discoideum]

gi|600159|gb|AAB60497.1|	96218.25	elongation factor 2
gi|56474887|gb|AAN04123.2|	94963.71	elongation factor-related protein 1 [Tetrahymena thermophila]
gi|2369714|emb|CAB09900.1|	94707.65	elongation factor 2 [Beta vulgaris subsp. vulgaris]
gi|3876400|emb|CAB02985.1|	95476.66	Hypothetical protein F25H5.4 [Caenorhabditis elegans]
gi|13938072|gb|AAH07152.1|	96222.25	Eukaryotic translation elongation factor 2 [Mus musculus]
gi|50542892|ref|XP_499612.1|	94027.3	hypothetical protein [Yarrowia lipolytica]
gi|50545473|ref|XP_500274.1|	94064.97	hypothetical protein [Yarrowia lipolytica]
gi|3642665|gb|AAC36522.1|	28866.59	elongation factor 2 [Mus musculus]
gi|4503483|ref|NP_001952.1|	96246.31	eukaryotic translation elongation factor 2 [Homo sapiens]
gi|50921395|ref|XP_471058.1|	94938.94	OSJNBa0020P07.3 [Oryza sativa (japonica cultivar-group)]
gi|24585713|ref|NP_724358.1|	94049.78	Elongation factor 2b CG2238-PC, isoform C [Drosophila melanogaster]
gi|156279|gb|AAD03339.1|	95326.51	elongation factor [Caenorhabditis elegans]
gi|29539334|dbj|BAC67668.1|	94958.54	elongation factor-2 [Cyanidioschyzon merolae]
gi|6066758|emb|CAB58373.1|	93798.81	SPCP31B10.07 [Schizosaccharomyces pombe]
gi|66360030|ref|XP_627193.1|	94127.1	Eft2p GTpase; translation elongation factor 2 (EF-2) [Cryptosporidium parvum Iowa II]
gi|30179014|gb|EAA03632.2|	94070.64	ENSANGP00000018623 [Anopheles gambiae str. PEST]
gi|55246389|gb|EAL42047.1|	22679.5	ENSANGP00000029149 [Anopheles gambiae str. PEST]
gi|9963972|gb|AAG09782.1|	93360.49	translation elongation factor 2 [Filobasidiella neoformans]
gi|68481380|ref|XP_715329.1|	92506.72	translation elongation factor EF-2 [Candida albicans SC5314]
gi|67540320|ref|XP_663934.1|	94085.97	elongation factor 2 [Aspergillus nidulans FGSC A4]
gi|67623439|ref|XP_668002.1|	93586.79	elongation factor 2 (EF-2) [Cryptosporidium hominis TU502]
gi|50909007|ref|XP_465992.1|	94986.92	putative elongation factor 2 [Oryza sativa (japonica cultivar-group)]
gi|23497558|gb|AAN37099.1|	94545.79	elongation factor 2 [Plasmodium falciparum 3D7]
gi|30696056|ref|NP_849818.1|	94742.58	LOS1; GTP binding / translation elongation factor/ translation factor, nucleic acid binding [Arabid
gi|8927040|gb|AAF81925.1|	90393.61	elongation factor 2 [Candida glabrata]
gi|8927044|gb|AAF81927.1|	90176.7	elongation factor 2 [Candida tropicalis]
gi|8927048|gb|AAF81929.1|	90304.9	elongation factor 2 [Candida parapsilosis]
gi|62752006|ref|NP_001015785.1|	96342.61	MGC108369 protein [Xenopus tropicalis]
gi|28564005|gb|AAO32381.1|	46361.15	EFT2 [Saccharomyces bayanus]
gi|28564219|gb|AAO32488.1|	50852.23	EFT [Saccharomyces castellii]
gi|12667408|gb|AAK01430.1|	95313.29	elongation factor 2 [Aedes aegypti]
gi|34910726|ref|NP_916710.1|	96021.51	putative elongation factor 2 [Oryza sativa (japonica cultivar-group)]
gi|15028587|gb|AAK77225.1|	95287.24	elongation factor 2 [Aedes aegypti]
gi|26324898|dbj|BAC26203.1|	96223.23	unnamed protein product [Mus musculus]
gi|26328763|dbj|BAC28120.1|	96165.16	unnamed protein product [Mus musculus]
gi|16554298|gb|AAK27414.1|	94356.67	elongation factor 2 [Monosiga brevicollis]
gi|13925370|gb|AAK49353.1|	93509.28	elongation factor 2 [Neurospora crassa]
gi|19335670|gb|AAL85604.1|	95306.15	elongation factor 2 [Aedes aegypti]
gi|19335672|gb|AAL85605.1|	95359.26	elongation factor 2 [Aedes aegypti]
gi|55728420|emb|CAH90954.1|	96218.28	hypothetical protein [Pongo pygmaeus]
gi|55730085|emb|CAH91767.1|	96186.31	hypothetical protein [Pongo pygmaeus]
gi|6090545|emb|CAB58724.1|	6782.42	SPAC513.01c [Schizosaccharomyces pombe]
gi|54035090|gb|AAH84061.1|	96603.38	Eukaryotic translation elongation factor 2 [Xenopus tropicalis]
gi|7919|emb|CAA33804.1|	95438.49	unnamed protein product [Drosophila melanogaster]
gi|37362212|gb|AAQ91234.1|	96463.16	eukaryotic translation elongation factor 2 [Danio rerio]

gi|13111488|gb|AAK12341.1|	81882.68	elongation factor-2 [Armadillidium vulgare]
gi|13111492|gb|AAK12343.1|	82284.64	elongation factor-2 [Eumesocampa frigilis]
gi|13111496|gb|AAK12345.1|	74472.81	elongation factor-2 [Hutchinsoniella macracantha]
gi|13111498|gb|AAK12346.1|	74233.13	elongation factor-2 [Limulus polyphemus]
gi|13111502|gb|AAK12348.1|	82376.04	elongation factor-2 [Mastigoproctus giganteus]
gi|13111504|gb|AAK12349.1|	81730.77	elongation factor-2 [Nipponopsalis abei]
gi|13111506|gb|AAK12350.1|	81963.23	elongation factor-2 [Cypridopsis vidua]
gi|13111508|gb|AAK12351.1|	74765.07	elongation factor-2 [Polyxenus fasciculatus]
gi|13111510|gb|AAK12352.1|	82226.03	elongation factor-2 [Scutigerella sp. 'Scu2']
gi|13111512|gb|AAK12353.1|	82681.09	elongation factor-2 [Scolopendra polymorpha]
gi|13111516|gb|AAK12355.1|	74213.62	elongation factor-2 [Tomocerus sp. jcrjws1]
gi|13111518|gb|AAK12356.1|	82185.53	elongation factor-2 [Tanystylum orbiculare]
gi|13111520|gb|AAK12357.1|	82218.76	elongation factor-2 [Chaetopleura apiculata]
gi|13111524|gb|AAK12359.1|	74215.84	elongation factor-2 [Nereis virens]
gi|13111526|gb|AAK12360.1|	82254.17	elongation factor-2 [Peripatus sp. Per2]
gi|84999038|ref|XP_954240.1|	93136.86	elongation factor 2 [Theileria annulata strain Ankara]
gi|68129664|emb|CAJ08970.1|	94927.93	elongation factor 2 [Leishmania major]
gi|34597146|gb|AAQ77148.1|	82709.21	elongation factor 2 [Australobius scabrior]
gi|34597148|gb|AAQ77149.1|	82235.12	elongation factor 2 [Ballophilus australiae]
gi|34597166|gb|AAQ77158.1|	82361.06	elongation factor 2 [Globotherium sp. 'Glo2']
gi|34597168|gb|AAQ77159.1|	82531.13	elongation factor 2 [Glomeris marginata]
gi|34597170|gb|AAQ77160.1|	82524.2	elongation factor 2 [Glomeridesmus trinidadensis]
gi|34597172|gb|AAQ77161.1|	82349.93	elongation factor 2 [Geophilus vittatus]
gi|34597178|gb|AAQ77164.1|	23897.24	elongation factor 2 [Hiltonius sp. 'Hil']
gi|34597182|gb|AAQ77166.1|	82498.38	elongation factor 2 [Ophyiulus pilosus]
gi|34597184|gb|AAQ77167.1|	82191.86	elongation factor 2 [Phryssonotus sp. 'jump']
gi|34597186|gb|AAQ77168.1|	82115.82	elongation factor 2 [Lamyctes fulvicornis]
gi|34597188|gb|AAQ77169.1|	-48453.86	elongation factor 2 [Lithobius forficatus]
gi|34597190|gb|AAQ77170.1|	82435.8	elongation factor 2 [Plesioproctus comans]
gi|34597192|gb|AAQ77171.1|	82644.14	elongation factor 2 [Narceus americanus]
gi|34597194|gb|AAQ77172.1|	23795.24	elongation factor 2 [Nemasoma varicorne]
gi|34597198|gb|AAQ77174.1|	82245.02	elongation factor 2 [Oxidus gracilus]
gi|34597204|gb|AAQ77177.1|	82588.47	elongation factor 2 [Uroblaniulus canadensis]
gi|34597206|gb|AAQ77178.1|	82503.12	elongation factor 2 [Pokabius bilabiatus]
gi|34597208|gb|AAQ77179.1|	82633.38	elongation factor 2 [Proteroiulus fuscus]
gi|34597214|gb|AAQ77182.1|	82277.03	elongation factor 2 [Platydesmus sp. 'Pla']
gi|34597216|gb|AAQ77183.1|	82493.97	elongation factor 2 [Pachymerium ferrugineum]
gi|34597224|gb|AAQ77187.1|	74705.11	elongation factor 2 [Scutigera coleoptrata]
gi|34597226|gb|AAQ77188.1|	82024.73	elongation factor 2 [Siphonocybe sp. 'Siph']
gi|34597232|gb|AAQ77191.1|	82550.19	elongation factor 2 [Orthocricus sp. 'Spi1']
gi|34597234|gb|AAQ77192.1|	82299.01	elongation factor 2 [Scolopocryptops sexspinosus]
gi|34597236|gb|AAQ77193.1|	82556.11	elongation factor 2 [Stemmiulus insulanus]
gi|34597238|gb|AAQ77194.1|	82125.89	elongation factor 2 [Striaria columbiana]
gi|34597240|gb|AAQ77195.1|	82680.07	elongation factor 2 [Scolopendra viridis]
gi|34597246|gb|AAQ77198.1|	82414.03	elongation factor 2 [Theatops posticus]
gi|37703915|gb|AAR01279.1|	82079.91	elongation factor-2 [Acanthocyclops vernalis]
gi|37703917|gb|AAR01280.1|	82157.17	elongation factor-2 [Abacion magnum]
gi|37703919|gb|AAR01281.1|	82381.87	elongation factor-2 [Anopsobius neozelandicus]

gi|37703925|gb|AAR01284.1|	82583.1	elongation factor-2 [Bothropolys multidentatus]
gi|37703929|gb|AAR01286.1|	82526.82	elongation factor-2 [Ctenolepisma lineata]
gi|37703933|gb|AAR01288.1|	74175.05	elongation factor-2 [Carcinoscorpius rotundicauda]
gi|37703937|gb|AAR01290.1|	81886.74	elongation factor-2 [Eurypauropus spinosus]
gi|37703939|gb|AAR01291.1|	23810.12	elongation factor-2 [Forficula auricularia]
gi|37703953|gb|AAR01298.1|	81917.42	elongation factor-2 [Libinia emarginata]
gi|37703959|gb|AAR01301.1|	82421.78	elongation factor-2 [Lynceus sp. JCR-2003]
gi|37703963|gb|AAR01303.1|	82383.76	elongation factor-2 [Mesocyclops edax]
gi|37703965|gb|AAR01304.1|	82008.43	elongation factor-2 [Neogonodactylus oerstedii]
gi|37703967|gb|AAR01305.1|	81972.77	elongation factor-2 [Nebalia hessleri]
gi|37703969|gb|AAR01306.1|	82464.8	elongation factor-2 [Nicoletia meinerti]
gi|37703971|gb|AAR01307.1|	23704.04	elongation factor-2 [Orchesella imitari]
gi|37703975|gb|AAR01309.1|	82316.81	elongation factor-2 [Periplaneta americana]
gi|37703979|gb|AAR01311.1|	82312.96	elongation factor-2 [Paralamyctes sp. JCR-2003]
gi|37703983|gb|AAR01313.1|	82191.03	elongation factor-2 [Rhinotus purpureus]
gi|37703991|gb|AAR01317.1|	82503.24	elongation factor-2 [Trachyiulus nordquisti]
gi|37703993|gb|AAR01318.1|	82330.78	elongation factor-2 [Streptocephalus seali]
gi|37704003|gb|AAR01323.1|	74479.19	elongation factor-2 [Ooperipatellus nanus]
gi|37704005|gb|AAR01324.1|	82058.09	elongation factor-2 [Richtersius coronifer]
gi|33869643|gb|AAH06547.1|	65366.05	EEF2 protein [Homo sapiens]
gi|57226782|gb|AAW43242.1|	91971.78	translation elongation factor 2 [Cryptococcus neoformans var. neoformans JEC21]
gi|27882475|gb|AAH44327.1|	96449.29	Eef2-prov protein [Xenopus laevis]
gi|38511951|gb|AAH60707.1|	94464.35	Eef2 protein [Mus musculus]
gi|28627569|gb|AAL83698.1|	95586.4	translation elongation factor 2 [Spodoptera exigua]
gi|6056373|gb|AAF02837.1|	95097.76	elongation factor EF-2 [Arabidopsis thaliana]
gi|37748712|gb|AAH60025.1|	39351.35	MGC68699 protein [Xenopus laevis]
gi|37590856|gb|AAH59523.1|	37893.47	Wu:fj53d02 protein [Danio rerio]
gi|39952199|ref|XP_363816.1|	96722.3	hypothetical protein MG01742.4 [Magnaporthe grisea 70-15]
gi|47559179|gb|AAT35592.1|	95084.16	elongation factor 2 [Trypanosoma cruzi]
gi|28278942|gb|AAH45488.1|	96415.15	Eukaryotic translation elongation factor 2, like [Danio rerio]
gi|52630939|gb|AAU84933.1|	95726.43	putative translation elongation factor 2 [Toxoptera citricida]
gi|50603727|gb|AAH77595.1|	95661.16	Eft-2-prov protein [Xenopus laevis]
gi|56474885|gb|AAN04122.2|	94292.56	elongation factor 2 [Tetrahymena thermophila]

394. Group probability: 0.9996. Peptides of the group

FKFPDNSLELYAEK	76.92	54.3502	1699.846	1700.142	1	2	distinct	1	0.958
AGKPFPLPDAVTILEPK	72.57	54.3163	1792.013	1792.897	1	2	distinct	0	0.9901

The equivalent proteins include

gi|71017745|ref|XP_759103.1|	26548.89	hypothetical protein UM02956.1 [Ustilago maydis 521]

395. Group probability: 0.9996. Peptides of the group

KPYNDMANR	55.39	55.419	1107.513	1107.749	1	2	distinct	0	0.9399
NANPEAGFGEVGR	46.35	55.4112	1316.611	1316.988	1	2	distinct	0	0.8839
RPLSAYMFFSQDQR	53.23	54.2767	1744.835	1746.123	1	2	distinct	0	0.9401

The equivalent proteins include

gi|71012570|ref|XP_758511.1|	13939.2	hypothetical protein UM02364.1 [Ustilago maydis 521]

396. Group probability: 0.9996. Peptides of the group

DHHWVAYNASK	54.73	55.3223	1326.61	1326.333	2	1	distinct	0	0.9403
MTAAYLDTNPHLLAK	77.09	54.9066	1657.85	1658.357	1	2	distinct	0	0.9928

The equivalent proteins include

gi|71004668|ref|XP_757000.1|	45586.68	hypothetical protein UM00853.1 [Ustilago maydis 521]

397. Group probability: 0.9996. Peptides of the group

IQDKEGIPPDQQR	47.88	54.643	1522.774	1523.197	1	2	shared(4)	1	0.8358

TISDYNIQKESTLHLVLR	54.37	53.2751	2129.148	2129.693	13	+2,+3	shared(2)	1	0.9929
TLSDYNNQKESTLHLVLR	58.97	53.2893	2130.107	2129.577	2	+2,+3	distinct	1	0.9917

The equivalent proteins include

gi|166336|gb|AAA72126.1|	51519.58	polyubiquitin

398. Group probability: 0.9996. Peptides of the group

HLFDTAQGLVDR	52.75	55.2198	1370.694	1370.835	1	2	distinct	0	0.9316
VAVISGGGAGHEPAQAGFVGK	75.52	53.9083	1907.985	1908.732	1	2	distinct	0	0.9934

The equivalent proteins include

gi|71003151|ref|XP_756256.1|	65208.78	hypothetical protein UM00109.1 [Ustilago maydis 521]

399. Group probability: 0.9995. Peptides of the group

HFVPGDQLPELADKIV	48.37	54.1226	1776.941	1778.083	1	2	distinct	1	0.9148
SGSAADTQAIADIVTYYLDMYAVESDSPPQTK	74.88	50.3559	3406.576	3407.435	6	3	distinct	0	0.9946

The equivalent proteins include

gi|71005512|ref|XP_757422.1|	24117.05	hypothetical protein UM01275.1 [Ustilago maydis 521]

400. Group probability: 0.9995. Peptides of the group

FVCGEVFSIDDIKEHGTEAAVK	56.93	52.5224	2450.179	2450.963	1	2	distinct	1	0.9686
AFDDAEVIHVEGDVNPIRDMEIISTELR	44.99	50.9585	3182.555	3183.854	1	3	distinct	1	0.7063
SEVPAFLTCIDIAGLTAGASTGAGLGNAFLSNVR	48.36	50.5977	3349.697	3351.001	1	3	distinct	0	0.9485

The equivalent proteins include

gi|71024069|ref|XP_762264.1|	51532	hypothetical protein UM06117.1 [Ustilago maydis 521]

401. Group probability: 0.9995. Peptides of the group

AYALTDHIHER	53.26	55.191	1324.652	1323.515	2	2	distinct	0	0.9323
ARPIPIGTFTAEYLDKDK	77.94	54.2938	2034.079	2035.284	1	3	distinct	1	0.9927

The equivalent proteins include

gi|71004852|ref|XP_757092.1|	100476.6	hypothetical protein UM00945.1 [Ustilago maydis 521]

402. Group probability: 0.9995. Peptides of the group

INLDGYVDCFLIHTPTSGPEGR	71.82	52.5695	2460.174	2460.913	3	+2,+3	distinct	0	0.9995

The equivalent proteins include

gi|71009633|ref|XP_758298.1|	32275.49	hypothetical protein UM02151.1 [Ustilago maydis 521]

403. Group probability: 0.9995. Peptides of the group

FPAIEHPGSTGVIYVTDR	73.25	53.6962	1957.99	1958.273	1	2	distinct	0	0.9911
MLQFDLSEFGEGVHEYAPNTGTMALR	50.17	51.55	2912.347	2913.696	1	3	distinct	0	0.9405

The equivalent proteins include

gi|71015650|ref|XP_758832.1|	57929.12	hypothetical protein UM02685.1 [Ustilago maydis 521]

404. Group probability: 0.9995. Peptides of the group

AANLGASTSNHTSTPNHLSTSASSR	67.49	52.5974	2468.164	2468.573	2	+2,+3	distinct	0	0.9995

The equivalent proteins include

gi|71004782|ref|XP_757057.1|	25615.73	hypothetical protein UM00910.1 [Ustilago maydis 521]

405. Group probability: 0.9995. Peptides of the group

RPIVISGPSGVGK	71.97	55.1362	1265.745	1265.796	1	2	distinct	0	0.9878
GQSYHYVSQQEFQDLVQQGAFLEHAK	53.74	51.4314	3036.436	3037.887	2	3	distinct	0	0.9566

The equivalent proteins include

gi|71017531|ref|XP_758996.1|	26305.31	hypothetical protein UM02849.1 [Ustilago maydis 521]

406. Group probability: 0.9995. Peptides of the group

THLSLSADPTKK	73.54	55.1846	1296.704	1296.438	1	1	distinct	1	0.989
SRDCTVTQVHSK	56.52	55.0207	1416.678	1417.376	1	2	distinct	1	0.9511

The equivalent proteins include

gi|71018473|ref|XP_759467.1|	102320.16	hypothetical protein UM03320.1 [Ustilago maydis 521]

407. Group probability: 0.9994. Peptides of the group

DSTIIMQLLR	45.88	55.6848	1188.654	1188.947	1	2	shared(4)	0	0.5759
HLIPSAASGESK	59.2	55.1838	1195.62	1196.088	1	2	shared(3)	0	0.9612
LAEQAERYEEMVENMK	62	53.6314	1968.892	1969.482	4	+2,+3	shared(3)	1	0.9973
LAFDDAIAELDTLSEESYKDSTLIMQLLR (00000000000000000000000100000)	64.57	50.8445	3299.648	3315.314	18	3	distinct	1	0.9851

The equivalent proteins include

gi|70989229|ref|XP_749464.1|	29197.65	hypothetical protein Afu2g03290 [Aspergillus fumigatus Af293]

408. Group probability: 0.9994. Peptides of the group

LYESLGAHAKPTIK	71.25	54.7127	1526.846	1527.608	6	+1,+2	distinct	0	0.9994

The equivalent proteins include

gi|89267123|emb|CAJ42004.1|	131023.7	alpha mannosidase [Ustilago hordei]
gi|71004076|ref|XP_756704.1|	131519.12	hypothetical protein UM00557.1 [Ustilago maydis 521]

409. Group probability: 0.9994. Peptides of the group

FLQVVAGHPLLQTGSK	105.16		54.2631	1693.951	1694.576	3	2	distinct	0	0.9994

The equivalent proteins include

gi|71023655|ref|XP_762057.1|	42042.27	hypothetical protein UM05910.1 [Ustilago maydis 521]

410. Group probability: 0.9994. Peptides of the group

NQVAMNPHNTVFDAK	91.76		54.3229	1684.799	1685.24	1	2	shared(2)	0	0.998
IINEPTAAAIAYGIDKK	71.85		54.6758	1786.983	1788.273	1	2	shared(14)	1	0.9837
NQVAMNPHNTVFDAKR	80.09		54.0539	1840.9	1841.223	1	2	shared(2)	1	0.9947
TQVFSTYADNQPGVLIQVFEGER	63.55		52.3905	2597.276	2598.243	1	2	distinct	0	0.7263

The equivalent proteins include

gi|88770694|gb|ABD51950.1|	71573.82	70 kDa heat shock protein [Rhodomonas salina]
gi|13812189|ref|NP_113319.1|	72839.27	heat shock protein 70KD [Guillardia theta]

411. Group probability: 0.9994. Peptides of the group

AVIALHGLINNR	66.01		55.4461	1289.757	1290.121	1	2	distinct	0	0.9785
TFMHVPSTIEAEEAEEIGVEHLLR	58.95		52.1917	2736.343	2737.136	2	3	distinct	0	0.97

The equivalent proteins include

gi|71005204|ref|XP_757268.1|	36861.03	hypothetical protein UM01121.1 [Ustilago maydis 521]

412. Group probability: 0.9993. Peptides of the group

LCIFAVAHGTPVAGIQK	103.55		54.1382	1780.966	1781.049	5	2	distinct	0	0.9993

The equivalent proteins include

gi|71023647|ref|XP_762053.1|	45282.93	hypothetical protein UM05906.1 [Ustilago maydis 521]

413. Group probability: 0.9993. Peptides of the group

AMAEICASHLSAVEGTPSRIPEEK	70.97		52.3965	2582.247	2583.223	2	+2,+3	distinct	1	0.9993

The equivalent proteins include

gi|71018721|ref|XP_759591.1|	90699.1	hypothetical protein UM03444.1 [Ustilago maydis 521]

414. Group probability: 0.9993. Peptides of the group

AEDGQFATIMVEYINNNHGR	67.27		52.9958	2278.044	2279.055	4	+2,+3	distinct	0	0.9993

The equivalent proteins include

gi|71022567|ref|XP_761513.1|	24205.76	hypothetical protein UM05366.1 [Ustilago maydis 521]

415. Group probability: 0.9993. Peptides of the group

GAPSSTSSSHAGLSHLR	103.29		54.6795	1650.807	1651.126	1	2	distinct	0	0.9993

The equivalent proteins include

gi|71022833|ref|XP_761646.1|	103290.66	hypothetical protein UM05499.1 [Ustilago maydis 521]

416. Group probability: 0.9993. Peptides of the group

MYGLGEHYNSLRPAPTA	73.78		54.0245	1875.894	1876.983	2	2	distinct	0	0.9912
HFLDYCDAVENTGVWGGQPEILALSR	47.28		51.3643	2946.397	2946.99	1	3	distinct	0	0.9236

The equivalent proteins include

gi|71020065|ref|XP_760263.1|	41670.44	hypothetical protein UM04116.1 [Ustilago maydis 521]

417. Group probability: 0.9993. Peptides of the group

APLVKPGTDVVNSLNR	56.76		54.2842	1678.937	1679.571	1	2	distinct	0	0.9591
VHHDDGTTEYVATPFQR	66.55		53.6677	1971.907	1972.205	1	2	distinct	0	0.9835

The equivalent proteins include

gi|71022933|ref|XP_761696.1|	62576.38	hypothetical protein UM05549.1 [Ustilago maydis 521]

418. Group probability: 0.9993. Peptides of the group

RVDVPLPDFWGGYR	57.92		54.831	1675.847	1677.273	2	2	distinct	1	0.9598
ATDATTTAITSHNQYR	66.53		54.1857	1749.828	1749.978	1	2	distinct	0	0.9827

The equivalent proteins include

gi|71017851|ref|XP_759156.1|	28607.32	hypothetical protein UM03009.1 [Ustilago maydis 521]

419. Group probability: 0.9992. Peptides of the group

SGKDFSALTHLPENK	70.87		54.5734	1642.831	1643.773	1	2	distinct	1	0.9876
GGLNQLAISPQCGFSSTVHGNEITPQTQFDK	47.66		50.7558	3330.594	3331.867	1	3	distinct	0	0.9389

The equivalent proteins include

gi|71020101|ref|XP_760281.1|	43562.12	hypothetical protein UM04134.1 [Ustilago maydis 521]

420. Group probability: 0.9992. Peptides of the group

RPDAVTPFALATPLFNK	101.86		54.6225	1857.015	1857.843	1	2	distinct	0	0.9992

The equivalent proteins include

gi|71005264|ref|XP_757298.1|	80800.47	hypothetical protein UM01151.1 [Ustilago maydis 521]								
421. Group probability: 0.9992. Peptides of the group										
HFMGPVIAK	44.91		55.6245	998.537	998.426	1	2	distinct	0	0.8486
EAGLPDGVIQFVPGPAPEIVGAAINHR	77.81		52.0176	2723.439	2724.487	1	3	distinct	0	0.9949
The equivalent proteins include										
gi|71005462|ref|XP_757397.1|	61478.95	hypothetical protein UM01250.1 [Ustilago maydis 521]								
422. Group probability: 0.9992. Peptides of the group										
GGSNVIVKPHR	62.59		55.5117	1162.657	1163.573	4	2	distinct	0	0.9699
NIAPGESVYGEKR	63.15		54.9514	1418.715	1418.596	1	2	distinct	1	0.9736
The equivalent proteins include										
gi|71019441|ref|XP_759951.1|	30740.01	hypothetical protein UM03804.1 [Ustilago maydis 521]								
423. Group probability: 0.9992. Peptides of the group										
LAHAMLSIPATK	64.81		55.424	1251.701	1252.124	1	2	distinct	0	0.9762
VDNVINTDHLTEEEAEEPLSQEFR	57.39		52.1278	2813.299	2813.877	1	3	distinct	0	0.9657
The equivalent proteins include										
gi|71005766|ref|XP_757549.1|	50007.32	hypothetical protein UM01402.1 [Ustilago maydis 521]								
424. Group probability: 0.9991. Peptides of the group										
DIESSALLQHLIPLFK	100.84		54.0131	1823.019	1823.517	2	2	distinct	0	0.9991
The equivalent proteins include										
gi|71003335|ref|XP_756348.1|	44167.95	hypothetical protein UM00201.1 [Ustilago maydis 521]								
425. Group probability: 0.9991. Peptides of the group										
AMAILNSFVQDIFER	100.75		54.1137	1752.887	1752.903	1	2	distinct	0	0.9991
The equivalent proteins include										
gi|71005972|ref|XP_757652.1|	15200.24	histone H2B [Ustilago maydis 521]								
426. Group probability: 0.9991. Peptides of the group										
IPSAVGYQPTLATDLGSLQER	68.33		53.1439	2215.148	2215.623	8	+2,+3	distinct	0	0.9991
The equivalent proteins include										
gi|71032549|ref|XP_765916.1|	63057.8	ATP synthase F1 subunit beta [Theileria parva strain Muguga]								
gi|84999258|ref|XP_954350.1|	63196.72	ATP synthase subunit beta, mitochondrial precursor [Theileria annulata strain Ankara]								
427. Group probability: 0.9991. Peptides of the group										
VGGSSEVEVGEKK	59.92		55.3897	1303.662	1304.054	1	2	shared(2)	1	0.9647
VEFEKPLILLSEK	55.23		54.7931	1543.886	1544.171	3	+2,+3	shared(2)	0	0.9947
VEFEKPLILLSEKK	54.37		54.5225	1671.981	1672.783	1	2	shared(2)	1	0.9455
SILGDIAVLTNGTVFTDELDVKLEK	46.73		52.0804	2689.442	2690.814	1	3	distinct	1	0.7096
The equivalent proteins include										
gi|39942170|ref|XP_360622.1|	63291.19	hypothetical protein MG03165.4 [Magnaporthe grisea 70-15]								
428. Group probability: 0.9991. Peptides of the group										
VISYNHLMPTR	61.42		55.3462	1329.686	1330.258	2	2	distinct	0	0.9668
GAVTQDTFKEPSQR	61.83		54.8236	1562.769	1563.187	1	2	distinct	1	0.9715
The equivalent proteins include										
gi|71022211|ref|XP_761336.1|	21681.51	hypothetical protein UM05189.1 [Ustilago maydis 521]								
429. Group probability: 0.9991. Peptides of the group										
VFDKDGDGFISAAELR	115.35		54.16	1738.853	1739.341	3	+2,+3	distinct	1	0.9963
EAFSLFDKDGDGTITTK	82.53		54.1901	1843.884	1844.047	4	2	shared(3)	1	0.9825
The equivalent proteins include										
gi|115518|sp|P02595|CALM_PATSP	16670.75	Calmodulin (CaM)								
gi|49037478|sp|P62184|CALM_RENRE	16697.8	Calmodulin (CaM)								
430. Group probability: 0.9990. Peptides of the group										
VAYGAPLPDTNDGPHR	53.13		54.4595	1678.806	1678.998	1	2	distinct	0	0.9435
ISSQTAAASSAATFGNNKK	65.61		53.9833	1852.928	1853.249	1	2	distinct	1	0.9832
The equivalent proteins include										
gi|71003614|ref|XP_756473.1|	30230.96	hypothetical protein UM00326.1 [Ustilago maydis 521]								
431. Group probability: 0.9990. Peptides of the group										
YLDPANAPGSAADKPDK	43.63		54.2723	1728.832	1729.841	1	3	distinct	0	0.8463
YLDPANAPGSAADKPDKVR	76.61		53.7584	1984.001	1984.453	2	2	distinct	1	0.9936
The equivalent proteins include										
gi|71023841|ref|XP_762150.1|	19441.68	hypothetical protein UM06003.1 [Ustilago maydis 521]								
432. Group probability: 0.9990. Peptides of the group										
TLDLGNPQLSMHSIR	49.44		54.265	1680.862	1680.948	1	2	distinct	0	0.9194

AIALFDNEEVGSVSSHGAESNMLPSLIQR	66.69	51.1989	3070.503	3071.99	1	3	distinct	0	0.9875

The equivalent proteins include

gi|71004598|ref|XP_756965.1|	157397.57	hypothetical protein UM00818.1 [Ustilago maydis 521]

433. Group probability: 0.9990. Peptides of the group

LLPLPSASKPTLR	59.04	55.0217	1391.85	1392.535	2	2	distinct	0	0.9621
AVGAEWAQLPAHLK	62.41	54.848	1489.804	1490.472	1	2	distinct	0	0.9729

The equivalent proteins include

gi|71019847|ref|XP_760154.1|	31421.77	hypothetical protein UM04007.1 [Ustilago maydis 521]

434. Group probability: 0.9990. Peptides of the group

GFEGENCIEEFFHLAHCAQECTAPK	61.64	51.2686	2980.258	2980.618	2	+2,+3	distinct	0	0.999

The equivalent proteins include

gi|71004842|ref|XP_757087.1|	14961.52	hypothetical protein UM00940.1 [Ustilago maydis 521]

435. Group probability: 0.9989. Peptides of the group

NMFASRPAGLASLGEDAEATSDSAQTPSTFHR	93.08	50.8428	3321.532	3322.834	3	3	distinct	0	0.9989

The equivalent proteins include

gi|71005402|ref|XP_757367.1|	155789.3	hypothetical protein UM01220.1 [Ustilago maydis 521]

436. Group probability: 0.9989. Peptides of the group

VINEPTAAAIAYGLDKK	87.08	54.2621	1772.967	1773.744	7	+2,+3	distinct	1	0.9989

The equivalent proteins include

gi|25527326|gb|AAN73310.1|	71783.57	heat-shock protein 70 [Cotesia rubecula]
gi|21427238|gb|AAM53144.1|	50697.31	Hsp70 protein [Carcharias taurus]
gi|21427240|gb|AAM53145.1|	50688.29	Hsp70 protein [Carcharias taurus]
gi|21427242|gb|AAM53146.1|	50636.32	Hsp70 protein [Carcharias taurus]
gi|21427244|gb|AAM53147.1|	50695.4	Hsp70 protein [Carcharias taurus]
gi|21427246|gb|AAM53148.1|	50785.37	Hsp70 protein [Carcharias taurus]
gi|21427248|gb|AAM53149.1|	50665.34	Hsp70 protein [Carcharias taurus]
gi|21427250|gb|AAM53150.1|	50695.27	Hsp70 protein [Odontaspis ferox]
gi|21427252|gb|AAM53151.1|	50680.27	Hsp70 protein [Odontaspis ferox]
gi|21427254|gb|AAM53152.1|	50809.53	Hsp70 protein [Odontaspis ferox]
gi|21427256|gb|AAM53153.1|	50744.31	Hsp70 protein [Alopias pelagicus]
gi|21427258|gb|AAM53154.1|	50660.28	Hsp70 protein [Alopias pelagicus]
gi|21427260|gb|AAM53155.1|	50645.2	Hsp70 protein [Alopias pelagicus]
gi|21427262|gb|AAM53156.1|	50528.22	Hsp70 protein [Alopias pelagicus]
gi|21427264|gb|AAM53157.1|	50654.23	Hsp70 protein [Alopias pelagicus]
gi|21427266|gb|AAM53158.1|	50630.29	Hsp70 protein [Alopias pelagicus]
gi|21427268|gb|AAM53159.1|	50528.22	Hsp70 protein [Alopias superciliosus]
gi|21427270|gb|AAM53160.1|	50617.21	Hsp70 protein [Alopias superciliosus]
gi|21427272|gb|AAM53161.1|	50780.39	Hsp70 protein [Alopias superciliosus]
gi|21427274|gb|AAM53162.1|	50828.43	Hsp70 protein [Alopias superciliosus]
gi|21427278|gb|AAM53164.1|	50771.29	Hsp70 protein [Alopias superciliosus]
gi|21427280|gb|AAM53165.1|	50746.46	Hsp70 protein [Alopias vulpinus]
gi|21427282|gb|AAM53166.1|	50617.33	Hsp70 protein [Alopias vulpinus]
gi|21427284|gb|AAM53167.1|	50620.35	Hsp70 protein [Alopias vulpinus]
gi|21427286|gb|AAM53168.1|	50853.6	Hsp70 protein [Alopias vulpinus]
gi|21427288|gb|AAM53169.1|	50704.4	Hsp70 protein [Alopias vulpinus]
gi|21427290|gb|AAM53170.1|	50718.23	Hsp70 protein [Lamna ditropis]
gi|21427292|gb|AAM53171.1|	50881.4	Hsp70 protein [Lamna ditropis]
gi|21427294|gb|AAM53172.1|	50842.31	Hsp70 protein [Lamna ditropis]
gi|21427296|gb|AAM53173.1|	50788.33	Hsp70 protein [Lamna ditropis]
gi|21427298|gb|AAM53174.1|	50722.32	Hsp70 protein [Lamna ditropis]
gi|21427300|gb|AAM53175.1|	50655.17	Hsp70 protein [Lamna ditropis]
gi|21427304|gb|AAM53177.1|	50798.35	Hsp70 protein [Lamna ditropis]
gi|21427306|gb|AAM53178.1|	50794.56	Hsp70 protein [Megachasma pelagios]
gi|21427308|gb|AAM53179.1|	50780.28	Hsp70 protein [Megachasma pelagios]
gi|21427310|gb|AAM53180.1|	50804.38	Hsp70 protein [Megachasma pelagios]
gi|21427312|gb|AAM53181.1|	50727.32	Hsp70 protein [Megachasma pelagios]
gi|21427314|gb|AAM53182.1|	50904.38	Hsp70 protein [Megachasma pelagios]
gi|21427316|gb|AAM53183.1|	50800.39	Hsp70 protein [Megachasma pelagios]
gi|21427318|gb|AAM53184.1|	50888.49	Hsp70 protein [Megachasma pelagios]
gi|21427320|gb|AAM53185.1|	50706.56	Hsp70 protein [Mitsukurina owstoni]
gi|21427322|gb|AAM53186.1|	50833.27	Hsp70 protein [Mitsukurina owstoni]
gi|21427326|gb|AAM53188.1|	50529.25	Hsp70 protein [Mitsukurina owstoni]
gi|21427328|gb|AAM53189.1|	50741.29	Hsp70 protein [Odontaspis ferox]
gi|21427330|gb|AAM53190.1|	50676.39	Hsp70 protein [Odontaspis ferox]
gi|21427332|gb|AAM53191.1|	50800.31	Hsp70 protein [Odontaspis ferox]

gi|21427334|gb|AAM53192.1|	50581.34	Hsp70 protein [Pseudocarcharias kamoharai]
gi|21427336|gb|AAM53193.1|	50807.45	Hsp70 protein [Pseudocarcharias kamoharai]
gi|21427338|gb|AAM53194.1|	50850.43	Hsp70 protein [Pseudocarcharias kamoharai]
gi|21427340|gb|AAM53195.1|	50743.35	Hsp70 protein [Pseudocarcharias kamoharai]
gi|21427344|gb|AAM53197.1|	50798.37	Hsp70 protein [Cetorhinus maximus]
gi|21427346|gb|AAM53198.1|	50921.29	Hsp70 protein [Cetorhinus maximus]
gi|21427348|gb|AAM53199.1|	50763.37	Hsp70 protein [Cetorhinus maximus]
gi|21427350|gb|AAM53200.1|	50755.27	Hsp70 protein [Cetorhinus maximus]
gi|21427352|gb|AAM53201.1|	50724.25	Hsp70 protein [Cetorhinus maximus]
gi|21427356|gb|AAM53203.1|	50712.13	Hsp70 protein [Cetorhinus maximus]
gi|50427305|ref|XP_462265.1|	73024.02	hypothetical protein DEHA0G17688g [Debaryomyces hansenii CBS767]
gi|1854623|gb|AAB48232.1|	23794.29	70-kDa heat shock protein [unidentified soil organism]

437. Group probability: 0.9989. Peptides of the group

GHYTEGAELVDSVLDIVR	93.41	53.6785	1971.99	1973.099	2	+2,+3	distinct	0	0.9946
GHYTEGAELVDSVLDIVRK	56.85	53.4582	2100.085	2101.066	1	3	distinct	1	0.7898

The equivalent proteins include

gi|68534412|gb|AAH99253.1|	50490.29	LOC446922 protein [Xenopus laevis]
gi|72006211|ref|XP_787610.1|	21252.75	PREDICTED: similar to tubulin, beta, 2, partial [Strongylocentrotus purpuratus]
gi|72180815|ref|XP_798940.1|	50958.47	PREDICTED: similar to tubulin, beta, 2 [Strongylocentrotus purpuratus]
gi|47228484|emb|CAG05304.1|	52771.52	unnamed protein product [Tetraodon nigroviridis]
gi|56118895|ref|NP_001008056.1|	50459.2	MGC79632 protein [Xenopus tropicalis]
gi|55239807|gb|EAA10161.3|	50270.03	ENSANGP00000013034 [Anopheles gambiae str. PEST]
gi|77748195|gb|AAI06693.1|	50559.25	MGC52834 protein [Xenopus laevis]
gi|51593543|gb|AAH78577.1|	50753.86	LOC446922 protein [Xenopus laevis]

438. Group probability: 0.9989. Peptides of the group

FPTQPQFAR	52.3	55.9521	1090.556	1090.94	1	2	distinct	0	0.9203
VLKPGGVFSCLEFGK	69.14	54.4555	1636.865	1637.663	4	2	distinct	0	0.9856

The equivalent proteins include

gi|71005138|ref|XP_757235.1|	42430.09	hypothetical protein UM01088.1 [Ustilago maydis 521]

439. Group probability: 0.9988. Peptides of the group

GLTEEALADLYPEAIIMKPGYLANAQR	58.1	51.3395	2946.516	2947.9	2	+2,+3	distinct	0	0.9988

The equivalent proteins include

gi|71004974|ref|XP_757153.1|	27846.4	hypothetical protein UM01006.1 [Ustilago maydis 521]

440. Group probability: 0.9988. Peptides of the group

IGGIGTVPVGR	66.14	55.3583	1024.603	1024.899	11	2	shared(36)	0	0.978
GSFRYAWVLDK	67.01	55.1741	1340.688	1340.443	11	+1,+2	distinct	1	0.9986

The equivalent proteins include

gi|55832354|gb|AAV66691.1|	37934.63	elongation factor 1 alpha [Battus polystictus]
gi|17027007|gb|AAL34049.1|	39648.71	elongation factor-1 alpha [Pycnocentrodes sp. UMSP-New Zealand]

441. Group probability: 0.9988. Peptides of the group

KTTQPSYVPTVTICHK	96.82	54.0342	1858.961	1859.743	1	2	distinct	1	0.9988

The equivalent proteins include

gi|71021579|ref|XP_761020.1|	41019.09	hypothetical protein UM04873.1 [Ustilago maydis 521]

442. Group probability: 0.9988. Peptides of the group

QNASPFLSSSDPEKGEMHPDAR	63.18	52.7309	2399.081	2399.683	2	+2,+3	distinct	1	0.9988

The equivalent proteins include

gi|71017585|ref|XP_759023.1|	13583.87	hypothetical protein UM02876.1 [Ustilago maydis 521]

443. Group probability: 0.9988. Peptides of the group

HYGQPVTTK	51.49	56.371	1029.524	1029.946	1	2	distinct	0	0.9137
LESGNFAWGSEHITAK	68.76	54.2386	1745.837	1746.807	1	2	distinct	0	0.9857

The equivalent proteins include

gi|71018855|ref|XP_759658.1|	23557.51	hypothetical protein UM03511.1 [Ustilago maydis 521]

444. Group probability: 0.9988. Peptides of the group

NLVQLHSYK	51.07		55.8688	1100.598	1100.795	2	+1,+2	distinct	0	0.988
RTAGAVSNVVAK	48.11		55.6917	1171.667	1171.992	1	2	distinct	1	0.8963

The equivalent proteins include

gi|71021849|ref|XP_761155.1|	24211.38	hypothetical protein UM05008.1 [Ustilago maydis 521]

445. Group probability: 0.9987. Peptides of the group

ISQAAIIGLK	58.13		55.9464	1012.628	1013.162	1	2	distinct	0	0.7663
KFFTLGVTPR	82.21		55.3674	1164.665	1165.033	4	2	distinct	1	0.9944

The equivalent proteins include

gi|71018433|ref|XP_759447.1|	16881.69	hypothetical protein UM03300.1 [Ustilago maydis 521]

446. Group probability: 0.9987. Peptides of the group

GIAAIYPITTMDHPFFLEK	94.48		53.8684	2163.107	2163.991	3	2	distinct	0	0.9987

The equivalent proteins include

gi|71009808|ref|XP_758314.1|	35516.89	hypothetical protein UM02167.1 [Ustilago maydis 521]

447. Group probability: 0.9987. Peptides of the group

AVDVVGQAGKPR	63.65		55.2554	1195.667	1195.99	1	2	distinct	0	0.9101
TISGFQTHTTPVR	69.67		54.9514	1443.747	1443.774	1	2	distinct	0	0.9851

The equivalent proteins include

gi|71017643|ref|XP_759052.1|	105333.72	hypothetical protein UM02905.1 [Ustilago maydis 521]

448. Group probability: 0.9985. Peptides of the group

FFEGHPQQMLSAMDR	63.34		54.3394	1792.802	1794.083	2	2	distinct	0	0.9761
LSSLPDHTLVYCGHEYTK	51.08		53.3753	2119.004	2119.453	1	2	distinct	0	0.9384

The equivalent proteins include

gi|71004140|ref|XP_756736.1|	29752.7	hypothetical protein UM00589.1 [Ustilago maydis 521]

449. Group probability: 0.9985. Peptides of the group

TGAPEYANGSDIVLDHNIK	47.15		53.5882	2012.98	2014.275	1	3	distinct	0	0.8963
CLRPTAYPIPYDGGAGDILK	66.84		53.2808	2176.099	2176.833	1	2	distinct	0	0.9856

The equivalent proteins include

gi|71023007|ref|XP_761733.1|	34509.94	hypothetical protein UM05586.1 [Ustilago maydis 521]

450. Group probability: 0.9985. Peptides of the group

KITMEQLK	49		56.5825	989.558	990.153	1	2	distinct	1	0.8921
EHGSHDDLWLLIDGK	69.33		54.2831	1733.837	1734.719	1	2	distinct	0	0.9859

The equivalent proteins include

gi|71005550|ref|XP_757441.1|	22671.8	hypothetical protein UM01294.1 [Ustilago maydis 521]

451. Group probability: 0.9985. Peptides of the group

STNANAHVAASKPEQK	94.25		54.5887	1651.828	1652.213	6	2	distinct	0	0.9985

The equivalent proteins include

gi|71022717|ref|XP_761588.1|	44562.56	hypothetical protein UM05441.1 [Ustilago maydis 521]

452. Group probability: 0.9984. Peptides of the group

DSTIIMQLLR	45.88		55.6848	1188.654	1188.947	1	2	shared(4)	0	0.5759
LDTLSEESYKDSTLIMQLLR	89.69		53.1616	2354.204	2355.033	2	2	distinct	1	0.9981

The equivalent proteins include

gi|109139601|ref|XP_001116299.1|	3830.82	PREDICTED: similar to tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein, parti

453. Group probability: 0.9984. Peptides of the group

HRYEVNPEYVER	50.38		54.7169	1589.759	1590.27	1	2	distinct	1	0.9167
LGLRPSIFQEGTEEWSK	64.83		53.7057	1976	1976.823	1	2	distinct	0	0.9808

The equivalent proteins include

gi|71004502|ref|XP_756917.1|	75836	hypothetical protein UM00770.1 [Ustilago maydis 521]

454. Group probability: 0.9984. Peptides of the group

YTAASQLEHLHSR	94.95		54.579	1511.748	1512.26	2	2	distinct	0	0.9984

The equivalent proteins include

gi|71004458|ref|XP_756895.1|	9825.8	hypothetical protein UM00748.1 [Ustilago maydis 521]

455. Group probability: 0.9984. Peptides of the group

HMTVSDLLLIAPDGSIVDGGRPER	92.34		52.5133	2547.311	2548.276	1	3	distinct	0	0.9984

The equivalent proteins include

gi|71003758|ref|XP_756545.1|	36297.25	hypothetical protein UM00398.1 [Ustilago maydis 521]

456. Group probability: 0.9983. Peptides of the group

SPDAVSEGAPSASALLGDKK	58.1		53.8467	1898.958	1899.743	1	3	distinct	1	0.9615

SGADTSFPHPMDSSAKPGEGAWSAPNPFA	50.13	51.4664	2915.282	2916.173	1	2	distinct	0	0.9564

The equivalent proteins include

gi|1346365|sp|P49605|KAPR_USTMA	56094.23	cAMP-dependent protein kinase regulatory subunit (PKA regulatory subunit)
gi|71024735|ref|XP_762597.1|	55337.68	cAMP-dependent protein kinase regulatory subunit [Ustilago maydis 521]

457. Group probability: 0.9983. Peptides of the group

KLGFTGAK	51.85	56.3648	820.481	820.781	2	+1,+2	distinct	1	0.9722
MIGNHLITK	59.75	55.3304	1025.569	1025.718	3	2	distinct	0	0.938

The equivalent proteins include

gi|71003698|ref|XP_756515.1|	49835.73	hypothetical protein UM00368.1 [Ustilago maydis 521]

458. Group probability: 0.9982. Peptides of the group

YRVEAHTGEVNALAFSPENENILVTGSSDK	88.53	50.9194	3246.579	3247.37	1	3	distinct	1	0.9982

The equivalent proteins include

gi|71021353|ref|XP_760907.1|	54193.57	hypothetical protein UM04760.1 [Ustilago maydis 521]

459. Group probability: 0.9982. Peptides of the group

ALFEQITEGLK	68.79	55.4682	1247.676	1248.541	2	+1,+2	distinct	0	0.9982

The equivalent proteins include

gi|71017843|ref|XP_759152.1|	14681.69	hypothetical protein UM03005.1 [Ustilago maydis 521]

460. Group probability: 0.9982. Peptides of the group

HGGADYIFALLTGYTDPPAGVK	89.54	53.0776	2262.132	2262.591	1	2	distinct	0	0.9982

The equivalent proteins include

gi|71021095|ref|XP_760778.1|	56448.55	hypothetical protein UM04631.1 [Ustilago maydis 521]

461. Group probability: 0.9981. Peptides of the group

VLTIGDGIAR	60.13	56.1474	1013.587	1014.314	1	2	shared(2)	0	0.9608
VVDALGNPIDGK	87.75	55.4031	1196.64	1197.823	1	2	shared(6)	0	0.9821
TAVAIDTIINQK	45.22	55.3925	1285.724	1285.683	1	1	shared(2)	0	0.8672
HAIIIYDDLSK	80.76	55.5162	1286.687	1287.158	9	+1,+2	shared(5)	0	0.9997
GIRPAINVGLSVSR	71.89	54.778	1437.842	1438.903	22	2	shared(4)	0	0.9882

The equivalent proteins include

gi|74096071|ref|NP_001027729.1|	60032.65	ATP synthase alpha-subunit [Ciona intestinalis]

462. Group probability: 0.9980. Peptides of the group

GPYESGSGHSSGLGHR	91.15	54.567	1583.708	1584.003	1	2	distinct	0	0.998

The equivalent proteins include

gi|88952458|ref|XP_942310.1|	197208.28	PREDICTED: similar to Hornerin [Homo sapiens]
gi|28557150|dbj|BAC57496.1|	48796.73	hornerin [Homo sapiens]
gi|55588478|ref|XP_524874.1|	126987.98	PREDICTED: hypothetical protein XP_524874 [Pan troglodytes]
gi|57546919|tpd|FAA00004.1|	283115.88	TPA: Hornerin [Homo sapiens]
gi|57864582|ref|NP_001009931.1|	283139.96	hornerin [Homo sapiens]
gi|40795897|gb|AAR91619.1|	283110.9	hornerin precursor [Homo sapiens]

463. Group probability: 0.9980. Peptides of the group

HKGVMVGMGQK (0000010000000)	70.83	55.6094	1170.6	1170.959	31	+1,+2	shared(8)	1	0.9992
SYELPDGKVITIGNER	64.43	54.1766	1789.921	1790.679	1	2	shared(14)	1	0.9686
YPIEHGIVTNWDDMEK	86.65	53.8856	1945.888	1946.228	3	+2,+3	shared(6)	0	0.9985
VAPEEHPVLLTEAPINPK	88.95	53.6979	1953.057	1953.863	9	2	shared(9)	0	0.9916
FRCPEALFQPSLLGLEAAGIHETTYNSIMK	54.07	50.4408	3392.69	3394.054	1	3	distinct	1	0.9641

The equivalent proteins include

gi|57222982|gb|AAW41026.1|	42307.21	actin [Cryptococcus neoformans var. neoformans JEC21]

464. Group probability: 0.9980. Peptides of the group

ATQGIFPLKDVYVR	68.57	54.5913	1605.888	1606.127	1	2	distinct	1	0.9843
IVEASLADLNKDDEQAYR	45.06	53.685	2049.001	2048.865	1	3	distinct	1	0.8707

The equivalent proteins include

gi|71021915|ref|XP_761188.1|	35677.88	hypothetical protein UM05041.1 [Ustilago maydis 521]

465. Group probability: 0.9980. Peptides of the group

LLVVVGPCSIHDVR	55.06	54.8539	1562.86	1564.283	4	2	distinct	0	0.9484
SIKPLIPPQILVEEYPLSLSAAQTVASGR	51.19	51.1666	3076.717	3077.475	2	2	distinct	0	0.9605

The equivalent proteins include

gi|71018153|ref|XP_759307.1|	56793.05	hypothetical protein UM03160.1 [Ustilago maydis 521]								
466. Group probability: 0.9980. Peptides of the group										
HAVLANPAVLFCGYK	91.49		54.9806	1658.86	1659.671	1	2	distinct	0	0.998
The equivalent proteins include										
gi|71011575|ref|XP_758471.1|	15841.02	hypothetical protein UM02324.1 [Ustilago maydis 521]								
467. Group probability: 0.9979. Peptides of the group										
VKDADGNEVFFK	66.3		54.9656	1367.672	1368.212	1	2	distinct	1	0.9793
AESDNAQPKPEGGEQLNIK	45.16		54.0061	2023.981	2024.102	1	2	distinct	0	0.8988
The equivalent proteins include										
gi|71023561|ref|XP_762010.1|	10389.08	hypothetical protein UM05863.1 [Ustilago maydis 521]								
468. Group probability: 0.9979. Peptides of the group										
GFGYVEFAAQESAQAAIDAMTGQELAGRPLR	86.08		51.0859	3253.582	3254.985	2	3	distinct	0	0.9979
The equivalent proteins include										
gi|71024221|ref|XP_762340.1|	48710.15	hypothetical protein UM06193.1 [Ustilago maydis 521]								
469. Group probability: 0.9979. Peptides of the group										
LLGDFQLTGLPPAPK	84.03		54.6564	1565.882	1565.076	66	2	distinct	0	0.9488
HAVITVPAYFNDSQR	78.66		54.337	1716.858	1717.543	9	+2,+3	shared(3)	0	0.9998
The equivalent proteins include										
gi|57230060|gb|AAW46461.1|	71594.17	heat shock protein, putative [Cryptococcus neoformans var. neoformans JEC21]								
470. Group probability: 0.9978. Peptides of the group										
RAPAAPPATAAPAVGAQK	89.44		54.5597	1643.911	1644.823	4	2	distinct	1	0.9978
The equivalent proteins include										
gi|71024287|ref|XP_762373.1|	86789.3	hypothetical protein UM06226.1 [Ustilago maydis 521]								
471. Group probability: 0.9978. Peptides of the group										
LVDLLTHPSTAVQTPALR	51.22		53.8028	1931.084	1931.336	1	2	distinct	0	0.9386
YLVSQGCIKPLCDLLSSMDNK	58.26		52.6176	2440.18	2440.917	1	3	distinct	0	0.9643
The equivalent proteins include										
gi|71021483|ref|XP_760972.1|	96727.71	hypothetical protein UM04825.1 [Ustilago maydis 521]								
472. Group probability: 0.9978. Peptides of the group										
EIVKVPQMAESITEGTLK	65.22		53.6598	1972.055	1972.323	1	2	distinct	1	0.9821
KPAPSADPQSRPSAASSSPPASK	43.51		53.1292	2220.113	2221.251	1	3	distinct	0	0.8774
The equivalent proteins include										
gi|71005996|ref|XP_757664.1|	66880.61	hypothetical protein UM01517.1 [Ustilago maydis 521]								
473. Group probability: 0.9978. Peptides of the group										
LALVTGGEIASTFDRPDLVK	88.18		53.4582	2101.142	2101.219	1	2	distinct	0	0.9978
The equivalent proteins include										
gi|71024305|ref|XP_762382.1|	56606.62	hypothetical protein UM06235.1 [Ustilago maydis 521]								
474. Group probability: 0.9978. Peptides of the group										
FESVFPLLVEELTAYLTSEK	88.09		53.1049	2314.198	2314.833	5	2	distinct	0	0.9978
The equivalent proteins include										
gi|71005854|ref|XP_757593.1|	46046.43	hypothetical protein UM01446.1 [Ustilago maydis 521]								
475. Group probability: 0.9978. Peptides of the group										
SIVLAALECLHDLAADSR	89.02		53.6981	1952.999	1953.631	1	2	distinct	0	0.9978
The equivalent proteins include										
gi|71006282|ref|XP_757807.1|	124963.58	hypothetical protein UM01660.1 [Ustilago maydis 521]								
476. Group probability: 0.9977. Peptides of the group										
LPTGEALSGNEPDSIYLAPGVDKLPFPAGTK	85.31		50.9569	3153.623	3154.667	1	3	distinct	1	0.9977
The equivalent proteins include										
gi|71018891|ref|XP_759676.1|	39759.94	hypothetical protein UM03529.1 [Ustilago maydis 521]								
477. Group probability: 0.9977. Peptides of the group										
SKPPIVIPGR	45.25		55.6642	1062.655	1063.283	1	2	distinct	0	0.857
AAAVGSNAQNAAVIAASNR	83.99		54.1694	1754.902	1755.811	1	2	distinct	0	0.9842
The equivalent proteins include										
gi|71019603|ref|XP_760032.1|	32403.81	hypothetical protein UM03885.1 [Ustilago maydis 521]								
478. Group probability: 0.9977. Peptides of the group										

EGLLSSHPSHQATR	68.03	54.885	1518.754	1518.852	4	2	distinct	0	0.9834
TASHPELFGPFAER	43.85	54.7099	1557.758	1557.92	1	2	distinct	0	0.8624

The equivalent proteins include

gi|71022407|ref|XP_761433.1|	30140.12	hypothetical protein UM05286.1 [Ustilago maydis 521]

479. Group probability: 0.9976. Peptides of the group

LLASGGAHILPSFGCK	89.36	54.6682	1626.855	1627.366	2	2	distinct	0	0.9976

The equivalent proteins include

gi|71004594|ref|XP_756963.1|	40326.86	hypothetical protein UM00816.1 [Ustilago maydis 521]

480. Group probability: 0.9976. Peptides of the group

TASVEIDTPANKGETK	68.4	54.9806	1659.831	1659.848	2	+2,+3	distinct	1	0.9976

The equivalent proteins include

gi|71019307|ref|XP_759884.1|	74427.42	hypothetical protein UM03737.1 [Ustilago maydis 521]

481. Group probability: 0.9976. Peptides of the group

ALGIMALLDEGETDWK (000001000000000000)	66.94	54.1671	1776.86	1775.713	3	2	distinct	0	0.6934
IPDGKPENQFAFSGEAK	90.8	54.0647	1833.89	1834.394	2	2	shared(2)	0	0.998
IYKIPDGKPENQFAFSGEAK	58.75	53.1024	2238.132	2238.973	2	2	shared(2)	1	0.9709

The equivalent proteins include

gi|230265|pdb|1PYP|	32076.43	Inorganic Pyrophosphatase (E.C.3.6.1.1)
gi|3114390|pdb|1HUJ|B	31806.31	Chain B, Refined Structure Of Yeast Inorganic Pyrophosphatase And Its K61r Mutant
gi|3114392|pdb|1HUK|B	31778.3	Chain B, Refined Structure Of Yeast Inorganic Pyrophosphatase And Its K61r Mutant
gi|1942887|pdb|1YPP|B	32148.45	Chain B, Acid Anhydride Hydrolase
gi|6729691|pdb|117E|B	32235.55	Chain B, The R78k And D117e Active Site Variants Of Saccharomyces Cerevisiae Soluble Inorganic Pyro
gi|6729856|pdb|8PRK|B	32324.57	Chain B, The R78k And D117e Active Site Variants Of Saccharomyces Cerevisiae Soluble Inorganic Pyro
gi|13787035|pdb|1E9G|A	32231.49	Chain A, Structure Of Inorganic Pyrophosphatase
gi|13787036|pdb|1E9G|B	32174.43	Chain B, Structure Of Inorganic Pyrophosphatase
gi|13787034|pdb|1E6A|B	32221.54	Chain B, Fluoride-Inhibited Substrate Complex Of Saccharomyces Cerevisiae Inorganic Pyrophosphatase
gi|6319483|ref|NP_009565.1|	32336.55	Cytoplasmic inorganic pyrophosphatase (PPase), catalyzes the rapid exchange of oxygens from Pi with
gi|4199|emb|CAA31629.1|	32352.58	unnamed protein product [Saccharomyces cerevisiae]

482. Group probability: 0.9975. Peptides of the group

TLIGHTENVCALDAGPHGQYLVSGSWDK	85.62	51.3011	3024.44	3025.727	1	3	distinct	0	0.9975

The equivalent proteins include

gi|71018451|ref|XP_759456.1|	87884.31	hypothetical protein UM03309.1 [Ustilago maydis 521]

483. Group probability: 0.9975. Peptides of the group

DGLTCAQCHQTENSVECNAK	56.91	53.0257	2320.947	2321.182	2	+2,+3	distinct	0	0.9975

The equivalent proteins include

gi|71022279|ref|XP_761369.1|	25781.4	hypothetical protein UM05222.1 [Ustilago maydis 521]

484. Group probability: 0.9974. Peptides of the group

EHNVDLAQVHGTGR	89.44	55.2527	1531.749	1532.335	1	2	distinct	0	0.9974

The equivalent proteins include

gi|71018229|ref|XP_759345.1|	163493.2	hypothetical protein UM03198.1 [Ustilago maydis 521]

485. Group probability: 0.9974. Peptides of the group

HGGGGGGFGGGGFGSR	60.18	55.3495	1319.575	1320.219	1	2	distinct	0	0.969
FLEQQNKVLQTK	86.32	54.9315	1474.814	1475.173	1	2	shared(2)	1	0.9933

The equivalent proteins include

gi|181402|gb|AAC83410.1|	66110.5	epidermal cytokeratin 2 [Homo sapiens]
gi|68563400|gb|AAH99643.1|	65678.32	Keratin 2A (epidermal ichthyosis bullosa of Siemens) [Homo sapiens]

486. Group probability: 0.9974. Peptides of the group

KNMNFILNNIQDLDNNQK (000100000000000000000)	58.45	53.7407	2191.069	2191.484	8	+2,+3	distinct	1	0.9974

The equivalent proteins include

gi|9757403|emb|CAC03103.1|	32521.89	erythrocyte membrane-associated antigen [Plasmodium falciparum]
gi|23498284|emb|CAD49256.1|	512529.66	erythrocyte membrane-associated antigen, putative [Plasmodium falciparum 3D7]

487. Group probability: 0.9974. Peptides of the group

LGANSLLDIVVFGR	117.51	54.9405	1472.835	1473.482	43	+1,+2	shared(3)	0	1
ANLPNQDLEFVQFHPTGIYGAGCLITEGSR	42.49	50.9929	3303.598	3304.644	1	3	distinct	0	0.8999

The equivalent proteins include

gi|66505480|ref|XP_623065.1|	73271.54	PREDICTED: similar to ENSANGP00000010243 [Apis mellifera]

488. Group probability: 0.9974. Peptides of the group

KFTPGYPTPSLGR	45.71	54.8868	1419.751	1420.5	3	2	distinct	1	0.8785
TVDAVAHTVQLEDGSSIK	65.63	53.9664	1868.948	1869.728	1	3	distinct	0	0.9786

The equivalent proteins include

gi|71018021|ref|XP_759241.1|	59043	hypothetical protein UM03094.1 [Ustilago maydis 521]

489. Group probability: 0.9974. Peptides of the group

MAQEIISHYPEQYKK	64.64	54.1447	1863.919	1864.233	5	+2,+3	distinct	1	0.9974

The equivalent proteins include

gi|71004230|ref|XP_756781.1|	29697.68	hypothetical protein UM00634.1 [Ustilago maydis 521]

490. Group probability: 0.9974. Peptides of the group

DKTCLLGCGVTTGWGAATHTAK	45.59	53.0213	2304.099	2305.281	1	3	distinct	1	0.8943
LGDKDIVSHLVDITDGGLDYTFDCTGNVK	58.76	51.1368	3166.513	3167.902	1	3	distinct	1	0.975

The equivalent proteins include

gi|71024323|ref|XP_762391.1|	34222.97	hypothetical protein UM06244.1 [Ustilago maydis 521]

491. Group probability: 0.9973. Peptides of the group

VFSGHSDAVSCGSFTPDGKR	64.39	53.3467	2109.954	2110.983	2	+2,+3	distinct	1	0.9973

The equivalent proteins include

gi|71024559|ref|XP_762509.1|	46822.68	hypothetical protein UM06362.1 [Ustilago maydis 521]

492. Group probability: 0.9973. Peptides of the group

KFFDASDASK	53.89	55.9175	1114.529	1115.232	1	2	distinct	1	0.9326
SPAFASFHAEK	59.41	55.5835	1190.572	1191.042	1	2	distinct	0	0.9602

The equivalent proteins include

gi|71021641|ref|XP_761051.1|	38717.67	hypothetical protein UM04904.1 [Ustilago maydis 521]

493. Group probability: 0.9973. Peptides of the group

YHLYCSTSPAPSAPPAK	53.28	54.0428	1845.872	1846.633	1	2	distinct	0	0.9466
MPDPVKPLSINIPINQEVAAQPSAELPK	51.22	51.3312	2995.605	2996.676	1	3	distinct	0	0.9497

The equivalent proteins include

gi|71019717|ref|XP_760089.1|	155797.09	hypothetical protein UM03942.1 [Ustilago maydis 521]

494. Group probability: 0.9972. Peptides of the group

VLANACGPCIGQWNR	61.75	54.2964	1714.803	1714.734	1	2	distinct	0	0.9726
TAIPSSVHCDHLIQAFEGAEADLKR	44.34	51.9797	2764.36	2765.54	1	3	distinct	1	0.8962

The equivalent proteins include

gi|71015753|ref|XP_758838.1|	112481.38	hypothetical protein UM02691.1 [Ustilago maydis 521]

495. Group probability: 0.9970. Peptides of the group

DLKDTLVTVHPTSFVEFPTGAVEGAVGFK	83.08	51.201	3060.581	3060.985	2	3	distinct	1	0.997

The equivalent proteins include

gi|71019281|ref|XP_759871.1|	52755.44	hypothetical protein UM03724.1 [Ustilago maydis 521]

496. Group probability: 0.9970. Peptides of the group

FRGNAPPAASSSNAPGGTSQVDPTSANQAGKP	81.65	51.2478	3038.444	3039.408	5	3	distinct	1	0.997

The equivalent proteins include

gi|71006756|ref|XP_758043.1|	10766.06	hypothetical protein UM01896.1 [Ustilago maydis 521]

497. Group probability: 0.9969. Peptides of the group

LPDGTVVEEWEFFR	87.15	54.2198	1722.825	1723.197	1	2	distinct	0	0.9969

The equivalent proteins include

gi|71019107|ref|XP_759784.1|	10913.15	hypothetical protein UM03637.1 [Ustilago maydis 521]							
498. Group probability: 0.9969. Peptides of the group									
QTQTFSTYADNQPGVLIQVFEGER	76.37	52.0329	2727.314	2727.613	7	+2,+3	distinct	0	0.9969
The equivalent proteins include									
gi|53829564|gb|AAU94661.1|	52385.94	HSP70 [Corallochytrium limacisporum]							
499. Group probability: 0.9968. Peptides of the group									
DTLLALHR	51.48	55.1176	937.534	938.152	1	2	distinct	0	0.9158
YTVATSDPPTGPAEDGERAPTTTSYHR	55.06	51.6092	2876.321	2877.598	1	3	distinct	1	0.9625
The equivalent proteins include									
gi|71021949|ref|XP_761205.1|	15835.32	hypothetical protein UM05058.1 [Ustilago maydis 521]							
500. Group probability: 0.9968. Peptides of the group									
TVVTEGLSQDPTYVPVIYDPSKPR	51.81	52.242	2660.37	2661.627	1	3	distinct	0	0.9439
GASQGQYHQQGWGEYHAGDAGAYYEDNTSR	48.97	50.9151	3302.367	3303.754	1	3	distinct	0	0.9434
The equivalent proteins include									
gi|71013128|ref|XP_758558.1|	92596.6	hypothetical protein UM02411.1 [Ustilago maydis 521]							
501. Group probability: 0.9968. Peptides of the group									
GVVASSQEHHAK	50.71	55.4723	1248.621	1249.162	2	2	distinct	0	0.9178
GQGAFQRPIQGGKEEK	57.4	54.2723	1728.891	1729.583	3	2	distinct	1	0.9613
The equivalent proteins include									
gi|71006290|ref|XP_757811.1|	40884.63	hypothetical protein UM01664.1 [Ustilago maydis 521]							
502. Group probability: 0.9968. Peptides of the group									
LIFETLDDQIKSELPQLVDLR	83.39	52.6677	2484.347	2485.303	1	2	distinct	1	0.9968
The equivalent proteins include									
gi|71022401|ref|XP_761430.1|	29704.06	hypothetical protein UM05283.1 [Ustilago maydis 521]							
503. Group probability: 0.9968. Peptides of the group									
VALTGLTIAEYFR	96.01	54.8052	1452.798	1453.379	17	2	shared(8)	0	0.9932
VALVFGQMNEPPGAR	76.13	54.7519	1584.808	1585.022	7	2	shared(6)	0	0.9745
LVLEVAQHLGENTVR	84.18	54.5381	1676.921	1677.711	15	+2,+3	shared(6)	0	0.9996
DEEGQDVLLFIDNIFR	112.41	54.0622	1921.942	1922.963	29	2	shared(3)	0	0.9935
SLQDIIAILGMDELSEQDKLTVER	74.18	52.0836	2715.4	2716.853	3	2	shared(3)	1	0.92
The equivalent proteins include									
gi|50307119|ref|XP_453538.1|	54035.37	ATPB_KLULA [Kluyveromyces lactis]							
gi|171110|gb|AAA34444.1|	54947	F1-ATPase beta-subunit precursor							
gi|6322581|ref|NP_012655.1|	54816.94	Beta subunit of the F1 sector of mitochondrial F1F0 ATP synthase, which is a large, evolutionarily							
504. Group probability: 0.9967. Peptides of the group									
IQDKEGIPPDQQR	47.88	54.643	1522.774	1523.197	1	2	shared(4)	1	0.8358
ECPSPECGAGIFMSWHR	51.64	54.0308	2019.839	2020.067	1	2	distinct	0	0.9384
TISDYNIQKESTLHLVLR	54.37	53.2751	2129.148	2129.693	13	+2,+3	shared(2)	1	0.9929
The equivalent proteins include									
gi|71021009|ref|XP_760735.1|	18501.85	hypothetical protein UM04588.1 [Ustilago maydis 521]							
505. Group probability: 0.9966. Peptides of the group									
HGGNIPLDEIVEIAR	85.78	54.6146	1631.863	1632.903	6	2	distinct	0	0.9966
The equivalent proteins include									
gi|71013111|ref|XP_758556.1|	27603.56	hypothetical protein UM02409.1 [Ustilago maydis 521]							
506. Group probability: 0.9966. Peptides of the group									
RPDKNDLVNR	48.94	55.2088	1225.653	1225.274	2	3	distinct	1	0.8192
NILKPGNLAPSLQAAR	65.69	54.5841	1661.958	1662.031	6	2	distinct	0	0.9812
The equivalent proteins include									
gi|71022033|ref|XP_761247.1|	21612.41	hypothetical protein UM05100.1 [Ustilago maydis 521]							
507. Group probability: 0.9966. Peptides of the group									
NHIITTQTEHK	60.3	55.3188	1320.679	1320.49	4	+1,+2	distinct	0	0.9633
GASKPFFHTDAAQAAGK	46.99	54.3846	1702.843	1703.609	1	2	distinct	0	0.9067
The equivalent proteins include									
gi|71023387|ref|XP_761923.1|	56220.62	hypothetical protein UM05776.1 [Ustilago maydis 521]							
508. Group probability: 0.9966. Peptides of the group									
VGGAQSIFLADMAGSVLPAVIAHGEGR	82.42	52.2649	2622.359	2623.793	2	3	distinct	0	0.9966
The equivalent proteins include									
gi|71022157|ref|XP_761309.1|	151318.94	hypothetical protein UM05162.1 [Ustilago maydis 521]							

509. Group probability: 0.9965. Peptides of the group

HFEIGGDKK	58.48	56.392	1029.524	1029.328	9	+1,+2	distinct	1	0.9965

The equivalent proteins include

gi|82621114|gb|ABB86245.1|	12242.51	ribosomal protein L41-like [Solanum tuberosum]
gi|4545319|gb|AAD22491.1|	11755.13	80S ribosomal protein L41 [Chlamydomonas reinhardtii]
gi|170920|gb|AAA34366.1|	12278.62	ribosomal protein L41
gi|15236469|ref|NP_193168.1|	12402.65	structural constituent of ribosome [Arabidopsis thaliana]
gi|2500380|sp|Q96499|RL44_GOSHI	12306.63	60S ribosomal protein L44
gi|34901296|ref|NP_911994.1|	12415.63	putative 60S ribosomal protein L44 [Oryza sativa (japonica cultivar-group)]
gi|51011508|gb|AAT92163.1|	12765.92	ribosomal protein L44 [Ixodes pacificus]
gi|15281775|gb|AAK94425.1|	14087.55	60S ribosomal protein L144 [Brassica rapa subsp. pekinensis]
gi|41152660|gb|AAR99579.1|	12372.64	60S ribosomal protein L44 [Phalaenopsis hybrid cultivar]
gi|1272508|dbj|BAA07784.1|	11534.24	L41 ribosomal protein [Candida maltosa]
gi|88185625|gb|EAQ93093.1|	12322.65	60S ribosomal protein L44 [Chaetomium globosum CBS 148.51]
gi|400999|sp|P31866|RL44_PICGU	12057.53	60S ribosomal protein L44 (60S ribosomal protein L41)
gi|90305903|gb|EAS35534.1|	12410.8	60S ribosomal protein L44 [Coccidioides immitis RS]
gi|85857576|gb|ABC86323.1|	14266.67	IP15820p [Drosophila melanogaster]
gi|62648306|ref|XP_575712.1|	92240.66	PREDICTED: similar to Elongation factor 1-gamma (EF-1-gamma) (eEF-1B gamma) [Rattus norvegicus]
gi|62659945|ref|XP_577295.1|	13693.23	PREDICTED: similar to large subunit ribosomal protein L36a [Rattus norvegicus]
gi|66506799|ref|XP_394987.2|	12812.96	PREDICTED: similar to CG7424-PA [Apis mellifera]
gi|12083868|gb|AAG48930.1|	12423.73	ribosomal protein L41 [Filobasidiella neoformans]
gi|61654698|gb|AAX48875.1|	12583.82	L44/L36a [Suberites domuncula]
gi|89047331|ref|XP_945426.1|	12642.73	PREDICTED: similar to large subunit ribosomal protein L36a [Homo sapiens]
gi|9438110|gb|AAF87576.1|	12822.02	putative large subunit ribosomal protein rpL44 [Aedes triseriatus]
gi|55729800|emb|CAH91628.1|	12773.97	hypothetical protein [Pongo pygmaeus]
gi|3128243|gb|AAC39456.1|	12476.68	ribosomal protein L41 [Phaffia rhodozyma]
gi|70909931|emb|CAJ17452.1|	12813.01	ribosomal protein L44e [Curculio glandium]
gi|70909933|emb|CAJ17453.1|	12828.99	ribosomal protein L44e [Dascillus cervinus]
gi|70909935|emb|CAJ17454.1|	12769	ribosomal protein L44e [Eucinetus sp. APV-2005]
gi|70909937|emb|CAJ17455.1|	12769.95	ribosomal protein L44e [Georissus sp. APV-2005]
gi|70909939|emb|CAJ17456.1|	12830.97	ribosomal protein L44e [Hister sp. APV-2005]
gi|70909941|emb|CAJ17457.1|	12798.95	ribosomal protein L44e [Platystomos albinus]
gi|70909943|emb|CAJ17458.1|	12751.84	ribosomal protein L44e [Scarabaeus laticollis]
gi|72144800|ref|XP_797556.1|	10382.61	PREDICTED: similar to CG7424-PA, partial [Strongylocentrotus purpuratus]
gi|9297119|sp|Q00477|RL44P_CANMA	12445.74	60S ribosomal protein L44 P (L41) (L41 P-type)
gi|46137331|ref|XP_390357.1|	13715.49	RL44_PICJA 60S RIBOSOMAL PROTEIN L44 (L41) [Gibberella zeae PH-1]
gi|73997305|ref|XP_852974.1|	12753.87	PREDICTED: similar to large subunit ribosomal protein L36a [Canis familiaris]
gi|94468496|gb|ABF18097.1|	12821.98	60S ribosomal protein L44 [Aedes aegypti]
gi|74008235|ref|XP_538108.2|	24720.87	PREDICTED: similar to large subunit ribosomal protein L36a [Canis familiaris]

gi|76609856|ref|XP_869482.1|	13588.35	PREDICTED: similar to large subunit ribosomal protein L36a [Bos taurus]
gi|50745650|ref|XP_420184.1|	12693.93	PREDICTED: similar to large subunit ribosomal protein L36a [Gallus gallus]
gi|76627666|ref|XP_869973.1|	17771.38	PREDICTED: similar to large subunit ribosomal protein L36a isoform 1 [Bos taurus]
gi|109072449|ref|XP_001088777.1|	17066.16	PREDICTED: similar to large subunit ribosomal protein L36a [Macaca mulatta]
gi|109076423|ref|XP_001089766.1|	13087.08	PREDICTED: similar to large subunit ribosomal protein L36a isoform 3 [Macaca mulatta]
gi|109076425|ref|XP_001089531.1|	10003.43	PREDICTED: similar to large subunit ribosomal protein L36a isoform 1 [Macaca mulatta]
gi|109076427|ref|XP_001089653.1|	13328.15	PREDICTED: similar to large subunit ribosomal protein L36a isoform 2 [Macaca mulatta]
gi|109079214|ref|XP_001102532.1|	12747.88	PREDICTED: similar to large subunit ribosomal protein L36a [Macaca mulatta]
gi|61825609|ref|XP_592570.1|	12741.9	PREDICTED: similar to large subunit ribosomal protein L36a [Bos taurus]
gi|109102188|ref|XP_001100013.1|	12786.75	PREDICTED: similar to large subunit ribosomal protein L36a [Macaca mulatta]
gi|109103955|ref|XP_001104426.1|	12729.96	PREDICTED: similar to large subunit ribosomal protein L36a [Macaca mulatta]
gi|109116135|ref|XP_001113675.1|	12717.88	PREDICTED: similar to large subunit ribosomal protein L36a [Macaca mulatta]
gi|109130491|ref|XP_001089096.1|	12762.87	PREDICTED: similar to large subunit ribosomal protein L36a [Macaca mulatta]
gi|109131574|ref|XP_001094570.1|	16269.81	PREDICTED: similar to large subunit ribosomal protein L36a [Macaca mulatta]
gi|27545275|ref|NP_775369.1|	12804.99	ribosomal protein L36A [Danio rerio]
gi|109499184|ref|XP_001063124.1|	13930.49	PREDICTED: similar to large subunit ribosomal protein L36a [Rattus norvegicus]
gi|109502147|ref|XP_001058998.1|	12703.9	PREDICTED: similar to large subunit ribosomal protein L36a [Rattus norvegicus]
gi|55635137|ref|XP_521714.1|	14043.53	PREDICTED: similar to large subunit ribosomal protein L36a [Pan troglodytes]
gi|109510028|ref|XP_001080446.1|	12666.89	PREDICTED: similar to large subunit ribosomal protein L36a [Rattus norvegicus]
gi|55645971|ref|XP_511676.1|	13390.26	PREDICTED: similar to large subunit ribosomal protein L36a [Pan troglodytes]
gi|55663764|ref|XP_521180.1|	18450.92	PREDICTED: similar to large subunit ribosomal protein L36a [Pan troglodytes]
gi|37622216|gb|AAQ95213.1|	12717.92	migration-inducing protein 6 [Homo sapiens]
gi|1710565|sp|P52809|RL44_PICJA	12459.76	60S ribosomal protein L44 (60S ribosomal protein L41)
gi|4506651|ref|NP_000992.1|	12745.92	ribosomal protein L36a-like protein [Homo sapiens]
gi|71000934|ref|XP_755148.1|	31547.44	ribosomal protein L41 [Aspergillus fumigatus Af293]
gi|24582672|ref|NP_609179.2|	12777.98	Ribosomal protein L36A CG7424-PA [Drosophila melanogaster]
gi|4889|emb|CAA50074.1|	12533.83	ribosomal protein L41 [Debaryomyces occidentalis]
gi|50545894|ref|XP_500485.1|	12579.78	hypothetical protein [Yarrowia lipolytica]
gi|51873963|gb|AAH78555.1|	12737.88	MGC85428 protein [Xenopus laevis]
gi|71004688|ref|XP_757010.1|	42244.67	hypothetical protein UM00863.1 [Ustilago maydis 521]
gi|67540022|ref|XP_663785.1|	12387.71	60S ribosomal protein L44 [Aspergillus nidulans FGSC A4]
gi|49532836|dbj|BAD26653.1|	12569.84	Ribosomal protein L44 [Plutella xylostella]
gi|38141518|emb|CAE53391.1|	12758.98	ribosomal protein L36A [Platichthys flesus]
gi|21435718|gb|AAM53948.1|	12630.8	ribosomal protein L44 [Choristoneura parallela]

gi|67005522|gb|AAY62379.1|	12407.74	ribosomal protein L41 [Candida glycerinogenes]
gi|30267873|gb|AAP21779.1|	12552.81	ribosomal protein L36a [Branchiostoma belcheri tsingtaunese]
gi|89034458|ref|XP_943996.1|	14156.53	PREDICTED: similar to large subunit ribosomal protein L36a [Homo sapiens]
gi|89038887|ref|XP_943182.1|	12633.82	PREDICTED: similar to large subunit ribosomal protein L36a [Homo sapiens]
gi|27500649|ref|XP_208185.1|	12614.69	PREDICTED: similar to large subunit ribosomal protein L36a [Homo sapiens]
gi|50424663|ref|XP_460921.1|	12516.81	hypothetical protein DEHA0F13937g [Debaryomyces hansenii CBS767]
gi|22203732|gb|AAM94276.1|	12756.89	ribosomal protein L44 [Chlamys farreri]
gi|56462198|gb|AAV91382.1|	12642.84	ribosomal protein 11 large subunit [Lonomia obliqua]
gi|29841127|gb|AAP06140.1|	12642.88	similar to GenBank Accession Number AF004672 ribosomal protein L41 in Phaffia rhodozyma [Schistosom
gi|38047529|gb|AAR09667.1|	12646.94	similar to Drosophila melanogaster CG7424 [Drosophila yakuba]
gi|54609267|gb|AAV34849.1|	12628.82	ribosomal protein L36A [Bombyx mori]

510. Group probability: 0.9964. Peptides of the group

IGGIGTVPVGR	66.14	55.3583	1024.603	1024.899	11	2	shared(36)	0	0.978
GYAPVLDCHTAHIACK	82.82	54.209	1811.845	1812.693	2	2	distinct	0	0.9958

The equivalent proteins include

gi|10140|emb|CAA41001.1|	49849.93	elongation factor 1 alpha [Stylonychia lemnae]
gi|4063596|gb|AAD03263.1|	45591.49	translation elongation factor 1-alpha [Stylonychia mytilus]
gi|46909351|gb|AAT06193.1|	45510.37	elongation factor 1 alpha [Priapulus caudatus]

511. Group probability: 0.9964. Peptides of the group

KDDEVLIVR	58.12	56.008	1085.608	1086.741	1	2	distinct	1	0.9521
TNGATVPLGIHPSNVVITSLK	47.5	53.3745	2117.184	2118.637	1	2	distinct	0	0.9242

The equivalent proteins include

gi|71021543|ref|XP_761002.1|	14547.03	hypothetical protein UM04855.1 [Ustilago maydis 521]

512. Group probability: 0.9962. Peptides of the group

LDVALVQNLPIALVFLPAADIPR	80.77	52.6301	2457.436	2457.933	4	2	distinct	0	0.9962

The equivalent proteins include

gi|71023869|ref|XP_762164.1|	32090	hypothetical protein UM06017.1 [Ustilago maydis 521]

513. Group probability: 0.9962. Peptides of the group

HVVFGEVVEGKDVVK	71.39	54.4269	1639.893	1640.463	24	+2,+3	distinct	1	0.9962

The equivalent proteins include

gi|84999520|ref|XP_954481.1|	25978.16	cyclophilin 1 [Theileria annulata strain Ankara]

514. Group probability: 0.9961. Peptides of the group

LNNHQLDQQVQLVEDALWK	82.2	53.1244	2290.171	2291.653	2	2	distinct	0	0.9961

The equivalent proteins include

gi|71006538|ref|XP_757935.1|	33837.99	hypothetical protein UM01788.1 [Ustilago maydis 521]

515. Group probability: 0.9961. Peptides of the group

QSLPPGLNVVEIGKPVK	83.2	54.2784	1774.035	1774.406	2	2	distinct	0	0.9961

The equivalent proteins include

gi|71017877|ref|XP_759169.1|	11833.69	hypothetical protein UM03022.1 [Ustilago maydis 521]

516. Group probability: 0.9960. Peptides of the group

IIGNTFIHVFEAEVAK	59.21	54.7994	1786.962	1787.465	1	2	distinct	0	0.9666
VDPDVFTAGVPVLGICYGLQEIAWNHGGK	40.94	51.164	3111.549	3112.763	1	3	distinct	0	0.8807

The equivalent proteins include

gi|71019933|ref|XP_760197.1|	60595.37	hypothetical protein UM04050.1 [Ustilago maydis 521]

517. Group probability: 0.9960. Peptides of the group

GIYRPPPSSQLVQPATAK	54.24	53.801	1909.042	1909.546	2	+2,+3	distinct	0	0.996

The equivalent proteins include

gi|71005090|ref|XP_757211.1|	17739.55	hypothetical protein UM01064.1 [Ustilago maydis 521]

518. Group probability: 0.9959. Peptides of the group

GHFNWSIVK	47.18	56.059	1086.561	1087.241	2	+1,+2	distinct	0	0.9532

HNPTYDWVILR	50.38	55.0623	1412.72	1413.104	3	2	distinct	0	0.9131

The equivalent proteins include

gi|71006908|ref|XP_758073.1|	64211.57	hypothetical protein UM01926.1 [Ustilago maydis 521]

519. Group probability: 0.9958. Peptides of the group

AYPAWGHSSVVGPLGDVK	81.76	53.923	1838.931	1838.88	1	2	distinct	0	0.9958

The equivalent proteins include

gi|71021897|ref|XP_761179.1|	40843.73	hypothetical protein UM05032.1 [Ustilago maydis 521]

520. Group probability: 0.9957. Peptides of the group

VALTGLTIAEYFR	96.01	54.8052	1452.798	1453.379	17	2	shared(8)	0	0.9932
VALVFGQMNEPPGAR	76.13	54.7519	1584.808	1585.022	7	2	shared(6)	0	0.9745
IPSAVGYQPTLATDMGTLQER (0000000000000010000000)	97.8	53.1308	2263.115	2263.623	6	2	distinct	0	0.9818

The equivalent proteins include

gi|91178114|gb|ABE27292.1|	36092.8	mitochondrial F-ATPase beta subunit [Candida haemulonii]

521. Group probability: 0.9956. Peptides of the group

VSQVVAAKDEAK	84	55.5998	1243.677	1243.934	1	2	distinct	1	0.9956

The equivalent proteins include

gi|71021855|ref|XP_761158.1|	32505.94	hypothetical protein UM05011.1 [Ustilago maydis 521]

522. Group probability: 0.9955. Peptides of the group

NAPSIIFIDEIDSIAPK	93.72	54.1176	1841.977	1842.723	4	2	shared(2)	0	0.9869
AVANETGAFFFLINGPEIMSK	92.86	52.9905	2255.13	2254.894	1	2	shared(2)	0	0.9986

The equivalent proteins include

gi|108706222|gb|ABF94017.1|	90429	Cell division cycle protein 48, putative, expressed [Oryza sativa (japonica cultivar-group)]
gi|66806375|ref|XP_636910.1|	89241.51	cell division cycle protein 48 [Dictyostelium discoideum]
gi|37534770|ref|NP_921687.1|	91598.76	putative endoplasmic reticulum membrane fusion protein [Oryza sativa (japonica cultivar-group)]
gi|68129784|emb|CAJ09090.1|	87582.32	Transitional endoplasmic reticulum ATPase, putative; valosin-containing protein homolog [Leishmania

523. Group probability: 0.9954. Peptides of the group

SITDPSKPAVAYSQHTQPTTVAR	49.72	52.6778	2454.25	2454.856	2	+2,+3	distinct	0	0.9954

The equivalent proteins include

gi|71023733|ref|XP_762096.1|	64406.69	hypothetical protein UM05949.1 [Ustilago maydis 521]

524. Group probability: 0.9953. Peptides of the group

AVIQVMQVQGVKPELLK	80.93	54.1784	1879.096	1879.619	4	2	distinct	0	0.9953

The equivalent proteins include

gi|71017567|ref|XP_759014.1|	18095.15	hypothetical protein UM02867.1 [Ustilago maydis 521]

525. Group probability: 0.9952. Peptides of the group

TTSAAAAQASKPAQR	81.78	54.9851	1457.759	1458.576	1	2	distinct	0	0.9952

The equivalent proteins include

gi|71018337|ref|XP_759399.1|	66175.39	hypothetical protein UM03252.1 [Ustilago maydis 521]

526. Group probability: 0.9950. Peptides of the group

VMGDLGQVVPMEWDLR	80.82	54.1923	1843.896	1844.212	1	2	distinct	0	0.995

The equivalent proteins include

gi|71003724|ref|XP_756528.1|	43582.44	hypothetical protein UM00381.1 [Ustilago maydis 521]

527. Group probability: 0.9949. Peptides of the group

TALNPISASAAAGAGSNKFPDTVWR	76.44	52.5758	2501.266	2501.896	2	2	distinct	1	0.9949

The equivalent proteins include

gi|71010445|ref|XP_758392.1|	38543.81	hypothetical protein UM02245.1 [Ustilago maydis 521]

528. Group probability: 0.9947. Peptides of the group

SCYNCGGVGHLSR	81.4	55.1135	1465.619	1466.01	1	2	distinct	0	0.9947

The equivalent proteins include

gi|71004674|ref|XP_757003.1|	20132.64	hypothetical protein UM00856.1 [Ustilago maydis 521]

529. Group probability: 0.9946. Peptides of the group

SKDELDPDHPNPCYPR	79.84	53.8004	1938.853	1938.756	2	2	distinct	1	0.9946

The equivalent proteins include

gi|71019409|ref|XP_759935.1|	11578.47	hypothetical protein UM03788.1 [Ustilago maydis 521]								
530. Group probability: 0.9946. Peptides of the group										
LGLLPQATHIIGYAR	80.4		54.5478	1621.93	1623.233	7	2	distinct	0	0.9946
The equivalent proteins include										
gi|71021693|ref|XP_761077.1|	57000.17	hypothetical protein UM04930.1 [Ustilago maydis 521]								
531. Group probability: 0.9946. Peptides of the group										
AKFEELNMDLFR	62.36		54.6765	1511.744	1512.824	2	2	shared(2)	1	0.9709
IINEPTAAAIAYGIDKK	71.85		54.6758	1786.983	1788.273	1	2	shared(14)	1	0.9837
VTHAVVTVPAYFNDAQR	63.11		53.9084	1886.964	1887.089	2	+2,+3	shared(2)	0	0.9983
The equivalent proteins include										
gi|4033394|sp|Q91883|GRP78_XENLA	72704.62	78 kDa glucose-regulated protein precursor (GRP 78) (Immunoglobulin heavy chain-binding protein) (B								
gi|66513713|ref|XP_393090.2|	72877.8	PREDICTED: similar to ENSANGP00000012893 [Apis mellifera]								
gi|91076646|ref|XP_970569.1|	63255.69	PREDICTED: similar to CG4147-PA, isoform A [Tribolium castaneum]								
gi|94468818|gb|ABF18258.1|	72356.26	heat shock cognate 70 [Aedes aegypti]								
gi|47218700|emb|CAG12424.1|	74152.06	unnamed protein product [Tetraodon nigroviridis]								
gi|3426021|dbj|BAA32395.1|	73165.66	heat shock 70 kD protein cognate [Bombyx mori]								
gi|1326169|gb|AAB41582.1|	72637.56	immunoglobulin binding protein [Xenopus laevis]								
gi|55241328|gb|EAA08691.3|	72440.32	ENSANGP00000012893 [Anopheles gambiae str. PEST]								
gi|27260894|gb|AAN86047.1|	73177.72	heat shock cognate 70 protein [Spodoptera frugiperda]								
gi|60223019|dbj|BAD90025.1|	69906.97	glucose-regulated protein 78kDa [Oncorhynchus mykiss]								
gi|50417653|gb|AAH77757.1|	72738.6	LOC397850 protein [Xenopus laevis]								
532. Group probability: 0.9945. Peptides of the group										
LRPYVFAGAPSDGGVSR	52.86		54.1982	1747.9	1748.77	2	+2,+3	distinct	0	0.9945
The equivalent proteins include										
gi|71005642|ref|XP_757487.1|	17698.26	hypothetical protein UM01340.1 [Ustilago maydis 521]								
533. Group probability: 0.9944. Peptides of the group										
LSNNVLDSLQETFETLLEEADVEALEEEAR	75.31		50.3142	3405.631	3406.357	6	3	distinct	0	0.9944
The equivalent proteins include										
gi|71020689|ref|XP_760575.1|	24575.38	hypothetical protein UM04428.1 [Ustilago maydis 521]								
534. Group probability: 0.9944. Peptides of the group										
IFLDKFDLAAESYQPFAVQLSQLASR	77.16		51.3122	2956.533	2957.946	2	3	distinct	1	0.9944
The equivalent proteins include										
gi|71024335|ref|XP_762397.1|	202951.08	hypothetical protein UM06250.1 [Ustilago maydis 521]								
535. Group probability: 0.9943. Peptides of the group										
VVDALGNPIDGK	87.75		55.4031	1196.64	1197.823	1	2	shared(6)	0	0.9821
TGEIVDVPVGPK	47.98		55.1025	1209.66	1209.174	1	2	distinct	0	0.6781
HAIIIYDDLSK	80.76		55.5162	1286.687	1287.158	9	+1,+2	shared(5)	0	0.9997
GIRPAINVGLSVSR	71.89		54.778	1437.842	1438.903	22	2	shared(4)	0	0.9882
EAYPGDVFYIHSR	58.88		54.6289	1552.731	1554.178	3	2	shared(8)	0	0.9619
The equivalent proteins include										
gi|67537828|ref|XP_662688.1|	73663.54	hypothetical protein AN5084.2 [Aspergillus nidulans FGSC A4]								
536. Group probability: 0.9943. Peptides of the group										
TFVLSHITPFAAR	51.64		55.0907	1458.798	1459.246	1	2	distinct	0	0.9274
YGTPPLLAVTDRIPGQLNDASIETR	47.48		52.0616	2696.413	2696.954	1	3	distinct	1	0.9211
The equivalent proteins include										
gi|71020397|ref|XP_760429.1|	61408.15	hypothetical protein UM04282.1 [Ustilago maydis 521]								
537. Group probability: 0.9941. Peptides of the group										
FRQEVAASSPGMLSYK	78.86		54.1375	1769.877	1770.923	1	2	distinct	1	0.9941
The equivalent proteins include										
gi|71023517|ref|XP_761988.1|	55082.61	hypothetical protein UM05841.1 [Ustilago maydis 521]								
538. Group probability: 0.9941. Peptides of the group										
VTILCDKFTGHPK	45.78		54.8201	1514.791	1515.843	1	2	distinct	1	0.8794

ELQQAAGEAGGAGLHPTEEEREEVDSR	51.95	51.7003	2864.317	2864.694	1	3	distinct	1	0.9507

The equivalent proteins include

gi|71013016|ref|XP_758548.1|	22240.87	hypothetical protein UM02401.1 [Ustilago maydis 521]

539. Group probability: 0.9940. Peptides of the group

LAEILANWETDPQTASLARPK	50.81	53.0045	2323.217	2324.188	1	3	distinct	0	0.9308
TFDALLNPGDVILVESPAYTGILPSLVMIK	41.78	50.896	3185.73	3186.383	1	2	distinct	0	0.9135

The equivalent proteins include

gi|71006570|ref|XP_757951.1|	54847.98	hypothetical protein UM01804.1 [Ustilago maydis 521]

540. Group probability: 0.9940. Peptides of the group

VKVAILGASGGVGQPLSLLLK	51.86	54.0307	2019.245	2019.826	5	+2,+3	distinct	1	0.994

The equivalent proteins include

gi|171918|gb|AAA34767.1|	37305.05	malate dehydrogenase
gi|6320125|ref|NP_010205.1|	37219.99	Cytoplasmic malate dehydrogenase, catalyzes interconversion of malate and oxaloacetate; involved in

541. Group probability: 0.9939. Peptides of the group

IPTTEAEVLALIDHTILAPNTTLNQIAAVCK	73.96	50.7731	3329.79	3331.288	6	3	distinct	0	0.9939

The equivalent proteins include

gi|71005358|ref|XP_757345.1|	29689.16	hypothetical protein UM01198.1 [Ustilago maydis 521]

542. Group probability: 0.9939. Peptides of the group

LVPNGLAHIGASLPASTVK	47.15	54.1513	1844.052	1845.287	1	2	distinct	0	0.9147
ISTAVDLSSPHPLASTASTASTLYGVSPAVASQPR	44.03	50.2139	3438.763	3439.517	1	3	distinct	0	0.9279

The equivalent proteins include

gi|71022595|ref|XP_761527.1|	29270.75	hypothetical protein UM05380.1 [Ustilago maydis 521]

543. Group probability: 0.9938. Peptides of the group

GGPGMPEMLKPTSLIMGAGLGQDVACLTDGR	73.91	51.1138	3128.513	3129.396	1	3	distinct	0	0.9938

The equivalent proteins include

gi|71023315|ref|XP_761887.1|	64972	hypothetical protein UM05740.1 [Ustilago maydis 521]

544. Group probability: 0.9938. Peptides of the group

QQAVEAIRDQFTLDKPLLESLVAR	76.94	52.0687	2739.492	2739.664	2	3	distinct	1	0.9938

The equivalent proteins include

gi|71009859|ref|XP_758320.1|	51626.17	hypothetical protein UM02173.1 [Ustilago maydis 521]

545. Group probability: 0.9938. Peptides of the group

HKGVMVGMGQK (0000010000000)	70.83	55.6094	1170.6	1170.959	31	+1,+2	shared(8)	1	0.9992
KEYDESGPSIVHR	51.92	54.8172	1515.732	1516.145	1	2	shared(3)	1	0.8424
SYELPDGKVITIGNER	64.43	54.1766	1789.921	1790.679	1	2	shared(14)	1	0.9686
YPNEHGIVTNWDDMEK	51.14	53.8585	1946.847	1947.563	1	2	distinct	0	0.9335
VAPEEHPVLLTEAPINPK	88.95	53.6979	1953.057	1953.863	9	2	shared(9)	0	0.9916

The equivalent proteins include

gi|109507063|ref|XP_001058533.1|	42108.88	PREDICTED: similar to Actin, cytoplasmic 2 (Gamma-actin) [Rattus norvegicus]

546. Group probability: 0.9937. Peptides of the group

QILDNAVAEIESLVK	78.58	54.4202	1640.898	1641.744	2	2	distinct	0	0.9937

The equivalent proteins include

gi|71022389|ref|XP_761424.1|	34254.2	hypothetical protein UM05277.1 [Ustilago maydis 521]

547. Group probability: 0.9937. Peptides of the group

DLATGEGTHFLVPWLQK	78.05	53.8295	1910.989	1911.873	4	2	distinct	0	0.9385
FAVPLGLGVMALQSSLYDVPGGYR	42.68	52.5168	2509.304	2509.963	1	2	distinct	0	0.8978

The equivalent proteins include

gi|71018839|ref|XP_759650.1|	40606.51	hypothetical protein UM03503.1 [Ustilago maydis 521]

548. Group probability: 0.9935. Peptides of the group

TGVLNEQEKDEIVAGLEK	76.76	53.6678	1971.016	1971.699	1	2	distinct	1	0.9935

The equivalent proteins include

gi|71020827|ref|XP_760644.1|	52324.32	hypothetical protein UM04497.1 [Ustilago maydis 521]

549. Group probability: 0.9933. Peptides of the group

GAPISIAYSPLHGVGAPSIER	75.21	53.3878	2091.111	2091.584	1	2	distinct	0	0.9933

The equivalent proteins include

gi|71006402|ref|XP_757867.1|	67457.88	hypothetical protein UM01720.1 [Ustilago maydis 521]							
550. Group probability: 0.9933. Peptides of the group									
LQLSSLFNWIGADFDSLAGSTVR	74.14	52.502	2496.265	2497.053	2	2	distinct	0	0.9933
The equivalent proteins include									
gi|71023783|ref|XP_762121.1|	76747.63	hypothetical protein UM05974.1 [Ustilago maydis 521]							
551. Group probability: 0.9932. Peptides of the group									
YYQPPHAANFALTATPAQQNAVASTTPQLAAK	72.18	50.5823	3340.684	3341.514	4	3	distinct	0	0.9932
The equivalent proteins include									
gi|71023115|ref|XP_761787.1|	23055.11	hypothetical protein UM05640.1 [Ustilago maydis 521]							
552. Group probability: 0.9931. Peptides of the group									
VHSIAVSDVDHVVASSQAALPGWR	73.49	52.5654	2500.282	2501.744	1	2	distinct	0	0.9931
The equivalent proteins include									
gi|71019925|ref|XP_760193.1|	54926.71	hypothetical protein UM04046.1 [Ustilago maydis 521]							
553. Group probability: 0.9931. Peptides of the group									
TSSGIFLPSSAASSPLPEASVIATGPGAPDKDGK	71.37	51.0127	3211.625	3213.074	5	3	distinct	1	0.9931
The equivalent proteins include									
gi|71023499|ref|XP_761979.1|	11284.1	hypothetical protein UM05832.1 [Ustilago maydis 521]							
554. Group probability: 0.9931. Peptides of the group									
VVDALGNPIDGK	87.75	55.4031	1196.64	1197.823	1	2	shared(6)	0	0.9821
EAYPGDVFYIHSR	58.88	54.6289	1552.731	1554.178	3	2	shared(8)	0	0.9619
VVDALGNPIDGKGPIVATER	88.37	54.0488	2020.095	2020.947	3	+2,+3	distinct	1	0.9786
The equivalent proteins include									
gi|77739663|ref|ZP_00808153.1|	55316.09	ATP synthase F1, alpha subunit [Rhodopseudomonas palustris BisA53]							
555. Group probability: 0.9930. Peptides of the group									
ATAGDTHLGGEDFDNR	68.44	54.7902	1674.723	1675.633	4	2	shared(13)	0	0.9851
EAVITVPAYFNDSQR	67.86	54.4754	1708.842	1708.239	1	2	distinct	0	0.9363
IINEPTAAAIAYGIDKK	71.85	54.6758	1786.983	1788.273	1	2	shared(14)	1	0.9837
SQVFTTYADNQPGVLIQVFEGER	65.73	52.3905	2597.276	2598.243	1	2	distinct	0	0.7739
The equivalent proteins include									
gi|67043503|gb|AAY63877.1|	47751.54	heat shock protein 70 [Cyclospora colobi]							
gi|35506383|gb|AAO66452.4|	47096.19	heat shock protein 70 [Cyclospora cayetanensis]							
556. Group probability: 0.9929. Peptides of the group									
LAEQGYPVHEGTAYLWAR	75.77	53.4823	2060.011	2060.483	2	2	distinct	0	0.9929
The equivalent proteins include									
gi|71010180|ref|XP_758357.1|	58536.43	hypothetical protein UM02210.1 [Ustilago maydis 521]							
557. Group probability: 0.9928. Peptides of the group									
WDPSVHGTSGPLEIGFTQIR	50.63	53.2187	2196.096	2197.063	2	+2,+3	distinct	0	0.9928
The equivalent proteins include									
gi|71018935|ref|XP_759698.1|	67252.41	hypothetical protein UM03551.1 [Ustilago maydis 521]							
558. Group probability: 0.9928. Peptides of the group									
VSQECLDKFQELK	77.87	54.5462	1622.797	1624.149	1	2	distinct	1	0.9928
The equivalent proteins include									
gi|71020461|ref|XP_760461.1|	15904.96	hypothetical protein UM04314.1 [Ustilago maydis 521]							
559. Group probability: 0.9925. Peptides of the group									
VFDKDGNGFISAAELR	84.69	54.1346	1737.869	1738.111	3	+2,+3	distinct	1	0.9711
EAFSLFDKDGDGTITTK	82.53	54.1901	1843.884	1844.047	4	2	shared(3)	1	0.9825
The equivalent proteins include									
gi|2392137|pdb|1AHR|	16452.71	Calmodulin Mutant With A Two Residue Deletion In The Central Helix							
gi|4930156|pdb|1VRK|A	16615.87	Chain A, The 1.9 Angstrom Structure Of E84k-Calmodulin Rs20 Peptide Complex							
gi|33358173|pdb|1QTX|A	16616.82	Chain A, The 1.65 Angstrom Structure Of Calmodulin Rs20 Peptide Complex							
gi|33358171|pdb|1QS7|C	16302.7	Chain C, The 1.8 Angstrom Structure Of Calmodulin Rs20 Peptide Complex							
gi|3561059|gb|AAC61858.1|	16746.91	calmodulin mutant SYNCAM28 [synthetic construct]							
gi|3561061|gb|AAC61859.1|	16746.91	calmodulin mutant SYNCAM29 [synthetic construct]							

gi|49035516|sp|O96081|CALMB_HALRO	16886.84	Calmodulin-B (CaM B)
gi|49035530|sp|Q95NI4|CALM_HALOK	16742.8	Calmodulin (CaM)
gi|49066052|sp|Q95NR9|CALM_METSE	16826.87	Calmodulin (CaM)
gi|49035528|sp|Q8STF0|CALM_STRIE	17585.21	Calmodulin (CaM)
gi|4959142|gb|AAD34239.1|	16740.91	calmodulin mutant SYNCAM2 [synthetic construct]
gi|4959143|gb|AAD34240.1|	16732.85	calmodulin mutant SYNCAM4 [synthetic construct]
gi|4959144|gb|AAD34241.1|	16698.86	calmodulin mutant SYNCAM6 [synthetic construct]
gi|4959146|gb|AAD34243.1|	16716.82	calmodulin mutant SYNCAM11 [synthetic construct]
gi|4959147|gb|AAD34244.1|	16816.93	calmodulin mutant SYNCAM30 [synthetic construct]
gi|4959148|gb|AAD34245.1|	17030.03	calmodulin mutant SYNCAM35 [synthetic construct]
gi|4959149|gb|AAD34246.1|	16745.97	calmodulin mutant SYNCAM46 [synthetic construct]
gi|4959150|gb|AAD34247.1|	16745.97	calmodulin mutant SYNCAM47 [synthetic construct]
gi|4959151|gb|AAD34248.1|	16745.97	calmodulin mutant SYNCAM48 [synthetic construct]
gi|4959152|gb|AAD34249.1|	16815.18	calmodulin mutant SYNCAM49 [synthetic construct]
gi|4959153|gb|AAD34250.1|	16757.17	calmodulin mutant SYNCAM50 [synthetic construct]
gi|4959154|gb|AAD34251.1|	16753.23	calmodulin mutant SYNCAM51 [synthetic construct]
gi|4959155|gb|AAD34252.1|	16800.18	calmodulin mutant SYNCAM52 [synthetic construct]
gi|4959157|gb|AAD34254.1|	16796.24	calmodulin mutant SYNCAM53 [synthetic construct]
gi|4959158|gb|AAD34255.1|	16771.19	calmodulin mutant SYNCAM53A [synthetic construct]
gi|4959159|gb|AAD34256.1|	16823.51	calmodulin mutant SYNCAM54 [synthetic construct]
gi|4959160|gb|AAD34257.1|	16746.91	calmodulin mutant SYNCAM55 [synthetic construct]
gi|4959161|gb|AAD34258.1|	16719.87	calmodulin mutant SYNCAM56 [synthetic construct]
gi|4959162|gb|AAD34259.1|	16690.8	calmodulin mutant SYNCAM57A [synthetic construct]
gi|4959163|gb|AAD34260.1|	16748.81	calmodulin mutant SYNCAM57B [synthetic construct]
gi|4959164|gb|AAD34261.1|	16676.79	calmodulin mutant SYNCAM57C [synthetic construct]
gi|4959165|gb|AAD34262.1|	16718.83	calmodulin mutant SYNCAM57D [synthetic construct]
gi|4959166|gb|AAD34263.1|	16734.79	calmodulin mutant SYNCAM58A [synthetic construct]
gi|4959167|gb|AAD34264.1|	16733.81	calmodulin mutant SYNCAM58C [synthetic construct]
gi|4959168|gb|AAD34265.1|	16746.88	calmodulin mutant SYNCAM62 [synthetic construct]
gi|4959169|gb|AAD34266.1|	16746.88	calmodulin mutant SYNCAM63A [synthetic construct]
gi|4959170|gb|AAD34267.1|	16489.78	calmodulin mutant SYNCAM64A [synthetic construct]
gi|4959171|gb|AAD34268.1|	16618.82	calmodulin mutant SYNCAM64B [synthetic construct]
gi|4959172|gb|AAD34269.1|	16703.85	calmodulin mutant SYNCAM71A [synthetic construct]
gi|4959588|gb|AAD34407.1|	16804.9	calmodulin mutant SYNCAM67 [synthetic construct]
gi|4959590|gb|AAD34408.1|	16775.87	calmodulin mutant SYNCAM3 [synthetic construct]
gi|4959593|gb|AAD34409.1|	16789.91	calmodulin mutant SYNCAM5 [synthetic construct]
gi|4959594|gb|AAD34410.1|	16782.83	calmodulin mutant SYNCAM16 [synthetic construct]

gi|4959598|gb|AAD34411.1|	16773.88	calmodulin mutant SYNCAM7 [synthetic construct]
gi|4959599|gb|AAD34412.1|	16689.86	calmodulin mutant SYNCAM60 [synthetic construct]
gi|4959602|gb|AAD34414.1|	16745.02	calmodulin mutant SYNCAM8 [synthetic construct]
gi|4959612|gb|AAD34416.1|	16741.08	calmodulin mutant SYNCAM12 [synthetic construct]
gi|4959613|gb|AAD34417.1|	16738.23	calmodulin mutant SYNCAM18 [synthetic construct]
gi|4959614|gb|AAD34418.1|	16760.02	calmodulin mutant SYNCAM24 [synthetic construct]
gi|4959615|gb|AAD34419.1|	16746.91	calmodulin mutant SYNCAM39 [synthetic construct]
gi|4959616|gb|AAD34420.1|	16803.02	calmodulin mutant SYNCAM43 [synthetic construct]
gi|4959617|gb|AAD34421.1|	16746.91	calmodulin mutant SYNCAM44 [synthetic construct]
gi|4959618|gb|AAD34422.1|	16746.91	calmodulin mutant SYNCAM45 [synthetic construct]
gi|4959621|gb|AAD34423.1|	16759.03	calmodulin mutant SYNCAM12A [synthetic construct]
gi|4959622|gb|AAD34424.1|	16756.19	calmodulin mutant SYNCAM18A [synthetic construct]
gi|4959625|gb|AAD34425.1|	16689.86	calmodulin mutant SYNCAM13 [synthetic construct]
gi|4959626|gb|AAD34426.1|	16689.86	calmodulin mutant SYNCAM14 [synthetic construct]
gi|4959629|gb|AAD34427.1|	17061.07	calmodulin mutant SYNCAM15 [synthetic construct]
gi|4959630|gb|AAD34428.1|	16745.97	calmodulin mutant SYNCAM40 [synthetic construct]
gi|4959640|gb|AAD34433.1|	16746.91	calmodulin mutant SYNCAM26 [synthetic construct]
gi|4959645|gb|AAD34434.1|	16846.91	calmodulin mutant SYNCAM31 [synthetic construct]
gi|4959647|gb|AAD34436.1|	16832.89	calmodulin mutant SYNCAM33 [synthetic construct]
gi|4959648|gb|AAD34437.1|	16805.88	calmodulin mutant SYNCAM34 [synthetic construct]
gi|3800849|gb|AAC68891.1|	16810.94	VU91C calmodulin [synthetic construct]
gi|62825400|gb|AAY16220.1|	14702.86	calmodulin [Silicularia rosea]
gi|62825406|gb|AAY16223.1|	14854.89	calmodulin [Orthopyxis integra]
gi|62825410|gb|AAY16225.1|	13282.29	calmodulin [Orthopyxis integra]
gi|62825430|gb|AAY16235.1|	12651.03	calmodulin [Clytia hummelincki]
gi|62825436|gb|AAY16238.1|	13937.61	calmodulin [Clytia gracilis]
gi|62825438|gb|AAY16239.1|	12640.94	calmodulin [Clytia gracilis]
gi|62825442|gb|AAY16241.1|	14022.66	calmodulin [Clytia gracilis]
gi|62825444|gb|AAY16242.1|	12521.98	calmodulin [Clytia hemisphaerica]
gi|62825460|gb|AAY16250.1|	14268.68	calmodulin [Laomedea flexuosa]
gi|62825470|gb|AAY16255.1|	13703.39	calmodulin [Obelia dichotoma]
gi|62825472|gb|AAY16256.1|	14839.88	calmodulin [Laomedea calceolifera]
gi|62825476|gb|AAY16258.1|	14826.89	calmodulin [Obelia geniculata]
gi|208092|gb|AAA72492.1|	16747.86	VU1 calmodulin [synthetic construct]
gi|64446704|gb|AAY41437.1|	16813.84	calmodulin 2 [Apostichopus japonicus]
gi|4468115|emb|CAB38169.1|	16813.8	calmodulin 2 [Branchiostoma lanceolatum]
gi|11121264|emb|CAC14791.1|	16829.82	calmodulin [Lumbricus rubellus]
gi|4150908|emb|CAA77069.1|	16787.79	calmodulin [Suberites domuncula]
gi|72009723|ref|XP_781705.1|	19409.27	PREDICTED: similar to CG8472-PA, isoform A [Strongylocentrotus purpuratus]
gi|72014310|ref|XP_781054.1|	16460.67	PREDICTED: similar to CG8472-PA, isoform A [Strongylocentrotus purpuratus]
gi|72067208|ref|XP_795681.1|	19395.25	PREDICTED: similar to CG8472-PA, isoform A [Strongylocentrotus purpuratus]
gi|72089282|ref|XP_789995.1|	16785.8	PREDICTED: similar to CG8472-PA, isoform A [Strongylocentrotus purpuratus]
gi|72089284|ref|XP_790017.1|	18665.71	PREDICTED: similar to CG8472-PA, isoform A [Strongylocentrotus purpuratus]
gi|71411704|ref|XP_808090.1|	16823.86	calmodulin [Trypanosoma cruzi strain CL Brener]

gi|71411702|ref|XP_808089.1|	23612.03	calmodulin [Trypanosoma cruzi strain CL Brener]
gi|74096311|ref|NP_001027633.1|	16825.81	calmodulin homologue [Ciona intestinalis]
gi|71068392|gb|AAZ23120.1|	13581.44	calmodulin [Clytia gracilis]
gi|71068394|gb|AAZ23121.1|	14166.68	calmodulin [Clytia gracilis]
gi|74053606|gb|AAZ95240.1|	13822.58	calmodulin [Clytia linearis]
gi|74053608|gb|AAZ95241.1|	13709.5	calmodulin [Clytia noliformis]
gi|74053610|gb|AAZ95242.1|	14856.98	calmodulin [Clytia elsaeoswaldae]
gi|76155399|gb|AAX26683.2|	15655.32	SJCHGC00574 protein [Schistosoma japonicum]
gi|51557667|gb|AAU06473.1|	16799.82	calmodulin [Culicoides sonorensis]
gi|2291247|gb|AAB65364.1|	16813.84	Calmodulin protein 1 [Caenorhabditis elegans]
gi|9858458|gb|AAG01043.1|	16813.87	calmodulin; CaM [Pythium splendens]
gi|7688|emb|CAA68327.1|	16668.78	unnamed protein product [Drosophila melanogaster]
gi|71405209|ref|XP_805243.1|	16813.84	calmodulin [Trypanosoma cruzi strain CL Brener]
gi|74025586|ref|XP_829359.1|	16827.85	calmodulin [Trypanosoma brucei TREU927]
gi|115500|sp|P05932|CALMB_ARBPU	15554.27	Calmodulin-beta (Cam B)
gi|115510|sp|P11118|CALM_EUGGR	16713.86	Calmodulin (CaM)
gi|728609|emb|CAA59418.1|	16797.88	calmodulin [Macrocystis pyrifera]
gi|115522|sp|P11121|CALM_PYUSP	16669.77	Calmodulin (CaM)
gi|71019653|ref|XP_760057.1|	16711.83	calmodulin [Ustilago maydis 521]
gi|55244362|gb|EAA05425.2|	17184.04	ENSANGP00000012700 [Anopheles gambiae str. PEST]
gi|33243604|gb|AAQ01510.1|	16769.83	calmodulin [Branchiostoma belcheri tsingtaunese]
gi|38048675|gb|AAR10240.1|	16483.65	similar to Drosophila melanogaster Cam [Drosophila yakuba]
gi|46517823|gb|AAQ20043.1|	16856.86	calmodulin [Pinctada fucata]
gi|56758390|gb|AAW27335.1|	16810.88	unknown [Schistosoma japonicum]

560. Group probability: 0.9924. Peptides of the group

DLELLALEYDLPLETIESLAK	73.61	52.7647	2387.272	2388.113	1	2	distinct	0	0.9924

The equivalent proteins include

gi|71006496|ref|XP_757914.1|	20579.37	hypothetical protein UM01767.1 [Ustilago maydis 521]

561. Group probability: 0.9924. Peptides of the group

VALTGLTIAEYFR	96.01	54.8052	1452.798	1453.379	17	2	shared(8)	0	0.9932
VALVFGQMNEPPGAR	76.13	54.7519	1584.808	1585.022	7	2	shared(6)	0	0.9745
LVLEVAQHLGENTVR	84.18	54.5381	1676.921	1677.711	15	+2,+3	shared(6)	0	0.9996
DEKGQDVLLFIDDIFR	75.52	54.0645	1921.978	1922.647	20	2	distinct	1	0.7062
SLQDIIAILGMDELSEQDKLTVER	74.18	52.0836	2715.4	2716.853	3	2	shared(3)	1	0.92

The equivalent proteins include

gi|45185400|ref|NP_983117.1|	54012.39	ABR169Wp [Eremothecium gossypii]

562. Group probability: 0.9923. Peptides of the group

DGQLATFEEYGGMVLANACGPCIGQWDRK	72.2	50.9851	3242.458	3241.924	1	3	distinct	1	0.9923

The equivalent proteins include

gi|39942882|ref|XP_360978.1|	85476.17	hypothetical protein MG03521.4 [Magnaporthe grisea 70-15]

563. Group probability: 0.9922. Peptides of the group

KPAAAPYSK	52.6	56.4718	931.513	931.225	2	+1,+2	distinct	0	0.9922

The equivalent proteins include

gi|71003770|ref|XP_756551.1|	35236.19	hypothetical protein UM00404.1 [Ustilago maydis 521]

564. Group probability: 0.9922. Peptides of the group

IDESAKADAPAPDVAAQK	74.86	54.0859	1795.895	1796.412	2	2	distinct	1	0.9922

The equivalent proteins include

gi|71010788|ref|XP_758414.1|	27786.24	hypothetical protein UM02267.1 [Ustilago maydis 521]

565. Group probability: 0.9922. Peptides of the group

LPDAIVACVGGGSNAIGIFHPFVQDK	49.4	52.1118	2681.363	2682.062	1	3	distinct	0	0.9356
LCTQLEGIIPALETSHALWSAFQIAK	42.08	51.507	2896.516	2897.834	1	3	distinct	0	0.8791

The equivalent proteins include

gi|71021001|ref|XP_760731.1|	77451.73	hypothetical protein UM04584.1 [Ustilago maydis 521]

566. Group probability: 0.9919. Peptides of the group

TTVTSEESGINESGLEHFPGASVSVGR	72.55	51.9762	2746.304	2747.027	1	3	distinct	0	0.9919

The equivalent proteins include

gi|71022387|ref|XP_761423.1|	17321.18	hypothetical protein UM05276.1 [Ustilago maydis 521]

567. Group probability: 0.9918. Peptides of the group

SYELPDGKVITIGNER	64.43		54.1766	1789.921	1790.679	1	2	shared(14)	1	0.9686
VAPEEHPVLLTEAPINPK	88.95		53.6979	1953.057	1953.863	9	2	shared(9)	0	0.9916
MNDEVQALVIDNGSGMCK	88.91		53.7979	1979.875	1979.89	1	2	distinct	0	0.9814

The equivalent proteins include

gi|33946349|gb|AAQ55800.1|	40885.34	actin [Platyamoeba placida]

568. Group probability: 0.9915. Peptides of the group

VLAIVTHGILSGPALDR	74.32		54.2302	1731.004	1732.333	1	2	distinct	0	0.9915

The equivalent proteins include

gi|71023995|ref|XP_762227.1|	46985.15	hypothetical protein UM06080.1 [Ustilago maydis 521]

569. Group probability: 0.9915. Peptides of the group

VQLGAYIDGLPAITAETFVVGADKSNPVEGR	70.16		50.926	3186.656	3188.054	2	3	distinct	1	0.9915

The equivalent proteins include

gi|71023165|ref|XP_761812.1|	41504.09	hypothetical protein UM05665.1 [Ustilago maydis 521]

570. Group probability: 0.9913. Peptides of the group

KAVITVPAYFNDSQR	86.78		54.4754	1707.894	1708.239	1	2	distinct	1	0.9879
IINEPTAAAIAYGIDKK	71.85		54.6758	1786.983	1788.273	1	2	shared(14)	1	0.9837

The equivalent proteins include

gi|70609372|gb|AAZ04921.1|	71352.43	heat-shock inducible Hsp70 [Volvox carteri f. nagariensis]

571. Group probability: 0.9913. Peptides of the group

NYYPSLGGLGWIVDNVADVFEMPWYK (0000000000000000000000100000)	69.66		51.3753	3048.437	3048.903	1	2	distinct	0	0.9913

The equivalent proteins include

gi|71004238|ref|XP_756785.1|	45098.92	hypothetical protein UM00638.1 [Ustilago maydis 521]

572. Group probability: 0.9911. Peptides of the group

FALAEAILLDQQTK	75.12		54.7859	1559.856	1560.282	1	2	distinct	0	0.9911

The equivalent proteins include

gi|71023785|ref|XP_762122.1|	143286.01	hypothetical protein UM05975.1 [Ustilago maydis 521]

573. Group probability: 0.9911. Peptides of the group

KNNPTPWNNVEPGTQTK	73.69		54.0423	1923.944	1924.336	1	2	distinct	1	0.9911

The equivalent proteins include

gi|71016985|ref|XP_758947.1|	21992.31	hypothetical protein UM02800.1 [Ustilago maydis 521]

574. Group probability: 0.9910. Peptides of the group

HALGALISYEMGK	75.51		55.2862	1388.712	1389.426	1	2	distinct	0	0.991

The equivalent proteins include

gi|71019163|ref|XP_759812.1|	58137.68	hypothetical protein UM03665.1 [Ustilago maydis 521]

575. Group probability: 0.9908. Peptides of the group

SAAAPTPVPASAPAPAPAPAAVPTPVR	68.94		52.5766	2431.322	2432.103	3	2	distinct	0	0.9908

The equivalent proteins include

gi|71020667|ref|XP_760564.1|	60267.51	hypothetical protein UM04417.1 [Ustilago maydis 521]

576. Group probability: 0.9908. Peptides of the group

VFQAHGDADPVVK	75.1		54.9061	1381.699	1382.127	1	2	distinct	0	0.9908

The equivalent proteins include

gi|71003193|ref|XP_756277.1|	26021.59	hypothetical protein UM00130.1 [Ustilago maydis 521]

577. Group probability: 0.9907. Peptides of the group

MSMNPFDEIAVEEAVR (000100000000000000)	100.37		54.0941	1852.833	1853.923	6	2	distinct	0	0.9907

The equivalent proteins include

gi|83745810|ref|ZP_00942867.1|	26596.48	Electron transfer flavoprotein beta-subunit [Ralstonia solanacearum UW551]
gi|83751615|ref|ZP_00948028.1|	27541.85	COG2086: Electron transfer flavoprotein, beta subunit [Bartonella bacilliformis KC583]
gi|67546787|ref|ZP_00424697.1|	26497.64	Electron transfer flavoprotein beta-subunit [Burkholderia vietnamiensis G4]
gi|84357135|ref|ZP_00981963.1|	25519.96	COG2086: Electron transfer flavoprotein, beta subunit [Burkholderia cenocepacia PC184]

gi|67548976|ref|ZP_00426853.1|	27565.09	Electron transfer flavoprotein beta-subunit [Burkholderia vietnamiensis G4]
gi|84361134|ref|ZP_00985814.1|	25562.99	COG2086: Electron transfer flavoprotein, beta subunit [Burkholderia dolosa AUO158]
gi|67665361|ref|ZP_00462625.1|	26552.68	Electron transfer flavoprotein beta-subunit [Burkholderia cenocepacia HI2424]
gi|84705019|ref|ZP_01018519.1|	27221.45	electron transfer flavoprotein beta chain, (ETFSS) [Parvularcula bermudensis HTCC2503]
gi|74015863|ref|ZP_00686490.1|	26551.66	Electron transfer flavoprotein beta-subunit [Burkholderia ambifaria AMMD]
gi|88938475|ref|ZP_01143928.1|	26642.41	Electron transfer flavoprotein beta subunit-like [Acidiphilium cryptum JF-5]
gi|47575022|ref|ZP_00245057.1|	26901.58	COG2086: Electron transfer flavoprotein, beta subunit [Rubrivivax gelatinosus PM1]
gi|91784795|ref|YP_560001.1|	26611.74	Electron transfer flavoprotein, beta-subunit [Burkholderia xenovorans LB400]
gi|77966392|gb|ABB07772.1|	26478.64	Electron transfer flavoprotein beta-subunit [Burkholderia sp. 383]
gi|82538334|ref|ZP_00897327.1|	25520.96	hypothetical protein Bpse110_02000025 [Burkholderia pseudomallei 1106b]
gi|1173889|gb|AAA86623.1|	26978.69	FlaX
gi|52428193|gb|AAU48786.1|	26553.67	electron transfer flavoprotein, beta subunit [Burkholderia mallei ATCC 23344]
gi|49238751|emb|CAF28011.1|	27227.57	Electron transfer flavoprotein beta-subunit [Bartonella henselae str. Houston-1]
gi|58001749|gb|AAW60643.1|	26571.15	Electron transfer flavoprotein beta-subunit [Gluconobacter oxydans 621H]
gi|34499273|ref|NP_903488.1|	26766.63	probable electron transfer flavoprotein, beta subunit [Chromobacterium violaceum ATCC 12472]
gi|59802248|ref|YP_208960.1|	27027.73	EtfB [Neisseria gonorrhoeae FA 1090]
gi|7227413|gb|AAF42463.1|	26987.66	electron transfer flavoprotein, beta subunit [Neisseria meningitidis MC58]
gi|7379004|emb|CAB83550.1|	26892.69	electron transfer flavoprotein beta-subunit [Neisseria meningitidis Z2491]
gi|33567206|emb|CAE31120.1|	26911.65	electron transfer flavoprotein beta-subunit [Bordetella bronchiseptica RB50]
gi|17427935|emb|CAD14625.1|	26678.54	probable electron transfer flavoprotein (beta-subunit) [Ralstonia solanacearum]
gi|72119648|gb|AAZ61911.1|	26696.55	Electron transfer flavoprotein beta-subunit [Ralstonia eutropha JMP134]
gi|77964961|gb|ABB06342.1|	26454.55	Electron transfer flavoprotein beta-subunit [Burkholderia sp. 383]
gi|77970200|gb|ABB11579.1|	26282.62	Electron transfer flavoprotein beta-subunit [Burkholderia sp. 383]
gi|91782264|ref|YP_557470.1|	26565.65	Putative electron transfer flavoprotein beta-subunit [Burkholderia xenovorans LB400]
gi|91780317|ref|YP_555524.1|	26548.67	Electron transfer flavoprotein beta-subunit, EtfB [Burkholderia xenovorans LB400]
gi|94309682|ref|YP_582892.1|	28931.56	electron transfer flavoprotein beta-subunit [Ralstonia metallidurans CH34]
gi|107022140|ref|YP_620467.1|	26568.71	electron transfer flavoprotein beta-subunit [Burkholderia cenocepacia AU 1054]

578. Group probability: 0.9907. Peptides of the group

LLPHLVGTIEQIAAR	74.17	54.5856	1629.957	1630.474	1	2	distinct	0	0.9907

The equivalent proteins include

gi|71022411|ref|XP_761435.1|	102972.81	hypothetical protein UM05288.1 [Ustilago maydis 521]

579. Group probability: 0.9907. Peptides of the group

RVVSQLLTLMDGIK	88.32	54.8838	1571.907	1572.247	3	2	shared(2)	1	0.9943
NAPSIIFIDEIDSIAPK	93.72	54.1176	1841.977	1842.723	4	2	shared(2)	0	0.9869

The equivalent proteins include

gi|71033633|ref|XP_766458.1|	90885.27	cell division cycle protein 48 [Theileria parva strain Muguga]
gi|84998232|ref|XP_953837.1|	92274.01	transitional endoplasmic reticulum ATPase [Theileria annulata strain Ankara]

580. Group probability: 0.9906. Peptides of the group

LVLEVAQHLGEDTVR	64.46	54.8187	1677.905	1677.391	15	+2,+3	distinct	0	0.9906

The equivalent proteins include

gi|23348660|gb|AAN30694.1|	54813.6	ATP synthase F1, beta subunit [Brucella suis 1330]
gi|62196796|gb|AAX75096.1|	54813.6	AtpD, ATP synthase F1, beta subunit [Brucella abortus biovar 1 str. 9-941]

581. Group probability: 0.9906. Peptides of the group

GHYTEGAELVDTVLDVVR	51.88	53.6785	1971.99	1973.099	1	2	distinct	0	0.3414
EAESCDCIQGFQITHSLGGGTGAGMGTLLISK	59.2	50.9654	3294.532	3294.716	1	3	distinct	0	0.962
KEAESCDCIQGFQLTHSLGGGTGAGMGTLLISK	40.31	50.3066	3422.627	3421.96	1	3	distinct	1	0.6238

The equivalent proteins include

gi|52626602|emb|CAG30544.1|	22329.93	beta tubulin [Gigaspora margarita]
gi|52626604|emb|CAG30545.1|	23659.62	beta tubulin [Scutellospora castanea]
gi|20429154|emb|CAD30550.1|	29575.46	putative beta-tubulin [Gigaspora margarita]

582. Group probability: 0.9904. Peptides of the group

AVHSIIAHVAGK	75.29	55.6564	1201.693	1202.05	2	2	distinct	0	0.9904

The equivalent proteins include

gi|71005888|ref|XP_757610.1|	33797.5	hypothetical protein UM01463.1 [Ustilago maydis 521]

583. Group probability: 0.9904. Peptides of the group

LTGTTMVTPR	53.93	55.9823	1075.57	1075.847	3	+1,+2	distinct	0	0.9904

The equivalent proteins include

gi|77743554|ref|ZP_00812016.1|	204785.33	IMP dehydrogenase/GMP reductase [Rhodopseudomonas palustris BisA53]

584. Group probability: 0.9904. Peptides of the group

SITIFNDAAPLGGWMVALPVDVHDVSTVVK	69.26	51.1414	3150.642	3151.499	1	3	distinct	0	0.9904

The equivalent proteins include

gi|71020761|ref|XP_760611.1|	123549.03	hypothetical protein UM04464.1 [Ustilago maydis 521]

585. Group probability: 0.9902. Peptides of the group

TVLIQELINNVAK	89.24	54.8364	1453.85	1454.973	12	2	shared(2)	0	0.9972
LVLEVAQHLGENTVR	84.18	54.5381	1676.921	1677.711	15	+2,+3	shared(6)	0	0.9996
IPSAVGYQPTLATDMGALQER	53.31	53.1474	2217.11	2215.892	2	3	shared(3)	0	0.6752

The equivalent proteins include

gi|68193203|gb|EAN07855.1|	55025.59	ATP synthase F1, beta subunit [Mesorhizobium sp. BNC1]

586. Group probability: 0.9901. Peptides of the group

ISQFGQNTLIGASGDMSDWQYVQHMLNK	69.69	51.142	3167.48	3167.981	1	3	distinct	0	0.9901

The equivalent proteins include

gi|71023555|ref|XP_762007.1|	29403.54	hypothetical protein UM05860.1 [Ustilago maydis 521]

587. Group probability: 0.9901. Peptides of the group

HKGVMVGMGQK (0000010000000)	70.83	55.6094	1170.6	1170.959	31	+1,+2	shared(8)	1	0.9992
YPIEHGIVTNWDDMEK	86.65	53.8856	1945.888	1946.228	3	+2,+3	shared(6)	0	0.9985
VAPEEHPVLLTEAPLDPK	47.48	53.6979	1954.041	1953.863	3	+2,+3	shared(2)	0	0.9549
TTGIVIDSGDGVTHTVPIYEGYALPHAIMR (00000000000000000000000000000100)	42.36	51.0553	3198.602	3198.047	1	3	shared(2)	0	0.5153

The equivalent proteins include

gi|62768595|gb|AAY00164.1|	21988.23	actin A1c [Haliotis iris]

588. Group probability: 0.9900. Peptides of the group

LHSFSIGLPGSPDLIAAR	71.89	53.9126	1850.005	1851.453	4	2	distinct	0	0.99

The equivalent proteins include

gi|71003584|ref|XP_756458.1|	71026.37	hypothetical protein UM00311.1 [Ustilago maydis 521]

589. Group probability: 0.9900. Peptides of the group

VGHDELVGEIIR	74.64	55.3217	1335.715	1336.317	1	2	distinct	0	0.99

The equivalent proteins include

gi|56754166|gb|AAW25271.1|	69182.05	SJCHGC09310 protein [Schistosoma japonicum]

590. Group probability: 0.9897. Peptides of the group

LLANGDRAEAEIAANIYADHLQR	71.65	52.4642	2523.283	2523.605	1	3	distinct	1	0.9897

The equivalent proteins include

gi|71004228|ref|XP_756780.1|	7512.51	hypothetical protein UM00633.1 [Ustilago maydis 521]

591. Group probability: 0.9896. Peptides of the group

MIPGQSTNFPLSGFVR (010000000000000000)	72.41	54.1861	1749.887	1750.084	10	2	distinct	0	0.9896

The equivalent proteins include

gi|71015924|ref|XP_758852.1|	12952.34	hypothetical protein UM02705.1 [Ustilago maydis 521]

592. Group probability: 0.9896. Peptides of the group

LVQWQNSISSIIESIAATR	70.97	53.3479	2115.132	2115.307	1	2	distinct	0	0.9896

The equivalent proteins include

gi|71005672|ref|XP_757502.1|	47778.67	hypothetical protein UM01355.1 [Ustilago maydis 521]

593. Group probability: 0.9889. Peptides of the group

TASAQVEGGVHGLHSYEK	70.73	53.8632	1868.902	1869.444	1	2	distinct	0	0.9889

The equivalent proteins include

gi|71014450|ref|XP_758713.1|	25866.27	hypothetical protein UM02566.1 [Ustilago maydis 521]

594. Group probability: 0.9888. Peptides of the group

HSEFISYPIQLVVTK	71.98	54.2529	1759.951	1759.833	1	2	distinct	0	0.9888

The equivalent proteins include

gi|57230624|gb|AAW46934.1|	79461.46	chaperone, putative [Cryptococcus neoformans var. neoformans JEC21]
gi|25990446|gb|AAN76524.1|	79417.5	heat-shock protein 90 [Cryptococcus bacillisporus]
gi|25990448|gb|AAN76525.1|	78395.07	heat-shock protein 90 [Cryptococcus neoformans var. grubii]

595. Group probability: 0.9886. Peptides of the group

VAHEINHGIGQAGK	72.37	55.0661	1429.743	1430.26	1	2	distinct	0	0.9886

The equivalent proteins include

gi|109124496|ref|XP_001111804.1|	29162.53	PREDICTED: similar to suprabasin [Macaca mulatta]
gi|37182524|gb|AAQ89064.1|	25376.77	HLAR698 [Homo sapiens]

596. Group probability: 0.9882. Peptides of the group

DAGAIAGLDVLR	60.42	55.74	1169.64	1169.723	1	1	shared(2)	0	0.9647
LVNHFVQEFK	64.36	55.6038	1259.666	1260.05	9	+1,+2	shared(3)	0	0.992
ATAGDTHLGGEDFDNR	68.44	54.7902	1674.723	1675.633	4	2	shared(13)	0	0.9851
IINEPTAAAIAYGIDKK	71.85	54.6758	1786.983	1788.273	1	2	shared(14)	1	0.9837
KSEVFSTYSDNQPGVLIQVFEGER	44.05	52.0305	2728.334	2727.381	2	+2,+3	distinct	1	0.3759

The equivalent proteins include

gi|50259091|gb|EAL21768.1|	69817.45	hypothetical protein CNBC4700 [Cryptococcus neoformans var. neoformans B-3501A]
gi|57225741|gb|AAW42202.1|	69538.28	heat shock protein 70, putative [Cryptococcus neoformans var. neoformans JEC21]
gi|57225777|gb|AAW42238.1|	69803.43	chaperone, putative [Cryptococcus neoformans var. neoformans JEC21]

597. Group probability: 0.9881. Peptides of the group

LDTLFDEIVTNPAAFNEHGALILQR	69.07	52.2002	2796.445	2797.755	1	3	distinct	0	0.9881

The equivalent proteins include

gi|71022241|ref|XP_761351.1|	29102.79	hypothetical protein UM05204.1 [Ustilago maydis 521]

598. Group probability: 0.9879. Peptides of the group

PLVIPDSSQIPTLVGDYSSVTHEALR	68.4	51.9144	2793.455	2794.334	1	3	distinct	0	0.9879

The equivalent proteins include

gi|71003756|ref|XP_756544.1|	16109.82	hypothetical protein UM00397.1 [Ustilago maydis 521]

599. Group probability: 0.9876. Peptides of the group

FIVTGADVIHDFAVPSLGIK	118.14	53.401	2098.146	2098.943	6	2	distinct	0	0.9876

The equivalent proteins include

gi|109627383|emb|CAK55145.1|	22632.8	cytochrome oxidase subunit II [Zygosaccharomyces rouxii]
gi|109627385|emb|CAK55138.1|	23649.33	cytochrome oxidase subunit II [Zygosaccharomyces pseudorouxii]
gi|109627387|emb|CAK55139.1|	22292.53	cytochrome oxidase subunit II [Zygosaccharomyces pseudorouxii]
gi|57335058|emb|CAF05619.1|	21427.25	cytochrome oxidase subunit 2 [Zygosaccharomyces rouxii]
gi|57335060|emb|CAF05620.1|	21441.24	cytochrome oxidase subunit 2 [Zygosaccharomyces rouxii]
gi|31581230|gb|AAP57815.1|	22079.59	cytochrome oxidase subunit 2 [Zygosaccharomyces rouxii]

gi|31581232|gb|AAP57816.1|	22093.58	cytochrome oxidase subunit 2 [Zygosaccharomyces mellis]
gi|31581234|gb|AAP57817.1|	22119.63	cytochrome oxidase subunit 2 [Zygosaccharomyces bailii]
gi|31581236|gb|AAP57818.1|	22077.61	cytochrome oxidase subunit 2 [Zygosaccharomyces bisporus]
gi|31581240|gb|AAP57820.1|	22139.57	cytochrome oxidase subunit 2 [Zygosaccharomyces lentus]

600. Group probability: 0.9876. Peptides of the group

VALTGLTIAEYFR	96.01	54.8052	1452.798	1453.379	17	2	shared(8)	0	0.9932
DVESQDVLLFIDNIFR	95.12	54.0622	1921.978	1922.963	29	2	distinct	0	0.9736

The equivalent proteins include

gi|56808123|ref|ZP_00365911.1|	43843.55	COG0055: F0F1-type ATP synthase, beta subunit [Streptococcus pyogenes M49 591]

601. Group probability: 0.9875. Peptides of the group

PEEHPVLLTEAPINPK	67.3	54.3162	1782.952	1783.583	2	2	distinct	0	0.9837
SYELPDGKVITIGNER	64.43	54.1766	1789.921	1790.679	1	2	shared(14)	1	0.9686

The equivalent proteins include

gi|83700630|gb|ABC41107.1|	23946.06	actin [Trichoderma koningiopsis]
gi|83700636|gb|ABC41110.1|	25557.96	actin [Trichoderma koningiopsis]
gi|84314104|gb|ABC55663.1|	22492.43	actin [Trichoderma ovalisporum]
gi|84314108|gb|ABC55665.1|	25671.05	actin [Trichoderma caribbaeum]
gi|84314110|gb|ABC55666.1|	24331.26	actin [Trichoderma ovalisporum]
gi|87133580|gb|ABD24432.1|	23815.02	actin [Trichoderma petersenii]

602. Group probability: 0.9873. Peptides of the group

ELEHAEEVPLHADVQELPYLQAVLSESLR	66.41	50.7511	3313.683	3314.776	3	3	distinct	0	0.9873

The equivalent proteins include

gi|71002943|ref|XP_756152.1|	60322.27	hypothetical protein UM00005.1 [Ustilago maydis 521]

603. Group probability: 0.9871. Peptides of the group

KPVFVAHSDQSR	71.71	55.0714	1369.71	1370.202	1	2	distinct	0	0.9871

The equivalent proteins include

gi|71021837|ref|XP_761149.1|	36788.51	hypothetical protein UM05002.1 [Ustilago maydis 521]

604. Group probability: 0.9870. Peptides of the group

VFDKDGNGFNSAAELR	87.82	54.16	1738.827	1739.341	3	+2,+3	distinct	1	0.9508
EAFSLFDKDGDGTITTK	82.53	54.1901	1843.884	1844.047	4	2	shared(3)	1	0.9825

The equivalent proteins include

gi|162032|gb|AAA30176.1|	16828.81	calmodulin C

605. Group probability: 0.9869. Peptides of the group

TFEKVDPSK	50.37	55.6716	1049.539	1049.93	2	+1,+2	distinct	1	0.9869

The equivalent proteins include

gi|71004518|ref|XP_756925.1|	13971.36	hypothetical protein UM00778.1 [Ustilago maydis 521]

606. Group probability: 0.9869. Peptides of the group

VLTIGDGIAR	60.13	56.1474	1013.587	1014.314	1	2	shared(2)	0	0.9608
VVDALGNPIDGK	87.75	55.4031	1196.64	1197.823	1	2	shared(6)	0	0.9821
HAIIIYDDLSK	80.76	55.5162	1286.687	1287.158	9	+1,+2	shared(5)	0	0.9997
EAYPGDVFYIHSR	58.88	54.6289	1552.731	1554.178	3	2	shared(8)	0	0.9619

The equivalent proteins include

gi|57227561|gb|AAW44019.1|	58177.63	ATP synthase alpha chain, mitochondrial precursor, putative [Cryptococcus neoformans var. neoforman

607. Group probability: 0.9867. Peptides of the group

DLVSADHSHVVYPLGDDADQGACPASHSVR	65.52	51.1188	3174.442	3175.219	2	3	distinct	0	0.9867

The equivalent proteins include

gi|71022673|ref|XP_761566.1|	47719.54	hypothetical protein UM05419.1 [Ustilago maydis 521]

608. Group probability: 0.9866. Peptides of the group

ELPAILSHHLPIDTSR	69.46	54.2859	1797.974	1798.329	2	2	distinct	0	0.9866

The equivalent proteins include

gi|71020693|ref|XP_760577.1|	31751.49	hypothetical protein UM04430.1 [Ustilago maydis 521]

609. Group probability: 0.9865. Peptides of the group

NRPAPSVDEVKK	71.21	55.0837	1338.725	1339.473	3	2	distinct	1	0.9865

The equivalent proteins include

gi|1399099|gb|AAB03213.1|	40548.91	aspartate semialdehyde dehydrogenase

gi|71021631|ref|XP_761046.1|	40575.68	hypothetical protein UM04899.1 [Ustilago maydis 521]

610. Group probability: 0.9864. Peptides of the group

DGYLLLPSFFDPTALLAHSK	67.45	53.217	2204.152	2205.113	1	2	distinct	0	0.9864

The equivalent proteins include

gi|71016325|ref|XP_758890.1|	38017.65	hypothetical protein UM02743.1 [Ustilago maydis 521]

611. Group probability: 0.9854. Peptides of the group

ICYVHQNQPGSLR	69.86	54.9078	1570.767	1571.548	4	2	distinct	0	0.9854

The equivalent proteins include

gi|71005428|ref|XP_757380.1|	53233.16	hypothetical protein UM01233.1 [Ustilago maydis 521]

612. Group probability: 0.9853. Peptides of the group

TDTNPGKNNTELHR	69.31	54.4497	1595.765	1596.175	2	2	distinct	1	0.9853

The equivalent proteins include

gi|71005098|ref|XP_757215.1|	13922.8	hypothetical protein UM01068.1 [Ustilago maydis 521]

613. Group probability: 0.9853. Peptides of the group

LGAGYPMGPFELADLVGLDTLSHIAK	63.89	52.1076	2684.388	2685.243	1	2	distinct	0	0.9853

The equivalent proteins include

gi|71005160|ref|XP_757246.1|	36799.36	hypothetical protein UM01099.1 [Ustilago maydis 521]

614. Group probability: 0.9851. Peptides of the group

QSASPTHTHVQSNASSPASPTK	68	53.2227	2219.057	2220.321	1	3	distinct	0	0.9851

The equivalent proteins include

gi|71020259|ref|XP_760360.1|	64931.04	hypothetical protein UM04213.1 [Ustilago maydis 521]

615. Group probability: 0.9851. Peptides of the group

FMVSHAPTLAASQK	69.23	54.9646	1486.76	1487.266	2	2	distinct	0	0.9851

The equivalent proteins include

gi|71021019|ref|XP_760740.1|	25506.54	hypothetical protein UM04593.1 [Ustilago maydis 521]

616. Group probability: 0.9848. Peptides of the group

TTTTTHSNPALIHR	69	54.7006	1548.801	1548.908	5	2	distinct	0	0.9848

The equivalent proteins include

gi|71020597|ref|XP_760529.1|	82193.83	hypothetical protein UM04382.1 [Ustilago maydis 521]

617. Group probability: 0.9846. Peptides of the group

LDLLKLAPGGHIGR	57.38	54.9851	1458.867	1458.928	5	+2,+3	distinct	1	0.9846

The equivalent proteins include

gi|94733357|emb|CAK04707.1|	20802.26	ribosomal protein L4 [Danio rerio]
gi|54261775|ref|NP_998272.1|	42810.18	ribosomal protein L4 [Danio rerio]

618. Group probability: 0.9846. Peptides of the group

KLDHELGIR	56.89	55.2145	1079.609	1080.282	2	2	distinct	1	0.8886
SLSDLTDHSIHR	44.69	55.0227	1379.679	1380.01	1	2	distinct	0	0.8619

The equivalent proteins include

gi|71021509|ref|XP_760985.1|	30431.37	hypothetical protein UM04838.1 [Ustilago maydis 521]

619. Group probability: 0.9844. Peptides of the group

KINPAVAQLQASR	69.28	55.443	1394.799	1394.966	2	2	distinct	1	0.9844

The equivalent proteins include

gi|71021719|ref|XP_761090.1|	13994.6	hypothetical protein UM04943.1 [Ustilago maydis 521]

620. Group probability: 0.9844. Peptides of the group

HPDNPFNQLSVAYDASKEEK	68.28	53.2343	2288.071	2289.143	3	3	distinct	1	0.9844

The equivalent proteins include

gi|71020913|ref|XP_760687.1|	24447.58	hypothetical protein UM04540.1 [Ustilago maydis 521]

621. Group probability: 0.9840. Peptides of the group

MGFNDQEIVALAGGHTLGR (010000000000000000000)	79.81	54.0993	1984.979	1986.274	9	+2,+3	distinct	0	0.984

The equivalent proteins include

gi|70992769|ref|XP_751233.1|	35180.72	cytochrome c peroxidase [Aspergillus fumigatus Af293]

622. Group probability: 0.9838. Peptides of the group

LPIGPSLAIPGTPVGDR	67.05	54.9001	1658.935	1658.975	2	2	distinct	0	0.9838

The equivalent proteins include

gi|71021931|ref|XP_761196.1|	12700.6	hypothetical protein UM05049.1 [Ustilago maydis 521]

623. Group probability: 0.9836. Peptides of the group

ILIEHLDDHALSVDIPAGEVIKPGDVK	64.47	51.6327	2892.56	2893.264	1	3	distinct	0	0.9836

The equivalent proteins include

gi|71016178|ref|XP_758875.1|	58936.01	hypothetical protein UM02728.1 [Ustilago maydis 521]

624. Group probability: 0.9832. Peptides of the group

VHDVAFKK	47.46	56.4368	942.529	942.91	3	+1,+2	distinct	1	0.9832

The equivalent proteins include

gi|71003329|ref|XP_756345.1|	20210.59	hypothetical protein UM00198.1 [Ustilago maydis 521]

625. Group probability: 0.9832. Peptides of the group

LPLPTNPSSSNSYSYSKPQTLSHLADAIDTTR	61.84	50.1509	3460.711	3461.236	1	3	distinct	0	0.9832

The equivalent proteins include

gi|71005656|ref|XP_757494.1|	12600.94	hypothetical protein UM01347.1 [Ustilago maydis 521]

626. Group probability: 0.9832. Peptides of the group

AATPDGFGPQAAVVAASGAAAYEQALDYIRPR	62	50.8761	3203.6	3204.858	1	3	distinct	0	0.9832

The equivalent proteins include

gi|71007635|ref|XP_758131.1|	39538.25	hypothetical protein UM01984.1 [Ustilago maydis 521]

627. Group probability: 0.9832. Peptides of the group

RFIPSISDAELPK	46.39	54.9688	1471.803	1472.147	1	2	distinct	1	0.8853
ELLDQINSGRPDAAVEK	44.11	54.0575	1853.948	1854.914	1	3	distinct	0	0.8533

The equivalent proteins include

gi|71017679|ref|XP_759070.1|	30456.33	hypothetical protein UM02923.1 [Ustilago maydis 521]

628. Group probability: 0.9831. Peptides of the group

HNDSVDKVGLFDAELINALPASLK	65.54	52.4113	2565.344	2566.001	2	3	distinct	1	0.9831

The equivalent proteins include

gi|71005106|ref|XP_757219.1|	35834.33	hypothetical protein UM01072.1 [Ustilago maydis 521]

629. Group probability: 0.9830. Peptides of the group

SAVKPGSESEATTPGAGSTEEIANSQGAYDGSR	61.54	51.066	3210.455	3211.603	2	3	distinct	0	0.983

The equivalent proteins include

gi|71008568|ref|XP_758227.1|	14831.12	hypothetical protein UM02080.1 [Ustilago maydis 521]

630. Group probability: 0.9830. Peptides of the group

VFDQCTSGKPFYFK	67.6	54.2209	1722.808	1723.213	1	2	distinct	0	0.983

The equivalent proteins include

gi|71002985|ref|XP_756173.1|	41338.4	hypothetical protein UM00026.1 [Ustilago maydis 521]

631. Group probability: 0.9828. Peptides of the group

SYTLQTASFDAR	68.55	55.4597	1358.647	1359.197	2	2	distinct	0	0.9828

The equivalent proteins include

gi|71015267|ref|XP_758790.1|	10659.82	hypothetical protein UM02643.1 [Ustilago maydis 521]

632. Group probability: 0.9821. Peptides of the group

DEQGQDVLLFIDNIFR	72.16	53.7914	1920.958	1922.383	8	2	distinct	0	0.8255
ELQDIIAILGMDELSEEDKLTVER	42.52	51.9557	2758.395	2759.358	1	2	distinct	1	0.8975

The equivalent proteins include

gi|68446657|dbj|BAE04241.1|	51544.18	ATP synthase beta chain [Staphylococcus haemolyticus JCSC1435]

633. Group probability: 0.9820. Peptides of the group

SNNLEAALQDFEHVLVHEPSNAFVQK	63.79	51.4567	2935.446	2935.929	1	3	distinct	0	0.982

The equivalent proteins include

gi|71022405|ref|XP_761432.1|	65506.98	hypothetical protein UM05285.1 [Ustilago maydis 521]

634. Group probability: 0.9819. Peptides of the group

DIKPEAIEFPR	48.11	55.3473	1313.698	1314.224	1	2	distinct	0	0.8933
IDKIDQEQLEK	60.51	55.3019	1357.709	1357.941	1	2	distinct	1	0.8305

The equivalent proteins include

gi|71016490|ref|XP_758901.1|	23061.06	hypothetical protein UM02754.1 [Ustilago maydis 521]

635. Group probability: 0.9819. Peptides of the group

QLEELKTELLNLR	67.35	54.5953	1597.904	1598.205	2	2	distinct	1	0.9819

The equivalent proteins include

gi|94468500|gb|ABF18099.1|	14339.42	60S ribosomal protein L35 [Aedes aegypti]

gi|71004454|ref|XP_756893.1|	25391.98	hypothetical protein UM00746.1 [Ustilago maydis 521]

636. Group probability: 0.9813. Peptides of the group

ILHLYEHASQSENR	66.52	54.294	1695.833	1696.539	2	2	distinct	0	0.9813

The equivalent proteins include

gi|71023189|ref|XP_761824.1|	45273.51	hypothetical protein UM05677.1 [Ustilago maydis 521]

637. Group probability: 0.9813. Peptides of the group

VVYKPDSQSTDEFMVIVNAEEYKK	64.19	51.6989	2818.373	2819.6	5	3	distinct	1	0.9813

The equivalent proteins include

gi|71024653|ref|XP_762556.1|	7593.75	hypothetical protein UM06409.1 [Ustilago maydis 521]

638. Group probability: 0.9807. Peptides of the group

LPVIAPYFEDKTHPADNAF	63.86	53.2606	2144.058	2145.113	2	2	distinct	1	0.9807

The equivalent proteins include

gi|71018885|ref|XP_759673.1|	22335.27	hypothetical protein UM03526.1 [Ustilago maydis 521]

639. Group probability: 0.9806. Peptides of the group

APAETPFSALAFAHLAEK	66.74	53.9666	1869.962	1871.21	1	3	distinct	0	0.9806

The equivalent proteins include

gi|71023055|ref|XP_761757.1|	54048.53	hypothetical protein UM05610.1 [Ustilago maydis 521]

640. Group probability: 0.9806. Peptides of the group

IAQFIDAGRDEYDVK	65.62	54.1337	1738.853	1739.436	1	2	distinct	1	0.9806

The equivalent proteins include

gi|71005506|ref|XP_757419.1|	19618.26	hypothetical protein UM01272.1 [Ustilago maydis 521]

641. Group probability: 0.9802. Peptides of the group

KVLGDTLVDHFGGTR	65.55	54.6768	1613.852	1614.594	1	2	distinct	1	0.9802

The equivalent proteins include

gi|71023777|ref|XP_762118.1|	53637.02	hypothetical protein UM05971.1 [Ustilago maydis 521]

642. Group probability: 0.9796. Peptides of the group

SAFKNEHSFEK	66.89	55.048	1322.625	1323.178	2	2	distinct	1	0.9796

The equivalent proteins include

gi|71022969|ref|XP_761714.1|	13723.17	hypothetical protein UM05567.1 [Ustilago maydis 521]

643. Group probability: 0.9794. Peptides of the group

LANIDYLRPIVADADTGHGGLTAVMK	62.39	52.0775	2710.411	2711.274	3	3	distinct	0	0.9794

The equivalent proteins include

gi|85099820|ref|XP_960854.1|	61631.04	ISOCITRATE LYASE (ISOCITRATASE) (ICL) [MIPS] [Neurospora crassa OR74A]
gi|2971|emb|CAA44573.1|	61660.03	isocitrate lyase [Neurospora crassa]

644. Group probability: 0.9793. Peptides of the group

LVNHFVQEFK	64.36	55.6038	1259.666	1260.05	9	+1,+2	shared(3)	0	0.992
TFTPEEISSMILVK	54.55	54.5124	1593.832	1594.697	1	2	distinct	0	0.7977
ATAGDTHLGGEDFDNR	68.44	54.7902	1674.723	1675.633	4	2	shared(13)	0	0.9851
IINEPTAAAIAYGIDKK	71.85	54.6758	1786.983	1788.273	1	2	shared(14)	1	0.9837

The equivalent proteins include

gi|50551349|ref|XP_503148.1|	70310.07	hypothetical protein [Yarrowia lipolytica]

645. Group probability: 0.9782. Peptides of the group

VIILDKTEGNAAR	65.38	55.3044	1398.783	1399.929	1	2	distinct	1	0.9782

The equivalent proteins include

gi|71005260|ref|XP_757296.1|	69067.2	hypothetical protein UM01149.1 [Ustilago maydis 521]

646. Group probability: 0.9781. Peptides of the group

NFGETPHEQDDVLSVWAPDVHAIPATSALR	59.86	51.0784	3271.59	3272.257	4	3	distinct	0	0.9781

The equivalent proteins include

gi|71019745|ref|XP_760103.1|	17735.89	hypothetical protein UM03956.1 [Ustilago maydis 521]

647. Group probability: 0.9781. Peptides of the group

ITFASGLGTHWDHENTYTAR	62	53.1574	2276.061	2277.183	1	2	distinct	0	0.9781

The equivalent proteins include

gi|71005844|ref|XP_757588.1|	33819.62	hypothetical protein UM01441.1 [Ustilago maydis 521]
gi|71004622|ref|XP_756977.1|	33834.59	hypothetical protein UM00830.1 [Ustilago maydis 521]

648. Group probability: 0.9780. Peptides of the group

KGMTPSQIGVQLR	65.23	55.1152	1413.776	1414.953	1	2	distinct	1	0.978

The equivalent proteins include

gi|71004278|ref|XP_756805.1|	17027.39	40S ribosomal protein S13 [Ustilago maydis 521]

649. Group probability: 0.9778. Peptides of the group

VAALLDHGSPFVELSR	63.71	54.2073	1709.91	1710.414	1	2	distinct	0	0.9778

The equivalent proteins include

gi|71017276|ref|XP_758969.1|	62646.59	hypothetical protein UM02822.1 [Ustilago maydis 521]

650. Group probability: 0.9776. Peptides of the group

LVISADQLSASPR	65.07	55.1451	1355.741	1356.22	1	2	distinct	0	0.9776

The equivalent proteins include

gi|71023599|ref|XP_762029.1|	35603.05	hypothetical protein UM05882.1 [Ustilago maydis 521]

651. Group probability: 0.9776. Peptides of the group

IVYAIHGGPMAGR	65.07	55.1742	1340.702	1340.961	3	2	distinct	0	0.9776

The equivalent proteins include

gi|71018803|ref|XP_759632.1|	20556.93	hypothetical protein UM03485.1 [Ustilago maydis 521]

652. Group probability: 0.9776. Peptides of the group

SYELPDGKVITIGNER	64.43	54.1766	1789.921	1790.679	1	2	shared(14)	1	0.9686
YPIEHGVITNWDDMEK	71.4	53.8856	1945.888	1946.228	1	2	distinct	0	0.9498
VAPEEHPVLLTEAPINPK	88.95	53.6979	1953.057	1953.863	9	2	shared(9)	0	0.9916

The equivalent proteins include

gi|19073082|gb|AAL84710.1|	36740.58	actin [Cercospora beticola]

653. Group probability: 0.9776. Peptides of the group

IGGIGTVPVGR	66.14	55.3583	1024.603	1024.899	11	2	shared(36)	0	0.978
SVEMHHEALTEAVPGDNVGFNVK (00001000000000000000000)	89.92	52.5434	2479.18	2479.493	7	+2,+3	distinct	0	0.9738

The equivalent proteins include

gi|83629359|gb|ABC26431.1|	27906.44	elongation factor-1alpha F2 [Endophytus anemones]
gi|83629431|gb|ABC26449.1|	27937.45	elongation factor-1alpha F2 [Amauronematus longicauda]
gi|83629551|gb|ABC26479.1|	27935.45	elongation factor-1alpha F2 [Diprion similis]
gi|83629559|gb|ABC26481.1|	27919.5	elongation factor-1alpha F2 [Sterictiphora sp. TN-2005]
gi|83629583|gb|ABC26487.1|	27935.45	elongation factor-1alpha F2 [Scolioneura betuleti]
gi|83629587|gb|ABC26488.1|	27919.46	elongation factor-1alpha F2 [Caliroa sp. TN-2005]
gi|83629599|gb|ABC26491.1|	27905.44	elongation factor-1alpha F2 [Phymatocera aterrima]
gi|66774450|gb|AAY56018.1|	31272.29	elongation factor 1 alpha [Pachypappa marsupialis]
gi|5670234|gb|AAD46637.1|	32795.1	elongation factor 1 alpha [Maculolachnus submacula]
gi|71273710|emb|CAH25445.1|	36133.68	elongation factor-1 alpha [Orygma luctuosum]
gi|71273712|emb|CAH25446.1|	36146.64	elongation factor-1 alpha [Nemopoda nitidula]
gi|71273714|emb|CAH25447.1|	36198.71	elongation factor-1 alpha [Saltella sphondylii]
gi|71273724|emb|CAH25449.1|	33868.44	elongation factor-1 alpha [Zuskamira inexpectata]
gi|71273726|emb|CAH25450.1|	25809.46	elongation factor-1 alpha [Themira annulipes]
gi|71273728|emb|CAH25451.1|	27003.1	elongation factor-1 alpha [Themira arctica]
gi|71273732|emb|CAH25453.1|	26794.89	elongation factor-1 alpha [Themira flavicoxa]
gi|71273734|emb|CAH25454.1|	27574.41	elongation factor-1 alpha [Themira lucida]
gi|71273736|emb|CAH25455.1|	36059.56	elongation factor-1 alpha [Themira minor]
gi|71273738|emb|CAH25456.1|	26764.91	elongation factor-1 alpha [Themira nigricornis]
gi|71273740|emb|CAH25457.1|	27428.34	elongation factor-1 alpha [Themira pusilla]
gi|71273742|emb|CAH25458.1|	36115.69	elongation factor-1 alpha [Themira putris]
gi|71273744|emb|CAH25459.1|	26669.8	elongation factor-1 alpha [Themira superba]
gi|71273730|emb|CAH25452.1|	27053.16	elongation factor-1 alpha [Themira biloba]
gi|73622745|gb|AAZ78411.1|	25358.1	elongation factor 1-alpha [Fagisuga triloba]

gi|73622801|gb|AAZ78439.1|	25418.18	elongation factor 1-alpha [Leucaspis ohakunensis]
gi|214113|gb|AAA49700.1|	50551.39	elongation factor-1 alpha-chain protein (EF-1-alpha)
gi|27735380|gb|AAH41196.1|	50524.28	Eef1a-s protein [Xenopus laevis]
gi|10100|emb|CAA46922.1|	44996.53	elongation factor 1-alpha [Rhynchosciara americana]
gi|2196948|gb|AAC03144.1|	40477.81	elongation factor-1 alpha [Aphonopelma chalcodes]
gi|2196950|gb|AAC03145.1|	40509.98	elongation factor-1 alpha [Armadillidium vulgare]
gi|2196952|gb|AAC03146.1|	40412.69	elongation factor-1 alpha [Dysdera crocata]
gi|2196964|gb|AAC03152.1|	39774.47	elongation factor-1 alpha [Narceus americanus]
gi|2196968|gb|AAC03154.1|	40000.66	elongation factor-1 alpha [Polyxenus fasciculatus]
gi|2196970|gb|AAC03155.1|	40224.76	elongation factor-1 alpha [Pedetontus saltator]
gi|2196976|gb|AAC03158.1|	40002.66	elongation factor-1 alpha [Tomocerus sp. 'jcrjws2']
gi|2196978|gb|AAC03159.1|	40378.78	elongation factor-1 alpha [Vonones ornata]
gi|18439|emb|CAA34769.1|	48981.43	unnamed protein product [Euglena gracilis]
gi|5670226|gb|AAD46629.1|	32654.09	elongation factor 1 alpha [Essigella fusca]
gi|5670227|gb|AAD46630.1|	31147.25	elongation factor 1 alpha [Eulachnus rileyi]
gi|5670228|gb|AAD46631.1|	31304.23	elongation factor 1 alpha [Eulachnus brevpilosus]
gi|5670229|gb|AAD46632.1|	30196.89	elongation factor 1 alpha [Cinara etsuhoe]
gi|5670230|gb|AAD46633.1|	32768.13	elongation factor 1 alpha [Cinara glabra]
gi|5670232|gb|AAD46635.1|	32665.98	elongation factor 1 alpha [Cinara ponderosae]
gi|5670235|gb|AAD46638.1|	31733.56	elongation factor 1 alpha [Pterochloroides persicae]
gi|5670236|gb|AAD46639.1|	32735.04	elongation factor 1 alpha [Lachnus roboris]
gi|5670238|gb|AAD46641.1|	30897.14	elongation factor 1 alpha [Lachnus takahashii]
gi|5670239|gb|AAD46642.1|	32052.5	elongation factor 1 alpha [Lachnus tropicalis]
gi|5670241|gb|AAD46644.1|	32748.17	elongation factor 1 alpha [Stomaphis fagi]
gi|5670242|gb|AAD46645.1|	32755.14	elongation factor 1 alpha [Stomaphis pini]
gi|5670243|gb|AAD46646.1|	32802.01	elongation factor 1 alpha [Stomaphis quercus]
gi|5670246|gb|AAD46649.1|	32749.1	elongation factor 1 alpha [Stomaphis yanonis]
gi|5670249|gb|AAD46652.1|	32782.15	elongation factor 1 alpha [Stomaphis japonica]
gi|5107120|gb|AAD39967.1|	32752.14	elongation factor 1 alpha [Stomaphis takahashii]
gi|5107121|gb|AAD39968.1|	28970.03	elongation factor 1 alpha [Nippolachnus piri]
gi|5107122|gb|AAD39969.1|	31492.47	elongation factor 1 alpha [Tuberolachnus salignus]
gi|5107123|gb|AAD39970.1|	32198.77	elongation factor 1 alpha [Protrama radicis]
gi|5107132|gb|AAD39979.1|	32810.15	elongation factor 1 alpha [Trama troglodytes]
gi|5107127|gb|AAD39974.1|	32664.27	elongation factor 1 alpha [Protrama ranunculi]
gi|5107128|gb|AAD39975.1|	31978.74	elongation factor 1 alpha [Trama maritima]
gi|5107130|gb|AAD39977.1|	32697.07	elongation factor 1 alpha [Trama rara]
gi|51951168|gb|AAU15053.1|	41120.28	elongation factor-1 alpha [Alocandrena porterae]
gi|51951276|gb|AAU15107.1|	41205.39	elongation factor-1 alpha [Haplomelitta griseonigra]
gi|51951302|gb|AAU15120.1|	41141.23	elongation factor-1 alpha [Isodontia mexicana]

gi|15808609|gb|AAL06605.1|	36006.68	elongation factor-1 alpha [Orygma luctuosum]
gi|15808617|gb|AAL06609.1|	35938.54	elongation factor-1 alpha [Helcomyza mirabilis]
gi|15808621|gb|AAL06611.1|	36205.68	elongation factor-1 alpha [Amma blancheae]
gi|15808625|gb|AAL06613.1|	36081.55	elongation factor-1 alpha [Chaetocoelopa littoralis]
gi|15808627|gb|AAL06614.1|	36179.67	elongation factor-1 alpha [Chaetocoelopa sydneyensis]
gi|15808629|gb|AAL06615.1|	35635.42	elongation factor-1 alpha [Coelopa alluaudi]
gi|15808633|gb|AAL06617.1|	36189.66	elongation factor-1 alpha [Coelopa frigida]
gi|15808635|gb|AAL06618.1|	36104.46	elongation factor-1 alpha [Coelopa pilipes]
gi|15808641|gb|AAL06621.1|	36147.68	elongation factor-1 alpha [Coelopa ursina]
gi|15808639|gb|AAL06620.1|	36195.65	elongation factor-1 alpha [Coelopa nebularum]
gi|15808645|gb|AAL06623.1|	35738.42	elongation factor-1 alpha [Coelopella curvipes]
gi|15808647|gb|AAL06624.1|	36179.67	elongation factor-1 alpha [Coelopella popeae]
gi|15808649|gb|AAL06625.1|	36177.69	elongation factor-1 alpha [Dasycoelopa australis]
gi|15808653|gb|AAL06627.1|	36219.7	elongation factor-1 alpha [Gluma musgravei]
gi|15808655|gb|AAL06628.1|	36219.7	elongation factor-1 alpha [Gluma nitida]
gi|15808657|gb|AAL06629.1|	36223.67	elongation factor-1 alpha [Icaridion debile]
gi|15808661|gb|AAL06631.1|	36063.53	elongation factor-1 alpha [Malacomyia sciomyzina]
gi|15808665|gb|AAL06633.1|	36105.57	elongation factor-1 alpha [This canus]
gi|50284525|dbj|BAD29728.1|	50487.25	elongation factor-1 alpha [Lethenteron japonicum]
gi|6467333|gb|AAF13139.1|	30160.54	elongation factor 1-a [Calliobothrium sp.]
gi|13122864|gb|AAK12673.1|	40370.82	elongation factor-1alpha [Astrobunus grallator]
gi|13122866|gb|AAK12674.1|	40298.78	elongation factor-1alpha [Caddo pepperella]
gi|13122872|gb|AAK12677.1|	41621.46	elongation factor-1alpha [Dicranolasma scabrum]
gi|13122874|gb|AAK12678.1|	40383.81	elongation factor-1alpha [Equitius doriae]
gi|13122898|gb|AAK12690.1|	40372.81	elongation factor-1alpha [Sodreana sodreana]
gi|13122880|gb|AAK12681.1|	41866.51	elongation factor-1alpha [Ischyropsalis luteipes]
gi|13122882|gb|AAK12682.1|	40354.85	elongation factor-1alpha [Laneosoares inermis]
gi|13122884|gb|AAK12683.1|	40352.84	elongation factor-1alpha [Proscotolemon sauteri]
gi|13122886|gb|AAK12684.1|	40344.77	elongation factor-1alpha [Progonyleptoidellus striatus]
gi|13122888|gb|AAK12685.1|	40324.84	elongation factor-1alpha [Pseudobiantes japonicus]
gi|13122890|gb|AAK12686.1|	40380.86	elongation factor-1alpha [Phalangium opilio]
gi|13122824|gb|AAK12653.1|	40386.82	elongation factor-1alpha [Discocyrtus areolatus]
gi|13122894|gb|AAK12688.1|	40309.82	elongation factor-1alpha [Sabacon imamurai]
gi|13122902|gb|AAK12692.1|	40443.84	elongation factor-1alpha [Taracus pallipes]
gi|6606185|gb|AAF19095.1|	41710.42	elongation factor-1 alpha [Eumesocampa frigilis]
gi|6606187|gb|AAF19097.1|	41825.53	elongation factor-1 alpha [Machiloides banksi]
gi|6606188|gb|AAF19098.1|	40248.81	elongation factor-1 alpha [Nipponopsalis abei]
gi|13122816|gb|AAK12649.1|	40328.79	elongation factor-1alpha [Caddo agilis]
gi|13123935|gb|AAK12652.2|	41865.49	elongation factor-1alpha [Chthonius tetrachelatus]
gi|13122830|gb|AAK12656.1|	40649.9	elongation factor-1alpha [Hadrurus arizonensis]

gi|13122836|gb|AAK12659.1|	41376.23	elongation factor-1alpha [Idiogaryops paludis]
gi|13122840|gb|AAK12661.1|	40405.87	elongation factor-1alpha [Odiellus pictus]
gi|13122856|gb|AAK12669.1|	40460.93	elongation factor-1alpha [Sclerobunus robustus]
gi|13122860|gb|AAK12671.1|	40443.76	elongation factor-1alpha [tachyuropodid 'Tac']
gi|14279585|gb|AAK58641.1|	39768.63	elongation factor-1 alpha [Lasioglossum albocinctum]
gi|14537406|gb|AAK66572.1|	39310.35	elongation factor-1 alpha [Lasioglossum erythrurum]
gi|14537409|gb|AAK66573.1|	39343.33	elongation factor-1 alpha [Lasioglossum florale]
gi|14537412|gb|AAK66574.1|	39340.36	elongation factor-1 alpha [Lasioglossum lanarium]
gi|14537415|gb|AAK66575.1|	39303.33	elongation factor-1 alpha [Lasioglossum mediopolitum]
gi|14537418|gb|AAK66576.1|	39359.37	elongation factor-1 alpha [Lasioglossum mirandum]
gi|14537427|gb|AAK66579.1|	39433.38	elongation factor-1 alpha [Lasioglossum olgae]
gi|14537430|gb|AAK66580.1|	39218.31	elongation factor-1 alpha [Lasioglossum sp. NDA(1)-A]
gi|14537433|gb|AAK66581.1|	39199.32	elongation factor-1 alpha [Lasioglossum olgae]
gi|14537436|gb|AAK66582.1|	39417.38	elongation factor-1 alpha [Lasioglossum cressonii]
gi|14537439|gb|AAK66583.1|	39483.46	elongation factor-1 alpha [Lasioglossum figueresi]
gi|14537524|gb|AAK66611.1|	39201.26	elongation factor-1 alpha [Lasioglossum pectorale]
gi|14537445|gb|AAK66585.1|	39425.41	elongation factor-1 alpha [Lasioglossum hyalinum]
gi|14537604|gb|AAK66637.1|	39215.27	elongation factor-1 alpha [Lasioglossum asteris]
gi|14537451|gb|AAK66587.1|	39233.25	elongation factor-1 alpha [Lasioglossum parvum]
gi|14537463|gb|AAK66591.1|	39381.4	elongation factor-1 alpha [Lasioglossum umbripenne]
gi|14537466|gb|AAK66592.1|	39387.39	elongation factor-1 alpha [Lasioglossum vierecki]
gi|14537475|gb|AAK66595.1|	39199.28	elongation factor-1 alpha [Lasioglossum albipes]
gi|14537478|gb|AAK66596.1|	39419.36	elongation factor-1 alpha [Lasioglossum apristum]
gi|14537487|gb|AAK66599.1|	39245.28	elongation factor-1 alpha [Lasioglossum cinctipes]
gi|14537490|gb|AAK66600.1|	39214.32	elongation factor-1 alpha [Lasioglossum comagenense]
gi|14537499|gb|AAK66603.1|	39432.28	elongation factor-1 alpha [Lasioglossum laticeps]
gi|14537539|gb|AAK66616.1|	39433.38	elongation factor-1 alpha [Lasioglossum subtropicum]
gi|14537505|gb|AAK66605.1|	39496.38	elongation factor-1 alpha [Lasioglossum mediterraneum]
gi|14537511|gb|AAK66607.1|	39231.27	elongation factor-1 alpha [Lasioglossum malachurum]
gi|14537514|gb|AAK66608.1|	39231.27	elongation factor-1 alpha [Lasioglossum morio]
gi|14537527|gb|AAK66612.1|	39447.4	elongation factor-1 alpha [Lasioglossum politum]
gi|14537530|gb|AAK66613.1|	39164.28	elongation factor-1 alpha [Lasioglossum puncticolle]
gi|14537613|gb|AAK66640.1|	39532.45	elongation factor-1 alpha [Lasioglossum noctivagum]
gi|14537536|gb|AAK66615.1|	39395.4	elongation factor-1 alpha [Lasioglossum gattaca]
gi|14537546|gb|AAK66618.1|	39197.23	elongation factor-1 alpha [Lasioglossum villosulum]
gi|14537550|gb|AAK66619.1|	39185.23	elongation factor-1 alpha [Lasioglossum lustrans]

gi|14537553|gb|AAK66620.1|	39400.39	elongation factor-1 alpha [Lasioglossum megastigmus]
gi|14537559|gb|AAK66622.1|	39146.26	elongation factor-1 alpha [Lasioglossum callizonium]
gi|14537562|gb|AAK66623.1|	39275.3	elongation factor-1 alpha [Lasioglossum coriaceum]
gi|14537565|gb|AAK66624.1|	39231.27	elongation factor-1 alpha [Lasioglossum desertum]
gi|14537580|gb|AAK66629.1|	39201.26	elongation factor-1 alpha [Lasioglossum lativentre]
gi|14537571|gb|AAK66626.1|	39441.43	elongation factor-1 alpha [Lasioglossum laevigatum]
gi|14537586|gb|AAK66631.1|	39431.4	elongation factor-1 alpha [Lasioglossum discum]
gi|14537601|gb|AAK66636.1|	39213.29	elongation factor-1 alpha [Lasioglossum zonulum]
gi|14537589|gb|AAK66632.1|	39348.33	elongation factor-1 alpha [Lasioglossum pavonotum]
gi|14537592|gb|AAK66633.1|	39518.43	elongation factor-1 alpha [Lasioglossum sisymbrii]
gi|14537595|gb|AAK66634.1|	39185.26	elongation factor-1 alpha [Lasioglossum sexnotatum]
gi|14537598|gb|AAK66635.1|	39419.36	elongation factor-1 alpha [Lasioglossum titusi]
gi|14537607|gb|AAK66638.1|	39257.3	elongation factor-1 alpha [Lasioglossum hybodinum]
gi|14537610|gb|AAK66639.1|	39419.36	elongation factor-1 alpha [Lasioglossum sp. 'Cobboboonee']
gi|14537616|gb|AAK66641.1|	39362.34	elongation factor-1 alpha [Lasioglossum oenotherae]
gi|14537619|gb|AAK66642.1|	39431.4	elongation factor-1 alpha [Lasioglossum alphenum]
gi|14010084|gb|AAK51842.1|	17451.06	elongation factor 1 alpha [Sandalodes sp. MCH-2001]
gi|19422986|gb|AAL88312.1|	17393.02	elongation factor 1-alpha [Habronattus sp. YUCUN]
gi|13446738|gb|AAK26505.1|	14621.58	elongation factor 1 alpha [Automate gardineri]
gi|13446740|gb|AAK26506.1|	14543.54	elongation factor 1 alpha [Alpheus cylindricus]
gi|13446742|gb|AAK26507.1|	14441.48	elongation factor 1 alpha [Alpheus saxidomus]
gi|13446746|gb|AAK26509.1|	14599.56	elongation factor 1 alpha [Alpheus lottini]
gi|13446748|gb|AAK26510.1|	13867.28	elongation factor 1 alpha [Alpheus chacei]
gi|13446750|gb|AAK26511.1|	14565.58	elongation factor 1 alpha [Alpheus hebes]
gi|13386688|gb|AAK21644.1|	14581.61	elongation factor-1 alpha [Alpheus rostratus]
gi|13386642|gb|AAK21621.1|	14525.59	elongation factor-1 alpha [Alpheus cylindricus]
gi|13386674|gb|AAK21637.1|	14515.57	elongation factor-1 alpha [Alpheus normanni A]
gi|13386646|gb|AAK21623.1|	14571.59	elongation factor-1 alpha [Alpheus estuarensis]
gi|13386622|gb|AAK21611.1|	14571.59	elongation factor-1 alpha [Alpheus bouvieri]
gi|13386660|gb|AAK21630.1|	14581.61	elongation factor-1 alpha [Alpheus hebes]
gi|13386710|gb|AAK21655.1|	14567.6	elongation factor-1 alpha [Alpheus websteri]
gi|13386712|gb|AAK21656.1|	14541.58	elongation factor-1 alpha [Alpheopsis trigonus]
gi|13386640|gb|AAK21620.1|	14511.57	elongation factor-1 alpha [Alpheus cylindricus]
gi|13386654|gb|AAK21627.1|	14571.59	elongation factor-1 alpha [Alpheus floridanus B]
gi|13386662|gb|AAK21631.1|	14557.58	elongation factor-1 alpha [Alpheus latus]
gi|11118907|gb|AAG30437.1|	37474.32	elongation factor-1 alpha [Diasemopsis dubia]
gi|11118909|gb|AAG30438.1|	37488.34	elongation factor-1 alpha [Diasemopsis silvatica]
gi|11118949|gb|AAG30458.1|	37516.37	elongation factor-1 alpha [Diasemopsis aethiopica]

gi|11118913|gb|AAG30440.1|	37473.37	elongation factor-1 alpha [Diasemopsis obstans]
gi|11118915|gb|AAG30441.1|	37436.28	elongation factor-1 alpha [Diasemopsis fasciata]
gi|11118917|gb|AAG30442.1|	36441.83	elongation factor-1 alpha [Diasemopsis signata]
gi|11118919|gb|AAG30443.1|	37456.27	elongation factor-1 alpha [Diasemopsis sp. M]
gi|11118921|gb|AAG30444.1|	37437.3	elongation factor-1 alpha [Diasemopsis munroi]
gi|11118927|gb|AAG30447.1|	37517.37	elongation factor-1 alpha [Diasemopsis hirsuta]
gi|11118925|gb|AAG30446.1|	37486.36	elongation factor-1 alpha [Trichodiopsis minuta]
gi|11118929|gb|AAG30448.1|	37444.38	elongation factor-1 alpha [Diasemopsis sp. W]
gi|11118931|gb|AAG30449.1|	37479.34	elongation factor-1 alpha [Sphyracephala munroi]
gi|11118973|gb|AAG30470.1|	37524.41	elongation factor-1 alpha [Cyrtodiopsis quinqueguttata]
gi|11118935|gb|AAG30451.1|	37165.97	elongation factor-1 alpha [Eurydiopsis argentifera]
gi|11118937|gb|AAG30452.1|	37291.22	elongation factor-1 alpha [Sphyracephala brevicornis]
gi|11118943|gb|AAG30455.1|	36406.86	elongation factor-1 alpha [Teleopsis quadriguttata]
gi|11118945|gb|AAG30456.1|	37510.39	elongation factor-1 alpha [Teleopsis rubicunda]
gi|11118947|gb|AAG30457.1|	37527.39	elongation factor-1 alpha [Sphyracephala bipunctipennis]
gi|11118951|gb|AAG30459.1|	37547.38	elongation factor-1 alpha [Sphyracephala beccarii]
gi|11118953|gb|AAG30460.1|	37487.36	elongation factor-1 alpha [Diasemopsis conjuncta]
gi|11118955|gb|AAG30461.1|	36619.91	elongation factor-1 alpha [Diasemopsis nebulosa]
gi|11118957|gb|AAG30462.1|	37474.36	elongation factor-1 alpha [Diasemopsis elongata]
gi|11118959|gb|AAG30463.1|	37420.28	elongation factor-1 alpha [Diasemopsis longipedunculata]
gi|11118967|gb|AAG30467.1|	37508.41	elongation factor-1 alpha [Diopsis longicornis]
gi|11118963|gb|AAG30465.1|	37508.41	elongation factor-1 alpha [Diopsis fumipennis]
gi|11118965|gb|AAG30466.1|	37538.42	elongation factor-1 alpha [Diopsis gnu]
gi|11118969|gb|AAG30468.1|	37472.35	elongation factor-1 alpha [Cyrtodiopsis currani]
gi|11118975|gb|AAG30471.1|	37539.44	elongation factor-1 alpha [Cyrtodiopsis whitei]
gi|14537556|gb|AAK66621.1|	39461.41	elongation factor-1 alpha [Lasioglossum punctatum]
gi|5739264|gb|AAD50389.1|	35915.58	elongation factor-1 alpha [Pherocera niger]
gi|5739265|gb|AAD50390.1|	35945.59	elongation factor-1 alpha [Stenogephrya sp.]
gi|5739266|gb|AAD50391.1|	35917.63	elongation factor-1 alpha [Ataenogera abdominalis]
gi|5739267|gb|AAD50392.1|	35890.62	elongation factor-1 alpha [Phycus niger]
gi|5739268|gb|AAD50393.1|	35916.64	elongation factor-1 alpha [Efflatouniella aegyptiaca]
gi|5739271|gb|AAD50396.1|	35959.61	elongation factor-1 alpha [Ruppellia basalis]
gi|5739272|gb|AAD50397.1|	35931.58	elongation factor-1 alpha [Neotabuda sp.]
gi|20335343|gb|AAM19287.1|	33860.44	elongation factor-1 alpha [Clinocera sp. NCSU-95051149]
gi|20335367|gb|AAM19299.1|	33568.15	elongation factor-1 alpha [Elmohardyia atlantica]
gi|55580853|emb|CAE53258.1|	37474.42	elongation factor 1-alpha [Polietina nigra]
gi|55580855|emb|CAE53259.1|	37564.5	elongation factor 1-alpha [Hydrotaea sp. Schuehli 10.xi.00]

gi|55580857|emb|CAE53260.1|	37611.47	elongation factor 1-alpha [Stomoxys calcitrans]
gi|55580861|emb|CAE53262.1|	23703.24	elongation factor 1-alpha [Biopyrellia bipuncta]
gi|55580865|emb|CAE53264.1|	37599.43	elongation factor 1-alpha [Morellia ochricornis]
gi|14531007|gb|AAK63115.1|	32528.9	elongation factor 1 alpha [Liriomyza huidobrensis]
gi|14530977|gb|AAK63100.1|	32528.9	elongation factor 1 alpha [Liriomyza bryoniae]
gi|4586210|emb|CAB40964.1|	40902.14	elongation factor 1 alpha [Lysiphlebus fabarum]
gi|7688237|emb|CAB89813.1|	35614.41	putative elongation factor 1-alpha [Leptoplana tremellaris]
gi|31295658|gb|AAP46308.1|	25352.1	elongation factor 1-alpha [Coelopa ursina]
gi|31295662|gb|AAP46310.1|	25366.12	elongation factor 1-alpha [Coelopa pilipes]
gi|31295664|gb|AAP46311.1|	25351.12	elongation factor 1-alpha [Coelopa vanduzeei]
gi|31295666|gb|AAP46312.1|	25352.1	elongation factor 1-alpha [Chaetocoelopa sydneyensis]
gi|31295670|gb|AAP46314.1|	25408.16	elongation factor 1-alpha [Gluma musgravei]
gi|31295674|gb|AAP46316.1|	25392.13	elongation factor 1-alpha [Gluma nitida]
gi|31295678|gb|AAP46318.1|	25366.12	elongation factor 1-alpha [Dasycoelopa australis]
gi|31295680|gb|AAP46319.1|	25141.02	elongation factor 1-alpha [Fucellia maritima]
gi|11526930|gb|AAG36834.1|	41448.45	elongation factor-1alpha [Glomeris marginata]
gi|11526934|gb|AAG36836.1|	41229.41	elongation factor-1alpha [Hiltonius sp. 'Hil']
gi|11526940|gb|AAG36839.1|	41171.36	elongation factor-1alpha [Nemasoma varicorne]
gi|11526958|gb|AAG36848.1|	41233.36	elongation factor-1alpha [Orthocricus sp. 'Spi1']
gi|11526962|gb|AAG36850.1|	41475.4	elongation factor-1alpha [Striaria columbiana]
gi|34596988|gb|AAQ77069.1|	41412.32	elongation factor 1 alpha [Ballophilus australiae]
gi|34596994|gb|AAQ77072.1|	41511.48	elongation factor 1 alpha [Glomeridesmus trinidadensis]
gi|34596998|gb|AAQ77074.1|	41508.4	elongation factor 1 alpha [Phryssonotus sp. 'jump']
gi|34597010|gb|AAQ77080.1|	41352.38	elongation factor 1 alpha [Siphonocybe sp. 'Siph']
gi|21105559|gb|AAM34703.1|	32175.88	elongation factor 1-alpha [Xyleborus justus]
gi|19422978|gb|AAL88308.1|	17363.01	elongation factor 1-alpha [Habronattus sp. NMEX]
gi|19880461|gb|AAM00345.1|	32477.95	elongation factor 1 alpha [Semotainia sp. JOS-2001]
gi|35395825|gb|AAQ84566.1|	18029.31	elongation factor 1 alpha [Amycus sp. MCH-2003]
gi|35395829|gb|AAQ84568.1|	18304.42	elongation factor 1 alpha [Telamonia masinloc]
gi|35395831|gb|AAQ84569.1|	17838.21	elongation factor 1 alpha [Chalcotropis luceroi]
gi|35395833|gb|AAQ84570.1|	18349.39	elongation factor 1 alpha [Eris militaris]
gi|35395835|gb|AAQ84571.1|	17380.02	elongation factor 1 alpha [Maevia intermedia]
gi|35395837|gb|AAQ84572.1|	18286.39	elongation factor 1 alpha [Marpissa pikei]
gi|35395839|gb|AAQ84573.1|	17494.05	elongation factor 1 alpha [Phanias sp. MCH-2003]
gi|35395841|gb|AAQ84574.1|	18177.31	elongation factor 1 alpha [Psecas aff. viridipurpureus MCH-2003]
gi|35395843|gb|AAQ84575.1|	18335.37	elongation factor 1 alpha [Terralonus mylothrus]
gi|35395845|gb|AAQ84576.1|	18375.46	elongation factor 1 alpha [Frigga crocuta]
gi|35395847|gb|AAQ84577.1|	17536.12	elongation factor 1 alpha [Orthrus bicolor]
gi|35395849|gb|AAQ84578.1|	18319.38	elongation factor 1 alpha [Salticidae sp. MCH-2003]

gi|37910491|gb|AAO72095.1|	40152.77	elongation factor-1 alpha [Andrena sp. Ansp643]
gi|6856299|gb|AAF29852.1|	34012.45	elongation factor-1 alpha [Alchisme sp. NYSM 96-09-16-68]
gi|41058513|gb|AAR99236.1|	32036.43	elongation factor-1 alpha [Camponotus sansabeanus]
gi|41058515|gb|AAR99237.1|	35279.39	elongation factor-1 alpha [Camponotus vafer]
gi|45385819|gb|AAR99238.2|	35271.83	elongation factor-1 alpha [Camponotus laevigatus]
gi|41058519|gb|AAR99239.1|	34746.26	elongation factor-1 alpha [Camponotus sayi]
gi|41058521|gb|AAR99240.1|	35500.99	elongation factor-1 alpha [Camponotus festinatus]
gi|41058523|gb|AAR99241.1|	35194.23	elongation factor-1 alpha [Camponotus ocreatus]
gi|41058525|gb|AAR99242.1|	35125.52	elongation factor-1 alpha [Camponotus schaefferi]
gi|41058527|gb|AAR99243.1|	33952.88	elongation factor-1 alpha [Camponotus vicinus]
gi|41058529|gb|AAR99244.1|	35391.06	elongation factor-1 alpha [Camponotus ulcerosus]
gi|41058531|gb|AAR99245.1|	33803.27	elongation factor-1 alpha [Camponotus pennsylvanicus]
gi|41058533|gb|AAR99246.1|	34125.42	elongation factor-1 alpha [Camponotus chromaiodes]
gi|41058535|gb|AAR99247.1|	35262.62	elongation factor-1 alpha [Camponotus castaneus]
gi|41058537|gb|AAR99248.1|	35405.6	elongation factor-1 alpha [Camponotus noveboracensis]
gi|41058539|gb|AAR99249.1|	37317.32	elongation factor-1 alpha [Camponotus americanus]
gi|41058541|gb|AAR99250.1|	35164.9	elongation factor-1 alpha [Camponotus nearcticus]
gi|41058543|gb|AAR99251.1|	34248.56	elongation factor-1 alpha [Camponotus floridanus]
gi|37048729|gb|AAQ88222.1|	41335.28	elongation factor-1 alpha [Eurypauropus spinosus]
gi|37048747|gb|AAQ88231.1|	41609.5	elongation factor-1 alpha [Nicoletia meinerti]
gi|37048755|gb|AAQ88235.1|	41227.31	elongation factor-1 alpha [Rhinotus purpureus]
gi|37048761|gb|AAQ88238.1|	41160.38	elongation factor-1 alpha [Trachyiulus nordquisti]
gi|4530087|gb|AAD21844.1|	41656.44	elongation factor 1-alpha [Ctenolepisma lineata]
gi|17530205|gb|AAL40750.1|	39688.55	elongation factor-1 alpha [Lasioglossum villosulum]
gi|17530197|gb|AAL40746.1|	39688.55	elongation factor-1 alpha [Lasioglossum interruptum]
gi|17530199|gb|AAL40747.1|	39642.56	elongation factor-1 alpha [Lasioglossum inconditum]
gi|17530207|gb|AAL40751.1|	41116.39	elongation factor-1 alpha [Agapostemon leunculus]
gi|17530209|gb|AAL40752.1|	41150.35	elongation factor-1 alpha [Lasioglossum lithuscum]
gi|17530213|gb|AAL40754.1|	41145.37	elongation factor-1 alpha [Chaetalictus sp. BND-2001]
gi|17530215|gb|AAL40755.1|	41114.41	elongation factor-1 alpha [Caenohalictus sp. BND-1]
gi|17530217|gb|AAL40756.1|	41084.4	elongation factor-1 alpha [Caenohalictus sp. BND-2]
gi|17530219|gb|AAL40757.1|	41132.35	elongation factor-1 alpha [Caenohalictus sp. BND-3]
gi|17530235|gb|AAL40765.1|	41138.32	elongation factor-1 alpha [Lasioglossum calceatum]
gi|17530227|gb|AAL40761.1|	41132.39	elongation factor-1 alpha [Dinagapostemon sp. BND-2]
gi|17530239|gb|AAL40767.1|	41145.37	elongation factor-1 alpha [Habralictus sp. BND-2001]

gi|17530241|gb|AAL40768.1|	41108.27	elongation factor-1 alpha [Lasioglossum lustrans]
gi|17530243|gb|AAL40769.1|	41166.35	elongation factor-1 alpha [Lasioglossum punctatum]
gi|17530245|gb|AAL40770.1|	41154.31	elongation factor-1 alpha [Lasioglossum athabascense]
gi|17530247|gb|AAL40771.1|	41136.34	elongation factor-1 alpha [Lasioglossum scitulum]
gi|17530251|gb|AAL40773.1|	41134.36	elongation factor-1 alpha [Lomatalictus sp. BND-2001]
gi|17530271|gb|AAL40783.1|	41188.4	elongation factor-1 alpha [Pseudagapostemon pissisi]
gi|17530275|gb|AAL40785.1|	41164.36	elongation factor-1 alpha [Rhinetula denticrus]
gi|17530277|gb|AAL40786.1|	41215.42	elongation factor-1 alpha [Ruizantheda mutabilis]
gi|17530279|gb|AAL40787.1|	41160.36	elongation factor-1 alpha [Ruizantheda proxima]
gi|17530283|gb|AAL40789.1|	41167.31	elongation factor-1 alpha [Sphecodes persimilis]
gi|49243046|gb|AAT58067.1|	34195.4	elongation factor 1 alpha [Prodinychus sp. AL7170]
gi|39986087|gb|AAR36896.1|	28166.62	elongation factor 1 alpha [Cinara villosa]
gi|39986077|gb|AAR36891.1|	25474.26	elongation factor 1 alpha [Cinara pseudotaxifoliae]
gi|39986063|gb|AAR36884.1|	24735.91	elongation factor 1 alpha [Cinara edulis]
gi|39986065|gb|AAR36885.1|	27840.49	elongation factor 1 alpha [Cinara cf. hirsuta/kuchea CF-2003]
gi|39986071|gb|AAR36888.1|	27414.21	elongation factor 1 alpha [Cinara aff. apini INHS 16456-16457]
gi|39986081|gb|AAR36893.1|	26277.64	elongation factor 1 alpha [Cinara strobi]
gi|39986075|gb|AAR36890.1|	25289.14	elongation factor 1 alpha [Cinara ponderosae]
gi|39986079|gb|AAR36892.1|	25543.32	elongation factor 1 alpha [Cinara schwarzii]
gi|39986083|gb|AAR36894.1|	28450.78	elongation factor 1 alpha [Cinara terminalis]
gi|39986089|gb|AAR36897.1|	27527.29	elongation factor 1 alpha [Cinara wahtolca]

654. Group probability: 0.9773. Peptides of the group

RVIITQPGLPR	65.74	55.3696	1248.767	1249.243	2	2	distinct	1	0.9773

The equivalent proteins include

gi|71003077|ref|XP_756219.1|	51127.58	hypothetical protein UM00072.1 [Ustilago maydis 521]

655. Group probability: 0.9772. Peptides of the group

GFGHLCVAVDDIHK	64.33	54.5537	1566.761	1566.898	1	2	distinct	0	0.9772

The equivalent proteins include

gi|71024491|ref|XP_762475.1|	304764.29	hypothetical protein UM06328.1 [Ustilago maydis 521]

656. Group probability: 0.9769. Peptides of the group

TVLAPHIGPLAQK	64.76	55.4401	1343.792	1344.423	1	2	distinct	0	0.9769

The equivalent proteins include

gi|71017789|ref|XP_759125.1|	40107.93	hypothetical protein UM02978.1 [Ustilago maydis 521]

657. Group probability: 0.9769. Peptides of the group

LAQDASFYDQIKPLSESELAQR	62.79	52.4912	2508.25	2509.457	1	3	distinct	0	0.9769

The equivalent proteins include

gi|71020183|ref|XP_760322.1|	117941.33	hypothetical protein UM04175.1 [Ustilago maydis 521]

658. Group probability: 0.9768. Peptides of the group

NAEAVPLDQALPILFSSLPLQK	60.48	52.8384	2363.31	2364.473	1	2	distinct	0	0.9768

The equivalent proteins include

gi|71020941|ref|XP_760701.1|	11418.89	hypothetical protein UM04554.1 [Ustilago maydis 521]

659. Group probability: 0.9767. Peptides of the group

YIELPAGLKPAGTPGSELLAYER	59.95	52.607	2444.295	2445.313	1	2	distinct	0	0.9767

The equivalent proteins include

gi|71010163|ref|XP_758355.1|	77971.3	hypothetical protein UM02208.1 [Ustilago maydis 521]

660. Group probability: 0.9765. Peptides of the group

FAHEVNYYVTTGEYAPGNDMGVSAFK	60.79	51.6953	2866.291	2866.942	1	3	distinct	0	0.9765

The equivalent proteins include

gi|71024507|ref|XP_762483.1|	41116.59	hypothetical protein UM06336.1 [Ustilago maydis 521]

661. Group probability: 0.9763. Peptides of the group

FIVSAADVIHDFAVPSLGIK	116.6	53.401	2098.146	2098.943	6	2	distinct	0	0.9763

The equivalent proteins include

gi|11466063|ref|NP_038222.1|	28133.46	cytochrome c oxidase subunit 2 [Pichia canadensis]

662. Group probability: 0.9762. Peptides of the group

IDLDKIESMQDEMEDLIEAANEVQETLGR	59.21	50.6489	3333.559	3334.96	2	3	distinct	1	0.9762

The equivalent proteins include

gi|71022399|ref|XP_761429.1|	24933.22	hypothetical protein UM05282.1 [Ustilago maydis 521]

663. Group probability: 0.9762. Peptides of the group

HKGVMVGMGQK (0000010000000)	70.83	55.6094	1170.6	1170.959	31	+1,+2	shared(8)	1	0.9992
KEYDESGPSIVHR	51.92	54.8172	1515.732	1516.145	1	2	shared(3)	1	0.8424
SYELPDGKVITIGNER	64.43	54.1766	1789.921	1790.679	1	2	shared(14)	1	0.9686
YPIEHGIVTNWDDMEK	86.65	53.8856	1945.888	1946.228	3	+2,+3	shared(6)	0	0.9985
VAPEEHPVLLTEAPINPK	88.95	53.6979	1953.057	1953.863	9	2	shared(9)	0	0.9916
TTGIVIDSGDGVTHTVPIYEGYALPHAIMR (00000000000000000000000000000100)	42.36	51.0553	3198.602	3198.047	1	3	shared(2)	0	0.5153

The equivalent proteins include

gi|90185696|emb|CAJ85786.1|	42019.89	actin [Haliotis tuberculata]
gi|14575743|gb|AAK68712.1|	42184.92	actin [Biomphalaria pfeifferi]
gi|14575745|gb|AAK68713.1|	42189.94	actin [Biomphalaria obstructa]
gi|14575747|gb|AAK68714.1|	42207.89	actin [Biomphalaria tenagophila]
gi|14575749|gb|AAK68715.1|	42239.88	actin [Helisoma trivolvis]
gi|483321|gb|AAA20641.1|	42163.83	actin
gi|60391980|gb|AAX19286.1|	42027.79	actin A1 [Haliotis iris]
gi|37528876|gb|AAQ92368.1|	42070.87	actin [Haliotis discus hannai]

664. Group probability: 0.9760. Peptides of the group

HKGVMVGMGQK (0000010000000)	70.83	55.6094	1170.6	1170.959	31	+1,+2	shared(8)	1	0.9992
SYELPDGKVITIGNER	64.43	54.1766	1789.921	1790.679	1	2	shared(14)	1	0.9686
YPIEHGIVTNWDDMEK	86.65	53.8856	1945.888	1946.228	3	+2,+3	shared(6)	0	0.9985
MDGEDVAALVIDNGSGMCK	60.16	53.7979	1980.859	1979.89	1	2	distinct	0	0.7769

The equivalent proteins include

gi|6746569|gb|AAF27627.1|	41892.89	actin [Pichia pastoris]

665. Group probability: 0.9759. Peptides of the group

RPDSAQHDFPGAR	64.15	54.8033	1452.686	1453.401	1	2	distinct	0	0.9759

The equivalent proteins include

gi|71022871|ref|XP_761665.1|	61646.96	hypothetical protein UM05518.1 [Ustilago maydis 521]

666. Group probability: 0.9757. Peptides of the group

ELISNSSDALDKVR	63.71	55.1866	1545.8	1545.907	1	2	distinct	1	0.9757

The equivalent proteins include

gi|75756312|gb|ABA27207.1|	81192.05	chaperone HSP90 [Bigelowiella natans]

667. Group probability: 0.9755. Peptides of the group

GGFSYFGSNLGSPEGYVIHR	60.74	53.1924	2143.012	2143.317	1	2	distinct	0	0.9755

The equivalent proteins include

gi|71021419|ref|XP_760940.1|	48195.79	hypothetical protein UM04793.1 [Ustilago maydis 521]

668. Group probability: 0.9755. Peptides of the group

RMSHDAVQEAPR	64.37	54.9398	1395.668	1396.59	1	2	distinct	1	0.9755

The equivalent proteins include

gi|71005884|ref|XP_757608.1|	98433.74	hypothetical protein UM01461.1 [Ustilago maydis 521]

669. Group probability: 0.9754. Peptides of the group

QTAHAPSVQGHVEPR	63.03	54.5246	1612.807	1613.441	1	2	distinct	0	0.9754

The equivalent proteins include

gi|71008408|ref|XP_758212.1|	63887.81	hypothetical protein UM02065.1 [Ustilago maydis 521]
gi|20257590|gb|AAM15960.1|	63859.81	histone deacetylase Hda1 [Ustilago maydis]

670. Group probability: 0.9753. Peptides of the group

IYHPNINSNGSICLDILR	61.49	53.414	2098.063	2098.523	1	2	distinct	0	0.9753

The equivalent proteins include

gi|54637955|gb|EAL27357.1|	48666.21	GA20418-PA [Drosophila pseudoobscura]
gi|56966680|pdb|1W4U|A	16932.47	Chain A, Nmr Solution Structure Of The Ubiquitin Conjugating Enzyme Ubch5b
gi|66360408|pdb|1X23|D	17688.84	Chain D, Crystal Structure Of Ubch5c

gi|62738886|pdb|1Z2U|A	17203.65	Chain A, The 1.1a Crystallographic Structure Of Ubiquitin- Conjugating Enzyme (Ubc-2) From Caenorha
gi|83754945|pdb|2ESK|A	17080.57	Chain A, Human Ubiquitin-Conjugating Enzyme (E2) Ubch5b, Wild-Type
gi|83754948|pdb|2ESO|A	17038.52	Chain A, Human Ubiquitin-Conjugating Enzyme (E2) Ubch5b Mutant Ile37ala
gi|83754950|pdb|2ESQ|A	17050.56	Chain A, Human Ubiquitin-Conjugating Enzyme (E2) Ubch5b Mutant Ser94gly
gi|93279754|pdb|2FUH|A	16773.42	Chain A, Solution Structure Of The Ubch5cUB NON-Covalent Complex
gi|90305516|gb|EAS35147.1|	16638.34	ubiquitin-conjugating enzyme E2 [Coccidioides immitis RS]
gi|3323498|gb|AAC39499.1|	16688.35	ubiquitin conjugating enzyme UBC1 [Glomerella cingulata]
gi|37915386|gb|AAP46141.1|	10874.33	UbcH5B [Ovis aries]
gi|5917672|gb|AAD55983.1|	16551.29	ubiquitin-conjugating protein [Magnaporthe grisea]
gi|87239722|emb|CAJ57640.1|	17007.6	putative ubiquitin conjugating enzyme 2 [Oesophagostomum dentatum]
gi|87239726|emb|CAJ57642.1|	16908.52	putative ubiquitin conjugating enzyme 2 [Oesophagostomum dentatum]
gi|87239724|emb|CAJ57641.1|	16896.49	putative ubiquitin conjugating enzyme 2 [Oesophagostomum dentatum]
gi|66507080|ref|XP_392336.2|	54627.48	PREDICTED: similar to GA20418-PA [Apis mellifera]
gi|68367240|ref|XP_709141.1|	15041.58	PREDICTED: similar to ubiquitin-conjugating enzyme E2D 4 (putative) isoform 2 [Danio rerio]
gi|74142433|dbj|BAE31970.1|	16903.51	unnamed protein product [Mus musculus]
gi|83773189|dbj|BAE63316.1|	16612.32	unnamed protein product [Aspergillus oryzae]
gi|84570589|dbj|BAE72681.1|	16652.35	hypothetical protein [Epichloe festucae]
gi|33621257|gb|AAQ23193.1|	10023.92	E2 ubiquitin conjugating enzyme UbcH5B [Bos taurus]
gi|48145949|emb|CAG33197.1|	16872.49	UBE2D3 [Homo sapiens]
gi|30584383|gb|AAP36440.1|	16932.51	Homo sapiens ubiquitin-conjugating enzyme E2D 1 (UBC4/5 homolog, yeast) [synthetic construct]
gi|44890748|gb|AAH66917.1|	16904.46	Ubiquitin-conjugating enzyme E2D 3, isoform 1 [Homo sapiens]
gi|72009072|ref|XP_782222.1|	36240.5	PREDICTED: similar to ubiquitin-conjugating enzyme E2D 3 isoform 2 [Strongylocentrotus purpuratus]
gi|72015542|ref|XP_781361.1|	17129.55	PREDICTED: similar to Ubiquitin-conjugating enzyme E2-17 kDa (Ubiquitin-protein ligase) (Ubiquitin
gi|72023587|ref|XP_791462.1|	16923.52	PREDICTED: similar to Ubiquitin-conjugating enzyme E2-17 kDa (Ubiquitin-protein ligase) (Ubiquitin
gi|72076311|ref|XP_795683.1|	15193.53	PREDICTED: similar to Ubiquitin-conjugating enzyme E2 D2 (Ubiquitin-protein ligase D2) (Ubiquitin c
gi|73949236|ref|XP_856020.1|	12782.47	PREDICTED: similar to Ubiquitin-conjugating enzyme E2 D2 (Ubiquitin-protein ligase D2) (Ubiquitin c
gi|46138581|ref|XP_390981.1|	15855.88	UBC1_COLGL Ubiquitin-conjugating enzyme E2-16 kDa (Ubiquitin-protein ligase) (Ubiquitin carrier pro
gi|51472295|gb|AAU04541.1|	16877.28	ubiquitin-conjugating enzyme E2D 2 isoform 1 [Oncorhynchus mykiss]
gi|33149324|ref|NP_871622.1|	17167.52	ubiquitin-conjugating enzyme E2D 3 isoform 3 [Homo sapiens]
gi|76622926|ref|XP_883226.1|	19730.05	PREDICTED: similar to Ubiquitin-conjugating enzyme E2 D2 (Ubiquitin-protein ligase D2) (Ubiquitin c
gi|76684482|ref|XP_589208.2|	17361.63	PREDICTED: similar to ubiquitin-conjugating enzyme E2D 4 (putative) [Bos taurus]
gi|81674232|gb|AAI09526.1|	17012.44	LOC511801 protein [Bos taurus]

gi|55624508|ref|XP_517826.1|	14925.51	PREDICTED: hypothetical protein XP_517826 [Pan troglodytes]
gi|55628490|ref|XP_519070.1|	13864.78	PREDICTED: similar to ubiquitin-conjugating enzyme HBUCE1 [Pan troglodytes]
gi|109509992|ref|XP_001080152.1|	43613.02	PREDICTED: similar to ubiquitin-conjugating enzyme E2D 1, UBC4/5 homolog [Rattus norvegicus]
gi|7327273|gb|AAB25489.2|	16922.54	ubiquitin-conjugating enzyme [Caenorhabditis elegans]
gi|47209518|emb|CAF93832.1|	11032.33	unnamed protein product [Tetraodon nigroviridis]
gi|47209021|emb|CAF89770.1|	18536.29	unnamed protein product [Tetraodon nigroviridis]
gi|47213200|emb|CAF95316.1|	13650.85	unnamed protein product [Tetraodon nigroviridis]
gi|47216207|emb|CAG01241.1|	16830.52	unnamed protein product [Tetraodon nigroviridis]
gi|765056|gb|AAC41750.1|	16952.47	ubiquitin conjugating enzyme
gi|71896625|ref|NP_001026324.1|	16904.46	ubiquitin-conjugating enzyme E2D 3 [Gallus gallus]
gi|85094665|ref|XP_959933.1|	16667.56	hypothetical protein ((XM_016084) hypothetical protein XP_016084 [Homo sapiens]) [Neurospora cras
gi|71000643|ref|XP_755003.1|	16682.36	ubiquitin conjugating enzyme UbcD [Aspergillus fumigatus Af293]
gi|37589809|gb|AAH59548.1|	16865.48	Hypothetical protein LOC335444 [Danio rerio]
gi|54637956|gb|EAL27358.1|	15940.95	GA20341-PA [Drosophila pseudoobscura]
gi|46561756|gb|AAT01083.1|	16895.53	putative ubiquitin-conjugating enzyme [Homalodisca coagulata]
gi|4507775|ref|NP_003330.1|	16952.51	ubiquitin-conjugating enzyme E2D 2 isoform 1 [Homo sapiens]
gi|477134|pir||A48145	16936.56	ubiquitin-conjugating enzyme ubc-2 - Caenorhabditis elegans
gi|37590333|gb|AAH59465.1|	16852.48	Hypothetical protein LOC324015 [Danio rerio]
gi|13812084|ref|NP_113222.1|	16670.53	ubiquitin conjugating enzyme [Guillardia theta]
gi|4507773|ref|NP_003329.1|	16819.43	ubiquitin-conjugating enzyme E2D 1 [Homo sapiens]
gi|49899030|gb|AAH76728.1|	16843.48	Ube2d2-prov protein [Xenopus laevis]
gi|2959363|emb|CAA17917.1|	16636.41	ubc4 [Schizosaccharomyces pombe]
gi|109066782|ref|XP_001096263.1|	16866.47	PREDICTED: similar to ubiquitin-conjugating enzyme E2D 4 (putative) [Macaca mulatta]
gi|4868141|gb|AAD31181.1|	12626.34	ubiquitin-conjugating enzyme 1 isoform [Homo sapiens]
gi|28189903|dbj|BAC56566.1|	14038.07	similar to phosphoarginine phosphatase [Bos taurus]
gi|71004926|ref|XP_757129.1|	16599.2	ubiquitin-conjugating enzyme E2-16 kDa [Ustilago maydis 521]
gi|6651017|gb|AAF22130.1|	10937.59	ubiquitin conjugating enzyme [Strongyloides stercoralis]
gi|67524607|ref|XP_660365.1|	16681.34	ubiquitin-conjugating enzyme E2-16 kDa [Aspergillus nidulans FGSC A4]
gi|34391575|gb|AAN46746.1|	11668.72	E2 ubiquitin-conjugating enzyme UbcH5B [Sus scrofa]
gi|41054778|ref|NP_957404.1|	16852.48	hypothetical protein LOC394085 [Danio rerio]
gi|33188456|ref|NP_862821.1|	13796.95	ubiquitin-conjugating enzyme E2D 2 isoform 2 [Homo sapiens]
gi|12843975|dbj|BAB26188.1|	16836.37	unnamed protein product [Mus musculus]
gi|12833659|dbj|BAB22614.1|	16846.46	unnamed protein product [Mus musculus]
gi|76619472|ref|XP_870557.1|	17002.53	PREDICTED: similar to ubiquitin-conjugating enzyme E2D 3 isoform 2 isoform 3 [Bos taurus]
gi|12311787|emb|CAC24487.1|	10952.44	putative ubiquitin-conjugating enzyme [Platichthys flesus]
gi|41055694|ref|NP_957253.1|	16961.51	ubiquitin-conjugating enzyme E2D 3 [Danio rerio]

gi|32400971|gb|AAP80691.1|	16760.38	ubiquitin-conjugating enzyme [Griffithsia japonica]
gi|38048037|gb|AAR09921.1|	12733.42	similar to Drosophila melanogaster eff [Drosophila yakuba]
gi|94391344|ref|XP_001003819.1|	9596.19	PREDICTED: similar to ubiquitin-conjugating enzyme E2D 4 (putative) isoform 1 [Mus musculus]
gi|94391346|ref|XP_001003835.1|	8130.26	PREDICTED: similar to ubiquitin-conjugating enzyme E2D 4 (putative) isoform 3 [Mus musculus]
gi|94408919|ref|XP_979481.1|	16953.54	PREDICTED: similar to ubiquitin-conjugating enzyme E2D 3 (UBC4/5 homolog, yeast) [Mus musculus]
gi|39977319|ref|XP_370047.1|	17618.1	hypothetical protein MG06562.4 [Magnaporthe grisea 70-15]
gi|41054637|ref|NP_955865.1|	16857.5	ubiquitin-conjugating enzyme E2D 2 [Danio rerio]
gi|56753179|gb|AAW24799.1|	16677.51	SJCHGC00720 protein [Schistosoma japonicum]

671. Group probability: 0.9749. Peptides of the group

VISWYDNEWGYSNR	96.97	54.223	1787.79	1788.634	13	2	distinct	0	0.9749

The equivalent proteins include

gi|6979054|gb|AAF34327.1|	36332.06	glyceraldehyde-3-phosphate dehydrogenase [Odontella sinensis]
gi|77918935|ref|YP_356750.1|	36062.57	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) [Pelobacter carbinolicus DSM 2380]
gi|76556199|emb|CAD48589.1|	35532.49	putative glyceraldehyde-3-phosphate dehydrogenase [Propionibacterium freudenreichii subsp. shermani
gi|50839905|gb|AAT82572.1|	36069.67	glyceraldehyde 3-phosphate dehydrogenase [Propionibacterium acnes KPA171202]

672. Group probability: 0.9749. Peptides of the group

LVSWYDNEWGYNSR	96.97	54.223	1787.79	1788.634	7	2	distinct	0	0.9749

The equivalent proteins include

gi|21593240|gb|AAM65189.1|	37080.16	glyceraldehyde-3-phosphate dehydrogenase C subunit (GapC) [Arabidopsis thaliana]

673. Group probability: 0.9745. Peptides of the group

SSDYNNSANHQDVAK	62.62	54.5897	1648.708	1649.036	1	2	distinct	0	0.9745

The equivalent proteins include

gi|71024263|ref|XP_762361.1|	12471.03	hypothetical protein UM06214.1 [Ustilago maydis 521]

674. Group probability: 0.9743. Peptides of the group

AQFTNVTSLHPTDPDHTLMLR	62.04	52.7912	2393.18	2393.939	3	3	distinct	0	0.9743

The equivalent proteins include

gi|71022819|ref|XP_761639.1|	135205.99	hypothetical protein UM05492.1 [Ustilago maydis 521]

675. Group probability: 0.9738. Peptides of the group

QLLSSPSTSEPLVAALGGAPIALISHIENDLR	57.08	51.5583	3268.767	3269.816	1	3	distinct	0	0.9738

The equivalent proteins include

gi|71019639|ref|XP_760050.1|	98354.42	hypothetical protein UM03903.1 [Ustilago maydis 521]

676. Group probability: 0.9733. Peptides of the group

VSGLIGHAVSANKK	62.59	54.871	1379.788	1380.27	1	2	distinct	1	0.9733

The equivalent proteins include

gi|71006210|ref|XP_757771.1|	86419.38	hypothetical protein UM01624.1 [Ustilago maydis 521]

677. Group probability: 0.9732. Peptides of the group

GMLTGPVTILLWSFPR (001000000000000000)	90.71	54.301	1786.98	1804.191	6	2	distinct	0	0.9732

The equivalent proteins include

gi|10038722|dbj|BAB12757.1|	88373.48	5-methyltetrahydropteroyltriglutamate-homocysteine S-methyltransferase [Buchnera aphidicola str. A

678. Group probability: 0.9732. Peptides of the group

ESTIEAILLSLR	74.95	55.4401	1343.766	1344.941	1	2	distinct	0	0.9732

The equivalent proteins include

gi|71020971|ref|XP_760716.1|	21895.71	hypothetical protein UM04569.1 [Ustilago maydis 521]

679. Group probability: 0.9728. Peptides of the group

MTGEFIETQCINPSFIVGHPQVMSPLAK	58.19		51.0564	3130.529	3131.766	3	3	distinct	0	0.9728

The equivalent proteins include

gi|71022075|ref|XP_761268.1|	107358.83	hypothetical protein UM05121.1 [Ustilago maydis 521]

680. Group probability: 0.9726. Peptides of the group

RNAPSNPAGAATAGAR	61.46		54.7696	1480.749	1482.163	1	2	distinct	1	0.9726

The equivalent proteins include

gi|71004026|ref|XP_756679.1|	56577.47	hypothetical protein UM00532.1 [Ustilago maydis 521]

681. Group probability: 0.9725. Peptides of the group

SGGGLGGLGGLGGLGGFGGSSHPTADEE DKYVINVK	54.67		50.4732	3358.643	3359.994	2	3	distinct	1	0.9725

The equivalent proteins include

gi|71004206|ref|XP_756769.1|	52470.95	hypothetical protein UM00622.1 [Ustilago maydis 521]

682. Group probability: 0.9715. Peptides of the group

DNPQANEAAMEKAGHDGTWVAHPALVK (000000000001000000000000000)	58.23		51.8362	2872.356	2871.641	3	3	distinct	1	0.9715

The equivalent proteins include

gi|71018373|ref|XP_759417.1|	38219.43	hypothetical protein UM03270.1 [Ustilago maydis 521]

683. Group probability: 0.9715. Peptides of the group

LDVMFNNAGIMHPADDNALNTDEK	59.67		52.8307	2644.19	2645.045	1	3	distinct	0	0.9715

The equivalent proteins include

gi|71023773|ref|XP_762116.1|	34675.09	hypothetical protein UM05969.1 [Ustilago maydis 521]

684. Group probability: 0.9712. Peptides of the group

AYQQHQAIR	63.83		55.6501	1113.568	1113.567	1	2	distinct	0	0.9712

The equivalent proteins include

gi|71021527|ref|XP_760994.1|	31813.6	hypothetical protein UM04847.1 [Ustilago maydis 521]

685. Group probability: 0.9711. Peptides of the group

TVDALGNPIDGK	77.39		55.4031	1198.619	1197.823	1	2	distinct	0	0.9557
EAYPGDVFYIHSR	58.88		54.6289	1552.731	1554.178	3	2	shared(8)	0	0.9619

The equivalent proteins include

gi|3861330|emb|CAA15229.1|	56543.86	ATP SYNTHASE ALPHA CHAIN (atpA) [Rickettsia prowazekii]
gi|2665936|gb|AAB88551.1|	56543.82	putative F1-ATP synthase alpha subunit [Rickettsia prowazekii]
gi|51460283|gb|AAU04246.1|	56552.87	H(+)-transporting two-sector ATPase F(1) alpha subunit; ATP synthase.; Chloroplast ATPase.; F(0)F(1

686. Group probability: 0.9707. Peptides of the group

AIELCHEAVHR	62.84		55.3268	1333.656	1335.133	2	2	distinct	0	0.9707

The equivalent proteins include

gi|71017885|ref|XP_759173.1|	12307.07	hypothetical protein UM03026.1 [Ustilago maydis 521]

687. Group probability: 0.9707. Peptides of the group

KIGRPVPSMDVDSVEAAEQVLK	60.18		52.9081	2367.247	2368.161	2	3	distinct	1	0.9707

The equivalent proteins include

gi|71021021|ref|XP_760741.1|	62308.89	hypothetical protein UM04594.1 [Ustilago maydis 521]

688. Group probability: 0.9706. Peptides of the group

IGGIGTVPVGR	66.14		55.3583	1024.603	1024.899	11	2	shared(36)	0	0.978
FMVTVIDAPGHR (00100000000000)	71.25		55.3019	1357.681	1357.971	17	+2,+3	distinct	0	0.9658

The equivalent proteins include

gi|82792178|gb|ABB90964.1|	40295.91	elongation factor 1-alpha [Phycomyces blakesleeanus]
gi|86451390|gb|ABC96908.1|	26913.27	elongation factor 1 alpha [Lyophyllum decastes]
gi|67005747|gb|AAY62530.1|	41737.8	translation elongation factor 1-alpha [Ganoderma tsugae]
gi|67005749|gb|AAY62531.1|	44414.96	translation elongation factor 1-alpha [Albatrellus higanensis]
gi|58618691|gb|AAW80840.1|	45785.78	translation elongation factor EF1-alpha [Hygrophoropsis aurantiaca]
gi|58618693|gb|AAW80841.1|	46058.88	translation elongation factor EF1-alpha [Strobilomyces floccopus]

gi|58758723|gb|AAW81760.1|	44633.25	translation elongation factor EF1-alpha [Climacodon septentrionalis]
gi|58758727|gb|AAW81762.1|	44499.15	translation elongation factor EF1-alpha [Grifola frondosa]
gi|66775566|gb|AAY56358.1|	44443.15	translation elongation factor 1-alpha [Sparassis crispa]
gi|11078214|gb|AAG29023.1|	46947.36	translation elongation factor 1-alpha [Parasitella parasitica]
gi|11078252|gb|AAG29042.1|	45783.78	translation elongation factor 1-alpha [Spinellus fusiger]

689. Group probability: 0.9695. Peptides of the group

IGGIGTVPVGR	66.14	55.3583	1024.603	1024.899	11	2	shared(36)	0	0.978
KIGGIGTVPVGR	60.21	55.2689	1152.698	1153.188	2	2	distinct	1	0.9644

The equivalent proteins include

gi|55580871|emb|CAE53267.1|	16188.37	elongation factor 1-alpha [Phaonia tuguriorum]
gi|32810515|gb|AAP87407.1|	19366.88	elongation factor 1-alpha [Cortinarius fulvo-ochrascens]

690. Group probability: 0.9690. Peptides of the group

DSSANNTSTTADASVIPAVSVGGGLGAVAGSGSHADR	52.95	50.5959	3355.587	3356.58	1	3	distinct	0	0.969

The equivalent proteins include

gi|71022901|ref|XP_761680.1|	159174.8	hypothetical protein UM05533.1 [Ustilago maydis 521]

691. Group probability: 0.9688. Peptides of the group

IGGIGTVPVGR	66.14	55.3583	1024.603	1024.899	11	2	shared(36)	0	0.978
SVEMHHESLAEGLPGDNVGFNVK (00001000000000000000000)	57.26	52.5558	2481.159	2482.365	1	3	distinct	0	0.9637

The equivalent proteins include

gi|82792146|gb|ABB90948.1|	43393.43	elongation factor 1-alpha [Polychytrium aggregatum]
gi|19386989|gb|AAL87074.1|	43160.05	translation elongation factor 1-alpha [Monoblepharis insignis]

692. Group probability: 0.9687. Peptides of the group

IGGIGTVPVGR	66.14	55.3583	1024.603	1024.899	11	2	shared(36)	0	0.978
NMITGTSQADCAVQIVAAGTGEFEAGISK	54.56	51.5357	2925.385	2926.757	1	3	distinct	0	0.9636

The equivalent proteins include

gi|74483561|gb|ABA10535.1|	45868.84	elongation factor 1 alpha [Napeogenes sylphis]

693. Group probability: 0.9686. Peptides of the group

WFAEEEAPARPEGFLEK	59.27	53.7576	2004.958	2006.073	5	2	distinct	0	0.9686

The equivalent proteins include

gi|71013394|ref|XP_758584.1|	15078.73	hypothetical protein UM02437.1 [Ustilago maydis 521]

694. Group probability: 0.9680. Peptides of the group

YAVVGASKDPSK	61.43	55.349	1220.64	1221.544	1	2	distinct	1	0.968

The equivalent proteins include

gi|71006504|ref|XP_757918.1|	16655.72	hypothetical protein UM01771.1 [Ustilago maydis 521]

695. Group probability: 0.9678. Peptides of the group

LAQMTLHNAAISASLHK	59.09	54.2565	1804.962	1805.473	1	2	distinct	0	0.9678

The equivalent proteins include

gi|71005426|ref|XP_757379.1|	62761.64	hypothetical protein UM01232.1 [Ustilago maydis 521]

696. Group probability: 0.9674. Peptides of the group

VLDSVYEHWWR	61.53	54.8587	1488.715	1488.433	1	2	distinct	0	0.9674

The equivalent proteins include

gi|71021071|ref|XP_760766.1|	65857.77	hypothetical protein UM04619.1 [Ustilago maydis 521]

697. Group probability: 0.9673. Peptides of the group

SKFTITPGSEQIR	47.97	55.0353	1462.778	1463.466	1	2	shared(3)	1	0.9
DGYAQILRDVGGIVLANACGPCIGQWDR	46.86	51.1539	3073.486	3073.109	1	3	distinct	1	0.9265

The equivalent proteins include

gi|74268076|gb|AAI02643.1|	85975.19	Aconitase 2, mitochondrial [Bos taurus]
gi|74211801|dbj|BAE29252.1|	86117.31	unnamed protein product [Mus musculus]
gi|74188189|dbj|BAE25770.1|	86036.2	unnamed protein product [Mus musculus]
gi|90970312|gb|ABE02803.1|	79185.46	mitochondrial aconitase 2 [Bos taurus]
gi|13435538|gb|AAH04645.1|	86151.3	Aco2 protein [Mus musculus]
gi|38541404|gb|AAH61999.1|	86121.25	Aconitase 2, mitochondrial [Rattus norvegicus]

gi|27806769|ref|NP_776402.1|	86045.26	aconitase 2, mitochondrial [Bos taurus]
gi|63101587|gb|AAH94462.1|	86185.28	Aconitase 2, mitochondrial [Mus musculus]
gi|10637996|emb|CAC11018.1|	86162.19	mitochondrial aconitase [Rattus norvegicus]

698. Group probability: 0.9673. Peptides of the group

SRPAVATSPLASPPSPTK	58.5	54.1501	1762.958	1763.973	1	2	distinct	0	0.9673

The equivalent proteins include

gi|71006630|ref|XP_757981.1|	53225.63	hypothetical protein UM01834.1 [Ustilago maydis 521]

699. Group probability: 0.9669. Peptides of the group

VASVQTISGTGANHLGAVFLQR	58.87	53.1426	2225.192	2226.352	1	3	distinct	0	0.9669

The equivalent proteins include

gi|71020957|ref|XP_760709.1|	46852.84	hypothetical protein UM04562.1 [Ustilago maydis 521]

700. Group probability: 0.9663. Peptides of the group

AIASQHAATQASR	60.4	55.1643	1310.669	1311.001	1	2	distinct	0	0.9663

The equivalent proteins include

gi|71018001|ref|XP_759231.1|	63905.91	hypothetical protein UM03084.1 [Ustilago maydis 521]

701. Group probability: 0.9659. Peptides of the group

YDDPAHAQTLAAINSGHAPLDLLNIR	56.63	52.0185	2785.415	2786.212	1	3	distinct	0	0.9659

The equivalent proteins include

gi|71017617|ref|XP_759039.1|	43249.6	hypothetical protein UM02892.1 [Ustilago maydis 521]

702. Group probability: 0.9656. Peptides of the group

KSATLDKPSTELQK	59.68	54.8796	1544.841	1545.059	1	2	distinct	1	0.9656

The equivalent proteins include

gi|71006384|ref|XP_757858.1|	67199.39	hypothetical protein UM01711.1 [Ustilago maydis 521]

703. Group probability: 0.9651. Peptides of the group

HGTTTGISAHDR	60.47	55.4241	1251.596	1252.125	2	2	distinct	0	0.9651

The equivalent proteins include

gi|49239499|emb|CAF25852.1|	41084.02	GTP cyclohydrolase II [Bartonella quintana str. Toulouse]
gi|49238035|emb|CAF27242.1|	41113.16	GTP cyclohydrolase II [Bartonella henselae str. Houston-1]
gi|71024307|ref|XP_762383.1|	26813.41	hypothetical protein UM06236.1 [Ustilago maydis 521]

704. Group probability: 0.9645. Peptides of the group

YNTTTSEDPVIHDISAK	60.25	53.9103	1889.901	1891.079	1	3	distinct	0	0.9645

The equivalent proteins include

gi|71005604|ref|XP_757468.1|	62957.32	hypothetical protein UM01321.1 [Ustilago maydis 521]

705. Group probability: 0.9644. Peptides of the group

IINEPTAAAIAYGIDKK	71.85	54.6758	1786.983	1788.273	1	2	shared(14)	1	0.9837
GVPQIEVTFDIDANGILNVTAADK	68.14	52.6387	2499.286	2499.723	1	2	distinct	0	0.9506

The equivalent proteins include

gi|92355|pir||S08211	69784.71	dnaK-type molecular chaperone hst70 - rat
gi|75775319|gb|AAI05157.1|	69981.85	Unknown (protein for MGC:127701) [Bos taurus]
gi|23271312|gb|AAH36107.1|	70186.95	HSPA2 protein [Homo sapiens]
gi|11177910|ref|NP_068635.1|	69770.7	heat shock protein 2 [Rattus norvegicus]
gi|57090217|ref|XP_537479.1|	70125.89	PREDICTED: similar to heat shock protein 2 isoform 1 [Canis familiaris]
gi|73963237|ref|XP_866274.1|	68295.97	PREDICTED: similar to heat shock protein 2 isoform 2 [Canis familiaris]
gi|41386699|ref|NP_776769.1|	69498.51	heat shock 70 kD protein 3 [Bos taurus]
gi|55640819|ref|XP_510002.1|	70319.99	PREDICTED: similar to heat shock 70kDa protein 2; Heat-shock 70kD protein-2; heat shock 70kD protei
gi|6063529|dbj|BAA85389.1|	70108.96	70 kDa heat shock protein [Capra hircus]
gi|123621|sp|P17156|HSP72_MOUSE	69982.87	Heat shock-related 70 kDa protein 2 (Heat shock protein 70.2)
gi|109946|pir||S10859	69968.86	dnaK-type molecular chaperone HSP70.2 - mouse
gi|4204880|gb|AAD11466.1|	70236.92	heat shock protein [Homo sapiens]
gi|12804655|gb|AAH01752.1|	70262.97	Heat shock 70kDa protein 2 [Homo sapiens]
gi|30481651|gb|AAH52350.1|	69883.79	Heat shock protein 2 [Mus musculus]

gi|49257558|gb|AAH74113.1|	69802.99	MGC81782 protein [Xenopus laevis]

706. Group probability: 0.9637. Peptides of the group

ATAGDTHLGGEDFDNR	68.44	54.7902	1674.723	1675.633	4	2	shared(13)	0	0.9851
ITNEPTAAAIAYGLDKK	73.62	54.2621	1774.946	1773.744	1	2	distinct	1	0.9473

The equivalent proteins include

gi|32394421|gb|AAM81602.1|	70659.95	muscle-specific heat shock protein Hsc70-1 [Cyprinus carpio]
gi|33598988|gb|AAP51387.1|	70887.08	constitutive heat shock protein HSC70-1 [Cyprinus carpio]

707. Group probability: 0.9632. Peptides of the group

KDPPHEDAGIQK	59.83	55.3297	1333.663	1334.643	2	2	distinct	1	0.9632

The equivalent proteins include

gi|71020507|ref|XP_760484.1|	15545.9	hypothetical protein UM04337.1 [Ustilago maydis 521]

708. Group probability: 0.9631. Peptides of the group

FFTMPARPDIDEVNK	58.3	54.1046	1778.866	1779.106	1	2	distinct	0	0.9631

The equivalent proteins include

gi|71003550|ref|XP_756441.1|	64626.96	hypothetical protein UM00294.1 [Ustilago maydis 521]

709. Group probability: 0.9626. Peptides of the group

RPALSSAEGVAATHAAGTR	56.52	54.0418	1821.944	1822.853	1	2	distinct	0	0.9626

The equivalent proteins include

gi|71020741|ref|XP_760601.1|	34938.43	hypothetical protein UM04454.1 [Ustilago maydis 521]

710. Group probability: 0.9623. Peptides of the group

AYAAHGGLTEVR	59.64	55.6195	1243.631	1244.11	1	2	distinct	0	0.9623

The equivalent proteins include

gi|71020425|ref|XP_760443.1|	55871.19	hypothetical protein UM04296.1 [Ustilago maydis 521]

711. Group probability: 0.9622. Peptides of the group

ADVISNASCTTNCLAPLAK	74.08	53.6564	2004.961	2004.921	2	2	distinct	0	0.9622

The equivalent proteins include

gi|77681317|dbj|BAE46581.1|	36249.57	glyceraldehyde 3-phosphate dehydrogenase [Microdochium nivale]
gi|452311|emb|CAA51721.1|	36120.53	glyceraldehyde-3-phosphate dehydrogenase [Claviceps purpurea]
gi|38492178|gb|AAR22391.1|	23096.68	glyceraldehyde-3-phosphate dehydrogenase [Metarhizium anisopliae]

712. Group probability: 0.9622. Peptides of the group

LNLGTWQGITLCEFR	58.08	54.3011	1806.909	1807.523	1	2	distinct	0	0.9622

The equivalent proteins include

gi|71005018|ref|XP_757175.1|	153366.58	hypothetical protein UM01028.1 [Ustilago maydis 521]

713. Group probability: 0.9618. Peptides of the group

IYESGHEVPFYQPLASLELFQR	57.02	52.2359	2622.312	2623.287	1	3	distinct	0	0.9618

The equivalent proteins include

gi|71019727|ref|XP_760094.1|	66236.47	hypothetical protein UM03947.1 [Ustilago maydis 521]

714. Group probability: 0.9617. Peptides of the group

TLELNPDKPVPDSLNLTFHSVDR	56.58	52.3151	2606.334	2606.708	1	3	distinct	0	0.9617

The equivalent proteins include

gi|71005744|ref|XP_757538.1|	40229.71	hypothetical protein UM01391.1 [Ustilago maydis 521]

715. Group probability: 0.9609. Peptides of the group

FAPASHDGQPR	59.53	55.2781	1181.558	1181.927	1	2	distinct	0	0.9609

The equivalent proteins include

gi|71013770|ref|XP_758659.1|	93694.94	hypothetical protein UM02512.1 [Ustilago maydis 521]

716. Group probability: 0.9607. Peptides of the group

SAIKPPPPPAAEQLTSR	56.82	54.2492	1758.963	1759.573	3	2	distinct	0	0.9607

The equivalent proteins include

gi|71006566|ref|XP_757949.1|	44823.07	hypothetical protein UM01802.1 [Ustilago maydis 521]

717. Group probability: 0.9605. Peptides of the group

NFVFLDKPSPSAAPVSFIQASEILDR	54.89	51.7222	2847.481	2848.824	2	3	distinct	0	0.9605

The equivalent proteins include

gi|71004168|ref|XP_756750.1|	57743.57	hypothetical protein UM00603.1 [Ustilago maydis 521]

718. Group probability: 0.9605. Peptides of the group

IAAGVVSPAEVVYTFESIIK	55.34	53.3919	2092.145	2092.311	2	2	distinct	0	0.9605

The equivalent proteins include

gi|71007887|ref|XP_758166.1|	48919.49	hypothetical protein UM02019.1 [Ustilago maydis 521]							
719. Group probability: 0.9600. Peptides of the group									
VALSALTIAEYFR	73.63	54.8052	1452.798	1453.379	9	2	distinct	0	0.9516
IPSAVGYQPTLSTEMGALQER (0000000000000010000000)	43.55	53.0828	2263.115	2264.072	1	2	distinct	0	0.1733
The equivalent proteins include									
gi|587526|emb|CAA54206.1|	51866.8	ATPase beta-subunit [Stigmatella aurantiaca]							
720. Group probability: 0.9597. Peptides of the group									
VALTGLTIAEYFR	96.01	54.8052	1452.798	1453.379	17	2	shared(8)	0	0.9932
LVLEVAQHLGENTVR	84.18	54.5381	1676.921	1677.711	15	+2,+3	shared(6)	0	0.9996
IPSAVGYQPTLATDMGALQER	53.31	53.1474	2217.11	2215.892	2	3	shared(3)	0	0.6752
SLQDIIAILGMDELSEQDKLTVER	74.18	52.0836	2715.4	2716.853	3	2	shared(3)	1	0.92
The equivalent proteins include									
gi|50545874|ref|XP_500475.1|	59931.27	hypothetical protein [Yarrowia lipolytica]							
721. Group probability: 0.9596. Peptides of the group									
TGTNHAEDQPVHLVVK	56.91	54.2543	1743.89	1744.25	3	2	distinct	0	0.9596
The equivalent proteins include									
gi|71005386|ref|XP_757359.1|	71766.86	hypothetical protein UM01212.1 [Ustilago maydis 521]							
722. Group probability: 0.9594. Peptides of the group									
SDEAKPAATLAATGDR	56.97	54.7382	1572.774	1573.322	1	2	distinct	0	0.9594
The equivalent proteins include									
gi|71004490|ref|XP_756911.1|	101880.72	hypothetical protein UM00764.1 [Ustilago maydis 521]							
723. Group probability: 0.9591. Peptides of the group									
FGIVEGLMSTIHATTATQK	84.63	53.6319	2004.035	2004.502	9	+2,+3	distinct	0	0.9591
The equivalent proteins include									
gi|929983|gb|AAB38369.1|	30863.12	glycerol-3-aldehyde dehydrogenase [Lactarius deterrimus]							
gi|20135844|emb|CAD29456.1|	36042.75	glyceraldehyde-3-phosphate dehydrogenase [Omphalotus olearius]							
gi|45421755|emb|CAF74786.1|	36369.82	glyceraldehyde 3-phosphate dehydrogenase [Armillariella tabescens]							
gi|34765757|gb|AAQ82456.1|	22655.68	glyceraldehyde 3-phosphate dehydrogenase [Armillariella tabescens]							
gi|47779429|gb|AAT38641.1|	26053.49	glyceraldehyde 3-phosphate dehydrogenase [Leccinum crocipodium]							
gi|47779431|gb|AAT38642.1|	26468.67	glyceraldehyde 3-phosphate dehydrogenase [Leccinum carpini]							
gi|57232460|gb|AAW47893.1|	25508.99	glyceraldehyde 3-phosphate dehydrogenase [Leccinum rotundifoliae]							
gi|57232466|gb|AAW47896.1|	25732.87	glyceraldehyde 3-phosphate dehydrogenase [Leccinum scabrum]							
gi|57232472|gb|AAW47899.1|	25779.38	glyceraldehyde 3-phosphate dehydrogenase [Leccinum scabrum]							
gi|57232482|gb|AAW47904.1|	25695.14	glyceraldehyde 3-phosphate dehydrogenase [Leccinum scabrum]							
724. Group probability: 0.9590. Peptides of the group									
AGGLVPLLSQR	58.98	55.1694	1109.656	1109.373	1	1	distinct	0	0.959
The equivalent proteins include									
gi|47115456|emb|CAG28509.1|	124377.93	TraA [Oligotropha carboxidovorans]							
725. Group probability: 0.9578. Peptides of the group									
TLAPLVESALPIIIEMLR	55.46	53.7065	1978.154	1979.553	1	2	distinct	0	0.9578
The equivalent proteins include									
gi|71012711|ref|XP_758522.1|	96518.22	hypothetical protein UM02375.1 [Ustilago maydis 521]							
726. Group probability: 0.9577. Peptides of the group									
GGPLGSLFRPDNFVFGQSGAGNNWAK	43.73	52.0635	2692.314	2693.733	1	2	distinct	0	0.8051
REAEGCDCLQGFQITHSLGGGTGAGMGTLLISK	46.59	50.3066	3420.622	3421.96	1	3	distinct	1	0.7831
The equivalent proteins include									
gi|57225882|gb|AAW42343.1|	50176.23	beta1-tubulin, putative [Cryptococcus neoformans var. neoformans JEC21]							
727. Group probability: 0.9576. Peptides of the group									
AIVEAVTHYNDPAK	57.25	54.5862	1526.773	1527.069	1	2	distinct	0	0.9576
The equivalent proteins include									
gi|71019481|ref|XP_759971.1|	34448.71	hypothetical protein UM03824.1 [Ustilago maydis 521]							
728. Group probability: 0.9574. Peptides of the group									

LQSESTSHQALISAVEPIEVLEKEYAANR	52.67	51.0661	3211.636	3211.753	1	3	distinct	1	0.9574

The equivalent proteins include

gi|71013528|ref|XP_758610.1|	38583.22	hypothetical protein UM02463.1 [Ustilago maydis 521]

729. Group probability: 0.9572. Peptides of the group

YAEPDLNKGESICIDR	56.19	54.0538	1878.878	1879.069	1	2	distinct	1	0.9572

The equivalent proteins include

gi|71008129|ref|XP_758183.1|	7276.46	hypothetical protein UM02036.1 [Ustilago maydis 521]

730. Group probability: 0.9570. Peptides of the group

LLGSLGSHDLSFMR	57.15	54.8558	1531.782	1533.163	1	2	distinct	0	0.957

The equivalent proteins include

gi|71018185|ref|XP_759323.1|	56059.1	hypothetical protein UM03176.1 [Ustilago maydis 521]

731. Group probability: 0.9568. Peptides of the group

IQFGGDEVVK	46.31	55.9513	1090.566	1090.78	1	2	shared(4)	0	0.638
INDYEESLLK	55.89	55.1929	1222.608	1222.808	1	2	distinct	0	0.9443

The equivalent proteins include

gi|4704283|emb|CAB41656.1|	35878.97	SPCC306.08c [Schizosaccharomyces pombe]

732. Group probability: 0.9567. Peptides of the group

WLCGIHNEVNQR	57.8	54.5776	1524.726	1525.008	1	2	distinct	0	0.9567

The equivalent proteins include

gi|71023575|ref|XP_762017.1|	37677.84	hypothetical protein UM05870.1 [Ustilago maydis 521]

733. Group probability: 0.9563. Peptides of the group

HKGVMVGMGQK (0000010000000)	70.83	55.6094	1170.6	1170.959	31	+1,+2	shared(8)	1	0.9992
IQDKEGIPPDQQR	47.88	54.643	1522.774	1523.197	1	2	shared(4)	1	0.8358
SYELPDGKVITIGNER	64.43	54.1766	1789.921	1790.679	1	2	shared(14)	1	0.9686
YPIEHGIVTNWDDMEK	86.65	53.8856	1945.888	1946.228	3	+2,+3	shared(6)	0	0.9985
VAPEEHPVLLTEAPINPK	88.95	53.6979	1953.057	1953.863	9	2	shared(9)	0	0.9916

The equivalent proteins include

gi|33346945|gb|AAP34634.1|	49579.96	ubiquitin/actin fusion protein [Gymnochlora stellata]

734. Group probability: 0.9561. Peptides of the group

FIPGLDSHLTFR	57.77	55.1275	1401.74	1402.356	1	2	distinct	0	0.9561

The equivalent proteins include

gi|71003021|ref|XP_756191.1|	56796.2	hypothetical protein UM00044.1 [Ustilago maydis 521]

735. Group probability: 0.9559. Peptides of the group

AHPGEELHAYIDR	57.22	54.7109	1506.721	1507.005	2	2	distinct	0	0.9559

The equivalent proteins include

gi|71005070|ref|XP_757201.1|	132950.35	hypothetical protein UM01054.1 [Ustilago maydis 521]

736. Group probability: 0.9556. Peptides of the group

LLNHDKDTVAASETR	56.27	54.3727	1668.843	1669.182	1	2	distinct	1	0.9556

The equivalent proteins include

gi|71019733|ref|XP_760097.1|	48779.46	hypothetical protein UM03950.1 [Ustilago maydis 521]

737. Group probability: 0.9555. Peptides of the group

KGNEGYFIEPTIFTDVPHDAK	53.44	52.815	2377.159	2377.923	1	2	distinct	1	0.9555

The equivalent proteins include

gi|71013736|ref|XP_758655.1|	54103.79	hypothetical protein UM02508.1 [Ustilago maydis 521]

738. Group probability: 0.9551. Peptides of the group

HLGPTFNETWAK	57.57	55.3129	1399.688	1400.377	2	2	distinct	0	0.9551

The equivalent proteins include

gi|71006468|ref|XP_757900.1|	37727.26	hypothetical protein UM01753.1 [Ustilago maydis 521]

739. Group probability: 0.9550. Peptides of the group

CAGLPLAAK	59.04	56.8499	899.49	900.113	1	2	distinct	0	0.955

The equivalent proteins include

gi|53793476|dbj|BAD53384.1|	53909.14	powdery mildew resistance protein PM3b-like protein [Oryza sativa (japonica cultivar-group)]

740. Group probability: 0.9547. Peptides of the group

LPDATKGPDHLR	55.68	55.2324	1318.699	1319.483	6	+2,+3	distinct	1	0.9547

The equivalent proteins include

gi|39939493|gb|AAR32786.1|	27420.82	ascorbate peroxidase [Pinus pinaster]

741. Group probability: 0.9547. Peptides of the group

FGIVQGLMTTVHATTATQK (000000001000000000000)	96.08	53.6319	2003.051	2004.502	10	2	distinct	0	0.9547

The equivalent proteins include

gi|283376|pir||S26974	36504.75	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - basidiomycete (Phaneroc

742. Group probability: 0.9543. Peptides of the group

TLAECFPNHAK	57.81	55.5295	1286.608	1287.199	1	2	distinct	0	0.9543

The equivalent proteins include

gi|71016212|ref|XP_758879.1|	8360.19	hypothetical protein UM02732.1 [Ustilago maydis 521]

743. Group probability: 0.9542. Peptides of the group

LVLEVAQHLGENTVR	84.18	54.5381	1676.921	1677.711	15	+2,+3	shared(6)	0	0.9996
DKEGQDVLLFIDNIFR	81.47	53.7914	1920.994	1922.383	24	2	shared(2)	1	0.9129
IPSAVGYQPTLATDMGTMQER	56.37	53.1154	2265.077	2263.592	2	2	shared(4)	0	0.5094

The equivalent proteins include

gi|47605558|sp|Q9PTY0|ATPB_CYPCA	55326.94	ATP synthase beta chain, mitochondrial precursor
gi|391913|dbj|BAA04178.1|	56211.01	H(+)-transporting ATPase beta subunit [Hemicentrotus pulcherrimus]
gi|68437443|ref|XP_699834.1|	65527.14	PREDICTED: similar to ATP synthase beta-subunit [Danio rerio]
gi|89574469|gb|ABD76365.1|	55778.13	putative ATP synthase beta subunit [Acyrthosiphon pisum]
gi|72008757|ref|XP_783293.1|	56110.98	PREDICTED: similar to CG11154-PA, isoform A [Strongylocentrotus purpuratus]
gi|95102938|gb|ABF51410.1|	55010.97	H+ transporting ATP synthase beta subunit isoform 1 [Bombyx mori]
gi|95102940|gb|ABF51411.1|	54858.82	H+ transporting ATP synthase beta subunit isoform 2 [Bombyx mori]
gi|71897237|ref|NP_001026562.1|	56649.74	ATP synthase, H+ transporting, mitochondrial F1 complex, beta subunit [Gallus gallus]
gi|47218629|emb|CAG04958.1|	55223.01	unnamed protein product [Tetraodon nigroviridis]
gi|45767611|gb|AAH67388.1|	56327.52	Hypothetical protein MGC76033 [Xenopus tropicalis]
gi|66267496|gb|AAH95620.1|	55079.83	Hypothetical protein LOC554135 [Danio rerio]
gi|28436792|gb|AAH46741.1|	56395.48	Atp5b-prov protein [Xenopus laevis]
gi|46909237|gb|AAT06136.1|	46034.02	ATP synthase beta subunit [Ephydatia cooperensis]
gi|46909239|gb|AAT06137.1|	45826.8	ATP synthase beta subunit [Dendraster excentricus]
gi|46909241|gb|AAT06138.1|	45867.83	ATP synthase beta subunit [Encope michelini]
gi|46909245|gb|AAT06140.1|	45884.78	ATP synthase beta subunit [Eucidaris tribuloides]

744. Group probability: 0.9540. Peptides of the group

ANEINKEVYDFLATATAK	87.33	53.5637	1997.01	1997.478	8	2	distinct	1	0.954

The equivalent proteins include

gi|3661614|gb|AAC61778.1|	84843.72	aconitase [Aspergillus terreus]

745. Group probability: 0.9539. Peptides of the group

MLRATTSAVPR	57.76	55.6694	1201.66	1201.684	1	2	distinct	1	0.9539

The equivalent proteins include

gi|418172|sp|P32307|V2R_PIG	41081.32	Vasopressin V2 receptor (Renal-type arginine vasopressin receptor) (Antidiuretic hormone receptor)

746. Group probability: 0.9539. Peptides of the group

IPVIMVGPGTGVAPFR	71.51	54.506	1609.901	1609.975	1	2	distinct	0	0.9539

The equivalent proteins include

gi|71024381|ref|XP_762420.1|	80370.88	hypothetical protein UM06273.1 [Ustilago maydis 521]

747. Group probability: 0.9537. Peptides of the group

AGGYTRPVFLPVPSDLLPAAISPAATQVPEEK	50.42	50.7491	3290.755	3291.579	1	3	distinct	0	0.9537

The equivalent proteins include

gi|71024257|ref|XP_762358.1|	111967.45	hypothetical protein UM06211.1 [Ustilago maydis 521]

748. Group probability: 0.9529. Peptides of the group

RFDILNLPLVPASER	55.55	54.1597	1738.973	1739.656	1	2	distinct	1	0.9529

The equivalent proteins include

gi|71003666|ref|XP_756499.1|	83467.9	hypothetical protein UM00352.1 [Ustilago maydis 521]

749. Group probability: 0.9529. Peptides of the group

ELGFDDDIYNVNGGAIAIGHPLGASGAR	52.18	52.1538	2798.362	2798.138	1	3	distinct	0	0.9529

The equivalent proteins include

gi|55232152|gb|AAV47571.1|	40504.79	acetyl-coA acetyltransferase [Haloarcula marismortui ATCC 43049]

750. Group probability: 0.9528. Peptides of the group

DSTIIMQLLR	45.88	55.6848	1188.654	1188.947	1	2	shared(4)	0	0.5759
QAFDDAIAELDTLSEDSYKDSTLIMQLLR (0000000000000000000000000100000)	49.08	50.8384	3316.602	3316.697	1	3	distinct	1	0.942

The equivalent proteins include

gi|34452065|gb|AAQ72489.1|	27960.81	14-3-3C1 protein [Oncorhynchus mykiss]

751. Group probability: 0.9526. Peptides of the group

LGCPPHAGGGIGLER	55.63	54.8808	1489.746	1490.215	2	2	distinct	0	0.9526

The equivalent proteins include

gi|71020373|ref|XP_760417.1|	63248.43	hypothetical protein UM04270.1 [Ustilago maydis 521]

752. Group probability: 0.9514. Peptides of the group

RTSATGALVAPHNSEPR	54.37	54.1451	1762.907	1763.313	1	2	distinct	1	0.9514

The equivalent proteins include

gi|71022581|ref|XP_761520.1|	89613.94	hypothetical protein UM05373.1 [Ustilago maydis 521]

753. Group probability: 0.9512. Peptides of the group

HGINHNIGQDGR	56.63	55.4051	1316.633	1317.311	2	2	distinct	0	0.9512

The equivalent proteins include

gi|71003251|ref|XP_756306.1|	35448.79	hypothetical protein UM00159.1 [Ustilago maydis 521]

754. Group probability: 0.9503. Peptides of the group

HVVFGQVVEGLDIVK	88.88	54.4105	1637.914	1639.299	4	2	distinct	0	0.9503

The equivalent proteins include

gi|21886603|emb|CAC84116.1|	18512.15	peptidylprolyl isomerase (cyclophilin) [Betula pendula]

755. Group probability: 0.9500. Peptides of the group

SNYNFEEPFLWLAR	45.91	54.291	1784.852	1784.804	2	+2,+3	distinct	0	0.95

The equivalent proteins include

gi|61366565|gb|AAX42876.1|	24692.71	RAN member RAS oncogene family [synthetic construct]
gi|74229915|gb|ABA00476.1|	24366.34	GTP-binding protein [Trichophyton rubrum]

756. Group probability: 0.9498. Peptides of the group

AAPALQNVLPGTGATGTTNATHTAAR	52.37	52.62	2461.267	2462.719	1	3	distinct	0	0.9498

The equivalent proteins include

gi|71023971|ref|XP_762215.1|	62322.51	hypothetical protein UM06068.1 [Ustilago maydis 521]

757. Group probability: 0.9498. Peptides of the group

IINEPTAAALSFGLDKK	58.99	54.6758	1786.983	1788.273	1	2	distinct	1	0.9498

The equivalent proteins include

gi|15828694|ref|NP_326054.1|	65480.66	molecular chaperone DnaK [Mycoplasma pulmonis UAB CTIP]

758. Group probability: 0.9497. Peptides of the group

ALSIQAHPDKPLGK	55.38	54.9358	1473.83	1474.953	3	2	distinct	0	0.9497

The equivalent proteins include

gi|71024169|ref|XP_762314.1|	51671.46	hypothetical protein UM06167.1 [Ustilago maydis 521]

759. Group probability: 0.9495. Peptides of the group

FASIPSEWHLPASILSDINEK	54.4	52.9472	2353.195	2354.443	1	3	distinct	0	0.9495

The equivalent proteins include

gi|71002955|ref|XP_756158.1|	61257.89	hypothetical protein UM00011.1 [Ustilago maydis 521]

760. Group probability: 0.9484. Peptides of the group

EAAADVKVEAHH	56	55.3976	1275.621	1275.906	1	2	distinct	1	0.9484

The equivalent proteins include

gi|71012536|ref|XP_758507.1|	13805.99	hypothetical protein UM02360.1 [Ustilago maydis 521]

761. Group probability: 0.9474. Peptides of the group

TVSSGYIEAHVPVSR	54.48	55.0375	1600.821	1601.339	1	2	distinct	0	0.9474

The equivalent proteins include

gi|71020247|ref|XP_760354.1|	28461.61	hypothetical protein UM04207.1 [Ustilago maydis 521]

S2. Protein assembly of peptide sequence matches made to tag-filtered P. sojae tandem mass spectra. The NCBI NR database was searched. Protein List with probabilities. The columns are arranged as follows: peptide sequence, Mascot Ions score, Mascot Identity score, computed peptide mass, observed precursor mass, number of tandem mass spectra assigned to same peptide sequence, the charge states observed for the peptide, whether the peptide is shared between protein groups with different probabilities (number in parentheses is number of other groups peptides are shared with) or is distinct (considered a unique identifier for proteins grouped with the same probability), the number of missed tryptic cleavages in this sequence, and the probability for a particular peptide sequence.

1. Group probability: 1.0000. Peptides of the group

AHGAQGIGLTR	68.34	55.2147	1079.584	1080.253	10	2	distinct	0	0.9819
GGMTSHAAVVAR (00010000000000)	91.33	55.6763	1155.582	1156.392	8	2	shared(2)	0	0.9737
TEHMFFSSAQR	50.12	55.1741	1339.598	1340.47	3	2	distinct	0	0.9109
LGIVHPGITEMQAK (0000000000010000)	62.94	54.6655	1492.807	1492.4	14	+1,+2	distinct	0	0.9993
IVFTAADAEAWFAR	89.72	54.5709	1566.783	1568.047	1	2	distinct	0	0.9975
HLDQLLHPSFANEK	103.93	54.5936	1647.837	1648.096	13	+2,+3	distinct	0	0.9998
QLDETVHTLETHFK	58.39	54.286	1696.842	1697.657	1	2	distinct	0	0.9619
RMEVFTNADTPEDAR	43.69	54.165	1750.794	1751.231	1	2	distinct	1	0.8668
IELGICGEHGGDPQSIEFFEK	87.53	52.8402	2361.095	2361.618	4	+2,+3	distinct	0	0.9997
HGVLEKDPFETLDQEGVGELVR	71.99	52.5273	2466.239	2466.788	5	+2,+3	distinct	1	0.9997

The equivalent proteins include

gi|16356689|gb|AAK74149.1|	98996.24	pyruvate phosphate dikinase [Phytophthora cinnamomi]
gi|16356691|gb|AAK74150.1|	99002.22	pyruvate phosphate dikinase [Phytophthora cinnamomi]

2. Group probability: 1.0000. Peptides of the group

FGSGWAWLGVK	81.22	55.3018	1206.619	1206.395	29	2	distinct	0	0.9942
SILEVVQSATEAPVR	109.51	54.7521	1597.867	1598.368	16	+2,+3	distinct	0	1
RPEYISAFWNVANWDK	95.56	53.7274	1994.964	1995.412	5	+2,+3	distinct	0	1
HHQAYVNNINNYISSDK	105.99	53.6002	2015.945	2016.447	27	+2,+3	distinct	0	1

The equivalent proteins include

gi|66865886|gb|AAY57577.1|	23956.74	manganese superoxide dismutase [Phytophthora nicotianae]

3. Group probability: 1.0000. Peptides of the group

LLADLIDYVPAR	84.07	55.3549	1357.76	1358.827	24	+1,+2	distinct	0	0.9998
SLLADAEAMDLSECILPVGDHIR (0000000001000000000000000)	116.84	52.5201	2524.23	2525.574	123	+2,+3	distinct	0	1

The equivalent proteins include

gi|81159502|gb|ABB56022.1|	20174.32	elicitin-like protein SOL2A [Phytophthora sojae]

4. Group probability: 1.0000. Peptides of the group

AVFPSIVGRPK	60.94	55.6087	1169.692	1170.277	8	2	distinct	0	0.8989
HLGIMVGMDQK (0000000010000)	79.27	55.5664	1227.61	1228.146	22	+1,+2	distinct	0	0.9997
TPEVLFQPSLIGK	59.88	54.9958	1427.802	1428.872	2	2	distinct	0	0.9648
AEYDESGPSIVHR	65.28	55.0678	1458.674	1459.218	3	+2,+3	shared(2)	0	0.9981
AEYDESGPSIVHRK	74.83	54.9453	1586.769	1587.119	5	2	shared(2)	1	0.9721
FRTPEVLFQPSLIGK	88.91	54.2421	1730.972	1731.667	11	+2,+3	distinct	1	0.9998
SYELPDGNVIVIGNER	105.1	54.2605	1773.89	1774.202	1	2	shared(2)	0	0.9923
YPIEHGIVTNWDDMEK (000000000000001000)	89.61	53.8859	1945.888	1946.177	23	+2,+3	shared(4)	0	0.9983
VAPEEHPVLLTEAPINPK	81.4	53.6978	1953.057	1953.885	13	2	shared(10)	0	0.9887
DLYCNIVLSGGTTMYPGIGER	47.6	53.0946	2315.093	2315.776	1	2	shared(2)	0	0.9253
KDLYCNIVLSGGTTMYPGIGER (00000000000000100000000)	89.96	52.8142	2443.187	2444.683	11	2	shared(2)	1	0.9983
TTGCVLDSGDGVSHTVPIYEGYALPHAIVR	72.64	50.9286	3183.566	3184.46	9	+2,+3	shared(3)	0	0.9878

The equivalent proteins include

gi|1085617|pir||S49007	41037.55	actin - Pythium irregulare (fragment)
gi|113223|sp|P22131|ACT1_PHYIN	42197.03	Actin-1
gi|9858460|gb|AAG01044.1|	42182.06	actin [Pythium splendens]

5. Group probability: 1.0000. Peptides of the group

FHVEEEGKGK	47.93	55.7364	1158.567	1159.423	2	2	shared(2)	1	0.8868
AKDSLAPVAVAVEQK	59.62	54.5754	1524.851	1525.17	2	2	distinct	1	0.9668
GVTLHLPVDFVIADK	62.28	54.4691	1622.903	1624.366	14	+2,+3	distinct	0	0.9989
VADKIQLIMNMLDK	90.88	54.6195	1630.879	1632.087	8	2	distinct	1	0.9939
LGDVYVNDAFGTAHR	79.59	54.5797	1633.785	1634.282	4	+2,+3	shared(3)	0	0.9548
AAGFLLDKELVYFAK	63.73	54.3276	1683.923	1685.182	1	2	distinct	1	0.977
IDAALPTVQYVLDQGAK	63.52	54.2851	1800.962	1802.369	2	2	distinct	0	0.9782
FNTEDKVSHVSTGGGASLELLEGK	76.84	52.5537	2474.229	2474.512	7	+2,+3	distinct	1	1

The equivalent proteins include

gi|23394369|gb|AAN31474.1|	43722.73	phosphoglycerate kinase [Phytophthora infestans]

6. Group probability: 1.0000. Peptides of the group

KFSDPIVQADIK	45.71		55.2978	1359.74	1360.845	1	2	distinct	1	0.873
SQVHEVVLVGGSTR	50.59		54.8716	1466.784	1467.846	3	2	distinct	0	0.8933
ARFEDMCGDYFR	51.41		54.6324	1565.639	1565.974	3	2	distinct	1	0.924
QKELEGVANPILQK	77.3		54.5536	1565.878	1566.538	5	2	distinct	1	0.9927
NQVAMNAHNTVFDAK	85		54.8918	1658.783	1659.309	6	2	distinct	0	0.9964
IINEPTAAAIAYGIDKK	113.47		54.7761	1786.983	1787.369	22	2	shared(6)	1	0.9981
NQVAMNAHNTVFDAKR	87.88		54.0716	1814.885	1815.33	3	2	distinct	1	0.9973
VQQLLSDFFNGKEPNK	72.42		54.1445	1862.953	1863.814	4	+2,+3	distinct	1	0.9985
SQTFSTYADNQPGVLIQVFEGER	63.02		52.394	2585.24	2585.586	2	2	distinct	0	0.8432

The equivalent proteins include

gi|38489930|gb|AAR21576.1|	71770.42	heat shock protein 70 [Phytophthora nicotianae]

7. Group probability: 1.0000. Peptides of the group

EFVASLARPR	58.29		55.7585	1144.635	1145.474	7	2	distinct	0	0.9543
SPDKVDATVQR	53.45		55.7212	1214.625	1215.293	1	2	distinct	1	0.9327
DFFGGHTYER	55.82		55.6068	1227.531	1228.536	1	2	distinct	0	0.9435
ERLPANLTQAQR	55.89		54.9397	1395.758	1396.461	7	2	distinct	1	0.9484
ICSYAQGLNLIR	48.18		54.9089	1406.734	1408.03	1	2	distinct	0	0.8986
GIHFVGMGVSGGEEGAR	86.07		54.9797	1658.783	1659.487	7	2	distinct	0	0.9969
ILSGPSEIPAVDKQQLIDDVR	64.57		53.0325	2292.232	2292.847	2	2	distinct	1	0.9832
MVHNGIEYGDMQLIAEAYDILK	81.23		52.4703	2522.218	2523.454	3	+2,+3	distinct	0	0.9989

The equivalent proteins include

gi|18644668|gb|AAL76320.1|	53625.12	6-phosphogluconate dehydrogenase [Phytophthora infestans]

8. Group probability: 1.0000. Peptides of the group

SHVTAGGTSLANFSFPGR	131.22		54.2501	1804.886	1805.289	4	2	distinct	0	0.9999
NAPAIIFIDEIDSIAPK	82.61		54.0448	1825.982	1826.739	16	2	shared(2)	0	0.9959
LGDVVGLHTCGDVPYGKR	71.31		53.6769	1941.973	1942.393	3	2	distinct	1	0.9895
GAAPCVLFFDELDSIAQQR	109.54		53.2257	2136.031	2137.284	8	2	distinct	0	0.9996
ELLELVQYPVEHPEKFEK	74.77		53.0949	2226.157	2226.594	7	2	distinct	1	0.9923

The equivalent proteins include

gi|66934627|gb|AAY58902.1|	89746.39	putative CDC48/ATPase [Hyaloperonospora parasitica]

9. Group probability: 1.0000. Peptides of the group

RALSAQAQAR	55.69		55.9636	1070.594	1071.446	3	2	distinct	1	0.8865
IINEPTAAAIAYGIDKK	113.47		54.7761	1786.983	1787.369	22	2	shared(6)	1	0.9981
LEIESLLDGEDFTESLSR	77.06		53.8276	2051.99	2052.789	2	2	distinct	0	0.9936
DVLLIDVVPLSQGIETVGGVMTK	96.73		52.8475	2382.308	2381.895	15	+2,+3	distinct	0	1
SQTFSTYQDNQPAVLIQVFEGER	81.72		52.3164	2656.277	2656.593	1	2	distinct	0	0.9966

The equivalent proteins include

gi|429116|emb|CAA53368.1|	55388.19	glucose regulated protein/BiP [Phytophthora cinnamomi]
gi|429118|emb|CAA53369.1|	72693.28	glucose regulated protein /BiP [Phytophthora cinnamomi]

10. Group probability: 1.0000. Peptides of the group

SLPLQLLVTAEHPDTK	124.59		54.2449	1760.967	1761.312	2	2	distinct	0	0.9999
EPNVDHCFLMNHDSK	52.36		54.1605	1841.782	1842.319	3	2	distinct	0	0.9378
SYDLIANDGVNSLHGGNTWGLK	77.51		52.9456	2330.129	2330.348	5	+2,+3	distinct	0	0.9994
SYDLIANDGVNSLHGGNTWGLKDFEGPFEVK	54.01		50.4843	3378.616	3379.444	2	3	distinct	1	0.9652

The equivalent proteins include

gi|21327106|gb|AAM48174.1|	36290.12	UDP-glucose 4-epimerase-like protein [Phytophthora sojae]

11. Group probability: 1.0000. Peptides of the group

KALIHDGLK	74.77		55.2942	993.597	994.593	6	2	distinct	1	0.9549
ALIHDGLKR	56.9		55.6184	1021.603	1022.506	1	2	distinct	1	0.8093
ALCEEHGVNLILVPSGK	86.85		54.1268	1834.961	1835.603	11	+2,+3	distinct	0	0.9994
VVSTSCAVITDFGEETHALNVLLDYLK	56.35		51.336	2993.505	2994.675	6	3	distinct	0	0.9667
KVVSTSCAVITDFGEETHALNVLLDYLK	94.97		51.1292	3121.6	3123.077	1	3	distinct	1	0.9989

The equivalent proteins include

gi|66270173|gb|AAY43416.1|	15491.87	ribosomal protein S12 [Phytophthora infestans]

12. Group probability: 1.0000. Peptides of the group

DSTIIMQLLR	62.92		55.6859	1188.654	1188.603	4	2	shared(5)	0	0.8101
AVANNHNVELTVEER	104.61		54.2917	1693.838	1694.333	3	2	distinct	0	0.9994
QASTIAMAELPPTHPIR (000000010000000000)	90.58		54.0263	1831.961	1832.424	21	+2,+3	distinct	0	0.9998
LAEQAERYDEMVDHMK	44.88		53.7655	1963.877	1964.27	1	2	distinct	1	0.8852
QAFDDAIAELDTLSEESYK	63.08		53.2605	2143.98	2145.265	2	2	shared(3)	0	0.9793
QAFDDAIAELDTLSEESYKDSTLIMQLLR	73.46		50.8352	3314.623	3315.694	3	3	shared(2)	1	0.9206

The equivalent proteins include

gi|23394350|gb|AAN31465.1|	28566.01	14-3-3-like protein [Phytophthora infestans]

13. Group probability: 1.0000. Peptides of the group

HAVIFYDDLSK	65.46	55.2897	1306.656	1306.456	12	+1,+2	distinct	0	0.9994
EAYPGDVFYIHSR	77.43	54.6324	1552.731	1553.625	13	2	shared(2)	0	0.9925
RTGSIVSVPVGPEVLGR	74.35	54.2236	1721.979	1722.923	22	2	distinct	1	0.9916
GMALNLEPDVVGVVVFSNDR (0010000000000000000000)	83.98	53.2714	2130.078	2131.325	6	2	distinct	0	0.9968

The equivalent proteins include

gi|9695382|ref|NP_037604.1|	56282.61	ATP synthase F1 subunit alpha [Phytophthora infestans]

14. Group probability: 1.0000. Peptides of the group

QLTDKDYYGNDIK	62.09	54.8712	1571.747	1572.512	3	2	distinct	1	0.9711
AYTFVNSNPGQPACYLK	71.72	53.8363	1928.909	1928.607	4	2	distinct	0	0.9895
AYTYINNNPGQPVCYLK	62.05	53.5883	2013.962	2014.14	3	2	distinct	0	0.9755
TVYVSLPSLCCDACASTAGCK	86	52.9532	2319	2319.384	1	2	distinct	0	0.9974

The equivalent proteins include

gi|2706495|emb|CAA65843.1|	29154.14	CBEL protein, formerly GP34 [Phytophthora parasitica]

15. Group probability: 1.0000. Peptides of the group

TKPIQGPYGTGMSGPSFGK (000000000000100000000)	94.9	53.8833	1908.94	1909.434	28	+2,+3	distinct	0	1
WTSIASTQPVGTTTFEHWPIR	97.97	52.7402	2414.202	2414.803	8	2	distinct	0	0.9991

The equivalent proteins include

gi|20270957|gb|AAM18483.1|	83857.32	putative exo-1,3-beta-glucanase [Phytophthora infestans]

16. Group probability: 1.0000. Peptides of the group

TACTATQQTAAYK	48.13	55.1313	1413.656	1414.142	1	2	distinct	0	0.9012
LMCASTACNTMIK (000000000001000)	67.83	55.0286	1499.66	1500.494	25	2	distinct	0	0.9825
LMCASTACNTMIKK	83.1	54.7144	1627.755	1629.112	14	2	distinct	1	0.9956
TLVSILSESSFSQCSK	80.12	54.2292	1771.866	1772.861	1	2	distinct	0	0.9947

The equivalent proteins include

gi|119287|sp|P15569|ELIB_PHYCI	10629.09	Beta-elicitin cinnamomin

17. Group probability: 1.0000. Peptides of the group

KTVAVGVIK	47.89	56.568	913.596	914.553	1	2	shared(2)	1	0.8811
IGGIGTVPVGR	47.13	55.1381	1024.603	1026.063	1	2	shared(8)	0	0.8842
EHALLAFTLGVK	64.61	55.1836	1297.739	1299.156	1	2	shared(5)	0	0.9343
VETGVIKPGMVATFGPVGLSTEVK (000000000010000000000000000)	112.1	52.7441	2415.308	2415.308	25	+2,+3	shared(2)	0	1
SVEMHHESLPEAVPGDNVGFNVK	76.04	52.5152	2491.18	2492.428	3	2	shared(2)	0	0.9814
SGDACMVILEPSKPMTVESFQEYPPLGR (0000001000000000100000000000000)	63.79	50.9984	3137.487	3169.855	11	+2,+3	distinct	0	0.9995

The equivalent proteins include

gi|74231225|gb|ABA00716.1|	48841.39	translation elongation factor 1 alpha [Phytophthora parasitica]
gi|6688977|emb|CAB65347.1|	47521.62	translation elongation factor 1 alpha [Phytophthora infestans]

18. Group probability: 1.0000. Peptides of the group

ITFELFADKVPK	85.33	54.9088	1406.781	1407.6	17	2	distinct	1	0.9858
VIPNFMCQGGDFTR	50.55	54.3672	1640.744	1641.291	1	2	shared(2)	0	0.9241
PNPQVFFDMTVGGAPAGR	98.26	54.0342	1859.899	1859.76	6	2	distinct	0	0.999
GNGTGGESIYGEKFPDENFLLK	69.33	52.8276	2371.133	2372.324	1	3	distinct	1	0.9869

The equivalent proteins include

gi|23394388|gb|AAN31483.1|	18536.13	peptidylprolyl isomerase [Phytophthora infestans]

19. Group probability: 1.0000. Peptides of the group

AVMHMALR	50.54	56.6865	927.478	928.136	4	2	shared(3)	0	0.9056
FLAGAHAMDK (000000001000)	67.37	56.0014	1059.517	1060.198	9	2	shared(3)	0	0.9478
ANIFGFWDWVGGR	81.96	54.5789	1523.731	1524.464	7	2	shared(3)	0	0.9939
FAAHIQQVDMESNGER	79.62	54.0538	1830.832	1831.328	5	2	distinct	0	0.963
KLQAIASGEHVNATEDR	112.31	53.9152	1837.928	1839.353	12	+2,+3	shared(2)	1	1
HMVAASSAVPLVQQFGIDR	63.53	53.4985	2025.047	2026.423	1	2	shared(3)	0	0.98
YSVTSAVGILPLALQYGFDITEK	71.42	52.6675	2484.315	2485.376	2	2	shared(3)	0	0.9915

The equivalent proteins include

gi|37960095|gb|AAP51072.1|	60840.39	glucose-6-phosphate isomerase [Phytophthora infestans]

20. Group probability: 1.0000. Peptides of the group

IGGIGTVPVGR	47.13	55.1381	1024.603	1026.063	1	2	shared(8)	0	0.8842
EHALLAFTLGVK	64.61	55.1836	1297.739	1299.156	1	2	shared(5)	0	0.9343
FFFTVIDAPGHR	72.18	55.0179	1405.714	1406.896	27	+2,+3	distinct	0	0.9995
VETGVIKPGMVATFGPVGLSTEVK (000000000010000000000000000)	112.1	52.7441	2415.308	2415.308	25	+2,+3	shared(2)	0	1
SVEMHHESLPEAVPGDNVGFNVK	76.04	52.5152	2491.18	2492.428	3	2	shared(2)	0	0.9814

The equivalent proteins include

gi|50660710|gb|AAT81037.1|	33463.06	translation elongation factor 1 alpha [Phytophthora sojae]
gi|50660720|gb|AAT81042.1|	34017.48	translation elongation factor 1 alpha [Phytophthora hybrid Dutch variant]
gi|50660722|gb|AAT81043.1|	34030.47	translation elongation factor 1 alpha [Phytophthora cinnamomi]
gi|50660730|gb|AAT81047.1|	34047.46	translation elongation factor 1 alpha [Phytophthora colocasiae]
gi|50660740|gb|AAT81052.1|	34055.39	translation elongation factor 1 alpha [Phytophthora fragariae var. fragariae]
gi|50660744|gb|AAT81054.1|	34043.42	translation elongation factor 1 alpha [Phytophthora fragariae var. rubi]
gi|50660768|gb|AAT81066.1|	34057.42	translation elongation factor 1 alpha [Phytophthora meadii]

21. Group probability: 1.0000. Peptides of the group

KVLAVTDPMLK	66.3	55.6104	1213.71	1214.831	5	+1,+2	distinct	1	0.999
KAALENIFLVK	73.25	55.8741	1244.749	1245.954	4	2	distinct	1	0.9881
SLFSEANPQPIKK	67.04	54.9851	1457.788	1458.784	9	2	distinct	1	0.9812

The equivalent proteins include

gi|23394358|gb|AAN31469.1|	31345.33	dihydrodipicolinate synthase [Phytophthora infestans]

22. Group probability: 1.0000. Peptides of the group

KDEYLNWAVDAFR	95.62	54.6437	1625.784	1626.84	4	2	distinct	1	0.9985
GMLTGPVTILNWSFPR (001000000000000000)	88.68	54.6791	1787.939	1788.136	12	2	distinct	0	0.996
DLGPGTYDIHSPVVPPKEEIVK	50.68	52.7876	2389.253	2389.698	4	2	distinct	1	0.9453

The equivalent proteins include

gi|56718247|gb|AAW24459.1|	31163.84	5-methyltetrahydropteroyl-triglutamate-homocystein S-methyltransferase [Phytophthora infestans]

23. Group probability: 1.0000. Peptides of the group

AVMHMALR	50.54	56.6865	927.478	928.136	4	2	shared(3)	0	0.9056
FLAGAHAMDK (000000001000)	67.37	56.0014	1059.517	1060.198	9	2	shared(3)	0	0.9478
ANIFGFWDWVGGR	81.96	54.5789	1523.731	1524.464	7	2	shared(3)	0	0.9939
FAAHIQQVDMESNGKR	69.79	54.0538	1829.884	1831.328	4	2	shared(2)	1	0.886
KLQAIASGEHVNATEDR	112.31	53.9152	1837.928	1839.353	12	+2,+3	shared(2)	1	1
HMVAASSAVPLVQQFGIDR	63.53	53.4985	2025.047	2026.423	1	2	shared(3)	0	0.98
YSVTSAVGILPLALQYGFDITEK	71.42	52.6675	2484.315	2485.376	2	2	shared(3)	0	0.9915

The equivalent proteins include

gi|37960107|gb|AAP51078.1|	60850.42	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960073|gb|AAP51061.1|	60861.39	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960081|gb|AAP51065.1|	60755.43	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960087|gb|AAP51068.1|	60776.38	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960091|gb|AAP51070.1|	60834.39	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960093|gb|AAP51071.1|	60842.35	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960105|gb|AAP51077.1|	60716.35	glucose-6-phosphate isomerase [Phytophthora erythroseptica]
gi|37960109|gb|AAP51079.1|	60859.42	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960111|gb|AAP51080.1|	60792.41	glucose-6-phosphate isomerase [Phytophthora infestans]

24. Group probability: 1.0000. Peptides of the group

ETHHVAGAAVR	54.14	55.7643	1146.589	1146.51	4	+1,+2	distinct	0	0.9947
RLTELIGAVGGK	63.93	55.5602	1212.719	1213.39	2	2	distinct	1	0.9742
ELIGTANQLAENNIDLLMPGFTHLQPAQPLR (0000000000000000001000000000000)	68.19	50.4487	3429.771	3429.395	12	3	distinct	0	0.99

The equivalent proteins include

gi|23394365|gb|AAN31472.1|	50896.16	argininosuccinate lyase [Phytophthora infestans]

25. Group probability: 1.0000. Peptides of the group

THTQDATPLTLGQEFSGYR	133.31	53.2814	2121.013	2121.651	10	+2,+3	distinct	0	1

The equivalent proteins include

gi|83751735|ref|ZP_00948148.1|	49983.55	COG0114: Fumarase [Bartonella bacilliformis KC583]

gi|49240103|emb|CAF26544.1|	50205.54	Fumarate hydratase c [Bartonella quintana str. Toulouse]

26. Group probability: 1.0000. Peptides of the group

SYLHLPAEIVPATLK	91.48	54.5848	1650.934	1652.162	4	2	distinct	0	0.998
SYLHLPAEIVPATLKK	98.28	54.1319	1779.029	1779.791	2	2	distinct	1	0.9989

The equivalent proteins include

gi|66270167|gb|AAY43413.1|	16478.54	ribosomal protein S10 [Phytophthora infestans]

27. Group probability: 1.0000. Peptides of the group

AVMHMALR	50.54	56.6865	927.478	928.136	4	2	shared(3)	0	0.9056
FLAGAHAMDK (000000001000)	67.37	56.0014	1059.517	1060.198	9	2	shared(3)	0	0.9478
GVWNSSFLGHSSR	81.59	55.0123	1432.685	1433.195	3	2	distinct	0	0.9948
ANIFGFWDWVGGR	81.96	54.5789	1523.731	1524.464	7	2	shared(3)	0	0.9939
FAAHIQQVDMESNGKR	69.79	54.0538	1829.884	1831.328	4	2	shared(2)	1	0.886
HMVAASSAVPLVQQFGIDR	63.53	53.4985	2025.047	2026.423	1	2	shared(3)	0	0.98
YSVTSAVGILPLALQYGFDITEK	71.42	52.6675	2484.315	2485.376	2	2	shared(3)	0	0.9915

The equivalent proteins include

gi|37960071|gb|AAP51060.1|	60801.41	glucose-6-phosphate isomerase [Phytophthora infestans]

28. Group probability: 1.0000. Peptides of the group

TMEINPLHPIIK	69.45	55.0576	1404.78	1405.284	6	2	distinct	0	0.9842
KTMEINPLHPIIK	66.31	54.8586	1532.875	1533.139	3	+2,+3	distinct	1	0.9968
VFIMDNCEELMPEYLSFVK	76.72	52.8125	2363.089	2363.453	1	2	shared(2)	0	0.9938

The equivalent proteins include

gi|22086550|gb|AAM90674.1|	80462.52	heat shock protein Hsp90 [Achlya ambisexualis]
gi|22086553|gb|AAM90675.1|	80476.53	heat shock protein Hsp90 [Achlya ambisexualis]

29. Group probability: 1.0000. Peptides of the group

HSEFIGFPIK	50.2	55.697	1173.618	1174.705	1	2	distinct	0	0.9073
KPEDVTHEEYASFYK	106.17	54.1194	1841.847	1842.568	2	2	distinct	0	0.9994
VFIMDNCEELMPEYLSFVK	76.72	52.8125	2363.089	2363.453	1	2	shared(2)	0	0.9938

The equivalent proteins include

gi|59894156|gb|AAX10946.1|	64423.44	heat shock protein 90 [Phytophthora palmivora]

30. Group probability: 1.0000. Peptides of the group

AEYDESGPSIVHR	65.28	55.0678	1458.674	1459.218	3	+2,+3	shared(2)	0	0.9981
AEYDESGPSIVHRK	74.83	54.9453	1586.769	1587.119	5	2	shared(2)	1	0.9721
YPIEHGIVTDWDDMEK	83.19	53.8466	1946.872	1946.691	15	+2,+3	distinct	0	0.9994

The equivalent proteins include

gi|50355625|dbj|BAD29953.1|	42035.79	actin [Ulva pertusa]

31. Group probability: 1.0000. Peptides of the group

IIVDAHYR	55.02	56.2684	985.534	986.243	8	2	distinct	0	0.888
EHIAAYGTGNER	55.87	55.4105	1316.611	1317.285	2	2	distinct	0	0.9478
RPASNMDPYVVTGR (0000001000000000)	67.39	54.8218	1561.767	1562.686	14	+2,+3	distinct	0	0.999

The equivalent proteins include

gi|23394346|gb|AAN31463.1|	39801.57	glutamine synthetase [Phytophthora infestans]

32. Group probability: 1.0000. Peptides of the group

LGGTCLNVGCIPSK	77	54.9253	1474.727	1475.148	1	2	distinct	0	0.9925
TCHAHPTLSEAFK	60.11	54.7306	1497.703	1497.461	5	+1,+2	distinct	0	0.9975

The equivalent proteins include

gi|83774859|dbj|BAE64982.1|	54922.59	unnamed protein product [Aspergillus oryzae]
gi|44985105|gb|AAS53883.1|	53811.88	AFR512Wp [Ashbya gossypii ATCC 10895]

33. Group probability: 1.0000. Peptides of the group

SLNNQFASFIDKVR	48.77	54.4749	1637.852	1638.84	1	2	distinct	1	0.7018
THNLEPYFESFINNLR	83.06	53.7483	1992.969	1993.391	17	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|109096823|ref|XP_001098292.1|	65340.78	PREDICTED: similar to keratin 1 isoform 7 [Macaca mulatta]
gi|109096825|ref|XP_001098082.1|	64503.44	PREDICTED: similar to keratin 1 isoform 5 [Macaca mulatta]
gi|109096827|ref|XP_001097902.1|	63150.85	PREDICTED: similar to keratin 1 isoform 3 [Macaca mulatta]
gi|109096829|ref|XP_001097988.1|	62009.39	PREDICTED: similar to keratin 1 isoform 4 [Macaca mulatta]
gi|109096831|ref|XP_001098182.1|	63139.76	PREDICTED: similar to keratin 1 isoform 6 [Macaca mulatta]
gi|109096833|ref|XP_001097800.1|	61737.33	PREDICTED: similar to keratin 1 isoform 2 [Macaca mulatta]

gi|109096835|ref|XP_001097706.1|	59017.2	PREDICTED: similar to keratin 1 isoform 1 [Macaca mulatta]
gi|55638143|ref|XP_522394.1|	98632.68	PREDICTED: similar to keratin 1B [Pan troglodytes]
gi|7331218|gb|AAF60327.1|	66149.05	keratin 1 [Homo sapiens]
gi|11935049|gb|AAG41947.1|	66198.07	keratin 1 [Homo sapiens]

34. Group probability: 1.0000. Peptides of the group

VYVQEGIYDEFVK	78.44	54.8276	1587.782	1588.458	3	2	distinct	0	0.9931
VYVQEGIYDEFVKR	78.67	54.2748	1743.883	1744.428	22	2	distinct	1	0.9936

The equivalent proteins include

gi|45238345|emb|CAD70567.1|	54808.42	aldehyde dehydrogenase [Crocus sativus]

35. Group probability: 1.0000. Peptides of the group

IPIFSAAGLPHNEIAAQIVR	88.58	53.3337	2116.179	2116.455	10	+2,+3	distinct	0	1

The equivalent proteins include

gi|39583624|emb|CAE65728.1|	56409.84	Hypothetical protein CBG10811 [Caenorhabditis briggsae]
gi|39597843|emb|CAE68535.1|	54855.11	Hypothetical protein CBG14362 [Caenorhabditis briggsae]
gi|7331730|gb|AAF60418.1|	56283.98	Temporarily assigned gene name protein 300 [Caenorhabditis elegans]

36. Group probability: 0.9999. Peptides of the group

AHSSMVGVDLPVK (000001000000000)	80.63	55.2955	1338.697	1339.061	22	+1,+2	distinct	0	0.9998
LGDVYVNDAFGTAHR	79.59	54.5797	1633.785	1634.282	4	+2,+3	shared(3)	0	0.9548

The equivalent proteins include

gi|3043929|gb|AAC13267.1|	43909.93	phosphoglycerate kinase [Aplysia californica]

37. Group probability: 0.9999. Peptides of the group

ACNALLLK	66.88	56.8385	901.505	902.794	1	2	shared(3)	0	0.9266
IGSEVYHNLK	60.26	55.7364	1158.603	1159.47	7	2	distinct	0	0.9616
IGSEVYHNLKK	47.26	55.4809	1286.698	1287.765	1	2	distinct	1	0.8847
VNQIGSITESIEAVTMAK	94.92	53.9105	1889.977	1890.696	2	2	shared(2)	0	0.9987

The equivalent proteins include

gi|23394379|gb|AAN31479.1|	49419.2	enolase [Phytophthora infestans]

38. Group probability: 0.9999. Peptides of the group

LVLEVAQHLGENTVR	99.26	54.5381	1676.921	1677.82	31	+2,+3	shared(2)	0	0.9998
TLQDIIAILGMDELSEDDKLTVAR	75.85	52.3696	2658.379	2657.719	20	2	distinct	1	0.9944

The equivalent proteins include

gi|46909245|gb|AAT06140.1|	45884.78	ATP synthase beta subunit [Eucidaris tribuloides]

39. Group probability: 0.9999. Peptides of the group

TVYHLNPSGR	45.36	55.7729	1142.583	1143.591	1	2	distinct	0	0.8581
NFDLRPGMIQK	49.48	55.3539	1317.686	1318.266	2	2	distinct	0	0.9044
FVIGGPHGDAGLTGR	79.38	54.7984	1452.747	1454.065	9	2	distinct	0	0.9941

The equivalent proteins include

gi|23394401|gb|AAN31489.1|	43150.8	S-adenosyl methionine synthetase [Phytophthora infestans]

40. Group probability: 0.9999. Peptides of the group

SYELPDGNVIVIGDER	89.05	54.2605	1774.874	1774.202	1	2	distinct	0	0.9686
DLYCNIVLSGGTTMYPGIGER	47.6	53.0946	2315.093	2315.776	1	2	shared(2)	0	0.9253
KDLYCNIVLSGGTTMYPGIGER (0000000000000100000000)	89.96	52.8142	2443.187	2444.683	11	2	shared(2)	1	0.9983
TTGCVLDSGDGVSHTVPIYEGYALPHAIVR	72.64	50.9286	3183.566	3184.46	9	+2,+3	shared(3)	0	0.9878

The equivalent proteins include

gi|57864652|gb|AAW56946.1|	29368.75	actin [Apodachlya brachynema]

41. Group probability: 0.9999. Peptides of the group

RLVQAPNSYFMDVK (0000000000010000)	88.99	54.3444	1666.85	1667.504	18	+2,+3	distinct	1	0.9999

The equivalent proteins include

gi|47225842|emb|CAF98322.1|	9793.08	unnamed protein product [Tetraodon nigroviridis]

42. Group probability: 0.9999. Peptides of the group

ACNALLLK	66.88	56.8385	901.505	902.794	1	2	shared(3)	0	0.9266
VPTPDVSVVDLTCR	100.87	54.7076	1556.787	1557.293	12	2	shared(2)	0	0.9926
LTGMAFRVPTPDVSVVDLTCR (0000100000000000000000)	64.95	52.8809	2333.187	2333.52	9	+2,+3	distinct	1	0.9972

The equivalent proteins include

gi|71000249|dbj|BAE07174.1|	86477.52	polyprotein [Heterocapsa triquetra]

43. Group probability: 0.9999. Peptides of the group

SDVLLFADQNHGWVHR	94.68	54.3504	1892.928	1893.02	16	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|20270963|gb|AAM18486.1|	32590.22	putative endo-1,3;1,4-beta-glucanase [Phytophthora infestans]

44. Group probability: 0.9999. Peptides of the group

AYTAAYTPCR	49.79	55.7421	1172.528	1173.727	1	2	distinct	0	0.9038
CILLGGVHGLVESLFR	96.62	54.1621	1768.966	1770.259	4	2	distinct	0	0.9988

The equivalent proteins include

gi|56718249|gb|AAW24460.1|	46429.08	ketol-acid reductoisomerase [Phytophthora infestans]

45. Group probability: 0.9999. Peptides of the group

QYTGVGSLK	45.87	55.2095	951.502	952.559	1	2	distinct	0	0.862
AYAEHLKR	65.71	56.3151	986.53	987.808	9	2	distinct	1	0.9678
SGKIELPAWWDVVK	77.54	54.7125	1626.877	1627.787	5	2	distinct	1	0.9728

The equivalent proteins include

gi|66270169|gb|AAY43414.1|	17459.17	ribosomal protein S19 [Phytophthora infestans]

46. Group probability: 0.9999. Peptides of the group

IAYVHSLKEEAIK	48.94	55.0312	1499.835	1500.569	1	2	distinct	1	0.9082
ESLNLSIVEAINQASEAWGIK	92.8	53.0647	2271.175	2271.854	8	2	distinct	0	0.9986

The equivalent proteins include

gi|23394406|gb|AAN31491.1|	40884.22	unknown [Phytophthora infestans]

47. Group probability: 0.9999. Peptides of the group

NLQGIIAILGMDELSEDDKLTVAR (000000000000100000000000000)	117.63	52.401	2613.368	2614.676	21	2	distinct	1	0.9999

The equivalent proteins include

gi|2116558|dbj|BAA20135.1|	60284.43	F1 ATPase [Pisum sativum]

48. Group probability: 0.9999. Peptides of the group

LAALVGAHK	50.61	55.7335	878.534	879.22	1	2	distinct	0	0.908
FDGLFGLAFDTISVDHLK	93.05	53.7301	1994.015	1995.319	2	2	distinct	0	0.9984

The equivalent proteins include

gi|66270071|gb|AAY43365.1|	42681.42	aspartic protease [Phytophthora infestans]

49. Group probability: 0.9998. Peptides of the group

VLDLIEHMVK	57.34	55.333	1195.663	1196.24	3	2	distinct	0	0.9508
NMHVVSNASCTTNCLAPLAK	83.89	53.2769	2187.023	2188.453	7	2	distinct	0	0.9968

The equivalent proteins include

gi|2266741|emb|CAA45835.1|	63675.17	triosephosphate isomerase + glyceraldehyde-3-phosphate dehydrogenase [Phytophthora infestans]
gi|120703|sp|P26988|G3P_PHYIN	36265.23	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)

50. Group probability: 0.9998. Peptides of the group

KIAVNLIPFPR	70.88	55.3215	1266.781	1267.527	5	2	shared(8)	1	0.9855
GHYTEGAELIDSVLDVVR	50.71	53.6785	1971.99	1972.76	1	2	shared(7)	0	0.7949
LTTPTYGDLNHLVCAAMSGITTCLR	82.51	51.98	2764.335	2765.271	4	2	shared(2)	0	0.997
AGPYGQIFRPDNFVFGQTGAGNNWAK	79.99	52.1825	2811.352	2812.533	7	+2,+3	shared(3)	0	0.9986
FWEVISDEHGVDPTGSYHGDSDLQLER	57.7	51.1678	3087.385	3088.854	1	3	shared(3)	0	0.9705
EAESCDCIQGFQLTHSLGGGTGSGMGTLLISK	75.02	50.7063	3310.527	3311.459	11	3	shared(4)	0	0.9947

The equivalent proteins include

gi|63333605|gb|AAY40458.1|	43811.33	beta-tubulin [Saprolegnia megasperma]
gi|63333607|gb|AAY40459.1|	43732.27	beta-tubulin [Saprolegnia megasperma]
gi|57903349|gb|AAW58086.1|	45720.09	beta-tubulin [Pythium graminicola]
gi|57903333|gb|AAW58079.1|	45648.06	beta-tubulin [Brevilegnia macrospora]
gi|57903344|gb|AAW58084.1|	45741.97	beta-tubulin [Phytophthora palmivora]

51. Group probability: 0.9998. Peptides of the group

AIVGSNAFAHESGIHQDGVLK	80.25	53.3022	2149.092	2149.306	13	+2,+3	distinct	0	0.9998

The equivalent proteins include

gi|33863392|ref|NP_894952.1|	58390.9	2-isopropylmalate synthase [Prochlorococcus marinus str. MIT 9313]

52. Group probability: 0.9998. Peptides of the group

GIYAYGFEKPSAIQKR	86.96	54.073	1826.968	1827.656	35	+2,+3	distinct	1	0.9998

The equivalent proteins include

gi|12381898|dbj|BAB21259.1|	47320.08	eukaryotic initiation factor 4A [Oryza sativa]
gi|108870174|gb|EAT34399.1|	39467.92	DEAD box ATP-dependent RNA helicase [Aedes aegypti]
gi|54638586|gb|EAL27988.1|	45912.76	GA20384-PA [Drosophila pseudoobscura]
gi|61367710|gb|AAX43036.1|	46491.78	eukaryotic translation initiation factor 4A isoform 1 [synthetic construct]
gi|60652753|gb|AAX29071.1|	47239.37	DEAD box polypeptide 48 [synthetic construct]
gi|48136057|ref|XP_393356.1|	46478.95	PREDICTED: similar to ENSANGP00000020417 [Apis mellifera]
gi|66509040|ref|XP_623693.1|	39986.8	PREDICTED: similar to ENSANGP00000020417 [Apis mellifera]

gi|66551110|ref|XP_623228.1|	39990.11	PREDICTED: similar to Eukaryotic initiation factor 4A (eIF4A) (eIF-4A) [Apis mellifera]
gi|66551115|ref|XP_623285.1|	48524.51	PREDICTED: similar to Eukaryotic initiation factor 4A (eIF4A) (eIF-4A) [Apis mellifera]
gi|68363414|ref|XP_709370.1|	38062.47	PREDICTED: similar to Eukaryotic translation initiation factor 4A, isoform 1A isoform 2 [Danio reri
gi|73695588|gb|AAZ80489.1|	47837.06	translation initiation factor 4A [Bombyx mori]
gi|67970988|dbj|BAE01836.1|	46615.87	unnamed protein product [Macaca fascicularis]
gi|67968411|dbj|BAE00567.1|	46324.61	unnamed protein product [Macaca fascicularis]
gi|67971846|dbj|BAE02265.1|	47126.29	unnamed protein product [Macaca fascicularis]
gi|74139596|dbj|BAE40935.1|	46380.65	unnamed protein product [Mus musculus]
gi|74142079|dbj|BAE41100.1|	47080.28	unnamed protein product [Mus musculus]
gi|74187427|dbj|BAE36681.1|	25025.58	unnamed protein product [Mus musculus]
gi|74151289|dbj|BAE38776.1|	41692.2	unnamed protein product [Mus musculus]
gi|74219920|dbj|BAE40541.1|	46338.62	unnamed protein product [Mus musculus]
gi|74187323|dbj|BAE22641.1|	46382.65	unnamed protein product [Mus musculus]
gi|55732624|emb|CAH93011.1|	46308.64	hypothetical protein [Pongo pygmaeus]
gi|50820|emb|CAA26846.1|	42385.99	unnamed protein product [Mus musculus]
gi|91082421|ref|XP_975873.1|	48126.25	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 2 [Tribolium castaneum]
gi|71051290|gb|AAH99392.1|	46221.6	Eif4a1 protein [Mus musculus]
gi|92873011|gb|ABE81518.1|	46974.18	Helicase, C-terminal [Medicago truncatula]
gi|72135799|ref|XP_801747.1|	48277.36	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 2 [Strongylocentrotus pu
gi|72135801|ref|XP_801813.1|	44075.07	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 3 [Strongylocentrotus pu
gi|72135803|ref|XP_801871.1|	48523.52	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 4 [Strongylocentrotus pu
gi|72135805|ref|XP_801921.1|	47678.61	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 5 [Strongylocentrotus pu
gi|72135807|ref|XP_801962.1|	48169.2	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 6 [Strongylocentrotus pu
gi|72135809|ref|XP_801994.1|	48227.42	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 7 [Strongylocentrotus pu
gi|72135811|ref|XP_802020.1|	48258.44	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 8 [Strongylocentrotus pu
gi|72135813|ref|XP_802037.1|	47943.6	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 9 [Strongylocentrotus pu
gi|72135815|ref|XP_802056.1|	49055.79	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 10 [Strongylocentrotus p
gi|72135817|ref|XP_802068.1|	48177.66	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 11 [Strongylocentrotus p
gi|72135819|ref|XP_802081.1|	49274.95	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 12 [Strongylocentrotus p
gi|72135821|ref|XP_802094.1|	49230.74	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 13 [Strongylocentrotus p
gi|72135823|ref|XP_802102.1|	47170.76	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 14 [Strongylocentrotus p
gi|72135825|ref|XP_780907.1|	47660.1	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 1 [Strongylocentrotus pu

gi|73964734|ref|XP_856667.1|	40634.1	PREDICTED: similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 isoform 2 [Canis familiaris]
gi|73964736|ref|XP_533130.2|	47066.27	PREDICTED: similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 isoform 1 [Canis familiaris]
gi|73966203|ref|XP_864489.1|	36288.67	PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 isoform 3 [Canis famil
gi|73966209|ref|XP_851852.1|	46339.6	PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 isoform 2 [Canis famil
gi|94377842|ref|XP_001002247.1|	31347.14	PREDICTED: similar to Probable ATP-dependent RNA helicase DDX48 (DEAD box protein 48) (Eukaryotic i
gi|83021886|ref|XP_923606.1|	47101.33	PREDICTED: similar to Probable ATP-dependent RNA helicase DDX48 (DEAD box protein 48) (Eukaryotic i
gi|74003454|ref|XP_860356.1|	8212.92	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 3 [Canis familiaris]
gi|74003470|ref|XP_860624.1|	38756.82	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 10 [Canis familiaris]
gi|74003486|ref|XP_860879.1|	34857.81	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 18 [Canis familiaris]
gi|94468792|gb|ABF18245.1|	45871.34	initiation factor EIF-4A [Aedes aegypti]
gi|95102876|gb|ABF51379.1|	47966.12	eukaryotic translation initiation factor 4A [Bombyx mori]
gi|16198386|gb|AAH15842.1|	46573.85	Eukaryotic translation initiation factor 4A, isoform 2 [Homo sapiens]
gi|79313227|ref|NP_001030693.1|	47376.2	EIF4A1; ATP-dependent helicase [Arabidopsis thaliana]
gi|76645556|ref|XP_887831.1|	40664.11	PREDICTED: similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 isoform 2 [Bos taurus]
gi|76645558|ref|XP_887836.1|	47377.4	PREDICTED: similar to DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 isoform 3 [Bos taurus]
gi|109052768|ref|XP_001102775.1|	43115.11	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 5 [Macaca mulatta]
gi|109052771|ref|XP_001102325.1|	41363.15	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 1 [Macaca mulatta]
gi|109052774|ref|XP_001102512.1|	41249.11	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 3 [Macaca mulatta]
gi|109052777|ref|XP_001102692.1|	43446.2	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 4 [Macaca mulatta]
gi|109052780|ref|XP_001103041.1|	37763.36	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 8 [Macaca mulatta]
gi|109092953|ref|XP_001085678.1|	46360.5	PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 isoform 7 [Macaca mula
gi|109092955|ref|XP_001085089.1|	42952.52	PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 isoform 3 [Macaca mula
gi|109092957|ref|XP_001085318.1|	43121.77	PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 isoform 4 [Macaca mula
gi|109092961|ref|XP_001084963.1|	39622.04	PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 isoform 2 [Macaca mula
gi|109092963|ref|XP_001085556.1|	39759.1	PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 isoform 6 [Macaca mula
gi|109092965|ref|XP_001085431.1|	39072.72	PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 isoform 5 [Macaca mula

gi|109113114|ref|XP_001109608.1|	39064.86	PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 isoform 1 [Macaca mula
gi|76691114|ref|XP_877148.1|	17679.88	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 3 [Bos taurus]
gi|76691116|ref|XP_591926.2|	36589.77	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 2 [Bos taurus]
gi|54696620|gb|AAV38682.1|	46465.72	eukaryotic translation initiation factor 4A, isoform 1 [synthetic construct]
gi|55646833|ref|XP_511961.1|	44303.78	PREDICTED: hypothetical protein XP_511961 [Pan troglodytes]
gi|39585896|emb|CAE61310.1|	45882.76	Hypothetical protein CBG05145 [Caenorhabditis briggsae]
gi|39595374|emb|CAE60412.1|	44858.16	Hypothetical protein CBG04018 [Caenorhabditis briggsae]
gi|47201178|emb|CAF89463.1|	17168.52	unnamed protein product [Tetraodon nigroviridis]
gi|47209111|emb|CAF90069.1|	47651.55	unnamed protein product [Tetraodon nigroviridis]
gi|485388|dbj|BAA06336.1|	46592.8	eukaryotic initiation factor 4AII [Homo sapiens]
gi|47227923|emb|CAF97552.1|	41968.88	unnamed protein product [Tetraodon nigroviridis]
gi|303844|dbj|BAA02152.1|	47186.99	eukaryotic initiation factor 4A [Oryza sativa (japonica cultivar-group)]
gi|17221661|dbj|BAB78485.1|	22223.81	eukaryotic initiation factor eIF-4A like protein [Marsupenaeus japonicus]
gi|4503529|ref|NP_001407.1|	46352.64	eukaryotic translation initiation factor 4A, isoform 1 [Homo sapiens]
gi|77404209|ref|NP_001029216.1|	46600.86	eukaryotic translation initiation factor 4A, isoform 2 [Bos taurus]
gi|82705769|ref|XP_727104.1|	45172.21	eukaryotic initiation factor 4a-3 [Plasmodium yoelii yoelii str. 17XNL]
gi|556308|gb|AAA50407.1|	46425.64	protein synthesis initiation factor 4A
gi|2500522|sp|Q41741|IF4A_MAIZE	46848.92	Eukaryotic initiation factor 4A (ATP-dependent RNA helicase eIF4A) (eIF-4A)
gi|2341061|gb|AAB67607.1|	47237.07	translational initiation factor eIF-4A [Zea mays]
gi|62087622|dbj|BAD92258.1|	7756.78	BM-010 variant [Homo sapiens]
gi|62088766|dbj|BAD92830.1|	42845.84	CD68 antigen variant [Homo sapiens]
gi|15277517|gb|AAH12862.1|	47095.26	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 [Mus musculus]
gi|18400210|ref|NP_566469.1|	46960.07	EIF4A1; ATP-dependent helicase [Arabidopsis thaliana]
gi|53792733|dbj|BAD53769.1|	47343.09	eukaryotic initiation factor 4A [Oryza sativa (japonica cultivar-group)]
gi|475216|emb|CAA55641.1|	47098.06	translation initiation factor (eIF-4A) [Nicotiana tabacum]
gi|485987|emb|CAA55737.1|	47157.1	unnamed protein product [Nicotiana tabacum]
gi|485941|emb|CAA55741.1|	40474.54	unnamed protein product [Nicotiana tabacum]
gi|485943|emb|CAA55742.1|	47131.08	unnamed protein product [Nicotiana tabacum]
gi|485945|emb|CAA55739.1|	46972.03	unnamed protein product [Nicotiana tabacum]
gi|31077172|sp|P29562|IF4A1_RABIT	45490.28	Eukaryotic initiation factor 4A-I (ATP-dependent RNA helicase eIF4A-1) (eIF4A-I) (eIF-4A-I)
gi|15221761|ref|NP_175829.1|	47075.05	EIF4A-2; ATP-dependent helicase [Arabidopsis thaliana]
gi|19697|emb|CAA43513.1|	47084.04	nicotiana eukaryotic translation initiation factor 4A [Nicotiana plumbaginifolia]
gi|485949|emb|CAA55738.1|	47152.12	unnamed protein product [Nicotiana tabacum]
gi|475221|emb|CAA55640.1|	47143.09	translation initiation factor (eIF-4A) [Nicotiana tabacum]
gi|485951|emb|CAA55736.1|	47081.02	unnamed protein product [Nicotiana tabacum]
gi|1170509|sp|P41378|IF4A_WHEAT	47183.05	Eukaryotic initiation factor 4A (ATP-dependent RNA helicase eIF4A) (eIF-4A)

gi|24645031|ref|NP_649788.2|	45900.69	eIF4AIII CG7483-PA [Drosophila melanogaster]
gi|5081253|gb|AAD39339.1|	6989.2	eukaryotic translation initiation factor Eif4a2 [Bos taurus]
gi|109118862|ref|XP_001110130.1|	47126.29	PREDICTED: DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 [Macaca mulatta]
gi|77748037|gb|AAI05876.1|	47096.28	Unknown (protein for MGC:125040) [Rattus norvegicus]
gi|58331980|ref|NP_001011139.1|	46233.51	hypothetical protein LOC496556 [Xenopus tropicalis]
gi|55241459|gb|EAA08469.3|	45846.59	ENSANGP00000020417 [Anopheles gambiae str. PEST]
gi|30174635|gb|EAA43551.1|	46029.37	ENSANGP00000023201 [Anopheles gambiae str. PEST]
gi|50905315|ref|XP_464146.1|	47393.09	putative translational initiation factor eIF-4A [Oryza sativa (japonica cultivar-group)]
gi|55297606|dbj|BAD68952.1|	45911.68	putative nicotiana eukaryotic translation initiation factor 4A [Oryza sativa (japonica cultivar-gro
gi|21555870|gb|AAM63951.1|	46972	Eukaryotic initiation factor 4A, putative [Arabidopsis thaliana]
gi|15218574|ref|NP_177417.1|	47082.89	ATP binding / ATP-dependent helicase/ helicase/ nucleic acid binding [Arabidopsis thaliana]
gi|23498289|emb|CAD49261.1|	45341.23	eukaryotic initiation factor, putative [Plasmodium falciparum 3D7]
gi|63139086|gb|AAY33860.1|	47277.04	eukaryotic initiation factor 4A [Pennisetum glaucum]
gi|28277876|gb|AAH45939.1|	46837.14	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 [Danio rerio]
gi|2773184|gb|AAB96704.1|	45623.64	Hypothetical protein F33D11.10 [Caenorhabditis elegans]
gi|31746585|gb|AAK29954.2|	45724.69	Hypothetical protein Y65B4A.6 [Caenorhabditis elegans]
gi|34896594|ref|NP_909641.1|	45941.69	putative translation initiation factor [Oryza sativa]
gi|29169170|gb|AAO66460.1|	11067.57	eukaryotic translation initiation factor 4A isoform 2-like protein [Homo sapiens]
gi|496902|emb|CAA56074.1|	47088.23	translation initiation factor [Homo sapiens]
gi|29294689|gb|AAH48899.1|	46451.77	Eukaryotic translation initiation factor 4A, isoform 1A [Danio rerio]
gi|26374621|dbj|BAB27678.2|	26381.39	unnamed protein product [Mus musculus]
gi|26344810|dbj|BAC36054.1|	47023.24	unnamed protein product [Mus musculus]
gi|109052765|ref|XP_001102871.1|	41492.24	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 6 [Macaca mulatta]
gi|40788956|dbj|BAA04879.2|	47239.37	KIAA0111 [Homo sapiens]
gi|19528517|gb|AAL90373.1|	45868.72	RE50350p [Drosophila melanogaster]
gi|19698881|gb|AAL91176.1|	46946.05	eukaryotic translation initiation factor [Arabidopsis thaliana]
gi|71897163|ref|NP_001025820.1|	47071.18	DEAD (Asp-Glu-Ala-Asp) box polypeptide 48 [Gallus gallus]
gi|45383077|ref|NP_989880.1|	46569.86	eukaryotic translation initiation factor 4A, isoform 2 [Gallus gallus]
gi|57997037|emb|CAI46218.1|	10768.07	hypothetical protein [Homo sapiens]
gi|3776021|emb|CAA09211.1|	50231.52	RNA helicase [Arabidopsis thaliana]
gi|14594802|emb|CAC43286.1|	42107.96	translation initiation factor eIF-4A1 [Arabidopsis thaliana]
gi|109113116|ref|XP_001109752.1|	44691.95	PREDICTED: similar to eukaryotic translation initiation factor 4A, isoform 1 isoform 3 [Macaca mula
gi|7305019|ref|NP_038534.1|	46571.88	eukaryotic translation initiation factor 4A2 [Mus musculus]
gi|15214821|gb|AAH12547.1|	46687.89	Eukaryotic translation initiation factor 4A, isoform 2 [Homo sapiens]
gi|2370591|emb|CAA73167.1|	46188.48	translation initiation factor eIF4A I [Xenopus laevis]
gi|2370593|emb|CAA73168.1|	47130.87	translation initiation factor eIF4A II [Xenopus laevis]
gi|3097266|emb|CAA76677.1|	46184.02	translation initiation factor [Pisum sativum]

gi|18419627|gb|AAL69381.1|	18046.85	putative DEAD/DEAH box helicase [Narcissus pseudonarcissus]
gi|29612461|gb|AAH49427.1|	46321.74	Eukaryotic translation initiation factor 4A, isoform 1B [Danio rerio]
gi|33327280|gb|AAQ08996.1|	11905.74	translation initiation factor 4A [Phaseolus vulgaris]
gi|25809054|gb|AAN74635.1|	47136.05	DEAD box RNA helicase [Pisum sativum]
gi|25809056|gb|AAN74636.1|	46863.79	DEAD box RNA helicase [Pisum sativum]
gi|94378803|ref|XP_980972.1|	47363.27	PREDICTED: similar to Probable ATP-dependent RNA helicase DDX48 (DEAD box protein 48) (Eukaryotic i
gi|38564733|gb|AAR23806.1|	46807.9	initiation factor eIF4A-15 [Helianthus annuus]
gi|94378994|ref|XP_981073.1|	47214.49	PREDICTED: similar to Probable ATP-dependent RNA helicase DDX48 (DEAD box protein 48) (Eukaryotic i
gi|94379208|ref|XP_993761.1|	47109.27	PREDICTED: similar to Probable ATP-dependent RNA helicase DDX48 (DEAD box protein 48) (Eukaryotic i
gi|74003484|ref|XP_860851.1|	38006.49	PREDICTED: similar to eukaryotic translation initiation factor 4A2 isoform 17 [Canis familiaris]
gi|28278797|gb|AAH45237.1|	46057.48	LOC444845 protein [Xenopus laevis]
gi|50603985|gb|AAH77641.1|	46275.55	LOC444845 protein [Xenopus laevis]
gi|76780122|gb|AAI06280.1|	46217.51	LOC443739 protein [Xenopus laevis]
gi|54311504|gb|AAH84859.1|	47349.34	Unknown (protein for MGC:85498) [Xenopus laevis]
gi|34911588|ref|NP_917141.1|	42206.63	putative RNA helicase RH2 [Oryza sativa (japonica cultivar-group)]

53. Group probability: 0.9998. Peptides of the group

IFGVTTLDVVR	66.68	55.5606	1218.697	1219.442	1	2	shared(2)	0	0.9569
RIFGVTTLDVVR	67.93	55.0941	1374.798	1375.471	35	+2,+3	distinct	1	0.9958
VAVLGAAGGIGQPLSLLMK	61	54.2107	1794.044	1794.864	2	2	distinct	0	0.6859

The equivalent proteins include

gi|5929964|gb|AAD56659.1|	36347.11	malate dehydrogenase [Glycine max]

54. Group probability: 0.9998. Peptides of the group

ACNALLLK	66.88	56.8385	901.505	902.794	1	2	shared(3)	0	0.9266
AGWAIMASHR (000000100000)	71.83	55.7416	1098.539	1099.712	8	2	distinct	0	0.9861
VNQIGSITESIEAVTMAK	94.92	53.9105	1889.977	1890.696	2	2	shared(2)	0	0.9987

The equivalent proteins include

gi|40949682|gb|AAR97552.1|	43085.69	enolase [Phytophthora palmivora]

55. Group probability: 0.9998. Peptides of the group

EGNDLYYEMIESGVNK	75.55	54.4166	1859.825	1859.155	6	2	distinct	0	0.9921
TREGNDLYYEMIESGVNK	60.23	53.3298	2116.973	2116.541	3	2	distinct	1	0.9724

The equivalent proteins include

gi|83944756|ref|ZP_00957122.1|	51401.29	ATP synthase subunit B [Oceanicaulis alexandrii HTCC2633]

56. Group probability: 0.9998. Peptides of the group

MGHAGAIVSGGK	83.38	55.6461	1083.549	1084.128	17	+1,+2	shared(2)	0	0.9984
MGIMPGYIHQK (0100000000000)	60.99	55.4363	1273.631	1274.066	14	+2,+3	distinct	0	0.9944

The equivalent proteins include

gi|46400572|emb|CAF24021.1|	31932.44	probable succinate-CoA ligase (ADP-forming) alpha chain [Parachlamydia sp. UWE25]

57. Group probability: 0.9997. Peptides of the group

IRLENEIQTYR	55.92	54.8356	1433.763	1434.654	3	2	shared(2)	1	0.9468
YCVQLSQIQAQISALEEQLQQIR	92.55	51.9821	2745.412	2745.865	6	2	distinct	0	0.9987

The equivalent proteins include

gi|307086|gb|AAA59468.1|	46472.64	keratin-10
gi|109115260|ref|XP_001100571.1|	62234.46	PREDICTED: similar to keratin 10 isoform 2 [Macaca mulatta]
gi|109115262|ref|XP_001100664.1|	57718.17	PREDICTED: similar to keratin 10 isoform 3 [Macaca mulatta]
gi|109115264|ref|XP_001100476.1|	56875.85	PREDICTED: similar to keratin 10 isoform 1 [Macaca mulatta]
gi|547749|sp|P13645|K1C10_HUMAN	59710.96	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)
gi|55645505|ref|XP_523631.1|	94764.75	PREDICTED: similar to keratin 25D; type I inner root sheath specific keratin 25 irs4 [Pan troglodyt
gi|186629|gb|AAA59199.1|	39832.12	keratin 10
gi|40354192|ref|NP_000412.2|	59019.73	keratin 10 [Homo sapiens]

58. Group probability: 0.9997. Peptides of the group

MGHAGAIVSGGK	83.38	55.6461	1083.549	1084.128	17	+1,+2	shared(2)	0	0.9984
LIGPNCPGIIKPGECK	75.63	54.0757	1751.906	1753.396	16	2	distinct	0	0.9922

The equivalent proteins include

gi|21593483|gb|AAM65450.1|	35738.5	succinyl-CoA synthetase, alpha subunit [Arabidopsis thaliana]
gi|92399543|gb|ABE76513.1|	35639.09	mitochondrial putative GDP-forming succinate-CoA ligase alpha subunit [Toxoplasma gondii]
gi|15237260|ref|NP_197716.1|	35750.54	catalytic/ succinate-CoA ligase (GDP-forming) [Arabidopsis thaliana]
gi|78191458|gb|ABB29950.1|	27366.37	succinyl-CoA ligase alpha 1 subunit-like [Solanum tuberosum]
gi|49617539|gb|AAT67464.1|	35751.57	succinyl-CoA ligase alpha 2 subunit [Lycopersicon esculentum]
gi|27357175|gb|AAN86619.1|	35118.32	succinyl-CoA ligase alpha 1 subunit [Lycopersicon esculentum]
gi|15241592|ref|NP_196447.1|	36584.82	catalytic/ succinate-CoA ligase (GDP-forming) [Arabidopsis thaliana]
gi|50938629|ref|XP_478842.1|	34566.85	putative succinyl-CoA ligase alpha subunit [Oryza sativa (japonica cultivar-group)]

59. Group probability: 0.9997. Peptides of the group

VFCMHGGLSPSIDTLDHAR	77.01	53.4291	2111.988	2112.481	3	2	distinct	0	0.9939
YFTDLFDHLPMTALIENR	52.74	53.2308	2195.072	2195.136	2	2	distinct	0	0.9469

The equivalent proteins include

gi|23394371|gb|AAN31475.1|	37225.02	serine/threonine protein phosphatase [Phytophthora infestans]

60. Group probability: 0.9997. Peptides of the group

VAVHEPTLHPNSEELIIGK	57.65	53.4848	2082.111	2082.786	1	2	distinct	0	0.9665
ELDTLLGYDELANVPFLVLGNK	70.07	52.5226	2432.284	2433.759	2	2	distinct	0	0.9901

The equivalent proteins include

gi|23394386|gb|AAN31482.1|	22024.34	GTP binding protein [Phytophthora infestans]

61. Group probability: 0.9996. Peptides of the group

GCIVGPDLSVLNLVVVK	110.38	54.3038	1781.012	1781.607	8	2	distinct	0	0.9996

The equivalent proteins include

gi|38512083|gb|AAH61437.1|	28353.53	40S ribosomal protein S6 [Xenopus tropicalis]

62. Group probability: 0.9996. Peptides of the group

HGVYSWPLCGNAPDALDHGVAAAGYGVYK	107.03	51.1952	3044.424	3045.78	1	3	distinct	0	0.9996

The equivalent proteins include

gi|66270081|gb|AAY43370.1|	42024.12	cathepsin-like cysteine protease [Phytophthora infestans]

63. Group probability: 0.9996. Peptides of the group

NLRPNYVDAIWDVVNWK	67.23	53.3922	2101.074	2101.88	18	+2,+3	distinct	0	0.9996

The equivalent proteins include

gi|108879548|gb|EAT43773.1|	24617.73	superoxide dismutase, Mn [Aedes aegypti]
gi|56417578|gb|AAV90730.1|	24554.64	cytoplasmic superoxide dismutase [Aedes albopictus]

64. Group probability: 0.9996. Peptides of the group

NSWGTYWGENGWFR	68.08	54.2544	1758.754	1760.171	1	2	distinct	0	0.9837
NQHIPKYCGSCWAQGTTSALSDR	61.7	52.17	2636.186	2637.502	6	3	distinct	1	0.9756

The equivalent proteins include

gi|66270083|gb|AAY43371.1|	71834.01	cathepsin-like cysteine protease [Phytophthora infestans]

65. Group probability: 0.9996. Peptides of the group

FFDELPADNTIEATQYLTHVQAGTEPFQGK	44.52	50.5407	3366.604	3368.08	1	3	distinct	0	0.917
KFFDELPADNTIEATQYLTHVQAGTEPFQGK	75.65	50.3024	3494.699	3495.464	6	3	distinct	1	0.9948

The equivalent proteins include

gi|49476326|gb|AAT66504.1|	26598.74	cell 12A endoglucanase [Phytophthora sojae]

66. Group probability: 0.9996. Peptides of the group

SKFDNIYGCR	50.4	55.6057	1258.576	1259.292	5	2	distinct	1	0.9091
WCSCNIFSTQDHAAAAIAR	79.72	53.2605	2177.973	2178.608	1	2	distinct	0	0.9952

The equivalent proteins include

gi|81075407|gb|ABB55380.1|	53522.03	S-adenosyl-L-homocysteine hydrolase-like [Solanum tuberosum]

gi|1710838|sp|P50246|SAHH_MEDSA	53744.18	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)
gi|6094228|sp|P93253|SAHH_MESCR	53771.21	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)
gi|417744|sp|Q01781|SAHH_PETCR	53774.09	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)
gi|68655456|emb|CAJ01706.1|	49960.23	S-adenosyl-L-homocysteine hydrolase [Hordeum vulgare subsp. vulgare]
gi|68655466|emb|CAJ01707.1|	53908.27	putative S-adenosylhomocystein hydrolase 2 [Hordeum vulgare subsp. vulgare]
gi|5917803|gb|AAD56048.1|	53805.24	S-adenosyl-L-homocysteinase [Lupinus luteus]
gi|21362943|sp|Q9SWF5|SAHH_LYCES	53876.21	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase)
gi|21553795|gb|AAM62888.1|	53995.3	adenosylhomocysteinase [Arabidopsis thaliana]
gi|16226776|gb|AAL16259.1|	53779.12	AT3g23810/MYM9_15 [Arabidopsis thaliana]
gi|71000473|dbj|BAE07182.1|	54052.41	S-adenosyl-L-homocysteine hydrolase [Beta vulgaris]
gi|84468348|dbj|BAE71257.1|	53967.29	putative adenosylhomocysteinase [Trifolium pratense]
gi|20453075|gb|AAM19782.1|	53751.13	AT3g23810/MYM9_15 [Arabidopsis thaliana]
gi|15292699|gb|AAK92718.1|	53828.18	putative S-adenosyl-L-homocysteinas protein [Arabidopsis thaliana]
gi|79325087|ref|NP_001031628.1|	48945.96	HOG1 (HOMOLOGY-DEPENDENT GENE SILENCING 1); adenosylhomocysteinase [Arabidopsis thaliana]
gi|77550704|gb|ABA93501.1|	49951.26	Adenosylhomocysteinase, putative, expressed [Oryza sativa (japonica cultivar-group)]
gi|108864354|gb|ABG22475.1|	43453.58	Adenosylhomocysteinase, putative, expressed [Oryza sativa (japonica cultivar-group)]
gi|78102508|sp|P68172|SAHH_NICSY	53640.16	Adenosylhomocysteinase (S-adenosyl-L-homocysteine hydrolase) (AdoHcyase) (Cytokinin binding protein
gi|2160322|dbj|BAA03710.1|	49797.31	cytokinin binding protein CBP57 [Nicotiana sylvestris]
gi|758247|emb|CAA56278.1|	53734.3	S-adenosylhomocysteine hydrolase [Phalaenopsis sp. 'pSPORT1']
gi|15236376|ref|NP_193130.1|	53971.33	HOG1 (HOMOLOGY-DEPENDENT GENE SILENCING 1); adenosylhomocysteinase [Arabidopsis thaliana]
gi|15229522|ref|NP_189023.1|	53809.13	SAHH2; adenosylhomocysteinase [Arabidopsis thaliana]
gi|60266727|gb|AAX15998.1|	53983.37	S-adenosyl-L-homocysteine hydrolase 1 mutant [Arabidopsis thaliana]
gi|60266729|gb|AAX15999.1|	54043.35	S-adenosyl-L-homocysteine hydrolase 1 mutant [Arabidopsis thaliana]
gi|60266731|gb|AAX16000.1|	53970.35	S-adenosyl-L-homocysteine hydrolase 1 mutant [Arabidopsis thaliana]
gi|6601496|gb|AAF19001.1|	34216.23	S-adenosylhomocysteine hydrolase [Allium cepa]
gi|92890678|gb|ABE90446.1|	53868.21	S-adenosyl-L-homocysteine hydrolase [Medicago truncatula]
gi|29691168|gb|AAO89238.1|	53790.19	adenosylhomocysteinase [Medicago truncatula]
gi|60219077|emb|CAI56440.1|	53923.34	S-adenosyl-L-homocysteine hydrolase [Cicer arietinum]
gi|29367605|gb|AAO72664.1|	53860.24	wheat adenosylhomocysteinase-like protein [Oryza sativa (japonica cultivar-group)]

67. Group probability: 0.9996. Peptides of the group

KIAVNLIPFPR	70.88	55.3215	1266.781	1267.527	5	2	shared(8)	1	0.9855
GHYTEGAELIDSVLDVVR	50.71	53.6785	1971.99	1972.76	1	2	shared(7)	0	0.7949
SGPFGQIFRPDNFVFGQTGAGNNWAK	79.99	52.1825	2811.352	2812.533	9	+2,+3	distinct	0	0.9989

The equivalent proteins include

gi|65428041|gb|AAY42541.1|	43730.52	beta-tubulin [Micromonas pusilla]

gi|65428055|gb|AAY42548.1|	43765.39	beta-tubulin [Micromonas pusilla]
gi|65428067|gb|AAY42554.1|	43753.39	beta-tubulin [Micromonas pusilla]
gi|65428069|gb|AAY42555.1|	43749.39	beta-tubulin [Micromonas pusilla]

68. Group probability: 0.9995. Peptides of the group

WTVLHEGTCSR	57.2	55.4057	1344.624	1345.372	5	+1,+2	distinct	0	0.9957
CVFDHENCNSGNK	46.95	54.7382	1579.614	1580.257	2	2	distinct	0	0.8913

The equivalent proteins include

gi|27922927|gb|AAO24652.1|	8659	unknown protein [Phytophthora sojae]

69. Group probability: 0.9995. Peptides of the group

VAVDAAVASSQPHNFLGLNEHGLASIVR	103.9	51.6145	2871.499	2872.958	1	3	distinct	0	0.9995

The equivalent proteins include

gi|23394399|gb|AAN31488.1|	41132.38	DAHP synthase [Phytophthora infestans]

70. Group probability: 0.9995. Peptides of the group

HLGIMVGMNQK (0000000010000)	58.19	55.5997	1242.621	1243.958	1	2	distinct	0	0.7895
SYELPDGNVIVIGNER	105.1	54.2605	1773.89	1774.202	1	2	shared(2)	0	0.9923
YPIEHGIVTNWDDMEK (0000000000000001000)	89.61	53.8859	1945.888	1946.177	23	+2,+3	shared(4)	0	0.9983
VAPEEHPVLLTEAPINPK	81.4	53.6978	1953.057	1953.885	13	2	shared(10)	0	0.9887
TTGCVLDSGDGVSHTVPIYEGYALPHAIVR	72.64	50.9286	3183.566	3184.46	9	+2,+3	shared(3)	0	0.9878

The equivalent proteins include

gi|3181|emb|CAA33907.1|	42303.02	unnamed protein product [Phytophthora megasperma]

71. Group probability: 0.9995. Peptides of the group

RVFGITTLDVVR	49.49	55.1643	1374.798	1374.764	4	+2,+3	distinct	1	0.9518
VAVLGAAGGIGQPMSLLLK	99.61	54.2107	1794.044	1794.864	3	2	distinct	0	0.9894

The equivalent proteins include

gi|57228274|gb|AAW44731.1|	35807.96	malate dehydrogenase, putative [Cryptococcus neoformans var. neoformans JEC21]

72. Group probability: 0.9994. Peptides of the group

VGLTGLTVAEYFR	105.09	54.934	1424.766	1425.451	8	2	shared(3)	0	0.9864
IPSAVGYQPTLATDLGALQER	110.91	53.1813	2199.153	2200.244	2	+2,+3	shared(2)	0	1

The equivalent proteins include

gi|89286974|gb|EAR84968.1|	63880.63	ATP synthase beta chain, mitochondrial precursor, putative [Tetrahymena thermophila SB210]

73. Group probability: 0.9994. Peptides of the group

KIAVNLIPFPR	70.88	55.3215	1266.781	1267.527	5	2	shared(8)	1	0.9855
EIVHIQGGQCGNQIGAK	70.47	54.3006	1807.9	1808.547	13	2	shared(3)	0	0.9519
LTTPTYGDLNHLVCAAMSGITTCLR	82.51	51.98	2764.335	2765.271	4	2	shared(2)	0	0.997
FWEVISDEHGVDPTGSYHGDSDLQLER	57.7	51.1678	3087.385	3088.854	1	3	shared(3)	0	0.9705
EAESCDCIQGFQLTHSLGGGTGSGMGTLLISK	75.02	50.7063	3310.527	3311.459	11	3	shared(4)	0	0.9947

The equivalent proteins include

gi|6653279|gb|AAF22655.1|	50702.01	beta-tubulin [Pythium ultimum]

74. Group probability: 0.9993. Peptides of the group

RTIQFVDWCPTGFK	68.04	54.1689	1753.861	1754.812	2	2	shared(3)	1	0.9837
IHFMLSSYAPVISAEK (000010000000000000)	84.73	54.3047	1807.918	1808.932	1	2	shared(2)	0	0.9876
QIYHPEQLISGKEDAANNYAR	44.31	52.6392	2416.177	2417.298	4	+2,+3	distinct	1	0.9761

The equivalent proteins include

gi|57903355|gb|AAW58089.1|	45228.32	alpha-tubulin [Apodachlya brachynema]
gi|57903369|gb|AAW58096.1|	45079.49	alpha-tubulin [Phytophthora palmivora]
gi|57903371|gb|AAW58097.1|	45063.5	alpha-tubulin [Plectospira myriandra]
gi|57903375|gb|AAW58099.1|	45054.51	alpha-tubulin [Pythium graminicola]
gi|57903377|gb|AAW58100.1|	45277.65	alpha-tubulin [Thraustotheca clavata]
gi|13649511|gb|AAK37433.1|	42984.51	alpha-tubulin [Reclinomonas americana]

75. Group probability: 0.9993. Peptides of the group

LGANSLLDIVVFGR	85.27	54.9407	1472.835	1473.587	5	2	shared(2)	0	0.9963
GSDWLGDQDAIHYMCR	71.32	54.0505	1922.804	1923.786	1	2	distinct	0	0.9886

The equivalent proteins include

gi|71005306|ref|XP_757319.1|	71954.79	hypothetical protein UM01172.1 [Ustilago maydis 521]
gi|57228890|gb|AAW45324.1|	70502.13	succinate dehydrogenase flavoprotein subunit precursor, putative [Cryptococcus neoformans var. neof

76. Group probability: 0.9993. Peptides of the group

LGANSLLDIVVFGR	85.27	54.9407	1472.835	1473.587	5	2	shared(2)	0	0.9963
FHSKNTVLATGGYGR	71.1	54.5765	1606.822	1607.473	7	2	distinct	1	0.9879

The equivalent proteins include

gi|66505480|ref|XP_623065.1|	73271.54	PREDICTED: similar to ENSANGP00000010243 [Apis mellifera]

77. Group probability: 0.9993. Peptides of the group

AEGADAIHPGYGFLSENAAFAR	71.58	53.0902	2263.066	2264.538	7	+2,+3	distinct	0	0.9993

The equivalent proteins include

gi|89099591|ref|ZP_01172466.1|	50699.49	acetyl-CoA carboxylase [Bacillus sp. NRRL B-14911]

78. Group probability: 0.9992. Peptides of the group

NMSVIAHVDHGK (00100000000000)	76.73	55.3766	1306.645	1307.194	11	2	distinct	0	0.9916
IGSPLFSVKAHLPVLESFGFTADLR	44.88	52.0145	2700.464	2700.796	1	3	distinct	1	0.901

The equivalent proteins include

gi|66805999|ref|XP_636721.1|	93511.92	elongation factor 2 [Dictyostelium discoideum AX4]

79. Group probability: 0.9991. Peptides of the group

DVEGQDVLLFVDNIFR	100.43	54.0563	1877.952	1879.303	48	2	distinct	0	0.9991

The equivalent proteins include

gi|71547504|ref|ZP_00668114.1|	50694.94	ATP synthase F1, beta subunit [Syntrophobacter fumaroxidans MPOB]
gi|85858477|ref|YP_460679.1|	51008.29	ATP synthase beta chain [Syntrophus aciditrophicus SB]
gi|18123|emb|CAA43808.1|	61954.03	H(+)-transporting ATP synthase; beta subunit of mitochondrial ATP synthase [Chlamydomonas reinhardt

80. Group probability: 0.9989. Peptides of the group

IINEPTAAAIAYGIDKK	113.47	54.7761	1786.983	1787.369	22	2	shared(6)	1	0.9981
EVLLLDVTPLSLGIETLGGVMTK (0000000000000000000001000)	122.84	52.8345	2413.339	2413.876	45	2	distinct	0	0.9963

The equivalent proteins include

gi|76884577|gb|ABA59258.1|	70024.14	Heat shock protein Hsp70 [Nitrosococcus oceani ATCC 19707]

81. Group probability: 0.9989. Peptides of the group

LNLLKLAPGGHIGR	71.61	54.9851	1457.883	1458.974	34	+2,+3	distinct	1	0.9989

The equivalent proteins include

gi|15293869|gb|AAK95127.1|	44099.05	ribosomal protein L4 [Ictalurus punctatus]
gi|4887131|gb|AAD32206.1|	44898.05	60S ribosomal protein L1 [Prunus armeniaca]
gi|84468330|dbj|BAE71248.1|	44765.09	putative 60S ribosomal protein L1 [Trifolium pratense]
gi|84468414|dbj|BAE71290.1|	44778.09	putative 60S ribosomal protein L1 [Trifolium pratense]
gi|92894088|gb|ABE92091.1|	44992.22	Ribosomal protein L4/L1e [Medicago truncatula]
gi|79313167|ref|NP_001030663.1|	44659.02	structural constituent of ribosome [Arabidopsis thaliana]
gi|15232723|ref|NP_187574.1|	44788.06	structural constituent of ribosome [Arabidopsis thaliana]
gi|77999245|gb|ABB16969.1|	45060.16	unknown [Solanum tuberosum]
gi|39589455|emb|CAE74484.1|	38657.2	Hypothetical protein CBG22235 [Caenorhabditis briggsae]
gi|66817212|ref|XP_642484.1|	40278.16	60S ribosomal protein L4 [Dictyostelium discoideum]
gi|17508669|ref|NP_491416.1|	38749.21	Ribosomal Protein, Large subunit family member (rpl-4) [Caenorhabditis elegans]
gi|15242558|ref|NP_195907.1|	44807.92	structural constituent of ribosome [Arabidopsis thaliana]
gi|26450328|dbj|BAC42280.1|	44810.87	putative 60S ribosomal protein [Arabidopsis thaliana]
gi|21593543|gb|AAM65510.1|	44744.06	60S ribosomal protein L4-B (L1) [Arabidopsis thaliana]
gi|28828239|gb|AAO50916.1|	40203.12	similar to Arabidopsis thaliana (Mouse-ear cress). AT3g09630/F11F8_22 [Dictyostelium discoideum]
gi|22137186|gb|AAM91438.1|	34448.7	AT5g02870/F9G14_180 [Arabidopsis thaliana]
gi|54609195|gb|AAV34813.1|	48195.24	ribosomal protein L4 [Bombyx mori]
gi|7630164|emb|CAB88236.1|	39942.81	rpl4 [Schizosaccharomyces pombe]
gi|3810827|emb|CAA21788.1|	39799.75	SPBP8B7.03c [Schizosaccharomyces pombe]
gi|71017629|ref|XP_759045.1|	36494.8	hypothetical protein UM02898.1 [Ustilago maydis 521]
gi|312177|emb|CAA51666.1|	38901.11	ribosomal protein L2 [Schizosaccharomyces pombe]

82. Group probability: 0.9989. Peptides of the group

GPYESGSGHSSGLGHR	97.92	54.5662	1583.708	1584.078	4	2	distinct	0	0.9989

The equivalent proteins include

gi|88952458|ref|XP_942310.1|	197208.28	PREDICTED: similar to Hornerin [Homo sapiens]
gi|28557150|dbj|BAC57496.1|	48796.73	hornerin [Homo sapiens]
gi|55588478|ref|XP_524874.1|	126987.98	PREDICTED: hypothetical protein XP_524874 [Pan troglodytes]
gi|57546919|tpd|FAA00004.1|	283115.88	TPA: Hornerin [Homo sapiens]
gi|57864582|ref|NP_001009931.1|	283139.96	hornerin [Homo sapiens]
gi|40795897|gb|AAR91619.1|	283110.9	hornerin precursor [Homo sapiens]

83. Group probability: 0.9987. Peptides of the group

TVEAEAAHGTVTR	67.95	55.2082	1340.668	1341.53	1	2	distinct	0	0.8681
FKDIFQEVYENEFK	73.99	54.1207	1834.878	1835.5	5	2	distinct	1	0.9903

The equivalent proteins include

gi|83858780|ref|ZP_00952302.1|	45770.19	isocitrate dehydrogenase [Oceanicaulis alexandrii HTCC2633]

84. Group probability: 0.9985. Peptides of the group

GIPLIFLQNITGFMVGK	93.89	54.0141	1847.038	1847.963	25	2	distinct	0	0.9985

The equivalent proteins include

gi|34497219|ref|NP_901434.1|	57419.54	probable propionyl-CoA carboxylase (beta subunit) [Chromobacterium violaceum ATCC 12472]
gi|82738392|ref|ZP_00901226.1|	57932.64	3-methylcrotonyl-CoA carboxylase, beta subunit, putative [Pseudomonas putida F1]
gi|84326696|ref|ZP_00974721.1|	58337.82	COG4799: Acetyl-CoA carboxylase, carboxyltransferase component (subunits alpha and beta) [Pseudomon
gi|88796986|ref|ZP_01112576.1|	58166.44	acetyl-CoA carboxylase beta chain [Reinekea sp. MED297]
gi|104782430|ref|YP_608928.1|	57968.55	3-methylcrotonyl-CoA carboxylase, beta subunit [Pseudomonas entomophila L48]
gi|26990766|ref|NP_746191.1|	57924.64	3-methylcrotonyl-CoA carboxylase, beta subunit, putative [Pseudomonas putida KT2440]

85. Group probability: 0.9984. Peptides of the group

AALVYGQMNEPPGAR	63.56	54.8744	1572.772	1573.149	1	2	shared(4)	0	0.9261
LVLEVAQHLGEDTVR	68.18	54.8144	1677.905	1677.486	18	+2,+3	distinct	0	0.9969

The equivalent proteins include

gi|23348660|gb|AAN30694.1|	54813.6	ATP synthase F1, beta subunit [Brucella suis 1330]
gi|62196796|gb|AAX75096.1|	54813.6	AtpD, ATP synthase F1, beta subunit [Brucella abortus biovar 1 str. 9-941]

86. Group probability: 0.9984. Peptides of the group

LLREELQLLQEPGSYVGEVVK	61.49	52.7612	2398.311	2399.497	3	+2,+3	distinct	1	0.9984

The equivalent proteins include

gi|71004628|ref|XP_756980.1|	46748.7	hypothetical protein UM00833.1 [Ustilago maydis 521]

87. Group probability: 0.9983. Peptides of the group

ILTDYGFEGHPLRK	68.88	54.6247	1644.862	1645.394	3	2	distinct	1	0.9847
DFPLSGFLEVFYNELK	45.53	53.8647	1916.956	1917.331	1	2	distinct	0	0.8913

The equivalent proteins include

gi|9695380|ref|NP_037602.1|	22914.22	NADH dehydrogenase subunit 9 [Phytophthora infestans]
gi|7545239|gb|AAA32025.2|	22795.14	NADH dehydrogenase [Phytophthora megasperma]
gi|56684557|gb|AAW21977.1|	22560.03	NADH dehydrogenase subunit 9 [Plasmopara viticola]

88. Group probability: 0.9982. Peptides of the group

TVQVVPHVTDAIQDWIER	91.53	53.311	2105.09	2105.917	1	2	distinct	0	0.9982

The equivalent proteins include

gi|15221525|ref|NP_174368.1|	66371.44	CTP synthase/ catalytic [Arabidopsis thaliana]
gi|4926827|gb|AAD32937.1|	72835.09	T17H7.12 [Arabidopsis thaliana]

89. Group probability: 0.9982. Peptides of the group

VGLTGLTVAEYFR	105.09	54.934	1424.766	1425.451	8	2	shared(3)	0	0.9864
AALVYGQMNEPPGAR	63.56	54.8744	1572.772	1573.149	1	2	shared(4)	0	0.9261
LVLEVAQHLGENTVR	99.26	54.5381	1676.921	1677.82	31	+2,+3	shared(2)	0	0.9998

The equivalent proteins include

gi|68193203|gb|EAN07855.1|	55025.59	ATP synthase F1, beta subunit [Mesorhizobium sp. BNC1]
gi|14024205|dbj|BAB50809.1|	50858.25	ATP synthase beta subunit [Mesorhizobium loti MAFF303099]

90. Group probability: 0.9982. Peptides of the group

VFSPHVLNLTLVDLPGITK	90.72	53.4159	2062.183	2063.219	5	2	distinct	0	0.9982

The equivalent proteins include

gi|710602|gb|AAA99998.1|	85764.53	dynamin-related protein
gi|6323028|ref|NP_013100.1|	85489.39	Dynamin-related GTPase required for mitochondrial fission and the maintenance of mitochondrial morp

91. Group probability: 0.9981. Peptides of the group

EIVHIQGGQCGNQIGAK	70.47	54.3006	1807.9	1808.547	13	2	shared(3)	0	0.9519
GHYTEGAELIDSVLDVVR	50.71	53.6785	1971.99	1972.76	1	2	shared(7)	0	0.7949
AGPYGQIFRPDNFVFGQTGAGNNWAK	79.99	52.1825	2811.352	2812.533	7	+2,+3	shared(3)	0	0.9986
FWEVISDEHGVDPTGSYHGDSDLQLER	57.7	51.1678	3087.385	3088.854	1	3	shared(3)	0	0.9705
EAESCDCIQGFQLTHSLGGGTGSGMGTLLISK	75.02	50.7063	3310.527	3311.459	11	3	shared(4)	0	0.9947

The equivalent proteins include

gi|2951981|gb|AAC05441.1|	50574.03	beta tubulin [Phytophthora cinnamomi]
gi|135475|sp|P20802|TBB_ACHKL	50445.97	Tubulin beta chain (Beta tubulin)

92. Group probability: 0.9981. Peptides of the group

TLYNELEVVEGMK	93.17	54.6158	1523.754	1523.955	1	2	distinct	0	0.9981

The equivalent proteins include

gi|108862364|gb|ABG21928.1|	14425.6	expressed protein [Oryza sativa (japonica cultivar-group)]
gi|24637539|gb|AAN63805.1|	58069.63	heat shock protein 60 [Prunus dulcis]
gi|56199652|gb|AAV84293.1|	20341.69	60 kDa chaperonin [Pythium aphanidermatum]

93. Group probability: 0.9981. Peptides of the group

SIVHPSYNSNTLNNDIMLIK (00000000000000000010000)	72.88	53.0635	2272.152	2272.395	15	+2,+3	distinct	0	0.9981

The equivalent proteins include

gi|1421532|pdb|1TGB|	24658.8	Trypsinogen-Ca From Peg
gi|230765|pdb|2TLD|E	23555.36	Chain E, Bovine Trypsin (E.C.3.4.21.4) Complex With A Modified SSI (Streptomyces Subtilisin Inhibit
gi|2392803|pdb|5PTP|	23998.54	Structure Of Hydrolase (Serine Proteinase)
gi|5542503|pdb|1ZZZ|A	25388.25	Chain A, Trypsin Inhibitors With Rigid Tripeptidyl Aldehydes
gi|13096615|pdb|1G3E|A	24562.78	Chain A, Bovine Beta-Trypsin Bound To Para-Amidino Schiff-Base Copper (Ii) Chelate
gi|34811715|pdb|1HJ9|A	23972.49	Chain A, Atomic Resolution Structures Of Trypsin Provide Insight Into Structural Radiation Damage
gi|34810822|pdb|1OPH|B	26076.68	Chain B, Non-Covalent Complex Between Alpha-1-Pi-Pittsburgh And S195a Trypsin
gi|49259462|pdb|1V2P|T	23979.59	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssyi)bt.A4
gi|49259463|pdb|1V2Q|T	24002.6	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Sswi)bt.B4
gi|49259464|pdb|1V2R|T	23972.63	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssri)bt.B4
gi|49259466|pdb|1V2T|T	24005.6	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssfi.Glu)bt.B4
gi|49259469|pdb|1V2W|T	23887.56	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssai)bt.B4
gi|71042446|pdb|1ZR0|C	23960.59	Chain C, Crystal Structure Of Kunitz Domain 1 Of Tissue Factor Pathway Inhibitor-2 With Bovine Tryp
gi|88193016|pdb|2FI4|E	23971.53	Chain E, Crystal Structure Of A Bpti Variant (Cys14->ser) In Complex With Trypsin
gi|88193018|pdb|2FI5|E	24086.56	Chain E, Crystal Structure Of A Bpti Variant (Cys38->ser) In Complex With Trypsin
gi|2507249|sp|P00760|TRY1_BOVIN	26092.68	Cationic trypsin precursor (Beta-trypsin) [Contains: Alpha-trypsin chain 1; Alpha-trypsin chain 2]
gi|76615876|ref|XP_883769.1|	26246.67	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 2 [Bos taurus]
gi|76615878|ref|XP_883804.1|	26537.88	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 3 [Bos taurus]

gi|76615880|ref|XP_871686.1|	26438.81	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 1 [Bos taurus]
gi|76615882|ref|XP_883865.1|	26551.93	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 2 [Bos taurus]
gi|61873128|ref|XP_584594.1|	26452.86	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 1 [Bos taurus]
gi|67549|pir||TRBOTR	24661.84	trypsin (EC 3.4.21.4) precursor - bovine
gi|90109720|pdb|2FX6|A	23974.57	Chain A, Bovine Trypsin Complexed With 2-Aminobenzamidazole

94. Group probability: 0.9981. Peptides of the group

LMCASTACNTMITK (0010000000000000)	92.46	54.9945	1600.708	1601.274	18	2	distinct	0	0.9981

The equivalent proteins include

gi|68137499|gb|AAY85678.1|	12640.04	acidic elicitin [Phytophthora alni subsp. alni]
gi|68137505|gb|AAY85681.1|	12606.05	acidic elicitin [Phytophthora alni subsp. alni]
gi|68137515|gb|AAY85686.1|	12530.02	acidic elicitin [Phytophthora fragariae var. fragariae]
gi|68137517|gb|AAY85687.1|	12564.01	acidic elicitin [Phytophthora fragariae var. fragariae]
gi|68137519|gb|AAY85688.1|	12546.02	acidic elicitin [Phytophthora fragariae var. rubi]
gi|68137521|gb|AAY85689.1|	12580	acidic elicitin [Phytophthora fragariae var. rubi]
gi|27462826|gb|AAO15602.1|	10501.94	alpha-elicitin capsicein [Phytophthora capsici]
gi|4138370|emb|CAA07710.1|	10519.91	sojein 1 protein [Phytophthora sojae]
gi|4138376|emb|CAA07713.1|	10461.91	sojein 4 protein [Phytophthora sojae]
gi|37783440|gb|AAP43023.1|	12496.96	elicitin [Phytophthora capsici]
gi|37783442|gb|AAP43024.1|	11767.76	elicitin [Phytophthora palmivora]

95. Group probability: 0.9979. Peptides of the group

VLGGEGGHGVIILSPR	90.86	54.7248	1559.878	1560.568	2	2	distinct	0	0.9979

The equivalent proteins include

gi|17742128|gb|AAL44517.1|	42698.08	phosphoserine aminotransferase [Agrobacterium tumefaciens str. C58]

96. Group probability: 0.9977. Peptides of the group

AALVYGQMNEPPGAR	63.56	54.8744	1572.772	1573.149	1	2	shared(4)	0	0.9261
IPSAVGYQPTLATDLGALQER	110.91	53.1813	2199.153	2200.244	2	+2,+3	shared(2)	0	1

The equivalent proteins include

gi|82793401|ref|XP_728025.1|	58109.38	ATP synthase F1subunit beta [Plasmodium yoelii yoelii str. 17XNL]
gi|23509039|ref|NP_701707.1|	58585.53	ATP synthase beta chain, mitochondrial precursor, putative [Plasmodium falciparum 3D7]

97. Group probability: 0.9977. Peptides of the group

LAGTQVFGHSGK	91.58	55.7461	1200.625	1201.161	10	2	distinct	0	0.9977

The equivalent proteins include

gi|66270077|gb|AAY43368.1|	56259.23	cysteine protease [Phytophthora infestans]

98. Group probability: 0.9974. Peptides of the group

EHAALEPR	45.39	55.5301	921.467	922.495	1	2	distinct	0	0.8551
CTTDHISMAGPWLK	67.23	54.7398	1615.749	1616.236	7	2	distinct	0	0.9823

The equivalent proteins include

gi|1351858|sp|P49609|ACON_GRAVE	84134.28	Aconitate hydratase, mitochondrial precursor (Citrate hydro-lyase) (Aconitase)
gi|66815883|ref|XP_641958.1|	83888.94	aconitase [Dictyostelium discoideum]
gi|4029334|emb|CAA76360.1|	82698.92	aconitate hydratase [Piromyces sp. E2]

99. Group probability: 0.9974. Peptides of the group

YVGSMVSDIHR	44.81	55.5853	1262.608	1263.203	1	2	distinct	0	0.8568
ILDLVPTDIHQR	54.68	54.9553	1418.788	1419.159	5	+2,+3	distinct	0	0.9821

The equivalent proteins include

gi|23394363|gb|AAN31471.1|	36904.33	fructose-1 6-biphosphatase [Phytophthora infestans]

100. Group probability: 0.9974. Peptides of the group

TFIAIKPDGVQR	46.94	55.4401	1343.756	1344.869	1	2	distinct	0	0.8857
NVCHGSDSVESAEK	64.42	54.8771	1517.642	1517.955	2	2	distinct	0	0.9773

The equivalent proteins include

gi|50306511|ref|XP_453229.1|	16961.93	unnamed protein product [Kluyveromyces lactis]

gi|50424677|ref|XP_460928.1|	17021.79	hypothetical protein DEHA0F14113g [Debaryomyces hansenii CBS767]

101. Group probability: 0.9974. Peptides of the group

TPGPGAQSALR	53.06	55.3723	1053.557	1054.389	1	2	distinct	0	0.9308
TKTPGPGAQSALR	59.17	55.2281	1282.699	1283.654	3	2	distinct	1	0.9624

The equivalent proteins include

gi|82623421|gb|ABB87125.1|	10677.75	hypothetical protein [Solanum tuberosum]
gi|83284009|gb|ABC01912.1|	16391.65	ribosomal protein S14-like protein [Solanum tuberosum]
gi|1762931|gb|AAC49968.1|	6995.95	ribosomal protein S14 [Nicotiana tabacum]
gi|61369149|gb|AAX43292.1|	16546.68	ribosomal protein S14 [synthetic construct]
gi|61654728|gb|AAX48890.1|	16282.67	S14 [Suberites domuncula]
gi|74268249|gb|AAI02537.1|	17050.85	Unknown (protein for MGC:127734) [Bos taurus]
gi|74226871|dbj|BAE27080.1|	16506.6	unnamed protein product [Mus musculus]
gi|91091798|ref|XP_970498.1|	16283.68	PREDICTED: similar to 40S ribosomal protein S14 [Tribolium castaneum]
gi|72015985|ref|XP_780390.1|	16159.63	PREDICTED: similar to 40S ribosomal protein S14 [Strongylocentrotus purpuratus]
gi|70909537|emb|CAJ17191.1|	16328.65	ribosomal protein S14e [Sphaerius sp. APV-2005]
gi|94468908|gb|ABF18303.1|	16302.67	40S ribosomal protein S141 [Aedes aegypti]
gi|109079317|ref|XP_001099589.1|	14487.5	PREDICTED: similar to ribosomal protein S14 [Macaca mulatta]
gi|76680427|ref|XP_584177.2|	16463.57	PREDICTED: similar to ribosomal protein S14 [Bos taurus]
gi|55625094|ref|XP_518037.1|	22706.67	PREDICTED: similar to 40S ribosomal protein S14 [Pan troglodytes]
gi|77745450|gb|ABB02624.1|	16405.67	ribosomal protein S14-like [Solanum tuberosum]
gi|71895291|ref|NP_001025790.1|	16433.6	ribosomal protein S14 [Gallus gallus]
gi|38048289|gb|AAR10047.1|	16311.71	similar to Drosophila melanogaster RpS14a [Drosophila yakuba]
gi|463857|gb|AAB60274.1|	16348.67	ribosomal protein S14
gi|730633|sp|Q08699|RS14_PODCA	16182.54	40S ribosomal protein S14
gi|5441523|emb|CAB46816.1|	8441.65	Ribosomal protein S14 [Canis familiaris]
gi|3097244|emb|CAA69615.1|	16461.6	ribosomal protein S14 [Mus musculus]
gi|458981|gb|AAC48301.1|	16352.69	Ribosomal protein, small subunit protein 14 [Caenorhabditis elegans]
gi|131772|sp|P19950|RS141_MAIZE	16304.65	40S ribosomal protein S14 (Clone MCH1)
gi|131773|sp|P19951|RS142_MAIZE	16309.64	40S ribosomal protein S14 (Clone MCH2)
gi|57129|emb|CAA33143.1|	16419.58	unnamed protein product [Rattus norvegicus]
gi|4588920|gb|AAD26263.1|	16276.64	ribosomal protein S14 [Stomoxys calcitrans]
gi|28189929|dbj|BAC56579.1|	15838.16	similar to ribosomal protein S14 [Bos taurus]
gi|15227588|ref|NP_181158.1|	16303.69	structural constituent of ribosome [Arabidopsis thaliana]
gi|15229775|ref|NP_187758.1|	16319.68	structural constituent of ribosome [Arabidopsis thaliana]
gi|15231260|ref|NP_190826.1|	16284.71	structural constituent of ribosome [Arabidopsis thaliana]
gi|55242989|gb|EAA06897.2|	16359.69	ENSANGP00000019074 [Anopheles gambiae str. PEST]
gi|55242445|gb|EAA08220.2|	16331.66	ENSANGP00000015417 [Anopheles gambiae str. PEST]
gi|62083507|gb|AAX62478.1|	16351.68	ribosomal protein S14 [Lysiphlebus testaceipes]
gi|50905421|ref|XP_464199.1|	16409.68	putative ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]
gi|54609311|gb|AAV34871.1|	16207.65	ribosomal protein S14 [Bombyx mori]
gi|50924099|ref|XP_472410.1|	16466.71	OJ000126_13.9 [Oryza sativa (japonica cultivar-group)]
gi|15213816|gb|AAK92183.1|	16264.67	ribosomal protein S14 [Spodoptera frugiperda]
gi|28436071|gb|AAO41731.1|	16361.64	cytoplasmic ribosomal protein S14 [Brassica napus]
gi|37748505|gb|AAH59561.1|	16405.59	Ribosomal protein S14 [Danio rerio]

gi|62362200|gb|AAX81537.1|	16046.47	S14e ribosomal protein-like protein [Philodina sp. NPS-2005]
gi|51011526|gb|AAT92172.1|	16166.56	ribosomal protein S14 [Ixodes pacificus]
gi|50344488|emb|CAH04330.1|	16267.68	S14e ribosomal protein [Dascillus cervinus]
gi|15294039|gb|AAK95196.1|	16376.56	40S ribosomal protein S14 [Ictalurus punctatus]
gi|94399883|ref|XP_001001619.1|	16537.67	PREDICTED: similar to ribosomal protein S14 [Mus musculus]
gi|82958328|ref|XP_913463.1|	16551.69	PREDICTED: similar to ribosomal protein S14 isoform 1 [Mus musculus]
gi|47935073|gb|AAT39883.1|	16218.46	ribosomal protein S14 [Branchiostoma belcheri tsingtaunese]
gi|51863346|gb|AAU11819.1|	16149.64	ribosomal protein S14 [Bombyx mori]
gi|51873216|gb|AAU12568.1|	12918.6	ribosomal protein S14 [Felis catus]

102. Group probability: 0.9972. Peptides of the group

YPNEHGIVTNWDDMEK	76.88	53.8456	1946.847	1946.612	11	+2,+3	distinct	0	0.9955
VAPEEHPVLLTEAPINPK	81.4	53.6978	1953.057	1953.885	13	2	shared(10)	0	0.9887

The equivalent proteins include

gi|109507063|ref|XP_001058533.1|	42108.88	PREDICTED: similar to Actin, cytoplasmic 2 (Gamma-actin) [Rattus norvegicus]

103. Group probability: 0.9971. Peptides of the group

LFQVEYAMEAINNAGSAVGILAK	83.6	52.7435	2408.241	2408.587	2	2	distinct	0	0.9971

The equivalent proteins include

gi|23394356|gb|AAN31468.1|	27615.7	proteasome subunit [Phytophthora infestans]

104. Group probability: 0.9966. Peptides of the group

IIGATNPAESPPGTIR	44.96	54.5892	1592.852	1594.088	1	2	distinct	0	0.884
KIIGATNPAESPPGTIR	60	54.232	1720.947	1721.467	9	2	distinct	1	0.9703

The equivalent proteins include

gi|2498076|sp|Q96559|NDK_HELAN	16206.47	Nucleoside diphosphate kinase (NDK) (NDP kinase)

105. Group probability: 0.9965. Peptides of the group

FGFVHLSAGDLLR	86.24	55.0134	1430.767	1431.178	7	2	distinct	0	0.9965

The equivalent proteins include

gi|72045720|ref|XP_786761.1|	21883.82	PREDICTED: similar to UMP-CMP kinase (Cytidylate kinase) (Deoxycytidylate kinase) (Cytidine monopho

106. Group probability: 0.9963. Peptides of the group

DILLLDVTPLSLGIETLGGVMTK (0000000000000000000001000)	122.84	52.8345	2413.339	2413.876	45	2	distinct	0	0.9963

The equivalent proteins include

gi|77747092|gb|ABB02935.1|	42049.98	DnaK [Candidatus Legionella jeonii]

107. Group probability: 0.9963. Peptides of the group

DILLLDVTPLSLGIETLGGVFTK	122.84	52.8345	2413.372	2413.876	136	2	distinct	0	0.9963

The equivalent proteins include

gi|82499691|ref|ZP_00885130.1|	66524.89	Heat shock protein Hsp70 [Caldicellulosiruptor saccharolyticus DSM 8903]
gi|76796920|ref|ZP_00779268.1|	66531.47	Heat shock protein Hsp70 [Thermoanaerobacter ethanolicus ATCC 33223]
gi|20515960|gb|AAM24211.1|	66045.37	Molecular chaperone [Thermoanaerobacter tengcongensis MB4]
gi|67873258|ref|ZP_00503537.1|	65755.18	Heat shock protein Hsp70 [Clostridium thermocellum ATCC 27405]
gi|22298333|ref|NP_681580.1|	70732.2	molecular chaperone DnaK [Thermosynechococcus elongatus BP-1]

108. Group probability: 0.9963. Peptides of the group

KVVISAPPK	67.38	55.1167	937.596	938.69	7	+1,+2	distinct	1	0.9963

The equivalent proteins include

gi|7274154|gb|AAF44719.1|	36307.1	glyceraldehyde-3-phosphate dehydrogenase [Achlya bisexualis]
gi|34329035|gb|AAQ63762.1|	34176.08	glyceraldehyde-3-phosphate dehydrogenase [Thraustotheca clavata]

109. Group probability: 0.9962. Peptides of the group

KLFHPEQLISGK	45.03	54.9397	1395.787	1396.404	1	2	distinct	1	0.8662
RTIQFVDWCPTGFK	68.04	54.1689	1753.861	1754.812	2	2	shared(3)	1	0.9837
IHFMLSSYAPVISAEK (000010000000000000)	84.73	54.3047	1807.918	1808.932	1	2	shared(2)	0	0.9876

The equivalent proteins include

gi|82400128|gb|ABB72803.1|	50580.75	alpha-tubulin-like protein [Solanum tuberosum]
gi|8928408|sp|Q9ZRB7|TBA_WHEAT	50395.6	Tubulin alpha chain
gi|1556446|gb|AAB08791.1|	50265.56	alpha tubulin [Hordeum vulgare]
gi|84105379|gb|ABC54661.1|	42854.46	alpha tubulin 1 [Trimastix marina]
gi|9965991|gb|AAG02564.1|	50293.58	alpha-tubulin [Daucus carota]
gi|3163944|emb|CAA06618.1|	50383.63	alpha-tubulin 1 [Eleusine indica]
gi|3163946|emb|CAA06619.1|	50395.67	alpha-tubulin 1 [Eleusine indica]
gi|1619297|emb|CAA69724.1|	50353.58	alpha-tubulin 2 [Hordeum vulgare subsp. vulgare]
gi|578450|emb|CAA77810.1|	50273.62	alpha-Tubulin [Oxytricha granulifera]
gi|71090024|gb|AAZ23863.1|	50082.49	alpha-tubulin [Sterkiella histriomuscorum]
gi|92896308|gb|ABE93145.1|	50206.55	Cell division protein FtsZ [Medicago truncatula]
gi|37529488|gb|AAQ92662.1|	50193.56	alpha-tubulin 2 [Gossypium hirsutum]
gi|37529490|gb|AAQ92663.1|	50223.57	alpha-tubulin 4 [Gossypium hirsutum]
gi|30683070|ref|NP_849388.1|	47889.17	TUA6 [Arabidopsis thaliana]
gi|76257841|gb|ABA41238.1|	44925.34	alpha-tubulin [Cyanophora paradoxa]
gi|76257847|gb|ABA41241.1|	44358.06	alpha-tubulin [Coleochaete scutata]
gi|76257849|gb|ABA41242.1|	44418.96	alpha-tubulin [Mantoniella squamata]
gi|76257861|gb|ABA41248.1|	44378.99	alpha-tubulin [Pterosperma cristatum]
gi|76257863|gb|ABA41249.1|	44312.96	alpha-tubulin [Pterosperma cristatum]
gi|77745465|gb|ABB02631.1|	50303.64	unknown [Solanum tuberosum]
gi|15222856|ref|NP_175423.1|	50193.56	TUA2 [Arabidopsis thaliana]
gi|15233627|ref|NP_193232.1|	50190.56	TUA6 [Arabidopsis thaliana]
gi|1174592|sp|P46259|TBA1_PEA	50305.62	Tubulin alpha-1 chain
gi|29423813|gb|AAO73546.1|	50375.6	alpha-tubulin [Ceratopteris richardii]
gi|296494|emb|CAA48927.1|	50381.68	alpha tubulin [Anemia phyllitidis]
gi|20413|emb|CAA47635.1|	50179.54	alpha-tubulin [Prunus dulcis]
gi|22147|emb|CAA33734.1|	50383.63	alpha1-tubulin [Zea mays]
gi|22148|emb|CAA33733.1|	50383.63	alpha2-tubulin [Zea mays]
gi|4165488|emb|CAA10663.1|	50381.61	alpha-tubulin 3 [Hordeum vulgare subsp. vulgare]
gi|25396550|dbj|BAC24800.1|	50222.58	alpha tubulin [Physcomitrella patens]
gi|1101025|gb|AAB36609.1|	42638.12	alpha-tubulin [Eucalyptus globulus subsp. bicostata]
gi|27819095|gb|AAO23139.1|	50261.58	alpha tubulin [Populus tremuloides]
gi|29124983|gb|AAO63781.1|	50276.59	alpha-tubulin 1 [Populus tremuloides]
gi|15029368|gb|AAK81858.1|	50379.67	alpha tubulin subunit [Rosa hybrid cultivar]
gi|16226462|gb|AAL16174.1|	50155.76	AT4g14960/dl3520c [Arabidopsis thaliana]
gi|51988174|emb|CAE52515.1|	50369.61	alpha tubulin [Setaria viridis]
gi|6723478|emb|CAB66336.1|	50227.6	alpha-tubulin [Betula pendula]
gi|17402467|emb|CAD13176.1|	50360.69	alpha-tubulin [Nicotiana tabacum]
gi|17402469|emb|CAD13177.1|	50387.7	alpha-tubulin [Nicotiana tabacum]
gi|17402471|emb|CAD13178.1|	50405.63	alpha-tubulin [Nicotiana tabacum]
gi|1743242|emb|CAA71141.1|	42363.19	alpha-tubulin [Histriculus cavicola]
gi|21632090|gb|AAL33695.1|	40779.4	alpha-tubulin [Halteria grandinella]
gi|21632086|gb|AAL33693.1|	40753.39	alpha-tubulin [Halteria grandinella]
gi|21632088|gb|AAL33694.1|	40749.42	alpha-tubulin [Halteria grandinella]
gi|21632092|gb|AAL33696.1|	40721.39	alpha-tubulin [Halteria grandinella]
gi|21632098|gb|AAL33699.1|	40837.4	alpha-tubulin [Halteria grandinella]
gi|34733239|gb|AAQ81585.1|	50089.48	putative tubulin alpha-2/alpha-4 chain [Brassica napus]
gi|22037131|gb|AAM89908.1|	40416.33	alpha-tubulin [Eutintinnus pectinis]
gi|22037135|gb|AAM89909.1|	41500.85	alpha-tubulin [Eutintinnus pectinis]
gi|23957214|gb|AAN40709.1|	40880.55	alpha-tubulin [Tintinnopsis tubulosoides]
gi|23957216|gb|AAN40710.1|	40901.59	alpha-tubulin [Tintinnopsis tubulosoides]
gi|23957221|gb|AAN40711.1|	41355.7	alpha-tubulin [Strombidium sp.]
gi|23957223|gb|AAN40712.1|	41334.81	alpha-tubulin [Strombidium sp.]
gi|23957225|gb|AAN40713.1|	40472.26	alpha-tubulin [Strombidium sp.]
gi|23957227|gb|AAN40714.1|	40634.37	alpha-tubulin [Strombidium sp.]
gi|23957263|gb|AAN40724.1|	41116.59	alpha-tubulin [Metacylis angulata]
gi|23957265|gb|AAN40725.1|	41480.9	alpha-tubulin [Metacylis angulata]
gi|23957267|gb|AAN40726.1|	40799.59	alpha-tubulin [Metacylis angulata]
gi|23957269|gb|AAN40727.1|	40730.52	alpha-tubulin [Metacylis angulata]
gi|23957275|gb|AAN40728.1|	41523.95	alpha-tubulin [Laboea strobila]
gi|23957277|gb|AAN40729.1|	41109.74	alpha-tubulin [Laboea strobila]
gi|23957281|gb|AAN40731.1|	41095.73	alpha-tubulin [Laboea strobila]
gi|23957251|gb|AAN40720.1|	40040.21	alpha-tubulin [Strombidinopsis sp.]
gi|23957257|gb|AAN40723.1|	40651.45	alpha-tubulin [Strombidinopsis sp.]
gi|23957290|gb|AAN40732.1|	40748.54	alpha-tubulin [Favella ehrenbergii]

gi|23957292|gb|AAN40733.1|	40617.43	alpha-tubulin [Favella ehrenbergii]
gi|62734655|gb|AAX96764.1|	50389.59	Tubulin/FtsZ family, GTPase domain, putative [Oryza sativa (japonica cultivar-group)]
gi|37789885|gb|AAP32191.1|	42754.39	alpha-tubulin [Trifolium repens]
gi|56481497|gb|AAV92379.1|	50294.6	alpha tubulin 1 [Pseudotsuga menziesii var. menziesii]
gi|54300498|gb|AAV32824.1|	43499.4	alpha-tubulin [Peridinium foliaceum]
gi|54300500|gb|AAV32825.1|	43469.43	alpha-tubulin [Kryptoperidinium foliaceum]

110. Group probability: 0.9961. Peptides of the group

KGLTPSQIGVILR	85.08	54.9183	1380.845	1381.505	5	2	distinct	1	0.9961

The equivalent proteins include

gi|54039304|sp|P62279|RS13_PIG	12026.78	40S ribosomal protein S13
gi|4633275|gb|AAD26692.1|	17181.66	40S ribosomal protein S13 [Cricetulus griseus]
gi|61369380|gb|AAX43326.1|	17324.75	ribosomal protein S13 [synthetic construct]
gi|67764864|gb|AAY79230.1|	12287.11	ribosomal protein S13 [Siniperca chuatsi]
gi|10121613|gb|AAG13286.1|	17151.61	ribosomal protein S13 [Gillichthys mirabilis]
gi|15450535|gb|AAK96445.1|	17115.53	AT3g60770/T4C21_180 [Arabidopsis thaliana]
gi|15294037|gb|AAK95195.1|	17139.64	40S ribosomal protein S13 [Ictalurus punctatus]
gi|70909527|emb|CAJ17186.1|	17052.51	ribosomal protein S13e [Agriotes lineatus]
gi|70909529|emb|CAJ17187.1|	17146.48	ribosomal protein S13e [Curculio glandium]
gi|70909531|emb|CAJ17188.1|	17152.5	ribosomal protein S13e [Georissus sp. APV-2005]
gi|54039308|sp|O77303|RS13_LUMRU	17104.68	40S ribosomal protein S13
gi|57089981|ref|XP_537358.1|	12731.13	PREDICTED: similar to ribosomal protein S13 [Canis familiaris]
gi|94391593|ref|XP_994773.1|	14265.94	PREDICTED: similar to ribosomal protein S13 [Mus musculus]
gi|44662862|gb|AAS47510.1|	17186.52	ribosomal protein S13 [Glycine max]
gi|68449762|gb|AAY97868.1|	17077.55	cytoplasmic ribosomal protein S13 [Lycopersicon esculentum]
gi|76607499|ref|XP_581041.2|	17038.46	PREDICTED: similar to ribosomal protein S13 [Bos taurus]
gi|18411716|ref|NP_567104.1|	17141.53	structural constituent of ribosome [Arabidopsis thaliana]
gi|18411224|ref|NP_567151.1|	17131.51	ATRPS13A (RIBOSOMAL PROTEIN S13A); structural constituent of ribosome [Arabidopsis thaliana]
gi|50805893|ref|XP_424367.1|	14633.33	PREDICTED: similar to ribosomal protein S13, partial [Gallus gallus]
gi|109081167|ref|XP_001084119.1|	18100.84	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109108275|ref|XP_001083923.1|	14235.02	PREDICTED: similar to ribosomal protein S13 isoform 4 [Macaca mulatta]
gi|109110588|ref|XP_001105971.1|	10903.08	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109120657|ref|XP_001097099.1|	17234.64	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109132315|ref|XP_001095630.1|	17177.54	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109139180|ref|XP_001119129.1|	17245.61	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109476367|ref|XP_001068232.1|	17762.03	PREDICTED: similar to ribosomal protein S13 [Rattus norvegicus]
gi|55642147|ref|XP_523078.1|	17270.5	PREDICTED: similar to ribosomal protein S13 [Pan troglodytes]
gi|47211519|emb|CAF90315.1|	17169.66	unnamed protein product [Tetraodon nigroviridis]
gi|8131699|dbj|BAA96366.1|	17164.58	cytoplasmic ribosomal protein S13 [Panax ginseng]
gi|77415468|gb|AAI06138.1|	17211.67	Ribosomal protein S13 [Mus musculus]
gi|7267097|emb|CAB80768.1|	16954.4	putative ribosomal protein S13 [Arabidopsis thaliana]
gi|7329687|emb|CAB82681.1|	16964.42	ribosomal protein S13-like [Arabidopsis thaliana]
gi|699581|gb|AAA91984.1|	17156.59	ribosomal S13 protein [Ictalurus punctatus]

gi|48209913|gb|AAT40507.1|	17107.56	cytoplasmic ribosomal protein S13 [Solanum demissum]
gi|417710|sp|P33192|RS13_CANMA	16931.31	40S ribosomal protein S13 (S15)
gi|396639|emb|CAA80974.1|	17162.61	ribosomal protein S13 [Pisum sativum]
gi|553640|gb|AAC15854.1|	13312.62	ribosomal protein S13 [Homo sapiens]
gi|62860010|ref|NP_001016602.1|	17239.67	ribosomal protein S13 [Xenopus tropicalis]
gi|48735394|gb|AAH72552.1|	17183.65	Zgc:91809 [Danio rerio]
gi|67084039|gb|AAY66954.1|	17255.66	40S ribosomal protein S13 [Ixodes scapularis]
gi|50344486|emb|CAH04329.1|	17136.46	S13e ribosomal protein [Timarcha balearica]
gi|50424883|ref|XP_461031.1|	17018.25	hypothetical protein DEHA0F16698g [Debaryomyces hansenii CBS767]
gi|22758884|gb|AAN05601.1|	16995.5	ribosomal protein S13 [Argopecten irradians]
gi|15029927|gb|AAH11192.1|	16132.15	Rps13 protein [Mus musculus]
gi|33585646|gb|AAH56028.1|	17237.69	Rps13-prov protein [Xenopus laevis]
gi|94385425|ref|XP_001004217.1|	17237.72	PREDICTED: similar to ribosomal protein S13 [Mus musculus]
gi|24266981|gb|AAN52387.1|	17109.6	ribosomal protein S13 [Branchiostoma belcheri]
gi|50555724|ref|XP_505270.1|	16851.25	hypothetical protein [Yarrowia lipolytica]
gi|6320269|ref|NP_010349.1|	17018.33	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 and rat S13 r
gi|44985849|gb|AAS54460.1|	16965.28	AGL030Wp [Ashbya gossypii ATCC 10895]
gi|50288301|ref|XP_446579.1|	17050.32	unnamed protein product [Candida glabrata]
gi|50311723|ref|XP_455889.1|	16758.29	unnamed protein product [Kluyveromyces lactis]

111. Group probability: 0.9954. Peptides of the group

VPTVDVSVVDLTCR	67.35	54.7099	1558.802	1557.818	5	2	distinct	0	0.8676
LTGMAFRVPTVDVSVVDLTCR	58.61	52.889	2335.203	2336.333	8	3	distinct	1	0.9651

The equivalent proteins include

gi|85860541|ref|YP_462743.1|	35966.36	glyceraldehyde 3-phosphate dehydrogenase [Syntrophus aciditrophicus SB]

112. Group probability: 0.9949. Peptides of the group

LGDLGVLEFTDLNPELTPFQR	78.09	52.784	2373.222	2374.295	1	2	distinct	0	0.9949

The equivalent proteins include

gi|62147616|emb|CAI72310.1|	96727.44	vacuolar proton translocating ATPase A subunit, putative [Phytophthora infestans]

113. Group probability: 0.9947. Peptides of the group

IRLENEIQTYR	55.92	54.8356	1433.763	1434.654	3	2	shared(2)	1	0.9468
YCVQLSQIQAQISALEEQLQEIR	48.8	51.9826	2746.396	2747.096	3	+2,+3	distinct	0	0.9771

The equivalent proteins include

gi|623409|gb|AAA60544.1|	57384.13	keratin 10

114. Group probability: 0.9944. Peptides of the group

LTGMAFCVPTPNVSVVDLTCR	79.39	52.929	2336.133	2336.782	6	3	distinct	0	0.9944

The equivalent proteins include

gi|94408078|ref|XP_978778.1|	22485.22	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]
gi|94408118|ref|XP_979290.1|	31442.78	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]

115. Group probability: 0.9943. Peptides of the group

VRLEPIISGGGQER	80.08	54.5666	1509.826	1511.012	1	2	distinct	1	0.9943

The equivalent proteins include

gi|88184850|gb|EAQ92318.1|	51016.23	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
gi|70998961|ref|XP_754202.1|	56891.13	tRNA splicing protein spl1 [Aspergillus fumigatus Af293]
gi|67524101|ref|XP_660112.1|	55635.41	hypothetical protein AN2508.2 [Aspergillus nidulans FGSC A4]
gi|3560214|emb|CAA20767.1|	55618.14	SPBC21D10.11c [Schizosaccharomyces pombe]
gi|10383773|ref|NP_009912.2|	54774.92	Cysteine desulfurase involved in iron-sulfur cluster (Fe/S) biogenesis; required for the post-trans
gi|172038|gb|AAA34814.1|	54800.93	nitrogen fixation-like protein

gi|50289061|ref|XP_446960.1|	53171.02	unnamed protein product [Candida glabrata]

116. Group probability: 0.9940. Peptides of the group

ESTIHLVLR	71.03	55.1556	1066.613	1067.325	13	2	shared(2)	0	0.9848
IQEKEGIPPDQQR	55.59	54.6181	1536.79	1537.455	2	2	distinct	1	0.9492

The equivalent proteins include

gi|73945898|ref|XP_852338.1|	11035.83	PREDICTED: similar to CG5271-PA [Canis familiaris]
gi|76638698|ref|XP_869731.1|	103189.67	PREDICTED: similar to ubiquitin C isoform 3 [Bos taurus]
gi|76638702|ref|XP_879056.1|	53447.48	PREDICTED: similar to ubiquitin C isoform 5 [Bos taurus]
gi|76638704|ref|XP_879141.1|	68981.2	PREDICTED: similar to ubiquitin C isoform 6 [Bos taurus]
gi|76638708|ref|XP_879323.1|	95909.61	PREDICTED: similar to ubiquitin C isoform 8 [Bos taurus]
gi|76638716|ref|XP_879643.1|	77522.8	PREDICTED: similar to ubiquitin C isoform 12 [Bos taurus]
gi|76638724|ref|XP_879987.1|	86106.45	PREDICTED: similar to ubiquitin C isoform 16 [Bos taurus]
gi|76638728|ref|XP_586525.2|	86064.41	PREDICTED: similar to ubiquitin C isoform 1 [Bos taurus]
gi|76638730|ref|XP_880223.1|	85894.1	PREDICTED: similar to ubiquitin C isoform 18 [Bos taurus]
gi|76638736|ref|XP_880428.1|	95205.37	PREDICTED: similar to ubiquitin C isoform 21 [Bos taurus]
gi|76638740|ref|XP_880581.1|	94648.06	PREDICTED: similar to ubiquitin C isoform 23 [Bos taurus]
gi|76638744|ref|XP_880724.1|	94606.01	PREDICTED: similar to ubiquitin C isoform 25 [Bos taurus]
gi|76638746|ref|XP_880794.1|	94648.06	PREDICTED: similar to ubiquitin C isoform 26 [Bos taurus]
gi|4102845|gb|AAD01603.1|	8074.37	ubiquitin [Entamoeba invadens]
gi|67479295|ref|XP_655029.1|	8692.69	ubiquitin [Entamoeba histolytica HM-1:IMSS]
gi|9295|emb|CAA46497.1|	7845.23	ubiquitin [Entamoeba histolytica]
gi|23451860|gb|AAN32889.1|	13290.07	ubiquitin extension protein [Heterodera glycines]

117. Group probability: 0.9932. Peptides of the group

SIVHPSYDSNTLNNDIMLIK (00000000000000000010000)	61.13	53.34	2273.136	2273.429	17	+2,+3	distinct	0	0.9932

The equivalent proteins include

gi|230196|pdb|1NTP|	23977.52	Modified Beta Trypsin (Monoisopropylphosphoryl Inhibited) (E.C.3.4.21.4) (Neutron Data)

118. Group probability: 0.9932. Peptides of the group

IALTTAEYLAYER	78.47	54.7249	1512.782	1513.951	3	2	distinct	0	0.9932

The equivalent proteins include

gi|8918242|dbj|BAA97567.1|	54346.11	vacuolar ATPase B subunit [Blastocystis hominis]
gi|27901531|emb|CAD61332.1|	45380.9	putative vacuolar H+ ATPase subunit B [Toxoplasma gondii]

119. Group probability: 0.9929. Peptides of the group

DSTIIMQLLR	62.92	55.6859	1188.654	1188.603	4	2	shared(5)	0	0.8101
LAFDDAIAELDTLSEESYKDSTLIMQLLR	69	50.825	3299.648	3300.563	9	3	distinct	1	0.9899

The equivalent proteins include

gi|83772732|dbj|BAE62860.1|	29229.67	unnamed protein product [Aspergillus oryzae]
gi|70989229|ref|XP_749464.1|	29197.65	hypothetical protein Afu2g03290 [Aspergillus fumigatus Af293]
gi|67534609|ref|XP_662105.1|	29211.63	hypothetical protein AN4501.2 [Aspergillus nidulans FGSC A4]
gi|13430385|gb|AAK25817.1|	29210.68	ARTA [Emericella nidulans]
gi|38490697|gb|AAR21678.1|	28585.52	14-3-3-like protein [Aspergillus flavus]

120. Group probability: 0.9928. Peptides of the group

SVLVDFLVSAGIKPTSIVSYNHLGNNDGK	72.96	51.2315	3043.598	3044.869	2	3	distinct	0	0.9928

The equivalent proteins include

gi|91088055|ref|XP_967186.1|	58604.27	PREDICTED: similar to CG11143-PA [Tribolium castaneum]
gi|93115136|gb|ABE98241.1|	57680.26	myo-inositol-1 phosphate synthase-like [Oreochromis mossambicus]

gi|47229914|emb|CAG10328.1|	59637.07	unnamed protein product [Tetraodon nigroviridis]

121. Group probability: 0.9927. Peptides of the group

YTLAGMEVSALLGR (0000001000000000)	77.37	54.693	1495.77	1496.39	6	2	distinct	0	0.9927

The equivalent proteins include

gi|73660119|emb|CAI82726.1|	50754.15	ATP synthase F1, beta subunit [Dehalococcoides sp. CBDB1]
gi|57225115|gb|AAW40172.1|	50764.11	ATP synthase F1, beta subunit [Dehalococcoides ethenogenes 195]

122. Group probability: 0.9922. Peptides of the group

KIAVNLIPFPR	70.88	55.3215	1266.781	1267.527	5	2	shared(8)	1	0.9855
EIVHIQGGQCGDQIGAK	58.29	54.3089	1808.884	1808.005	5	2	distinct	0	0.8285
GHYTEGAELIDSVLDVVR	50.71	53.6785	1971.99	1972.76	1	2	shared(7)	0	0.7949
AGPYGQIFRPDNFVFGQTGAGNNWAK	79.99	52.1825	2811.352	2812.533	7	+2,+3	shared(3)	0	0.9986

The equivalent proteins include

gi|1067181|emb|CAA91942.1|	50961.07	beta-tubulin [oomycete-like MacKay2000]

123. Group probability: 0.9921. Peptides of the group

YPIKHGIVTNWDDMEK	70.94	53.889	1944.94	1946.416	2	+2,+3	distinct	1	0.9873
VAPEEHPVLLTEAPINPK	81.4	53.6978	1953.057	1953.885	13	2	shared(10)	0	0.9887

The equivalent proteins include

gi|113239|sp|P27132|ACT2_NAEFO	41468.59	Actin-2 (Actin II)

124. Group probability: 0.9921. Peptides of the group

HYGALTGLNK	64.39	56.0578	1072.566	1073.339	9	+1,+2	shared(3)	0	0.998
HYGALTGLNKIETVEK	49.61	54.2222	1771.947	1773.258	1	2	distinct	1	0.9234

The equivalent proteins include

gi|88603570|ref|YP_503748.1|	28916.95	phosphoglycerate mutase 1 family [Methanospirillum hungatei JF-1]

125. Group probability: 0.9919. Peptides of the group

QILGPLAMAGQLGGAESATR	49.51	53.7326	1940.015	1940.445	3	+2,+3	distinct	0	0.9919

The equivalent proteins include

gi|92911051|ref|ZP_01279825.1|	81636.38	ATP-dependent DNA helicase RecG [Mycobacterium sp. JLS]
gi|108798904|ref|YP_639101.1|	81658.45	ATP-dependent DNA helicase RecG [Mycobacterium sp. MCS]

126. Group probability: 0.9919. Peptides of the group

IINQPTAAAIAYGLDKK	97.09	54.7761	1785.999	1787.369	3	2	distinct	1	0.9919

The equivalent proteins include

gi|640325|pdb|1NGB|	42542.9	Heat-Shock Cognate 70kd Protein (44kd Atpase N-Terminal Fragment) (E.C.3.6.1.3) Mutant With Glu 17

127. Group probability: 0.9918. Peptides of the group

HLLALINDILDLSKIEAGK	76.1	53.4489	2075.199	2073.811	28	3	distinct	1	0.9918

The equivalent proteins include

gi|67930180|ref|ZP_00523355.1|	87462.27	Response regulator receiver:ATP-binding region, ATPase-like:Histidine kinase, HAMP region:Histidine

128. Group probability: 0.9918. Peptides of the group

KFLDGIYVSEK	77.32	55.2315	1297.692	1298.372	16	2	distinct	1	0.9918

The equivalent proteins include

gi|3088347|dbj|BAA25830.1|	5147.66	ribosomal protein L9 [Homo sapiens]
gi|687602|gb|AAA85685.1|	19793.72	ribosomal protein L9, mutant
gi|88183391|gb|EAQ90859.1|	21731.65	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
gi|88183394|gb|EAQ90862.1|	25489.13	hypothetical protein CHGG_02797 [Chaetomium globosum CBS 148.51]
gi|90302055|gb|EAS31686.1|	21933.76	hypothetical protein CIMG_07165 [Coccidioides immitis RS]
gi|62510945|sp|Q5IFJ7|RL9_MACFA	21977.86	60S ribosomal protein L9
gi|84569966|gb|AAI11371.1|	21860.75	Unknown (protein for MGC:131531) [Homo sapiens]
gi|60653317|gb|AAX29353.1|	22076.92	ribosomal protein L9 [synthetic construct]
gi|62641949|ref|XP_577847.1|	24602.72	PREDICTED: similar to 60S ribosomal protein L9 [Rattus norvegicus]
gi|62658097|ref|XP_221450.2|	38201.97	PREDICTED: similar to 60S ribosomal protein L9 [Rattus norvegicus]
gi|62659405|ref|XP_223094.3|	30892.72	PREDICTED: similar to 60S ribosomal protein L9 [Rattus norvegicus]
gi|15293883|gb|AAK95134.1|	21890.85	ribosomal protein L9 [Ictalurus punctatus]
gi|62901872|gb|AAY18887.1|	24882.14	RPL9 [synthetic construct]
gi|68354498|ref|XP_707613.1|	21320.36	PREDICTED: similar to Rpl9 protein isoform 4 [Danio rerio]
gi|74267804|gb|AAI03428.1|	21976.83	RPL9 protein [Bos taurus]

gi|6015604|emb|CAA65987.2|	22109.87	ribosomal protein L9 [Pisum sativum]
gi|92878660|gb|ABE85179.1|	21852.74	Ribosomal protein L6, signature 2 [Medicago truncatula]
gi|51767763|ref|XP_484272.1|	22090.85	PREDICTED: similar to ribosomal protein L9 [Mus musculus]
gi|94397040|ref|XP_930828.2|	20495.5	PREDICTED: similar to ribosomal protein L9 isoform 2 [Mus musculus]
gi|94397413|ref|XP_995580.1|	20395.47	PREDICTED: similar to ribosomal protein L9 [Mus musculus]
gi|94398019|ref|XP_987698.1|	23645.24	PREDICTED: similar to ribosomal protein L9 [Mus musculus]
gi|15144375|gb|AAK84469.1|	21551.62	Ribosomal protein, large subunit protein 9 [Caenorhabditis elegans]
gi|76607197|ref|XP_584460.2|	21760.57	PREDICTED: similar to ribosomal protein L9 isoform 1 [Bos taurus]
gi|50774641|ref|XP_423225.1|	21935.82	PREDICTED: similar to ribosomal protein L9; 60S ribosomal protein L9 [Gallus gallus]
gi|109049123|ref|XP_001106717.1|	21476.5	PREDICTED: similar to ribosomal protein L9 [Macaca mulatta]
gi|109099634|ref|XP_001094980.1|	22069.92	PREDICTED: similar to ribosomal protein L9 [Macaca mulatta]
gi|109105720|ref|XP_001116116.1|	22003.95	PREDICTED: similar to ribosomal protein L9 isoform 2 [Macaca mulatta]
gi|109125246|ref|XP_001107304.1|	19189.5	PREDICTED: similar to ribosomal protein L9 [Macaca mulatta]
gi|55622598|ref|XP_526551.1|	38966.11	PREDICTED: similar to ribosomal protein L9; 60S ribosomal protein L9 [Pan troglodytes]
gi|109477682|ref|XP_001074676.1|	21957.76	PREDICTED: similar to 60S ribosomal protein L9 [Rattus norvegicus]
gi|109511464|ref|XP_001056263.1|	22091.54	PREDICTED: similar to 60S ribosomal protein L9 [Rattus norvegicus]
gi|77416921|gb|ABA81856.1|	22019.93	unknown [Solanum tuberosum]
gi|78191472|gb|ABB29957.1|	21943.87	unknown [Solanum tuberosum]
gi|39582015|emb|CAE64446.1|	21552.57	Hypothetical protein CBG09153 [Caenorhabditis briggsae]
gi|109074023|ref|XP_001092114.1|	21963.84	PREDICTED: similar to ribosomal protein L9 [Macaca mulatta]
gi|47210906|emb|CAF94210.1|	21497.69	unnamed protein product [Tetraodon nigroviridis]
gi|85116829|ref|XP_965129.1|	21795.77	hypothetical protein [Neurospora crassa OR74A]
gi|67591332|ref|XP_665544.1|	21558.39	ribosomal protein [Cryptosporidium hominis TU502]
gi|20727|emb|CAA46273.1|	21852.77	GA [Pisum sativum]
gi|687604|gb|AAA85686.1|	19769.75	ribosomal protein L9
gi|49618939|gb|AAT68054.1|	22009.88	60S ribosomal protein L9 [Danio rerio]
gi|1107489|emb|CAA63024.1|	22571.96	60S ribosomal protein L9 [Arabidopsis thaliana]
gi|607793|gb|AAB01041.1|	21977.86	ribosomal protein L9
gi|3355662|emb|CAA08792.1|	21070.11	ribosomal protein L9 [Podocoryne carnea]
gi|50554253|ref|XP_504535.1|	21552.36	hypothetical protein [Yarrowia lipolytica]
gi|15235114|ref|NP_192783.1|	22073.89	structural constituent of ribosome [Arabidopsis thaliana]
gi|54035458|gb|AAH83329.1|	21981.85	Ribosomal protein L9 [Mus musculus]
gi|18398761|ref|NP_564418.1|	22117.91	structural constituent of ribosome [Arabidopsis thaliana]
gi|55824704|gb|AAH86561.1|	21993.85	Ribosomal protein L9 [Rattus norvegicus]
gi|44982321|gb|AAS51630.1|	21593.56	ADL290Wp [Ashbya gossypii ATCC 10895]
gi|56541102|gb|AAH86937.1|	22055.83	Ribosomal protein L9 [Mus musculus]
gi|66792784|ref|NP_001019640.1|	12795.75	ribosomal protein L9 [Bos taurus]
gi|21554945|gb|AAM63736.1|	22141.88	ribosomal protein L9, putative [Arabidopsis thaliana]
gi|62657857|ref|XP_573277.1|	13499.42	PREDICTED: similar to 60S ribosomal protein L9 [Rattus norvegicus]
gi|68354504|ref|XP_707615.1|	21754.75	PREDICTED: similar to Rpl9 protein isoform 6 [Danio rerio]
gi|38051904|gb|AAH60589.1|	22021.86	Ribosomal protein L9 [Rattus norvegicus]
gi|67083791|gb|AAY66830.1|	21903.78	60S ribosomal protein L9 [Ixodes scapularis]

gi|62321620|dbj|BAD95213.1|	11214.98	ribosomal protein L9 [Arabidopsis thaliana]
gi|55729544|emb|CAH91503.1|	21892.77	hypothetical protein [Pongo pygmaeus]
gi|60417194|emb|CAH59397.1|	21859.76	60S ribosomal protein L9 [Platichthys flesus]
gi|50308713|ref|XP_454360.1|	21724.73	unnamed protein product [Kluyveromyces lactis]
gi|50310527|ref|XP_455283.1|	21737.79	unnamed protein product [Kluyveromyces lactis]
gi|22758894|gb|AAN05606.1|	21220.24	ribosomal protein L9 [Argopecten irradians]
gi|28436778|gb|AAH46581.1|	22055.86	Rpl9-prov protein [Xenopus laevis]
gi|94368927|ref|XP_982482.1|	22535.97	PREDICTED: similar to ribosomal protein L9 [Mus musculus]
gi|94391522|ref|XP_988370.1|	21737.54	PREDICTED: similar to 60S ribosomal protein L9 [Mus musculus]
gi|37779100|gb|AAP20210.1|	21915.8	ribosomal protein L9 [Pagrus major]
gi|54640261|gb|EAL29296.1|	21523.38	GA19385-PA [Drosophila pseudoobscura]
gi|14994664|gb|AAK76989.1|	21509.66	ribosomal protein L9 [Spodoptera frugiperda]
gi|66565444|ref|XP_623506.1|	21621.73	PREDICTED: similar to ribosomal protein L9 [Apis mellifera]
gi|70909653|emb|CAJ17250.1|	21496.59	ribosomal protein L9e [Cicindela litorea]
gi|70909655|emb|CAJ17273.1|	21164.47	ribosomal protein L9e [Hister sp. APV-2005]
gi|70909657|emb|CAJ17251.1|	21548.55	ribosomal protein L9e [Meladema coriacea]
gi|46108544|ref|XP_381330.1|	28332	hypothetical protein FG01154.1 [Gibberella zeae PH-1]
gi|94468812|gb|ABF18255.1|	21537.52	ribosomal protein L9 [Aedes aegypti]
gi|24583602|ref|NP_723644.1|	21549.4	Ribosomal protein L9 CG6141-PB, isoform B [Drosophila melanogaster]
gi|55244076|gb|EAA05902.2|	21632.62	ENSANGP00000011018 [Anopheles gambiae str. PEST]
gi|75859014|ref|XP_868847.1|	21884.68	hypothetical protein AN9465.2 [Aspergillus nidulans FGSC A4]
gi|1208910|emb|CAA64319.1|	21563.41	ribosomal protein L9 [Drosophila melanogaster]
gi|56462202|gb|AAV91384.1|	21595.67	ribosomal protein 13 [Lonomia obliqua]
gi|38047669|gb|AAR09737.1|	21538.36	similar to Drosophila melanogaster RpL9 [Drosophila yakuba]
gi|54609207|gb|AAV34819.1|	21477.7	ribosomal protein L9 [Bombyx mori]
gi|56199512|gb|AAV84245.1|	22195.82	ribosomal protein L9 [Culicoides sonorensis]
gi|71032597|ref|XP_765940.1|	21320.57	60S ribosomal protein L6 [Theileria parva strain Muguga]
gi|84999220|ref|XP_954331.1|	19960.83	ribosomal protein l6 [Theileria annulata strain Ankara]

129. Group probability: 0.9916. Peptides of the group

IINEPTAAALSFGLDKK	96.71	54.7761	1786.983	1787.369	4	2	distinct	1	0.9916

The equivalent proteins include

gi|15828694|ref|NP_326054.1|	65480.66	molecular chaperone DnaK [Mycoplasma pulmonis UAB CTIP]

130. Group probability: 0.9913. Peptides of the group

GVLIHGPPGTGK	54.48	56.1829	1131.64	1132.141	1	2	distinct	0	0.8715
NAPAIIFIDEIDSIAPK	82.61	54.0448	1825.982	1826.739	16	2	shared(2)	0	0.9959

The equivalent proteins include

gi|21226350|ref|NP_632272.1|	84695.37	Cell division cycle protein [Methanosarcina mazei Go1]
gi|72396736|gb|AAZ71009.1|	84500.49	cell division cycle protein [Methanosarcina barkeri str. fusaro]
gi|85375691|ref|YP_459753.1|	84366.01	Cell division cycle protein [Erythrobacter litoralis HTCC2594]

131. Group probability: 0.9909. Peptides of the group

SIKHAVVTVPAYFNDSQR	72.97	53.5482	2031.054	2031.48	5	2	distinct	1	0.9909

The equivalent proteins include

gi|50427305|ref|XP_462265.1|	73024.02	hypothetical protein DEHA0G17688g [Debaryomyces hansenii CBS767]

132. Group probability: 0.9909. Peptides of the group

VATLIVRPR	76.89	55.3578	1023.655	1024.259	7	2	distinct	0	0.9909

The equivalent proteins include

gi|84355044|ref|ZP_00979935.1|	59378.51	COG2225: Malate synthase [Burkholderia cenocepacia PC184]

gi|84362169|ref|ZP_00986803.1|	59651.72	COG2225: Malate synthase [Burkholderia dolosa AUO158]
gi|74017829|ref|ZP_00688452.1|	59302.49	Malate synthase A [Burkholderia ambifaria AMMD]
gi|77967575|gb|ABB08955.1|	59331.44	Malate synthase A [Burkholderia sp. 383]
gi|107028768|ref|YP_625863.1|	59478.58	Malate synthase A [Burkholderia cenocepacia AU 1054]
gi|91784154|ref|YP_559360.1|	60113.75	Malate synthase A [Burkholderia xenovorans LB400]

133. Group probability: 0.9908. Peptides of the group

GMSIMNSFINDIFER	91.12	54.2602	1772.823	1773.621	5	2	distinct	0	0.9908

The equivalent proteins include

gi|108885310|sp|P82887|H2B_OLILU	12653.81	Histone H2B

134. Group probability: 0.9908. Peptides of the group

KSLLVHTK	65.66	55.1836	924.576	925.126	2	2	distinct	1	0.8739
VACIGAWHPSR	70.32	55.37	1252.613	1253.064	9	2	shared(2)	0	0.9848

The equivalent proteins include

gi|66566113|ref|XP_624821.1|	47520.2	PREDICTED: similar to ribosomal protein L3 [Apis mellifera]
gi|91089565|ref|XP_971875.1|	50625.78	PREDICTED: similar to CG4863-PA, isoform A [Tribolium castaneum]
gi|70909597|emb|CAJ17224.1|	20201.81	ribosomal protein L3e [Micromalthus debilis]
gi|70909599|emb|CAJ17225.1|	32449.4	ribosomal protein L3e [Mycetophagus quadripustulatus]
gi|70909601|emb|CAJ17226.1|	47147.16	ribosomal protein L3e [Scarabaeus laticollis]
gi|94468802|gb|ABF18250.1|	47151.22	ribosomal protein L3 [Aedes aegypti]
gi|55241021|gb|EAA08849.2|	48255.91	ENSANGP00000011028 [Anopheles gambiae str. PEST]
gi|62083395|gb|AAX62422.1|	47239.05	ribosomal protein L3 variant 1 [Lysiphlebus testaceipes]

135. Group probability: 0.9898. Peptides of the group

IPTLAIHLDR	75.36	55.6298	1147.671	1149.098	3	2	distinct	0	0.9898

The equivalent proteins include

gi|83766225|dbj|BAE56368.1|	54186.72	unnamed protein product [Aspergillus oryzae]
gi|92871439|gb|ABE80427.1|	58773.68	Peptidase M18, aminopeptidase I [Medicago truncatula]
gi|77554110|gb|ABA96906.1|	52866.65	Aspartyl aminopeptidase, putative, expressed [Oryza sativa (japonica cultivar-group)]
gi|71000136|ref|XP_754785.1|	55081.05	aspartyl aminopeptidase [Aspergillus fumigatus Af293]
gi|6321905|ref|NP_011981.1|	54368.04	Cytoplasmic aspartyl aminopeptidase; cleaves unblocked N-terminal acidic amino acid residues from p
gi|50545992|ref|XP_500533.1|	53199.83	hypothetical protein [Yarrowia lipolytica]
gi|57226693|gb|AAW43153.1|	56224.38	aminopeptidase, putative [Cryptococcus neoformans var. neoformans JEC21]
gi|68484212|ref|XP_713998.1|	55302.47	hypothetical protein CaO19.9871 [Candida albicans SC5314]
gi|15238629|ref|NP_200824.1|	53019.5	aminopeptidase I/ aspartyl aminopeptidase [Arabidopsis thaliana]
gi|21537290|gb|AAM61631.1|	53086.48	aspartyl aminopeptidase-like protein [Arabidopsis thaliana]
gi|50289759|ref|XP_447311.1|	53855.59	hypothetical protein CAGL0I01298g [Candida glabrata CBS138]
gi|50309801|ref|XP_454914.1|	55475.33	unnamed protein product [Kluyveromyces lactis]

136. Group probability: 0.9891. Peptides of the group

LDLLKLAPGGHIGR	60.34	54.9851	1458.867	1458.974	7	+2,+3	distinct	1	0.9891

The equivalent proteins include

gi|94733357|emb|CAK04707.1|	20802.26	ribosomal protein L4 [Danio rerio]
gi|54261775|ref|NP_998272.1|	42810.18	ribosomal protein L4 [Danio rerio]

137. Group probability: 0.9888. Peptides of the group

RTQQQLELEIENMGGHLNAYTSR	70.52	52.0949	2687.308	2688.653	1	3	distinct	1	0.9888

The equivalent proteins include

gi|46107960|ref|XP_381039.1|	52746.69	hypothetical protein FG00863.1 [Gibberella zeae PH-1]

138. Group probability: 0.9884. Peptides of the group

RTIQFVDWCPTGFK	68.04	54.1689	1753.861	1754.812	2	2	shared(3)	1	0.9837
ELYHPEQLISGKEDAANNYAR	55.64	52.6394	2417.161	2417.37	2	3	distinct	1	0.955

The equivalent proteins include

gi|26419422|gb|AAN78301.1|	51014.93	alpha-tubulin [Encephalitozoon intestinalis]

139. Group probability: 0.9872. Peptides of the group

AEPSLHWIDYLGSMVK	69.96	54.1459	1844.913	1846.146	2	2	distinct	0	0.9872

The equivalent proteins include

gi|66270177|gb|AAY43418.1|	22365.38	20S proteasome subunit [Phytophthora infestans]

140. Group probability: 0.9871. Peptides of the group

MSMNPFCEIAVEEAIR	85.91	53.8365	1895.858	1897.246	9	2	distinct	0	0.9871

The equivalent proteins include

gi|83859194|ref|ZP_00952715.1|	26885.32	electron transfer flavoprotein beta subunit [Oceanicaulis alexandrii HTCC2633]
gi|23394375|gb|AAN31477.1|	27072.63	electron transfer flavoprotein beta subunit [Phytophthora infestans]
gi|50930317|ref|XP_474686.1|	27565.83	OSJNBb0006L01.5 [Oryza sativa (japonica cultivar-group)]

141. Group probability: 0.9871. Peptides of the group

VPTPNVSVVDLTCR	73.06	54.7076	1555.803	1557.293	3	2	distinct	0	0.897
ITGMAFRVPTPNVSVVDLTCR	55.82	52.8809	2332.203	2333.52	1	3	distinct	1	0.8744

The equivalent proteins include

gi|229279|prf||681085A	35915.24	dehydrogenase,glyceraldehydephosphate
gi|54635963|gb|EAL25366.1|	37437.25	GA21475-PA [Drosophila pseudoobscura]
gi|40889053|pdb|1J0X|R	35849.25	Chain R, Crystal Structure Of The Rabbit Muscle Glyceraldehyde-3- Phosphate Dehydrogenase (Gapdh)
gi|1066045|gb|AAA81516.1|	11749.82	glyceraldehyde-3-phosphate dehydrogenase
gi|1218048|gb|AAA91804.1|	30745.73	glyceraldehyde-3-phosphate dehydrogenase
gi|65987|pir||DEPGG3	35914.25	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - pig
gi|1841758|gb|AAB47507.1|	33731.22	glyceraldehyde-phosphate-dehydrogenase [Bos taurus]
gi|2687661|gb|AAB88869.1|	35972.41	glyceraldehyde-3-phosphate dehydrogenase [Columba livia]
gi|2623288|gb|AAC16069.1|	19975.13	glyceraldehyde-3-phosphate dehydrogenase [Ovis aries]
gi|1730158|sp|P51640|G3P_MESAU	33739.32	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|3445501|gb|AAC32447.1|	13071.82	glyceraldehyde-3-phosphate dehydrogenase [Cavia porcellus]
gi|89272932|emb|CAJ82888.1|	36098.28	glyceraldehyde 3 phosphate dehydrogenase [Xenopus tropicalis]
gi|2506441|sp|P00355|G3P_PIG	36041.36	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|6166169|sp|Q28554|G3P_SHEEP	34937.79	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|1730164|sp|P51469|G3P_XENLA	36017.26	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|6679939|ref|NP_032111.1|	48096.38	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic [Mus musculus]
gi|62652560|ref|XP_576287.1|	22717.37	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - m
gi|50978862|ref|NP_001003142.1|	36066.26	glyceraldehyde-3-phosphate dehydrogenase [Canis familiaris]
gi|57163839|ref|NP_001009307.1|	36018.31	glyceraldehyde-3-phosphate dehydrogenase [Felis catus]
gi|4105596|gb|AAD02474.1|	35909.37	glyceraldehyde-3-phosphate dehydrogenase [Gallus gallus]
gi|1773078|gb|AAB40155.1|	16172.25	glyceraldehyde-3-phosphate dehydrogenase [Sus scrofa]
gi|55741036|gb|AAV64182.1|	35999.29	glyceraldehyde-3-phosphate dehydrogenase [Spermophilus citellus]
gi|72496432|dbj|BAE19661.1|	17001.93	glyceraldehyde 3-phosphate dehydrogenase [Oryctolagus cuniculus]
gi|74212012|dbj|BAE40174.1|	36074.21	unnamed protein product [Mus musculus]
gi|74137577|dbj|BAE35822.1|	15638.9	unnamed protein product [Mus musculus]
gi|74141423|dbj|BAE35989.1|	36044.36	unnamed protein product [Mus musculus]
gi|74194852|dbj|BAE26016.1|	36102.33	unnamed protein product [Mus musculus]

gi|74203253|dbj|BAE20812.1|	25339.9	unnamed protein product [Mus musculus]
gi|63401|emb|CAA23697.1|	14687.46	unnamed protein product [Gallus gallus]
gi|2623266|gb|AAB86435.1|	29991.26	glyceraldehyde 3-phosphate dehydrogenase [Ovis aries]
gi|73997649|ref|XP_854083.1|	17391.78	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Canis familiaris]
gi|74004878|ref|XP_852254.1|	44356.63	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Canis familiaris]
gi|84626361|gb|ABC59721.1|	7922.26	glyceraldehyde-3-phosphate dehydrogenase [Spermophilus parryii]
gi|70673311|gb|AAZ06800.1|	22296.24	glyceraldehyde-3-phosphate dehydrogenase [Oxalis stricta]
gi|37698402|gb|AAR00508.1|	35030.96	glyceraldehyde-3-phosphate dehydrogenase; GAPDH [Passer domesticus]
gi|109484558|ref|XP_001065101.1|	36045.19	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|109503243|ref|XP_001070609.1|	33300.03	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase isoform 1 [Rattus norvegicus]
gi|6978952|dbj|BAA90773.1|	36298.41	glyceraldehyde-3-phosphate dehydrogenase [Spirometra erinaceieuropaei]
gi|109476813|ref|XP_001059327.1|	36090.27	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|13702286|dbj|BAB43824.1|	34889.76	glyceraldehyde 3-phosphate dehydrogenase [Cavia porcellus]
gi|55154587|gb|AAH85275.1|	36072.32	Similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]
gi|211797|gb|AAA48774.1|	35989.41	glyceraldehyde-3-phosphate dehydrogenase
gi|1628381|emb|CAA23698.1|	35967.38	glyceraldehyde-3-phosphate dehydrogenase [Gallus gallus]
gi|2494630|sp|Q64467|G3PT_MOUSE	48367.48	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific (Spermatogenic cell-specific glyceraldehy
gi|1169794|sp|P46406|G3P_RABIT	36025.3	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|62616|emb|CAA79512.1|	35863.34	glyceraldehydephosphate dehydrogenase [Coturnix coturnix]
gi|77404273|ref|NP_001029206.1|	36073.38	glyceraldehyde-3-phosphate dehydrogenase [Bos taurus]
gi|49435|emb|CAA36368.1|	35953.3	unnamed protein product [Cricetulus griseus]
gi|62318276|dbj|BAD93764.1|	36059.28	Glyceraldehyde-3-phosphate dehydrogenase [Meriones unguiculatus]
gi|1100225|gb|AAD10214.1|	46324.43	glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
gi|1100223|gb|AAD10215.1|	46339.43	glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
gi|4966351|gb|AAD34682.1|	43648.17	Similar to gb|AJ001706 NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (GapCp1) from Pinus s
gi|5052383|gb|AAD38527.1|	20110.47	glyceraldehyde-3-phosphate dehydrogenase GAPDH [Sus scrofa]
gi|3219753|gb|AAC23533.1|	11813.23	glyceraldehyde-3-phosphate dehydrogenase [Sus scrofa]
gi|5712111|gb|AAD47370.1|	18687.6	glyceraldehyde 3-phosphate dehydrogenase [Mustela vison]
gi|3452462|gb|AAC32882.1|	14706.46	glyceraldehyde-3-phosphate dehydrogenase [Equus caballus]
gi|15219206|ref|NP_173080.1|	44988.94	NAD binding / glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphat
gi|18072805|emb|CAC80377.1|	44689.85	glyceraldehyde-3-phosphate dehydrogenase [Capsicum annuum]
gi|56188|emb|CAA26150.1|	36098.37	glyceraldehyde 3-phosphate-dehydrogenase [Rattus norvegicus]

gi|56611127|gb|AAH87743.1|	36056.29	Glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|39652292|dbj|BAD04859.1|	17342.06	glyceraldehyde-3-phosphate dehydrogenase [Laticauda semifasciata]
gi|50905605|ref|XP_464291.1|	43461.25	putative glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)]
gi|8575565|gb|AAF78051.1|	16838.72	glyceraldehyde-3-phosphate dehydrogenase; GAPDH [Taeniopygia guttata]
gi|52076528|dbj|BAD45405.1|	43752.23	putative glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)]
gi|21618027|gb|AAM67077.1|	45002.95	putative glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]
gi|1667605|gb|AAB18821.1|	7965.31	glyceraldehyde-3-phosphate dehydrogenase [Cavia porcellus]
gi|109504062|ref|XP_001073242.1|	36085.25	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|9838358|gb|AAF68961.2|	18681.56	glyceraldehyde 3-phosphate dehydrogenase GAPDH [Marmota monax]
gi|27754473|gb|AAO22684.1|	44961.93	putative glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]
gi|62201487|gb|AAH92267.1|	36100.35	Similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]
gi|49522602|gb|AAH75438.1|	31638.89	MGC89215 protein [Xenopus tropicalis]
gi|5163490|gb|AAD40684.1|	29650.02	glyceraldehyde-3-phosphate dehydrogenase [Equus caballus]
gi|56377786|dbj|BAD74117.1|	36049.37	glyceraldehyde-3-phosphate dehydrogenase (GAPDH) homologue [Pelodiscus sinensis]
gi|21070959|gb|AAK50815.2|	10679.71	glyceraldehyde-3-phosphate dehydrogenase [Capreolus capreolus]
gi|2285903|emb|CAA03875.1|	28908.03	glyceraldehyde 3-phosphate dehydrogenase [Bos taurus]
gi|3059140|emb|CAA04942.1|	39298.06	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
gi|3059122|emb|CAA06030.1|	39352.13	glyeraldehyde-3-phosphate dehydrogenase [Marsilea quadrifolia]
gi|18076096|emb|CAC80386.1|	45945.31	glyceraldehyde-3-phosphate dehydrogenase [Marchantia polymorpha]
gi|21218402|gb|AAM44068.1|	31038.79	glyceraldehyde-3-phosphate dehydrogenase [Sigmodon hispidus]
gi|13027414|ref|NP_076454.1|	47362.02	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic [Rattus norvegicus]
gi|66990025|gb|AAH98095.1|	36102.33	LOC654472 protein [Mus musculus]
gi|27882192|gb|AAH43972.1|	36097.31	Gapd-prov protein [Xenopus laevis]
gi|94397810|ref|XP_988049.1|	36074.26	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]
gi|94399312|ref|XP_978477.1|	36092.36	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]
gi|16304127|gb|AAL16930.1|	13856.15	glyceraldehyde 3-phosphate dehydrogenase 1 [Fragaria x ananassa]
gi|16226113|gb|AAL16077.1|	13870.16	glyceraldehyde 3-phosphate dehydrogenase [Fragaria x ananassa]
gi|49616580|gb|AAT67150.1|	20734.78	glyceraldehyde-3-phosphate dehydrogenase [Cervus elaphus]
gi|50086895|gb|AAT70328.1|	34343.55	glyceraldehyde 3-phosphate dehydrogenase [Petromyzon marinus]
gi|27356782|gb|AAL49972.1|	35974.29	glyceraldehyde-3-phosphate dehydrogenase [Meriones unguiculatus]
gi|55153885|gb|AAH85315.1|	36093.23	Similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]
gi|62653546|ref|XP_576394.1|	36045.19	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]

gi|62658024|ref|XP_573304.1|	36277.38	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|57232588|gb|AAW47939.1|	6830.78	GAPDH [Tupaia belangeri]
gi|56783068|gb|AAW28862.1|	29980.23	glyceraldehyde-3-phosphate dehydrogenase [Peromyscus maniculatus]

142. Group probability: 0.9871. Peptides of the group

ENIAKIMNESLMLVTALNPHIGYDK (0000000100000000000000000)	68.04	51.8396	2829.44	2829.072	4	3	distinct	1	0.9871

The equivalent proteins include

gi|24640177|ref|NP_572339.1|	53826.85	lethal (1) G0255 CG4094-PA, isoform A [Drosophila melanogaster]
gi|24640179|ref|NP_727108.1|	50713.05	lethal (1) G0255 CG4094-PB, isoform B [Drosophila melanogaster]
gi|19528365|gb|AAL90297.1|	53811.88	LD46083p [Drosophila melanogaster]
gi|38047607|gb|AAR09706.1|	12956.77	similar to Drosophila melanogaster CG4094 [Drosophila yakuba]

143. Group probability: 0.9868. Peptides of the group

EAYPGDVFYIHSR	77.43	54.6324	1552.731	1553.625	13	2	shared(2)	0	0.9925
CTGRILEVPVGESLLGR	44.5	54.2635	1854.998	1855.895	1	3	distinct	1	0.8576

The equivalent proteins include

gi|78702137|ref|ZP_00866579.1|	55692.65	ATP synthase F1, alpha subunit [Alkalilimnicola ehrlichei MLHE-1]

144. Group probability: 0.9866. Peptides of the group

VNTLIRPDGKK	48.33	55.1724	1239.73	1240.209	3	2	distinct	1	0.8957
VNTLIRPDGQKK	50.66	55.0842	1367.788	1368.689	3	2	distinct	1	0.8714

The equivalent proteins include

gi|61654660|gb|AAX48856.1|	17374.73	L23a [Suberites domuncula]
gi|72145683|ref|XP_792948.1|	17866.11	PREDICTED: similar to 60S ribosomal protein L23a [Strongylocentrotus purpuratus]
gi|24266954|gb|AAN52376.1|	18528.63	ribosomal protein L23a [Branchiostoma belcheri]

145. Group probability: 0.9864. Peptides of the group

KTVAVGVIK	47.89	56.568	913.596	914.553	1	2	shared(2)	1	0.8811
IGGIGTVPVGR	47.13	55.1381	1024.603	1026.063	1	2	shared(8)	0	0.8842
EHALLAFTLGVK	64.61	55.1836	1297.739	1299.156	1	2	shared(5)	0	0.9343
SVEMHHEALIEAVPGDNVGFNVK	57.63	52.5152	2491.216	2492.428	3	2	distinct	0	0.9066

The equivalent proteins include

gi|90265663|dbj|BAE91879.1|	50435.44	elongation factor 1-alpha [Athalia rosae]

146. Group probability: 0.9863. Peptides of the group

GGMTSHAAVVAR (00010000000000)	91.33	55.6763	1155.582	1156.392	8	2	shared(2)	0	0.9737
SGAAISMPGMMDTVLNLGLNDETVKGLAK	45.32	51.3953	2932.471	2932.507	1	3	distinct	1	0.9184

The equivalent proteins include

gi|4980770|gb|AAD35361.1|	98387.3	pyruvate,orthophosphate dikinase [Thermotoga maritima MSB8]

147. Group probability: 0.9862. Peptides of the group

AMGIMNSFINDIFER (001000000000000000)	85.48	54.2621	1772.823	1774.034	17	2	distinct	0	0.9862

The equivalent proteins include

gi|76644398|ref|XP_875437.1|	25340.43	PREDICTED: similar to Histone H2B 291B [Bos taurus]
gi|61888730|ref|XP_604423.1|	15998.07	PREDICTED: similar to H2B histone family, member C [Bos taurus]
gi|76678151|ref|XP_609308.2|	9756.19	PREDICTED: similar to Histone H2B 291B, partial [Bos taurus]
gi|109079443|ref|XP_001110898.1|	13913.59	PREDICTED: similar to H2B histone family, member T [Macaca mulatta]
gi|50261574|gb|AAT72343.1|	21971.36	H2B/t variant [Homo sapiens]
gi|49659929|gb|AAT68256.1|	18405.62	histone H2B/s [Homo sapiens]

148. Group probability: 0.9856. Peptides of the group

MAMNPFCEIAVEEAIR (010000000000000000)	84.65	53.8365	1895.858	1897.246	10	2	distinct	0	0.9856

The equivalent proteins include

gi|88859195|ref|ZP_01133835.1|	25728.88	Electron transfer flavoprotein beta-subunit [Pseudoalteromonas tunicata D2]

149. Group probability: 0.9851. Peptides of the group

YKIVLLR	50.4	56.611	903.591	903.581	1	1	shared(2)	1	0.834
HYGALTGLDK	51.04	56.1766	1073.551	1074.046	2	+1,+2	distinct	0	0.8365
VIIAAHGNSIR	55.36	55.3388	1149.662	1150.474	5	2	shared(2)	0	0.9435

The equivalent proteins include

gi|88796704|ref|ZP_01112360.1|	27940.36	phosphoglyceromutase [Alteromonas macleodii 'Deep ecotype']

150. Group probability: 0.9846. Peptides of the group

DSTIIMQLLR	62.92	55.6859	1188.654	1188.603	4	2	shared(5)	0	0.8101
TASEIATTELPPTHPIR	49.19	54.0258	1832.963	1833.15	2	2	distinct	0	0.7237
QAFDDAIAELDTLSEESYK	63.08	53.2605	2143.98	2145.265	2	2	shared(3)	0	0.9793
QAFDDAIAELDTLSEESYKDSTLIMQLLR	73.46	50.8352	3314.623	3315.694	3	3	shared(2)	1	0.9206

The equivalent proteins include

gi|6320304|ref|NP_010384.1|	31099.36	14-3-3 protein, minor isoform; binds proteins and DNA, involved in regulation of many processes inc
gi|6321025|ref|NP_011104.1|	30186.84	14-3-3 protein, major isoform; binds proteins and DNA, involved in regulation of many processes inc
gi|832919|emb|CAA50656.1|	22136.03	BMH1 [Saccharomyces cerevisiae]
gi|50293761|ref|XP_449292.1|	28405.09	unnamed protein product [Candida glabrata]
gi|671634|emb|CAA46959.1|	30271.9	BMH1 [Saccharomyces cerevisiae]
gi|683696|emb|CAA59275.1|	31262.41	BMH2 [Saccharomyces cerevisiae]

151. Group probability: 0.9837. Peptides of the group

AGMTHIMR	70.54	56.6773	915.442	915.808	7	2	distinct	0	0.9837

The equivalent proteins include

gi|55627178|ref|XP_518669.1|	47690.1	PREDICTED: similar to ribosomal protein L3; 60S ribosomal protein L3; HIV-1 TAR RNA-binding protein

152. Group probability: 0.9835. Peptides of the group

ESTIHLVLR	71.03	55.1556	1066.613	1067.325	13	2	shared(2)	0	0.9848
YPIEHGIVTNWDDMEK (000000000000001000)	89.61	53.8859	1945.888	1946.177	23	+2,+3	shared(4)	0	0.9983
VAPEEHPVLLTEAPINPK	81.4	53.6978	1953.057	1953.885	13	2	shared(10)	0	0.9887

The equivalent proteins include

gi|33346927|gb|AAP34624.1|	26433.21	ubiquitin/actin fusion protein 1 [Bigelowiella natans]
gi|33346937|gb|AAP34630.1|	26017.09	ubiquitin/actin fusion protein 3 [Lotharella amoeboformis]
gi|33346935|gb|AAP34629.1|	26031.11	ubiquitin/actin fusion protein 2 [Lotharella amoeboformis]
gi|33346941|gb|AAP34632.1|	26075.11	ubiquitin/actin fusion protein 2 [Lotharella globosa]
gi|33346943|gb|AAP34633.1|	26332.2	ubiquitin/actin fusion protein 3 [Lotharella globosa]
gi|33346945|gb|AAP34634.1|	49579.96	ubiquitin/actin fusion protein [Gymnochlora stellata]

153. Group probability: 0.9826. Peptides of the group

IIIEPTAAAIAYGLDKK	88.42	54.7761	1786.024	1787.369	3	2	distinct	1	0.9826

The equivalent proteins include

gi|15620767|emb|CAC69880.1|	72796.99	heat shock protein (Hsp70) [Moneuplotes crassus]

154. Group probability: 0.9825. Peptides of the group

VPTPDVSVVDLTCR	100.87	54.7076	1556.787	1557.293	12	2	shared(2)	0	0.9926
LTGMSFRVPTPDVSVVDLTCR	58.7	53.012	2349.182	2350.082	2	3	distinct	1	0.8138

The equivalent proteins include

gi|48853581|ref|ZP_00307749.1|	36124.38	COG0057: Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Cytophaga hu

155. Group probability: 0.9819. Peptides of the group

SGKPLHYK	48.26	56.7303	928.513	929.188	1	2	shared(2)	0	0.8846
ANPRVFFDMTVGGAPAGR	68.76	53.999	1861.926	1860.659	5	2	distinct	1	0.9405

The equivalent proteins include

gi|829148|emb|CAA48638.1|	18565.23	cyclophilin [Zea mays]
gi|13925734|gb|AAK49427.1|	18709.18	cyclophilin A-2 [Triticum aestivum]
gi|13925737|gb|AAK49428.1|	18721.19	cyclophilin A-3 [Triticum aestivum]

156. Group probability: 0.9814. Peptides of the group

VVSWYDNEWGYSNR	66.58	54.2603	1773.775	1773.614	2	2	distinct	0	0.9814

The equivalent proteins include

gi|67925626|ref|ZP_00518948.1|	11174.39	similar to Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Crocosphae
gi|76797229|ref|ZP_00779563.1|	36920.09	Glyceraldehyde-3-phosphate dehydrogenase, type I [Thermoanaerobacter ethanolicus ATCC 33223]

gi|77687068|ref|ZP_00802362.1|	31226.17	Glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Alkaliphilus metalliredigenes QYMF]
gi|88946476|ref|ZP_01149554.1|	36708.19	Glyceraldehyde-3-phosphate dehydrogenase, type I [Desulfotomaculum reducens MI-1]
gi|89341241|ref|ZP_01193486.1|	38782.28	Glyceraldehyde-3-phosphate dehydrogenase, type I [Mycobacterium flavescens PYR-GCK]
gi|90204185|ref|ZP_01206829.1|	36998.22	Glyceraldehyde-3-phosphate dehydrogenase, type I [Mycobacterium vanbaalenii PYR-1]
gi|13092768|emb|CAC30078.1|	36221.9	glyceraldehyde 3-phosphate dehydrogenase [Mycobacterium leprae]
gi|13881096|gb|AAK45745.1|	36104.85	glyceraldehyde 3-phosphate dehydrogenase [Mycobacterium tuberculosis CDC1551]
gi|66965925|ref|ZP_00413489.1|	35921.58	Glyceraldehyde-3-phosphate dehydrogenase, type I [Arthrobacter sp. FB24]
gi|71677692|ref|ZP_00675427.1|	37023.86	Glyceraldehyde-3-phosphate dehydrogenase, type I [Trichodesmium erythraeum IMS101]
gi|870798|gb|AAC37245.1|	38377.72	glyceraldehyde-3-phosphate dehydrogenase
gi|3323159|gb|AAC65812.1|	38344.7	glyceraldehyde 3-phosphate dehydrogenase (gap) [Treponema pallidum subsp. pallidum str. Nichols]
gi|20516773|gb|AAM24956.1|	36775.02	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Thermoanaerobacter te
gi|51856472|dbj|BAD40630.1|	36348.86	glyceraldehyde-3-phosphate dehydrogenase [Symbiobacterium thermophilum IAM 14863]
gi|108799371|ref|YP_639568.1|	36231.88	glyceraldehyde-3-phosphate dehydrogenase, type I [Mycobacterium sp. MCS]
gi|20549|emb|CAA42902.1|	36462.75	glyceraldehyde 3-phosphate dehydrogenase [Petroselinum crispum]
gi|2749881|gb|AAB95084.1|	36186.95	glyceraldehyde-3-phosphate dehydrogenase homolog [Mycobacterium avium]
gi|520887|emb|CAA52631.1|	39455.46	glyceraldehyde-3-phosphate dehydrogenase [Trypanoplasma borreli]
gi|520888|emb|CAA52632.1|	39614.38	glyceraldehyde-3-phosphate dehydrogenase [Trypanoplasma borreli]

157. Group probability: 0.9813. Peptides of the group

ALGLPIERPK	48.28	55.3438	1092.665	1093.804	1	2	distinct	0	0.8911
VIPGYGHAVLR	61.31	55.1426	1180.672	1181.166	7	2	distinct	0	0.8286

The equivalent proteins include

gi|28564950|gb|AAO32559.1|	37394.97	CIT3 [Saccharomyces kluyveri]

158. Group probability: 0.9808. Peptides of the group

WSGAVVSDIDPPAHRIR	43.71	54.4336	1874.975	1874.292	2	+2,+3	distinct	1	0.9808

The equivalent proteins include

gi|76260198|ref|ZP_00767837.1|	30981	hypothetical protein CaurDRAFT_3259 [Chloroflexus aurantiacus J-10-fl]

159. Group probability: 0.9801. Peptides of the group

GVNWASFHPTLPLIVSGADDR	51.78	53.5097	2251.138	2251.779	8	+2,+3	distinct	0	0.9801

The equivalent proteins include

gi|108868541|gb|EAT32766.1|	140260.25	coatomer [Aedes aegypti]
gi|108870473|gb|EAT34698.1|	140791.43	coatomer [Aedes aegypti]
gi|54641517|gb|EAL30267.1|	141311.63	GA20724-PA [Drosophila pseudoobscura]
gi|24655452|ref|NP_728648.1|	140951.6	-coatomer protein CG7961-PB, isoform B [Drosophila melanogaster]
gi|50918233|ref|XP_469513.1|	137434.92	putative alpha-coat protein [Oryza sativa]
gi|50918235|ref|XP_469514.1|	137418.94	putative alpha-coat protein [Oryza sativa]
gi|15226538|ref|NP_179734.1|	137407.07	protein transporter/ transporter [Arabidopsis thaliana]
gi|45357045|gb|AAS58474.1|	136808.66	coatomer alpha subunit [Hordeum vulgare subsp. vulgare]

160. Group probability: 0.9796. Peptides of the group

LVDLVNKLNLADK	45.61	54.7989	1453.850	1453.758	2	+2,+3	distinct	1	0.9796

The equivalent proteins include

gi|15076994|gb|AAK83019.1|	42486.33	putative glycosyl transferase WbdM [Salmonella enterica]

161. Group probability: 0.9784. Peptides of the group

TTGCVLDSGDGVSHTVPIYEGYALPHAVIR	66.63	50.9288	3183.566	3184.421	9	+2,+3	distinct	0	0.9784

The equivalent proteins include

gi|57864662|gb|AAW56951.1|	29293.65	actin [Phaeodactylum tricornutum]
gi|54300518|gb|AAV32834.1|	27066.67	actin [Phaeodactylum tricornutum]

162. Group probability: 0.9775. Peptides of the group

NVLFVISKPDVFK	64.93	54.7602	1504.865	1505.666	3	2	distinct	0	0.9775

The equivalent proteins include

gi|4115918|gb|AAD03429.1|	25580.32	similar to nascent polypeptide associated complex alpha chain [Arabidopsis thaliana]
gi|15235122|ref|NP_192786.1|	23157.29	unknown protein [Arabidopsis thaliana]

163. Group probability: 0.9773. Peptides of the group

PEEHPVLLTEAPINPK	63.51	54.3057	1782.952	1784.318	4	2	distinct	0	0.9773

The equivalent proteins include

gi|83700630|gb|ABC41107.1|	23946.06	actin [Trichoderma koningiopsis]
gi|83700636|gb|ABC41110.1|	25557.96	actin [Trichoderma koningiopsis]
gi|84314104|gb|ABC55663.1|	22492.43	actin [Trichoderma ovalisporum]
gi|84314108|gb|ABC55665.1|	25671.05	actin [Trichoderma caribbaeum]
gi|84314110|gb|ABC55666.1|	24331.26	actin [Trichoderma ovalisporum]
gi|87133580|gb|ABD24432.1|	23815.02	actin [Trichoderma petersenii]

164. Group probability: 0.9771. Peptides of the group

HGGGGGGFGGGGFGSR	63.66	55.3841	1319.575	1320.155	1	2	distinct	0	0.9771

The equivalent proteins include

gi|181402|gb|AAC83410.1|	66110.5	epidermal cytokeratin 2 [Homo sapiens]
gi|68563400|gb|AAH99643.1|	65678.32	Keratin 2A (epidermal ichthyosis bullosa of Siemens) [Homo sapiens]

165. Group probability: 0.9758. Peptides of the group

EHIILAR	50.08	55.9587	850.502	850.484	13	+1,+2	distinct	0	0.9758

The equivalent proteins include

gi|84494790|ref|ZP_00993909.1|	43889.46	elongation factor [Janibacter sp. HTCC2649]
gi|44982911|gb|AAS52141.1|	68617.07	ADR221Cp [Ashbya gossypii ATCC 10895]
gi|82499264|ref|ZP_00884712.1|	44217.72	Translation elongation factor Tu:Small GTP-binding protein domain [Caldicellulosiruptor saccharolyt
gi|82527417|ref|ZP_00886831.1|	36039.34	COG0050: GTPases - translation elongation factors [Burkholderia pseudomallei 1106a]
gi|82527894|ref|ZP_00887194.1|	26368.23	COG0050: GTPases - translation elongation factors [Burkholderia pseudomallei 1106a]
gi|94493157|ref|ZP_01300361.1|	43726.31	hypothetical protein Rgryl_01000989 [Rickettsiella grylli]
gi|94498474|ref|ZP_01305030.1|	42980.2	translation elongation factor [Sphingomonas sp. SKA58]
gi|94502270|ref|ZP_01308753.1|	43892.13	translation elongation factor Tu [Candidatus Sulcia muelleri str. Hc (Homalodisca coagulata)]
gi|640371|pdb|1EFT|	44698.17	Elongation Factor Tu (Ef-Tu) Complexed With Guanosine-5'-(Beta,Gamma-Imido) Triphosphate (Gdpnp)
gi|62512633|ref|ZP_00384258.1|	43546.34	COG0050: GTPases - translation elongation factors [Lactobacillus casei ATCC 334]
gi|83622553|ref|ZP_00932862.1|	19091.57	COG0050: GTPases - translation elongation factors [Burkholderia mallei JHU]
gi|83749364|ref|ZP_00946360.1|	43296.24	Protein Translation Elongation Factor Tu (EF-TU) [Ralstonia solanacearum UW551]
gi|83751218|ref|ZP_00947632.1|	42833.13	COG0050: GTPases - translation elongation factors [Bartonella bacilliformis KC583]
gi|83751314|ref|ZP_00947727.1|	42817.1	COG0050: GTPases - translation elongation factors [Bartonella bacilliformis KC583]
gi|2624676|pdb|1AIP|F	44710.11	Chain F, Ef-Tu Ef-Ts Complex From Thermus Thermophilus

gi|83750553|ref|ZP_00946984.1|	42399.86	COG0050: GTPases - translation elongation factors [Bartonella bacilliformis KC583]
gi|83858582|ref|ZP_00952104.1|	43146.89	translation elongation factor Tu [Oceanicaulis alexandrii HTCC2633]
gi|14488802|pdb|1HA3|B	44680.13	Chain B, Elongation Factor Tu In Complex With Aurodox
gi|84356469|ref|ZP_00981314.1|	29018.7	COG0050: GTPases - translation elongation factors [Burkholderia cenocepacia PC184]
gi|67644743|ref|ZP_00443119.1|	19861	COG0050: GTPases - translation elongation factors [Burkholderia mallei NCTC 10247]
gi|67645167|ref|ZP_00443471.1|	36595.63	COG0050: GTPases - translation elongation factors [Burkholderia mallei NCTC 10247]
gi|71482396|ref|ZP_00662089.1|	36824.9	Translation elongation factor Tu:Small GTP-binding protein domain [Prosthecochloris vibrioformis DS
gi|67734561|ref|ZP_00485683.1|	28147.24	COG0050: GTPases - translation elongation factors [Burkholderia pseudomallei 668]
gi|666130|gb|AAA62238.1|	43634.47	elongation factor Tu
gi|71548897|ref|ZP_00669121.1|	43025.33	Translation elongation factor Tu:Small GTP-binding protein domain [Nitrosomonas eutropha C71]
gi|71549903|ref|ZP_00670075.1|	43011.31	Translation elongation factor Tu:Small GTP-binding protein domain [Nitrosomonas eutropha C71]
gi|84685515|ref|ZP_01013413.1|	42984.82	translation elongation factor Tu [Rhodobacterales bacterium HTCC2654]
gi|84703916|ref|ZP_01017744.1|	43213.85	probable elongation factor tu protein [Parvularcula bermudensis HTCC2503]
gi|71839071|ref|ZP_00678825.1|	43109.3	Translation elongation factor Tu:Small GTP-binding protein domain [Pelobacter propionicus DSM 2379]
gi|84714770|ref|ZP_01022062.1|	43204.13	Translation elongation factor Tu:Small GTP-binding protein domain [Polaromonas naphthalenivorans CJ
gi|67919959|ref|ZP_00513499.1|	43170.53	Translation elongation factor Tu:Small GTP-binding protein domain [Chlorobium limicola DSM 245]
gi|67934428|ref|ZP_00527483.1|	43636.56	Translation elongation factor Tu:Small GTP-binding protein domain [Solibacter usitatus Ellin6076]
gi|67935584|ref|ZP_00528604.1|	43318.58	Translation elongation factor Tu:Small GTP-binding protein domain [Chlorobium phaeobacteroides DSM
gi|85709060|ref|ZP_01040126.1|	42363.57	translation elongation factor [Erythrobacter sp. NAP1]
gi|74020391|ref|ZP_00690984.1|	16238.05	Protein synthesis factor, GTP-binding [Burkholderia ambifaria AMMD]
gi|24987755|pdb|1MJ1|A	46011.24	Chain A, Fitting The Ternary Complex Of Ef-TuTRNAGTP AND RIBOSOMAL Proteins Into A 13 A Cryo-Em Map
gi|67940771|ref|ZP_00533113.1|	43140.27	Translation elongation factor Tu:Small GTP-binding protein domain [Chlorobium phaeobacteroides BS1]
gi|85715133|ref|ZP_01046117.1|	43408.35	elongation factor Tu [Nitrobacter sp. Nb-311A]
gi|68550993|ref|ZP_00590425.1|	42973.39	Translation elongation factor Tu:Small GTP-binding protein domain [Pelodictyon phaeoclathratiforme
gi|68553824|ref|ZP_00593176.1|	43129.25	Translation elongation factor Tu:Small GTP-binding protein domain [Prosthecochloris aestuarii DSM 2
gi|76261707|ref|ZP_00769307.1|	44218.91	Translation elongation factor Tu:Small GTP-binding protein domain [Chloroflexus aurantiacus J-10-fl
gi|88812771|ref|ZP_01128017.1|	43604.06	Translation elongation factor Tu [Nitrococcus mobilis Nb-231]

gi|77740844|ref|ZP_00809330.1|	43563.36	Translation elongation factor Tu:Small GTP-binding protein domain [Rhodopseudomonas palustris BisA5
gi|88937672|ref|ZP_01143224.1|	43028.24	Translation elongation factor Tu:Small GTP-binding protein domain [Geobacter uraniumreducens Rf4]
gi|88938871|ref|ZP_01144323.1|	42772.91	translation elongation factor Tu [Acidiphilium cryptum JF-5]
gi|88950284|ref|ZP_01152892.1|	43268.91	Translation elongation factor Tu:Small GTP-binding protein domain [Halorhodospira halophila SL1]
gi|88950296|ref|ZP_01152904.1|	43282.93	Translation elongation factor Tu:Small GTP-binding protein domain [Halorhodospira halophila SL1]
gi|78698562|ref|ZP_00863063.1|	43683.55	Translation elongation factor Tu:Small GTP-binding protein domain [Bradyrhizobium sp. BTAi1]
gi|78702842|ref|ZP_00867264.1|	43460.74	Translation elongation factor Tu:Small GTP-binding protein domain [Alkalilimnicola ehrlichei MLHE-1
gi|89211479|ref|ZP_01189843.1|	43550.01	Translation elongation factor Tu:Small GTP-binding protein domain [Halothermothrix orenii H 168]
gi|89359809|ref|ZP_01197629.1|	43520.4	Translation elongation factor Tu:Small GTP-binding protein domain [Xanthobacter autotrophicus Py2]
gi|90409551|ref|ZP_01217578.1|	42383.68	Translation elongation factor EF-Tu [Psychromonas sp. CNPT3]
gi|90417780|ref|ZP_01225692.1|	43046.87	translation elongation factor Tu [Aurantimonas sp. SI85-9A1]
gi|82533616|ref|ZP_00892677.1|	19235.55	hypothetical protein Bpse110_02005085 [Burkholderia pseudomallei 1106b]
gi|91221631|ref|ZP_01257346.1|	30466.52	elongation factor Tu [Psychroflexus torquis ATCC 700755]
gi|82407272|pdb|1OB5|E	44712.18	Chain E, T. Aquaticus Elongation Factor Ef-Tu Complexed With The Antibiotic Enacyloxin Iia, A Gtp A
gi|93278983|pdb|2C77|A	44696.12	Chain A, Ef-Tu Complexed With A Gtp Analog And The Antibiotic Ge2270 A
gi|93278984|pdb|2C78|A	44652.1	Chain A, Ef-Tu Complexed With A Gtp Analog And The Antibiotic Pulvomycin
gi|2654449|gb|AAB87734.1|	43227.32	elongation factor Tu [Thiomonas cuprina]
gi|93449979|gb|EAT01385.1|	43563.11	Translation elongation factor Tu:Small GTP-binding protein domain [delta proteobacterium MLMS-1]
gi|93450012|gb|EAT01401.1|	43063.93	Translation elongation factor Tu:Small GTP-binding protein domain [delta proteobacterium MLMS-1]
gi|93453181|gb|EAT03645.1|	43526.09	Translation elongation factor Tu:Small GTP-binding protein domain [delta proteobacterium MLMS-1]
gi|93453272|gb|EAT03721.1|	43523.14	Translation elongation factor Tu:Small GTP-binding protein domain [delta proteobacterium MLMS-1]
gi|31541275|gb|AAP56576.1|	43834.39	TufB [Mycoplasma gallisepticum R]
gi|71796439|gb|AAZ41190.1|	43984.61	elongation factor Tu [Candidatus Blochmannia pennsylvanicus str. BPEN]
gi|33301059|sp|Q822I4|EFTU_CHLCV	43427.19	Elongation factor Tu (EF-Tu)
gi|13626414|sp|Q9PK73|EFTU_CHLMU	43547.29	Elongation factor Tu (EF-Tu)
gi|23014093|ref|ZP_00053930.1|	43312.17	COG0050: GTPases - translation elongation factors [Magnetospirillum magnetotacticum MS-1]
gi|23013732|ref|ZP_00053596.1|	21017.49	COG0050: GTPases - translation elongation factors [Magnetospirillum magnetotacticum MS-1]
gi|23011810|ref|ZP_00052061.1|	47168.3	COG0050: GTPases - translation elongation factors [Magnetospirillum magnetotacticum MS-1]
gi|23024624|ref|ZP_00063827.1|	39816.25	COG0050: GTPases - translation elongation factors [Leuconostoc mesenteroides subsp. mesenteroides A

gi|47574116|ref|ZP_00244152.1|	43346.15	COG0050: GTPases - translation elongation factors [Rubrivivax gelatinosus PM1]
gi|17430065|emb|CAD16750.1|	43425.23	probable elongation factor tu (ef-tu protein) [Ralstonia solanacearum]
gi|14021291|dbj|BAB47904.1|	42800.28	elongation factor Tu [Mesorhizobium loti MAFF303099]
gi|35214501|dbj|BAC91869.1|	44846.19	protein synthesis elongation factor Tu [Gloeobacter violaceus PCC 7421]
gi|74099607|gb|AAZ99038.1|	25085.7	Tuf [Lactobacillus helveticus]
gi|74099617|gb|AAZ99041.1|	19519.16	elongation factor Tu [Lactobacillus helveticus]
gi|74099627|gb|AAZ99045.1|	22477.73	elongation factor Tu [Lactobacillus helveticus]
gi|17982679|gb|AAL51923.1|	44540.89	Protein Translation Elongation Factor Tu (EF-TU) [Brucella melitensis 16M]
gi|21648234|gb|AAM73407.1|	42929.2	translation elongation factor TU [Chlorobium tepidum TLS]
gi|74316421|ref|YP_314161.1|	43166.21	translation elongation factor Tu [Thiobacillus denitrificans ATCC 25259]
gi|7190634|gb|AAF39428.1|	44223.63	translation elongation factor Tu [Chlamydia muridarum Nigg]
gi|83415018|dbj|BAE53773.1|	24375.72	elongation factor Tu [uncultured bacterium]
gi|83415020|dbj|BAE53774.1|	24272.7	elongation factor Tu [uncultured bacterium]
gi|85539926|dbj|BAE78421.1|	40628.63	elongation factor TU [Thorea hispida]
gi|85539928|dbj|BAE78422.1|	40645.72	elongation factor TU [Thorea hispida]
gi|85539930|dbj|BAE78423.1|	40610.65	elongation factor TU [Thorea okadae]
gi|86357289|ref|YP_469181.1|	42782.05	elongation factor EF-Tu protein [Rhizobium etli CFN 42]
gi|86357303|ref|YP_469195.1|	42925.1	elongation factor EF-Tu protein [Rhizobium etli CFN 42]
gi|89257965|gb|ABD65253.1|	39767.49	elongation factor TU [Aster yellows phytoplasma]
gi|89898120|ref|YP_515230.1|	43392.19	translation elongation factor Tu [Chlamydophila felis Fe/C-56]
gi|89574437|gb|ABD77430.1|	33998.35	elongation factor Tu [Candidatus Phytoplasma solani]
gi|89574439|gb|ABD77431.1|	34024.43	elongation factor Tu [Candidatus Phytoplasma solani]
gi|89574441|gb|ABD77432.1|	33990.45	elongation factor Tu [Candidatus Phytoplasma solani]
gi|89574443|gb|ABD77433.1|	34029.31	elongation factor Tu [Candidatus Phytoplasma solani]
gi|83648866|ref|YP_437301.1|	43501.09	translation elongation factor Tu [Hahella chejuensis KCTC 2396]
gi|83814995|ref|YP_445165.1|	43815.64	translation elongation factor Tu [Salinibacter ruber DSM 13855]
gi|85858144|ref|YP_460346.1|	43998.72	protein translation Elongation Factor Tu (EF-TU) [Syntrophus aciditrophicus SB]
gi|86605983|ref|YP_474746.1|	45199.35	translation elongation factor Tu [Synechococcus sp. JA-3-3Ab]
gi|86608401|ref|YP_477163.1|	44884.14	translation elongation factor Tu [Synechococcus sp. JA-2-3B'a(2-13)]
gi|28271577|emb|CAD64482.1|	43350.13	elongation factor Tu [Lactobacillus plantarum WCFS1]
gi|82701898|ref|YP_411464.1|	43012.15	translation elongation factor Tu [Nitrosospira multiformis ATCC 25196]
gi|77918300|ref|YP_356115.1|	43957.98	translation elongation factor Tu [Pelobacter carbinolicus DSM 2380]
gi|77918313|ref|YP_356128.1|	43983.03	translation elongation factor Tu [Pelobacter carbinolicus DSM 2380]
gi|44357|emb|CAA40415.1|	43625.67	elongation factor Tu [Mycoplasma hominis]
gi|45658705|ref|YP_002791.1|	43660.53	elongation factor Tu [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]
gi|560825|emb|CAA54322.1|	42729.02	elongation factor Tu [Prosthecochloris vibrioformis]
gi|587581|emb|CAA54325.1|	43125.02	elongation factor Tu [Taxeobacter ocellatus]
gi|587579|emb|CAA54198.1|	43227.32	elongation factor Tu [Thiomonas cuprina]

gi|1666548|emb|CAA67991.1|	42771	elongation factor EF-Tu [Agrobacterium tumefaciens]
gi|83312247|ref|YP_422511.1|	43311.15	GTPase - translation elongation factor [Magnetospirillum magneticum AMB-1]
gi|83591278|ref|YP_431287.1|	44438.66	translation elongation factor Tu [Moorella thermoacetica ATCC 39073]
gi|61676020|gb|AAX51675.1|	29665.31	translation elongation factor TU [Neochlamydia hartmannellae]
gi|91774633|ref|YP_544389.1|	43037.19	translation elongation factor Tu [Methylobacillus flagellatus KT]
gi|15074287|emb|CAC45933.1|	42893.13	PROBABLE ELONGATION FACTOR TU PROTEIN [Sinorhizobium meliloti]
gi|71026283|ref|XP_762822.1|	49470.44	elongation factor Tu [Theileria parva strain Muguga]
gi|32186878|gb|AAP72171.1|	43787.49	reconstructed ancestral elongation factor Tu ML-meso [synthetic construct]
gi|32186880|gb|AAP72172.1|	43660.77	reconstructed ancestral elongation factor Tu ML-stem [synthetic construct]
gi|71912293|gb|AAZ53217.1|	31020.88	Tu elongation factor protein [Green leafhopper phytoplasma]
gi|90961619|ref|YP_535535.1|	43303.98	Protein Translation Elongation Factor Tu [Lactobacillus salivarius subsp. salivarius UCC118]
gi|94676917|ref|YP_588930.1|	43572.71	translation elongation factor Tu [Baumannia cicadellinicola str. Hc (Homalodisca coagulata)]
gi|94987377|ref|YP_595310.1|	43847.41	GTPases-translation elongation factors [Lawsonia intracellularis PHE/MN1-00]
gi|74420424|gb|ABA04623.1|	43380.32	translation elongation factor Tu [Nitrobacter winogradskyi Nb-255]
gi|89902557|ref|YP_525028.1|	43178.09	translation elongation factor Tu [Rhodoferax ferrireducens T118]
gi|20517297|gb|AAM25437.1|	44293.73	GTPases - translation elongation factors [Thermoanaerobacter tengcongensis MB4]
gi|20517312|gb|AAM25451.1|	44265.73	GTPases - translation elongation factors [Thermoanaerobacter tengcongensis MB4]
gi|104530284|gb|ABF72846.1|	31655.24	translation elongation factor TU [Wheat blue dwarf phytoplasma]
gi|108712132|gb|ABF99927.1|	33977.76	Elongation factor Tu, mitochondrial precursor, putative, expressed [Oryza sativa (japonica cultivar
gi|26553484|ref|NP_757418.1|	43218.21	elongation factor Tu [Mycoplasma penetrans HF-2]
gi|108758449|ref|YP_631497.1|	43445.58	translation elongation factor Tu [Myxococcus xanthus DK 1622]
gi|104773860|ref|YP_618840.1|	43311.01	Elongation factor Tu [Lactobacillus delbrueckii subsp. bulgaricus ATCC 11842]
gi|76884115|gb|ABA58796.1|	43760.3	Translation elongation factor Tu [Nitrosococcus oceani ATCC 19707]
gi|77997279|gb|ABB16178.1|	44450.84	translation elongation factor Tu [Carboxydothermus hydrogenoformans Z-2901]
gi|77997296|gb|ABB16195.1|	44422.83	translation elongation factor Tu [Carboxydothermus hydrogenoformans Z-2901]
gi|71725852|gb|AAZ39051.1|	43487.46	elongation factor EF-Tu [Candidatus Phytoplasma australiense]
gi|73333688|gb|AAZ74785.1|	30344.57	elongation factor EF-Tu [Candidatus Phytoplasma australiense]
gi|73333732|gb|AAZ74786.1|	30330.56	elongation factor EF-Tu [Candidatus Phytoplasma australiense]
gi|73333897|gb|AAZ74787.1|	30360.57	elongation factor EF-Tu [Candidatus Phytoplasma australiense]
gi|73334102|gb|AAZ74788.1|	30392.57	elongation factor EF-Tu [Candidatus Phytoplasma australiense]
gi|73334150|gb|AAZ74789.1|	30348.57	elongation factor EF-Tu [Candidatus Phytoplasma australiense]
gi|73334222|gb|AAZ74791.1|	30344.57	elongation factor EF-Tu [Candidatus Phytoplasma australiense]

gi|73334285|gb|AAZ74792.1|	30345.52	elongation factor EF-Tu [Candidatus Phytoplasma australiense]
gi|78165970|gb|ABB23068.1|	43102.34	Translation elongation factor Tu [Pelodictyon luteolum DSM 273]
gi|78172008|gb|ABB29104.1|	43132.4	Translation elongation factor Tu [Chlorobium chlorochromatii CaD3]
gi|6539452|dbj|BAA88134.1|	43798.17	EF-Tu [Porphyromonas gingivalis]
gi|34540215|ref|NP_904694.1|	43842.24	elongation factor Tu [Porphyromonas gingivalis W83]
gi|6539456|dbj|BAA88136.1|	43870.23	EF-Tu [Porphyromonas gingivalis]
gi|6539460|dbj|BAA88138.1|	43812.23	EF-Tu [Porphyromonas gingivalis]
gi|6539462|dbj|BAA88139.1|	43839.19	EF-Tu [Tannerella forsythensis]
gi|150141|gb|AAA25411.1|	43595.66	elongation factor Tu
gi|55773076|dbj|BAD71517.1|	44811.14	elongation factor Tu (EF-Tu) [Thermus thermophilus HB8]
gi|52427292|gb|AAU47885.1|	43192.14	translation elongation factor Tu [Burkholderia mallei ATCC 23344]
gi|119203|sp|P26184|EFTU_FLESI	44157.4	Elongation factor Tu (EF-Tu)
gi|312960|emb|CAA43956.1|	44811.17	elongation factor Tu [Thermus thermophilus]
gi|95931444|ref|ZP_01314150.1|	43244.92	translation elongation factor Tu [Desulfuromonas acetoxidans DSM 684]
gi|95930700|ref|ZP_01313433.1|	43172.9	translation elongation factor Tu [Desulfuromonas acetoxidans DSM 684]
gi|99906675|ref|ZP_01315221.1|	18482.19	hypothetical protein Bpse1_03005450 [Burkholderia pseudomallei 1655]
gi|99907582|ref|ZP_01315465.1|	29476.98	hypothetical protein Bpse1_03005186 [Burkholderia pseudomallei 1655]
gi|100057078|ref|ZP_01320582.1|	40309.56	hypothetical protein BpseP_03005680 [Burkholderia pseudomallei Pasteur]
gi|90290117|ref|ZP_01209794.1|	39584.18	hypothetical protein Bpse17_02005171 [Burkholderia pseudomallei 1710a]
gi|100119128|ref|ZP_01326161.1|	32851.73	hypothetical protein BpseS_03005803 [Burkholderia pseudomallei S13]
gi|100120311|ref|ZP_01326530.1|	27590.98	hypothetical protein BpseS_03005437 [Burkholderia pseudomallei S13]
gi|100230799|ref|ZP_01332429.1|	18780.3	hypothetical protein Bpse4_03005114 [Burkholderia pseudomallei 406e]
gi|100263073|ref|ZP_01337950.1|	35731.2	hypothetical protein Bmal2_03004290 [Burkholderia mallei 2002721280]
gi|68245310|gb|EAN27438.1|	43281.14	Translation elongation factor Tu:Small GTP-binding protein domain [Magnetococcus sp. MC-1]
gi|9957206|gb|AAG09263.1|	42824.07	Eftu [EDTA-degrading bacterium BNC1]
gi|100916325|ref|ZP_01344808.1|	25718.97	hypothetical protein Bmal10_03002154 [Burkholderia mallei 10399]
gi|99082274|ref|YP_614428.1|	42848.63	translation elongation factor Tu [Silicibacter sp. TM1040]
gi|12045310|ref|NP_073121.1|	43191.42	elongation factor Tu [Mycoplasma genitalium G37]
gi|77965667|gb|ABB07047.1|	43135.12	translation elongation factor Tu [Burkholderia sp. 383]
gi|67550114|ref|ZP_00427922.1|	23790.91	Small GTP-binding protein domain [Burkholderia vietnamiensis G4]
gi|67550028|ref|ZP_00427854.1|	43234.15	Translation elongation factor Tu:Small GTP-binding protein domain [Burkholderia vietnamiensis G4]
gi|71899537|ref|ZP_00681693.1|	43091.14	Translation elongation factor Tu:Small GTP-binding protein domain [Xylella fastidiosa Ann-1]
gi|71899977|ref|ZP_00682123.1|	28571.32	Small GTP-binding protein domain [Xylella fastidiosa Ann-1]
gi|14279524|gb|AAK58633.1|	42989.29	elongation factor Tu [Ureaplasma parvum serovar 14]
gi|67876169|ref|ZP_00505128.1|	44274.61	Translation elongation factor Tu:Small GTP-binding protein domain [Clostridium thermocellum ATCC 27
gi|28199874|ref|NP_780188.1|	43164.14	elongation factor Tu [Xylella fastidiosa Temecula1]
gi|108763678|ref|YP_631272.1|	43459.6	translation elongation factor Tu [Myxococcus xanthus DK 1622]
gi|89893215|ref|YP_516702.1|	44066.31	hypothetical protein DSY0469 [Desulfitobacterium hafniense Y51]

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<tr><td>gi|91977671|ref|YP_570330.1|</td><td>43586.24</td><td>translation elongation factor Tu [Rhodopseudomonas palustris BisB5]</td></tr>
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<tr><td>gi|17935855|ref|NP_532645.1|</td><td>42770.02</td><td>elongation factor Tu [Agrobacterium tumefaciens str. C58]</td></tr>
<tr><td>gi|50875998|emb|CAG35838.1|</td><td>43683.01</td><td>probable elongation factor Tu [Desulfotalea psychrophila LSv54]</td></tr>
<tr><td>gi|50876011|emb|CAG35851.1|</td><td>43557.95</td><td>probable translation elongation factor EF-Tu [Desulfotalea psychrophila LSv54]</td></tr>
<tr><td>gi|23348072|gb|AAN30154.1|</td><td>42748.99</td><td>translation elongation factor Tu [Brucella suis 1330]</td></tr>
<tr><td>gi|62148348|emb|CAH64115.1|</td><td>43414.2</td><td>putative elongation factor Tu [Chlamydophila abortus S26/3]</td></tr>
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<tr><td>gi|60494891|emb|CAH09698.1|</td><td>43780.28</td><td>Elongation factor Tu [Bacteroides fragilis NCTC 9343]</td></tr>
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<tr><td>gi|22203350|gb|AAM92281.1|</td><td>42896.22</td><td>elongation factor TU [Bartonella henselae]</td></tr>
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gi|37901246|gb|AAO53238.1|	41768.6	elongation factor TU [Lepocinclis spirogyroides]
gi|4263511|gb|AAD15337.1|	49606.67	mitochondrial elongation factor Tu [Arabidopsis thaliana]
gi|13424877|gb|AAK25161.1|	43540.29	translation elongation factor EF-Tu [Caulobacter crescentus CB15]
gi|59802179|ref|YP_208891.1|	43195.99	putative translation elongation factor Tu [Neisseria gonorrhoeae FA 1090]
gi|46450746|gb|AAS97392.1|	43664.4	translation elongation factor Tu [Desulfovibrio vulgaris subsp. vulgaris str. Hildenborough]
gi|56313635|emb|CAI08280.1|	43462.27	Elongation factor Tu [Azoarcus sp. EbN1]
gi|7225357|gb|AAF40598.1|	43182.92	translation elongation factor Tu [Neisseria meningitidis MC58]
gi|29340052|gb|AAO77846.1|	43892.22	elongation factor Tu [Bacteroides thetaiotaomicron VPI-5482]
gi|39984907|gb|AAR36263.1|	43248.35	translation elongation factor Tu [Geobacter sulfurreducens PCA]
gi|48855335|ref|ZP_00309494.1|	43108.19	COG0050: GTPases - translation elongation factors [Cytophaga hutchinsonii]
gi|48865307|ref|ZP_00319169.1|	44197.68	COG0050: GTPases - translation elongation factors [Oenococcus oeni PSU-1]
gi|945204|gb|AAB84063.1|	36353.64	elongation factor EF-TU [non-culturable plant pathogenic bacterial sp.]
gi|945202|gb|AAB84061.1|	37141.12	elongation factor EF-TU [non-culturable plant pathogenic bacterial sp.]
gi|939760|gb|AAB84062.1|	37435.2	elongation factor EF-TU [non-culturable plant pathogenic bacterial sp.]
gi|48288|emb|CAA29397.1|	44797.13	unnamed protein product [Thermus thermophilus]
gi|86158370|ref|YP_465155.1|	43360.59	translation elongation factor Tu [Anaeromyxobacter dehalogenans 2CP-C]
gi|22299293|ref|NP_682540.1|	44974.16	elongation factor Tu [Thermosynechococcus elongatus BP-1]
gi|27380513|ref|NP_772042.1|	43568.58	elongation factor Tu [Bradyrhizobium japonicum USDA 110]
gi|50920113|ref|XP_470417.1|	48564.31	translational elongation factor Tu [Oryza sativa (japonica cultivar-group)]
gi|11181616|gb|AAG32661.1|	48746.33	translational elongation factor EF-TuM [Zea mays]
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gi|53804631|ref|YP_113534.1|	43190.22	translation elongation factor Tu [Methylococcus capsulatus str. Bath]
gi|13272297|gb|AAK17080.1|	44370.23	elongation factor Tu [Candidatus Carsonella ruddii]
gi|13310843|gb|AAK18635.1|	34482.24	elongation factor Tu [Candidatus Carsonella ruddii]
gi|13310852|gb|AAK18643.1|	34667.42	elongation factor Tu [Candidatus Carsonella ruddii]
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gi|7688111|emb|CAB89785.1|	39692.47	elongation factor TU [Aster yellows phytoplasma]
gi|7688117|emb|CAB89788.1|	39738.43	elongation factor TU [Aster yellows phytoplasma]
gi|7688119|emb|CAB89789.1|	39689.47	elongation factor TU [Aster yellows phytoplasma]
gi|7688123|emb|CAB89791.1|	39661.49	elongation factor TU [Aster yellows phytoplasma]
gi|7688127|emb|CAB89793.1|	39584.44	elongation factor TU [Aster yellows phytoplasma]
gi|7688129|emb|CAB89794.1|	39623.54	elongation factor TU [Aster yellows phytoplasma]
gi|8250492|emb|CAB93624.1|	12325.27	elongation factor Tu (EF-Tu) [Mycoplasma hominis]
gi|8250484|emb|CAB93620.1|	12295.26	elongation factor Tu (EF-Tu) [Mycoplasma hominis]
gi|22266008|emb|CAD11457.2|	28196.5	putative elongation factor Tu [Lactobacillus acidophilus]
gi|22266010|emb|CAD11458.2|	28195.48	putative elongation factor Tu [Lactobacillus helveticus]
gi|22266012|emb|CAD11459.2|	28206.57	putative elongation factor Tu [Lactobacillus amylovorus]
gi|22266014|emb|CAD11460.2|	28207.52	putative elongation factor Tu [Lactobacillus crispatus]
gi|22266016|emb|CAD11461.2|	28207.52	putative elongation factor Tu [Lactobacillus gallinarum]
gi|22266018|emb|CAD11462.2|	28195.48	putative elongation factor Tu [Lactobacillus gasseri]
gi|22266020|emb|CAD11463.2|	28182.37	putative elongation factor Tu [Lactobacillus johnsonii]
gi|22266022|emb|CAD11464.2|	28195.45	putative elongation factor Tu [Lactobacillus jensenii]
gi|22266024|emb|CAD11465.2|	27926.28	putative elongation factor Tu [Lactobacillus delbrueckii subsp. bulgaricus]
gi|22266026|emb|CAD11466.2|	28016.33	putative elongation factor Tu [Lactobacillus delbrueckii subsp. delbrueckii]
gi|22266146|emb|CAD30665.1|	28210.54	putative elongation factor Tu [Lactobacillus paracasei subsp. paracasei]
gi|22266030|emb|CAD11468.2|	28163.5	putative elongation factor Tu [Lactobacillus ruminis]
gi|22266032|emb|CAD11469.2|	28068.37	putative elongation factor Tu [Lactobacillus mali]
gi|22266034|emb|CAD11470.2|	27969.42	putative elongation factor Tu [Lactobacillus sharpeae]
gi|22266040|emb|CAD11473.2|	28329.38	putative elongation factor Tu [Lactobacillus coryniformis subsp. coryniformis]
gi|22266042|emb|CAD11474.2|	28002.31	putative elongation factor Tu [Lactobacillus delbrueckii subsp. lactis]
gi|22266044|emb|CAD11475.2|	28119.43	putative elongation factor Tu [Lactobacillus pentosus]
gi|22266046|emb|CAD11476.2|	28133.45	putative elongation factor Tu [Lactobacillus plantarum]
gi|22266054|emb|CAD11480.2|	28078.23	putative elongation factor Tu [Lactobacillus reuteri]
gi|22266056|emb|CAD11481.2|	28284.43	putative elongation factor Tu [Weissella confusa]
gi|22266064|emb|CAD11485.2|	28149.34	putative elongation factor Tu [Lactobacillus agilis]
gi|22266062|emb|CAD11484.2|	28291.51	putative elongation factor Tu [Lactobacillus murinus]
gi|22266068|emb|CAD11487.2|	28208.3	putative elongation factor Tu [Lactobacillus brevis]

gi|22266128|emb|CAD30656.1|	28241.59	putative elongation factor Tu [Lactobacillus casei]
gi|22266072|emb|CAD11489.2|	28173.5	putative elongation factor Tu [Lactobacillus suebicus]
gi|22266074|emb|CAD11490.2|	28341.66	putative elongation factor Tu [Lactobacillus malefermentans]
gi|22266076|emb|CAD11491.2|	28152.46	putative elongation factor Tu [Lactobacillus vaccinostercus]
gi|22266080|emb|CAD11493.2|	28053.17	putative elongation factor Tu [Lactobacillus fermentum]
gi|22266152|emb|CAD30868.1|	28196.53	putative elongation factor Tu [Lactobacillus rhamnosus]
gi|22266148|emb|CAD30703.1|	28147.46	putative elongation factor Tu [Lactobacillus paraplantarum]
gi|33520007|ref|NP_878839.1|	43732.48	elongation factor Tu (EF-Tu) [Candidatus Blochmannia floridanus]
gi|30249992|ref|NP_842062.1|	43015.24	GTPase-translation elongation factors and sulfate adenylate transferase subunit 1 [Nitrosomonas eur
gi|38422326|emb|CAE45328.1|	43333.07	unnamed protein product [Magnetospirillum gryphiswaldense]
gi|39936346|ref|NP_948622.1|	43594.31	elongation factor Tu [Rhodopseudomonas palustris CGA009]
gi|939971|emb|CAA54197.1|	41341.6	elongation factor Tu [Stigmatella aurantiaca]
gi|1149571|emb|CAA61511.1|	51637.41	mitochondrial elongation factor Tu [Arabidopsis thaliana]
gi|3766292|emb|CAA77086.1|	29861.41	elongation factor EF-Tu [Papaya dieback phytoplasma]
gi|72120293|gb|AAZ62556.1|	43289.19	Translation elongation factor Tu:Small GTP-binding protein domain [Ralstonia eutropha JMP134]
gi|71845580|gb|AAZ45076.1|	43419.08	Translation elongation factor Tu:Small GTP-binding protein domain [Dechloromonas aromatica RCB]
gi|21702609|gb|AAM76005.1|	43540.25	elongation factor Tu [Candidatus Tremblaya princeps]
gi|78220434|gb|ABB39783.1|	43692.3	translation elongation factor Tu [Desulfovibrio desulfuricans G20]
gi|91785480|ref|YP_560686.1|	43259.16	Translation elongation factor Tu [Burkholderia xenovorans LB400]
gi|91790282|ref|YP_551234.1|	43198.08	translation elongation factor Tu [Polaromonas sp. JS666]
gi|91774621|ref|YP_544377.1|	43009.18	translation elongation factor Tu [Methylobacillus flagellatus KT]
gi|92117096|ref|YP_576825.1|	43382.32	translation elongation factor Tu [Nitrobacter hamburgensis X14]
gi|78193099|gb|ABB30866.1|	43237.35	Translation elongation factor Tu [Geobacter metallireducens GS-15]
gi|85001349|ref|XP_955393.1|	49576.46	elongation factor tu [Theileria annulata strain Ankara]
gi|431279|gb|AAA19798.1|	43451.3	elongation factor Tu [Chlamydia trachomatis]
gi|37913004|gb|AAR05333.1|	43506	predicted translation elongation factor Tu [uncultured marine alpha proteobacterium HOT2C01]
gi|94312272|ref|YP_585482.1|	43346.21	translation elongation factor Tu [Ralstonia metallidurans CH34]
gi|38426823|gb|AAR20453.1|	32149.54	elongation factor EF-Tu [Candidatus Phytoplasma australiense]
gi|38426821|gb|AAR20452.1|	28251.58	elongation factor EF-Tu [Candidatus Phytoplasma australiense]
gi|38426825|gb|AAR20454.1|	28479.74	elongation factor EF-Tu [Candidatus Phytoplasma australiense]
gi|38426862|gb|AAR20476.1|	29957.42	elongation factor EF-Tu [Candidatus Phytoplasma australiense]
gi|38426829|gb|AAR20456.1|	18016.4	elongation factor EF-Tu [Candidatus Phytoplasma australiense]
gi|38488993|gb|AAR21227.1|	25918.83	Tuf [Lactobacillus rhamnosus]
gi|38606869|gb|AAR25425.1|	25607.46	Tuf [Lactobacillus gallinarum]
gi|38606871|gb|AAR25426.1|	25619.36	Tuf [Lactobacillus helveticus]
gi|38606873|gb|AAR25427.1|	25659.46	Tuf [Lactobacillus crispatus]
gi|38606875|gb|AAR25428.1|	25994.38	Tuf [Lactobacillus gasseri]

gi|38606877|gb|AAR25429.1|	25741.34	Tuf [Lactobacillus johnsonii]
gi|38606881|gb|AAR25431.1|	26085.55	Tuf [Lactobacillus casei]
gi|38606885|gb|AAR25433.1|	25967.47	Tuf [Lactobacillus paracasei]
gi|38606899|gb|AAR25440.1|	26008.43	Tuf [Lactobacillus gasseri]
gi|85057736|ref|YP_456652.1|	43494.57	protein translation elongation factor Tu [Aster yellows witches'-broom phytoplasma AYWB]
gi|94985969|ref|YP_605333.1|	44300.65	translation elongation factor Tu [Deinococcus geothermalis DSM 11300]
gi|46242585|gb|AAS83410.1|	25441.17	elongation factor Tu [Lactobacillus suntoryeus]
gi|108804989|ref|YP_644926.1|	44102.6	translation elongation factor Tu [Rubrobacter xylanophilus DSM 9941]
gi|38195601|gb|AAR13464.1|	41152.8	protein chain elongation factor EF-Tu [Candidatus Liberibacter asiaticus]
gi|14279518|gb|AAK58630.1|	43005.29	elongation factor Tu [Ureaplasma urealyticum serovar 13]
gi|6137417|pdb|1D2E|D	43986.9	Chain D, Crystal Structure Of Mitochondrial Ef-Tu In Complex With Gdp
gi|108871455|gb|EAT35680.1|	49695.14	elongation factor tu (ef-tu) [Aedes aegypti]
gi|54641072|gb|EAL29823.1|	199734.07	GA16901-PA [Drosophila pseudoobscura]
gi|88183134|gb|EAQ90602.1|	48944.13	hypothetical protein CHGG_02537 [Chaetomium globosum CBS 148.51]
gi|2119917|pir||S62768	49718.14	translation elongation factor EF-Tu precursor - bovine
gi|56967054|pdb|1XB2|A	45114.17	Chain A, Crystal Structure Of Bos Taurus Mitochondrial Elongation Factor TuTS COMPLEX
gi|7676153|sp|O83217|EFTU_TREPA	43461.46	Elongation factor Tu (EF-Tu)
gi|90298167|gb|EAS27798.1|	48477.98	hypothetical protein CIMG_09002 [Coccidioides immitis RS]
gi|88909611|sp|P84172|EFTU_CHICK	38511.34	Elongation factor Tu, mitochondrial precursor (EF-Tu)
gi|83766720|dbj|BAE56860.1|	46811.02	unnamed protein product [Aspergillus oryzae]
gi|46125609|ref|XP_387358.1|	49393.2	hypothetical protein FG07182.1 [Gibberella zeae PH-1]
gi|73958590|ref|XP_536924.2|	63603.4	PREDICTED: similar to Tu translation elongation factor, mitochondrial [Canis familiaris]
gi|32425705|gb|AAH01633.2|	50185.44	Tu translation elongation factor, mitochondrial [Homo sapiens]
gi|109128036|ref|XP_001103438.1|	49356.99	PREDICTED: Tu translation elongation factor, mitochondrial isoform 2 [Macaca mulatta]
gi|109128038|ref|XP_001103519.1|	50257.43	PREDICTED: Tu translation elongation factor, mitochondrial isoform 3 [Macaca mulatta]
gi|109128040|ref|XP_001103284.1|	35199.52	PREDICTED: Tu translation elongation factor, mitochondrial isoform 1 [Macaca mulatta]
gi|55643661|ref|XP_510904.1|	57697.28	PREDICTED: hypothetical protein XP_510904 [Pan troglodytes]
gi|91178547|gb|ABE27739.1|	26517.57	mitochondrial GTPase elongation factor Tu [Candida albicans]
gi|91178549|gb|ABE27740.1|	26173.64	mitochondrial GTPase elongation factor Tu [Candida catenulata]
gi|91178551|gb|ABE27741.1|	26469.61	mitochondrial GTPase elongation factor Tu [Candida dubliniensis]
gi|91178553|gb|ABE27742.1|	26583.69	mitochondrial GTPase elongation factor Tu [Debaryomyces hansenii]
gi|91178555|gb|ABE27743.1|	26710.77	mitochondrial GTPase elongation factor Tu [Candida glabrata]
gi|91178557|gb|ABE27744.1|	26505.76	mitochondrial GTPase elongation factor Tu [Pichia guilliermondii]
gi|91178559|gb|ABE27745.1|	26568.66	mitochondrial GTPase elongation factor Tu [Candida haemulonii]
gi|91178561|gb|ABE27746.1|	26617.83	mitochondrial GTPase elongation factor Tu [Candida inconspicua]
gi|91178563|gb|ABE27747.1|	26621.71	mitochondrial GTPase elongation factor Tu [Kluyveromyces marxianus]

gi|91178565|gb|ABE27748.1|	26791.88	mitochondrial GTPase elongation factor Tu [Issatchenkia orientalis]
gi|91178567|gb|ABE27749.1|	26605.82	mitochondrial GTPase elongation factor Tu [Pichia fermentans]
gi|91178569|gb|ABE27750.1|	26388.52	mitochondrial GTPase elongation factor Tu [Yarrowia lipolytica]
gi|91178571|gb|ABE27751.1|	26562.68	mitochondrial GTPase elongation factor Tu [Clavispora lusitaniae]
gi|91178575|gb|ABE27753.1|	26505.7	mitochondrial GTPase elongation factor Tu [Pichia anomala]
gi|91178577|gb|ABE27754.1|	26557.5	mitochondrial GTPase elongation factor Tu [Candida rugosa]
gi|91178579|gb|ABE27755.1|	26584.49	mitochondrial GTPase elongation factor Tu [Kluyveromyces lactis]
gi|91178581|gb|ABE27756.1|	26514.37	mitochondrial GTPase elongation factor Tu [Candida tropicalis]
gi|91178583|gb|ABE27757.1|	26587.52	mitochondrial GTPase elongation factor Tu [Candida viswanathii]
gi|91178585|gb|ABE27758.1|	26548.61	mitochondrial GTPase elongation factor Tu [Candida zeylanoides]
gi|39585273|emb|CAE57516.1|	54746.5	Hypothetical protein CBG00491 [Caenorhabditis briggsae]
gi|47219666|emb|CAG02711.1|	43932.85	unnamed protein product [Tetraodon nigroviridis]
gi|47219667|emb|CAG02712.1|	49256.2	unnamed protein product [Tetraodon nigroviridis]
gi|13559775|gb|AAK29979.1|	54885.54	Tu elongation factor (ef-tu), mitochondrial protein 1 [Caenorhabditis elegans]
gi|1181593|dbj|BAA07492.1|	54754.5	elongation factor Tu homologue precursor [Caenorhabditis elegans]
gi|85103402|ref|XP_961513.1|	48103.5	hypothetical protein ((AL513467) probable translation elongation factor EF-Tu precursor, mitochond
gi|70995660|ref|XP_752585.1|	48426.93	translation elongation factor EF-Tu [Aspergillus fumigatus Af293]
gi|833999|gb|AAC60647.1|	49844.25	P43 [Homo sapiens]
gi|3322451|gb|AAC65172.1|	54839.21	translation elongation factor TU (tuf) [Treponema pallidum subsp. pallidum str. Nichols]
gi|704416|gb|AAB00499.1|	49851.32	elongation factor Tu
gi|27806367|ref|NP_776632.1|	49709.14	Tu translation elongation factor, mitochondrial [Bos taurus]
gi|5105535|dbj|BAA80848.1|	48631.85	437aa long hypothetical elongation factor 1-alpha [Aeropyrum pernix K1]
gi|6324761|ref|NP_014830.1|	48112.76	Mitochondrial translation elongation factor Tu; comprises both GTPase and guanine nucleotide exchan
gi|42526277|ref|NP_971375.1|	43931.64	translation elongation factor Tu [Treponema denticola ATCC 35405]
gi|50556838|ref|XP_505827.1|	46741.08	hypothetical protein [Yarrowia lipolytica]
gi|899285|emb|CAA59169.1|	49852.31	mitochondrial elongation factor Tu [Homo sapiens]
gi|4760342|emb|CAB42365.1|	48593.9	SPBC9B6.04c [Schizosaccharomyces pombe]
gi|44980576|gb|AAS50509.1|	47485.33	AAR143Wp [Ashbya gossypii ATCC 10895]
gi|55240516|gb|EAA09467.2|	43767.7	ENSANGP00000010016 [Anopheles gambiae str. PEST]
gi|57228256|gb|AAW44713.1|	51012.5	translation elongation factor, putative [Cryptococcus neoformans var. neoformans JEC21]
gi|68473812|ref|XP_719009.1|	46904.07	translation elongation factor Tu [Candida albicans SC5314]
gi|67517809|ref|XP_658688.1|	51076.21	hypothetical protein AN1084.2 [Aspergillus nidulans FGSC A4]
gi|61806580|ref|NP_001013523.1|	49669.49	hypothetical protein LOC541378 [Danio rerio]
gi|50288693|ref|XP_446776.1|	47755.42	unnamed protein product [Candida glabrata]
gi|50302533|ref|XP_451201.1|	47443.25	unnamed protein product [Kluyveromyces lactis]
gi|50420633|ref|XP_458853.1|	46954.11	hypothetical protein DEHA0D09889g [Debaryomyces hansenii CBS767]

gi|39946084|ref|XP_362579.1|	49070.24	hypothetical protein MG08162.4 [Magnaporthe grisea 70-15]

166. Group probability: 0.9756. Peptides of the group

QAFDDAIAELDTLSEESYK	63.08	53.2605	2143.98	2145.265	2	2	shared(3)	0	0.9793
QAFDDAIAELDTLSEESYKDSTLIMQLPR (0000000000000000000000000100000)	72.53	50.8352	3314.586	3315.694	3	3	distinct	1	0.9138

The equivalent proteins include

gi|62420901|gb|AAX82172.1|	28911.23	14-3-3 1 protein [Phanerochaete chrysosporium]

167. Group probability: 0.9733. Peptides of the group

NMIIVPEMIGSVVGVYNGK	60.26	53.6352	2019.053	2019.174	1	2	distinct	0	0.9733

The equivalent proteins include

gi|44983159|gb|AAS52341.1|	15969.59	AEL343Cp [Ashbya gossypii ATCC 10895]
gi|50310825|ref|XP_455435.1|	15947.6	unnamed protein product [Kluyveromyces lactis]

168. Group probability: 0.9732. Peptides of the group

HEQGAGHMAQGYAR	82.64	54.6807	1511.669	1512.416	8	2	distinct	0	0.9732

The equivalent proteins include

gi|90302929|gb|EAS32560.1|	75884.24	conserved hypothetical protein [Coccidioides immitis RS]
gi|46108408|ref|XP_381262.1|	75384.74	hypothetical protein FG01086.1 [Gibberella zeae PH-1]

169. Group probability: 0.9731. Peptides of the group

RIDALSR	51.57	57.2568	829.477	830.829	1	2	distinct	1	0.789
RVTLEIGGK	51.91	56.327	971.576	972.261	3	2	distinct	1	0.8724

The equivalent proteins include

gi|11320879|gb|AAG33935.1|	56822.05	aldehyde dehydrogenase-6 [Mus musculus]
gi|109082542|ref|XP_001083856.1|	56820.15	PREDICTED: aldehyde dehydrogenase 1A3 [Macaca mulatta]
gi|4502041|ref|NP_000684.1|	56772.04	aldehyde dehydrogenase 1A3 [Homo sapiens]
gi|46621670|gb|AAH69274.1|	56871.12	Aldehyde dehydrogenase 1A3 [Homo sapiens]
gi|37194683|gb|AAH58277.1|	56863.08	Aldh1a3 protein [Mus musculus]
gi|31874128|emb|CAD97973.1|	45919.6	hypothetical protein [Homo sapiens]

170. Group probability: 0.9725. Peptides of the group

DSTIIMQLLR	62.92	55.6859	1188.654	1188.603	4	2	shared(5)	0	0.8101
QAFDDAIAELDTLSEDSYKDSTLIMQLLR (0000000000000000000000000100000)	53.63	50.7835	3316.602	3317.565	3	3	distinct	1	0.9611

The equivalent proteins include

gi|34452065|gb|AAQ72489.1|	27960.81	14-3-3C1 protein [Oncorhynchus mykiss]

171. Group probability: 0.9721. Peptides of the group

VLITASDVLHSWAIPSLGIK	68.02	53.267	2119.204	2119.855	1	2	distinct	0	0.9721

The equivalent proteins include

gi|7545164|gb|AAA32022.2|	30698.59	cytochrome c oxidase subunit II [Phytophthora megasperma]
gi|71063523|gb|AAZ22193.1|	21691.22	cytochrome oxidase subunit II [Pythium graminicola]
gi|71063533|gb|AAZ22198.1|	21627.22	cytochrome oxidase subunit II [Pythium irregulare]
gi|71063547|gb|AAZ22205.1|	21649.17	cytochrome oxidase subunit II [Pythium nunn]
gi|71063559|gb|AAZ22211.1|	21691.22	cytochrome oxidase subunit II [Pythium rostratum]
gi|71063565|gb|AAZ22214.1|	21675.22	cytochrome oxidase subunit II [Pythium sylvaticum]
gi|71063569|gb|AAZ22216.1|	21645.23	cytochrome oxidase subunit II [Pythium nodosum]
gi|71063571|gb|AAZ22217.1|	21661.21	cytochrome oxidase subunit II [Pythium violae]
gi|71063581|gb|AAZ22222.1|	21650.14	cytochrome oxidase subunit II [Phytophthora cactorum]
gi|71063583|gb|AAZ22223.1|	21622.07	cytochrome oxidase subunit II [Phytophthora cactorum]
gi|71063587|gb|AAZ22225.1|	21619.15	cytochrome oxidase subunit II [Phytophthora cinnamomi]
gi|71063589|gb|AAZ22226.1|	21660.23	cytochrome oxidase subunit II [Phytophthora citricola]
gi|71063593|gb|AAZ22228.1|	21517.16	cytochrome oxidase subunit II [Phytophthora citricola]

gi|71063595|gb|AAZ22229.1|	21631.2	cytochrome oxidase subunit II [Phytophthora megasperma]
gi|71063597|gb|AAZ22230.1|	21634.18	cytochrome oxidase subunit II [Phytophthora megasperma]
gi|71063599|gb|AAZ22231.1|	21634.18	cytochrome oxidase subunit II [Phytophthora megasperma]
gi|71063601|gb|AAZ22232.1|	21650.17	cytochrome oxidase subunit II [Phytophthora nicotianae]
gi|71063605|gb|AAZ22234.1|	21644.25	cytochrome oxidase subunit II [Phytophthora sojae]
gi|71063607|gb|AAZ22235.1|	21644.24	cytochrome oxidase subunit II [Phytophthora sojae]
gi|71063609|gb|AAZ22236.1|	21660.25	cytochrome oxidase subunit II [Phytophthora undulata]
gi|9695376|ref|NP_037598.1|	29827.11	cytochrome c oxidase subunit 2 [Phytophthora infestans]
gi|60203149|gb|AAX14746.1|	19484.84	cytochrome oxidase subunit II [Pythium irregulare]
gi|60203100|gb|AAX14722.1|	19355.78	cytochrome oxidase subunit II [Pythium irregulare]
gi|60203151|gb|AAX14747.1|	19512.87	cytochrome oxidase subunit II [Pythium irregulare]
gi|60203121|gb|AAX14732.1|	19466.75	cytochrome oxidase subunit II [Pythium irregulare]
gi|60203147|gb|AAX14745.1|	19494.86	cytochrome oxidase subunit II [Pythium irregulare]
gi|8885659|gb|AAF80240.1|	22174.47	cytochrome c oxidase subunit II [Peronophythora litchii]
gi|9587834|gb|AAF89404.1|	26228.38	cytochrome c oxidase subunit II [Pythium insidiosum]
gi|9587890|gb|AAF89432.1|	26214.39	cytochrome c oxidase subunit II [Pythium sylvaticum]
gi|9587846|gb|AAF89410.1|	26228.41	cytochrome c oxidase subunit II [Pythium iwagamai]
gi|9587858|gb|AAF89416.1|	26230.39	cytochrome c oxidase subunit II [Pythium nunn]
gi|9587868|gb|AAF89421.1|	26181.39	cytochrome c oxidase subunit II [Pythium pulchrum]
gi|9587870|gb|AAF89422.1|	26167.38	cytochrome c oxidase subunit II [Pythium rostratum]
gi|15428384|gb|AAK97844.1|	22170.49	cytochrome c oxidase subunit II [Lagenidium myophilum]
gi|31158504|gb|AAN01348.1|	21792.21	cytochrome c oxidase subunit II [Phytophthora palmivora]
gi|31158418|gb|AAN01305.1|	21771.35	cytochrome c oxidase subunit II [Phytophthora boehmeriae]
gi|31158424|gb|AAN01308.1|	21764.18	cytochrome c oxidase subunit II [Phytophthora cactorum]
gi|38348785|gb|AAR17798.1|	21747.21	cytochrome c oxidase subunit II [Phytophthora cinnamomi]
gi|31158432|gb|AAN01312.1|	21788.29	cytochrome c oxidase subunit II [Phytophthora citricola]
gi|31158438|gb|AAN01315.1|	21774.27	cytochrome c oxidase subunit II [Phytophthora colocasiae]
gi|31158440|gb|AAN01316.1|	21750.16	cytochrome c oxidase subunit II [Phytophthora cryptogea]
gi|38348787|gb|AAR17799.1|	21748.22	cytochrome c oxidase subunit II [Phytophthora erythroseptica]
gi|31158454|gb|AAN01323.1|	21797.38	cytochrome c oxidase subunit II [Phytophthora fragariae var. fragariae]
gi|31158456|gb|AAN01324.1|	21799.4	cytochrome c oxidase subunit II [Phytophthora fragariae var. rubi]
gi|31158458|gb|AAN01325.1|	21730.27	cytochrome c oxidase subunit II [Phytophthora gonapodyides]
gi|31158460|gb|AAN01326.1|	21748.24	cytochrome c oxidase subunit II [Phytophthora heveae]
gi|31158466|gb|AAN01329.1|	21790.27	cytochrome c oxidase subunit II [Phytophthora hibernalis]
gi|38348789|gb|AAR17800.1|	21793.21	cytochrome c oxidase subunit II [Phytophthora ilicis]
gi|31158470|gb|AAN01331.1|	21821.25	cytochrome c oxidase subunit II [Phytophthora ilicis]

gi|31158476|gb|AAN01334.1|	21790.27	cytochrome c oxidase subunit II [Phytophthora infestans]
gi|38348795|gb|AAR17803.1|	21751.16	cytochrome c oxidase subunit II [Phytophthora lateralis]
gi|31158482|gb|AAN01337.1|	21792.25	cytochrome c oxidase subunit II [Phytophthora megakarya]
gi|31158484|gb|AAN01338.1|	21702.23	cytochrome c oxidase subunit II [Phytophthora megasperma]
gi|31158486|gb|AAN01339.1|	21730.27	cytochrome c oxidase subunit II [Phytophthora megasperma]
gi|31158488|gb|AAN01340.1|	21716.25	cytochrome c oxidase subunit II [Phytophthora megasperma]
gi|38348799|gb|AAR17805.1|	21778.23	cytochrome c oxidase subunit II [Phytophthora nicotianae]
gi|31158500|gb|AAN01346.1|	21792.25	cytochrome c oxidase subunit II [Phytophthora palmivora]
gi|31158508|gb|AAN01350.1|	21763.23	cytochrome c oxidase subunit II [Phytophthora pseudotsugae]
gi|31158510|gb|AAN01351.1|	21772.31	cytochrome c oxidase subunit II [Phytophthora sojae]
gi|38348805|gb|AAR17808.1|	21795.23	cytochrome c oxidase subunit II [Phytophthora syringae]
gi|33350990|gb|AAP49016.1|	22166.57	cytochrome oxidase subunit II [Hyaloperonospora parasitica]
gi|38016575|gb|AAR07621.1|	25606.14	cytochrome c oxidase subunit II [Phytophthora nemorosa]
gi|38373703|gb|AAR19106.1|	25592.13	cytochrome c oxidase subunit II [Phytophthora pseudosyringae]
gi|38373707|gb|AAR19108.1|	25568.03	cytochrome c oxidase subunit II [Phytophthora lateralis]
gi|38373715|gb|AAR19112.1|	25593.12	cytochrome c oxidase subunit II [Phytophthora ramorum]
gi|38373717|gb|AAR19113.1|	25612.09	cytochrome c oxidase subunit II [Phytophthora syringae]
gi|38373719|gb|AAR19114.1|	25592.13	cytochrome c oxidase subunit II [Phytophthora syringae]
gi|38348779|gb|AAR17795.1|	21776.25	cytochrome c oxidase subunit II [Phytophthora ramorum]
gi|38348781|gb|AAR17796.1|	21772.31	cytochrome c oxidase subunit II [Phytophthora cambivora]
gi|38348797|gb|AAR17804.1|	21777.24	cytochrome c oxidase subunit II [Phytophthora nemorosa]
gi|38348803|gb|AAR17807.1|	21763.22	cytochrome c oxidase subunit II [Phytophthora pseudosyringae]
gi|93280090|gb|ABF06688.1|	25593.12	cytochrome c oxidase subunit II [Phytophthora capsici]
gi|93280098|gb|ABF06692.1|	25577.13	cytochrome c oxidase subunit II [Phytophthora tropicalis]
gi|71063555|gb|AAZ22209.1|	21622.3	cytochrome oxidase subunit II [Pythium periplocum]
gi|71063577|gb|AAZ22220.1|	21632.2	cytochrome oxidase subunit II [Phytophthora capsici]
gi|9587864|gb|AAF89419.1|	26201.54	cytochrome c oxidase subunit II [Pythium oligandrum]
gi|38348783|gb|AAR17797.1|	21760.26	cytochrome c oxidase subunit II [Phytophthora capsici]
gi|33350982|gb|AAP49012.1|	22166.53	cytochrome oxidase subunit II [Pythium acanthicum]

172. Group probability: 0.9718. Peptides of the group

VIRPAKVGVVK	63.26	55.2224	1164.771	1165.228	34	2	distinct	1	0.9718

The equivalent proteins include

gi|44981559|gb|AAS51344.1|	23340.25	ACR118Wp [Ashbya gossypii ATCC 10895]
gi|50290879|ref|XP_447872.1|	26282.67	unnamed protein product [Candida glabrata]
gi|19113469|ref|NP_596677.1|	25375.21	hypothetical protein SPBC3B9.19 [Schizosaccharomyces pombe 972h-]
gi|39942268|ref|XP_360671.1|	28033.49	hypothetical protein MG03214.4 [Magnaporthe grisea 70-15]
gi|50419777|ref|XP_458420.1|	27213.99	hypothetical protein DEHA0C18084g [Debaryomyces hansenii CBS767]

gi|68475146|ref|XP_718291.1|	27388.82	putative mitochondrial presequence-associated import motor subunit [Candida albicans SC5314]
gi|50057227|emb|CAH03211.1|	31560.47	Co-chaperone GrpE, putative [Paramecium tetraurelia]
gi|85082684|ref|XP_956965.1|	26924.94	probable heat shock protein MGE1 precursor [MIPS] [Neurospora crassa OR74A]

173. Group probability: 0.9714. Peptides of the group

DPTQQTAIDNFMVHELDGTQNEWGWCK	57.97	50.8411	3219.403	3218.014	1	3	distinct	0	0.9714

The equivalent proteins include

gi|90194338|gb|ABD92697.1|	47812.23	los [Brassica rapa subsp. chinensis]
gi|15227987|ref|NP_181192.1|	47974.44	LOS2; phosphopyruvate hydratase [Arabidopsis thaliana]
gi|34597330|gb|AAQ77240.1|	47631.1	enolase [Brassica rapa]
gi|15809970|gb|AAL06912.1|	47959.47	At2g36530/F1O11.16 [Arabidopsis thaliana]
gi|16226235|gb|AAL16111.1|	35062.72	At2g36530/F1O11.16 [Arabidopsis thaliana]
gi|20260174|gb|AAM12985.1|	48032.44	enolase (2-phospho-D-glycerate hydroylase) [Arabidopsis thaliana]
gi|18175728|gb|AAL59917.1|	47983.44	putative enolase (2-phospho-D-glycerate hydroylase) [Arabidopsis thaliana]
gi|34597332|gb|AAQ77241.1|	47635.23	enolase [Brassica napus]
gi|45477377|gb|AAS66001.1|	47949.34	LOS2 [Capsella bursa-pastoris]

174. Group probability: 0.9713. Peptides of the group

MQVIPLKPLDNK (01000000000000)	62.57	54.9294	1410.79	1410.652	2	2	distinct	0	0.9713

The equivalent proteins include

gi|107836434|gb|ABF84303.1|	45503.37	glutathione spermidine synthetase [Helicobacter pylori HPAG1]
gi|109946923|ref|YP_664151.1|	45640.41	conserved hypothetical protein [Helicobacter acinonychis str. Sheeba]
gi|4154744|gb|AAD05805.1|	45533.5	putative [Helicobacter pylori J99]
gi|15644861|ref|NP_207031.1|	45517.38	hypothetical protein HP0233 [Helicobacter pylori 26695]
gi|58979124|gb|AAW83323.1|	45505.35	GSP synthase [Helicobacter pylori]
gi|58979132|gb|AAW83324.1|	45491.33	GSP synthase [Helicobacter pylori]
gi|58979167|gb|AAW83326.1|	45591.38	GSP synthase [Helicobacter pylori]

175. Group probability: 0.9702. Peptides of the group

LTLHGLQQYYIK	62.14	54.802	1475.814	1476.534	9	2	distinct	0	0.9702

The equivalent proteins include

gi|90297820|gb|EAS27451.1|	50197.6	hypothetical protein CIMG_10056 [Coccidioides immitis RS]
gi|91208173|sp|Q6BME5|SUB2_DEBHA	49600.22	ATP-dependent RNA helicase SUB2
gi|83772640|dbj|BAE62768.1|	49981.5	unnamed protein product [Aspergillus oryzae]
gi|50293331|ref|XP_449077.1|	50299.68	unnamed protein product [Candida glabrata]
gi|46128571|ref|XP_388839.1|	62549.72	hypothetical protein FG08663.1 [Gibberella zeae PH-1]
gi|70984615|ref|XP_747814.1|	50801.99	ATP dependent RNA helicase [Aspergillus fumigatus Af293]
gi|50309861|ref|XP_454944.1|	50132.56	unnamed protein product [Kluyveromyces lactis]
gi|67903470|ref|XP_681991.1|	51052.01	hypothetical protein AN8722.2 [Aspergillus nidulans FGSC A4]
gi|6320119|ref|NP_010199.1|	50619.85	Component of the TREX complex required for nuclear mRNA export; DEAD-box RNA helicase involved in e
gi|68485395|ref|XP_713375.1|	33772.35	hypothetical protein CaO19.13092 [Candida albicans SC5314]
gi|50424083|ref|XP_460626.1|	41861.56	hypothetical protein DEHA0F06688g [Debaryomyces hansenii CBS767]

176. Group probability: 0.9700. Peptides of the group

HYGALTGLNK	64.39	56.0578	1072.566	1073.339	9	+1,+2	shared(3)	0	0.998
VIIAAHGNSIR	55.36	55.3388	1149.662	1150.474	5	2	shared(2)	0	0.9435

The equivalent proteins include

gi|71895985|ref|NP_001026727.1|	29050.91	phosphoglycerate mutase 1 (brain) [Gallus gallus]

177. Group probability: 0.9691. Peptides of the group

YPIEHGIVTNWDDMEK (000000000000001000)	89.61	53.8859	1945.888	1946.177	23	+2,+3	shared(4)	0	0.9983

VAPEEHPVLLTEAPLDPK	58.57	53.685	1954.041	1953.494	4	2	distinct	0	0.8585

The equivalent proteins include

gi|62768595|gb|AAY00164.1|	21988.23	actin A1c [Haliotis iris]

178. Group probability: 0.9685. Peptides of the group

IQGIGAGFVPR	62.09	55.634	1113.629	1114.006	4	2	distinct	0	0.9685

The equivalent proteins include

gi|88937508|ref|ZP_01143072.1|	11749.11	cysteine synthase/cystathionine beta-synthase [Geobacter uraniumreducens Rf4]
gi|68343196|gb|AAY90802.1|	39584.32	cysteine synthase A [Pseudomonas fluorescens Pf-5]
gi|92889440|gb|ABE89872.1|	40971.46	Pyridoxal-5-phosphate-dependent enzyme, beta subunit [Medicago truncatula]
gi|68247248|gb|EAN29335.1|	33687.48	Cysteine synthase K/M:Cysteine synthase A [Magnetococcus sp. MC-1]
gi|57899533|dbj|BAD87047.1|	42103.78	putative plastidic cysteine synthase 1 [Oryza sativa (japonica cultivar-group)]
gi|34906120|ref|NP_914407.1|	43956.56	putative plastidic cysteine synthase 1 [Oryza sativa (japonica cultivar-group)]
gi|55540797|gb|AAV52904.1|	15552.14	chloroplast O-acetylserine thiollyase [Populus alba x Populus tremula]

179. Group probability: 0.9685. Peptides of the group

NTAIVLAAK	79.15	55.8501	899.544	898.135	3	2	distinct	0	0.9685

The equivalent proteins include

gi|82738292|ref|ZP_00901128.1|	23426.53	conserved hypothetical protein [Pseudomonas putida F1]

180. Group probability: 0.9680. Peptides of the group

TIQQLETLLGEPLQSYF	61.41	53.7071	1979.025	1978.335	1	3	distinct	0	0.968

The equivalent proteins include

gi|76630190|ref|XP_583512.2|	72654.93	PREDICTED: similar to HEAT repeat containing protein 1 (Protein BAP28) [Bos taurus]

181. Group probability: 0.9668. Peptides of the group

IGPALAAGNSVILKPSEKSPLSALR	57.44	52.4989	2488.438	2489.481	5	3	distinct	1	0.9668

The equivalent proteins include

gi|91796404|gb|ABE58543.1|	54679.45	Aldehyde dehydrogenase (NAD+) [Chromohalobacter salexigens DSM 3043]
gi|83587439|ref|ZP_00926067.1|	53594.49	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli 101-1]
gi|75179045|ref|ZP_00699063.1|	53587.55	COG1012: NAD-dependent aldehyde dehydrogenases [Shigella boydii BS512]
gi|75190386|ref|ZP_00703653.1|	53601.55	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli E24377A]
gi|75212739|ref|ZP_00712737.1|	53667.64	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli B171]
gi|75240055|ref|ZP_00724016.1|	54064.73	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli E110019]
gi|75259412|ref|ZP_00730731.1|	53722.68	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli E22]
gi|74312330|ref|YP_310749.1|	48454.99	aldehyde dehydrogenase [Shigella sonnei Ss046]
gi|82544244|ref|YP_408191.1|	53631.58	aldehyde dehydrogenase [Shigella boydii Sb227]
gi|145224|gb|AAA23428.1|	53682.6	aldehyde dehydrogenase
gi|16129261|ref|NP_415816.1|	53613.53	gamma-Glu-gamma-aminobutyraldehyde dehydrogenase, NAD(P)H-dependent [Escherichia coli K12]
gi|30041068|gb|AAP16798.1|	53488.67	aldehyde dehydrogenase [Shigella flexneri 2a str. 2457T]
gi|56383426|gb|AAN42916.2|	53474.66	aldehyde dehydrogenase [Shigella flexneri 2a str. 301]

182. Group probability: 0.9666. Peptides of the group

LIEAFQFHEEHGDVCPANWK	57.1	52.7057	2426.111	2427.278	3	2	distinct	0	0.9666

The equivalent proteins include

gi|23394396|gb|AAN31487.1|	23732.16	thioredoxin peroxidase [Phytophthora infestans]

183. Group probability: 0.9666. Peptides of the group

DMVLLDVTPLSLGIETLGGVMTK (00000000000000000000001000)	55.86	52.6443	2417.28	2416.029	2	2	distinct	0	0.9666

The equivalent proteins include

gi|51573343|gb|AAU07368.1|	69363.74	heat shock protein 70 [Borrelia garinii PBi]
gi|39376|emb|CAA47888.1|	69346.75	heat-shock protein [Borrelia burgdorferi]

184. Group probability: 0.9663. Peptides of the group

TLERGAHIVVGTPGR	59.51	54.8218	1561.869	1562.893	6	2	distinct	1	0.9663

The equivalent proteins include

gi|83951704|ref|ZP_00960436.1|	83864.94	ATP-dependent RNA helicase, DEAD/DEAH box family protein [Roseovarius nubinhibens ISM]
gi|15073360|emb|CAC41868.1|	69320.08	PUTATIVE ATP-DEPENDENT RNA HELICASE PROTEIN [Sinorhizobium meliloti]
gi|56680381|gb|AAV97047.1|	76031.23	ATP-dependent RNA helicase, DEAD/DEAH box family [Silicibacter pomeroyi DSS-3]

185. Group probability: 0.9662. Peptides of the group

RVLVIGGGDGGVLR	59.94	55.0017	1366.804	1367.928	2	2	distinct	1	0.9662

The equivalent proteins include

gi|50552163|ref|XP_503556.1|	34430.22	hypothetical protein [Yarrowia lipolytica]

186. Group probability: 0.9661. Peptides of the group

IYQRPFGGQSKDFGK	59.33	54.2603	1726.879	1726.834	3	2	distinct	1	0.9661

The equivalent proteins include

gi|84328157|ref|ZP_00976166.1|	26815.39	COG1053: Succinate dehydrogenase/fumarate reductase, flavoprotein subunit [Pseudomonas aeruginosa 2
gi|87119170|ref|ZP_01075068.1|	64361.96	succinate dehydrogenase [Marinomonas sp. MED121]
gi|88703464|ref|ZP_01101180.1|	62721.07	succinate dehydrogenase, flavoprotein subunit [gamma proteobacterium KT 71]
gi|90416067|ref|ZP_01224000.1|	63752.44	succinate dehydrogenase [marine gamma proteobacterium HTCC2207]
gi|32041626|ref|ZP_00139209.1|	62188.26	COG1053: Succinate dehydrogenase/fumarate reductase, flavoprotein subunit [Pseudomonas aeruginosa U
gi|83647434|ref|YP_435869.1|	64186.94	succinate dehydrogenase, flavoprotein subunit [Hahella chejuensis KCTC 2396]
gi|104782663|ref|YP_609161.1|	64038.04	succinate dehydrogenase, flavoprotein subunit [Pseudomonas entomophila L48]
gi|71558353|gb|AAZ37564.1|	63883.94	succinate dehydrogenase, flavoprotein subunit [Pseudomonas syringae pv. phaseolicola 1448A]
gi|26990883|ref|NP_746308.1|	63979.06	succinate dehydrogenase [Pseudomonas putida KT2440]
gi|9947546|gb|AAG04972.1|	64062.23	succinate dehydrogenase (A subunit) [Pseudomonas aeruginosa PAO1]
gi|91796431|gb|ABE58570.1|	64732.74	succinate dehydrogenase, flavoprotein subunit [Chromohalobacter salexigens DSM 3043]
gi|28852640|gb|AAO55713.1|	63980.96	succinate dehydrogenase, flavoprotein subunit [Pseudomonas syringae pv. tomato str. DC3000]
gi|63255954|gb|AAY37050.1|	63867.91	Succinate dehydrogenase or fumarate reductase, flavoprotein subunit:Succinate dehydrogenase, flavop

187. Group probability: 0.9650. Peptides of the group

DKFENMGAQLVR	60.33	54.9089	1406.698	1407.764	3	2	distinct	1	0.965

The equivalent proteins include

gi|49531857|emb|CAG69569.1|	57192.64	chaperone Hsp60, peptide-dependent ATPase, heat shock protein [Acinetobacter sp. ADP1]

188. Group probability: 0.9636. Peptides of the group

IWHPNISSQTGAICLDILK	56.65	53.2692	2165.13	2165.992	1	2	distinct	0	0.9636

The equivalent proteins include

gi|89289672|gb|EAR87660.1|	32701.32	Ubiquitin-conjugating enzyme family protein [Tetrahymena thermophila SB210]
gi|85544593|pdb|2F4Z|B	21517.82	Chain B, Toxoplasma Gondii Ubiquitin Conjugating Enzyme Tgtwinscan_2721- E2 Domain

gi|66356904|ref|XP_625630.1|	22824.81	Ubc1p like ubiquitin-conjugating enzyme E2 fused to a UBA domain (UBC+UBA) [Cryptosporidium parvum
gi|67597699|ref|XP_666164.1|	17433.84	ubiquitin-conjugating enzyme [Cryptosporidium hominis TU502]
gi|50057428|emb|CAH03412.1|	22492.48	Ubiquitin-conjugating enzyme, putative [Paramecium tetraurelia]

189. Group probability: 0.9630. Peptides of the group

IVATGEGLIAEEIIALAK	57.06		54.1397	1810.045	1810.465	2	2	distinct	0	0.963

The equivalent proteins include

gi|82742248|ref|ZP_00904947.1|	11687.14	FlhB domain protein [Shewanella sp. W3-18-1]
gi|68541552|ref|ZP_00581295.1|	11451.94	FlhB domain protein [Shewanella baltica OS155]
gi|77814111|ref|ZP_00813377.1|	11588.06	FlhB domain protein [Shewanella putrefaciens CN-32]

190. Group probability: 0.9626. Peptides of the group

YGSVPHAGFGLGFER	58.28		54.5812	1592.773	1593.442	6	2	distinct	0	0.9626

The equivalent proteins include

gi|89073955|ref|ZP_01160461.1|	52604.11	asparaginyl-tRNA synthetase [Photobacterium sp. SKA34]
gi|90579564|ref|ZP_01235373.1|	52629.16	asparaginyl-tRNA synthetase [Vibrio angustum S14]
gi|20141643|sp|P52276|SYN_SYNY3	52893.74	Asparaginyl-tRNA synthetase (Asparagine--tRNA ligase) (AsnRS)
gi|89257628|gb|ABD65116.1|	80060.65	asparaginyl-tRNA synthetase, putative [Brassica oleracea]
gi|83645055|ref|YP_433490.1|	52854.38	asparaginyl-tRNA synthetase [Hahella chejuensis KCTC 2396]
gi|84623953|ref|YP_451325.1|	52144.45	asparaginyl-tRNA synthetase [Xanthomonas oryzae pv. oryzae MAFF 311018]
gi|2664210|emb|CAA10904.1|	64089.43	asparaginyl-tRNA synthetase [Arabidopsis thaliana]
gi|21107804|gb|AAM36486.1|	52063.39	asparaginyl-tRNA synthetase [Xanthomonas axonopodis pv. citri str. 306]
gi|28199814|ref|NP_780128.1|	52851.82	asparaginyl-tRNA synthetase [Xylella fastidiosa Temecula1]
gi|92872084|gb|ABE80885.1|	66025.3	Aspartyl-tRNA synthetase, class IIb; tRNA synthetase, class II (D, K and N) [Medicago truncatula]
gi|78047215|ref|YP_363390.1|	52178.45	asparaginyl-tRNA synthetase [Xanthomonas campestris pv. vesicatoria str. 85-10]
gi|108761851|ref|YP_630519.1|	52890.86	asparaginyl-tRNA synthetase [Myxococcus xanthus DK 1622]
gi|22300015|ref|NP_683262.1|	52681.25	asparaginyl-tRNA synthetase [Thermosynechococcus elongatus BP-1]
gi|81299641|ref|YP_399849.1|	52457.35	asparaginyl-tRNA synthetase [Synechococcus elongatus PCC 7942]
gi|71898278|ref|ZP_00680452.1|	52909.9	Asparaginyl-tRNA synthetase, class IIb [Xylella fastidiosa Ann-1]
gi|71899836|ref|ZP_00681986.1|	52897.86	Asparaginyl-tRNA synthetase, class IIb [Xylella fastidiosa Ann-1]
gi|16332045|ref|NP_442773.1|	58350.54	asparaginyl-tRNA synthetase [Synechocystis sp. PCC 6803]
gi|9107777|gb|AAF85360.1|	52943.88	asparaginyl-tRNA synthetase [Xylella fastidiosa 9a5c]
gi|21112638|gb|AAM40856.1|	52165.46	asparaginyl-tRNA synthetase [Xanthomonas campestris pv. campestris str. ATCC 33913]
gi|15236037|ref|NP_193462.1|	64171.45	NS1 [Arabidopsis thaliana]
gi|58582041|ref|YP_201057.1|	52130.39	asparaginyl-tRNA synthetase [Xanthomonas oryzae pv. oryzae KACC10331]
gi|50937183|ref|XP_478119.1|	65030.86	putative asparaginyl-tRNA synthetase, chloroplast/mitochondrial precursor [Oryza sativa (japonica c
gi|56750719|ref|YP_171420.1|	52337.32	asparaginyl-tRNA synthetase [Synechococcus elongatus PCC 6301]

191. Group probability: 0.9608. Peptides of the group

VIAWYDNEWGYSNR	85.68		54.2143	1771.795	1771.999	13	2	distinct	0	0.9608

The equivalent proteins include

gi|90585446|ref|ZP_01241155.1|	37141.23	Glyceraldehyde-3-phosphate dehydrogenase, type I [Staphylococcus aureus subsp. aureus JH9]
gi|27315825|gb|AAO04960.1|	37240.2	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus epidermidis ATCC 12228]
gi|82751275|ref|YP_417016.1|	37153.29	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus RF122]
gi|53687157|ref|ZP_00107108.2|	36947.96	COG0057: Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Nostoc punct
gi|68446963|dbj|BAE04547.1|	37303.14	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus haemolyticus JCSC1435]
gi|49483929|ref|YP_041153.1|	37151.22	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus MRSA252]
gi|73662387|ref|YP_301168.1|	37276.99	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus saprophyticus subsp. saprophyticus ATCC
gi|57637827|gb|AAW54615.1|	37256.16	glyceraldehyde 3-phosphate dehydrogenase [Staphylococcus epidermidis RP62A]
gi|77995878|gb|ABB14777.1|	36250.11	glyceraldehyde-3-phosphate dehydrogenase, type I [Carboxydothermus hydrogenoformans Z-2901]
gi|56751277|ref|YP_171978.1|	38965.41	glyceraldehyde 3-phosphate dehydrogenase [Synechococcus elongatus PCC 6301]
gi|87127690|gb|ABD22204.1|	37127.22	glyceraldehyde-3-phosphate dehydrogenase, type I [Staphylococcus aureus subsp. aureus USA300]
gi|6979050|gb|AAF34325.1|	35682.03	cytosolic glyceraldehyde-3-phosphate dehydrogenase [Phaeodactylum tricornutum]
gi|38195941|gb|AAR13671.1|	37070.2	GapB [Staphylococcus aureus]
gi|89894253|ref|YP_517740.1|	36707.21	hypothetical protein DSY1507 [Desulfitobacterium hafniense Y51]
gi|81300748|ref|YP_400956.1|	36323.85	glyceraldehyde-3-phosphate dehydrogenase, type I [Synechococcus elongatus PCC 7942]
gi|109649322|ref|ZP_01373210.1|	36579.19	glyceraldehyde-3-phosphate dehydrogenase, type I [Desulfitobacterium hafniense DCB-2]
gi|89894355|ref|YP_517842.1|	37131.45	glyceraldehyde 3-phosphate dehydrogenase [Desulfitobacterium hafniense Y51]
gi|56752164|ref|YP_172865.1|	37270.32	glyceraldehyde 3-phosphate dehydrogenase [Synechococcus elongatus PCC 6301]

192. Group probability: 0.9608. Peptides of the group

LVAWYDNEWGYSNR	85.68	54.2143	1771.795	1771.999	7	2	distinct	0	0.9608

The equivalent proteins include

gi|2055380|gb|AAC49702.1|	41799.18	glyceraldehyde-3-phosphate dehydrogenase precursor
gi|74272661|gb|ABA01126.1|	20899.77	glyceraldehyde-3-phosphate dehydrogenase [Chlamydomonas incerta]
gi|296131|emb|CAA51071.1|	36909.74	glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Physcomitrella patens]
gi|968996|gb|AAA82047.1|	36640.86	glyceraldehyde-3-phosphate dehydrogenase
gi|1346064|sp|P49644|G3PC_CHLRE	36706.8	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic
gi|1730194|sp|P54270|G3PC_GRAVE	36406.39	Glyceraldehyde-3-phosphate dehydrogenase, cytosolic
gi|297454|emb|CAA51515.1|	36373.35	glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Chondrus crispus]

gi|50940735|ref|XP_479895.1|	36560.87	glyceraldehyde 3-phosphate dehydrogenase, cytosolic [Oryza sativa (japonica cultivar-group)]
gi|30525878|gb|AAP32470.1|	36061.41	cytosolic glyceraldehyde 3-phosphate dehydrogenase [Porphyra yezoensis]
gi|440395|emb|CAA51517.1|	36403.36	glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Chondrus crispus]

193. Group probability: 0.9607. Peptides of the group

CAVVNLPYGGAKGGIGFNPK	55.46	53.6349	2018.041	2019.113	3	2	distinct	1	0.9607

The equivalent proteins include

gi|89307282|gb|EAS05270.1|	68836.23	Glutamate/Leucine/Phenylalanine/Valine dehydrogenase family protein [Tetrahymena thermophila SB210]

194. Group probability: 0.9603. Peptides of the group

DILLLDVTPLSLGIETMGGVMTK	65.14	52.8396	2415.3	2414.453	7	2	distinct	0	0.9603

The equivalent proteins include

gi|57340176|gb|AAW50075.1|	73604.53	hypothetical protein FTT1269 [synthetic construct]
gi|3122002|sp|O32482|DNAK_LEGPN	70215.33	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70)
gi|53751737|emb|CAH13159.1|	70245.36	Chaperone protein DnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) [Legionella pneu
gi|53754755|emb|CAH16242.1|	70217.33	Chaperone protein DnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) [Legionella pneu
gi|56604821|emb|CAG45902.1|	69382.76	Chaperone protein dnaK (heat shock protein family 70 protein) [Francisella tularensis subsp. tulare
gi|52629353|gb|AAU28094.1|	70873.61	chaperone protein DnaK, heat shock protein Hsp70 [Legionella pneumophila subsp. pneumophila str. Ph

195. Group probability: 0.9593. Peptides of the group

EFGIDEKNMFGFWDWVGGR	57.73	53.2047	2289.031	2287.732	3	3	distinct	1	0.9593

The equivalent proteins include

gi|66499293|ref|XP_623552.1|	63155.85	PREDICTED: similar to glucosephosphate isomerase [Apis mellifera]

196. Group probability: 0.9588. Peptides of the group

SSMSDMEQVIDDLK (0000001000000000)	57.56	54.5156	1612.696	1614.053	2	2	distinct	0	0.9588

The equivalent proteins include

gi|56783954|dbj|BAD81391.1|	77715.32	hypothetical protein [Oryza sativa (japonica cultivar-group)]
gi|34904404|ref|NP_913549.1|	84981.03	unnamed protein product [Oryza sativa (japonica cultivar-group)]

197. Group probability: 0.9585. Peptides of the group

EEAIAKMIEWLEVTGAGNQK	57.09	53.1302	2216.115	2214.789	7	3	distinct	1	0.9585

The equivalent proteins include

gi|89201262|ref|ZP_01180007.1|	91705.9	Leucyl-tRNA synthetase bacterial/mitochondrial, class Ia [Bacillus cereus subsp. cytotoxis NVH 391-

198. Group probability: 0.9582. Peptides of the group

IHTFIATSDIHLK	66.27	54.7078	1494.819	1495.513	7	2	distinct	0	0.9582

The equivalent proteins include

gi|98661215|dbj|GAA01713.1|	55806.58	unnamed protein product [Pelotomaculum thermopropionicum SI]
gi|67928966|ref|ZP_00522151.1|	42997.96	HMG-CoA lyase-like [Solibacter usitatus Ellin6076]
gi|88944101|ref|ZP_01147434.1|	55440.56	2-isopropylmalate synthase [Desulfotomaculum reducens MI-1]
gi|39931403|sp|Q7VBG1|LEU1_PROMA	58142.27	2-isopropylmalate synthase (Alpha-isopropylmalate synthase) (Alpha-IPM synthetase)
gi|77996366|gb|ABB15265.1|	55813.19	2-isopropylmalate synthase [Carboxydothermus hydrogenoformans Z-2901]
gi|78712959|gb|ABB50136.1|	59615.8	2-isopropylmalate synthase [Prochlorococcus marinus str. MIT 9312]
gi|67924197|ref|ZP_00517638.1|	58365.1	2-isopropylmalate synthase [Crocosphaera watsonii WH 8501]

gi|33861622|ref|NP_893183.1|	59609.74	2-isopropylmalate synthase [Prochlorococcus marinus subsp. pastoris str. CCMP1986]							
gi|26452162|dbj|BAC43169.1|	37151.21	putative 2-isopropylmalate synthase [Arabidopsis thaliana]							
gi|15221125|ref|NP_177544.1|	68493.03	IMS1 [Arabidopsis thaliana]							
gi|71490967|gb|EAO23309.1|	56263.8	2-isopropylmalate synthase [Syntrophomonas wolfei subsp. wolfei str. Goettingen]							
199. Group probability: 0.9564. Peptides of the group									
AEGLWAGIVIPEAGR	56.52	54.6028	1537.825	1537.225	1	2	distinct	0	0.9564
The equivalent proteins include									
gi|108797038|ref|YP_637235.1|	11080.64	transcription factor WhiB [Mycobacterium sp. MCS]							
200. Group probability: 0.9556. Peptides of the group									
KIAVNLIPFPR	70.88	55.3215	1266.781	1267.527	5	2	shared(8)	1	0.9855
EILHVQGGQCGNQIGAK	66.3	54.3047	1807.9	1808.677	4	2	distinct	0	0.9178
The equivalent proteins include									
gi|296498|emb|CAA48929.1|	50334.78	beta tubulin 1 [Anemia phyllitidis]							
201. Group probability: 0.9555. Peptides of the group									
NPPPPPSSSADTPPPPPSSSSSTSSSAESLR	51.42	51.3446	3004.39	3005.713	1	3	distinct	0	0.9555
The equivalent proteins include									
gi|66932877|gb|AAY58271.1|	53995.63	cell cycle switch protein CCS52A [Lotus corniculatus var. japonicus]							
202. Group probability: 0.9552. Peptides of the group									
IKLEDAGFDWK	58	55.3095	1320.671	1321.151	2	2	distinct	1	0.9552
The equivalent proteins include									
gi|73913050|gb|AAZ91463.1|	61505.65	delta-1-pyrroline-5-carboxylate dehydrogenase [Triticum turgidum]							
gi|927428|emb|CAA60412.1|	61335.65	fis1 [Linum usitatissimum]							
gi|18449337|gb|AAL70106.1|	61494.57	putative aldehyde dehydrogenase BIS1 [Hordeum vulgare]							
gi|18449343|gb|AAL70109.1|	61416.65	putative aldehyde dehydrogenase WIS1 [Triticum aestivum]							
gi|50932489|ref|XP_475772.1|	56764.18	putative aldehyde dehydrogenase [Oryza sativa (japonica cultivar-group)]							
203. Group probability: 0.9538. Peptides of the group									
MVLPSNITK (01000000000)	58.57	56.1535	1017.553	1018.433	1	2	distinct	0	0.9538
The equivalent proteins include									
gi|90585996|ref|ZP_01241700.1|	67819.01	conserved hypothetical protein [Staphylococcus aureus subsp. aureus JH9]							
gi|87127959|gb|ABD22473.1|	122034.25	conserved hypothetical protein [Staphylococcus aureus subsp. aureus USA300]							
gi|21203232|dbj|BAB93933.1|	122052.31	MW0068 [Staphylococcus aureus subsp. aureus MW2]							
gi|49243416|emb|CAG41836.1|	122053.29	hypothetical protein [Staphylococcus aureus subsp. aureus MSSA476]							
gi|14245860|dbj|BAB56255.1|	122103.27	hypothetical protein [Staphylococcus aureus subsp. aureus Mu50]							
204. Group probability: 0.9538. Peptides of the group									
MKSYDIVVIGGGPGGYVAAIK	53.14	53.3483	2094.118	2094.557	1	2	distinct	1	0.9538
The equivalent proteins include									
gi|10173393|dbj|BAB04498.1|	49550.26	dihydrolipoamide dehydrogenase [Bacillus halodurans C-125]							
205. Group probability: 0.9532. Peptides of the group									
SDGIFIGNFVGGDSLK	55.3	54.5067	1624.81	1625.841	1	2	distinct	0	0.9532
The equivalent proteins include									
gi|3861015|emb|CAA14915.1|	25786.51	unknown [Rickettsia prowazekii]							
gi|51459959|gb|AAU03922.1|	25929.56	conserved hypothetical protein [Rickettsia typhi str. Wilmington]							
206. Group probability: 0.9531. Peptides of the group									
MNIDTDTQWAYWDGIR	55.1	53.7562	1983.878	1984.426	2	2	distinct	0	0.9531
The equivalent proteins include									
gi|21684695|gb|AAM66752.1|	44195.58	fructose-1,6-bisphosphate aldolase precursor [Odontella sinensis]							
207. Group probability: 0.9522. Peptides of the group									
IFAQIWHTGR	57.73	55.6027	1227.651	1228.24	13	2	distinct	0	0.9522
The equivalent proteins include									

gi|87122066|ref|ZP_01077950.1|	39182.78	NADH-dependent flavin oxidoreductase, Oye family protein [Marinomonas sp. MED121]
gi|69952897|ref|ZP_00640225.1|	37973.03	NADH:flavin oxidoreductase/NADH oxidase [Shewanella frigidimarina NCIMB 400]
gi|87118359|ref|ZP_01074258.1|	38338.54	putative NADH-dependent flavin oxidoreductase [Marinomonas sp. MED121]
gi|75815197|ref|ZP_00745719.1|	38374.3	COG1902: NADH:flavin oxidoreductases, Old Yellow Enzyme family [Vibrio cholerae V52]
gi|68545953|ref|ZP_00585502.1|	38513.42	NADH:flavin oxidoreductase/NADH oxidase [Shewanella amazonensis SB2B]
gi|75824824|ref|ZP_00754268.1|	20894.55	COG1902: NADH:flavin oxidoreductases, Old Yellow Enzyme family [Vibrio cholerae RC385]
gi|75825153|ref|ZP_00754589.1|	38406.28	COG1902: NADH:flavin oxidoreductases, Old Yellow Enzyme family [Vibrio cholerae O395]
gi|78366646|ref|ZP_00836924.1|	38049.11	NADH:flavin oxidoreductase/NADH oxidase [Shewanella sp. PV-4]
gi|89074607|ref|ZP_01161072.1|	39287.43	hypothetical protein SKA34_06979 [Photobacterium sp. SKA34]
gi|90411245|ref|ZP_01219257.1|	39794.91	putative NADH-dependent flavin oxidoreductase [Photobacterium profundum 3TCK]
gi|90580490|ref|ZP_01236296.1|	39241.47	hypothetical protein VAS14_08930 [Vibrio angustum S14]
gi|71146590|gb|AAZ27063.1|	38543.4	oxidoreductase, FAD/FMN-binding [Colwellia psychrerythraea 34H]
gi|9658440|gb|AAF96894.1|	38335.29	NADH-dependent flavin oxidoreductase, Oye family [Vibrio cholerae O1 biovar eltor str. N16961]
gi|54303040|ref|YP_133033.1|	38678.38	putative NADH-dependent flavin oxidoreductase [Photobacterium profundum SS9]
gi|91792588|ref|YP_562239.1|	37771	NADH:flavin oxidoreductase/NADH oxidase [Shewanella denitrificans OS217]

208. Group probability: 0.9521. Peptides of the group

GVKAILAAR	58.07	55.7627	897.576	898.985	3	2	distinct	1	0.9521

The equivalent proteins include

gi|19887888|gb|AAM02489.1|	49542.49	Fusion of at least two uncharacterized domain specific for M.kandleri, MK-12 family [Methanopyrus k

209. Group probability: 0.9517. Peptides of the group

FHVEEEGKGK	47.93	55.7364	1158.567	1159.423	2	2	shared(2)	1	0.8868
VADKIQLINNMLDK (0000000000010000)	44.36	54.6152	1629.876	1631.294	1	2	distinct	1	0.6376
LGDVYVNDAFGTAHR	79.59	54.5797	1633.785	1634.282	4	+2,+3	shared(3)	0	0.9548

The equivalent proteins include

gi|22219037|pdb|1KF0|A	44837.26	Chain A, Crystal Structure Of Pig Muscle Phosphoglycerate Kinase Ternary Complex With Amp-Pcp And 3
gi|47169449|pdb|1VJD|A	44802.18	Chain A, Structure Of Pig Muscle Pgk Complexed With Atp
gi|66893|pir||KIHOG	44865.26	phosphoglycerate kinase (EC 2.7.2.3) - horse
gi|266755|sp|P29408|PGK1_MACEU	45405.38	Phosphoglycerate kinase 1
gi|52783777|sp|P00559|PGK1_HORSE	44973.29	Phosphoglycerate kinase 1
gi|61354676|gb|AAX41039.1|	45101.31	phosphoglycerate kinase 1 [synthetic construct]
gi|74216774|dbj|BAE37790.1|	44907.12	unnamed protein product [Mus musculus]
gi|74219103|dbj|BAE26693.1|	44949.14	unnamed protein product [Mus musculus]
gi|56403927|emb|CAI29748.1|	44929.2	hypothetical protein [Pongo pygmaeus]
gi|48145549|emb|CAG32997.1|	44973.24	PGK1 [Homo sapiens]
gi|50513041|gb|AAT77773.1|	44929.23	phosphoglycerate kinase 1 [Sus scrofa]
gi|109131308|ref|XP_001100787.1|	44957.23	PREDICTED: similar to phosphoglycerate kinase 1 isoform 4 [Macaca mulatta]
gi|109131310|ref|XP_001100617.1|	40724	PREDICTED: similar to phosphoglycerate kinase 1 isoform 2 [Macaca mulatta]
gi|109131312|ref|XP_001100332.1|	41653.74	PREDICTED: similar to phosphoglycerate kinase 1 isoform 1 [Macaca mulatta]

gi|109131314|ref|XP_001100701.1|	41773.47	PREDICTED: similar to phosphoglycerate kinase 1 isoform 3 [Macaca mulatta]
gi|55663594|ref|XP_529051.1|	46230.42	PREDICTED: phosphoglycerate kinase 1 [Pan troglodytes]
gi|41350401|gb|AAS00488.1|	44985.28	migration-inducing gene 10 protein [Homo sapiens]
gi|129906|sp|P16617|PGK1_RAT	44925.09	Phosphoglycerate kinase 1
gi|129903|sp|P09411|PGK1_MOUSE	44907.08	Phosphoglycerate kinase 1
gi|987048|emb|CAA86028.1|	44933.17	phosphoglycerate kinase [Cricetulus griseus]
gi|38649310|gb|AAH63161.1|	44909.14	Phosphoglycerate kinase 1 [Rattus norvegicus]
gi|80477474|gb|AAI08373.1|	44921.14	Phosphoglycerate kinase 1 [Mus musculus]
gi|55733484|emb|CAH93420.1|	44985.26	hypothetical protein [Pongo pygmaeus]
gi|1150|emb|CAA45574.1|	45274.34	phosphoglycerate kinase [Macropus eugenii]

210. Group probability: 0.9513. Peptides of the group

IHGGLLGVR	57.93	55.962	920.556	921.119	5	2	distinct	0	0.9513

The equivalent proteins include

gi|31789439|gb|AAP58553.1|	61927.46	putative AICAR transformylase [uncultured Acidobacteria bacterium]

211. Group probability: 0.9513. Peptides of the group

VAILTLNRPK	64	55.2114	1123.708	1124.61	12	2	distinct	0	0.9513

The equivalent proteins include

gi|90420908|ref|ZP_01228813.1|	28428.41	enoyl-CoA hydratase [Aurantimonas sp. SI85-9A1]

212. Group probability: 0.9512. Peptides of the group

VKEVGSLLANLAHDQNK	56.69	54.1269	1834.99	1835.72	2	3	distinct	1	0.9512

The equivalent proteins include

gi|90962347|ref|YP_536263.1|	24674.35	ABC transporter, ATP-binding protein [Lactobacillus salivarius subsp. salivarius UCC118]

213. Group probability: 0.9508. Peptides of the group

KYYDFLSAYSAVNQGHCHPK	52.7	52.8295	2384.101	2385.252	4	2	distinct	1	0.9508

The equivalent proteins include

gi|83858025|ref|ZP_00951552.1|	47131.51	acetylornithine aminotransferase, putative [Croceibacter atlanticus HTCC2559]
gi|86133210|ref|ZP_01051792.1|	47259.83	acetylornithine aminotransferase, putative [Tenacibaculum sp. MED152]
gi|88712789|ref|ZP_01106874.1|	45702.42	acetylornithine aminotransferase, putative [Flavobacteriales bacterium HTCC2170]
gi|88802990|ref|ZP_01118517.1|	46973.69	acetylornithine aminotransferase, putative [Polaribacter irgensii 23-P]

214. Group probability: 0.9505. Peptides of the group

VADVYVNDAFGTAHR	78.55	54.5797	1633.785	1634.282	4	+2,+3	distinct	0	0.9505

The equivalent proteins include

gi|51860718|gb|AAU11483.1|	105253.61	chloroplast phosphoglycerate kinase precursor [Euglena gracilis]

215. Group probability: 0.9499. Peptides of the group

QATINIGTIGHVAHGK	54.58	54.8191	1615.879	1616.708	1	2	distinct	0	0.9499

The equivalent proteins include

gi|108872932|gb|EAT37157.1|	78606.33	histone-lysine n-methyltransferase [Aedes aegypti]
gi|54639643|gb|EAL29045.1|	72650.02	GA19622-PA [Drosophila pseudoobscura]
gi|88185753|gb|EAQ93221.1|	56170.49	hypothetical protein CHGG_01456 [Chaetomium globosum CBS 148.51]
gi|82802708|gb|ABB92405.1|	51695.4	eFI-2-gamma [Homo sapiens]
gi|82802710|gb|ABB92406.1|	51696.44	eFI-2-gamma [Pan troglodytes]
gi|82802712|gb|ABB92407.1|	51735.55	eFI-2-gamma [Gorilla gorilla]
gi|82802714|gb|ABB92408.1|	51591.42	eFI-2-gamma [Pongo pygmaeus]
gi|82802716|gb|ABB92409.1|	51701.51	eFI-2-gamma [Hylobates lar]
gi|90298719|gb|EAS28350.1|	57582.8	hypothetical protein CIMG_09554 [Coccidioides immitis RS]
gi|84310029|emb|CAJ18344.1|	68663.33	putative H3K9 methyltransferase [Bombyx mori]
gi|84310031|emb|CAJ18345.1|	67156.39	putative H3K9 methyltransferase [Cercopis vulnerata]
gi|84310033|emb|CAJ18346.1|	45956.34	putative translation initiation factor 2 gamma subunit [Drosophila nasutoides]
gi|84310034|emb|CAJ18347.1|	73704.71	putative H3K9 methyltransferase [Drosophila nasutoides]

S3. Protein assembly of peptide sequence matches made to tag-filtered P. sojae tandem mass spectra. The NCBI NR database appended with P. sojae protein sequences was searched. Protein List with probabilities. The columns are arranged as follows: peptide sequence, Mascot Ions score, Mascot Identity score, computed peptide mass, observed precursor mass, number of tandem mass spectra assigned to same peptide sequence, the charge states observed for the peptide, whether the peptide is shared between protein groups with different probabilities (number in parentheses is number of other groups peptides are shared with) or is distinct (considered a unique identifier for proteins grouped with the same probability), the number of missed tryptic cleavages in this sequence, and the probability for a particular peptide sequence.

1. Group probability: 1.0000. Peptides of the group

ILGYLNIDDLVGITK	110.28	54.5596	1645.929	1646.85	8	2	distinct	0	0.9989
VQGDAPVWHPEVGQWLSK	77.09	53.6782	2032.017	2032.627	20	+2,+3	distinct	0	0.9992
SGCGAFTWTSYNGGTCWLK	91.93	53.2568	2151.914	2151.965	5	2	distinct	0	0.9983
SGCGAFTWTNYNGGTCWLK	93.92	53.3042	2178.925	2179.37	5	2	shared(2)	0	0.9986
APYPNNYWCSFPNSCAQK	57.23	53.2103	2202.925	2203.323	2	2	distinct	0	0.9642
YYENHNPLEYGDFVAMDGAK (000000000000000100000)	76.61	52.9531	2332.011	2332.033	7	+2,+3	distinct	0	0.9999
GFEVEQSIDFWKNPGDQNANANR	85.19	52.1849	2635.205	2636.526	1	3	distinct	1	0.9969
GSATSNPGAISGVVQGSSSNNNNNNSGAWSMKPVK (0000000000000000000000000000001000 00)	98.69	50.3726	3417.597	3418.909	4	3	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|140695|estExt_fgenesh1_pg.C_880067	0	No title.

2. Group probability: 1.0000. Peptides of the group

KIGYPVIIK	55	56.4215	1029.659	1030.666	6	2	distinct	1	0.9185
LGPAPAAESYLNYAK	51.06	54.6854	1563.793	1564.936	1	2	distinct	0	0.9294
ALGAVSLLLLEQLKR	69.2	54.5872	1623.008	1624.251	2	2	distinct	1	0.9857
KLQLSHDDDEAPVTVK	92.8	54.3688	1793.916	1794.136	2	2	distinct	1	0.9983
ALHEYQIVGLPTNIEFVAR	84.01	53.5044	2169.158	2169.666	20	+2,+3	distinct	0	0.9999
LSGAEAVHPGYGFLSENAAFAR	84.14	53.1197	2263.102	2264.538	17	+2,+3	distinct	0	0.9992
IYAENPYNDFLPGSGTLQHIR	74.38	52.7236	2404.181	2404.726	10	+2,+3	distinct	0	0.9999
AGVPVTPGYHGEDQSFETLQSEAR	66.4	52.3647	2574.199	2574.47	1	2	distinct	0	0.9873

The equivalent proteins include

jgi|Physo1_1|109683|estExt_fgenesh1_pm.C_2750001	0	No title.

3. Group probability: 1.0000. Peptides of the group

FHVEEEGKGK	47.93	55.7704	1158.567	1159.423	2	2	shared(2)	1	0.8866
AHSSMVGVDLPVK (000001000000000)	80.63	55.3244	1338.697	1339.061	22	+1,+2	distinct	0	0.9998
AKDSLAPVAVAVEQK	59.62	54.6065	1524.851	1525.17	2	2	distinct	1	0.9667
GVTLHLPVDFVIADK	62.28	54.5002	1622.903	1624.366	14	+2,+3	distinct	0	0.9989
VADKIQLIMNMLDK	90.88	54.6512	1630.879	1632.087	8	2	distinct	1	0.9939
LGDVYVNDAFGTAHR	79.59	54.6124	1633.785	1634.282	4	+2,+3	shared(2)	0	0.9548
AAGFLLDKELVYFAK	63.73	54.3597	1683.923	1685.182	1	2	distinct	1	0.9769
ALDNPQRPFVSILGGAK	69.11	54.3006	1781.979	1783.172	15	+2,+3	distinct	0	0.998
IDAALPTVQYVLDQGAK	63.52	54.3132	1800.962	1802.369	2	2	distinct	0	0.9781
TVVWNGPMGVFEFEAFAHGTK (000000000100000000000000)	72.79	52.9889	2323.109	2340.277	4	2	distinct	0	0.9918
GVTLHLPVDFVIADKFAPDAAQK	94.15	52.5539	2451.316	2450.995	13	+2,+3	distinct	1	0.9999
FNTEDKVSHVSTGGGASLELLEGK	76.84	52.583	2474.229	2474.512	7	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|109468|estExt_fgenesh1_pm.C_1120004	0	No title.

4. Group probability: 1.0000. Peptides of the group

HLGAELALVAR	54.97	55.6328	1148.667	1148.529	5	+1,+2	shared(2)	0	0.9959
YYYHAVGTPR	68.16	55.3938	1225.588	1226.374	13	2	shared(2)	0	0.9809
SKDYFAGMAWK	47.88	55.4109	1302.607	1304.091	2	2	shared(2)	1	0.8909
KTQSNVSKPFPK	83.59	55.3325	1359.751	1360.299	6	+1,+2	shared(2)	1	0.9996
KLFVPYDNVIPPSAK	50.79	54.4324	1686.934	1687.763	1	2	shared(2)	1	0.9281
ILIVGGGPAGIAVAQALAADLTAK	136.7	53.7579	2189.278	2189.943	8	+2,+3	distinct	0	1
VEVVGTMLPLGPNGGVSQLPVMGGVVMGNLITK	66.41	50.8794	3262.749	3264.041	1	3	shared(2)	0	0.989
ILIVGGGPAGIAVAQALAADLTAKDDTEVLVLEK	61.75	50.7098	3330.865	3330.616	14	3	distinct	1	0.984

The equivalent proteins include

jgi|Physo1_1|142200|estExt_fgenesh1_pg.C_1090056	0	No title.

5. Group probability: 1.0000. Peptides of the group

AIDQEFGSFDNFKK	52.34	54.5843	1644.778	1645.808	1	2	distinct	1	0.9348
SVGVQGSGWGWLGYSPETK	84.63	53.7663	1993.953	1995.393	2	2	distinct	0	0.9968

NVRPDYLNAIWDVVNWK	106.34	53.4183	2101.074	2102.42	34	+2,+3	distinct	0	0.9999
HHQTYVNNYNAALEQYAEAEAK	101.8	52.5139	2563.173	2563.647	22	+2,+3	distinct	0	1
LPDLAYDFGALEPSISGQIMEIHHQK (0000000000000000000010000000)	97.87	51.6668	2908.443	2909.811	14	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109207|estExt_fgenesh1_pm.C_730003	0	No title.

6. Group probability: 1.0000. Peptides of the group

FGSGWAWLGVK	81.22	55.3329	1206.619	1206.395	29	2	distinct	0	0.9941
SILEVVQSATEAPVR	109.51	54.7835	1597.867	1598.368	16	+2,+3	distinct	0	1
RPEYISAFWNVANWDK	95.56	53.7625	1994.964	1995.412	5	+2,+3	distinct	0	1
HHQAYVNNINNYISSDK	105.99	53.6315	2015.945	2016.447	27	+2,+3	distinct	0	1

The equivalent proteins include

gi|66865886|gb|AAY57577.1|	23956.74	manganese superoxide dismutase [Phytophthora nicotianae]

7. Group probability: 1.0000. Peptides of the group

ACNALLLK	66.88	56.8713	901.505	902.794	1	2	shared(3)	0	0.9266
AGWAIMASHR (000000100000)	71.83	55.7775	1098.539	1099.712	8	2	distinct	0	0.9861
IGSEVYHNLK	60.26	55.7704	1158.603	1159.47	7	2	distinct	0	0.9616
IGSEVYHNLKK	47.26	55.5128	1286.698	1287.765	1	2	distinct	1	0.8846
ISADKLQEVYEGFIAK	74.71	54.1949	1809.951	1811.098	6	2	distinct	1	0.9758
VNQIGSITESIEAVTMAK	94.92	53.9432	1889.977	1890.696	2	2	distinct	0	0.9987
YMVEELDGTQNEWGWCK	111.36	53.2921	2143.898	2145.342	4	2	distinct	0	0.9997
IVSIEDPFDQDDWASWVK	121.37	53.3287	2149	2149.761	7	2	distinct	0	0.9999
LAMQEFMILPVGATSFTEAMK	55.27	53.161	2314.141	2315.238	6	+2,+3	distinct	0	0.9889

The equivalent proteins include

jgi|Physo1_1|108827|estExt_fgenesh1_pm.C_340027	0	No title.
jgi|Physo1_1|109759|estExt_fgenesh1_pm.C_19660001	0	No title.
jgi|Physo1_1|109760|estExt_fgenesh1_pm.C_19710001	0	No title.

8. Group probability: 1.0000. Peptides of the group

RPSFVGR	47.76	56.8238	817.456	818.17	2	2	distinct	0	0.8656
IRPTGVSMNVLK	55.01	55.3434	1313.749	1314.392	2	2	distinct	0	0.9437
GTELGMEHLVIGMPHR	77.79	54.1552	1775.881	1776.481	4	+2,+3	distinct	0	0.999
APAAAPATGYNAVHQIEQDR	131.54	53.6551	2079.013	2079.351	10	+2,+3	distinct	0	1
FGHNEVDNPFFTQPLMYK	84.19	53.462	2183.015	2183.803	9	+2,+3	distinct	0	0.9998
WVQEEPLNMGFWTYVSPR	98.16	53.1342	2238.057	2239.01	4	2	distinct	0	0.999

The equivalent proteins include

jgi|Physo1_1|109505|estExt_fgenesh1_pm.C_1210001	0	No title.

9. Group probability: 1.0000. Peptides of the group

KVVISAPPK	67.38	55.1514	937.596	938.69	7	+1,+2	shared(2)	1	0.9963
LEKPASMDAIK (0000000100000)	51.85	55.6378	1201.638	1218.516	5	+2,+3	shared(2)	0	0.9735
LVDLVLHMATVDK	83.6	54.833	1452.801	1453.832	9	+2,+3	distinct	0	0.9972
VPTPDVSVVDLTCR	100.87	54.7391	1556.787	1557.293	12	2	shared(4)	0	0.9926
YDSTHGKFDGSVETK	66.7	54.3734	1669.758	1670.296	7	2	shared(2)	1	0.9822
LVAWYDNEWGYSNR	85.68	54.2461	1771.795	1771.999	7	2	shared(2)	0	0.9608
DGNLVVNGEVIHVFAAR	103.49	54.2738	1808.953	1809.9	8	+2,+3	shared(2)	0	1
VVAINDPFMDLEYMAYLFK (000000000000001000000)	122.87	53.0299	2278.105	2278.884	310	+2,+3	shared(2)	0	1
VVISAPPKDDTPMYVMGVNHK (00000000000000001000000)	91.26	52.9717	2297.155	2297.687	18	+2,+3	shared(2)	1	0.9999
LTGMAFRVPTPDVSVVDLTCR (00001000000000000000000)	64.95	52.9126	2333.187	2333.52	9	+2,+3	shared(3)	1	0.9972
EYNGSAHVVSNASCTTNCLAPLAK	82.61	52.505	2563.179	2563.344	2	2	distinct	0	0.9969
VINDQFGIVEGLMTTVHATTATQLPVDGPAK (000000000000010000000000000000000)	85.4	51.379	3222.659	3223.996	58	3	shared(2)	0	0.9977

The equivalent proteins include

jgi|Physo1_1|109003|estExt_fgenesh1_pm.C_510003	0	No title.

10. Group probability: 1.0000. Peptides of the group

VTASEVNGDVVK	62.07	55.7177	1216.63	1217.854	1	2	distinct	0	0.9695
KQGLEFQFGTK	77.57	55.1659	1281.672	1282.3	7	+1,+2	distinct	1	0.9994
TLTGGIESLFKK	64.65	55.2371	1292.734	1293.931	1	2	distinct	1	0.9759
TQVPGIFAIGDVIK	68.39	54.9724	1456.829	1457.52	5	+1,+2	distinct	0	0.9995
LGGTCLNVGCIPSK	77	54.96	1474.727	1475.148	1	2	distinct	0	0.9924
TCHAHPTLSEAFK	60.11	54.762	1497.703	1497.461	5	+1,+2	distinct	0	0.9975
RAFTAGLGLEQMGIQTDK	122.8	53.7904	1934.988	1935.801	8	2	distinct	1	0.9999
AEGIEYNVGKFPMMANSR	81.68	53.5439	2012.945	2013.424	8	2	distinct	1	0.9958

AFTAGLGLEQMGIQTDKLGR (00000000000010000000000)	110.97	53.3393	2105.094	2105.702	9	+2,+3	distinct	1	1
VTVVEFQDAACPGMDKESVK	60.55	53.2396	2209.039	2210.472	1	3	distinct	1	0.9693
GAMLAHKAEEEGVACVENIAGK (0001000000000000000000)	82.86	52.9929	2283.099	2283.718	13	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|109642|estExt_fgenesh1_pm.C_1910001	0	No title.

11. Group probability: 1.0000. Peptides of the group

MLDHAAALLK	73.29	55.2928	1081.595	1082.454	11	+1,+2	distinct	0	0.9984
RMLDHAAALLK	50.73	55.1205	1237.696	1238.587	2	2	distinct	1	0.9155
IKLEDAGFDWK	58	55.3406	1320.671	1321.151	2	2	distinct	1	0.9552
YGAIKPTAIYVPLK	61.27	54.7709	1532.897	1533.739	10	+1,+2,+3	distinct	0	0.9996
KLSDLTIGPVLTVTTK	94.97	54.3831	1684.997	1685.426	3	2	distinct	1	0.9986
SFGVPGDHQGQASHGYR	71.53	54.4336	1798.813	1799.661	3	2	distinct	0	0.9891
TTGAPQNHWFGPAGDPCAGGIGTPEAIK	67.2	51.8218	2806.313	2807.417	9	+2,+3	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|109579|estExt_fgenesh1_pm.C_1480002	0	No title.

12. Group probability: 1.0000. Peptides of the group

NHCIMLAR	49.24	55.9686	1013.49	1013.341	1	1	distinct	0	0.8957
NRDEISQMR	47.18	55.6322	1147.54	1148.265	2	2	distinct	1	0.8758
FEFASPFELHR	64.6	55.0557	1378.667	1379.471	11	+2,+3	distinct	0	0.9979
RMEITNDNEYK	44.64	55.0479	1411.64	1412.041	1	2	distinct	1	0.8561
SSFNTDYYTMGNKIPGIK	75.3	54.3179	2034.972	2036.408	10	2	distinct	1	0.9925
KWCGEDNGPIFVEMNTYR	72.85	53.1765	2214.983	2215.929	2	2	distinct	1	0.9909
LPAIFCIENNHYGMGTSTAR	97.39	53.5349	2251.051	2251.562	14	+2,+3	distinct	0	0.9999
GFCHLYDGQEAVATGVEAALDR	103.78	52.7803	2378.096	2379.378	8	+2,+3	distinct	0	1
KANFYGGQGIVGAQVPVGAGLAFASK	80.82	52.481	2506.333	2506.767	8	2	distinct	1	0.9966
GFCHLYDGQEAVATGVEAALDRTDSWITSYR	61.12	50.1799	3487.61	3488.495	2	3	distinct	1	0.9814

The equivalent proteins include

jgi|Physo1_1|108775|estExt_fgenesh1_pm.C_300026	0	No title.

13. Group probability: 1.0000. Peptides of the group

HRPSVSELEEK	45.2	55.174	1309.663	1310.578	1	2	distinct	0	0.8627
NKTPTSTPTPPAGK	56.94	54.9697	1395.736	1396.96	1	2	distinct	1	0.9561
DHAIVHGADGVAPSLQATQEK	123.4	53.2266	2143.066	2143.234	5	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|132189|estExt_fgenesh1_pg.C_190139	0	No title.

14. Group probability: 1.0000. Peptides of the group

LGAAHFYIK	72.28	56.2275	1018.56	1019.977	10	2	distinct	0	0.9861
AKFESLNEELFK	76.63	54.8729	1453.745	1454.401	6	2	distinct	1	0.9916
SFTPEEISSMVLLR	58.33	54.5581	1607.823	1608.688	1	2	distinct	0	0.9615
ERGNAAFASGDHATAIK	73.88	54.2934	1714.839	1715.314	4	2	distinct	1	0.9912
MKPEDVTELVLVGGSTR	93.05	54.0987	1829.956	1830.897	6	2	distinct	0	0.9984
EFTTAIAYEPTNVIYYSNR	70.32	53.5365	2251.08	2251.349	2	2	distinct	0	0.989
SINPDEAVAYGAAVQGAILDGIR	93.23	53.087	2299.181	2300.524	2	2	distinct	0	0.9987
RIINEPTAAALAYGLDTNAGTDGK	53.38	52.6084	2431.234	2432.374	1	2	distinct	1	0.9599
NDATNSLLLVDVTPLSLGIETVGK	74.06	52.7205	2468.337	2469.493	4	2	distinct	0	0.9934

The equivalent proteins include

jgi|Physo1_1|143782|estExt_fgenesh1_pg.C_1510018	0	No title.

15. Group probability: 1.0000. Peptides of the group

YGVLVEEAGVALR	94.44	55.1269	1374.751	1375.339	1	2	distinct	0	0.9983
SGKPMVADFMAPWCGK (000000000010000000)	84.95	54.3353	1780.81	1781.973	13	2	distinct	0	0.9965
ALQFVEEHGEVCPANWQPGDK	93.34	52.7186	2410.101	2410.609	8	+2,+3	distinct	0	0.9999
ALNTQLIAVSCDSPESHLAWTR	93.16	52.6293	2468.212	2468.601	11	+2,+3	distinct	0	0.9999
CSQILPFVEDLAEAHPDVTFAK	104.86	52.6798	2486.215	2486.63	2	2	distinct	0	0.9995
LDVSIPEIEQLKDELEVGAYPEFR	75.57	51.8952	2788.417	2789.696	8	2	distinct	1	0.9944
VQHQAPQFTAQAVLDGDITDISLDTYR	99.26	51.3292	3001.478	3002.583	8	3	distinct	0	0.9992

The equivalent proteins include

jgi|Physo1_1|141953|estExt_fgenesh1_pg.C_1060012	0	No title.

16. Group probability: 1.0000. Peptides of the group

AYEALDMLDTILAK	56.31	54.6639	1565.801	1565.994	1	1	distinct	0	0.9539
HLTEYPNVVAYLR	48.17	54.7552	1573.825	1574.282	3	+2,+3	distinct	0	0.9872
YHLYVTYSCPFACR	65.75	54.1562	1835.812	1836.185	3	2	distinct	0	0.9801
SDKHLTEYPNVVAYLR	66.13	53.9561	1903.979	1905.384	1	2	distinct	1	0.9821
APHVAAEGPFVDYDAAHER	108.65	53.8993	2050.95	2051.215	11	+2,+3	distinct	0	1

NLLGLEDAIGLSVAHPVFQK	118.13	53.2774	2120.163	2121.186	17	+2,+3	distinct	0	1
TKPNDPNDEHKGWTFVDPEK	51.42	52.9482	2353.097	2353.574	1	2	distinct	1	0.9447

The equivalent proteins include

jgi|Physo1_1|130534|estExt_fgenesh1_pg.C_110203	0	No title.

17. Group probability: 1.0000. Peptides of the group

EHADVEHQVTMDR	66.89	54.6629	1565.689	1566.103	4	2	distinct	0	0.9811
FTNKPCNPSSPNQIFK	64.36	54.0854	1877.909	1878.644	10	2	distinct	0	0.979
FTDKPCNPDSPNQVYK	60.87	53.846	1908.868	1910.012	3	+2,+3	distinct	0	0.9987
LGLTPYDILTSGQEIMLR	73.42	54.0561	2019.071	2019.976	2	2	distinct	0	0.9912
TGPTPYDMLLSGEEIMFR	106.95	53.5505	2055.965	2056.967	8	2	distinct	0	0.9995
IAAGNTAVDILATGQEIMLR	96.28	53.5434	2056.099	2056.636	3	+2,+3	distinct	0	0.9999
NPAKPNLCFDDGGGTTAGATK	82.65	53.4007	2090.969	2090.758	6	+2,+3	distinct	0	1
NPAKPNLCFDDGGGMTPGASK (00000000000000010000000)	89.31	53.3031	2132.962	2134.11	14	+2,+3	distinct	0	1
YVMWTCDENNPNQHFEVLPR	98.55	52.5514	2548.126	2549.119	2	2	distinct	0	0.9991
FVDKTCNPSSPNQIFTYDANTR	43	52.3638	2574.181	2575.326	1	3	distinct	1	0.8691
FEDQPCDPTSPNQIFTYDTVTHQFK	43.31	51.2972	3014.339	3015.525	1	3	distinct	0	0.8879
AHLWYCDPNNQNQWFVMDPNTLMLK (000000000000000001000000000)	54.26	51.1014	3134.42	3135.416	4	3	distinct	0	0.9573
YWLWGCDNNNPNQHFEVLSAAAMAAEK	72.36	51.0991	3135.397	3136.623	4	3	distinct	0	0.9919
YWLWTCDNANQNQHFEIVSPASMPALK (00000000000000000000000100000)	51.16	50.9723	3235.485	3236.896	2	3	distinct	0	0.9479

The equivalent proteins include

jgi|Physo1_1|142672|estExt_fgenesh1_pg.C_1190042	0	No title.

18. Group probability: 1.0000. Peptides of the group

EHAALEPR	45.39	55.5645	921.467	922.495	1	2	distinct	0	0.8549
TFTPGKPLTLR	47.72	55.7045	1229.713	1230.185	3	2	distinct	0	0.8887
IIYGHLDDATTK	71.53	55.3308	1345.688	1346.334	2	2	distinct	0	0.9868
KTNGNKPLTLAEK	61.19	55.1327	1412.799	1414.211	2	2	distinct	1	0.9686
CTTDHISMAGPWLK	67.23	54.7686	1615.749	1616.236	7	2	distinct	0	0.9823
FKVPYYVTPGSEQVR	53.97	54.1395	1768.915	1769.357	2	2	distinct	1	0.9459
TAVPTTIHCDHLITAEK	101.21	53.9773	1905.962	1906.421	9	2	distinct	0	0.9992
VAMQDATAQMAVLQFISSGLPK	89.12	52.9979	2305.181	2306.117	2	2	distinct	0	0.9981
LALLSAFDEWNGEDFTDMPVLIK	66.53	52.2513	2623.288	2624.459	2	2	distinct	0	0.987
GHLDNISNNLLIGAENAETGETNSVK	73.59	52.1069	2709.32	2710.113	2	3	distinct	0	0.9923
DGILDTFLESGATVLANACGPCIGQWNR	60.05	51.3401	3034.428	3035.84	2	3	distinct	0	0.9768

The equivalent proteins include

jgi|Physo1_1|109018|estExt_fgenesh1_pm.C_520011	0	No title.

19. Group probability: 1.0000. Peptides of the group

RMTPAEIFAR	47.69	55.4643	1190.623	1191.758	2	2	distinct	1	0.8849
LHETAFMGNGLGR	51.64	55.2594	1401.682	1402.259	2	2	distinct	0	0.9272
KSDLQDYIATHYTAPR	131.51	54.0868	1877.927	1878.565	8	+2,+3	distinct	1	1
YETTQNNGAAHFLEHMAFK	69.34	53.1497	2208.006	2208.627	3	2	distinct	0	0.9881
EHALAATGPIHELPDYNFIR	84.86	53.1268	2263.138	2263.509	2	+2,+3	distinct	0	0.9999
RTQQQLELEIENMGGHLNAYTSR	70.52	52.124	2687.308	2688.653	1	3	distinct	1	0.9887
TADEVINDKEHALAATGPIHELPDYNFIR	86.07	50.89	3248.61	3249.713	1	3	distinct	1	0.9977

The equivalent proteins include

jgi|Physo1_1|108442|estExt_fgenesh1_pm.C_100001	0	No title.

20. Group probability: 1.0000. Peptides of the group

AVFPSIVGRPK	60.94	55.6417	1169.692	1170.277	8	2	distinct	0	0.8988
HLGIMVGMDQK (0000000010000)	79.27	55.5998	1227.61	1228.146	22	+1,+2	distinct	0	0.9997
TPEVLFQPSLIGK	59.88	55.0276	1427.802	1428.872	2	2	distinct	0	0.9648
AEYDESGPSIVHR	65.28	55.0979	1458.674	1459.218	3	+2,+3	shared(2)	0	0.998
AEYDESGPSIVHRK	74.83	54.9745	1586.769	1587.119	5	2	shared(2)	1	0.9721
FRTPEVLFQPSLIGK	88.91	54.2738	1730.972	1731.667	11	+2,+3	distinct	1	0.9998
SYELPDGNVIVIGNER	105.1	54.2914	1773.89	1774.202	1	2	shared(2)	0	0.9923
YPIEHGIVTNWDDMEK (000000000000001000)	89.61	53.9187	1945.888	1946.177	23	+2,+3	shared(4)	0	0.9983
VAPEEHPVLLTEAPINPK	81.4	53.7297	1953.057	1953.885	13	2	shared(10)	0	0.9887
DLYCNIVLSGGTTMYPGIGER	47.6	53.1241	2315.093	2315.776	1	2	shared(2)	0	0.9252
KDLYCNIVLSGGTTMYPGIGER (000000000000000100000000)	89.96	52.8441	2443.187	2444.683	11	2	shared(2)	1	0.9983
TTGCVLDSGDGVSHTVPIYEGYALPHAIVR	72.64	50.9575	3183.566	3184.46	9	+2,+3	shared(3)	0	0.9878

The equivalent proteins include

gi|1085617|pir||S49007	41037.55	actin - Pythium irregulare (fragment)
gi|113223|sp|P22131|ACT1_PHYIN	42197.03	Actin-1
gi|9858460|gb|AAG01044.1|	42182.06	actin [Pythium splendens]

jgi|Physo1_1|108986|estExt_fgenesh1_pm.C_490003	0	No title.

21. Group probability: 1.0000. Peptides of the group

YDAAGISYTHR	59.04	55.4556	1252.584	1253.271	4	2	distinct	0	0.959
TVEAEAAHGTVTR	67.95	55.2417	1340.668	1341.53	1	2	shared(2)	0	0.868
AKYDAAGISYTHR	92.57	54.737	1451.716	1452.476	10	+2,+3	distinct	1	1
KTSTNPIASIYAWTR	107.05	54.4586	1707.894	1708.844	4	2	distinct	1	0.9995
VHKPIVELDGDEMTR (00000000000001000)	74.46	54.1803	1737.872	1738.472	14	+2,+3	distinct	0	0.9987
FKDIFEEVYQNEFK	96.36	54.1512	1834.878	1835.5	8	+2,+3	distinct	1	0.9986
NILNGTVFREPIVISNVPR	65.05	53.3226	2137.201	2138.382	12	+2,+3	distinct	1	0.9989
LDGNQELIDFSLGLEDAVIK	71.69	53.2809	2188.126	2188.951	1	2	distinct	0	0.9906
GKLDGNQELIDFSLGLEDAVIK	115.86	52.813	2373.243	2374.4	13	+2,+3	distinct	1	1
DATNDQVTIDAAHAIQEHHVGIK	80.64	52.5891	2482.22	2482.751	5	+2,+3	distinct	0	0.9998
STDFIAPGPGKFEVVYTPADGSEK	81.92	52.5214	2511.217	2511.103	6	2	distinct	1	0.9967
DLAICIHGSNVTPDHYLYTEDFMDK	76.51	51.4835	2953.326	2953.969	3	3	distinct	0	0.9939

The equivalent proteins include

jgi|Physo1_1|109565|estExt_fgenesh1_pm.C_1440001	0	No title.

22. Group probability: 1.0000. Peptides of the group

AHGAQGIGLTR	68.34	55.2464	1079.584	1080.253	10	2	distinct	0	0.9819
GGMTSHAAVVAR (00010000000000)	91.33	55.7078	1155.582	1156.392	7	2	shared(2)	0	0.9737
TEHMFFSSAQR	50.12	55.2069	1339.598	1340.47	3	2	distinct	0	0.9107
LGIVHPGITEMQAK (0000000000010000)	62.94	54.6973	1492.807	1492.4	14	+1,+2	distinct	0	0.9993
IVFTAADAEAWFAR	89.72	54.6017	1566.783	1568.047	1	2	distinct	0	0.9975
HLDQLLHPSFANEK	103.93	54.6251	1647.837	1648.096	13	+2,+3	distinct	0	0.9998
QLDETVHTLETHFK	58.39	54.3196	1696.842	1697.657	1	2	distinct	0	0.9618
RMEVFTNADTPEDAR	43.69	54.1966	1750.794	1751.231	1	2	distinct	1	0.8667
ALGVTFADAANPLLVSVR	57.41	54.1823	1813.01	1813.874	2	2	distinct	0	0.964
IELGICGEHGGDPQSIEFFEK	87.53	52.8688	2361.095	2361.618	4	+2,+3	distinct	0	0.9997
HGVLEKDPFETLDQEGVGELVR	71.99	52.5628	2466.239	2466.788	5	+2,+3	distinct	1	0.9997

The equivalent proteins include

jgi|Physo1_1|108954|estExt_fgenesh1_pm.C_460001	0	No title.

23. Group probability: 1.0000. Peptides of the group

ELHNQSLR	53.69	55.3273	995.515	994.391	2	2	distinct	0	0.9303
AAAHEFSGDAEK	48.11	55.6498	1231.547	1232.151	2	2	distinct	0	0.8963
YKELHNQSLR	52.09	55.5128	1286.673	1287.772	3	2	distinct	1	0.9217
LLASPLPEAEAGILR	76.33	54.6941	1548.887	1550.158	3	2	distinct	0	0.9923
LLASPLPEAEAGILRK	88.53	54.5673	1676.982	1677.577	6	2	distinct	1	0.9975
GLGTKEDLIYPIVVGR	87.53	54.3032	1728.977	1729.61	5	2	distinct	1	0.9972
MITEPLDLLAELFESAMK (000000000000000000100)	133.2	53.5896	2050.037	2066.811	112	+2,+3	distinct	0	1
IAEEVSGDYGELLLSVFDAR	89.12	53.4799	2182.079	2183.549	5	2	distinct	0	0.998
MGTDEEGFVSVLVASPPEHLR	97.15	53.0661	2269.105	2269.312	8	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|140346|estExt_fgenesh1_pg.C_840073	0	No title.

24. Group probability: 1.0000. Peptides of the group

KIFVGGDDFK	56	55.3485	1124.587	1125.308	6	+1,+2	distinct	1	0.9945
VIVLWSANTER	66.55	55.5128	1286.698	1287.469	1	2	distinct	0	0.9787
RAQVLDHDLQR	50.26	55.1836	1349.716	1351.185	3	+2,+3	distinct	1	0.9894
ENEHPDHVVVIK	54.16	55.1384	1414.72	1415.44	2	2	distinct	0	0.9396
ACVGLAPESHMLLENK (000000000001000000)	73.83	54.1878	1767.865	1768.785	12	2	distinct	0	0.9908
LLYKENEHPDHVVVIK	72.16	53.8276	1932.047	1932.439	2	2	distinct	1	0.9895
FSDIVEGVNDTSANLLESIK	111.59	53.2336	2150.074	2151.402	1	2	distinct	0	0.9997
IKPLPSIYYPDFIAANQADR	74.8	53.1439	2291.195	2291.947	24	+2,+3	distinct	0	0.9998
TGVMIVGLGGNNGSTLLASILANK	117.8	53.0739	2299.257	2299.637	7	2	distinct	0	0.9999
SVLVDFLVSAGIKPTSIVSYNHLGNNDGK	72.96	51.2624	3043.598	3044.869	2	3	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|108192|estExt_fgenesh1_pm.C_20024	0	No title.

25. Group probability: 1.0000. Peptides of the group

IGSWVTLEYR	61.08	55.2266	1222.635	1222.589	1	2	distinct	0	0.9646
LIHYVNQDAR	65.17	55.5174	1227.636	1227.479	4	1	distinct	0	0.9751
DLEFIWRPSK	47	55.4108	1289.677	1290.951	1	2	distinct	0	0.8779
SAAATVLSGDASIR	49.07	55.3772	1317.689	1318.875	1	2	distinct	0	0.9117
ELNEVLFVIGEK	57.82	55.3159	1388.755	1389.845	2	2	distinct	0	0.9561
TTVQTVSIPITHK	68.3	54.8838	1423.803	1424.778	5	+2,+3	distinct	0	0.9977
QIDALYQSHHSSK	72.95	54.7082	1512.732	1512.865	4	2	distinct	0	0.9889
NKDLEFIWRPSK	81.37	54.8916	1531.815	1532.786	7	2	distinct	1	0.9945

QFMFVEQSFFQR	60.1		54.5932	1592.745	1593.401	2	2	distinct	0	0.9645
MESQFFRPLTAYR	48.95		54.5842	1644.808	1645.695	5	+2,+3	distinct	0	0.9897
AVGLVQHHDGLSGTEK	87.37		54.5986	1646.838	1647.305	14	2	distinct	0	0.9972
VQYILDTAVEELVR	81.49		54.625	1646.888	1647.694	2	2	distinct	0	0.9949
NSVVSEVTELVLTGTK	89.52		54.82	1674.904	1676.012	4	2	distinct	0	0.9977
DDYWSGFFTSRPTLK	64.52		54.1734	1818.858	1819.112	5	2	distinct	0	0.9786
ASQVFTGEIIDHYCPPGK	68.3		53.6611	2017.957	2018.614	2	2	distinct	0	0.9863
GNHVFIPMGCDFQFDNSR (00000000100000000000)	96.2		53.2701	2139.925	2141.339	15	+2,+3	distinct	0	1
NIQIPLSLDVAYYQAFQGDGPK	107.3		52.6056	2436.232	2436.478	3	2	distinct	0	0.9996
VPWLTVGEFPPSVGLTTVQELSK	50.73		52.583	2483.331	2483.591	1	2	distinct	0	0.9476
AKVPWLTVGEFPPSVGLTTVQELSK	69.17		52.1308	2682.463	2682.801	20	+2,+3	distinct	1	0.9996

The equivalent proteins include

jgi|Physo1_1|131780|estExt_fgenesh1_pg.C_170122	0	No title.

26. Group probability: 1.0000. Peptides of the group

LLADLIDYVPAR	84.07		55.3864	1357.76	1358.827	24	+1,+2	distinct	0	0.9998
SLLADAEAMDLSECILPVGDHIR (00000000001000000000000000)	116.84		52.5481	2524.23	2525.574	123	+2,+3	distinct	0	1

The equivalent proteins include

gi|81159502|gb|ABB56022.1|	20174.32	elicitin-like protein SOL2A [Phytophthora sojae]
jgi|Physo1_1|108732|estExt_fgenesh1_pm.C_280002	0	No title.

27. Group probability: 1.0000. Peptides of the group

SHVTAGGTSLANFSFPGR	131.22		54.2809	1804.886	1805.289	4	2	distinct	0	0.9999
LDQLIFIPMPDFESR	62.59		54.241	1819.918	1820.723	1	2	distinct	0	0.9746
NAPAIIFIDEIDSIAPK	82.61		54.0767	1825.982	1826.739	16	2	shared(2)	0	0.9959
LGDVVGIHTCGDVPYGKR	71.31		53.7099	1941.973	1942.393	5	2	distinct	1	0.9895
GAAPCVLFFDELDSIAQQR	109.54		53.2598	2136.031	2137.284	8	2	distinct	0	0.9996
ELLELVQYPVEHPEKFEK	74.77		53.1252	2226.157	2226.594	7	2	distinct	1	0.9923
VVETEPAPYCIVAPDTIIHCEGEPVR	47.84		51.3873	2950.42	2950.769	1	3	distinct	0	0.9272
VVETEPAPYCIVAPDTIIHCEGEPVRR	51.07		51.1379	3106.521	3107.843	1	3	distinct	1	0.9473

The equivalent proteins include

jgi|Physo1_1|109633|estExt_fgenesh1_pm.C_1820001	0	No title.

28. Group probability: 1.0000. Peptides of the group

LHPEILGDFQK	58.26		55.2175	1295.687	1296.285	5	2	distinct	0	0.9563
LLPWFDGMLEADEK	45.26		54.4831	1662.796	1663.888	1	2	distinct	0	0.8789
LHEAYHNLNCVNVL	62.95		54.3035	1694.82	1695.553	13	2	distinct	0	0.9744
NQNGSILGAIAAAYHVR	109.37		54.1995	1753.922	1754.905	8	+2,+3	distinct	0	1
KLLPWFDGMLEADEK (000000000010000000)	73.98		54.3215	1790.891	1792.099	20	+2,+3	distinct	1	0.9994
GYLQGQIGNPEGPDAPNKK	70.24		53.7723	1981.986	1982.802	10	+2,+3	distinct	1	0.9989
MNIDTDTQWAYWNGLR	77.83		53.7976	1982.894	1983.612	1	2	distinct	0	0.9786
MNIDTDTQWAYWNGLRK	74.4		53.4684	2110.989	2112.422	1	2	distinct	1	0.9917
YAQEHNFAIPAVNVTSSSTANAALQAAR	94.53		51.5156	2901.437	2902.552	9	+2,+3	distinct	0	1
EHGVPLWSSHMLDLSEEPMEENVAISK	55.17		51.2442	3063.432	3064.815	3	3	distinct	0	0.9632

The equivalent proteins include

jgi|Physo1_1|157135|C_scaffold_35000027	0	No title.

29. Group probability: 1.0000. Peptides of the group

RGVQEFELK	45.12		55.8446	1104.593	1105.548	1	2	distinct	1	0.2706
IHYDNWVSEK	47.41		55.4658	1289.604	1289.373	2	1	distinct	0	0.8821
FGLSFWADFLK	66.1		55.3466	1329.676	1330.324	10	+1,+2	distinct	0	0.9975
HGEASMFSQDSGVFK (0000010000000000)	89.3		54.5145	1625.714	1626.205	5	2	distinct	0	0.9975
TKPIQGPYGTGMSGPSFGK (0000000000000100000000)	94.9		53.9167	1908.94	1909.434	28	+2,+3	distinct	0	1
WTSIASTQPVGTTTFEHWPIR	97.97		52.7716	2414.202	2414.803	8	2	distinct	0	0.9991
GHNAIIGLEPVNEPWELTPIEVLK	69.7		52.1296	2667.427	2668.76	17	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|109097|estExt_fgenesh1_pm.C_600003	0	No title.

30. Group probability: 1.0000. Peptides of the group

RVTLEIGGK	51.91		56.3588	971.576	972.261	3	2	shared(3)	1	0.8722
HLAQHPNVDK	47.99		55.7939	1157.594	1158.743	3	2	distinct	0	0.8872
VGELIVEAGFPK	78.95		55.4942	1257.697	1258.863	1	2	shared(2)	0	0.9931
LLINNEFVPSVSGK	68.47		54.911	1515.83	1516.785	2	2	distinct	0	0.984
VYVQEGIYDEFVK	78.44		54.8581	1587.782	1588.458	3	2	distinct	0	0.9931
VYVQEGIYDEFVKR	78.67		54.308	1743.883	1744.428	22	2	distinct	1	0.9936
GWFIEPTVFADVTDDMTIAR (00000000000000000100000)	97.86		52.9995	2283.088	2284.084	13	2	shared(2)	0	0.9991

TGTVYVNCYDVFDGNTPFGGFK	107.51		52.6838	2457.095	2456.854	9	2	distinct	0	0.9996
LGPALAAGNTVVLKPAEQTPLSALR	85.32		52.6066	2486.422	2487.772	31	+2,+3	distinct	0	1
TGTVYVNCYDVFDGNTPFGGFKDSGIGR	63.95		51.1905	3042.382	3043.621	1	3	distinct	1	0.9836

The equivalent proteins include

jgi|Physo1_1|120743|estExt_Genewise1.C_810091	0	No title.

31. Group probability: 1.0000. Peptides of the group

KAGVFSAFTQGK	80.52		55.2276	1239.661	1240.284	3	2	distinct	1	0.994
AKLPGTFGNYIK	50.86		55.3464	1307.724	1308.364	6	2	distinct	1	0.919
KAAFEALAEDLR	46.48		55.3853	1332.704	1334.022	1	3	distinct	1	0.3626
EAEVFTSHHSALVK	77.54		54.756	1553.784	1554.627	12	2	distinct	0	0.9928
SQEPGTHEEIIEFVK	67.5		54.2353	1741.852	1742.632	4	2	distinct	0	0.9835
LVYGDKFELLNLVTK	106.36		54.2005	1750.987	1751.089	13	+2,+3	distinct	1	0.9999
HDVNGSNARPIFTYLK	66.61		54.0678	1830.938	1831.582	1	2	distinct	0	0.9828
DTAVWNVVDGAIYASQLK	78.74		53.8492	1948.989	1950.089	1	2	distinct	0	0.9945
YQEEGLVVLGFPCNQFK	80.8		53.5385	2026.982	2027.709	5	2	distinct	0	0.9953
DTAVWNVVDGAIYASQLKR	78.82		53.3409	2105.09	2105.86	4	2	distinct	1	0.9948

The equivalent proteins include

jgi|Physo1_1|132609|estExt_fgenesh1_pg.C_210169	0	No title.

32. Group probability: 1.0000. Peptides of the group

QIFDFHAIKK	58.75		55.8124	1245.687	1246.433	2	2	distinct	1	0.9561
FFGNLMDSHVVFGK (0000001000000000)	52.62		54.5887	1596.776	1597.069	6	+2,+3	distinct	0	0.9924
TSPFQDQKPGTSGLR	59.29		54.644	1617.811	1618.622	7	+2,+3	distinct	0	0.9951
KLNVPFFEVPTGWK	69.72		54.5459	1660.898	1662.394	10	2	distinct	1	0.9858
EWCPPGHGDLYASLAGSGK	118.43		53.8833	2000.905	2001.097	6	+2,+3	distinct	0	1
LWIGKDGLLSTPCVSAVVR	63.87		53.6656	2070.13	2071.199	2	2	distinct	1	0.9805
EDFTFVVDAMSGVNGPYAR	77.58		53.5069	2073.947	2074.775	2	2	distinct	0	0.9942
SDAYVITEDYRPVIAPER	53.6		53.4123	2093.043	2094.317	1	3	distinct	0	0.9392
TFMSDNYLQNFVASVFEALPAK (00010000000000000000000)	125.42		52.5472	2491.209	2492.633	43	2	distinct	0	0.9999
FFVTPSDSLAIIAANCTVIPFFK	108		52.4712	2557.329	2557.827	14	2	distinct	0	0.9997

The equivalent proteins include

jgi|Physo1_1|158882|C_scaffold_167000003	0	No title.

33. Group probability: 1.0000. Peptides of the group

TVAAVDHIR	54.21		55.2255	980.54	981.259	1	2	distinct	0	0.9335
LMFESHASLR	61.48		55.6051	1189.591	1190.318	2	2	distinct	0	0.9656
FGSELPKPASFLTR	55.54		54.7	1548.83	1549.95	4	3	distinct	0	0.9393
MTGGGFGGCIVALVQQQHAQK	83.89		53.2882	2186.072	2186.685	1	2	distinct	0	0.9969
VNLIGEHTDYNDGFVCPLALDK	83.48		52.5281	2489.19	2489.088	5	2	distinct	0	0.9969
LMDTLDAGYPADKFGSELPKPASFLTR	78.17		51.4445	2939.474	2940.865	12	+2,+3	distinct	1	0.9999
AGSDNVDVVEQAVTLFYSTFSQYANLPR	104.58		51.1596	3090.493	3090.842	4	2	distinct	0	0.9996
ALLCQAAEHEYCNVPCGIMDQFISSCGK	65.64		51.4275	3257.407	3258.227	3	3	distinct	0	0.9857
ALLCQAAEHEYCNVPCGIMDQFISSCGKK	54.76		50.4566	3385.502	3386.878	4	3	distinct	1	0.965

The equivalent proteins include

jgi|Physo1_1|157829|C_scaffold_63000007	0	No title.

34. Group probability: 1.0000. Peptides of the group

IAELTKPGDKK	52.88		55.628	1198.692	1199.56	2	2	distinct	1	0.9293
HTLAYHSDEGK	58.09		55.7464	1256.579	1257.953	2	2	distinct	0	0.9551
LGANSLLDIVVFGR	85.27		54.9751	1472.835	1473.587	5	2	shared(2)	0	0.9963
FHTNNTVLATGGYGR	93.88		54.6092	1606.785	1607.473	8	2	distinct	0	0.985
IYQRPFGGQSLEFGK	72.66		54.2615	1725.884	1726.233	11	+2,+3	distinct	0	0.9983
NLLACASCTMHGAEAR	45.35		54.2742	1760.776	1761.086	1	2	distinct	0	0.8886
GSDWLGDQDAIHYMCR	71.32		54.0797	1922.804	1923.786	1	2	distinct	0	0.9886
IVPGLFAAGEAACASVHGANR	114		53.5896	2067.032	2066.891	18	+2,+3	distinct	0	1
AGIPLQDPEFVQFHPTGIYGAGCLITEGSR	58.9		50.9975	3229.587	3230.987	8	3	distinct	0	0.9762

The equivalent proteins include

jgi|Physo1_1|108636|estExt_fgenesh1_pm.C_210010	0	No title.

35. Group probability: 1.0000. Peptides of the group

MPGVNYNSR	44.68		55.5253	1036.476	1036.627	1	2	shared(2)	0	0.8457
KGPDWAPDSSK	55.08		55.8357	1186.562	1187.198	2	2	shared(2)	1	0.9415
SNFQGLTIGWKDPK	44.44		54.6776	1589.82	1590.597	1	2	distinct	1	0.8694
HLGFCLAFDNLNNK	93.19		54.5312	1661.798	1663.044	10	2	distinct	0	0.9982
HQGFCLDTDPAQNNK	68.1		54.2857	1743.763	1743.906	3	2	distinct	0	0.9843

FYTMESSKPFAQVVR (00001000000000000)	72.69		54.2399	1788.887	1789.876	11	+2,+3	distinct	0	0.9982
CLDAYQAWDGGIVHVYR	91.89		54.0762	2021.942	2022.857	2	2	distinct	0	0.9982
LQLWGCLLNNNNQVWR	82.43		53.539	2027.016	2028.148	6	2	distinct	0	0.9958
KIVISETGWSSGGSDPAAGVASPANQAK	42.6		52.1359	2684.34	2685.048	1	3	shared(2)	1	0.8909
SGDNVAIGFGGSNVAGSQWFYDPSTHLVK	56.21		51.4261	3009.426	3010.855	2	3	distinct	0	0.9686

The equivalent proteins include

jgi|Physo1_1|128780|estExt_fgenesh1_pg.C_50277	0	No title.

36. Group probability: 1.0000. Peptides of the group

IIGQEHYDVAR	74.12		55.3194	1299.657	1300.042	12	+1,+2	distinct	0	0.9988
FVPLVDTISSFK	64.81		55.1598	1351.739	1352.434	2	2	distinct	0	0.9763
IMNVIGESVDER	59.1		55.2764	1360.666	1362.105	1	2	distinct	0	0.9608
VGLTGLTVAEYFR	105.09		54.9675	1424.766	1425.451	8	2	shared(2)	0	0.9864
DNLPPILNALEIK	62.54		55.0508	1448.824	1449.583	2	2	distinct	0	0.9721
AALVYGQMNEPPGAR	63.56		54.9075	1572.772	1573.149	1	2	shared(3)	0	0.926
IVLEVAQHLGENTVR	99.26		54.5673	1676.921	1677.82	61	+2,+3	shared(2)	0	0.9998
FMSQPLHVAEVFTGK (00100000000000000)	106.28		54.783	1689.855	1691.189	30	2	distinct	0	0.9994
QISELGIYPAVDPLDSK	70.7		54.2446	1843.957	1845.105	2	2	distinct	0	0.9884
EGNDLYYEMIESGVIK	84.54		54.4459	1858.866	1859.066	7	2	distinct	0	0.9886
DVEGQDVLLFVDNIFR	100.43		54.0866	1877.952	1879.303	48	2	distinct	0	0.9991
TREGNDLYYEMIESGVIK	85.01		53.4052	2116.015	2116.626	2	2	distinct	1	0.9844
IPSAVGYQPTLATDLGALQER	110.91		53.2112	2199.153	2200.244	2	+2,+3	distinct	0	1
GLQDIIAILGMDELSEDDKLTVAR	117.8		52.4295	2614.352	2614.676	38	+2,+3	distinct	1	1
YAPIHTSAPLLTEQGSGAEILVTGMK	90.55		52.1137	2683.389	2684.372	23	+2,+3	distinct	0	1
DIIAGNYDDLPEAAFYMVGGIEEVK	71.85		52.032	2728.294	2728.551	2	2	distinct	0	0.9924

The equivalent proteins include

jgi|Physo1_1|109375|estExt_fgenesh1_pm.C_960005	0	No title.

37. Group probability: 1.0000. Peptides of the group

AHAIGSGSEGALNNLK	101.2		54.6473	1537.785	1538.404	5	+2,+3	distinct	0	0.9999
RLTSPLLEPGSIEK	64.28		54.6789	1538.867	1539.617	3	2	distinct	1	0.9771
VEATNHWFSYNEPVR	66.8		54.0212	1847.859	1848.367	5	2	distinct	0	0.9825
HVGAAMSGITADAQTLIDHAR (000000100000000000000)	116.68		53.2989	2134.059	2135.242	8	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108388|estExt_fgenesh1_pm.C_70033	0	No title.

38. Group probability: 1.0000. Peptides of the group

VFAHAAAR	47.15		56.5467	841.456	842.316	1	2	distinct	0	0.8732
LGGQNFVFWGGR	70.83		55.3608	1336.668	1336.88	5	2	distinct	0	0.9859
MELDHMAAFFK	76.31		55.115	1338.61	1339.812	2	2	distinct	0	0.9809
CLWGTTNLFGHR	66.87		55.0716	1460.698	1461.211	6	2	distinct	0	0.9802
KIVEIGGLAPGGLNFDAK	51.86		54.2815	1797.999	1798.729	2	+2,+3	distinct	1	0.9919
ESTDLEDIFIAHIGSMDCFAR	47.53		52.7339	2426.088	2427.271	1	3	distinct	0	0.9081
FAVCYWHTFGNTGGDPFGSETYTNR	81.26		51.6641	2883.235	2884.197	16	+2,+3	distinct	0	0.9999
LNVEPNHTTLAGHDYEHDIYYAASYK	82.29		51.487	3020.394	3021.447	4	3	distinct	0	0.9964
MLGSVDCNTGDPLVGWDTDQFLMDEKK	61.52		51.2443	3070.372	3071.505	1	3	distinct	1	0.9789

The equivalent proteins include

jgi|Physo1_1|109314|estExt_fgenesh1_pm.C_890003	0	No title.

39. Group probability: 1.0000. Peptides of the group

HLTPEIYDKLK	48.96		55.3499	1355.745	1357.213	3	3	distinct	1	0.8781
SKYNNYPVLTPK	84.3		54.8231	1422.751	1423.255	4	2	distinct	1	0.9957
TFLVWVNEEDHMR	51.8		54.8201	1674.782	1675.886	1	2	distinct	0	0.9288
GEHSPPGPGGVYDVSNK	101.38		54.3295	1695.785	1696.462	17	+2,+3	distinct	0	1
GSKGEHSPPGPGGVYDVSNK	93.26		53.7652	1967.934	1969.175	10	+2,+3	distinct	1	1
IGFSEVELVQTMIDGIWK	106.06		53.6361	2064.06	2064.749	28	2	distinct	0	0.9995
DLMDPVIEGWHGYKPTDTHK	82.2		52.9994	2338.105	2339.456	7	2	distinct	0	0.9963
EEEQQLIDDHFLFQKPGGGTLLTNAGAAR	81.96		51.0028	3154.568	3155.5	5	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|108967|estExt_fgenesh1_pm.C_470006	0	No title.

40. Group probability: 1.0000. Peptides of the group

IIGSYVGNR	57.66		55.83	977.529	978.913	2	2	shared(2)	0	0.9503
KDWPVTQQK	50.64		55.8113	1128.593	1129.379	3	2	distinct	1	0.908
ELKPGEVLVR	45.1		55.3176	1138.671	1139.408	1	2	distinct	0	0.856
VIAIDTGADKHK	64.31		55.3512	1266.693	1267.501	7	2	distinct	1	0.9751

VTADVFGSVLNAHR	88.03		54.9852	1484.773	1485.885	6	+2,+3	distinct	0	0.9998
WIANSCLGCEDCRK	60.07		54.2013	1767.749	1767.977	7	2	shared(2)	1	0.9672
LAYSGVCHSDLHIWK	64.18		54.3205	1784.867	1785.115	3	2	distinct	0	0.9778
IIGSYVGNRQDSIEALK	45.98		54.1221	1861.99	1862.754	2	2	shared(2)	1	0.8986
TQTAVIFDKLNGPLQVR	100.97		53.8805	1899.058	1899.621	4	2	distinct	1	0.9992
LPCVGGHEGAGYVAAIGDHTR	125.92		53.2613	2136.017	2136.3	7	+2,+3	distinct	0	1
VAAGGDVSTNYSIEKLDNLPSVFER	41.82		52.1819	2680.334	2681.752	1	3	distinct	1	0.87
EINGVCGDSVVIPGAGGGLGHYACQYAR	71.37		51.6403	2876.333	2877.764	8	3	distinct	0	0.9913

The equivalent proteins include

jgi|Physo1_1|109125|estExt_fgenesh1_pm.C_620002	0	No title.

41. Group probability: 1.0000. Peptides of the group

HVAALLLCVLGGNATPSVADLEK	111.1		53.0143	2347.257	2347.962	33	+2,+3	distinct	0	1
LATVSVGAAPAAGAAAGGAAPAKEEEK	95.87		52.8691	2364.228	2364.354	8	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|108694|estExt_fgenesh1_pm.C_240025	0	No title.

42. Group probability: 1.0000. Peptides of the group

KPVCIMAR	48.31		56.6448	973.52	974.005	1	2	distinct	0	0.8852
AHVANWFFK	48.86		55.8199	1118.566	1119.8	1	2	distinct	0	0.8924
YAAEVEALRK	55.95		55.6072	1148.619	1149.101	4	2	distinct	1	0.9441
LGAVIVAVVDPMVAK	90.3		54.7837	1480.869	1480.814	2	2	distinct	0	0.9977
IGVVKPYSETPTLK	69.49		55.2529	1530.866	1531.313	20	+1,+2,+3	distinct	0	0.9999
VPVDETAIPAENRVPR	46.77		54.1579	1761.937	1762.478	2	2	distinct	1	0.9019
AGAHLFLEKPLSNAPVDEVTK	95.15		53.1121	2235.19	2236.593	11	+2,+3	distinct	0	1
VALVGAGAVNFGGAEGPWDHASR	117.07		53.0985	2237.098	2237.589	16	+2,+3	distinct	0	1
SGALGNLVHGALLQGEAYDASLEIMADGLR (000000000000000000000001000000)	52.21		51.107	3056.524	3057.839	1	3	distinct	0	0.9572

The equivalent proteins include

jgi|Physo1_1|139835|estExt_fgenesh1_pg.C_790014	0	No title.

43. Group probability: 1.0000. Peptides of the group

RPSPFAER	56.28		56.5249	958.498	959.406	3	2	distinct	0	0.9431
VPAGLAQYFAMAR (000000000001000)	92.18		55.58	1393.718	1393.523	10	2	distinct	0	0.9979
NWAVYYEKNPAK	59.1		54.7131	1481.73	1482.576	3	2	distinct	1	0.9612
EFVVAQSFTSKPVK	84.73		54.5852	1565.845	1566.662	1	2	distinct	0	0.9962
KDEYLNWAVDAFR	95.62		54.676	1625.784	1626.84	4	2	distinct	1	0.9985
TVPIILGPLTYLALSK	53.53		54.3562	1698.033	1698.747	1	2	distinct	0	0.9455
GMLTGPVTILNWSFPR (001000000000000000)	88.68		54.7079	1787.939	1788.136	12	2	distinct	0	0.996
WFDSNYHYEVPELNAK	65.55		53.6197	2010.911	2011.234	2	2	distinct	0	0.9813
DLGPGTYDIHSPVVPPKEEIVK	50.68		52.8181	2389.253	2389.698	4	2	distinct	1	0.9452
LTSFLNLLPAEQVVVNPDCGLK	76.95		52.7328	2426.288	2427.2	1	2	distinct	0	0.9945
KLTSFLNLLPAEQVVVNPDCGLK	104.16		52.4869	2554.383	2554.986	12	2	distinct	1	0.9995

The equivalent proteins include

jgi|Physo1_1|108148|estExt_fgenesh1_pm.C_10013	0	No title.

44. Group probability: 1.0000. Peptides of the group

ATGFGVAFIQSLLK	88.38		54.8996	1450.818	1451.31	6	2	distinct	0	0.9972
DMGGAAALLGAFEAACHAK	72.12		54.0328	1859.866	1860.763	3	+2,+3	distinct	0	0.9993
GVDALHVTLHALPTQVSR	77.11		53.8276	1913.048	1913.248	9	+2,+3	distinct	0	0.9991
WLHVDMAFPSFTGDDER	92.47		54.0762	2021.894	2023.057	10	+2,+3	distinct	0	0.9999
LVDAPPNELHSDAFIAEAR	47.93		53.6005	2064.028	2064.405	1	2	distinct	0	0.9212
ANAQVSCAGQFIANHLGEFENTGK	82.28		52.4969	2562.192	2563.018	6	+2,+3	distinct	0	0.9999
LQVVYQTPLSGEQTTLVQHTADAIQLAAR	50.97		51.1705	3150.667	3151.899	2	3	distinct	0	0.9505

The equivalent proteins include

jgi|Physo1_1|140692|estExt_fgenesh1_pg.C_880064	0	No title.

45. Group probability: 1.0000. Peptides of the group

HYFIEVNPR	49		55.7299	1173.593	1174.399	2	2	distinct	0	0.894
FVGPTPENLHR	58.83		55.1504	1265.652	1266.122	8	2	distinct	0	0.9585
VKDEAAGVSTVAKPK	111.39		54.7462	1498.835	1499.122	15	+2,+3	distinct	1	1
SFLTNVLNHPDFIK	77.43		54.5892	1643.867	1645.095	12	2	distinct	0	0.9928
FKDEYGSMHFLDTR (0000000010000000)	99.03		54.2842	1744.788	1745.183	6	2	distinct	1	0.9989
YLNAGTVEFLVDQQGR	57.49		54.2737	1808.906	1809.789	1	2	distinct	0	0.9616
VPVVPGTDGPVHTLEQAR	94		54.1605	1870.99	1871.743	18	+2,+3	distinct	0	1
DMAGLLKPQAAQILISAIR	70.48		54.2728	2008.15	2008.717	5	+2,+3	distinct	0	0.9995
DVDVISHAIYPDVFAGFMK	93.16		53.3718	2123.04	2123.666	3	2	distinct	0	0.9985

IAGGETFEDLGLSQDKIKPR	42.66	53.2915	2173.138	2173.425	1	2	distinct	1	0.88
LDDGPGFVGAHITPHYDSLLVK	77.05	53.0416	2350.196	2349.203	7	+2,+3	distinct	0	0.9997
ALGATGPAPSKVDPLVPTLEAPPASTEK	49.31	52.0058	2713.454	2714.66	4	+2,+3	distinct	1	0.9968
VLPNGHEMFEGRPGAEMEPYDFEAAEK	44.72	51.4284	3049.358	3050.402	1	3	distinct	0	0.9075

The equivalent proteins include

jgi|Physo1_1|108780|estExt_fgenesh1_pm.C_310004	0	No title.

46. Group probability: 1.0000. Peptides of the group

IMWMLENVPGLR	60.4	54.9967	1457.752	1458.252	7	2	distinct	0	0.9652
GGIELSQLQAIGITNQR	48.27	54.3159	1796.974	1797.672	1	2	distinct	0	0.9167
ATGKPLYNAIVWHDTR	94.11	54.0831	1840.958	1841.248	8	2	distinct	0	0.9985
LSGGVHGGVHVTDVTNASR	105.43	54.0986	1861.939	1862.352	1	2	distinct	0	0.9995
AEAGDALFGNMDTWLIWK	93.63	53.7429	2036.967	2037.086	4	2	distinct	0	0.9985
QIYQQPGWCEHDADEITR	73.84	53.2635	2244.986	2245.248	5	2	distinct	0	0.9916
NTYGTGCFFMMNTGTKPTPSTK	91.5	52.6999	2440.086	2440.275	9	+2,+3	distinct	0	0.9998
AALEATAFQTQEVVAAMEGDSGVHLTK	68.65	51.8806	2773.359	2774.748	1	3	distinct	0	0.9886

The equivalent proteins include

jgi|Physo1_1|108295|estExt_fgenesh1_pm.C_50010	0	No title.

47. Group probability: 1.0000. Peptides of the group

NLDFLLGGGR	46.89	55.9369	1060.566	1061.166	1	2	distinct	0	0.8754
GVHENTYLNK	59.6	55.7735	1173.578	1173.46	6	+1,+2	distinct	0	0.9962
NLDFLLGGGRK	55.71	55.6688	1188.661	1189.295	6	2	distinct	1	0.9448
GMVTGMIVTCR (0010000000000)	82.43	55.1424	1223.582	1224.353	9	2	distinct	0	0.9948
HGYFVMIEGSR (0000001000000)	70.97	55.1535	1294.613	1295.506	8	2	distinct	0	0.9857
VDHAGHSNDPGTMAK	62.26	54.6928	1535.679	1535.409	10	+1,+2,+3	distinct	0	0.9998
VTHATPASFASHVIDR	72.54	54.6224	1707.869	1707.289	13	+2,+3	distinct	0	0.9998
EPSLPEMVDIVLSLLR (000000010000000000)	88.18	54.1947	1809.991	1810.786	91	+2,+3	distinct	0	0.9998
DLEDVMIELGHVISLR (000000100000000000)	98.54	53.954	1837.961	1838.943	69	+2,+3	distinct	0	1
LFGLFHEDHMSYEVDR (000000000010000000)	74.87	53.7757	1993.899	1994.349	6	+2,+3	distinct	0	0.9994
SVIMMIPDGTGPNVFTLAR	91.66	53.6645	2018.033	2018.835	14	2	distinct	0	0.9946
LMTNFLGLEHQQELVTLK (00100000000000000000)	84.49	53.3891	2113.124	2114.175	39	+2,+3	distinct	0	0.9997
TYDSAIAVDTYEQPLGTVLEAAK	79.46	52.7199	2454.217	2455.097	2	2	distinct	0	0.9958
VTHATPASFASHVIDRDSEDDIAAQYVANK	57.76	50.9849	3227.548	3228.269	5	3	distinct	1	0.9737

The equivalent proteins include

jgi|Physo1_1|137262|estExt_fgenesh1_pg.C_520052	0	No title.

48. Group probability: 1.0000. Peptides of the group

KGLSPDVPPLDR	61.24	55.2388	1292.709	1294.013	1	2	distinct	1	0.9675
NMSVIAHVDHGK (00100000000000)	76.73	55.4054	1306.645	1307.194	11	2	shared(2)	0	0.9916
SGTITTSETGHTIR	75.68	55.094	1459.727	1460.104	4	2	distinct	0	0.9915
GTVAFGSGLHQWGFTLK	98.91	54.3089	1804.926	1805.431	10	+2,+3	distinct	0	0.9999
KIWGYGPDGTGANVFVDATK	113.65	53.7176	2095.037	2095.742	17	+2,+3	distinct	1	1
ALLELHLEPEDCYQSFTR	67.32	53.1588	2220.052	2220.965	3	+2,+3	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|109259|estExt_fgenesh1_pm.C_810006	0	No title.

49. Group probability: 1.0000. Peptides of the group

EADGILFGFPTR	75.45	55.3158	1321.667	1322.724	6	2	distinct	0	0.9906
KDHPVATTDVLK	78.16	55.2209	1322.719	1323.69	18	+1,+2	distinct	1	0.9999
QPSKLELTVATTQGK	68.19	55.1252	1599.883	1600.406	4	2	distinct	1	0.9841
IAIIYYSTYGHIAK	69.13	54.4993	1611.866	1611.918	16	2	distinct	0	0.9851
APELFNMDEIHGGSPWGAGTLANGDGSR (0000000100000000000000000000)	94.89	51.8637	2855.293	2856.792	7	+2,+3	distinct	0	1
EGAESVEGVTAEIYQIQETLPEEVLTK	68.69	51.3708	2961.471	2961.745	4	2	distinct	0	0.9908

The equivalent proteins include

jgi|Physo1_1|156135|C_scaffold_11000030	0	No title.
jgi|Physo1_1|156136|C_scaffold_11000031	0	No title.

50. Group probability: 1.0000. Peptides of the group

LCDLAEAAVKR	58.78	55.9043	1244.655	1245.368	1	2	distinct	1	0.9576
CLWNGWLDAHAR	89.28	54.7678	1497.694	1498.377	17	+2,+3	distinct	0	0.9999
AFHFILDPFQQEK	74.72	54.553	1618.814	1620.082	13	2	distinct	0	0.9905
LYAASAGYFHDVADDMLDVR	90.07	53.2668	2228.021	2229.28	3	+2,+3	distinct	0	1
TFSPDYDHYNFAPQGEQSIFHAR	62.07	52.0678	2726.215	2727.704	5	+2,+3	distinct	0	0.9979

DLVAYVGGVDLTNDRWDTLEHDQAELR	48.48	51.1495	3099.49	3100.85	1	3	distinct	1	0.9339

The equivalent proteins include

jgi|Physo1_1|127024|estExt_fgenesh1_pg.C_10004	0	No title.

51. Group probability: 1.0000. Peptides of the group

APGFGDNRK	48.36	56.4075	960.478	961.69	1	2	distinct	1	0.8863
NAGHEGAVVVGK	60.41	55.3501	1136.594	1136.385	8	+1,+2	distinct	0	0.9979
DKFENMGAQLVR	60.33	54.9405	1406.698	1407.764	2	2	distinct	1	0.965
TLYNELEVVEGMK	93.17	54.6484	1523.754	1523.955	1	2	distinct	0	0.9981
GIQMAVDHVVDGLQK	46.83	54.5089	1608.829	1610.274	1	3	distinct	0	0.8747
VSSLQSIIPMLETVVK	45.52	54.2861	1742.985	1744.109	1	2	distinct	0	0.8902
RGIQMAVDHVVDGLQK (000001000000000000)	79.91	54.1654	1764.93	1765.526	12	+2,+3	distinct	1	0.9994
KVSSLQSIIPMLETVVK	65.42	54.1606	1871.08	1871.972	6	+2,+3	distinct	1	0.9992

The equivalent proteins include

jgi|Physo1_1|109597|estExt_fgenesh1_pm.C_1550001	0	No title.

52. Group probability: 1.0000. Peptides of the group

KGVHVTYGGMGK	68.39	55.5568	1232.633	1233.641	3	+1,+2	distinct	1	0.9991
FKELISDLPAPK	66.31	55.335	1356.765	1357.762	1	2	distinct	1	0.9791
YAEFGHPLNVLK	74.63	55.3092	1386.73	1387.403	12	+2,+3	distinct	0	0.9983
EAVAVGTGSLIFHDITLK	78.86	53.9957	1870.02	1870.318	1	2	distinct	0	0.9945
IKIEDAATLAVNPATAYR	101.01	53.9022	1916.037	1917.09	3	+2,+3	distinct	1	0.9998
TINIIRDDGDYDVTVQHLK	74.96	53.1735	2214.128	2214.186	2	2	distinct	1	0.9927

The equivalent proteins include

jgi|Physo1_1|136873|estExt_fgenesh1_pg.C_490011	0	No title.

53. Group probability: 1.0000. Peptides of the group

LFFTAFAQNWCEK	64.2	54.6157	1660.771	1661.582	1	2	distinct	0	0.9761
FAEAFSCPVGAPMNPEKK	83.84	53.7771	1978.928	1979.128	17	+2,+3	distinct	1	0.9999
IGMVMGHELSHGFDDQGR (00010000000000000000)	95.19	54.1271	1984.888	1985.999	13	+2,+3	distinct	0	0.9999
LFVGADPEDPSTNVLQLAQGGLTLPSR	81.98	51.9548	2794.45	2794.681	2	2	distinct	0	0.9971
NYIGGPDDVPPLPFELQADAFFNNVK	55.97	51.6252	2876.402	2876.673	1	2	distinct	0	0.9708
AIGKPVDEQAWDMFPSTVNAYYDPSANK (000000000000010000000000000000)	68.59	51.1804	3113.444	3114.447	2	3	distinct	0	0.9891

The equivalent proteins include

jgi|Physo1_1|139557|estExt_fgenesh1_pg.C_750054	0	No title.

54. Group probability: 1.0000. Peptides of the group

HQMNNANLGR	54.11	55.2493	1153.541	1154.125	4	2	distinct	0	0.9348
LNLLKLAPGGHIGR	71.61	55.0162	1457.883	1458.974	34	+2,+3	distinct	1	0.9989
RGPLIVYANANGAEK	90.44	54.9384	1571.842	1572.18	11	2	distinct	1	0.9978
EAGHQHSAESWGTGR	52.73	54.5586	1608.703	1609.115	6	2	distinct	0	0.9392
IQGGGNQSSGQAAFGNMCR	88.09	53.8316	1938.842	1938.995	2	2	distinct	0	0.9977
RFAVASALAASAVPALVMAR	100.54	53.7223	1971.109	1972.584	5	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|121586|estExt_Genewise1.C_930071	0	No title.

55. Group probability: 1.0000. Peptides of the group

FRPALVFQPK	50.77	55.6711	1201.697	1202.728	2	2	distinct	0	0.9118
LLGCLSTTHSK	58	55.6911	1215.628	1216.255	1	2	distinct	0	0.9548
AGLHELAAEFPTLVSNVR	95.69	54.0799	1923.021	1923.719	8	+2,+3	distinct	0	0.9999
LRYPLDVHQAANEAEEAR	79.61	53.572	2081.029	2081.729	8	2	distinct	1	0.9949
FLDVYGGQIASLPIGYNHPK	72.4	53.3029	2131.11	2131.39	13	+2,+3	distinct	0	0.9995
IAGMIIEPIQAEGGDNHASPAFFR	70.71	52.4635	2540.248	2540.779	1	2	distinct	0	0.9913
ALPSTPAPAFPDEYAHAEIVTGQVPGPK	43.9	51.7184	2859.444	2860.449	1	3	distinct	0	0.9035

The equivalent proteins include

jgi|Physo1_1|157659|C_scaffold_55000043	0	No title.

56. Group probability: 1.0000. Peptides of the group

SLQGTLMHQLK	63.91	55.6625	1254.675	1255.6	5	2	distinct	0	0.9731
ITGLTFPGDRVHSEK	62.4	54.4126	1655.863	1656.158	4	2	distinct	1	0.974
LIKPGNTNLQVTEALTK	83.23	54.0191	1839.046	1839.788	2	2	distinct	0	0.9961
HDLLQAYPILEGRPGDK	69.86	53.8308	1921.006	1921.326	9	+2,+3	distinct	0	0.9995
LAAEIAQSALEGVLSQLEAGKDVVELCK	104.81	51.4776	2940.548	2942.043	3	3	distinct	1	0.9995
GVAFPTSISANEIICHFSPLQNESLVLK	66.16	51.2426	3070.58	3071.853	6	+2,+3	distinct	0	0.9989

The equivalent proteins include

jgi|Physo1_1|109304|estExt_fgenesh1_pm.C_870001	0	No title.

57. Group probability: 1.0000. Peptides of the group

TPLYDLHVALGGK	84.77	55.0388	1382.756	1383.563	1	2	distinct	0	0.996

KTPLYDLHVALGGK	64.44	54.6467	1510.851	1512.307	1	2	distinct	1	0.9774
DLEFMHGVFTPLTLK	46.15	54.2572	1746.901	1748.173	2	2	distinct	0	0.8924
REEGGFPGHAIIMDQLK	74.56	53.8399	1896.952	1897.396	4	2	distinct	1	0.9918
EQGCASLFDVSHMGQLR	57.09	53.8099	1933.877	1934.72	1	2	distinct	0	0.962
ALVALQGPGAADVVELLKPNMNLK	105.79	52.6032	2460.377	2460.627	15	+2,+3	distinct	0	1
EGAELYDADDNVVGHVTSGTFSPSLKK	68.43	51.7803	2835.356	2836.342	1	3	distinct	1	0.9884

The equivalent proteins include

jgi|Physo1_1|155812|C_scaffold_8000018	0	No title.

58. Group probability: 1.0000. Peptides of the group

IPTLAIHLDR	75.36	55.6633	1147.671	1149.098	3	2	distinct	0	0.9898
HASVLLQLIAK	77.25	55.3407	1191.734	1192.472	1	2	distinct	0	0.9917
LLLVDRPILR	47.9	55.2008	1206.781	1207.672	3	2	distinct	0	0.8877
GNGFHVIGAHTDSPCLK	71.19	54.1366	1808.863	1810.36	2	2	distinct	0	0.9889
LDNLCCSWLATQALIK	60.16	53.9789	1904.949	1905.839	1	2	distinct	0	0.9698
SFMVSADMAHGVHPNYSEK	88.02	53.3434	2105.93	2106.381	3	2	distinct	0	0.9977
LTLSPHTPQTVGAFLQFINK	76.94	53.2726	2211.205	2211.276	6	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|109605|estExt_fgenesh1_pm.C_1640002	0	No title.

59. Group probability: 1.0000. Peptides of the group

KYAEGIHK	45.86	56.5459	944.508	945.082	2	2	distinct	1	0.858
ALGLPIERPK	48.28	55.3784	1092.665	1093.804	1	2	distinct	0	0.8909
VIPGYGHAVLR	61.31	55.1755	1180.672	1181.166	7	2	distinct	0	0.8285
AIGVLSQLFWDR	62.68	55.1386	1403.756	1405.09	1	2	distinct	0	0.9714
SVTSEWINNHFANQK	105.39	54.2388	1773.843	1774.662	5	2	distinct	0	0.9994
SLLWETSLLDAEEGIR	68.1	54.0724	1830.936	1831.818	1	2	distinct	0	0.9849
IVDTIYQVMPGVLTEHGK	70.67	53.7365	1999.045	1999.404	12	+2,+3	distinct	0	0.9998
TKNPYPNVDSHSGVLLQYYGLTQK	77.52	52.1593	2721.376	2722.503	4	3	distinct	1	0.9941

The equivalent proteins include

jgi|Physo1_1|109571|estExt_fgenesh1_pm.C_1450006	0	No title.

60. Group probability: 1.0000. Peptides of the group

HWIGYSK	47.45	56.7742	889.445	889.946	1	2	distinct	0	0.8621
VIAVLVGGRPR	67.25	55.3501	1135.719	1136.627	12	2	distinct	0	0.9801
ETVMLFLTQPFR	62.21	54.8287	1480.775	1481.906	2	2	distinct	0	0.9704
VYETFGEDPYLVSVIAESLIK	113.8	52.858	2371.22	2372.058	47	+2,+3	distinct	0	1
DTLAAGTPWIFGPMLEISQNPLWPR	56.35	51.9033	2809.426	2810.345	5	2	distinct	0	0.9706
TPTGHDKDGVTLSDYDLLNYFLPPFK	58.8	51.4537	2952.454	2952.741	8	+2,+3	distinct	1	0.9993

The equivalent proteins include

jgi|Physo1_1|131903|estExt_fgenesh1_pg.C_180012	0	No title.

61. Group probability: 1.0000. Peptides of the group

GVLTAALNAAQYR	55.67	55.2526	1346.731	1348.029	1	2	distinct	0	0.9489
NIKPHVVNVAEDGAGVDK	74.88	54.1121	1860.969	1861.504	3	2	distinct	0	0.9922
CIQHGTPLVTASYVSPEMK	80.25	53.4379	2117.029	2117.524	7	2	distinct	0	0.9954
GLEGDDGIMMMGVDILPSELAR	97.32	52.8982	2318.096	2318.046	3	2	distinct	0	0.9991
EDANGFLQWLGAFDHSTPVVR	56.77	52.8714	2358.139	2359.099	1	2	distinct	0	0.9667
ILYGTVIDNPDYFVKPQPGFSGTPSR	84.25	51.7242	2867.449	2868.561	15	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|108801|estExt_fgenesh1_pm.C_340001	0	No title.

62. Group probability: 1.0000. Peptides of the group

EFVASLARPR	58.29	55.7916	1144.635	1145.474	7	2	distinct	0	0.9543
SPDKVDATVQR	53.45	55.7524	1214.625	1215.293	1	2	distinct	1	0.9326
DFFGGHTYER	55.82	55.6386	1227.531	1228.536	1	2	distinct	0	0.9434
ERLPANLTQAQR	55.89	54.9697	1395.758	1396.461	7	2	distinct	1	0.9483
AKDEGNLPLVGYK	44.93	55.1186	1402.746	1403.533	1	2	distinct	1	0.8692
ICSYAQGLNLIR	48.18	54.9406	1406.734	1408.03	1	2	distinct	0	0.8984
GIHFVGMGVSGGEEGAR	86.07	55.0071	1658.783	1659.487	7	2	distinct	0	0.9969
ILSGPSEIPAVDKQQLIDDVR	64.57	53.0633	2292.232	2292.847	2	2	distinct	1	0.9831
MVHNGIEYGDMQLIAEAYDILK	81.23	52.5002	2522.218	2523.454	3	+2,+3	distinct	0	0.9989

The equivalent proteins include

jgi|Physo1_1|108585|estExt_fgenesh1_pm.C_170009	0	No title.

63. Group probability: 1.0000. Peptides of the group

GFKDQIYEVFR	60.19	55.2155	1400.709	1401.772	2	2	distinct	1	0.8571
TLQQGVHIVVGTPGR	83.8	54.8812	1560.874	1561.39	7	2	distinct	0	0.9844
KGVAINFLTHNDVR	71.29	54.6081	1582.858	1583.431	2	2	distinct	1	0.9876
GIYAYGFEKPSAIQKR	86.96	54.1071	1826.968	1827.656	35	+2,+3	distinct	1	0.9998
VQVALFSATMPLDVLEVTR	57.32	53.3807	2088.129	2088.722	2	2	distinct	0	0.9656
AVKPILLGHDCIAQAQSGTGK	98.78	53.93	2163.147	2164.645	12	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109443|estExt_fgenesh1_pm.C_1080002	0	No title.

64. Group probability: 1.0000. Peptides of the group

KFSDPIVQADIK	45.71	55.3295	1359.74	1360.845	1	2	distinct	1	0.8729
SQVHEVVLVGGSTR	50.59	54.902	1466.784	1467.846	3	2	distinct	0	0.8932
ARFEDMCGDYFR	51.41	54.6639	1565.639	1565.974	3	2	distinct	1	0.9239
QKELEGVANPILQK	77.3	54.5852	1565.878	1566.538	5	2	distinct	1	0.9927
NQVAMNAHNTVFDAK	85	54.9199	1658.783	1659.309	6	2	distinct	0	0.9964
IINEPTAAAIAYGIDKK	113.47	54.8034	1786.983	1787.369	22	2	shared(7)	1	0.9981
NQVAMNAHNTVFDAKR	87.88	54.1038	1814.885	1815.33	3	2	distinct	1	0.9973
VQQLLSDFFNGKEPNK	72.42	54.1743	1862.953	1863.814	4	+2,+3	distinct	1	0.9985
SQTFSTYADNQPGVLIQVFEGER	63.02	52.4235	2585.24	2585.586	2	2	distinct	0	0.7566

The equivalent proteins include

gi|38489930|gb|AAR21576.1|	71770.42	heat shock protein 70 [Phytophthora nicotianae]

65. Group probability: 1.0000. Peptides of the group

KTVAVGVIK	47.89	56.6012	913.596	914.553	1	2	shared(2)	1	0.881
IGGIGTVPVGR	47.13	55.1691	1024.603	1026.063	1	2	shared(7)	0	0.8841
EHALLAFTLGVK	64.61	55.2154	1297.739	1299.156	1	2	shared(4)	0	0.9343
FFFTVIDAPGHR	72.18	55.051	1405.714	1406.896	27	+2,+3	distinct	0	0.9995
VETGVIKPGMVATFGPVGLSTEVK (0000000000100000000000000)	112.1	52.7752	2415.308	2415.308	25	+2,+3	distinct	0	1
SVEMHHESLPEAVPGDNVGFNVK	76.04	52.5443	2491.18	2492.428	3	2	distinct	0	0.9814
SGDACMVILEPSKPMTVESFQEYPPLGR (0000001000000000100000000000000)	63.79	51.0271	3137.487	3169.855	11	+2,+3	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|109384|estExt_fgenesh1_pm.C_970007	0	No title.

66. Group probability: 1.0000. Peptides of the group

RVQANLGAK	48.16	56.4284	955.556	956.8	2	2	distinct	1	0.6865
SKEWVHDIVQK	69.99	55.1181	1367.72	1368.388	7	+2,+3	distinct	1	0.9992
AISFVGGNQAGEYIHSR	102.71	54.2515	1804.886	1805.655	12	2	distinct	0	0.9993
NHAVIMPDCDKEQAVGALAGAAFGAAGQR (000000100000000000000000000000)	69.04	51.6239	2924.402	2925.636	12	+2,+3	distinct	1	0.9999
EAGLPDGVLNIIHGAHDTVNFICDAPEIK	75.46	51.1391	3114.544	3115.925	6	+2,+3	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|108308|estExt_fgenesh1_pm.C_50023	0	No title.

67. Group probability: 1.0000. Peptides of the group

HCWYIPADGTQGR	53.41	54.7579	1559.694	1560.623	2	2	distinct	0	0.9383
VIIGHGDNFYWSGINSR	98.35	53.7998	1933.943	1934.531	11	2	distinct	0	0.999
SGCGAFTWTNYNGGTCWLK	93.92	53.3042	2178.925	2179.37	5	2	shared(2)	0	0.9986
IVNSHYSTYNDYAEHNMK	100.95	53.4591	2184.953	2186.365	15	+2,+3	distinct	0	1
MQYHTTDNNWQFGENFQSTK	55.12	52.479	2475.055	2474.809	1	2	distinct	0	0.9604
TIPWVNVLGNHDYGGASFICENNSR	44.4	51.7301	2819.308	2819.526	1	2	distinct	0	0.9165
SSSYSNYDVVAEDVVASLMNTQAGNQAVKPK	49.9	51.1665	3271.567	3273.007	1	3	distinct	0	0.9493

The equivalent proteins include

jgi|Physo1_1|140694|estExt_fgenesh1_pg.C_880066	0	No title.

68. Group probability: 1.0000. Peptides of the group

KVVISAPPK	67.38	55.1514	937.596	938.69	7	+1,+2	shared(2)	1	0.9963
LEKPASMDAIK (0000000100000)	51.85	55.6378	1201.638	1218.516	5	+2,+3	shared(2)	0	0.9735
LVDLVLHMATIDN	52.39	54.8331	1452.765	1453.451	7	2	distinct	0	0.74
VPTPDVSVVDLTCR	100.87	54.7391	1556.787	1557.293	12	2	shared(4)	0	0.9926
YDSTHGKFDGSVETK	66.7	54.3734	1669.758	1670.296	7	2	shared(2)	1	0.9822
LVAWYDNEWGYSNR	85.68	54.2461	1771.795	1771.999	7	2	shared(2)	0	0.9608
DGNLVVNGEVIHVFAAR	103.49	54.2738	1808.953	1809.9	8	+2,+3	shared(2)	0	1
VVAINDPFMDLEYMAYLFK (000000000000001000000)	122.87	53.0299	2278.105	2278.884	310	+2,+3	shared(2)	0	1
VVISAPPKDDTPMYVMGVNHK (0000000000000001000000)	91.26	52.9717	2297.155	2297.687	18	+2,+3	shared(2)	1	0.9999
LTGMAFRVPTPDVSVVDLTCR (00001000000000000000000)	64.95	52.9126	2333.187	2333.52	9	+2,+3	shared(3)	1	0.9972
VINDQFGIVEGLMTTVHATTATQLPVDGPAK (000000000000010000000000000000000)	85.4	51.379	3222.659	3223.996	58	3	shared(2)	0	0.9977

The equivalent proteins include

jgi|Physo1_1|109002|estExt_fgenesh1_pm.C_510002	0	No title.

69. Group probability: 1.0000. Peptides of the group

VVCALYEGGEAGKR	50.07	54.7029	1507.745	1508.007	2	2	distinct	1	0.9202

RNPDILGCVENELGLR	74.13	54.0867	1853.942	1854.799	6	+2,+3	distinct	1	0.9997
HAMTPHYSGTTLDAQAR (0001000000000000000)	84.98	54.514	1855.864	1856.441	15	+2,+3	distinct	0	0.9998
FFDGKPQRPEYLIAEGGK	54.25	53.9108	2051.048	2051.588	2	2	distinct	0	0.9528
GHEYVVTSDKDGDQSEFVR	99.34	53.4681	2166.982	2167.961	8	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|144953|estExt_fgenesh1_pg.C_3530001	0	No title.

70. Group probability: 1.0000. Peptides of the group

HLLQLIVAGGK	68.26	55.7891	1147.708	1147.564	4	+1,+2	distinct	0	0.9956
TIITQCQQHGFQR	99.96	54.8538	1615.789	1616.433	9	2	distinct	0	0.999
FSKPVQSGEEFVIR	56.13	54.572	1621.846	1622.698	3	2	distinct	0	0.9532
LLANPSFNPAQSSHGR	72.18	54.3027	1694.849	1695.67	11	+2,+3	distinct	0	0.9984
TIPSRDDLSHHYAEVK	48.03	53.9364	1866.922	1867.539	2	2	distinct	1	0.9125
LVIPDVAEEPDFLSFAR	51.28	53.9022	1916.988	1917.155	1	2	distinct	0	0.9366
LCEAAHPGPHVEQFQER	53.05	53.652	2003.927	2004.389	3	+2,+3	distinct	0	0.9914

The equivalent proteins include

jgi|Physo1_1|127575|estExt_fgenesh1_pg.C_20151	0	No title.

71. Group probability: 1.0000. Peptides of the group

TVVIHGMAK	45.05	55.7885	954.532	955.373	1	2	distinct	0	0.8499
LGNKPATTTTSFR	44.09	55.0597	1392.736	1393.091	1	2	distinct	0	0.8593
EHQSFATLPGMYER (0000000000010000)	63.32	54.4575	1664.762	1665.441	7	2	distinct	0	0.9752
ITSGEHNHVMDNFLR	85.53	54.1638	1768.831	1769.282	4	2	distinct	0	0.9966
TLEAVGAYQANPVTASPAVAPQEHKPVR	109.28	51.58	2900.514	2901.557	1	3	distinct	0	0.9997
SLMLCNPSNPAGTVHSPAQLESIAAVLR (0001000000000000000000000000)	77.42	51.4271	2932.49	2932.725	11	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|129035|estExt_fgenesh1_pg.C_60192	0	No title.

72. Group probability: 1.0000. Peptides of the group

AGKPQEVTVYVSPVVVK	62.85	54.3148	1799.019	1799.457	2	2	distinct	0	0.9768
HSNVIASISGATNLVNVR	65.63	53.9963	1850.996	1852.058	1	2	distinct	0	0.9826
LGFGGVVKPADIPTVGISR	81.6	53.9412	1882.068	1882.753	18	+2,+3	distinct	0	0.9999
ASVPLTMQPDYEAHFYVR	75.14	53.3865	2123.015	2123.57	1	2	distinct	0	0.9925
ALVANFMPEIVQLLEQHPDVR	83.75	52.682	2418.273	2419.24	2	2	distinct	0	0.9969
SDNLDSSAYVGPGAGRFPTANSVMNDIIQLAR	57.3	50.717	3335.62	3336.947	1	3	distinct	1	0.9747

The equivalent proteins include

jgi|Physo1_1|108556|estExt_fgenesh1_pm.C_150025	0	No title.

73. Group probability: 1.0000. Peptides of the group

KYTFTEDFAPR	78.58	55.1971	1373.662	1374.69	1	2	distinct	1	0.9926
KAGNTNIYVTGPATSK	114.56	54.5396	1620.847	1621.439	5	2	distinct	1	0.9997
SDVLLFADQNHGWVHR	94.68	54.3793	1892.928	1893.02	16	+2,+3	distinct	0	0.9999
VPQLLMAAGDDPDFVKPDGSVHK (0000001000000000000000000)	80.33	52.5983	2435.215	2435.07	8	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|108414|estExt_fgenesh1_pm.C_90010	0	No title.

74. Group probability: 1.0000. Peptides of the group

KDIFLNSMFDK	79.97	55.2572	1356.675	1356.993	2	2	shared(3)	1	0.9935
GAHYYAYQLLHTGA	89.7	54.6856	1563.747	1564.523	19	+1,+2,+3	distinct	0	1
IISGPGLATIYEFLAK	95.06	54.6159	1691.95	1692.384	32	2	shared(3)	0	0.9986
ACPVYLVLTEELGER	64.68	54.2299	1747.881	1748.953	3	+2,+3	distinct	0	0.9993
TNELCNQTLEIFVGAYGR	96.66	53.5559	2084	2084.793	8	2	shared(3)	0	0.9989
YLNEEHASFNEVCHLFMNEAK	62.05	52.4523	2581.137	2581.619	2	2	distinct	0	0.9792

The equivalent proteins include

jgi|Physo1_1|138630|estExt_fgenesh1_pg.C_650049	0	No title.

75. Group probability: 1.0000. Peptides of the group

SERPDLASAR	45.83	55.9053	1100.557	1101.995	1	2	distinct	0	0.8633
LITVRPTGFEK	48.77	55.6672	1259.724	1260.737	1	2	distinct	0	0.8986
YDHLVAEEVAELLVAAQK	125.93	53.6151	1997.047	1998.055	4	+2,+3	distinct	0	1
VVAPELYVAAGISGAIQHLAGMK (00000000000000000000100)	83.31	52.9764	2294.246	2294.851	31	+2,+3	distinct	0	0.9998
VVAPELYVAAGISGAIQHLAGMKDSK	62.27	52.2918	2624.399	2625.873	1	3	distinct	1	0.9791
LDVAPISDILAVADKDTFFRPTYAGNAIAQVK	55.49	50.3465	3418.814	3419.326	5	3	distinct	1	0.9705

The equivalent proteins include

jgi|Physo1_1|108676|estExt_fgenesh1_pm.C_240007	0	No title.

76. Group probability: 1.0000. Peptides of the group

KLQITTQGR	46.45	56.1759	1043.609	1045.015	1	2	distinct	1	0.8662
VSGGFTHGASGVVFK	69.8	55.0509	1448.741	1449.486	14	+1,+2	distinct	0	0.9994
VSGGFTHGASGVVFKK	60.91	54.8369	1576.836	1577.424	3	2	distinct	1	0.9712
VVTEAELPNVLTQGLK	83.68	54.2394	1709.956	1710.35	1	2	distinct	0	0.9961
SAIVQHNVGASYTGADFVTSLVTK	105.91	52.6142	2464.26	2464.832	6	2	distinct	0	0.9996
SAIVQHNVGASYTGADFVTSLVTKK	66.94	52.3406	2592.355	2593.65	5	3	distinct	1	0.9856

The equivalent proteins include

jgi|Physo1_1|141609|estExt_fgenesh1_pg.C_1010022	0	No title.

77. Group probability: 1.0000. Peptides of the group

NSLMLVTALNPHIGYDK	95.39	53.9245	1884.977	1886.048	5	+2,+3	distinct	0	1
THTQDATPLTLGQEFSGYR	133.31	53.3121	2121.013	2121.651	10	+2,+3	distinct	0	1
LDDHFPLVVFQTGSGTQSNMNTNEVISNR	87.25	50.9323	3219.525	3220.545	1	3	distinct	0	0.998

The equivalent proteins include

jgi|Physo1_1|109373|estExt_fgenesh1_pm.C_960003	0	No title.

78. Group probability: 1.0000. Peptides of the group

IIGSYVGNR	57.66	55.83	977.529	978.913	2	2	shared(2)	0	0.9503
WIANSCLGCEDCRK	60.07	54.2013	1767.749	1767.977	7	2	shared(2)	1	0.9672
IIGSYVGNRQDSIEALK	45.98	54.1221	1861.99	1862.754	2	2	shared(2)	1	0.8986
ELPMHAAAPILCAGVTVYK (0000100000000000000000)	76.32	53.6078	2040.054	2040.054	13	+2,+3	distinct	0	0.9994
KDWPVTQPEELKPGEVLVR	84.02	53.1821	2219.195	2219.449	10	+2,+3	distinct	1	0.9998
EIGGVCGDSVVIPGAGGGLGHLACQYAR	74.84	52.1649	2769.333	2770.756	3	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|132859|estExt_fgenesh1_pg.C_230002	0	No title.
jgi|Physo1_1|138265|estExt_fgenesh1_pg.C_620001	0	No title.

79. Group probability: 1.0000. Peptides of the group

KDYPVATPDVLK	53.44	55.4379	1344.729	1345.796	2	2	distinct	1	0.9353
TNVAIIYYSTYGHIATMAESVK	86.46	52.6143	2431.209	2432.565	6	2	distinct	0	0.9976
SPLLFNMEEIHGGSPWGAGTLAGADGSR (00000001000000000000000000000)	97.15	51.9887	2826.339	2826.773	34	+2,+3	distinct	0	1
EGVESVEGVTAEIYQVQETLSEEILGK	95.26	51.4813	2935.455	2935.692	33	2	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|130452|estExt_fgenesh1_pg.C_110121	0	No title.

80. Group probability: 1.0000. Peptides of the group

IVLSPTPARPAPTP	71.15	55.1389	1415.814	1416.084	3	2	distinct	0	0.9873
FVNLLHSMADPER	51.88	54.7946	1527.75	1529.014	3	2	distinct	0	0.9293
NLGNAQVDHVQGIAK	89.8	54.8978	1562.816	1563.923	11	2	distinct	0	0.9976
FVNLLHSMADPERK	58.52	54.4127	1655.845	1656.094	5	2	distinct	1	0.9622
DKIVLSPTPARPAPTP	62.39	54.9451	1658.936	1659.386	9	2	distinct	1	0.9747
GREFEGMGLGGTCVNFGCVPK	68.22	53.0753	2271.023	2271.363	1	2	distinct	1	0.9877
ADFDNIVAIHPTAAEELVTMAPWGMIK	70.43	51.4617	2939.456	2940.203	6	2	distinct	0	0.9921

The equivalent proteins include

jgi|Physo1_1|108729|estExt_fgenesh1_pm.C_270014	0	No title.

81. Group probability: 1.0000. Peptides of the group

NVGAIGFELWQVK	81.48	55.1286	1459.782	1460.159	3	2	distinct	0	0.9947
WVASTWKPAAEVGK	59.44	54.7875	1528.804	1529.238	8	2	distinct	0	0.9649
GKDLYLSYLVQHEQK	87.45	54.2409	1819.947	1820.73	5	2	distinct	1	0.9971
THAILNYARPGEDAVNMDHK	96.23	53.5361	2251.08	2251.117	2	2	distinct	0	0.9989
LLPADVDQANFGGESPYAVMFGPDICGSNKK (0000000000000000000001000000000000)	105.72	50.8831	3296.548	3297.458	5	3	distinct	1	0.9996

The equivalent proteins include

jgi|Physo1_1|109612|estExt_fgenesh1_pm.C_1680002	0	No title.

82. Group probability: 1.0000. Peptides of the group

YVGSMVSDIHR	44.81	55.6153	1262.608	1263.203	1	2	distinct	0	0.8566
ILDLVPTDIHQR	54.68	54.9886	1418.788	1419.159	5	+2,+3	distinct	0	0.982
KLDVLANDIFVNSLK	98.08	54.4945	1687.951	1688.937	3	2	distinct	1	0.9989
TIYSCNEGNYAHWDR	80.41	53.9165	1884.785	1885.401	7	2	distinct	0	0.9947
GVHCFTLDPTIGAFILSQK	94.88	53.3858	2103.082	2103.428	16	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109566|estExt_fgenesh1_pm.C_1450001	0	No title.

83. Group probability: 1.0000. Peptides of the group

HLVGEIIK	47.93	55.669	907.549	908.665	5	2	distinct	0	0.6906
HLVGEIIKR	53.48	55.5769	1063.65	1064.415	3	2	distinct	1	0.9271
TYIMVKPDGVQR	53.91	55.0493	1405.739	1407.063	19	2	distinct	0	0.9384
NVCHGSDSVESAEK	64.42	54.9095	1517.642	1517.955	2	2	shared(2)	0	0.9772
MLGATKPTESALGTIR (010000000000000000)	102.51	54.618	1644.887	1661.27	23	2	distinct	0	0.9978
KMLGATKPTESALGTIR (0010000000000000000)	72.93	54.2928	1772.982	1773.647	5	2	distinct	1	0.9904
YMSSGPVTCMVWEGTNVVLEGR	120.01	52.9227	2471.128	2471.359	30	2	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|108873|estExt_fgenesh1_pm.C_370013	0	No title.

84. Group probability: 1.0000. Peptides of the group

HAWADKR	45.36	54.9856	882.446	883	1	2	shared(2)	1	0.8403
HFLYHSVDYK	50.41	55.4026	1307.63	1308.106	2	2	distinct	0	0.9095
HTVFYTGVTALPISWK	123.42	54.2682	1818.967	1820.266	26	+2,+3	distinct	0	1
KPYLFGEHVVYATTEDGGK	113	53.337	2110.037	2110.253	18	+2,+3	distinct	0	1
DINDVDSHLVGKGDWIVSDSK	68.51	53.0468	2298.113	2299.533	1	3	shared(2)	1	0.9853

The equivalent proteins include

jgi|Physo1_1|137803|estExt_fgenesh1_pg.C_570068	0	No title.

85. Group probability: 1.0000. Peptides of the group

TAAFTQVSQHHVDSK	79.89	54.3737	1654.806	1655.104	7	2	distinct	0	0.9944
VSAFKPVLDQALISLPLK	96.94	53.8308	1938.155	1938.65	6	2	distinct	0	0.9989
TFVDFFTNQTELPHTFWK	87.4	53.3099	2257.084	2258.051	5	+2,+3	distinct	0	0.9999
VSAFKPVLDQALISLPLKDQLR	90.19	52.553	2450.426	2450.975	5	+2,+3	distinct	1	0.9993

The equivalent proteins include

jgi|Physo1_1|109348|estExt_fgenesh1_pm.C_930003	0	No title.

86. Group probability: 1.0000. Peptides of the group

IHTTIGLGSK	64.2	55.3626	1025.587	1025.524	9	+1,+2	distinct	0	0.997
LENTHSVHGAPLKPDDLSATK	93.53	53.3026	2229.139	2229.613	6	+2,+3	distinct	0	0.9999
AMPNMYVYRPADGNETVGAYIAAVENTHK	69.8	51.1556	3181.496	3182.087	4	3	distinct	0	0.9905
APGHPENFCTPGVEVSTGPLGQGISNAVGLAIAEK	97.98	50.1055	3473.725	3474.435	6	3	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|108201|estExt_fgenesh1_pm.C_20033	0	No title.

87. Group probability: 1.0000. Peptides of the group

IFGVTTLDVVR	66.68	55.5937	1218.697	1219.442	1	2	shared(3)	0	0.9568
RIFGVTTLDVVR	67.93	55.1294	1374.798	1375.471	35	+2,+3	shared(2)	1	0.9958
VAVLGAAGGIGQPMSLLLK	99.61	54.2417	1794.044	1794.864	3	2	shared(2)	0	0.9894
VIGGHAGTTILPLLSQLEGAK	122.92	53.4794	2074.179	2074.196	36	+2,+3	distinct	0	1
VTGHVGMEQAGEALEGADVVVIPAGVPR	82.16	51.991	2757.412	2757.703	3	+2,+3	distinct	0	0.9997

The equivalent proteins include

jgi|Physo1_1|109054|estExt_fgenesh1_pm.C_550007	0	No title.

88. Group probability: 1.0000. Peptides of the group

KLAGMFVDNFK	80.1	55.3554	1268.659	1269.171	2	2	distinct	1	0.9935
KLGDIPENVLNPR	85.61	54.9573	1463.81	1464.409	7	2	distinct	1	0.9963
LSDGQAMYHFLSGYTAK	70.11	53.9584	1887.882	1889.379	4	2	distinct	0	0.9878
HNTSVYLVNTGWTSGGYGVGK	121.51	53.2717	2196.06	2196.415	3	2	distinct	0	0.9999
GVTEPTATFSACFGAAFLPLHPTK	55.79	52.6668	2519.252	2519.53	1	2	distinct	0	0.9675

The equivalent proteins include

jgi|Physo1_1|109616|estExt_fgenesh1_pm.C_1690003	0	No title.

89. Group probability: 1.0000. Peptides of the group

KAVSATSVYFESLPYR	88.61	54.182	1816.936	1817.315	3	2	distinct	1	0.9975
EHASPFDYCDIVTTTTHK	76.3	53.2774	2120.947	2121.177	1	2	distinct	0	0.9933
YYGGNEIIDKIEILCQQR	78.36	53.265	2211.099	2211.731	2	2	distinct	1	0.9828
LAEQAALFKPALIVCGGSAYPR	58.7	52.9531	2331.241	2331.992	6	+2,+3	distinct	0	0.9984
TLTDLGYSMCTGGTDNHLILWDLRPQK	84.59	51.1257	3104.506	3105.579	4	3	distinct	0	0.9972

The equivalent proteins include

jgi|Physo1_1|142228|estExt_fgenesh1_pg.C_1100022	0	No title.

90. Group probability: 1.0000. Peptides of the group

KLVVALGSPK	70.65	55.4912	1010.649	1011.248	10	+1,+2	distinct	1	0.9993
HNPALIAER	61.61	56.0279	1019.551	1020.495	2	2	distinct	0	0.9647

ETQLALVLNAIVNDAALAEHEAFK	91.42	52.4424	2579.359	2580.797	6	+2,+3	distinct	0	1
ETQLALVLNAIVNDAALAEHEAFKK	88.12	52.1156	2707.454	2708.363	8	3	distinct	1	0.9978

The equivalent proteins include

jgi|Physo1_1|158121|C_scaffold_82000017	0	No title.

91. Group probability: 1.0000. Peptides of the group

LQLFGLHAR	51.43	55.4048	1053.608	1054.398	1	2	distinct	0	0.9149
VQIGNYFIDLSLATK	102.61	54.2702	1680.909	1682.002	1	2	distinct	0	0.9992
LLLETVVDPEILGGLK	82.19	54.4586	1708.002	1708.797	3	2	distinct	0	0.9956
EPNFASFLHDPTIAR	67.75	54.327	1713.847	1715.094	2	2	distinct	0	0.9838
FSKPVAGLFEVLAENGR	110.57	54.057	1832.978	1833.005	3	2	distinct	0	0.9996

The equivalent proteins include

jgi|Physo1_1|108488|estExt_fgenesh1_pm.C_110019	0	No title.

92. Group probability: 1.0000. Peptides of the group

IGVNQPKR	52.51	55.3906	910.535	911.453	3	2	distinct	1	0.9226
RIHEDPEFLEK	57.4	55.0969	1411.71	1412.573	3	2	distinct	1	0.7598
AYSSVGAIHAYFQK	100.69	54.7032	1540.767	1541.794	3	2	distinct	0	0.9991
FPQYGTDNGVLRPK	70.52	54.6189	1590.815	1591.835	8	2	distinct	0	0.9868
AGASWEKFEELMHVTK	59.87	54.125	1861.903	1862.656	3	+2,+3	distinct	1	0.9981
ENEVVIPSLMFVESLDAILEDLAK (00000000000100000000000000)	76.81	52.1936	2673.382	2674.064	20	2	distinct	0	0.9949

The equivalent proteins include

jgi|Physo1_1|108461|estExt_fgenesh1_pm.C_100020	0	No title.

93. Group probability: 1.0000. Peptides of the group

GIPLIFLQNITGFMVGK	93.89	54.0446	1847.038	1847.963	25	2	distinct	0	0.9985
TSGVTDHYANNDAHALDITR	76.59	53.3159	2170.004	2171.437	2	+2,+3	distinct	0	0.9999
TSGVTDHYANNDAHALDITRR	47.51	52.985	2326.105	2327.114	1	3	distinct	1	0.9075
KQPAVTQTPIEEPLYSPDELGGVIPVDSR	66.34	51.1204	3134.613	3134.558	7	+2,+3	distinct	1	0.9997

The equivalent proteins include

jgi|Physo1_1|109115|estExt_fgenesh1_pm.C_610005	0	No title.

94. Group probability: 1.0000. Peptides of the group

IHTFIATSDIHLK	66.27	54.7396	1494.819	1495.513	7	2	distinct	0	0.9582
MVSHYTGMSIQPNK	71.84	54.6189	1591.749	1591.875	5	2	distinct	0	0.9882
SDPDFLCEVLAEVIK	75.06	54.3163	1733.855	1735.186	2	2	distinct	0	0.9915
HQATYEIMLPESVGLSENK	83.6	53.2999	2145.041	2146.257	2	2	distinct	0	0.9966
AIVGSNAFAHESGIHQDGVLK	80.25	53.333	2149.092	2149.306	13	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|108956|estExt_fgenesh1_pm.C_460003	0	No title.

95. Group probability: 1.0000. Peptides of the group

FDEVYHVHFK	68.7	55.3324	1319.63	1320.273	7	2	distinct	0	0.9818
GLQDIIGLSVVHPVFQR	82.97	54.2093	1877.052	1877.826	19	+2,+3	distinct	0	1
TRPNDPEDQHMSWAFADPK	59.47	53.1342	2240.991	2241.413	4	2	distinct	0	0.9716
MFNSSFDALAPSKLDLYPAEFR	79.35	52.5996	2518.22	2517.92	5	2	distinct	1	0.9956
KTPWLPGPSGLGEYSSEGSIPDTVNNAQYVR	50.85	50.7695	3318.616	3319.967	3	3	distinct	1	0.9538

The equivalent proteins include

jgi|Physo1_1|129851|estExt_fgenesh1_pg.C_90128	0	No title.

96. Group probability: 1.0000. Peptides of the group

STSTPSPAPAPKPR	67.27	55.0566	1392.736	1393.018	7	2	distinct	0	0.9822
AVTHEYQIHEER	76.14	54.6007	1510.716	1510.782	2	2	distinct	0	0.9913
SNPASRPYPSPAAPR	51.13	54.6016	1566.79	1567.637	3	2	distinct	0	0.93
SLLQQLAEAFEMLTNR	86.92	54.1221	1862.956	1862.78	6	+2,+3	distinct	0	1
LADAVHPSEQWIVELLK	75.7	53.8962	1947.046	1948.521	5	2	distinct	0	0.9925

The equivalent proteins include

jgi|Physo1_1|142023|estExt_fgenesh1_pg.C_1070014	0	No title.

97. Group probability: 1.0000. Peptides of the group

VVCMPGVQDHKR	55.68	54.854	1424.702	1425.251	1	2	distinct	1	0.9475
AKEYLDSINHNIVVK	73.2	54.2355	1741.936	1742.915	1	2	distinct	1	0.99
AGLINALAHITGGGLLENVPR	73.38	53.4434	2085.169	2086.167	5	+2,+3	distinct	0	0.9999
FGDPETQVVLPLLHSDLFEIMR	63.35	52.4473	2555.309	2556.694	4	3	distinct	0	0.978
APSTPLVVLCGDRAPDALVQTAAALQAGGLR	75.02	51.2018	3087.65	3088.83	4	3	distinct	1	0.9944

The equivalent proteins include

jgi|Physo1_1|129332|estExt_fgenesh1_pg.C_70157	0	No title.

98. Group probability: 1.0000. Peptides of the group

FGSHVFVGK	66.35	56.1179	976.513	977.407	4	2	distinct	0	0.9767
LRAPEVAAFDFK	70.83	55.1314	1362.73	1363.805	5	+2,+3	distinct	1	0.9977
TCQFGYAHVDTPK	73.26	54.6166	1522.687	1523.342	1	2	distinct	0	0.9892
LNPLTLITLTYPTK	61.32	54.866	1586.928	1587.86	1	2	distinct	0	0.9702
GLTVFCQFYDNPGR	78.31	54.5605	1672.767	1673.349	2	2	distinct	0	0.9933
TPGTLFGIPDNADHISYDLWDSR	48.44	52.3588	2589.214	2590.705	1	2	distinct	0	0.9363

The equivalent proteins include

jgi|Physo1_1|140046|estExt_fgenesh1_pg.C_810035	0	No title.

99. Group probability: 1.0000. Peptides of the group

KDPIQLNHR	64.75	55.6755	1119.615	1120.319	5	2	distinct	1	0.9734
IFAQIWHTGR	57.73	55.6346	1227.651	1228.24	13	2	distinct	0	0.9521
GWQAVTEAVHAK	76.17	55.2159	1295.662	1296.731	2	2	distinct	0	0.9912
HADGVDTPVNGVAHHFR	64.14	54.0428	1827.876	1829.306	3	2	distinct	0	0.9794
VGHPLNQPDGQLPVSSSATSMDNVK (00000000000000000000000100000)	78.18	52.4393	2577.249	2577.951	16	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109429|estExt_fgenesh1_pm.C_1050001	0	No title.

100. Group probability: 1.0000. Peptides of the group

LLQVLTPNLDHAR	62.06	54.8877	1488.841	1490.148	4	2	distinct	0	0.971
ALEHYTELADLKR	74.58	54.7815	1557.815	1558.329	3	2	distinct	1	0.9904
MESIELARPVLMQGR	53.75	54.3033	1728.901	1729.956	1	2	distinct	0	0.9447
AINFYLEQHPLELTR	71.42	54.1325	1842.963	1843.42	6	2	distinct	0	0.9883
LDLPGAEELYFTEFNR	75.37	53.8093	1912.921	1913.346	1	2	distinct	0	0.9921
IYITLNKDPQQFLINNQFYDSEVVGK	74.93	51.2199	3085.576	3086.849	3	3	distinct	1	0.9933

The equivalent proteins include

jgi|Physo1_1|143969|estExt_fgenesh1_pg.C_1600014	0	No title.

101. Group probability: 1.0000. Peptides of the group

QNFSALTR	59.34	55.6459	935.482	936.9	5	2	distinct	0	0.9036
AQGAAIDKYASR	49.88	55.434	1249.641	1249.93	1	2	distinct	1	0.9116
LSSAMSAAAAIGAHLR	89.65	54.6349	1525.803	1526.381	2	2	distinct	0	0.9977
ATATELTEEKADAVEILAR	52.49	53.5544	2030.053	2030.881	1	3	distinct	1	0.9351
MELQDCAFNLVDAIVPTSNLETAFK	51.69	51.9022	2825.361	2825.889	1	2	distinct	0	0.9558
VVIWGNHSSTQVPDVTYAEVQGQPLDK	73.43	51.4457	2966.477	2967.012	9	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|109232|estExt_fgenesh1_pm.C_780001	0	No title.

102. Group probability: 1.0000. Peptides of the group

RQALLAAR	51.54	55.8796	897.551	898.552	1	2	distinct	1	0.5601
VATLIVRPR	76.89	55.3903	1023.655	1024.259	13	2	distinct	0	0.9909
RVEITGPVDR	48.61	55.333	1140.625	1141.063	2	2	distinct	1	0.8941
KTISYTHPQTGK	46.46	55.3296	1359.715	1360.615	1	2	distinct	1	0.881
FLAFLHEQFEPR	71.73	54.7709	1532.778	1533.76	3	2	distinct	0	0.9872
EVAAGHDGTWVAHPGLVK	89.44	54.1448	1842.938	1843.306	12	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108758|estExt_fgenesh1_pm.C_300009	0	No title.

103. Group probability: 1.0000. Peptides of the group

HSEFIGFPIK	50.2	55.7298	1173.618	1174.705	1	2	distinct	0	0.9072
TMEINPLHPIIK	69.45	55.0895	1404.78	1405.284	6	2	distinct	0	0.9842
KTMEINPLHPIIK	66.31	54.8905	1532.875	1533.139	3	+2,+3	distinct	1	0.9968
KPEDVTHEEYASFYK	106.17	54.1493	1841.847	1842.568	2	2	distinct	0	0.9994
VFIMDNCEELMPEYLSFVK	76.72	52.8422	2363.089	2363.453	1	2	distinct	0	0.9938

The equivalent proteins include

jgi|Physo1_1|108777|estExt_fgenesh1_pm.C_310001	0	No title.

104. Group probability: 1.0000. Peptides of the group

FHVLTPAEVK	47.44	55.3176	1139.634	1139.377	4	+1,+2	distinct	0	0.9796
YKEHAPASILVR	45.43	55.0426	1382.767	1383.361	1	2	distinct	1	0.8705
KLPTILVDEDSHK	68.79	54.6435	1493.809	1494.067	5	+2,+3	distinct	1	0.9989
KIAVLSEPAGIVYSGLGPDYR	77.68	53.242	2204.184	2204.729	1	2	distinct	1	0.9946
YNDDLEIEDAIHTALLTLR	95.94	53.1735	2214.117	2214.158	3	2	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|109244|estExt_fgenesh1_pm.C_790006	0	No title.

105. Group probability: 1.0000. Peptides of the group

VQHIEIHGK	53.42	56.0369	1059.582	1060.719	11	+1,+2	distinct	0	0.9919
NTAYGATVKPR	75.48	55.6036	1176.625	1177.154	8	2	distinct	0	0.9903
HNPNVAFVVYR	62.41	55.397	1314.683	1315.842	10	+2,+3	distinct	0	0.998
VIYLSIVDGKPVGR	82.74	54.8526	1514.882	1515.573	12	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|138074|estExt_fgenesh1_pg.C_600033	0	No title.

106. Group probability: 1.0000. Peptides of the group

KFTPLLDVVYNDIK	91.25	54.5381	1663.918	1664.905	4	2	distinct	1	0.9979
VIGLYFSGHYCPPCR	56.56	54.0464	1824.844	1825.75	1	2	distinct	0	0.957
HFVTDNSQDIDAILSHLR	115.96	53.8043	2080.034	2080.321	5	+2,+3	distinct	0	1
FTEYYEEMPWIALPYAR	61.1	53.2956	2178.013	2178.561	1	2	distinct	0	0.9735

The equivalent proteins include

jgi|Physo1_1|142576|estExt_fgenesh1_pg.C_1170035	0	No title.

107. Group probability: 1.0000. Peptides of the group

VAHQLIKDELALDGNPK	117.22	54.0664	1860.01	1860.12	6	2	distinct	1	0.9998
CVTMLANLYHAPLEPGQK	78.27	53.6108	2041.012	2040.325	2	2	distinct	0	0.9943
KNYIDLDQYPQTAEIHNR	105.26	53.1771	2217.081	2217.593	3	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|109436|estExt_fgenesh1_pm.C_1070001	0	No title.

108. Group probability: 1.0000. Peptides of the group

MLAVDYENVKPDIVILGK	90.31	53.6337	2016.096	2016.295	4	2	distinct	0	0.998
EYYDFLSAYSAVNQGHCHPK	61.95	52.8415	2385.048	2386.032	8	2	distinct	0	0.9781
AFYNNVLGEYQEYMTQLLGFDR	116.73	52.1488	2670.242	2670.343	31	2	distinct	0	0.9998
GLLNAIIINERPNQPDALQLCMNLAK	80.94	51.4646	2918.547	2919.912	2	3	distinct	0	0.996

The equivalent proteins include

jgi|Physo1_1|109298|estExt_fgenesh1_pm.C_860005	0	No title.

109. Group probability: 1.0000. Peptides of the group

GPIGCGVHATEK	61.42	55.2381	1224.592	1225.391	3	2	distinct	0	0.968
SPSNKPSVEVHR	65.83	55.3026	1335.689	1336.21	5	2	distinct	0	0.9782
HGIPDQTCQAYQAK	90.33	54.7722	1615.741	1616.25	7	2	distinct	0	0.9977
NSWGSFWGEDGWMR	56.24	54.3271	1713.699	1714.699	1	2	distinct	0	0.9539
NSWGTYWGENGWFR	68.08	54.2866	1758.754	1760.171	1	2	distinct	0	0.9837
NQHIPKYCGSCWAQGTTSALSDR	61.7	52.2008	2636.186	2637.502	11	3	distinct	1	0.9756

The equivalent proteins include

jgi|Physo1_1|128333|estExt_fgenesh1_pg.C_40177	0	No title.

110. Group probability: 1.0000. Peptides of the group

RALSAQAQAR	55.69	55.9949	1070.594	1071.446	3	2	distinct	1	0.8863
IINEPTAAAIAYGIDKK	113.47	54.8034	1786.983	1787.369	22	2	shared(7)	1	0.9981
LEIESLLDGEDFTESLSR	77.06	53.8572	2051.99	2052.789	2	2	distinct	0	0.9936
DVLLIDVVPLSQGIETVGGVMTK	96.73	52.8794	2382.308	2381.895	15	+2,+3	distinct	0	1
SQTFSTYQDNQPAVLIQVFEGER	81.72	52.3464	2656.277	2656.593	1	2	distinct	0	0.9966

The equivalent proteins include

gi|429116|emb|CAA53368.1|	55388.19	glucose regulated protein/BiP [Phytophthora cinnamomi]
gi|429118|emb|CAA53369.1|	72693.28	glucose regulated protein /BiP [Phytophthora cinnamomi]
jgi|Physo1_1|109481|estExt_fgenesh1_pm.C_1170002	0	No title.

111. Group probability: 1.0000. Peptides of the group

VLLSSPPEHLR	51.91	55.7945	1246.703	1247.741	6	+2,+3	distinct	0	0.9912
GVGTSDHLLYSVLMGR	80.17	54.4583	1703.866	1704.895	3	2	distinct	0	0.9947
ALQEPMVEYKPSFHTK (000000100000000000)	69.28	53.9698	1903.95	1904.244	10	2	distinct	0	0.9864
IQEEVGGEYQELLLQLLEAPR	80.6	52.7358	2426.269	2427.64	5	2	distinct	0	0.9959
LSLNAWPFLAEHIEGTMAGIGTDETALSAAIVR	63.34	50.2557	3453.76	3455.221	2	3	distinct	0	0.9857

The equivalent proteins include

jgi|Physo1_1|155769|C_scaffold_7000098	0	No title.

112. Group probability: 1.0000. Peptides of the group

KVLAVTDPMLK	66.3	55.6411	1213.71	1214.831	5	+1,+2	distinct	1	0.999
KAALENIFLVK	73.25	55.9032	1244.749	1245.954	4	2	distinct	1	0.9881
SLFSEANPQPIKK	67.04	55.0163	1457.788	1458.784	9	2	distinct	1	0.9812
TNVNLSPQTIAELNKLPNIVAIK	84.88	52.4027	2489.422	2490.89	12	+2,+3	distinct	1	0.9998

The equivalent proteins include

jgi|Physo1_1|108407|estExt_fgenesh1_pm.C_90003	0	No title.

113. Group probability: 1.0000. Peptides of the group

QSLELAEHQKK	64.53	55.1451	1309.699	1310.219	4	2	distinct	1	0.9748
KQECTQSYIR	45.62	55.306	1311.624	1312.339	1	2	distinct	1	0.8625
RQSLELAEHQK	47.09	55.3249	1337.705	1338.551	1	2	distinct	1	0.8833
DELIHHALQGVR	63.93	55.3096	1386.737	1387.455	2	2	distinct	0	0.9743
RPYGVGLLVAGVDK	63.82	54.9854	1442.824	1443.958	6	2	distinct	0	0.9704
GVHLYQTCPSGNYYEYK	81.42	53.4182	2077.92	2078.457	8	2	distinct	0	0.9955

NQYDTDVTVWSPQGHLHQIDYAMEAVK (000000000000000000000000100000)	57.08	51.0358	3144.461	3145.817	8	3	distinct	0	0.969

The equivalent proteins include

jgi|Physo1_1|109262|estExt_fgenesh1_pm.C_810009	0	No title.
jgi|Physo1_1|109746|estExt_fgenesh1_pm.C_12150001	0	No title.

114. Group probability: 1.0000. Peptides of the group

HGTDPLVVCAR	53.48	55.1424	1223.608	1224.546	1	2	distinct	0	0.9336
FALDQKPEQVK	66.09	55.4578	1301.698	1302.682	2	2	distinct	0	0.9347
KILTNVCQLVPSDCK	84.21	54.2884	1773.912	1774.258	4	2	distinct	1	0.9962
AIIGDLCDAMAADSMCHTFLK	82.16	52.9887	2339.042	2340.233	1	2	distinct	0	0.9964
MFDEAAADLQAGKEPHEICQALK	92.66	52.506	2571.21	2571.487	2	2	distinct	1	0.9987

The equivalent proteins include

jgi|Physo1_1|144660|estExt_fgenesh1_pg.C_2300010	0	No title.

115. Group probability: 1.0000. Peptides of the group

KLEELGYTLPAVAEPK	92.84	54.2113	1756.961	1758.379	2	2	distinct	1	0.9983
SGNTIYLAGHLPQPAGGELILGK	77.31	52.9981	2305.243	2305.984	10	+2,+3	distinct	0	1
DLTPEQGYDAAHYVALSLMATLK	91.85	52.5151	2506.241	2506.413	12	2	distinct	0	0.9986

The equivalent proteins include

jgi|Physo1_1|156147|C_scaffold_11000042	0	No title.

116. Group probability: 1.0000. Peptides of the group

LGQLVHKK	68.45	55.5645	921.576	922.745	7	2	distinct	1	0.9398
FGLNHVTSLIENK	73.84	55.0095	1470.783	1471.849	2	2	distinct	0	0.9897
NAAVVALTHVNKEDK	90.3	54.5584	1607.863	1608.502	9	2	distinct	1	0.9977
NIAAGKEEASAPPAVVK	81.02	54.7096	1650.894	1651.067	1	2	distinct	1	0.9952
LKVPPSINQFSNTLEK	69.6	54.1246	1813.994	1814.952	2	2	distinct	1	0.9868

The equivalent proteins include

jgi|Physo1_1|156835|C_scaffold_30000010	0	No title.

117. Group probability: 1.0000. Peptides of the group

SVVFKDHLR	63.38	55.9023	1099.614	1100.756	3	2	distinct	1	0.9698
AYTAAYTPCR	49.79	55.7735	1172.528	1173.727	1	2	distinct	0	0.9037
CILLGGVHGLVESLFR	96.62	54.1935	1768.966	1770.259	4	2	distinct	0	0.9988
QVGVIGWGSQGPAQAQNLR	98.03	53.8251	1965.018	1965.09	7	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|136278|estExt_fgenesh1_pg.C_440079	0	No title.

118. Group probability: 1.0000. Peptides of the group

SLPLQLLVTAEHPDTK	124.59	54.2764	1760.967	1761.312	2	2	distinct	0	0.9999
EPNVDHCFLMNHDSK	52.36	54.1889	1841.782	1842.319	3	2	distinct	0	0.9377
SYDLIANDGVNSLHGGNTWGLK	77.51	52.9791	2330.129	2330.348	5	+2,+3	distinct	0	0.9994
SYDLIANDGVNSLHGGNTWGLKDFEGPFEVK	54.01	50.5147	3378.616	3379.444	2	3	distinct	1	0.9651

The equivalent proteins include

gi|21327106|gb|AAM48174.1|	36290.12	UDP-glucose 4-epimerase-like protein [Phytophthora sojae]

119. Group probability: 1.0000. Peptides of the group

IEIVHQATR	59.9	55.3005	1065.593	1066.832	2	2	distinct	0	0.9596
LSFSWYDFPDMQLGAR	49.4	53.8054	1931.888	1932.938	1	2	distinct	0	0.9226
SLAATGAPCLGETGQAPTHSLR	108.42	53.2602	2194.08	2195.498	4	2	distinct	0	0.9997
AHLPEGATFEVPDGGYFVLVR	74.17	53.3678	2273.148	2273.425	9	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|133120|estExt_fgenesh1_pg.C_240089	0	No title.

120. Group probability: 1.0000. Peptides of the group

KALIHDGLK	74.77	55.3273	993.597	994.593	6	2	distinct	1	0.9548
ALIHDGLKR	56.9	55.6514	1021.603	1022.506	1	2	distinct	1	0.8092
ALCEEHGVNLILVPSGK	86.85	54.1576	1834.961	1835.603	11	+2,+3	distinct	0	0.9994
VVSTSCAVITDFGEETHALNVLLDYLK	56.35	51.3669	2993.505	2994.675	6	3	distinct	0	0.9667
KVVSTSCAVITDFGEETHALNVLLDYLK	94.97	51.1588	3121.6	3123.077	1	3	distinct	1	0.9989

The equivalent proteins include

gi|66270173|gb|AAY43416.1|	15491.87	ribosomal protein S12 [Phytophthora infestans]
jgi|Physo1_1|109491|estExt_fgenesh1_pm.C_1190004	0	No title.

121. Group probability: 1.0000. Peptides of the group

VLVSVQEHIQR	86.9	55.3683	1306.736	1308.047	3	2	distinct	0	0.9964
RGMLAYVEGVQR	49.31	55.0822	1377.719	1378.413	1	2	distinct	1	0.9077
GAAGIHLEDQKPGTKK	54.95	54.5499	1648.89	1649.548	2	2	distinct	1	0.9517

AYGEYADLIWMETAKPGVPLAR (0000000000010000000000000)	89.94	52.5394	2450.23	2451.625	3	2	distinct	0	0.9983
TPPTDFLRPIVADADTGHGGLTAVMK	75.09	52.1222	2679.369	2680.59	3	3	distinct	0	0.9932

The equivalent proteins include

jgi|Physo1_1|109161|estExt_fgenesh1_pm.C_660003	0	No title.

122. Group probability: 1.0000. Peptides of the group

LAWHSSGSYSK	47.81	55.3841	1221.578	1221.409	1	1	distinct	0	0.8903
DIVALVGAHAIGR	85.27	55.3845	1290.741	1291.371	7	2	distinct	0	0.9946
FDPEINHGGNAGLHLAVK	58.89	53.9328	1887.959	1888.645	5	2	distinct	0	0.9686
EIVEIFDDDNYMGPTLVR	72.51	53.3292	2125.004	2125.808	2	2	distinct	0	0.9906
SGYSGPWTNAEWTFSNEFFR	95	52.8805	2382.034	2382.059	11	2	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|108469|estExt_fgenesh1_pm.C_100028	0	No title.

123. Group probability: 1.0000. Peptides of the group

SGKPLHYK	48.26	56.7639	928.513	929.188	1	2	shared(2)	0	0.8844
ITFELFADKVPK	85.33	54.9404	1406.781	1407.6	17	2	distinct	1	0.9858
NIEAVGSQSGQTKK	55.14	55.098	1445.747	1446.405	4	2	distinct	1	0.9485
VIPNFMCQGGDFTR	50.55	54.4	1640.744	1641.291	1	2	distinct	0	0.924
PNPQVFFDMTVGGAPAGR	98.26	54.0665	1859.899	1859.76	6	2	distinct	0	0.999
GNGTGGESIYGEKFPDENFLLK	69.33	52.8585	2371.133	2372.324	1	3	distinct	1	0.9869

The equivalent proteins include

jgi|Physo1_1|108795|estExt_fgenesh1_pm.C_320007	0	No title.

124. Group probability: 1.0000. Peptides of the group

NVAAHLSPAFR	62.82	55.4193	1181.63	1183.049	6	2	distinct	0	0.9706
EGDVVTIGQCRPLAK	46.43	54.4543	1641.851	1642.067	1	2	distinct	0	0.8946
VKEGDVVTIGQCRPLAK	87.2	53.9308	1869.014	1869.335	7	+2,+3	distinct	1	0.9992
FNVLEVEPASETKPINVR	98.43	53.5525	2041.084	2041.623	10	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|109522|estExt_fgenesh1_pm.C_1260002	0	No title.
jgi|Physo1_1|142976|estExt_fgenesh1_pg.C_1260022	0	No title.

125. Group probability: 1.0000. Peptides of the group

HMIFGPGFYEGYK	55.55	55.217	1544.712	1546.172	3	+2,+3	distinct	0	0.9953
AYASVPHPAGSHQDYK	67.22	54.3248	1726.806	1727.632	7	+2,+3	distinct	0	0.9975
TIPHIPTLPLSYGQAR	60.11	54.1795	1762.973	1764.306	8	+2,+3	distinct	0	0.9978
AEIVEYYPLLSLPIHR	70.03	53.8264	1912.046	1913.12	6	2	distinct	0	0.9873

The equivalent proteins include

jgi|Physo1_1|143291|estExt_fgenesh1_pg.C_1340023	0	No title.

126. Group probability: 1.0000. Peptides of the group

HTHCEFTGDVLK	48.57	54.9733	1442.661	1444.118	3	+2,+3	distinct	0	0.9866
IALTTAEYLAYER	78.47	54.7567	1512.782	1513.951	3	2	distinct	0	0.9931
TISGVNGPLVILENVKLPK	47.48	53.6628	1990.183	1991.037	1	2	distinct	1	0.9179
IPIFSAAGLPHNEIAAQIVR	88.58	53.3671	2116.179	2116.455	19	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108790|estExt_fgenesh1_pm.C_320002	0	No title.

127. Group probability: 1.0000. Peptides of the group

LLVWIGNR	46.43	55.9944	969.576	971.004	1	2	distinct	0	0.6345
VSADLGNVAQQPFHPR	71.72	54.2087	1734.88	1735.517	8	2	distinct	0	0.989
MVHVSSLLAQPNSPSEWAASK	74.07	53.1255	2238.11	2238.579	8	+2,+3	distinct	0	0.9993
NPSLVNLPLPVAQAIGYFCEQFPDPK	77.73	51.4966	2913.473	2914.891	3	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|142305|estExt_fgenesh1_pg.C_1110046	0	No title.

128. Group probability: 1.0000. Peptides of the group

INNVNSHDAIYNK	80.71	55.0612	1500.732	1500.95	1	2	distinct	0	0.9943
LPLDVIWSDIDYMR	69.35	54.2066	1734.865	1735.677	1	2	distinct	0	0.9854
SYHDFTLDPTNFPQAK	78.11	54.0405	1879.874	1880.823	2	2	distinct	0	0.9937
YASNKLPLDVIWSDIDYMR	101.36	53.0432	2298.135	2298.86	3	2	distinct	1	0.9993

The equivalent proteins include

jgi|Physo1_1|130344|estExt_fgenesh1_pg.C_110013	0	No title.
jgi|Physo1_1|130345|estExt_fgenesh1_pg.C_110014	0	No title.

129. Group probability: 1.0000. Peptides of the group

FTHVALALPTVGR	80.64	54.9491	1380.788	1382.048	23	+1,+2,+3	distinct	0	1
YSVSVLPDQLEAAAEILAETTLAPK	66.1	52.8587	2628.39	2628.942	2	2	distinct	0	0.9873

YVNTANAALVGAGVAHNTLTDLANAYFGDLTK	89.33	50.8782	3264.641	3264.341	1	3	distinct	0	0.9985

The equivalent proteins include

jgi|Physo1_1|142149|estExt_fgenesh1_pg.C_1090005	0	No title.

130. Group probability: 1.0000. Peptides of the group

KYWATHDAQAQAK	90.68	54.9241	1516.742	1517.248	3	2	distinct	1	0.9976
LEGVDKYGNLFGSVVHPSGR	69.97	53.3084	2130.086	2130.573	2	2	distinct	1	0.9891
SVLPFQKPVVDGLLNAQEIAK	62.16	53.5058	2265.273	2265.969	5	+2,+3	distinct	0	0.9972
VILKPSLQLVNFGLSGVQCPR	76.38	52.9612	2324.304	2324.682	1	2	distinct	0	0.994

The equivalent proteins include

jgi|Physo1_1|141509|estExt_fgenesh1_pg.C_990054	0	No title.

131. Group probability: 1.0000. Peptides of the group

QITDKDYYGNDIK	62.09	54.9044	1571.747	1572.512	5	2	distinct	1	0.9711
AYTFVNSNPGQPACYLK	71.72	53.8683	1928.909	1928.607	4	2	distinct	0	0.9894
AYTYINNNPGQPVCYLK	62.05	53.6194	2013.962	2014.14	3	2	distinct	0	0.9755
TVYVSLPSLCCDACASTAGCK	86	52.9843	2319	2319.384	1	2	distinct	0	0.9974
AYTYINNNPGQPVCYLKSAAGTPTTK	57.17	51.8765	2828.38	2829.004	1	3	distinct	1	0.9675

The equivalent proteins include

jgi|Physo1_1|108819|estExt_fgenesh1_pm.C_340019	0	No title.

132. Group probability: 1.0000. Peptides of the group

KLTPEYAAAAK	45.22	55.5879	1161.639	1162.977	1	2	distinct	1	0.8618
LLHVIMPSTEK	47.04	55.3547	1266.701	1267.294	1	2	distinct	0	0.8827
LLHVIMPSTEKR	49.76	54.8865	1422.802	1423.546	3	+2,+3	distinct	1	0.9885
GFPTLIFFPAKDK	56.85	54.7837	1479.813	1480.772	3	2	distinct	1	0.9543
IVDYFGLKDEEMPAVMLVNMAGSMK	91.42	51.9856	2787.335	2787.442	7	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|108791|estExt_fgenesh1_pm.C_320003	0	No title.

133. Group probability: 1.0000. Peptides of the group

DSTIIMQLLR	62.92	55.7197	1188.654	1188.603	4	2	shared(5)	0	0.81
AVANNHNVELTVEER	104.61	54.3237	1693.838	1694.333	3	2	distinct	0	0.9994
QASTIAMAELPPTHPIR (0000000100000000000)	90.58	54.0587	1831.961	1832.424	21	+2,+3	distinct	0	0.9998
LAEQAERYDEMVDHMK	44.88	53.7972	1963.877	1964.27	1	2	distinct	1	0.885
QAFDDAIAELDTLSEESYK	63.08	53.2907	2143.98	2145.265	2	2	shared(3)	0	0.9793
QAFDDAIAELDTLSEESYKDSTLIMQLLR	73.46	50.8644	3314.623	3315.694	3	3	shared(2)	1	0.9205

The equivalent proteins include

gi|23394350|gb|AAN31465.1|	28566.01	14-3-3-like protein [Phytophthora infestans]
jgi|Physo1_1|108926|estExt_fgenesh1_pm.C_430006	0	No title.

134. Group probability: 1.0000. Peptides of the group

LFLHEDIHDEFLNR	88.01	54.1599	1796.885	1797.274	3	2	distinct	0	0.9972
VVAAMDNAKPQWCDLPAPAR	83.33	53.2522	2209.077	2210.289	4	+2,+3	distinct	0	0.9997
IGDPLEDGVLCGPLHNTQAVK	62.29	53.2648	2232.121	2232.879	3	+2,+3	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|108413|estExt_fgenesh1_pm.C_90009	0	No title.

135. Group probability: 1.0000. Peptides of the group

YTQQHWTYELDTGR	64.72	54.1615	1796.812	1797.031	2	2	distinct	0	0.9782
EIPWQGHQGLLVDCR	80.76	54.3373	1806.883	1807.552	10	2	distinct	0	0.9948
AALDYSPSMLNSAKPIGLK	85.29	53.6822	1975.045	1975.9	2	2	distinct	0	0.997
FLLATESCNCPDVGHGDLAWFR	87.66	52.5077	2564.158	2564.748	2	2	distinct	0	0.9979

The equivalent proteins include

jgi|Physo1_1|138217|estExt_fgenesh1_pg.C_610051	0	No title.

136. Group probability: 1.0000. Peptides of the group

GKIDAIADFRPK	61.25	55.4141	1329.74	1331.209	5	+2,+3	distinct	1	0.9947
KYNYGLTTWSPLASGVLTGK	104.15	53.3087	2155.131	2155.676	25	+2,+3	distinct	1	1
FDLDYVDLVFCHRPDPSTPIEETVR	41.17	51.5298	3019.439	3020.544	1	3	distinct	0	0.8642

The equivalent proteins include

jgi|Physo1_1|108826|estExt_fgenesh1_pm.C_340026	0	No title.

137. Group probability: 1.0000. Peptides of the group

NLVHGSDGPDSAK	48.53	55.0862	1295.611	1296.218	1	2	distinct	0	0.9047
TFIAIKPDGVQR	46.94	55.4709	1343.756	1344.869	1	2	shared(2)	0	0.8855
ILGATNPNQAAPGTLR	72.97	54.6426	1592.863	1592.886	4	2	distinct	0	0.99
KILGATNPNQAAPGTLR	102.98	54.2624	1720.958	1721.467	16	+2,+3	distinct	1	0.9997
HEITMWFKPEEVSNYER (0000010000000000000)	75.18	53.2632	2194.015	2194.313	12	2	distinct	0	0.9923

The equivalent proteins include

jgi|Physo1_1|156590|C_scaffold_22000045	0	No title.

138. Group probability: 1.0000. Peptides of the group

LTSNAIEPLHVFVPR	98.38	54.57	1691.936	1692.419	8	2	distinct	0	0.9989
FHPTANNVLASTSSDFSVR	87.95	53.7693	2048.992	2050.213	2	2	distinct	0	0.9976
HVYVEPAKLEYCYTNVR	68.27	53.3472	2140.041	2140.371	1	2	distinct	1	0.9859
IWGIPEGGLAETCVDPLVDLTGHGR	60.08	52.2764	2661.322	2661.585	1	2	distinct	0	0.9786

The equivalent proteins include

jgi|Physo1_1|108182|estExt_fgenesh1_pm.C_20014	0	No title.

139. Group probability: 1.0000. Peptides of the group

ADGQVIHFQAPK	93.74	55.3163	1309.678	1310.03	6	2	distinct	0	0.9981
KLGVTPIPGVEEVNLFK	91.37	54.0214	1839.05	1839.616	16	+2,+3	distinct	1	0.9999
SLQELLPGIINQLGPDNLANLK	73.29	52.884	2359.311	2360.091	4	2	distinct	0	0.9924

The equivalent proteins include

jgi|Physo1_1|108876|estExt_fgenesh1_pm.C_370016	0	No title.

140. Group probability: 1.0000. Peptides of the group

AIVIFVPFR	50.14	55.9301	1060.643	1061.495	3	2	distinct	0	0.9036
TLTHVQEQILDDLVFPTEIVGK	82.45	52.7759	2494.332	2494.614	20	+2,+3	distinct	0	0.9995
TLTHVQEQILDDLVFPTEIVGKR	87.72	52.1855	2650.433	2651.889	2	3	distinct	1	0.9975
IVKPEGQTADEFELQVAQELVNLEQSAAEIK	71.09	50.3649	3425.756	3426.532	14	3	distinct	0	0.9922

The equivalent proteins include

jgi|Physo1_1|109563|estExt_fgenesh1_pm.C_1420002	0	No title.

141. Group probability: 1.0000. Peptides of the group

APYPGNYWFSFPNSCAQK	63.42	53.3301	2132.941	2133.278	7	2	distinct	0	0.9791
YYESHTPPEYGEFVAMDGAK (0000000000000000100000)	73.43	53.0957	2289.989	2290.085	9	+2,+3	distinct	0	0.9999
ATNTGSGFEVDEAIDFWEKPGDEDANSER	75.63	50.9219	3185.37	3185.825	2	3	distinct	0	0.9943
TDECRAEYPGGLCPMGTSPDGVTCTFGYK	41.42	51.0958	3225.351	3226.2	1	3	distinct	1	0.8857

The equivalent proteins include

jgi|Physo1_1|131361|estExt_fgenesh1_pg.C_150132	0	No title.

142. Group probability: 1.0000. Peptides of the group

HAVIFYDDLSK	65.46	55.3208	1306.656	1306.456	12	+1,+2	distinct	0	0.9994
EAYPGDVFYIHSR	77.43	54.6655	1552.731	1553.625	13	2	shared(2)	0	0.9925
RTGSIVSVPVGPEVLGR	74.35	54.2544	1721.979	1722.923	22	2	distinct	1	0.9916
GMALNLEPDVVGVVVFSNDR (0010000000000000000000)	83.98	53.3046	2130.078	2131.325	6	2	distinct	0	0.9968

The equivalent proteins include

gi|9695382|ref|NP_037604.1|	56282.61	ATP synthase F1 subunit alpha [Phytophthora infestans]

143. Group probability: 1.0000. Peptides of the group

KPVVIYDYPK	47.16	55.3841	1220.68	1221.646	1	2	distinct	0	0.8797
YGSVPHAGFGLGFER	58.28	54.6106	1592.773	1593.442	6	2	distinct	0	0.9626
NAMAFATHEFFNQR	79.69	54.3304	1682.762	1683.883	10	2	distinct	0	0.9941
FSVKPVWGTDFGSEHER	82.9	53.7503	1976.938	1977.511	7	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108671|estExt_fgenesh1_pm.C_240002	0	No title.

144. Group probability: 1.0000. Peptides of the group

WVAFGGSYPGNLAAWVR	95.86	53.9892	1849.926	1851.096	4	2	distinct	0	0.9987
KFDDANPFAGDDSKPASGAYR	75.44	53.2668	2228.013	2229.228	1	3	distinct	1	0.992
VDVNANGWGPTALPEQFLNIPYAPFNKGDK	68.7	51.1934	3271.63	3272.486	1	3	distinct	1	0.9899
YFGGGECYHEVEQAITQLGQLMDGGKEDR	65.03	51.0186	3286.466	3287.342	1	3	distinct	1	0.9856

The equivalent proteins include

jgi|Physo1_1|141581|estExt_fgenesh1_pg.C_1000067	0	No title.

145. Group probability: 1.0000. Peptides of the group

FTIGHAWR	50.68	56.3488	986.509	987.549	4	2	distinct	0	0.9073
LFFAHGISR	56.64	55.9374	1046.566	1047.253	4	2	distinct	0	0.9455
RGDLVETLHGVQVADPYR	61.02	54.0194	2024.044	2024.553	11	+2,+3	distinct	1	0.9988
LVDNMDSAYSYILNDGDYYYFK	57.98	52.175	2668.168	2668.642	1	2	distinct	0	0.9715
NANMIHVADLSDFDNFLKGPSDSTIPVIK	69.86	50.9588	3157.575	3158.87	1	3	distinct	1	0.9906

The equivalent proteins include

jgi|Physo1_1|108684|estExt_fgenesh1_pm.C_240015	0	No title.

146. Group probability: 1.0000. Peptides of the group

AFEASGNDVAAYVAPLFADLLAR	98.49	52.855	2380.206	2381.697	18	+2,+3	distinct	0	1
FLAGPSAGAAPAAGAAAAGETTAKVEEK	70.17	52.6155	2513.276	2514.679	6	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|134110|estExt_fgenesh1_pg.C_300021	0	No title.

147. Group probability: 1.0000. Peptides of the group

MNAGRPFTAWLDNVK	78.93	54.3844	1718.856	1719.828	14	2	distinct	0	0.9936
KQIDGVQDHSQIFVIGDK	46.6	53.5409	2026.048	2026.282	1	2	distinct	1	0.9084
MAAMENATTNAEDLIGSLTLVYNK	131.73	52.3882	2569.24	2569.784	3	2	distinct	0	1
SLAVQPDSDAFDLYELEPDNKDELLADLK	46.88	50.9119	3262.577	3263.221	1	3	distinct	1	0.9295

The equivalent proteins include

jgi|Physo1_1|109105|estExt_fgenesh1_pm.C_600011	0	No title.

148. Group probability: 1.0000. Peptides of the group

IQGIGAGFVPR	62.09	55.6657	1113.629	1114.006	4	2	distinct	0	0.9685
IHFETTGPEVWR	61.83	55.0095	1470.726	1471.703	13	2	distinct	0	0.9693
DMTALIGNTPLVYLNR	63.91	54.2085	1789.94	1791.101	1	2	shared(2)	0	0.9781
IIAVEPEESPVLSGGNPAPHK	99.6	53.3155	2140.116	2140.571	15	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109172|estExt_fgenesh1_pm.C_670004	0	No title.

149. Group probability: 1.0000. Peptides of the group

IVGTLIHILK	66.81	55.6114	1105.722	1106.945	15	2	distinct	0	0.9784
VNVNGGAVAIGHPIGVSGAR	79.08	54.2396	1844.002	1844.568	9	2	distinct	0	0.995
TPIACFNGSFAPLSGPELGAVANAEAVRR	106.7	51.3525	2971.497	2972.3	7	3	distinct	1	0.9996
LGNGTLVDGVIHDGLWDPYNNQHMGMCGEK	51.84	50.6919	3326.491	3327.158	4	3	distinct	0	0.9561

The equivalent proteins include

jgi|Physo1_1|109674|estExt_fgenesh1_pm.C_2560001	0	No title.

150. Group probability: 1.0000. Peptides of the group

KIAVNLIPFPR	70.88	55.3512	1266.781	1267.527	5	2	shared(6)	1	0.9855
EIVHIQGGQCGNQIGAK	70.47	54.3297	1807.9	1808.547	13	2	distinct	0	0.9519
GHYTEGAELIDSVLDVVR	50.71	53.7106	1971.99	1972.76	1	2	shared(5)	0	0.7948
LTTPTYGDLNHLVCAAMSGITTCLR	82.51	52.0121	2764.335	2765.271	4	2	distinct	0	0.997
AGPYGQIFRPDNFVFGQTGAGNNWAK	79.99	52.2124	2811.352	2812.533	7	+2,+3	shared(2)	0	0.9986
FWEVISDEHGVDPTGSYHGDSDLQLER	57.7	51.2026	3087.385	3088.854	1	3	distinct	0	0.9705
EAESCDCIQGFQLTHSLGGGTGSGMGTLLISK	75.02	50.7346	3310.527	3311.459	11	3	shared(2)	0	0.9946

The equivalent proteins include

jgi|Physo1_1|109498|estExt_fgenesh1_pm.C_1190011	0	No title.

151. Group probability: 1.0000. Peptides of the group

MGHAGAIVSGGK	83.38	55.6797	1083.549	1084.128	17	+1,+2	distinct	0	0.9984
MGIMPGYIHQK (0100000000000)	60.99	55.4665	1273.631	1274.066	14	+2,+3	distinct	0	0.9944
LIGPNCPGIIKPGECK	75.63	54.1064	1751.906	1753.396	16	2	distinct	0	0.9922
QGTFHSQQAIEYGTNMVGGVTPK	57.06	52.5758	2449.17	2449.358	2	2	distinct	0	0.9699

The equivalent proteins include

jgi|Physo1_1|143975|estExt_fgenesh1_pg.C_1600020	0	No title.

152. Group probability: 1.0000. Peptides of the group

AGGDRQELHEAIR	58.91	54.9433	1450.728	1451.482	1	2	distinct	1	0.9617
AVHDHMDALLDPSLFIGR (00000010000000000000)	91.85	54.1736	2006.004	2006.91	7	+2,+3	distinct	0	0.9999
CPQQVEEFISEEIAPILK	106.03	53.3109	2129.071	2130.212	1	2	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|109266|estExt_fgenesh1_pm.C_810013	0	No title.

153. Group probability: 1.0000. Peptides of the group

NMAHFAQGIR (001000000000)	54.53	55.8086	1143.561	1143.422	20	+1,+2	distinct	0	0.9959
AVYGAFEPPSFDLGTIKYPR	90.18	53.1991	2227.131	2227.956	5	+2,+3	distinct	1	0.9998
MGFYTGSDDWLATSTDISQLR	87.06	52.8691	2363.074	2364.309	1	2	distinct	0	0.9977

The equivalent proteins include

jgi|Physo1_1|108318|estExt_fgenesh1_pm.C_60008	0	No title.

154. Group probability: 1.0000. Peptides of the group

IVNSHYSPSVHYAETGMK (00000000000000000100)	81.92	53.6562	2018.952	2019.443	18	+2,+3	distinct	0	0.9999
AILSHGDNFYWTGINSEDGR	136.05	53.536	2251.029	2251.912	1	2	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|127847|estExt_fgenesh1_pg.C_30056	0	No title.

155. Group probability: 1.0000. Peptides of the group

FHGVSFGAK	56.88	56.1178	948.482	948.299	3	1	distinct	0	0.9464
RIYQIAQALK	55.51	55.8044	1202.713	1203.385	2	2	distinct	1	0.6742
VMGTHPTMIDSAEDR	54.1	54.9894	1658.739	1659.423	1	2	distinct	0	0.9456
SKPMLGLEPDSLFDYYKR	52.98	53.2664	2158.077	2158.849	3	2	distinct	1	0.9479
VMVGESTENDNLPPLDGPKRPEGYVGIK	62.39	51.315	3010.507	3011.719	1	3	distinct	1	0.9811
ALELQGDNVKPIFGICLGNQLLSLAAGANTYK	80.44	50.4318	3387.786	3388.727	2	3	distinct	0	0.9967

The equivalent proteins include

jgi|Physo1_1|109206|estExt_fgenesh1_pm.C_730002	0	No title.

156. Group probability: 1.0000. Peptides of the group

LCLPQVEDIIAATKR	72.64	54.2858	1725.945	1727.28	5	+2,+3	distinct	1	0.9992
GSNGPAAGVAAQHSQCYAAWYGSVPGLK	43.45	51.7982	2803.314	2804.641	2	3	distinct	0	0.8995
AAIRDPNPVVVLENELVYGVSFPVSK	90.38	52.2148	2811.517	2812.163	17	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|122568|estExt_Genewise1.C_1080034	0	No title.

157. Group probability: 1.0000. Peptides of the group

RQGVDVSPFR	51.49	55.8665	1159.61	1160.106	1	2	distinct	1	0.9169
AATFLPHTAQR	47.57	55.3738	1211.641	1212.598	3	2	distinct	0	0.888
VNQALYLIATGAR	82.71	55.3159	1388.778	1389.838	2	2	distinct	0	0.9952
RVNQALYLIATGAR	81.13	55.2153	1544.879	1545.98	14	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|109358|estExt_fgenesh1_pm.C_950003	0	No title.

158. Group probability: 1.0000. Peptides of the group

HAEEFYQSLNLPYR	102.89	54.185	1765.842	1766.938	2	2	distinct	0	0.9992
YLIATSEQPICGYHR	59.69	54.3343	1806.872	1807.543	1	2	distinct	0	0.9671
VPEVLVPFMGGVTYLPFTR	87.41	53.3121	2121.133	2122.16	3	2	distinct	0	0.9975
VHQFDKVEQFCITDPESSVAMHEEMLR	50.45	50.9186	3261.489	3262.099	1	3	distinct	1	0.9446

The equivalent proteins include

jgi|Physo1_1|108754|estExt_fgenesh1_pm.C_300005	0	No title.

159. Group probability: 1.0000. Peptides of the group

SFSWTNLNGGTCWLK	89.18	54.1939	1769.819	1769.518	28	2	distinct	0	0.9975
TPGDCCGICNNWSGCR	81.58	53.8265	1912.707	1913.022	2	2	distinct	0	0.9954
AYTGCHAFSWSNYNGGTCWLK	81.59	52.5182	2479.047	2479.717	46	+2,+3	distinct	0	0.9997

The equivalent proteins include

jgi|Physo1_1|134006|estExt_fgenesh1_pg.C_290073	0	No title.

160. Group probability: 1.0000. Peptides of the group

HGDALVVNSQKPVK	79.18	54.8797	1490.82	1491.065	7	+2,+3	distinct	0	0.9994
LGGSLIPHKSDENDGIVEYK	63.61	53.511	2170.091	2170.274	5	+2,+3	distinct	1	0.9995
FGNKYDDTFYLTGLNHADTAFR	71.07	52.4359	2565.192	2566.412	1	3	distinct	1	0.9888

The equivalent proteins include

jgi|Physo1_1|145331|estExt_fgenesh1_pg.C_10590002	0	No title.

161. Group probability: 1.0000. Peptides of the group

IHGGLLGVR	57.93	55.9942	920.556	921.119	5	2	distinct	0	0.9513
YGCNPHQNPAAILSR	72.42	54.3104	1696.81	1697.284	4	+2,+3	distinct	0	0.999
TGVVELATYLSQHGVELLSTGGTAK	79.76	52.5882	2530.328	2530.982	2	2	distinct	0	0.9962
LPFTVLNGTPGYINLLDAANAYQLVR	58.74	51.7295	2832.517	2833.63	1	2	distinct	0	0.9771

The equivalent proteins include

jgi|Physo1_1|109486|estExt_fgenesh1_pm.C_1170007	0	No title.

162. Group probability: 1.0000. Peptides of the group

WDYSMFVKPK	73.68	55.3784	1299.632	1300.488	5	2	distinct	0	0.9882
HWRPDMEEAEAR	49.44	54.5952	1525.673	1526.335	1	2	distinct	0	0.9097
YKGGVLMAADTLGSYGSLAR	107.13	53.5992	2029.03	2029.895	2	2	distinct	1	0.9996
LTAVHNTTLLGAGGDFSDFQFIK	70.4	52.6038	2451.243	2452.591	2	2	distinct	0	0.9907

The equivalent proteins include

jgi|Physo1_1|158871|C_scaffold_162000014	0	No title.

163. Group probability: 1.0000. Peptides of the group

NFDPGFFVEHFVK	58.47		54.5335	1581.762	1582.491	1	2	distinct	0	0.9606
KVFLDPEWGVLSSIK	74.19		54.3722	1716.945	1718.001	6	2	distinct	1	0.9781
VSDIVFGIVGYPSDVR	53.23		54.2543	1721.899	1722.725	1	2	distinct	0	0.9442
VGWIGTGVMGASMVGHILK	90.44		53.8255	1912.006	1912.791	3	2	distinct	0	0.9981
MNLSLPGLALANQLYVAVK	50.73		53.6359	2014.128	2015.623	1	2	distinct	0	0.9383

The equivalent proteins include

jgi|Physo1_1|120688|estExt_Genewise1.C_810036	0	No title.

164. Group probability: 1.0000. Peptides of the group

QYTGVGSLK	45.87		55.2449	951.502	952.559	1	2	distinct	0	0.8618
AYAEHLKR	65.71		56.3486	986.53	987.808	9	2	distinct	1	0.9678
ISSHGQQDLDR	51.24		55.2386	1254.595	1255.005	3	2	distinct	0	0.919
HILHQLEEMK (000000000100)	56.42		55.3212	1276.66	1293.137	3	2	distinct	0	0.9466
KISSHGQQDLDR	71		54.9357	1382.69	1383.156	6	2	distinct	1	0.9863
SGKIELPAWWDVVK	77.54		54.7445	1626.877	1627.787	5	2	distinct	1	0.9728

The equivalent proteins include

jgi|Physo1_1|109411|estExt_fgenesh1_pm.C_1010005	0	No title.

165. Group probability: 1.0000. Peptides of the group

LISGKPVYVALAQR	88.73		54.7778	1513.898	1514.684	11	+2,+3	distinct	0	0.9996
RQDRPDADDWTNCYVK	49.6		53.6234	2037.896	2039.321	1	3	distinct	1	0.9068
VPGAPAPGGYPMPGYGMPMQQQR	42.77		52.8448	2386.102	2386.479	1	2	distinct	0	0.8942
ITGMLLEMDNGELLHLLESPEALEAK	88.95		51.7445	2865.45	2866.857	2	3	distinct	0	0.998

The equivalent proteins include

jgi|Physo1_1|108322|estExt_fgenesh1_pm.C_60012	0	No title.

166. Group probability: 1.0000. Peptides of the group

VVHDKFGIK	49.37		55.6701	1041.597	1041.469	1	1	distinct	1	0.8975
VLDLIEHMVK	57.34		55.3685	1195.663	1196.24	3	2	distinct	0	0.9507
NMHVVSNASCTTNCLAPLAK	83.89		53.3077	2187.023	2188.453	7	2	distinct	0	0.9968
FGGEISHDEQHIFVDGKPIR	81.55		52.9644	2280.129	2281.328	2	+2,+3	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|108305|estExt_fgenesh1_pm.C_50020	0	No title.

167. Group probability: 1.0000. Peptides of the group

AGMTHIMR	70.54		56.7097	915.442	915.808	7	2	distinct	0	0.9836
KSLLVHTK	65.66		55.2178	924.576	925.126	2	2	distinct	1	0.8739
APHLTAFMGYK	68.42		55.4108	1234.617	1234.323	4	1	distinct	0	0.982
VACIGAWHPSR	70.32		55.4025	1252.613	1253.064	9	2	shared(2)	0	0.9848
DDASKAPHLTAFMGYK	48.59		54.2004	1750.835	1750.943	1	3	distinct	1	0.897
DITPLGGFPHYGIINEDWLMIK	54.43		52.5209	2528.277	2528.36	2	2	distinct	0	0.9608

The equivalent proteins include

jgi|Physo1_1|109017|estExt_fgenesh1_pm.C_520010	0	No title.

168. Group probability: 1.0000. Peptides of the group

HDGNLSLDQVIGVAR	100.51		54.6186	1592.827	1593.781	2	+2,+3	distinct	0	0.9999
NIKHDGNLSLDQVIGVAR	83.71		53.9627	1948.049	1948.428	6	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|108649|estExt_fgenesh1_pm.C_220010	0	No title.

169. Group probability: 1.0000. Peptides of the group

LHAASYLLPGEDILFAFESAK	82.7		53.0828	2291.184	2292.627	3	+2,+3	distinct	0	0.9999
ISAGHDLVSQATSAAEWLENAFNQR	117.74		52.0119	2714.305	2714.448	6	2	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|129572|estExt_fgenesh1_pg.C_80083	0	No title.

170. Group probability: 1.0000. Peptides of the group

RGVKPADLISGLEFACGNPDK	77.14		53.2533	2243.137	2243.741	4	+2,+3	distinct	1	0.9998
WTSIGSTQPIGTTTFEHWPLR	80.89		52.8623	2414.202	2414.591	2	2	distinct	0	0.996
YAEHPAIIGLEPVNEPWELTPIDLLK	60.32		51.355	2956.559	2957.693	2	2	distinct	0	0.9802

The equivalent proteins include

jgi|Physo1_1|116268|estExt_Genewise1.C_320049	0	No title.

171. Group probability: 1.0000. Peptides of the group

AHSYIDKVNSR	46.3		55.4659	1288.652	1289.683	1	2	distinct	1	0.8746
RPLVVMAPNPECLR	70.3		54.7089	1650.87	1651.21	2	2	distinct	0	0.9865
LSVAPMLAELIQAEHFK	70.65		53.8666	1896.018	1897.222	1	2	distinct	0	0.9884
WLPDSPAQFAMFFHGTGK	99.55		53.7432	2035.961	2036.791	2	2	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|129878|estExt_fgenesh1_pg.C_90155	0	No title.

172. Group probability: 1.0000. Peptides of the group

FVLDKEFR	44.97		55.2696	1052.565	1053.733	1	2	distinct	1	0.8504

LRPDTGLYGK	47.03	55.8199	1118.608	1119.597	3	2	distinct	0	0.8772
AAPKEEAPKPK	54.89	55.3632	1164.65	1165.085	4	2	distinct	1	0.9411
KVEHPLAVLNR	53.51	55.429	1274.746	1275.771	2	2	distinct	1	0.9334
HMVEANPDAEYYTWTK	114.67	53.7337	1953.857	1954.586	7	2	distinct	0	0.9997

The equivalent proteins include

jgi|Physo1_1|142260|estExt_fgenesh1_pg.C_1110001	0	No title.

173. Group probability: 1.0000. Peptides of the group

SSFEAPHEPR	47.32	55.4648	1155.531	1156.058	1	2	distinct	0	0.8812
LHSGDSYIFLK	53.08	55.4899	1278.661	1278.982	1	2	distinct	0	0.9307
AASALLATFLDDSLGGNPVQVR	88.47	53.156	2214.164	2214.716	3	+2,+3	distinct	0	0.9999
AASQSEEDIGVDPNGDGKHEITVWR	62.77	52.1098	2709.263	2710.376	1	3	distinct	1	0.9793

The equivalent proteins include

jgi|Physo1_1|136639|estExt_fgenesh1_pg.C_470053	0	No title.

174. Group probability: 1.0000. Peptides of the group

ETHHVAGAAVR	54.14	55.7971	1146.589	1146.51	3	+1,+2	shared(2)	0	0.9946
RLTELIGAVGGK	63.93	55.5899	1212.719	1213.39	2	2	shared(2)	1	0.9741
NKPLSSLTFEELSTLHPK	99.39	53.6109	2040.089	2040.337	8	2	distinct	0	0.9991
ELIGTANQLAENNIELLMPGFTHLQPAQPLR (0000000000000000000100000000000000)	90.53	50.4448	3427.792	3428.389	9	3	distinct	0	0.998

The equivalent proteins include

jgi|Physo1_1|109558|estExt_fgenesh1_pm.C_1380002	0	No title.

175. Group probability: 1.0000. Peptides of the group

LLGDVTIASGGVMPNIHSVLLPK (00000000000000100000000000)	96.27	52.9384	2330.303	2331.179	48	+2,+3	distinct	0	1
IGGGAPVYMAAVLEYLCAEILELAGNAAR	46.46	51.3874	2991.52	2993.001	1	3	distinct	0	0.7282
NDEELNKLLGDVTIASGGVMPNIHSVLLPK	69.4	51.0584	3172.68	3173.206	5	3	distinct	1	0.9905

The equivalent proteins include

jgi|Physo1_1|158257|C_scaffold_93000012	0	No title.

176. Group probability: 1.0000. Peptides of the group

IPCHVLAK	51.67	55.46	936.521	937.267	3	2	distinct	0	0.9165
HITIFSPEGR	54.99	55.7078	1155.604	1156.336	6	2	distinct	0	0.939
IDPAGHFWGYK	63.77	55.411	1289.619	1290.383	9	2	distinct	0	0.9729
LRYEAHEFENK	62.11	54.8619	1434.689	1435.107	6	2	distinct	1	0.931
RIADVAQVYTQHASMR	55.52	54.177	1844.932	1845.869	4	+2,+3	distinct	1	0.9974

The equivalent proteins include

jgi|Physo1_1|108340|estExt_fgenesh1_pm.C_60030	0	No title.

177. Group probability: 1.0000. Peptides of the group

GAPSVLGIHPK	51.34	56.1399	1074.619	1075.066	3	2	distinct	0	0.9183
FTFGGAKPQVK	68	55.3915	1178.645	1178.989	9	2	distinct	0	0.9813
VQGMWVFHSTR	61.38	55.2517	1346.655	1347.575	5	2	distinct	0	0.9667
VWSYDNPEHTLK	45.53	54.8909	1487.704	1488.394	1	2	distinct	0	0.872
VFMWDTGNSIGEIVGHQK	82.91	53.6343	2016.973	2018.057	2	2	distinct	0	0.9962

The equivalent proteins include

jgi|Physo1_1|129331|estExt_fgenesh1_pg.C_70156	0	No title.

178. Group probability: 1.0000. Peptides of the group

RVTLEIGGK	51.91	56.3588	971.576	972.261	3	2	shared(3)	1	0.8722
VGELIVEAGFPK	78.95	55.4942	1257.697	1258.863	1	2	shared(2)	0	0.9931
IHGSVIPISGPYLCYTK	62.15	53.9495	1903.987	1905.377	4	2	distinct	0	0.9755
GWFIEPTVFADVTDDMTIAR (00000000000000000100000)	97.86	52.9995	2283.088	2284.084	13	2	shared(2)	0	0.9991
TGTVYYVNCYDVFDSNTPFGGFK	97.26	52.6068	2487.105	2488.234	1	2	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|109263|estExt_fgenesh1_pm.C_810010	0	No title.

179. Group probability: 1.0000. Peptides of the group

AVAHHTDCTFIR	51.4	54.9512	1426.678	1427.199	2	2	distinct	0	0.9234
LLREELQLLQEPGSYVGEVVK	61.49	52.7905	2398.311	2399.497	3	+2,+3	distinct	1	0.9984
EVIELPIKHPELFDALGVAQPK	75.85	52.8315	2442.352	2443.482	7	+2,+3	distinct	1	0.9997

The equivalent proteins include

jgi|Physo1_1|109338|estExt_fgenesh1_pm.C_920004	0	No title.

180. Group probability: 1.0000. Peptides of the group

IVVHDLQPEVEEPK	48.73	54.6497	1630.857	1631.508	1	2	distinct	0	0.9104
LYSLVAGDVIHALVFSPNR	115.9	53.6684	2070.126	2070.592	4	2	distinct	0	0.9998

SLLVWQLSNDGEEYGFAR	90.91		53.5612	2083.001	2083.574	2	2	distinct	0	0.9981

The equivalent proteins include

jgi|Physo1_1|109389|estExt_fgenesh1_pm.C_980005	0	No title.

181. Group probability: 1.0000. Peptides of the group

TFGHAPFTFK	56.45		55.3102	1151.576	1152.031	4	2	distinct	0	0.9468
ITHHFGGSCYASSNTADSNR	89.04		53.2584	2180.929	2181.576	7	+2,+3	distinct	0	1
NLFDTNVVFASFSHPQMSSFQFK	55.27		52.1352	2677.263	2677.551	1	2	distinct	0	0.9651

The equivalent proteins include

jgi|Physo1_1|144141|estExt_fgenesh1_pg.C_1690006	0	No title.

182. Group probability: 1.0000. Peptides of the group

QISQYFSSFR	46.99		55.8539	1261.609	1261.943	2	2	distinct	0	0.8767
VKECTGNAVPVGTVQR	80		54.3238	1713.883	1714.494	11	2	distinct	1	0.9947
CGVNIYPFFTQGELKPVDK	58.3		53.2648	2211.103	2211.718	9	+2,+3	distinct	0	0.9979
VAVGVQMNDLSGVDAEIQAVCDGYKR	59.59		51.9604	2793.342	2794.839	1	3	distinct	1	0.9737

The equivalent proteins include

jgi|Physo1_1|131139|estExt_fgenesh1_pg.C_140137	0	No title.

183. Group probability: 1.0000. Peptides of the group

LVQHGVTNTAGSLK	59.88		54.8855	1423.778	1424.054	5	2	distinct	0	0.9661
DYVRPGMVGNIFEK	53.01		54.5418	1623.808	1624.786	2	2	distinct	0	0.9386
HLPCFGLTGPSSGSDAANMR	96.74		53.4829	2073.936	2074.481	4	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108276|estExt_fgenesh1_pm.C_40027	0	No title.

184. Group probability: 1.0000. Peptides of the group

TACTATQQTAAYK	48.13		55.1623	1413.656	1414.142	1	2	distinct	0	0.9011
LMCASTACNTMIK (000000000001000)	67.83		55.0587	1499.66	1500.494	25	2	distinct	0	0.9825
LMCASTACNTMIKK	83.1		54.7455	1627.755	1629.112	14	2	distinct	1	0.9956
TLVSILSESSFSQCSK	80.12		54.26	1771.866	1772.861	1	2	distinct	0	0.9947

The equivalent proteins include

gi|119287|sp|P15569|ELIB_PHYCI	10629.09	Beta-elicitin cinnamomin

185. Group probability: 1.0000. Peptides of the group

TVSAPPPAPPTHSLLETK	47.6		54.1344	1841.989	1841.88	2	2	distinct	0	0.915
HLAAVLGQHENDAVVIPK	78.94		53.8215	1910.037	1910.474	10	+2,+3	distinct	0	0.9995
LMLSFYLLDPEGTGFITK	94.94		53.5363	2044.059	2045.297	4	2	distinct	0	0.9987

The equivalent proteins include

jgi|Physo1_1|156081|C_scaffold_10000100	0	No title.

186. Group probability: 1.0000. Peptides of the group

KSYMDGHNILK	50.2		55.3786	1304.655	1305.342	1	2	distinct	1	0.9111
IPPLTPEQAELVESLEQVQIIAR	50.83		52.3837	2572.411	2573.623	1	2	distinct	0	0.9483
TLGSGQALIDGLFPVDGTLSLELHR	69.12		52.3038	2608.386	2608.805	3	+2,+3	distinct	0	0.9997
MIFHGEPQQLPDCHDTLCDIEEFSK	56.54		51.2664	3045.331	3046.508	1	3	distinct	0	0.9649

The equivalent proteins include

jgi|Physo1_1|158580|C_scaffold_119000001	0	No title.

187. Group probability: 1.0000. Peptides of the group

YGSANALHFK	59.83		55.4553	1106.551	1107.394	3	2	distinct	0	0.9603
ETRPTFFFGVPR	62.88		54.8329	1452.751	1453.597	3	2	distinct	0	0.9721
VTESGAGARPAITAPQAFQNTLAK	85.04		52.7544	2398.26	2399.708	13	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|132768|estExt_fgenesh1_pg.C_220116	0	No title.

188. Group probability: 1.0000. Peptides of the group

HLGAELALVAR	54.97		55.6328	1148.667	1148.529	5	+1,+2	shared(2)	0	0.9959
YYYHAVGTPR	68.16		55.3938	1225.588	1226.374	13	2	shared(2)	0	0.9809
SKDYFAGMAWK	47.88		55.4109	1302.607	1304.091	2	2	shared(2)	1	0.8909
KTQSNVSKPFPK	83.59		55.3325	1359.751	1360.299	6	+1,+2	shared(2)	1	0.9996
KLFVPYDNVIPPSAK	50.79		54.4324	1686.934	1687.763	1	2	shared(2)	1	0.9281
IVPGANEVEYAPIDEAGDLLADPVK	52.22		52.4331	2594.311	2595.065	1	2	distinct	0	0.9573
VEVVGTMLPLGPNGGVSQLPVMGGVVMGNLITK	66.41		50.8794	3262.749	3264.041	1	3	shared(2)	0	0.989

The equivalent proteins include

jgi|Physo1_1|144990|estExt_fgenesh1_pg.C_3690001	0	No title.

189. Group probability: 1.0000. Peptides of the group

ESYPACGGTHQSPINIPVR	76.53		53.5169	2081.995	2082.95	8	2	distinct	0	0.9936
DLSHNDWGMFHAPLTYGGDCSK	90.78		52.4862	2507.063	2507.469	9	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|132952|estExt_fgenesh1_pg.C_230095	0	No title.

190. Group probability: 1.0000. Peptides of the group

LGDFAPVAPAIQNFHTR	72.94	54.0013	1852.958	1853.431	12	+2,+3	distinct	0	0.9986
LNTWGGSLALGHPFGATGSR	85.43	53.747	1998.007	1998.741	11	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|108326|estExt_fgenesh1_pm.C_60016	0	No title.

191. Group probability: 1.0000. Peptides of the group

LVRPFVVSAVLR	57.15	55.1677	1354.845	1355.657	2	2	distinct	0	0.9535
LGTFGVLHPQVLK	58.39	54.8487	1407.824	1408.463	6	2	distinct	0	0.96
FKPLSQDKEFEAK	45.81	54.6388	1565.809	1566.274	1	2	distinct	1	0.8801
ETQGQDKDHSAHSDAVLYK	44.68	53.3589	2127.982	2128.161	1	2	distinct	1	0.8957
RICAAYTGPTDGFEVIHGLVDR	85.78	52.6312	2446.206	2447.559	1	3	distinct	1	0.9969

The equivalent proteins include

jgi|Physo1_1|108453|estExt_fgenesh1_pm.C_100012	0	No title.

192. Group probability: 1.0000. Peptides of the group

VAGLAAGAIGAAGVIGSAVSATR	110.28	53.8113	1939.085	1939.715	17	+2,+3	distinct	0	1
SVLEPVELLAELFDTTLK	56.7	53.593	2016.103	2017.413	1	2	distinct	0	0.9622

The equivalent proteins include

jgi|Physo1_1|144346|estExt_fgenesh1_pg.C_1800007	0	No title.

193. Group probability: 1.0000. Peptides of the group

LAALVGAHK	50.61	55.7678	878.534	879.22	1	2	distinct	0	0.9078
FGSHNVYDHDASSTYK	105.31	54.0794	1826.786	1827.443	9	2	distinct	0	0.9994
FDGLFGLAFDTISVDHLK	93.05	53.7646	1994.015	1995.319	2	2	distinct	0	0.9984

The equivalent proteins include

jgi|Physo1_1|158318|C_scaffold_95000019	0	No title.

194. Group probability: 1.0000. Peptides of the group

VYADAVVNHMSGGGNDVLSHR	62.01	53.2564	2197.033	2197.983	3	+2,+3	distinct	0	0.9985
HSPYYTHSYTYGVNEYTK	92.87	53.2525	2208.975	2209.873	1	2	distinct	0	0.9984
TGWAAPYIHYNSGTGWTTSPGQAITK	54.84	52.0292	2764.324	2765.768	1	3	distinct	0	0.9601

The equivalent proteins include

jgi|Physo1_1|129859|estExt_fgenesh1_pg.C_90136	0	No title.

195. Group probability: 1.0000. Peptides of the group

AHHNTSQSDAAESELR	103.42	54.1549	1751.782	1751.944	5	+2,+3	distinct	0	1
ILGPESDFFANLVVDAVSSVK	82.75	53.3003	2206.152	2206.484	6	2	distinct	0	0.9966

The equivalent proteins include

jgi|Physo1_1|109440|estExt_fgenesh1_pm.C_1070005	0	No title.

196. Group probability: 1.0000. Peptides of the group

ALHAQLAQLLADNQDGK	126.41	54.2853	1804.943	1805.049	2	2	distinct	0	0.9999
TQFTALLNAAAAHPVAAQSDVFK	60.95	52.8885	2370.233	2370.628	2	+2,+3	distinct	0	0.9989

The equivalent proteins include

jgi|Physo1_1|140120|estExt_fgenesh1_pg.C_820021	0	No title.

197. Group probability: 1.0000. Peptides of the group

AFTFTTHNGGTCWLK	71.93	54.2021	1739.809	1740.547	9	2	distinct	0	0.9888
MLKPLSCCSACSNFPGCR (01000000000000000000)	75.78	53.27	2143.909	2144.284	13	+2,+3	distinct	0	0.9989
SGCNAFSWSDLNGGTCWFK	74.2	53.2242	2192.904	2193.612	2	2	distinct	0	0.9922

The equivalent proteins include

jgi|Physo1_1|135818|estExt_fgenesh1_pg.C_410009	0	No title.

198. Group probability: 1.0000. Peptides of the group

TYFVDGLHFSQK	60.43	54.9027	1440.704	1441.596	3	2	distinct	0	0.9653
WVLQHAMPIYEK (00000001000000)	74.16	54.7778	1513.775	1514.587	26	+1,+2	distinct	0	0.9987
KTYFVDGLHFSQK	66.81	54.7853	1568.799	1569.437	5	+2,+3	distinct	1	0.9975

The equivalent proteins include

jgi|Physo1_1|135534|estExt_fgenesh1_pg.C_390021	0	No title.

199. Group probability: 1.0000. Peptides of the group

MYVFDGHCGVNEK	76.69	54.7561	1554.659	1555.028	2	2	distinct	0	0.992
LSAGQAQYHFLSGYTAK	91.74	54.1345	1840.911	1841.734	7	2	distinct	0	0.9982
GNHPNAVIFLTCDAYGVLPPVSK	71.84	52.7178	2468.252	2469.546	1	2	distinct	0	0.9918

The equivalent proteins include

jgi|Physo1_1|108707|estExt_fgenesh1_pm.C_260008	0	No title.
jgi|Physo1_1|108708|estExt_fgenesh1_pm.C_260009	0	No title.

200. Group probability: 1.0000. Peptides of the group

YHGNGVVAQHGGEAKE	83.8	54.6037	1651.77	1652.662	1	2	distinct	1	0.9961

ISYSHNFLPENVETLIK	62.59		53.6638	2003.036	2004.334	2	2	distinct	0	0.9766
TILPHHATEECFPTIEK	67.35		54.0775	2021.988	2022.656	7	+2,+3	distinct	0	0.9986

The equivalent proteins include

jgi|Physo1_1|130464|estExt_fgenesh1_pg.C_110133	0	No title.

201. Group probability: 1.0000. Peptides of the group

HEAVEVPNLQVIK	54.07		55.0424	1474.814	1475.282	3	2	distinct	0	0.9414
SYLHLPAEIVPATLK	91.48		54.6178	1650.934	1652.162	4	2	distinct	0	0.998
SYLHLPAEIVPATLKK	98.28		54.1649	1779.029	1779.791	2	2	distinct	1	0.9989

The equivalent proteins include

jgi|Physo1_1|108449|estExt_fgenesh1_pm.C_100008	0	No title.

202. Group probability: 1.0000. Peptides of the group

IGGDVIIHELDTLIESLR	93.03		53.7839	1992.089	1992.831	8	2	distinct	0	0.9984
DNAYHPHVTVGGFQLDPDTGR	79		53.0199	2295.067	2295.581	3	2	distinct	0	0.9952
DTGLFPILVHGAGPQMNAELDK	62.97		53.059	2322.168	2322.747	1	2	distinct	0	0.9813

The equivalent proteins include

jgi|Physo1_1|139358|estExt_fgenesh1_pg.C_730027	0	No title.

203. Group probability: 1.0000. Peptides of the group

VGQAVEIVGQAGRPK	79.26		54.6303	1507.847	1508.842	3	2	distinct	0	0.9941
SITGFQTHTTPVLLNVK	75.46		54.0816	1855.02	1855.359	9	2	distinct	0	0.9924
LLGNSTDLGSWGHEFVR	85.4		53.9754	1886.927	1888.008	2	2	distinct	0	0.9968

The equivalent proteins include

jgi|Physo1_1|109208|estExt_fgenesh1_pm.C_730004	0	No title.

204. Group probability: 1.0000. Peptides of the group

FHGIKPDQEK	53.11		55.491	1197.614	1198.564	2	2	distinct	0	0.9284
HLSAFGLALQR	59.71		55.3738	1211.677	1212.656	1	2	distinct	0	0.9614
LVGQFPNHLPAMQAK	58.77		54.7099	1649.871	1650.987	4	2	distinct	0	0.9635
FITPPAGATWADIIFTR	94.35		54.0542	1875.988	1877.247	2	2	distinct	0	0.9985

The equivalent proteins include

jgi|Physo1_1|137699|estExt_fgenesh1_pg.C_560073	0	No title.

205. Group probability: 1.0000. Peptides of the group

FQPALDLITELLYEIK	118.73		53.9789	1905.05	1905.905	12	2	distinct	0	0.9998
TYTSGLGVIENVGHIVDNLFR	97.96		53.0688	2303.191	2303.423	7	2	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|108149|estExt_fgenesh1_pm.C_10014	0	No title.

206. Group probability: 1.0000. Peptides of the group

RFDLEDADFK	58.8		55.6625	1254.588	1255.43	1	2	distinct	1	0.9564
FGGEMIASYFDER	89.22		54.7074	1520.661	1521.396	2	2	distinct	0	0.9973
AAAILGEHNAVEDANLNLAK	92.09		53.6609	2033.054	2033.391	1	2	distinct	0	0.9984

The equivalent proteins include

jgi|Physo1_1|158411|C_scaffold_104000007	0	No title.

207. Group probability: 1.0000. Peptides of the group

KALAPYLQLTNAVR	57.35		54.7406	1556.904	1558.097	1	2	distinct	1	0.9578
VGNLEDFNVVLAQHGPVFK	72.76		53.572	2082.09	2082.195	1	2	distinct	0	0.9911
TLSVAQLQQAVEQLLPSQNASKPALLALLAK	102.29		51.0842	3242.86	3243.775	4	3	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|136709|estExt_fgenesh1_pg.C_470123	0	No title.

208. Group probability: 1.0000. Peptides of the group

KLFNITK	53.64		56.309	862.528	863.13	4	2	distinct	1	0.8649
VLEVDDEHKLR	84.67		55.1382	1351.71	1351.921	11	2	distinct	1	0.9957
GCIVGPDLSVLNLVVVK	110.38		54.3351	1781.012	1781.607	8	2	distinct	0	0.9996

The equivalent proteins include

jgi|Physo1_1|108459|estExt_fgenesh1_pm.C_100018	0	No title.

209. Group probability: 1.0000. Peptides of the group

KLQVTTHGR	61.11		55.2447	1038.593	1039.622	5	2	distinct	1	0.9637
SAVVDHNVALSYR	58.69		55.0353	1429.731	1430.17	2	2	distinct	0	0.9609
LSGSFTHASSGVVFK	72.18		54.6484	1522.778	1523.848	5	2	distinct	0	0.9889
LSGSFTHASSGVVFKK	68.87		54.6195	1650.873	1651.599	6	2	distinct	1	0.9857

The equivalent proteins include

jgi|Physo1_1|141610|estExt_fgenesh1_pg.C_1010023	0	No title.

210. Group probability: 1.0000. Peptides of the group

LNAVSELAPISWPEFTNVHPFVPK	45.56		52.0859	2691.406	2692.148	1	2	distinct	0	0.9213
HILENPGWYTSYTPYQAEVSQGR	59.09		52.1014	2695.267	2696.596	3	+2,+3	distinct	0	0.9992

ATSNICTAQALLANMAAAYAIYHGPEGLDK	80.06	51.1019	3134.516	3135.456	1	3	distinct	0	0.9963

The equivalent proteins include

jgi|Physo1_1|109239|estExt_fgenesh1_pm.C_790001	0	No title.

211. Group probability: 1.0000. Peptides of the group

GIQAATSHMLGQNFGK	105.14	54.99	1658.82	1659.424	4	2	distinct	0	0.9994
EKEHLEGFAPEVAWVTK	75.72	53.7655	1968.994	1969.338	2	2	distinct	1	0.9926
ALVDAAQVNCHPLRNDQTYSLK	53.41	52.559	2512.249	2513.569	2	3	distinct	1	0.9473

The equivalent proteins include

jgi|Physo1_1|132096|estExt_fgenesh1_pg.C_190046	0	No title.

212. Group probability: 1.0000. Peptides of the group

KVSLGVGAYR	80.5	55.6996	1048.603	1049.288	2	2	distinct	1	0.9935
ITGVQTISGTGGVR	58.48	55.4451	1344.736	1345.284	1	2	distinct	0	0.9613
EGHNIFLSQSYAK	47.08	54.6422	1492.731	1493.448	2	2	distinct	0	0.8927
HVPFFDCAYQGFASGDATR	72.92	53.2827	2144.937	2145.452	4	2	distinct	0	0.9913

The equivalent proteins include

jgi|Physo1_1|108281|estExt_fgenesh1_pm.C_40032	0	No title.

213. Group probability: 1.0000. Peptides of the group

LGGSGCQHVPIPTDNYVSDK	68.09	53.2712	2143	2144.166	5	+2,+3	distinct	0	0.999
LGGSGCQHVPIPTDNYVSDKR	49.86	53.0905	2299.101	2300.32	2	+2,+3	distinct	1	0.9922
LLATTTDFADYFPTDHNGVDATDVVFWR	56.51	50.9682	3186.493	3187.825	1	3	distinct	0	0.9686

The equivalent proteins include

jgi|Physo1_1|132826|estExt_fgenesh1_pg.C_220174	0	No title.

214. Group probability: 1.0000. Peptides of the group

SRDLLHPSAAEEASK	87.65	54.4518	1609.806	1610.336	5	2	distinct	1	0.9972
RLVQAPNSYFMDVK (0000000000010000)	88.99	54.3768	1666.85	1667.504	18	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|111303|estExt_Genewise1.C_50149	0	No title.

215. Group probability: 1.0000. Peptides of the group

FFEHYLEAK	58.96	55.8205	1182.571	1183.717	1	2	distinct	0	0.9556
ILHLVDPVDKK	55.43	55.5014	1275.755	1276.179	3	2	distinct	1	0.9436
GEYDGHHVCIHIDR	45.74	54.513	1706.758	1707.536	1	2	distinct	0	0.8838
TLPVTNDVEGVAQGFPFLVYPCRPGIAQGISR	95.01	50.266	3457.782	3458.399	1	3	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|136340|estExt_fgenesh1_pg.C_450031	0	No title.

216. Group probability: 1.0000. Peptides of the group

VQVTPVIRPK	48.82	55.3501	1135.708	1136.337	3	2	distinct	0	0.896
MPNVGYGSNKK	44.73	55.2177	1193.586	1194.34	1	2	distinct	1	0.8568
KYCAEIAHNVSGR	106.64	54.7957	1503.725	1504.504	19	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|109525|estExt_fgenesh1_pm.C_1260005	0	No title.

217. Group probability: 1.0000. Peptides of the group

VGIDSPLAGAGKK	65.46	55.3089	1211.687	1211.927	18	+1,+2,+3	distinct	1	0.9999
DLNPAYFHIAAANILGK	96.39	54.1067	1826.968	1827.611	10	2	distinct	0	0.9962

The equivalent proteins include

jgi|Physo1_1|142753|estExt_fgenesh1_pg.C_1210020	0	No title.

218. Group probability: 1.0000. Peptides of the group

FYINNIVGGTGAYGHSK	113.79	54.1158	1796.884	1797.44	4	2	distinct	0	0.9997
QVLALVNVPGLVDRPEIK	72.15	53.775	1959.152	1960.13	7	+2,+3	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|108810|estExt_fgenesh1_pm.C_340010	0	No title.

219. Group probability: 1.0000. Peptides of the group

HVTQAVVTVPAYFNDSQR	105.63	53.5807	2031.017	2031.48	6	2	distinct	0	0.9946
DILLLDVTPLSLGIETLGGVFTK	122.84	52.8653	2413.372	2413.876	136	2	distinct	0	0.9963
AQQGEGAASDDSKDENVHDAEFK	65.97	52.5799	2447.047	2448.163	1	3	distinct	1	0.9831

The equivalent proteins include

jgi|Physo1_1|108503|estExt_fgenesh1_pm.C_120013	0	No title.

220. Group probability: 1.0000. Peptides of the group

NPGHPLEQFIPLLK	69.26	54.9778	1601.893	1603.234	1	2	distinct	0	0.9851

NVAAMSLELGLPTLASIPHSIANAFK (0000010000000000000000000000)	78.87		52.1222	2664.431	2680.701	36	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109515|estExt_fgenesh1_pm.C_1240001	0	No title.

221. Group probability: 1.0000. Peptides of the group

HFVGYSK	48.7		55.2337	836.418	837.687	4	+1,+2	distinct	0	0.9809
TYETFGEDPYLCSVLGDAIIR	84.8		52.6817	2418.141	2419.423	3	2	distinct	0	0.9972
DTEAAGIPWIFGPILDLAQNPLWAR	73.61		52.0011	2763.438	2764.321	8	2	distinct	0	0.9935

The equivalent proteins include

jgi|Physo1_1|133710|estExt_fgenesh1_pg.C_270122	0	No title.

222. Group probability: 1.0000. Peptides of the group

HAWADKR	45.36		54.9856	882.446	883	1	2	shared(2)	1	0.8403
GSNYILVAGGIHDVGPR	46.11		54.2288	1723.9	1724.968	2	2	distinct	0	0.8995
KPYLFGEHVVYATTDDGGK	97.06		53.7145	2096.021	2096.058	7	+2,+3	distinct	0	0.9999
DINDVDSHLVGKGDWIVSDSK	68.51		53.0468	2298.113	2299.533	1	3	shared(2)	1	0.9853

The equivalent proteins include

jgi|Physo1_1|137802|estExt_fgenesh1_pg.C_570067	0	No title.

223. Group probability: 1.0000. Peptides of the group

ISCHVTIR	60.18		56.4065	984.517	985.089	5	2	distinct	0	0.9597
FEGIVLDEPRK	66.67		55.4712	1301.698	1303.143	1	2	distinct	1	0.979
VLEQLTGQKPVYSK	73.63		54.747	1588.882	1589.463	6	2	distinct	0	0.9899
LVINCCVGESGDKLTR	54.86		54.2611	1819.892	1820.108	1	2	distinct	1	0.9516

The equivalent proteins include

jgi|Physo1_1|108498|estExt_fgenesh1_pm.C_120008	0	No title.

224. Group probability: 1.0000. Peptides of the group

RTPFGNFGGK	50.97		55.2461	1079.551	1080.319	4	2	distinct	1	0.9141
ELQIDPEIVNQAGGAIALGHPLGASGSR	41.51		52.1785	2769.441	2770.387	1	3	distinct	0	0.8799
VVSYQVSGVDPTIMGIGPVPAITGALKR	100.71		51.9131	2824.552	2825.896	10	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|109594|estExt_fgenesh1_pm.C_1540002	0	No title.

225. Group probability: 1.0000. Peptides of the group

VAIITLNRPK	64		55.2461	1123.708	1124.61	23	2	distinct	0	0.9512
EGMAAFVEKR	69.21		55.3143	1136.565	1137.496	1	2	distinct	1	0.8594
VVPADQLLDEALK	77.34		54.9608	1409.777	1411.029	2	2	distinct	0	0.9924
VSKPVIAAVNGYALGGGCELAMLCDLIIAGDSAK	68.34		50.2428	3432.745	3433.488	9	3	distinct	0	0.9911

The equivalent proteins include

jgi|Physo1_1|108294|estExt_fgenesh1_pm.C_50009	0	No title.

226. Group probability: 1.0000. Peptides of the group

WEYMNKPAPGSWEEK	66.34		53.9965	1850.83	1851.639	7	2	distinct	0	0.9818
KIGWFGGGADLTPSYLFEEDAR	104.44		52.7464	2428.17	2428.844	9	2	distinct	1	0.9995
TLDVLKNPVDWLDVPAVDLEALSTGDLLK	48.25		51.3582	3148.691	3149.923	2	3	distinct	1	0.9369

The equivalent proteins include

jgi|Physo1_1|132630|estExt_fgenesh1_pg.C_210190	0	No title.

227. Group probability: 1.0000. Peptides of the group

HYGALTGLNK	64.39		56.0887	1072.566	1073.339	9	+1,+2	shared(4)	0	0.998
IVIAAHGNSLR	56.51		55.3716	1149.662	1150.474	2	2	distinct	0	0.9092
FTGWHDVQLSEK	64		55.1002	1445.694	1446.904	2	2	distinct	0	0.9746
HYGALTGLNKQETVDK	94.29		54.251	1772.906	1773.271	7	2	distinct	1	0.9985

The equivalent proteins include

jgi|Physo1_1|108887|estExt_fgenesh1_pm.C_390003	0	No title.

228. Group probability: 1.0000. Peptides of the group

LFLAPWSPPAWMK (000000000000100)	68.44		54.8274	1542.806	1544.145	14	2	distinct	0	0.9775
YVDGMAFHWYEDGGER	68.26		53.8439	1930.794	1931.672	2	2	distinct	0	0.9852
VQVTNTPFCLNLVPTASEGHEVR	47.87		52.443	2567.28	2568.595	1	3	distinct	0	0.9174
VTADKCEDEVVPHQQWTFNAEDGTLR	60.99		51.2279	3044.393	3045.428	1	3	distinct	1	0.9771

The equivalent proteins include

jgi|Physo1_1|138213|estExt_fgenesh1_pg.C_610047	0	No title.

229. Group probability: 1.0000. Peptides of the group

VLSALPGVHIR	50.83		55.6559	1160.703	1161.536	1	2	distinct	0	0.9154
EQQAGLIWQHLFVDR	72.08		53.95	1838.943	1839.311	1	2	distinct	0	0.989
HWLGDPASNTPPPAWSR	75.23		53.9756	1887.902	1888.232	4	2	distinct	0	0.9922
VDQILLGDWASIGPTLDVFK	46.14		53.2861	2186.162	2186.787	1	2	distinct	0	0.9116

The equivalent proteins include

jgi|Physo1_1|131558|estExt_fgenesh1_pg.C_160102	0	No title.

230. Group probability: 1.0000. Peptides of the group

GVCPFHGDCIEGMVASGSIAAR	49.02	53.1528	2290.029	2291.125	1	3	distinct	0	0.9215
SPTYGYITSTPKPNWGNTDVVGVFK	70.23	52.0252	2727.354	2728.678	8	+2,+3	distinct	0	0.9995
KSPTYGYITSTPKPNWGNTDVVGVFK	64.23	51.8648	2855.449	2856.86	1	3	distinct	1	0.9825

The equivalent proteins include

jgi|Physo1_1|158834|C_scaffold_159000001	0	No title.
jgi|Physo1_1|158835|C_scaffold_159000002	0	No title.

231. Group probability: 1.0000. Peptides of the group

KIEFISFK	49.73	55.2779	1010.58	1010.471	3	1	distinct	1	0.6861
GEPGLVFTHGK	52.16	55.6273	1140.593	1141.495	2	2	distinct	0	0.9247
TAAALTLTHKPK	74.8	55.4442	1250.735	1251.19	9	2	distinct	0	0.9901
VTHVSNLFHSK	46.04	55.4148	1267.667	1268.585	1	2	distinct	0	0.8718
EAFMPLVPGVHYAEFNDIESVK	59.65	52.4261	2491.209	2491.453	2	2	distinct	0	0.9753

The equivalent proteins include

jgi|Physo1_1|130851|estExt_fgenesh1_pg.C_130042	0	No title.

232. Group probability: 1.0000. Peptides of the group

VDLTPNYGSSHPWEICK	74.13	53.7497	2001.925	2002.378	3	2	distinct	0	0.9915
SLEELYADAVAEGGNLVMYHGGDFK	89.78	52.1134	2684.243	2684.492	17	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|108716|estExt_fgenesh1_pm.C_270001	0	No title.
jgi|Physo1_1|133594|estExt_fgenesh1_pg.C_270006	0	No title.

233. Group probability: 1.0000. Peptides of the group

AVMHMALR	50.54	56.7184	927.478	928.136	4	2	shared(4)	0	0.9055
FLAGAHAMDK (000000001000)	67.37	56.0363	1059.517	1060.198	9	2	shared(3)	0	0.9477
ANIFGFWDWVGGR	81.96	54.61	1523.731	1524.464	7	2	shared(3)	0	0.9938
FAAHIQQVDMESNGER	79.62	54.0851	1830.832	1831.328	5	2	distinct	0	0.963
KLQAIASGEHVNATEDR	112.31	53.9465	1837.928	1839.353	12	+2,+3	shared(3)	1	1
HMVAASSAVPLVQQFGIDR	63.53	53.5301	2025.047	2026.423	1	2	shared(3)	0	0.98
YSVTSAVGILPLALQYGFDITEK	71.42	52.6969	2484.315	2485.376	2	2	shared(3)	0	0.9914

The equivalent proteins include

gi|37960095|gb|AAP51072.1|	60840.39	glucose-6-phosphate isomerase [Phytophthora infestans]

234. Group probability: 1.0000. Peptides of the group

LSQLHFLLR	62.37	55.4905	1125.666	1126.528	5	2	distinct	0	0.9214
HQHSGASTLGEPDAAAAK	99.96	54.2715	1746.828	1746.686	6	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109023|estExt_fgenesh1_pm.C_530005	0	No title.

235. Group probability: 1.0000. Peptides of the group

IADNKDSFDWGCSHSGYER	62.6	53.2488	2242.934	2243.359	2	2	distinct	1	0.9784
VPMNDFADIYADKNGFVILGTR	74.96	52.7761	2455.22	2456.164	1	3	distinct	1	0.992
APHLAPIGNDGMLAMWEGSSSGGDLQEGGDR	77.15	51.1538	3124.398	3125.848	4	3	distinct	0	0.9954

The equivalent proteins include

jgi|Physo1_1|135613|estExt_fgenesh1_pg.C_390100	0	No title.

236. Group probability: 1.0000. Peptides of the group

RPAIETVR	66.47	56.0786	940.545	941.91	4	2	distinct	0	0.941
YGVDANTQSFMGHAMALMR	100.51	53.4349	2098.939	2099.294	3	2	distinct	0	0.9992
VLIVDRNPYYGGECASPNLTNLYK	65.07	52.0654	2755.364	2756.559	3	3	distinct	1	0.9825

The equivalent proteins include

jgi|Physo1_1|109350|estExt_fgenesh1_pm.C_930005	0	No title.

237. Group probability: 1.0000. Peptides of the group

FAVGNAEHTTK	60.67	55.8314	1173.578	1174.123	1	2	distinct	0	0.9642
KHDASIDEHVK	62.4	55.4899	1277.636	1278.547	5	2	distinct	1	0.9694
TQVVHASSSTYGTVK	57.44	54.8978	1563.789	1564.03	1	2	distinct	0	0.9595
TLFDIDEAWVGPGLNALDNK	63.43	53.311	2187.085	2187.781	2	2	distinct	0	0.9806

The equivalent proteins include

jgi|Physo1_1|156530|C_scaffold_21000020	0	No title.

238. Group probability: 1.0000. Peptides of the group

LLDLNHEELMDLVNAR (000000000010000000)	109.09	53.9226	1893.962	1895.345	15	+2,+3	distinct	0	1
NMIIVPEMIGSVVGVYNGK	60.26	53.6648	2019.053	2019.174	1	2	distinct	0	0.9732

The equivalent proteins include

jgi|Physo1_1|109596|estExt_fgenesh1_pm.C_1540004	0	No title.

239. Group probability: 1.0000. Peptides of the group

LLQLISRPLPEGEASILR	66.19	53.6858	2004.173	2004.931	13	+2,+3	distinct	0	0.9991
VLLAALQAPLEQFNPALHTAQR	96.32	52.8246	2400.328	2400.726	4	2	distinct	0	0.999

The equivalent proteins include

jgi|Physo1_1|108858|estExt_fgenesh1_pm.C_360012	0	No title.

240. Group probability: 1.0000. Peptides of the group

AQDVDHELPMKPITMMR	44.96	53.6116	2010.969	2011.416	2	+2,+3	distinct	0	0.9825
LNMVAITQANAHMLMSDYEAR	79.79	52.7801	2378.118	2379.35	3	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|138196|estExt_fgenesh1_pg.C_610030	0	No title.

241. Group probability: 1.0000. Peptides of the group

YTDFATAFADAGHSWSTDFCGK	119.54	52.7213	2454.022	2454.586	11	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|137332|estExt_fgenesh1_pg.C_530025	0	No title.

242. Group probability: 1.0000. Peptides of the group

KIIAESGIK	50.47	56.7732	957.586	958.811	1	2	distinct	1	0.7482
LNLHEFQSLEIMK	71.99	55.0234	1600.828	1602.188	1	2	distinct	0	0.9878
GGVHMCTKPEQAEDFAK	69.37	53.9936	1903.856	1904.426	11	2	distinct	0	0.987
LNLHEFQSLEIMKDFGVATPQGIPADTPAEAK	56.91	50.4043	3466.744	3467.412	1	3	distinct	1	0.974

The equivalent proteins include

jgi|Physo1_1|108575|estExt_fgenesh1_pm.C_160014	0	No title.

243. Group probability: 1.0000. Peptides of the group

FFLGTDSAPHVASK	78.12	54.8775	1475.741	1476.298	1	2	distinct	0	0.9932
KFFLGTDSAPHVASK	80.04	54.6313	1603.836	1604.521	3	+2,+3	distinct	1	0.9998

The equivalent proteins include

jgi|Physo1_1|108496|estExt_fgenesh1_pm.C_120006	0	No title.

244. Group probability: 1.0000. Peptides of the group

LFANALATALHVQNK	101.05	54.5057	1609.894	1610.952	6	2	distinct	0	0.9991
AMYPHDVALVYEVK	69.17	54.736	1633.817	1634.694	1	2	distinct	0	0.985
VSEQQKLPAGQTFTLQQAIK	49.3	53.1628	2214.201	2215.116	1	3	distinct	1	0.9178

The equivalent proteins include

jgi|Physo1_1|137070|estExt_fgenesh1_pg.C_500106	0	No title.

245. Group probability: 1.0000. Peptides of the group

YLTHILTMR	45.12	55.789	1146.622	1147.499	2	2	distinct	0	0.8508
RSELVQDVAGDTAGTTFFR	90.7	53.4876	2069.018	2069.686	6	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|127310|estExt_fgenesh1_pg.C_10290	0	No title.

246. Group probability: 1.0000. Peptides of the group

HPEVQQEIAQLAYK	51.73	54.3508	1652.852	1653.688	1	2	distinct	0	0.9315
DYNSQVTLEEFEELIAPLLTR	71.91	52.5445	2479.248	2479.683	10	2	distinct	0	0.9912
HLAEVLGLDKEQQNYGLSTTLNADESVAR	87.58	50.9557	3170.584	3171.876	1	3	distinct	1	0.998

The equivalent proteins include

jgi|Physo1_1|144810|estExt_fgenesh1_pg.C_2700005	0	No title.

247. Group probability: 1.0000. Peptides of the group

LFQVEYAMEAINNAGSAVGILAK	83.6	52.7743	2408.241	2408.587	2	2	distinct	0	0.9971
LDDHLICAVAGLTSDANILVNYAR	104.51	52.4466	2613.322	2613.857	6	2	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|109494|estExt_fgenesh1_pm.C_1190007	0	No title.

248. Group probability: 1.0000. Peptides of the group

KLAEVWGSDLPR	65.14	55.2166	1369.735	1371.209	2	2	distinct	1	0.9769
TLFVASIEDSPKPPPQR	92.26	54.0584	1881	1881.586	3	2	distinct	0	0.9982
TPPLPAANVKPTDGVVYWFIDEDAAAK	56.18	51.6715	2884.465	2885.83	3	3	distinct	0	0.966

The equivalent proteins include

jgi|Physo1_1|132192|estExt_fgenesh1_pg.C_190142	0	No title.

249. Group probability: 1.0000. Peptides of the group

IQHSALWENQALR	77.5	54.6854	1564.811	1564.984	2	2	distinct	0	0.9925
GGIPHDVYGMTTHSVR	77.84	54.2667	1725.826	1725.817	6	2	distinct	0	0.9936
LNTYTESQILDHILSSAEIVK	58.12	52.8519	2373.243	2373.6	1	2	distinct	0	0.9704

The equivalent proteins include

jgi|Physo1_1|143791|estExt_fgenesh1_pg.C_1510027	0	No title.

250. Group probability: 1.0000. Peptides of the group

LIVAILPSFGER	45.66	55.3542	1313.771	1314.299	1	2	distinct	0	0.8722
DMTALIGNTPLVYLNR	63.91	54.2085	1789.94	1791.101	1	2	shared(2)	0	0.9781
ALSLGQFDNPANPQIHFETTGPEIWR	83.39	51.5314	2937.441	2937.67	11	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|109755|estExt_fgenesh1_pm.C_17080001	0	No title.

251. Group probability: 1.0000. Peptides of the group

FPFGSLVPLWSR	52.51	55.1215	1404.755	1405.301	4	2	distinct	0	0.9303
LSHDPIHDNAYYGK	78.52	54.6364	1628.758	1629.616	2	2	distinct	0	0.9934
CMIGGILSCGLTHTGITPLDVVK	82.38	52.8523	2441.248	2441.798	5	2	distinct	0	0.9967

The equivalent proteins include

jgi|Physo1_1|109646|estExt_fgenesh1_pm.C_1930002	0	No title.

252. Group probability: 1.0000. Peptides of the group

EHIILAR	50.08	55.9941	850.502	850.484	13	+1,+2	distinct	0	0.9757
GQVLCKPGTINPHTK	71.26	54.6197	1648.872	1649.023	1	2	distinct	0	0.9276
DFEKPFLMPVEDVFSISGR	68.55	53.1707	2212.087	2212.759	6	+2,+3	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|109196|estExt_fgenesh1_pm.C_720005	0	No title.

253. Group probability: 1.0000. Peptides of the group

HLGLLDNWLR	54.66	55.2306	1235.677	1236.454	3	2	distinct	0	0.9379
VPAEEITGLAPGEMFVHR	84.83	53.7435	1951.982	1952.672	8	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|143382|estExt_fgenesh1_pg.C_1370031	0	No title.

254. Group probability: 1.0000. Peptides of the group

LNVAIKPEGSEK	52.86	55.3465	1283.708	1284.93	1	2	distinct	0	0.9321
RPYGQLQADKTDPSK	62.39	54.3807	1702.864	1703.295	3	+2,+3	distinct	1	0.9965
NFATTISPWVVPLAALEPFR	73.84	53.2667	2228.199	2229.183	9	2	distinct	0	0.9922

The equivalent proteins include

jgi|Physo1_1|108641|estExt_fgenesh1_pm.C_220002	0	No title.

255. Group probability: 1.0000. Peptides of the group

LSVGESLTNMVWAALGGR	85.34	54.0669	1859.956	1861.387	2	2	distinct	0	0.9969
MTQQVYDKPLASFWHGK	55.62	54.2949	2034.999	2036.428	2	2	distinct	0	0.9563
TLDSHLLLTAETHNFPSGVAPFPGAETGTGGR	64.45	50.8526	3249.605	3250.199	3	3	distinct	0	0.9864

The equivalent proteins include

jgi|Physo1_1|108492|estExt_fgenesh1_pm.C_120002	0	No title.

256. Group probability: 1.0000. Peptides of the group

IFAVHVAEHMK	56.79	55.1931	1280.67	1281.752	1	2	distinct	0	0.9503
VHEAIREDPSPAAK	53.35	54.9153	1518.779	1519.143	3	2	distinct	1	0.9399
GAADAGLDIPHSEKR	62.77	54.7123	1535.769	1536.139	9	+2,+3	distinct	1	0.996
TYFVEEVADEKRPFR	44.35	53.9098	1884.937	1886.351	1	3	distinct	1	0.8461

The equivalent proteins include

jgi|Physo1_1|108494|estExt_fgenesh1_pm.C_120004	0	No title.

257. Group probability: 1.0000. Peptides of the group

HAGIFIAR	45.61	55.4508	883.503	883.448	1	1	distinct	0	0.5138
IVALNASHFLK	71.69	55.3738	1211.703	1212.584	4	2	distinct	0	0.9865
DHAVVVGAYRVPK	58.8	54.9605	1409.778	1410.487	1	2	distinct	1	0.9614
KLQQEQFKPAEQLTLEPYER	51.94	52.5867	2474.28	2474.379	4	+2,+3	distinct	1	0.9927

The equivalent proteins include

jgi|Physo1_1|111761|estExt_Genewise1.C_70003	0	No title.

258. Group probability: 1.0000. Peptides of the group

NFPSLIEHCIEWSR	57.7	54.7084	1786.846	1787.891	2	2	distinct	0	0.9591
ILQLIHNFPEDHLTNSGEK	93.24	53.2455	2204.123	2204.359	7	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|157877|C_scaffold_66000007	0	No title.

259. Group probability: 1.0000. Peptides of the group

GNVIITYQHPDFAHSDK	56.36	53.7281	1940.938	1942.13	1	2	distinct	0	0.9595
TVAYVGSHMDVVPANPEGWQR	52.91	52.9665	2312.101	2312.675	1	2	distinct	0	0.9532
LFHSGLPNLGINGIELGMDAFTK	44.85	52.8479	2443.257	2444.212	1	3	distinct	0	0.8915
ALYSAISDVLGEAKPFSISGSLPLVR	66.87	52.0721	2689.469	2689.804	3	2	distinct	0	0.9887

The equivalent proteins include

jgi|Physo1_1|123133|estExt_Genewise1.C_1200039	0	No title.

260. Group probability: 1.0000. Peptides of the group

YAQVMTATLACDHR	88.04	54.6653	1635.75	1635.956	1	2	distinct	0	0.9971
LEVPHYHLSTNLTLDK	76.27	54.2083	1878.984	1879.748	10	+2,+3	distinct	0	0.9992

The equivalent proteins include

jgi|Physo1_1|110502|estExt_Genewise1.C_30032	0	No title.

261. Group probability: 1.0000. Peptides of the group

KVYIEDIR	45.12	55.6717	1034.576	1035.273	3	2	distinct	1	0.8511
YLLGTSLARPVIAK	69.01	55.0878	1500.903	1501.536	13	2	distinct	0	0.9847
HAHLDLEGLCMDR	46.55	54.5853	1565.708	1566.965	1	3	distinct	0	0.8619
TPELTGALDLFLELNK	75.89	54.3001	1772.956	1774.37	1	2	distinct	0	0.9923

The equivalent proteins include

jgi|Physo1_1|108409|estExt_fgenesh1_pm.C_90005	0	No title.

262. Group probability: 1.0000. Peptides of the group

YGAHSATDVTGFGILAHAR	88.25	53.7996	1942.965	1944.266	3	+2,+3	distinct	0	0.9999
LLGYLDNLANDLKPNETPGMDSSVVK	64.03	51.81	2802.411	2803.412	1	3	distinct	0	0.9822

The equivalent proteins include

jgi|Physo1_1|127317|estExt_fgenesh1_pg.C_10297	0	No title.

263. Group probability: 1.0000. Peptides of the group

VVLQQFHATPGAKDEK	70.35	54.1833	1766.931	1767.258	1	2	distinct	1	0.9876
AYVCHQSKPEIEASR	72.51	54.2806	1773.847	1774.332	4	2	distinct	0	0.9893
KQPELYSQFDAEGLPTHNAAGEELTK	62.65	51.6561	2872.388	2873.07	2	3	distinct	1	0.98

The equivalent proteins include

jgi|Physo1_1|136103|estExt_fgenesh1_pg.C_430036	0	No title.

264. Group probability: 1.0000. Peptides of the group

SMLDKHPEQEAR	73.44	54.8132	1439.683	1439.998	3	2	distinct	1	0.9889
YVVAIKPDTWCDVYWGGAK	82.94	53.1164	2227.077	2227.122	4	2	distinct	0	0.9964
DTEAAGIPWIFGPILDISQNTLWAR	45.52	52.0502	2783.428	2784.789	1	2	distinct	0	0.9238

The equivalent proteins include

jgi|Physo1_1|142760|estExt_fgenesh1_pg.C_1210027	0	No title.

265. Group probability: 1.0000. Peptides of the group

LVIIANNTPPLRK	55.82	54.9822	1447.887	1448.852	15	2	shared(2)	1	0.9498
TGVHHFTGNNNDLGTACGK	97.56	53.7309	1998.897	1999.496	20	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108147|estExt_fgenesh1_pm.C_10012	0	No title.

266. Group probability: 1.0000. Peptides of the group

FSHLAWINTPR	56.59	55.2424	1340.699	1341.333	3	2	shared(2)	0	0.9494
KLGCEVLGCSVDSK	81.41	54.6304	1550.743	1551.343	2	2	distinct	1	0.9949
LVEAFQFTDEHGEVCPAGWK	85.65	52.9844	2319.063	2319.419	1	2	distinct	0	0.9973

The equivalent proteins include

jgi|Physo1_1|108745|estExt_fgenesh1_pm.C_290008	0	No title.

267. Group probability: 1.0000. Peptides of the group

LAGTQVFGHSGK	91.58	55.7782	1200.625	1201.161	10	2	distinct	0	0.9977
LDHGVLAVGYGNDNGQK	93.55	54.2007	1755.854	1756.144	3	2	distinct	0	0.9984

The equivalent proteins include

jgi|Physo1_1|142383|estExt_fgenesh1_pg.C_1130020	0	No title.

268. Group probability: 1.0000. Peptides of the group

RWAGSAFGGFK	63.54	55.8205	1182.593	1183.381	2	2	distinct	1	0.9721
VGDHVVPCYTPQCR	50.94	54.4323	1686.761	1687.73	2	2	distinct	0	0.9265
FDLPQINEAFHAMHQGDCIR	55.63	52.7941	2398.095	2399.348	1	3	distinct	0	0.9532
SGADPEGIFPVIMGHEGAGIVESVGPDVTSLK	52.96	51.4413	3164.57	3165.533	1	3	distinct	0	0.9624

The equivalent proteins include

jgi|Physo1_1|108408|estExt_fgenesh1_pm.C_90004	0	No title.

269. Group probability: 1.0000. Peptides of the group

AVMHMALR	50.54	56.7184	927.478	928.136	4	2	shared(4)	0	0.9055
FLAGAHAMDK (000000001000)	67.37	56.0363	1059.517	1060.198	9	2	shared(3)	0	0.9477
GVWNSSFLGHSSR	81.59	55.0468	1432.685	1433.195	3	2	distinct	0	0.9948
ANIFGFWDWVGGR	81.96	54.61	1523.731	1524.464	7	2	shared(3)	0	0.9938
FAAHIQQVDMESNGKR	69.79	54.0851	1829.884	1831.328	4	2	shared(2)	1	0.8859
HMVAASSAVPLVQQFGIDR	63.53	53.5301	2025.047	2026.423	1	2	shared(3)	0	0.98
YSVTSAVGILPLALQYGFDITEK	71.42	52.6969	2484.315	2485.376	2	2	shared(3)	0	0.9914

The equivalent proteins include

gi|37960071|gb|AAP51060.1|	60801.41	glucose-6-phosphate isomerase [Phytophthora infestans]							
270. Group probability: 1.0000. Peptides of the group									
MPGVNYNSR	44.68	55.5253	1036.476	1036.627	1	2	shared(2)	0	0.8457
KGPDWAPDSSK	55.08	55.8357	1186.562	1187.198	2	2	shared(2)	1	0.9415
HQGFCLDTDPAQGNK	55.66	54.4243	1686.742	1687.104	1	2	distinct	0	0.9531
CLDAYQPWNGGIVHVYR	87.62	53.7061	2046.973	2047.896	9	2	distinct	0	0.9974
KIVISETGWSSGGSDPAAGVASPANQAK	42.6	52.1359	2684.34	2685.048	1	3	shared(2)	1	0.8909
The equivalent proteins include									
jgi|Physo1_1|128781|estExt_fgenesh1_pg.C_50278	0	No title.							
271. Group probability: 1.0000. Peptides of the group									
FSHLAWINTPR	56.59	55.2424	1340.699	1341.333	3	2	shared(2)	0	0.9494
GLFIIDKEGILR	55.31	55.2434	1372.808	1373.33	2	2	distinct	1	0.8324
KLNTQVIGASIDSK	86.63	54.9815	1472.82	1473.269	1	2	distinct	1	0.9968
LIEAFQFHEEHGDVCPANWK	57.1	52.7339	2426.111	2427.278	3	2	distinct	0	0.9666
The equivalent proteins include									
jgi|Physo1_1|108742|estExt_fgenesh1_pm.C_290005	0	No title.							
272. Group probability: 1.0000. Peptides of the group									
AEYDESGPSIVHR	65.28	55.0979	1458.674	1459.218	3	+2,+3	shared(2)	0	0.998
AEYDESGPSIVHRK	74.83	54.9745	1586.769	1587.119	5	2	shared(2)	1	0.9721
YPIEHGIVTDWDDMEK	83.19	53.8796	1946.872	1946.691	15	+2,+3	distinct	0	0.9994
The equivalent proteins include									
gi|50355625|dbj|BAD29953.1|	42035.79	actin [Ulva pertusa]							
273. Group probability: 1.0000. Peptides of the group									
AWGSTEAAQLAYFEEK	91.16	54.2842	1799.837	1800.666	1	2	distinct	0	0.998
IAFSPAQDIMYITNSQK	89.59	53.8267	1925.956	1927.356	1	2	distinct	0	0.9978
The equivalent proteins include									
jgi|Physo1_1|142894|estExt_fgenesh1_pg.C_1240014	0	No title.							
274. Group probability: 1.0000. Peptides of the group									
GALASRPHK	51.01	55.6313	935.53	936.217	1	2	distinct	0	0.6781
ANIAGKPVVTATQMLESMIK	59.63	53.4027	2101.127	2102.528	1	3	shared(2)	0	0.9666
IFCTLGPACWSQEGIGELIDAGMNVAR	69.77	51.3102	2964.393	2964.516	13	+2,+3	distinct	0	0.9999
The equivalent proteins include									
jgi|Physo1_1|109368|estExt_fgenesh1_pm.C_950013	0	No title.							
275. Group probability: 1.0000. Peptides of the group									
AVGHILAK	47.93	55.6115	807.497	808.139	1	2	distinct	0	0.8838
LYGDGGVKPWSNSIATR	50.85	54.2652	1819.922	1820.372	2	+2,+3	distinct	0	0.9926
VNILRDPVTGNYWQSYSEDPFLNAR	45.84	51.4877	2953.436	2954.925	1	3	distinct	1	0.9099
VSLVHGAVDEDGNQQQAGYSVPITSQGIPAIR	47.12	50.9023	3305.664	3306.357	2	3	distinct	0	0.9379
The equivalent proteins include									
jgi|Physo1_1|135218|estExt_fgenesh1_pg.C_360134	0	No title.							
276. Group probability: 1.0000. Peptides of the group									
GVLIHGPPGTGK	54.48	56.2125	1131.64	1132.141	1	2	shared(2)	0	0.8714
KIELPHPTEEAR	65.33	54.9856	1418.752	1419.04	5	+2,+3	distinct	1	0.9981
VIAATNRPDVLDPALLR	49.97	54.0924	1833.047	1834.226	5	+2,+3	distinct	0	0.9928
The equivalent proteins include									
jgi|Physo1_1|108207|estExt_fgenesh1_pm.C_20039	0	No title.							
277. Group probability: 1.0000. Peptides of the group									
DVHPFYFATQYHPEFK	58.41	53.5425	2024.942	2025.932	3	2	distinct	0	0.9651
TVQVVPHVTDAIQDWIER	91.53	53.3407	2105.09	2105.917	1	2	distinct	0	0.9982
VGPENFCLVHVSLVPVLGSVGEQK	44.53	52.5189	2563.347	2563.982	1	2	distinct	0	0.9131
The equivalent proteins include									
jgi|Physo1_1|109608|estExt_fgenesh1_pm.C_1650001	0	No title.							
278. Group probability: 1.0000. Peptides of the group									
KEYGPSQPLK	48.63	55.7971	1145.608	1146.399	2	2	distinct	1	0.8933
SKFDNIYGCR	50.4	55.6365	1258.576	1259.292	5	2	distinct	1	0.909
CKGVSEETTTGVHR	45.84	54.7579	1559.736	1560.756	1	2	distinct	1	0.8843
WCSCNIFSTQDHAAAAIAR	79.72	53.2948	2177.973	2178.608	1	2	distinct	0	0.9952
The equivalent proteins include									
jgi|Physo1_1|109095|estExt_fgenesh1_pm.C_600001	0	No title.							
279. Group probability: 1.0000. Peptides of the group									
LYANLISQPSR	48.46	55.8533	1260.683	1261.977	1	2	shared(2)	0	0.8954
LGWTDLYPADAR	52.46	55.1221	1376.672	1377.186	1	2	distinct	0	0.93

AVPLHDEIHEPLDQFLSSLGLK	72.03	52.6626	2457.29	2457.579	20	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|131470|estExt_fgenesh1_pg.C_160014	0	No title.
jgi|Physo1_1|131473|estExt_fgenesh1_pg.C_160017	0	No title.

280. Group probability: 1.0000. Peptides of the group

LGDAFHPK	57.12	55.4508	883.455	883.49	2	2	distinct	0	0.6819
SNLVALLEGK	47.24	56.1036	1042.602	1043.22	1	2	distinct	0	0.4754
LKQEEAATTGR	72.71	55.8044	1202.625	1203.739	3	2	distinct	1	0.9875
RYEDQLSELK	50.18	55.2695	1279.641	1281.004	1	2	distinct	1	0.9079
LVVPTDDGYVPVVVPK	60.62	54.3254	1695.945	1696.805	1	2	distinct	0	0.9708

The equivalent proteins include

jgi|Physo1_1|139774|estExt_fgenesh1_pg.C_780035	0	No title.

281. Group probability: 1.0000. Peptides of the group

IIVDAHYR	55.02	56.3036	985.534	986.243	8	2	distinct	0	0.8879
EHIAAYGTGNER	55.87	55.442	1316.611	1317.285	2	2	distinct	0	0.9477
RPASNMDPYVVTGR (0000001000000000)	67.39	54.8526	1561.767	1562.686	14	+2,+3	distinct	0	0.999

The equivalent proteins include

gi|23394346|gb|AAN31463.1|	39801.57	glutamine synthetase [Phytophthora infestans]

282. Group probability: 1.0000. Peptides of the group

LYANLISQPSR	48.46	55.8533	1260.683	1261.977	1	2	shared(2)	0	0.8954
LFTINIVRPEISK	71.43	55.168	1528.898	1529.694	2	2	distinct	0	0.9872
GVDHELVPCNPGSDFFK	47.09	53.903	1916.873	1917.297	1	2	distinct	0	0.9084
TQPFNEEIHVPLVGFIK	65.47	53.7421	1967.052	1967.625	4	2	distinct	0	0.9818

The equivalent proteins include

jgi|Physo1_1|131502|estExt_fgenesh1_pg.C_160046	0	No title.

283. Group probability: 1.0000. Peptides of the group

ELLQGQHVVAVR	74.97	55.2404	1347.762	1348.822	6	2	distinct	0	0.9902
VFEKPIVVDCR	58.46	55.2887	1360.717	1361.223	3	2	distinct	0	0.957
VFAENSELKPTLAK	68.11	55.2699	1545.84	1546.271	3	2	distinct	0	0.9834

The equivalent proteins include

jgi|Physo1_1|109046|estExt_fgenesh1_pm.C_540020	0	No title.

284. Group probability: 1.0000. Peptides of the group

AHALAVQK	53.75	55.9306	836.487	836.369	2	1	distinct	0	0.9298
NTYIVTHNLLR	63.48	55.4143	1342.736	1344.031	6	2	distinct	0	0.9722
MVPNPAGIAFYHDLIDEMTK	82.51	53.2854	2261.086	2261.414	16	2	distinct	0	0.9964

The equivalent proteins include

jgi|Physo1_1|137835|estExt_fgenesh1_pg.C_580008	0	No title.

285. Group probability: 1.0000. Peptides of the group

AVMHMALR	50.54	56.7184	927.478	928.136	4	2	shared(4)	0	0.9055
FLAGAHAMDK (000000001000)	67.37	56.0363	1059.517	1060.198	9	2	shared(3)	0	0.9477
ANIFGFWDWVGGR	81.96	54.61	1523.731	1524.464	7	2	shared(3)	0	0.9938
FAAHIQQVDMESNGKR	69.79	54.0851	1829.884	1831.328	4	2	shared(2)	1	0.8859
KLQAIASGEHVNATEDR	112.31	53.9465	1837.928	1839.353	12	+2,+3	shared(3)	1	1
HMVAASSAVPLVQQFGIDR	63.53	53.5301	2025.047	2026.423	1	2	shared(3)	0	0.98
YSVTSAVGILPLALQYGFDITEK	71.42	52.6969	2484.315	2485.376	2	2	shared(3)	0	0.9914

The equivalent proteins include

gi|37960107|gb|AAP51078.1|	60850.42	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960073|gb|AAP51061.1|	60861.39	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960081|gb|AAP51065.1|	60755.43	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960087|gb|AAP51068.1|	60776.38	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960091|gb|AAP51070.1|	60834.39	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960093|gb|AAP51071.1|	60842.35	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960105|gb|AAP51077.1|	60716.35	glucose-6-phosphate isomerase [Phytophthora erythroseptica]
gi|37960109|gb|AAP51079.1|	60859.42	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960111|gb|AAP51080.1|	60792.41	glucose-6-phosphate isomerase [Phytophthora infestans]

286. Group probability: 1.0000. Peptides of the group

GVNALQNPHDPVVIPR	82.31	54.2289	1724.932	1725.118	3	2	distinct	0	0.9956
VLVPVVPSQILGIGLNYR	58.57	53.7638	1936.151	1937.134	3	2	distinct	0	0.9678
NPPLFLAPGDMVEIEIER	53.14	53.6078	2039.04	2040.126	2	2	distinct	0	0.9483
The equivalent proteins include									
jgi|Physo1_1|135798|estExt_fgenesh1_pg.C_400135	0	No title.							
287. Group probability: 1.0000. Peptides of the group									
ADHSLVDKYSTR	52.14	55.132	1390.684	1391.285	1	2	distinct	1	0.928
LTDNIAGSLVNASKPVQAR	52.92	53.7482	1953.064	1953.358	1	2	distinct	0	0.949
NPSNYFAEIEQIAFSPSHMVPGIEPSPDK	87.32	50.9661	3200.512	3199.973	5	3	distinct	0	0.998
The equivalent proteins include									
jgi|Physo1_1|129552|estExt_fgenesh1_pg.C_80063	0	No title.							
288. Group probability: 1.0000. Peptides of the group									
TAPLHVSVHDR	57.97	55.6399	1230.647	1231.82	8	2	distinct	0	0.9548
GTHFQELPVSGCPK	61.5	54.7997	1555.745	1556.465	4	2	distinct	0	0.9707
RVSLDMLDWADPHAR	45.89	54.1737	1780.868	1781.239	1	2	distinct	1	0.8901
LIPVSYGIWFLDSTVPLLDDR	51.46	52.6819	2418.283	2419.077	1	2	distinct	0	0.9472
The equivalent proteins include									
jgi|Physo1_1|131019|estExt_fgenesh1_pg.C_140017	0	No title.							
289. Group probability: 1.0000. Peptides of the group									
RFMSQVWTR	52.53	55.2653	1209.608	1210.257	1	2	distinct	1	0.9229
RVEAYAGDNNQHGPR	81.15	54.2627	1682.787	1683.341	16	+2,+3	distinct	1	0.9999
The equivalent proteins include									
jgi|Physo1_1|135217|estExt_fgenesh1_pg.C_360133	0	No title.							
290. Group probability: 1.0000. Peptides of the group									
KVVVLCNLK	49.82	55.9949	1071.647	1071.485	2	1	distinct	1	0.9008
VKSDVYSSPIVFSQLDLR	93.77	53.8567	2052.089	2052.922	3	2	distinct	1	0.9985
VDIGKGEELEMVMEHQPYFAEEELVDR (00000000000100000000000000000)	49.37	51.0136	3191.479	3192.615	4	3	distinct	1	0.939
The equivalent proteins include									
jgi|Physo1_1|144562|estExt_fgenesh1_pg.C_1980006	0	No title.							
jgi|Physo1_1|144563|estExt_fgenesh1_pg.C_1980007	0	No title.							
291. Group probability: 1.0000. Peptides of the group									
RFFDFLPLNNK	60.06	54.9605	1409.745	1410.652	3	2	distinct	1	0.8955
DIINQIVDSFDFFEIMPDYAK	83.77	52.6673	2519.193	2519.253	15	2	distinct	0	0.9969
FCDSFNIPIVTLVDVPGFLPGTDQEYGGIIR	56.34	50.246	3438.717	3439.55	1	3	distinct	0	0.9717
The equivalent proteins include									
jgi|Physo1_1|109606|estExt_fgenesh1_pm.C_1640003	0	No title.							
292. Group probability: 1.0000. Peptides of the group									
VHPADLKPCLTK	53.55	55.0982	1377.744	1378.016	1	2	distinct	0	0.9364
THPIAYDGFEPSGR	60.38	55.1846	1545.721	1546.764	1	2	distinct	0	0.9674
HAGAYWSQVLDGAGR	82.65	54.9623	1586.759	1587.336	2	2	distinct	0	0.9956
The equivalent proteins include									
jgi|Physo1_1|136606|estExt_fgenesh1_pg.C_470020	0	No title.							
293. Group probability: 1.0000. Peptides of the group									
IVTGDASQAWHALCR	98.41	54.3258	1683.815	1684.212	11	+2,+3	shared(2)	0	0.9999
YKAPCVAVVQSSGFGK	80.63	54.3098	1696.861	1697.291	1	2	distinct	1	0.9949
MGRPMWYSTCPNPADR	55.96	53.777	1937.833	1937.898	1	2	shared(2)	0	0.9565
The equivalent proteins include									
jgi|Physo1_1|137148|estExt_fgenesh1_pg.C_510032	0	No title.							
jgi|Physo1_1|141989|estExt_fgenesh1_pg.C_1060048	0	No title.							
294. Group probability: 1.0000. Peptides of the group									
GMCDYGTGHCTCFPGYEGK	77.61	53.2746	2195.817	2195.839	4	2	distinct	0	0.9942
HMGCYCDQGYRGPDCSLK	47.67	53.2089	2202.87	2202.883	1	2	distinct	1	0.9171
TCPYGDAWVQVPTATNTAHSLVECSNR	62.08	51.377	3033.371	3034.715	2	3	distinct	0	0.9798
The equivalent proteins include									
jgi|Physo1_1|156623|C_scaffold_24000001	0	No title.							
295. Group probability: 1.0000. Peptides of the group									
RPDHNNDALYFR	46.99	54.9566	1516.717	1518.184	1	3	distinct	0	0.8613
FQINLDNLEPQVALFPSPDNVKPVSEVVGMK	123.95	50.3638	3423.775	3424.897	2	3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|141550|estExt_fgenesh1_pg.C_1000036	0	No title.

296. Group probability: 1.0000. Peptides of the group

KPAALNPEHLK	54.74	55.7176	1216.693	1217.371	3	2	distinct	0	0.9399
KDYKPEGDVPTPAAPAAIK	75.49	53.7044	1967.036	1967.532	2	2	distinct	1	0.993
SSEMNVAFPAGAGSDDYVEKPIPEQFVHK	58.53	51.3686	3148.481	3149.711	1	3	distinct	0	0.9744

The equivalent proteins include

jgi|Physo1_1|158145|C_scaffold_85000011	0	No title.

297. Group probability: 1.0000. Peptides of the group

SPVILVLDEIHDPQNFGAILR	89.9	52.9176	2345.274	2346.538	9	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|140510|estExt_fgenesh1_pg.C_860048	0	No title.

298. Group probability: 1.0000. Peptides of the group

AEMHAVGDHELR	53.62	55.0308	1363.63	1364.552	2	2	distinct	0	0.9369
YQAYPTYDLACPIVDSIEGVTHALR	42.66	51.7579	2851.385	2852.648	1	3	distinct	0	0.8802
AGVADESPAGAAAHAAPAAVAAATPAAAAPAGKK	89.25	51.6374	2879.489	2880.652	3	3	distinct	1	0.9985

The equivalent proteins include

jgi|Physo1_1|133964|estExt_fgenesh1_pg.C_290031	0	No title.

299. Group probability: 1.0000. Peptides of the group

ACNALLLK	66.88	56.8713	901.505	902.794	1	2	shared(3)	0	0.9266
GVPLYQHFADLIGNK	86.24	54.5609	1670.878	1671.671	15	2	distinct	0	0.9968
NLVLPVPSFNVINGGSHAGNK	83.65	53.2903	2133.133	2133.605	5	2	distinct	0	0.9914

The equivalent proteins include

jgi|Physo1_1|109144|estExt_fgenesh1_pm.C_630010	0	No title.

300. Group probability: 1.0000. Peptides of the group

FNANVTQKPLK	86.68	55.4914	1258.703	1258.98	5	2	distinct	0	0.996
TIIDSVHPLENVMEAFK	58.78	53.7488	1941.987	1943.368	1	2	distinct	0	0.9672
YVAPKPSSMSWNEAAGVPLAGQTSWQALVTYGK	42.63	50.7258	3493.734	3493.704	1	3	distinct	0	0.9115

The equivalent proteins include

jgi|Physo1_1|133480|estExt_fgenesh1_pg.C_260086	0	No title.

301. Group probability: 1.0000. Peptides of the group

LVNIDQVIQWLMK	91.01	54.8196	1598.885	1600.257	2	2	distinct	0	0.9977
ELNLDYIVDNPWLVIPISALR	77.8	52.6404	2452.337	2452.815	5	2	distinct	0	0.9948

The equivalent proteins include

jgi|Physo1_1|141248|estExt_fgenesh1_pg.C_960012	0	No title.

302. Group probability: 1.0000. Peptides of the group

GGLDASSHNYPPHGK	61.75	54.6695	1535.712	1536.584	2	2	distinct	0	0.9724
HEYMEYLQTHQSR	80.66	54.3352	1720.763	1721.11	2	+2,+3	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|142184|estExt_fgenesh1_pg.C_1090040	0	No title.

303. Group probability: 1.0000. Peptides of the group

VVDGVIAGQFLQVFK	46.84	54.5475	1618.908	1619.476	1	2	distinct	0	0.8981
LKPEEFQGGSFTVSNLGSFGIDQFR	58.06	51.9519	2759.355	2760.386	1	3	distinct	0	0.9688
TQSVKPNPSVDVSVAVATPTGLITPIVPK	76.43	51.5531	2914.638	2914.781	3	2	distinct	0	0.9956

The equivalent proteins include

jgi|Physo1_1|158966|C_scaffold_188000005	0	No title.

304. Group probability: 1.0000. Peptides of the group

AVEHVLLDGVR	47.63	55.2009	1206.672	1207.428	2	2	distinct	0	0.889
DFANPIAQILSAALLLR	133.45	53.9706	1825.046	1825.424	16	2	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|109069|estExt_fgenesh1_pm.C_560007	0	No title.

305. Group probability: 1.0000. Peptides of the group

AWLGPDNQIAGYHQR	83.67	54.2275	1724.838	1725.365	2	2	distinct	0	0.996
WITEDNGLALKPASPWR	83.13	53.7295	1953.011	1953.755	6	2	distinct	0	0.9961

The equivalent proteins include

jgi|Physo1_1|141365|estExt_fgenesh1_pg.C_970053	0	No title.

306. Group probability: 1.0000. Peptides of the group

LSHEQFPELK	53.66	55.5174	1226.629	1227.649	1	2	distinct	0	0.9318

VKEWYSLPHDTSK	64.94	54.7509	1588.789	1589.589	3	2	distinct	1	0.9775
TGRPGTPVDIADSYEHLLQVYDQVK	69.89	51.9789	2800.403	2801.672	4	3	distinct	0	0.989

The equivalent proteins include

jgi|Physo1_1|133628|estExt_fgenesh1_pg.C_270040	0	No title.

307. Group probability: 1.0000. Peptides of the group

VPAYSPYAVAEHAAALMMTLNR (0000000000000000001100000)	82.95	52.8258	2375.177	2376.169	5	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|137917|estExt_fgenesh1_pg.C_580090	0	No title.

308. Group probability: 1.0000. Peptides of the group

KLEPDIFHTKPDTSK	69.05	54.2006	1754.92	1755.967	2	2	distinct	1	0.9856
YLHELYGDSVKYPVLK	96.18	54.0859	1923.014	1923.434	6	2	distinct	1	0.9987

The equivalent proteins include

jgi|Physo1_1|138303|estExt_fgenesh1_pg.C_620039	0	No title.

309. Group probability: 1.0000. Peptides of the group

QVMALYDKRPK	65.75	55.2403	1347.733	1348.449	4	2	distinct	1	0.9773
RIPSGQLWAGNPAK	76.36	54.6194	1493.81	1494.482	10	+2,+3	distinct	1	0.9991

The equivalent proteins include

jgi|Physo1_1|109006|estExt_fgenesh1_pm.C_510006	0	No title.

310. Group probability: 1.0000. Peptides of the group

KVHLFDIDVPGK	69.51	54.9455	1366.761	1367.241	5	+2,+3	distinct	1	0.9986
ELLNEKDHPSTYALSQLAAK	67.13	53.2052	2227.148	2227.672	5	2	distinct	1	0.986

The equivalent proteins include

jgi|Physo1_1|108421|estExt_fgenesh1_pm.C_90017	0	No title.

311. Group probability: 1.0000. Peptides of the group

LLTPAQVIDYIAAHPMAK (000000000000000001000)	103.02	53.7855	1951.06	1951.264	45	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|158374|C_scaffold_101000017	0	No title.

312. Group probability: 1.0000. Peptides of the group

SRPYLFSNSLGPSVVGASLK	97.87	53.6543	2078.116	2078.725	9	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108830|estExt_fgenesh1_pm.C_340030	0	No title.

313. Group probability: 1.0000. Peptides of the group

AVMHMALR	50.54	56.7184	927.478	928.136	4	2	shared(4)	0	0.9055
ATAGLNPEETLVVVVSK	82.55	54.2934	1725.951	1726.653	3	2	distinct	0	0.9959
KLQAIASGEHVNATEDR	112.31	53.9465	1837.928	1839.353	12	+2,+3	shared(3)	1	1

The equivalent proteins include

jgi|Physo1_1|157608|C_scaffold_54000010	0	No title.

314. Group probability: 1.0000. Peptides of the group

AHLDVVKDPK	52.56	55.5109	1120.624	1121.6	2	2	distinct	1	0.9249
AFISSKPDAGFNHK	65.52	54.9173	1517.763	1518.45	5	2	distinct	0	0.9793
IMETLEHEQHLPLASR	68.32	53.9165	1902.962	1902.894	2	2	distinct	0	0.9852

The equivalent proteins include

jgi|Physo1_1|132830|estExt_fgenesh1_pg.C_220178	0	No title.

315. Group probability: 1.0000. Peptides of the group

SLNNQFASFIDKVR	48.77	54.5076	1637.852	1638.84	1	2	distinct	1	0.7016
THNLEPYFESFINNLR	83.06	53.7821	1992.969	1993.391	17	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|109096823|ref|XP_001098292.1|	65340.78	PREDICTED: similar to keratin 1 isoform 7 [Macaca mulatta]
gi|109096825|ref|XP_001098082.1|	64503.44	PREDICTED: similar to keratin 1 isoform 5 [Macaca mulatta]
gi|109096827|ref|XP_001097902.1|	63150.85	PREDICTED: similar to keratin 1 isoform 3 [Macaca mulatta]
gi|109096829|ref|XP_001097988.1|	62009.39	PREDICTED: similar to keratin 1 isoform 4 [Macaca mulatta]
gi|109096831|ref|XP_001098182.1|	63139.76	PREDICTED: similar to keratin 1 isoform 6 [Macaca mulatta]
gi|109096833|ref|XP_001097800.1|	61737.33	PREDICTED: similar to keratin 1 isoform 2 [Macaca mulatta]
gi|109096835|ref|XP_001097706.1|	59017.2	PREDICTED: similar to keratin 1 isoform 1 [Macaca mulatta]

gi|55638143|ref|XP_522394.1|	98632.68	PREDICTED: similar to keratin 1B [Pan troglodytes]
gi|7331218|gb|AAF60327.1|	66149.05	keratin 1 [Homo sapiens]
gi|11935049|gb|AAG41947.1|	66198.07	keratin 1 [Homo sapiens]

316. Group probability: 1.0000. Peptides of the group

AQMAPWIKPK	57.87	55.7713	1168.643	1169.471	1	2	distinct	0	0.9526
LIVEKPFGHDLASFDK	106.92	54.1652	1814.957	1815.532	9	2	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|109499|estExt_fgenesh1_pm.C_1190012	0	No title.

317. Group probability: 1.0000. Peptides of the group

IKTEHDFNLEK	67.39	55.3557	1372.699	1373.242	2	2	distinct	1	0.9803
LDQIYYDLKPTVR	68.76	54.5794	1622.867	1624.183	2	+2,+3	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|138060|estExt_fgenesh1_pg.C_600019	0	No title.

318. Group probability: 1.0000. Peptides of the group

KLSTELHAR	70.19	55.1439	1053.593	1053.999	8	2	distinct	1	0.9837
LCNNLALAIQMASVAEAMNLGTTLGIDPK	88.21	51.2372	3028.539	3028.547	2	2	distinct	0	0.9985

The equivalent proteins include

jgi|Physo1_1|142005|estExt_fgenesh1_pg.C_1060064	0	No title.

319. Group probability: 1.0000. Peptides of the group

KFLDGIYVSEK	77.32	55.2627	1297.692	1298.372	16	2	distinct	1	0.9918
RVALSEGVSYVR	60.59	55.3626	1334.731	1336.137	4	2	distinct	1	0.9655
FVYAHFPINVTFENNTVEIR	45.75	52.7059	2409.212	2410.666	1	2	distinct	0	0.9096

The equivalent proteins include

jgi|Physo1_1|108722|estExt_fgenesh1_pm.C_270007	0	No title.

320. Group probability: 1.0000. Peptides of the group

DYTINIHKR	54.36	55.7704	1158.615	1159.535	5	2	distinct	1	0.9337
LYTLVQHVQVASFK	110.15	54.6471	1631.903	1632.662	1	2	distinct	0	0.9996

The equivalent proteins include

jgi|Physo1_1|109268|estExt_fgenesh1_pm.C_820002	0	No title.

321. Group probability: 1.0000. Peptides of the group

CYQCGETGHWAR	70.95	54.61	1523.603	1524.466	4	2	distinct	0	0.9863
RDCPEAPSQEGFSGYGGPCFGCGK	89.88	52.2433	2619.058	2619.765	1	3	distinct	1	0.998

The equivalent proteins include

jgi|Physo1_1|109617|estExt_fgenesh1_pm.C_1690004	0	No title.

322. Group probability: 1.0000. Peptides of the group

KDIFLNSMFDK	79.97	55.2572	1356.675	1356.993	2	2	shared(3)	1	0.9935
GAHYYAYQLLQEA	47.42	54.6268	1525.72	1526.065	1	2	distinct	0	0.8959
NTVDFTNVEFGWR	45.83	54.7821	1583.737	1584.768	3	2	distinct	0	0.8799
IISGPGLATIYEFLAK	95.06	54.6159	1691.95	1692.384	32	2	shared(3)	0	0.9986
TNELCNQTLEIFVGAYGR	96.66	53.5559	2084	2084.793	8	2	shared(3)	0	0.9989

The equivalent proteins include

jgi|Physo1_1|138629|estExt_fgenesh1_pg.C_650048	0	No title.

323. Group probability: 1.0000. Peptides of the group

VVAFLHAPGAQSGLSR	70.74	54.5591	1608.874	1609.185	6	2	distinct	0	0.9879
HLYVTSLFPTSDPPLPPTR	44.52	53.2808	2137.121	2137.61	1	2	distinct	0	0.8944
IMHSGSEDPTGDAAEEDHRYPFAGAANPK	60.11	51.2167	3069.352	3070.173	2	3	distinct	1	0.9778

The equivalent proteins include

jgi|Physo1_1|140047|estExt_fgenesh1_pg.C_810036	0	No title.

324. Group probability: 1.0000. Peptides of the group

DKPITMNNHEMGITPER	86.22	53.8248	1981.935	1982.366	5	2	distinct	0	0.997
FNQYSSLTDFYTVLATNVDR	70.64	52.9315	2353.123	2353.37	2	2	distinct	0	0.9898

The equivalent proteins include

jgi|Physo1_1|108369|estExt_fgenesh1_pm.C_70014	0	No title.

325. Group probability: 1.0000. Peptides of the group

IIGADHPTLSAR	59.03	55.2977	1249.678	1250.525	2	2	distinct	0	0.9605
FAGQFGNDTHGDALQK	101.51	54.4989	1704.786	1705.393	2	2	distinct	0	0.9992

The equivalent proteins include

jgi|Physo1_1|136766|estExt_fgenesh1_pg.C_480045	0	No title.

326. Group probability: 1.0000. Peptides of the group

KGAALHALK	53.62	55.669	907.56	908.627	1	2	distinct	1	0.9294

VLQEIQSDPSKINEHIK	56.46	53.7381	1977.053	1978.335	2	3	distinct	1	0.9092
SAAYLSLDDAAHALEDAELCIETKPDWAK	76.75	50.884	3202.513	3203.87	1	3	distinct	0	0.9949

The equivalent proteins include

jgi|Physo1_1|140327|estExt_fgenesh1_pg.C_840054	0	No title.

327. Group probability: 1.0000. Peptides of the group

RPTTAEAIAHAK	61.84	55.1691	1264.689	1265.607	5	+2,+3	distinct	0	0.998
KGVNLPGLIVELPALSEK	66.04	54.0985	1876.103	1877.438	1	2	distinct	1	0.9832

The equivalent proteins include

jgi|Physo1_1|108888|estExt_fgenesh1_pm.C_390004	0	No title.

328. Group probability: 1.0000. Peptides of the group

KGGFIMIK	58.35	55.8262	892.52	893.447	2	2	distinct	1	0.847
CNFTALDIFTNK	68.97	54.9854	1442.686	1443.695	3	2	distinct	0	0.9797
EDIKLPTFPETFADEIR	70.85	54.0419	2020.015	2020.401	1	2	distinct	1	0.9886

The equivalent proteins include

jgi|Physo1_1|155602|C_scaffold_6000033	0	No title.

329. Group probability: 1.0000. Peptides of the group

RNPYSWTER	44.92	55.2009	1207.573	1207.957	1	2	distinct	1	0.85
QVGPFAFQQVYEAGHMVPLDQPK	74.18	52.3965	2585.274	2585.768	5	2	distinct	0	0.9933
EVGDDMFHFLQDFFQAKPEYQK	57.81	52.1932	2718.242	2719.477	2	3	distinct	0	0.9644

The equivalent proteins include

jgi|Physo1_1|109077|estExt_fgenesh1_pm.C_580002	0	No title.

330. Group probability: 1.0000. Peptides of the group

RNDGIHIINVGK	83.54	55.197	1334.742	1335.536	9	2	distinct	1	0.9907
FAQHTGCQAIASR	60.66	55.0505	1445.683	1446.108	5	+1,+2	distinct	0	0.9961

The equivalent proteins include

jgi|Physo1_1|109027|estExt_fgenesh1_pm.C_540001	0	No title.

331. Group probability: 1.0000. Peptides of the group

IGSVVAPTPAHAAEIKR	50.06	54.371	1715.968	1716.747	1	2	distinct	1	0.9287
SVQPGGWRPGGTLTQYK	53.69	54.0724	1830.938	1831.708	5	2	distinct	0	0.9485
SYIETHCPDDHTIIIDESMQPWVGPQWR	69.35	50.4461	3409.55	3410.542	1	3	distinct	0	0.9899

The equivalent proteins include

jgi|Physo1_1|135234|estExt_fgenesh1_pg.C_370003	0	No title.

332. Group probability: 1.0000. Peptides of the group

HLVFQGGSVLADLMK	88.74	54.7063	1613.86	1615.013	4	2	distinct	0	0.9974
NIVLSGGSSMYPGLPSRLEK	66.66	53.3253	2104.099	2104.745	1	2	distinct	1	0.9854

The equivalent proteins include

jgi|Physo1_1|109297|estExt_fgenesh1_pm.C_860004	0	No title.

333. Group probability: 1.0000. Peptides of the group

LNRPPVNSLNTALIQELDATIK	89.46	52.706	2419.343	2419.829	10	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|134968|estExt_fgenesh1_pg.C_350020	0	No title.

334. Group probability: 1.0000. Peptides of the group

GLVDHGLSLPK	56.18	55.7316	1134.64	1135.954	2	2	distinct	0	0.947
RNPDFDIPLEEAIKP	56.01	54.1729	1752.905	1753.841	3	2	distinct	1	0.9548
SPESDVFVAAPIIEAAKGESAYPAINLTWDGK	62.48	50.5952	3345.677	3346.97	1	3	distinct	1	0.984

The equivalent proteins include

jgi|Physo1_1|132215|estExt_fgenesh1_pg.C_190165	0	No title.

335. Group probability: 1.0000. Peptides of the group

AIAPFRDEDTLILCSGQATHNLR	59.9	52.4166	2597.302	2598.694	1	3	distinct	1	0.9713
ANRDPNSPIMDWAAAFQGWLDNTLTAESK (00000000001000000000000000000)	91.5	50.8598	3218.509	3219.993	8	3	distinct	1	0.9986

The equivalent proteins include

jgi|Physo1_1|129924|estExt_fgenesh1_pg.C_90201	0	No title.

336. Group probability: 1.0000. Peptides of the group

TIRPDSSVHSFK	51.82	55.2442	1372.71	1373.333	2	2	distinct	0	0.9257
LEDELPVHYFTMAHNR	59.92	53.7142	1970.931	1971.568	1	2	distinct	0	0.9693
LTLGPWSHVGVDNADPFAVSK	63.79	53.2502	2209.117	2209.732	1	2	distinct	0	0.9819

The equivalent proteins include

jgi|Physo1_1|140714|estExt_fgenesh1_pg.C_880086	0	No title.

337. Group probability: 1.0000. Peptides of the group

VNFYHTGPNGER	47.65	55.3159	1389.642	1389.958	1	2	distinct	0	0.8928
WWNDDHAAANQTEAMR	86.12	53.8677	1914.807	1914.971	2	2	distinct	0	0.9969
QQISPWHDIPLYNPDGTVNFICEIPK	40.59	51.5862	3080.507	3081.87	1	3	distinct	0	0.8619

The equivalent proteins include

jgi|Physo1_1|138692|estExt_fgenesh1_pg.C_660011	0	No title.

338. Group probability: 1.0000. Peptides of the group

VSRPLAQTIAAK	64.2	55.2393	1253.746	1254.823	3	2	distinct	0	0.9749
IVTGDASQAWHALCR	98.41	54.3258	1683.815	1684.212	11	+2,+3	shared(2)	0	0.9999
MGRPMWYSTCPNPADR	55.96	53.777	1937.833	1937.898	1	2	shared(2)	0	0.9565

The equivalent proteins include

jgi|Physo1_1|138900|estExt_fgenesh1_pg.C_670102	0	No title.

339. Group probability: 1.0000. Peptides of the group

IAMQAFDITRPPVAIGAVGLAR(0001000000000000000000)	77.18	53.5049	2266.262	2265.802	5	+2,+3	distinct	0	0.9994
GITFEDVVVPEENVLGDPGYGFK	45.93	52.5791	2480.211	2481.285	2	2	distinct	0	0.9202

The equivalent proteins include

jgi|Physo1_1|114335|estExt_Genewise1.C_190173	0	No title.

340. Group probability: 1.0000. Peptides of the group

LMGINHTR	49.78	56.006	940.491	941.059	1	2	distinct	0	0.9004
VPTPNVSLAILNLQLDPTKAEGITK	76.44	52.2552	2631.485	2632.961	6	+2,+3	distinct	1	0.9995

The equivalent proteins include

jgi|Physo1_1|108355|estExt_fgenesh1_pm.C_60045	0	No title.

341. Group probability: 0.9999. Peptides of the group

GLSGEHLTVAQLVHNAAFQK	85.9	53.2955	2119.117	2119.701	2	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|141307|estExt_fgenesh1_pg.C_960071	0	No title.

342. Group probability: 0.9999. Peptides of the group

KDIFLNSMFDK	79.97	55.2572	1356.675	1356.993	2	2	shared(3)	1	0.9935
GAHFYAYQLLHQ	63.5	55.0488	1446.704	1447.697	5	2	distinct	0	0.9734
IISGPGLATIYEFLAK	95.06	54.6159	1691.95	1692.384	32	2	shared(3)	0	0.9986
TNELCNQTLEIFVGAYGR	96.66	53.5559	2084	2084.793	8	2	shared(3)	0	0.9989

The equivalent proteins include

jgi|Physo1_1|138625|estExt_fgenesh1_pg.C_650044	0	No title.

343. Group probability: 0.9999. Peptides of the group

VFSPHVLNLTLVDLPGITK	90.72	53.4476	2062.183	2063.219	5	2	distinct	0	0.9982
LEQPGLQCVDLVFDELQR	57.84	53.2483	2158.073	2158.333	1	2	distinct	0	0.966

The equivalent proteins include

jgi|Physo1_1|109490|estExt_fgenesh1_pm.C_1190003	0	No title.

344. Group probability: 0.9999. Peptides of the group

TTPEVLAHLNANR	63.5	54.7537	1434.758	1435.296	2	2	distinct	0	0.9745
NLSAAAHLIHGSSEGR	88.71	54.543	1618.817	1619.443	7	2	distinct	0	0.9975

The equivalent proteins include

jgi|Physo1_1|141649|estExt_fgenesh1_pg.C_1010062	0	No title.

345. Group probability: 0.9999. Peptides of the group

KVAGLYQK	50.12	56.4737	905.533	905.769	1	2	distinct	1	0.9024
SYLPDEIQAIQRPLEFYVSDK	44.19	52.5073	2510.269	2510.881	1	2	distinct	0	0.9004
SYLPDEIQAIQRPLEFYVSDKVVEAEK	74.55	51.2523	3165.623	3166.843	4	3	distinct	1	0.9933

The equivalent proteins include

jgi|Physo1_1|155238|C_scaffold_1000042	0	No title.

346. Group probability: 0.9999. Peptides of the group

SASNIVFSNGLLDPWSSAGVLHAPK	82.96	52.4412	2566.318	2567.758	3	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|142831|estExt_fgenesh1_pg.C_1220058	0	No title.

347. Group probability: 0.9999. Peptides of the group

ILSTSLPAFNLNKR	55.94	54.7493	1572.899	1574.277	1	2	distinct	1	0.9523
ELNVGIIGPATVGGIKPGCLR	92.63	53.302	2120.177	2120.53	5	2	distinct	0	0.9986

The equivalent proteins include

jgi|Physo1_1|108913|estExt_fgenesh1_pm.C_420007	0	No title.

348. Group probability: 0.9999. Peptides of the group

IVLEVAQHLGENTVR	99.26	54.5673	1676.921	1677.82	61	+2,+3	shared(2)	0	0.9998
TLQDIIAILGMDELSEDDKLTVAR	75.85	52.3988	2658.379	2657.719	20	2	distinct	1	0.9944

The equivalent proteins include

gi|46909245|gb|AAT06140.1|	45884.78	ATP synthase beta subunit [Eucidaris tribuloides]

349. Group probability: 0.9999. Peptides of the group

KVPAVYETAHTR	66.91	55.295	1370.731	1371.36	3	2	distinct	1	0.9802
YPSAININWYGVLPGNWGPR	82.68	53.4052	2273.138	2274.14	1	2	distinct	0	0.9964

The equivalent proteins include

jgi|Physo1_1|130440|estExt_fgenesh1_pg.C_110109	0	No title.

350. Group probability: 0.9999. Peptides of the group

SHVIVLPGGK	67.64	56.12	1005.597	1005.447	9	+1,+2	distinct	0	0.9971
VGQIEHNISPQDSVSK	62.31	54.164	1736.869	1737.222	3	2	distinct	0	0.9749

The equivalent proteins include

jgi|Physo1_1|140949|estExt_fgenesh1_pg.C_920012	0	No title.

351. Group probability: 0.9999. Peptides of the group

TVYHLNPSGR	45.36	55.8086	1142.583	1143.591	1	2	distinct	0	0.8579
NFDLRPGMIQK	49.48	55.3853	1317.686	1318.266	2	2	distinct	0	0.9043
FVIGGPHGDAGLTGR	79.38	54.8325	1452.747	1454.065	9	2	distinct	0	0.9941

The equivalent proteins include

gi|23394401|gb|AAN31489.1|	43150.8	S-adenosyl methionine synthetase [Phytophthora infestans]
jgi|Physo1_1|108486|estExt_fgenesh1_pm.C_110017	0	No title.

352. Group probability: 0.9999. Peptides of the group

SYELPDGNVIVIGDER	89.05	54.2914	1774.874	1774.202	1	2	distinct	0	0.9686
DLYCNIVLSGGTTMYPGIGER	47.6	53.1241	2315.093	2315.776	1	2	shared(2)	0	0.9252
KDLYCNIVLSGGTTMYPGIGER (0000000000000000100000000)	89.96	52.8441	2443.187	2444.683	11	2	shared(2)	1	0.9983
TTGCVLDSGDGVSHTVPIYEGYALPHAIVR	72.64	50.9575	3183.566	3184.46	9	+2,+3	shared(3)	0	0.9878

The equivalent proteins include

gi|57864652|gb|AAW56946.1|	29368.75	actin [Apodachlya brachynema]

353. Group probability: 0.9999. Peptides of the group

ARLECQSYR	52.09	55.4534	1181.561	1182.72	2	2	distinct	1	0.9196
AITVFSPDGHLFQVEYAMEAVK	95.64	52.5984	2451.214	2451.977	4	2	distinct	0	0.9989

The equivalent proteins include

jgi|Physo1_1|140976|estExt_fgenesh1_pg.C_920039	0	No title.

354. Group probability: 0.9999. Peptides of the group

LQGYGYDHLILK	49.25	54.9365	1418.756	1420.136	1	2	distinct	0	0.9075
LEWAKPSNKPANEDAGSMGTTFR	59.2	52.4856	2506.191	2507.207	4	+2,+3	distinct	0	0.999

The equivalent proteins include

jgi|Physo1_1|108333|estExt_fgenesh1_pm.C_60023	0	No title.

355. Group probability: 0.9999. Peptides of the group

VPPAAADCPSVAHVGPIAGSVR	52.69	53.3578	2127.089	2128.325	2	3	distinct	0	0.9429
KFAASIPDLPLYYPYLDPK	50.69	53.2726	2210.166	2211.274	1	2	distinct	1	0.9386
AAGAIILGTTNMHEVGSGVTGYNMHYGTAR	57.61	51.4768	3048.454	3049.597	1	3	distinct	0	0.9731

The equivalent proteins include

jgi|Physo1_1|139844|estExt_fgenesh1_pg.C_790023	0	No title.

356. Group probability: 0.9999. Peptides of the group

YIWLGDFYHTTR	64.84	54.9768	1570.757	1571.06	7	2	distinct	0	0.9764
KLALGSAPTIASTDYTK	81.95	54.1461	1735.936	1736.387	5	2	distinct	1	0.9957

The equivalent proteins include

jgi|Physo1_1|127729|estExt_fgenesh1_pg.C_20305	0	No title.

357. Group probability: 0.9999. Peptides of the group

SDIISLHCPLFPSTK	74.74	54.3124	1713.876	1715.263	1	2	distinct	0	0.9912
VPAYSPYAVAEHAATLMMTLNR	77.54	52.6957	2405.187	2406.511	3	3	distinct	0	0.9883

The equivalent proteins include

jgi|Physo1_1|109081|estExt_fgenesh1_pm.C_580006	0	No title.

358. Group probability: 0.9999. Peptides of the group

NSWSTHWGEDGYVK	60.23	54.5382	1664.722	1665.132	2	2	distinct	0	0.9674
NAPDYCHFNANNAIGR	85.82	54.0941	1832.801	1833.363	6	2	distinct	0	0.9968

The equivalent proteins include

jgi|Physo1_1|140951|estExt_fgenesh1_pg.C_920014	0	No title.

359. Group probability: 0.9999. Peptides of the group

HELEQHALTK	57.58	55.6455	1204.62	1206.032	2	2	distinct	0	0.9515
IRPVPFFGAPCSDAAGGQVDYADVQR	88.11	51.8946	2792.334	2793.317	2	3	distinct	0	0.9978

The equivalent proteins include

jgi|Physo1_1|128818|estExt_fgenesh1_pg.C_50315	0	No title.
jgi|Physo1_1|128819|estExt_fgenesh1_pg.C_50316	0	No title.

360. Group probability: 0.9999. Peptides of the group

YCGKDNFHMR	55.9	55.3871	1326.56	1327.638	1	2	distinct	1	0.9441
ASVDAFPFVAHLVSDEKEQLSSEALEAAR	88.26	51.0981	3115.546	3116.407	2	3	distinct	1	0.9981

The equivalent proteins include

jgi|Physo1_1|109444|estExt_fgenesh1_pm.C_1080003	0	No title.

361. Group probability: 0.9999. Peptides of the group

ITMPNIHNNPIDLSR	95.57	54.3276	1733.888	1734.431	5	2	distinct	0	0.9986
RVLLETFAGPADAGVPSPAVQFTLYK	47.4	51.9959	2746.469	2747.691	1	3	distinct	1	0.9234

The equivalent proteins include

jgi|Physo1_1|158534|C_scaffold_114000011	0	No title.

362. Group probability: 0.9999. Peptides of the group

RPTIQGIWQPDLDFPEFK	74.23	53.4599	2186.116	2186.345	9	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|128268|estExt_fgenesh1_pg.C_40112	0	No title.

363. Group probability: 0.9999. Peptides of the group

ETHHVAGAAVR	54.14	55.7971	1146.589	1146.51	3	+1,+2	shared(2)	0	0.9946
RLTELIGAVGGK	63.93	55.5899	1212.719	1213.39	2	2	shared(2)	1	0.9741
ELIGTANQLAENNIDLLMPGFTHLQPAQPLR (000000000000000000100000000000000)	68.19	50.4775	3429.771	3429.395	12	3	distinct	0	0.99

The equivalent proteins include

gi|23394365|gb|AAN31472.1|	50896.16	argininosuccinate lyase [Phytophthora infestans]

364. Group probability: 0.9999. Peptides of the group

KILFVLGGPGAGK	60.34	55.7537	1255.765	1256.776	1	2	distinct	1	0.9657
FGFVHLSAGDLLR	86.24	55.0477	1430.767	1431.178	7	2	distinct	0	0.9965

The equivalent proteins include

jgi|Physo1_1|109056|estExt_fgenesh1_pm.C_550009	0	No title.

365. Group probability: 0.9999. Peptides of the group

IFSPDHPEAPVLR	52.34	54.8162	1476.772	1477.411	5	2	distinct	0	0.9321
VAWTRPIFETLEPVWNEK	69.03	53.1568	2214.147	2214.631	16	+2,+3	distinct	0	0.9981

The equivalent proteins include

jgi|Physo1_1|139685|estExt_fgenesh1_pg.C_770024	0	No title.

366. Group probability: 0.9999. Peptides of the group

LTVSILDLVQQATNYK	85.92	54.252	1804.993	1805.757	5	2	distinct	0	0.9968
ACGVSRPVISASITSNDASQLGPQIQSMR (0000000000000000000000000000100)	53.21	51.2445	3029.502	3030.737	14	3	distinct	0	0.9592

The equivalent proteins include

jgi|Physo1_1|108166|estExt_fgenesh1_pm.C_10031	0	No title.

367. Group probability: 0.9999. Peptides of the group

VLGGEGGHGVIILSPR	90.86	54.7579	1559.878	1560.568	3	2	distinct	0	0.9979
QGVLVMNTPFGNTLSAAELTLGLISAVSR	48.39	51.3959	2958.585	2959.809	1	3	distinct	0	0.9376

The equivalent proteins include

jgi|Physo1_1|142688|estExt_fgenesh1_pg.C_1190058	0	No title.

368. Group probability: 0.9999. Peptides of the group

RIDAISR	51.57	57.2891	829.477	830.829	1	2	shared(2)	1	0.826
YEPVGVVAAIIPWNYPALMALWK	44.25	52.3107	2600.386	2600.772	3	2	distinct	0	0.9081
YIDVVNPATEEVIQQVAAASAADVDLAVQAAKR	76.36	50.3501	3424.784	3426.136	1	3	distinct	1	0.9954

The equivalent proteins include

jgi|Physo1_1|108817|estExt_fgenesh1_pm.C_340017	0	No title.

369. Group probability: 0.9999. Peptides of the group

IAYVHSLKEEAIK	48.94	55.0613	1499.835	1500.569	1	2	distinct	1	0.9081
ESLNLSIVEAINQASEAWGIK	92.8	53.0964	2271.175	2271.854	8	2	distinct	0	0.9986

The equivalent proteins include

gi|23394406|gb|AAN31491.1|	40884.22	unknown [Phytophthora infestans]
jgi|Physo1_1|108840|estExt_fgenesh1_pm.C_350008	0	No title.

370. Group probability: 0.9999. Peptides of the group

GTKPAGFILNPELFMR	53.71		54.2071	1789.955	1790.475	1	2	distinct	0	0.9465
RHVDEDDNAAAEGSTQPQDEPPEAPSPAK	84.69		51.1258	3057.355	3058.052	1	3	distinct	1	0.9974

The equivalent proteins include

jgi|Physo1_1|136250|estExt_fgenesh1_pg.C_440051	0	No title.

371. Group probability: 0.9999. Peptides of the group

GPQKGEDLTHPLK	49.47		54.9756	1418.752	1419.245	2	2	distinct	1	0.9124
HIAPGMVQQMQSVCPDCR	92.58		53.3891	2112.933	2114.179	5	2	distinct	0	0.9984

The equivalent proteins include

jgi|Physo1_1|109267|estExt_fgenesh1_pm.C_820001	0	No title.

372. Group probability: 0.9999. Peptides of the group

SHMQYWQFGIK (0001000000000)	58.35		54.873	1423.671	1424.332	2	2	distinct	0	0.9569
KAGKPVVLEEYGIK	86.15		55.2074	1529.882	1530.863	6	2	distinct	1	0.9966

The equivalent proteins include

jgi|Physo1_1|130996|estExt_fgenesh1_pg.C_130187	0	No title.

373. Group probability: 0.9999. Peptides of the group

KIWLDPNESNEIALANSR	95.33		53.7019	2069.054	2069.951	4	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|109394|estExt_fgenesh1_pm.C_980010	0	No title.

374. Group probability: 0.9998. Peptides of the group

IAKPSVDMNSHQR	51.47		54.6177	1481.741	1482.252	1	2	distinct	0	0.927
LQIWGLSGGGNPACRPPK	89.87		54.0276	1906.984	1907.597	1	2	distinct	0	0.9979

The equivalent proteins include

jgi|Physo1_1|157072|C_scaffold_34000036	0	No title.

375. Group probability: 0.9998. Peptides of the group

VCLIGDGQVSLGHTVVKPNAK	85.11		53.7638	2191.178	2192.318	4	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|120016|estExt_Genewise1.C_700075	0	No title.

376. Group probability: 0.9998. Peptides of the group

VIMATNAIESLDPALIRPGR	84.99		53.2662	2136.172	2137.474	1	3	distinct	0	0.9964
EAVELPLTHPELYEGIGIRPPK	55.41		52.643	2457.327	2458.578	1	3	distinct	0	0.9557

The equivalent proteins include

jgi|Physo1_1|108382|estExt_fgenesh1_pm.C_70027	0	No title.

377. Group probability: 0.9998. Peptides of the group

QVHPETGISKR	45.47		55.4787	1250.673	1251.306	1	2	distinct	1	0.8651
RVESYSTYIYK	45.73		54.94	1407.703	1408.053	1	2	distinct	1	0.8695
GMSIMNSFINDIFER	91.12		54.2912	1772.823	1773.621	5	2	distinct	0	0.9908

The equivalent proteins include

jgi|Physo1_1|108804|estExt_fgenesh1_pm.C_340004	0	No title.
jgi|Physo1_1|108813|estExt_fgenesh1_pm.C_340013	0	No title.

378. Group probability: 0.9998. Peptides of the group

LTHTGFTHTGPCEVWCDDTK	78.06		52.8575	2361.015	2361.493	13	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|131638|estExt_fgenesh1_pg.C_160182	0	No title.

379. Group probability: 0.9998. Peptides of the group

AQSSHQMVLKPK	52.96		55.0992	1352.723	1353.869	1	2	distinct	0	0.933
AYFQQLLKPESVLTDADDTEPYTVDWLKK	85.14		50.4183	3412.708	3414.135	2	3	distinct	1	0.9976

The equivalent proteins include

jgi|Physo1_1|108284|estExt_fgenesh1_pm.C_40035	0	No title.

380. Group probability: 0.9998. Peptides of the group

HIEENPEFLQPEVR	62.62		54.1644	1735.853	1736.581	1	2	distinct	0	0.9738
IAQTAEAAGVTPQQLVDKYAGIFQQLTK	74.86		51.3717	2988.592	2990.073	3	3	distinct	1	0.9937

The equivalent proteins include

jgi|Physo1_1|158682|C_scaffold_127000002	0	No title.

381. Group probability: 0.9998. Peptides of the group

RVLIVGGGDGGVLR	74.95		55.0343	1366.804	1367.928	4	2	distinct	1	0.9507
YYSAQIHEAAFVLPAFAER	82.61		53.2452	2182.085	2183.357	14	2	distinct	0	0.9963

The equivalent proteins include

jgi|Physo1_1|109524|estExt_fgenesh1_pm.C_1260004	0	No title.							
382. Group probability: 0.9998. Peptides of the group									
LGALPHGGGGIGLER	54.78	55.1807	1402.768	1404.245	11	+2,+3	distinct	0	0.9962
AAAAAAGPTLTDTYGELPLIQSQERPNK	51.46	51.6655	2882.477	2883.525	2	3	distinct	0	0.9503
The equivalent proteins include									
jgi|Physo1_1|108386|estExt_fgenesh1_pm.C_70031	0	No title.							
383. Group probability: 0.9998. Peptides of the group									
SFDLVVIPGGMPGAEHLR	84.43	53.9269	1893.977	1894.831	11	+2,+3	distinct	0	0.9998
The equivalent proteins include									
jgi|Physo1_1|142787|estExt_fgenesh1_pg.C_1220014	0	No title.							
384. Group probability: 0.9998. Peptides of the group									
KGGSSFLQR	73.94	55.5785	978.525	979.138	4	2	distinct	1	0.9264
QIQSSVGSLKDEMIAQNAALSK	54.16	52.9259	2317.195	2318.557	2	+2,+3	distinct	1	0.9972
The equivalent proteins include									
jgi|Physo1_1|155469|C_scaffold_4000037	0	No title.							
385. Group probability: 0.9998. Peptides of the group									
LVNSEHVGLIHVK	68.51	54.9991	1443.82	1444.229	2	2	distinct	0	0.9835
MTNPVNVEFISDKLTQFLR	68.83	53.5364	2251.167	2252.026	2	2	distinct	1	0.9874
The equivalent proteins include									
jgi|Physo1_1|134211|estExt_fgenesh1_pg.C_300122	0	No title.							
386. Group probability: 0.9998. Peptides of the group									
HAVEDVKDVAAK	77.92	55.193	1280.672	1281.49	2	2	distinct	1	0.9925
QEEHVVWNAAPKPNATTTEK	59.13	53.1666	2249.108	2249.555	3	2	distinct	0	0.9718
The equivalent proteins include									
jgi|Physo1_1|129292|estExt_fgenesh1_pg.C_70117	0	No title.							
387. Group probability: 0.9998. Peptides of the group									
NADLKPHQQLVTSEPCVR	79.43	53.4117	2091.053	2091.497	1	2	distinct	0	0.9949
TPEVLQLSVDHKPDLEFEK	57.4	53.1847	2223.142	2224.152	1	3	distinct	0	0.9581
The equivalent proteins include									
jgi|Physo1_1|108204|estExt_fgenesh1_pm.C_20036	0	No title.							
388. Group probability: 0.9998. Peptides of the group									
KGMDVLTSHPR	80.69	55.2219	1239.639	1240.49	3	2	distinct	1	0.9939
MELSLHGQGSHR	60.3	55.1382	1350.646	1351.577	2	2	distinct	0	0.9648
The equivalent proteins include									
jgi|Physo1_1|155940|C_scaffold_9000120	0	No title.							
389. Group probability: 0.9998. Peptides of the group									
QRPLHMSYDIDAVDPLVAPSTGTR	52.51	52.2173	2638.317	2639.345	1	3	distinct	0	0.9472
NALLSLPHAVSVIGAPMTYGQPLLGTDGGPDLLR	77.21	50.411	3442.828	3443.719	2	3	distinct	0	0.9959
The equivalent proteins include									
jgi|Physo1_1|141130|estExt_fgenesh1_pg.C_940041	0	No title.							
390. Group probability: 0.9998. Peptides of the group									
FAAHDVLR	48.68	56.7164	927.493	928.221	1	2	distinct	0	0.8887
SHLHDLEEK	46.67	55.3924	1106.536	1107.121	2	2	distinct	0	0.8708
LSSAGLVYNHFGR	69.47	54.9217	1419.726	1420.464	8	2	distinct	0	0.9849
The equivalent proteins include									
jgi|Physo1_1|108501|estExt_fgenesh1_pm.C_120011	0	No title.							
391. Group probability: 0.9998. Peptides of the group									
DMVVLPGFVDAHTHPVWSGNR (00100000000000000000000)	83.76	52.856	2333.137	2333.835	5	+2,+3	distinct	0	0.9998
The equivalent proteins include									
jgi|Physo1_1|109335|estExt_fgenesh1_pm.C_920001	0	No title.							
392. Group probability: 0.9998. Peptides of the group									
LFADVNIQPLHLK	76.23	54.7472	1506.856	1506.986	8	2	distinct	0	0.9917
HCQPETCTLCPGDMATTTCCIPLKGGR	58.6	51.1158	3120.338	3121.296	1	3	distinct	1	0.9728
The equivalent proteins include									
jgi|Physo1_1|156853|C_scaffold_30000028	0	No title.							
393. Group probability: 0.9998. Peptides of the group									
IIGHGDNIYWNGAGPDDIDYR	91.18	52.8783	2360.082	2360.561	4	+2,+3	distinct	0	0.9998
The equivalent proteins include									
jgi|Physo1_1|130258|estExt_fgenesh1_pg.C_100216	0	No title.							
394. Group probability: 0.9998. Peptides of the group									

TLYTPSVSGIVDVLHVDIGADDSAK	111.16	52.5088	2571.307	2572.386	2	2	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|137030|estExt_fgenesh1_pg.C_500066	0	No title.

395. Group probability: 0.9998. Peptides of the group

YISELHANAVNAYHDK	73.26	54.2424	1843.885	1844.443	1	2	distinct	0	0.9904
YISELHANAVNAYHDKK	61.63	53.6928	1971.98	1972.306	2	2	distinct	1	0.9745

The equivalent proteins include

jgi|Physo1_1|130818|estExt_fgenesh1_pg.C_130009	0	No title.

396. Group probability: 0.9997. Peptides of the group

AVLTCKPEYAYGASGSPPK	74.69	53.7686	1994.977	1995.387	1	2	distinct	0	0.9924
AVLTCKPEYAYGASGSPPKIPANATLK	55.74	51.7967	2803.458	2804.813	3	3	distinct	1	0.9646

The equivalent proteins include

jgi|Physo1_1|121523|estExt_Genewise1.C_930008	0	No title.

397. Group probability: 0.9997. Peptides of the group

TKPFPWPESNCDLLDFDCK	69.17	52.9385	2368.05	2368.213	14	+2,+3	distinct	0	0.9997

The equivalent proteins include

jgi|Physo1_1|157932|C_scaffold_70000016	0	No title.

398. Group probability: 0.9997. Peptides of the group

FHAAPFAEFAMLESR	59.09	54.2272	1722.819	1723.621	3	3	distinct	0	0.9575
YVDEHFGGPAVLAPAANRPEIK	49.21	53.0327	2350.207	2350.567	4	+2,+3	distinct	0	0.9931

The equivalent proteins include

jgi|Physo1_1|145035|estExt_fgenesh1_pg.C_4180004	0	No title.

399. Group probability: 0.9997. Peptides of the group

IRLENEIQTYR	55.92	54.8709	1433.763	1434.654	3	2	shared(2)	1	0.9467
YCVQLSQIQAQISALEEQLQQIR	92.55	52.0118	2745.412	2745.865	6	2	distinct	0	0.9987

The equivalent proteins include

gi|307086|gb|AAA59468.1|	46472.64	keratin-10
gi|109115260|ref|XP_001100571.1|	62234.46	PREDICTED: similar to keratin 10 isoform 2 [Macaca mulatta]
gi|109115262|ref|XP_001100664.1|	57718.17	PREDICTED: similar to keratin 10 isoform 3 [Macaca mulatta]
gi|109115264|ref|XP_001100476.1|	56875.85	PREDICTED: similar to keratin 10 isoform 1 [Macaca mulatta]
gi|547749|sp|P13645|K1C10_HUMAN	59710.96	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)
gi|55645505|ref|XP_523631.1|	94764.75	PREDICTED: similar to keratin 25D; type I inner root sheath specific keratin 25 irs4 [Pan troglodyt
gi|186629|gb|AAA59199.1|	39832.12	keratin 10
gi|40354192|ref|NP_000412.2|	59019.73	keratin 10 [Homo sapiens]

400. Group probability: 0.9997. Peptides of the group

SMHQGHTAAGQGETSTTQQSAGATR	111.06	52.6421	2499.116	2500.441	6	3	distinct	0	0.9997

The equivalent proteins include

jgi|Physo1_1|145389|estExt_fgenesh1_pg.C_11390001	0	No title.

401. Group probability: 0.9997. Peptides of the group

ALGWNGHVAGTR	69.86	55.1258	1237.632	1238.288	6	2	distinct	0	0.9848
VEWLLQEGDEVKPSSVPGGKVPVAR	63.06	52.1079	2675.428	2676.475	3	3	distinct	1	0.9798

The equivalent proteins include

jgi|Physo1_1|158900|C_scaffold_173000011	0	No title.

402. Group probability: 0.9997. Peptides of the group

KIAVNLIPFPR	70.88	55.3512	1266.781	1267.527	5	2	shared(6)	1	0.9855
GHYTEGAELIDSVLDVVR	50.71	53.7106	1971.99	1972.76	1	2	shared(5)	0	0.7948
SGPFGQIFRPDNFVFGQTGAGNNWAK	79.99	52.2124	2811.352	2812.533	9	+2,+3	distinct	0	0.9989

The equivalent proteins include

gi|65428041|gb|AAY42541.1|	43730.52	beta-tubulin [Micromonas pusilla]
gi|65428055|gb|AAY42548.1|	43765.39	beta-tubulin [Micromonas pusilla]
gi|65428067|gb|AAY42554.1|	43753.39	beta-tubulin [Micromonas pusilla]
gi|65428069|gb|AAY42555.1|	43749.39	beta-tubulin [Micromonas pusilla]

403. Group probability: 0.9997. Peptides of the group

VFCMHGGLSPSIDTLDHAR	77.01	53.4613	2111.988	2112.481	3	2	distinct	0	0.9939
YFTDLFDHLPMTALIENR	52.74	53.2648	2195.072	2195.136	2	2	distinct	0	0.9468

The equivalent proteins include

gi|23394371|gb|AAN31475.1|	37225.02	serine/threonine protein phosphatase [Phytophthora infestans]

jgi|Physo1_1|109080|estExt_fgenesh1_pm.C_580005	0	No title.

404. Group probability: 0.9997. Peptides of the group

VAVHEPTLHPNSEELIIGK	57.65	53.5168	2082.111	2082.786	1	2	distinct	0	0.9665
ELDTLLGYDELANVPFLVLGNK	70.07	52.5533	2432.284	2433.759	2	2	distinct	0	0.9901

The equivalent proteins include

gi|23394386|gb|AAN31482.1|	22024.34	GTP binding protein [Phytophthora infestans]
jgi|Physo1_1|109427|estExt_fgenesh1_pm.C_1040002	0	No title.

405. Group probability: 0.9997. Peptides of the group

FAADVVAPHAR	63.01	55.2021	1152.604	1154.096	1	2	distinct	0	0.9712
VDPVVGLLCDLQNTVVNNVFLVHGSQAQK	67.39	51.3359	3162.649	3164.003	5	3	distinct	0	0.9882

The equivalent proteins include

jgi|Physo1_1|109319|estExt_fgenesh1_pm.C_900005	0	No title.

406. Group probability: 0.9997. Peptides of the group

LQVLTAPHPVFTR	59.59	54.741	1477.84	1478.286	4	2	distinct	0	0.9641
RVGPGFIQQFQTTCDK	73.12	54.0388	1880.92	1881.363	1	2	distinct	1	0.9903

The equivalent proteins include

jgi|Physo1_1|140557|estExt_fgenesh1_pg.C_870004	0	No title.

407. Group probability: 0.9996. Peptides of the group

MYLHDHEQFLSTAR	73.87	54.2546	1746.815	1747.538	1	2	distinct	0	0.9902
IWHPNISSQTGAICLDILK	56.65	53.2999	2165.13	2165.992	1	2	distinct	0	0.9636

The equivalent proteins include

jgi|Physo1_1|136669|estExt_fgenesh1_pg.C_470083	0	No title.
jgi|Physo1_1|142734|estExt_fgenesh1_pg.C_1210001	0	No title.
jgi|Physo1_1|143955|estExt_fgenesh1_pg.C_1590030	0	No title.

408. Group probability: 0.9996. Peptides of the group

HGVYSWPLCGNAPDALDHGVAAAGYGVYK	107.03	51.2263	3044.424	3045.78	1	3	distinct	0	0.9996

The equivalent proteins include

gi|66270081|gb|AAY43370.1|	42024.12	cathepsin-like cysteine protease [Phytophthora infestans]
jgi|Physo1_1|108512|estExt_fgenesh1_pm.C_130003	0	No title.

409. Group probability: 0.9996. Peptides of the group

GGHIPGSLNVPFGK	46.6	55.0558	1378.736	1379.46	1	2	distinct	0	0.8911
YFGHDSVHILNGGITK	85.33	54.223	1756.89	1757.615	5	2	distinct	0	0.9967

The equivalent proteins include

jgi|Physo1_1|144222|estExt_fgenesh1_pg.C_1730012	0	No title.

410. Group probability: 0.9996. Peptides of the group

GPYASMYTAKPWTVR	76.41	54.3396	1726.85	1727.484	5	2	distinct	0	0.9924
TPEGIPIKPLYTQGDLEGLDVAQAPGTFPFTR	49.46	50.4551	3427.766	3428.978	4	3	distinct	0	0.9499

The equivalent proteins include

jgi|Physo1_1|108209|estExt_fgenesh1_pm.C_20041	0	No title.

411. Group probability: 0.9996. Peptides of the group

HIGGCDAVMALHAK	75.35	54.8914	1478.712	1479.416	8	+2,+3	distinct	0	0.9996

The equivalent proteins include

jgi|Physo1_1|135082|estExt_fgenesh1_pg.C_350134	0	No title.
jgi|Physo1_1|139165|estExt_fgenesh1_pg.C_700100	0	No title.

412. Group probability: 0.9996. Peptides of the group

VFSSSIFKPGFK	53.04	55.4165	1342.728	1343.431	2	2	distinct	0	0.933
MLAQLLEHGTTGAPIEEDPASHPLFK (01000000000000000000000000000)	76.84	51.8739	2801.406	2802.899	5	3	distinct	0	0.9942

The equivalent proteins include

jgi|Physo1_1|138999|estExt_fgenesh1_pg.C_690008	0	No title.

413. Group probability: 0.9996. Peptides of the group

KLLGMAGIEDCYTSAR	109.69	54.3187	1783.86	1785.246	1	2	distinct	1	0.9996

The equivalent proteins include

jgi|Physo1_1|109513|estExt_fgenesh1_pm.C_1230003	0	No title.

414. Group probability: 0.9996. Peptides of the group

RPETSFQAADR	65.26	55.5157	1276.616	1277.376	1	2	distinct	0	0.9762
SAPALAFGNSMVFKPSEETPLTALK	62.85	52.3666	2605.346	2606.745	1	2	distinct	0	0.9832

The equivalent proteins include

jgi|Physo1_1|157598|C_scaffold_53000023	0	No title.

415. Group probability: 0.9996. Peptides of the group

IPVVASSGAGKPEHFTEVFEK	64.34	53.2729	2228.148	2229.527	3	+2,+3	distinct	0	0.9996

The equivalent proteins include

jgi|Physo1_1|109060|estExt_fgenesh1_pm.C_550013	0	No title.

416. Group probability: 0.9996. Peptides of the group

FFDELPADNTIEATQYLTHVQAGTEPFQGK	44.52	50.5707	3366.604	3368.08	1	3	distinct	0	0.9169
KFFDELPADNTIEATQYLTHVQAGTEPFQGK	75.65	50.3293	3494.699	3495.464	6	3	distinct	1	0.9948

The equivalent proteins include

gi|49476326|gb|AAT66504.1|	26598.74	cell 12A endoglucanase [Phytophthora sojae]
jgi|Physo1_1|109281|estExt_fgenesh1_pm.C_840003	0	No title.

417. Group probability: 0.9995. Peptides of the group

CDDEGCHEALHSLVEDEVR	69.33	53.0223	2268.938	2270.266	4	+2,+3	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|137720|estExt_fgenesh1_pg.C_560094	0	No title.

418. Group probability: 0.9995. Peptides of the group

NNPPHILVGTPGR	69.27	55.2725	1370.742	1371.227	10	2	distinct	0	0.9845
LTLHGLQQYYIK	62.14	54.8351	1475.814	1476.534	9	2	distinct	0	0.9702

The equivalent proteins include

jgi|Physo1_1|108807|estExt_fgenesh1_pm.C_340007	0	No title.

419. Group probability: 0.9995. Peptides of the group

TTRPPEAPGAASVQPAVIGFDMGGTSTDVSR	103.45	51.2415	3071.498	3072.567	4	3	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|108268|estExt_fgenesh1_pm.C_40019	0	No title.

420. Group probability: 0.9995. Peptides of the group

HGIVSCSQPLASEIGLR	107.41	54.0425	1822.936	1823.532	2	2	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|109055|estExt_fgenesh1_pm.C_550008	0	No title.

421. Group probability: 0.9995. Peptides of the group

HGHTDQLYPEEALELQR	79.43	54.3219	2034.976	2034.876	5	+2,+3	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|128423|estExt_fgenesh1_pg.C_40267	0	No title.

422. Group probability: 0.9995. Peptides of the group

WTVLHEGTCSR	57.2	55.4374	1344.624	1345.372	5	+1,+2	distinct	0	0.9956
CVFDHENCNSGNK	46.95	54.7688	1579.614	1580.257	2	2	distinct	0	0.8912

The equivalent proteins include

gi|27922927|gb|AAO24652.1|	8659	unknown protein [Phytophthora sojae]

423. Group probability: 0.9995. Peptides of the group

RLDACSSLK	52.75	55.6995	1048.533	1049.64	1	2	distinct	1	0.9237
SACQSQLVHYR	52.91	55.252	1347.635	1347.992	2	2	distinct	0	0.9301
EVLPRPDLFNHCGQGFNQGK	45.77	53.0024	2312.112	2313.27	1	2	distinct	0	0.9092

The equivalent proteins include

jgi|Physo1_1|128351|estExt_fgenesh1_pg.C_40195	0	No title.

424. Group probability: 0.9995. Peptides of the group

VAVDAAVASSQPHNFLGLNEHGLASIVR	103.9	51.6434	2871.499	2872.958	1	3	distinct	0	0.9995

The equivalent proteins include

gi|23394399|gb|AAN31488.1|	41132.38	DAHP synthase [Phytophthora infestans]
jgi|Physo1_1|108202|estExt_fgenesh1_pm.C_20034	0	No title.
jgi|Physo1_1|109603|estExt_fgenesh1_pm.C_1630002	0	No title.

425. Group probability: 0.9995. Peptides of the group

HLGIMVGMNQK (0000000010000)	58.19	55.632	1242.621	1243.958	1	2	distinct	0	0.7894
SYELPDGNVIVIGNER	105.1	54.2914	1773.89	1774.202	1	2	shared(2)	0	0.9923
YPIEHGIVTNWDDMEK (0000000000001000)	89.61	53.9187	1945.888	1946.177	23	+2,+3	shared(4)	0	0.9983

VAPEEHPVLLTEAPINPK	81.4		53.7297	1953.057	1953.885	13	2	shared(10)	0	0.9887
TTGCVLDSGDGVSHTVPIYEGYALPHAIVR	72.64		50.9575	3183.566	3184.46	9	+2,+3	shared(3)	0	0.9878

The equivalent proteins include

gi|3181|emb|CAA33907.1|	42303.02	unnamed protein product [Phytophthora megasperma]
jgi|Physo1_1|108972|estExt_fgenesh1_pm.C_480001	0	No title.

426. Group probability: 0.9995. Peptides of the group

VLAAQPSKPATSGGQK	50.37		54.6824	1538.842	1539.455	3	2	distinct	0	0.9277
EHNIDLHDVEGTGPQGR	76.49		54.4456	1872.871	1873.198	1	2	distinct	0	0.993

The equivalent proteins include

jgi|Physo1_1|108462|estExt_fgenesh1_pm.C_100021	0	No title.

427. Group probability: 0.9995. Peptides of the group

TYLGRPGNNVK	44.9		55.6378	1217.652	1218.494	1	2	distinct	0	0.8577
LHIPAENFPFCTIDPNDAVVPLPDQR	49.54		51.3287	2974.465	2975.956	2	3	distinct	0	0.9373
FNWLVDKYQPASVVPPVISITDIAGLVR	49.75		51.5612	3096.701	3097.932	1	3	distinct	1	0.9424

The equivalent proteins include

jgi|Physo1_1|108759|estExt_fgenesh1_pm.C_300010	0	No title.

428. Group probability: 0.9995. Peptides of the group

MYSEHHLVPSVADAVR	63.16		54.1909	1809.883	1810.525	4	2	distinct	0	0.9767
TGDLLGSMALPAGQLWYLEELTR	60.32		52.5891	2533.289	2533.614	1	2	distinct	0	0.9774

The equivalent proteins include

jgi|Physo1_1|134170|estExt_fgenesh1_pg.C_300081	0	No title.

429. Group probability: 0.9995. Peptides of the group

LLLAYESYLR	60.02		55.146	1239.686	1239.858	1	2	distinct	0	0.9612
RLLLAYESYLR	51.23		54.9735	1395.787	1396.328	3	+2,+3	distinct	1	0.9863

The equivalent proteins include

jgi|Physo1_1|135245|estExt_fgenesh1_pg.C_370014	0	No title.

430. Group probability: 0.9994. Peptides of the group

LLHAPQLWAQGAK	57.81		55.0314	1431.799	1432.918	4	2	distinct	0	0.9578
YVIKPDFVAPGVGIR	70.22		54.6171	1629.924	1631.052	7	2	distinct	0	0.9869

The equivalent proteins include

jgi|Physo1_1|132390|estExt_fgenesh1_pg.C_200162	0	No title.

431. Group probability: 0.9994. Peptides of the group

VISDSPLVALFAQSLLVR	104.81		53.8804	1927.114	1928.03	4	2	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|141161|estExt_fgenesh1_pg.C_950009	0	No title.

432. Group probability: 0.9994. Peptides of the group

HIITTQIEHK	49.43		55.5937	1218.672	1219.546	2	2	distinct	0	0.901
VRLEPIISGGGQER	80.08		54.6007	1509.826	1511.012	1	2	distinct	1	0.9943

The equivalent proteins include

jgi|Physo1_1|108984|estExt_fgenesh1_pm.C_490001	0	No title.

433. Group probability: 0.9994. Peptides of the group

IIDLHAPSDIVK	52.91		55.35	1319.745	1320.987	2	2	distinct	0	0.9324
RIIDLHAPSDIVK	45.7		54.8319	1475.846	1476.418	2	2	distinct	1	0.8784
KSPCGEGTNTWDR	52.04		54.7473	1506.652	1506.975	1	2	distinct	1	0.9304

The equivalent proteins include

jgi|Physo1_1|108371|estExt_fgenesh1_pm.C_70016	0	No title.

434. Group probability: 0.9994. Peptides of the group

HAAWYATMSQMPGSR (00000000100000000)	105.79		54.3324	1692.75	1693.708	11	2	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|108424|estExt_fgenesh1_pm.C_90020	0	No title.

435. Group probability: 0.9994. Peptides of the group

IYKPVLPPSVTPMFDAYNDR	43.41		53.0813	2322.172	2323.527	2	+2,+3	distinct	0	0.9837
EALANAADAEPLNDADLQEVEQLVHQLLQK	53.7		50.9305	3284.652	3285.924	2	3	distinct	0	0.9626

The equivalent proteins include

jgi|Physo1_1|142328|estExt_fgenesh1_pg.C_1120012	0	No title.

436. Group probability: 0.9994. Peptides of the group

GFTLGTPVALFVPNENVRPK	73.51		53.2449	2155.179	2156.657	4	2	distinct	0	0.992
RGSEHNDPFCAGSEAERPEK	50.04		53.3684	2271.993	2273.342	1	3	distinct	1	0.9226

The equivalent proteins include

jgi|Physo1_1|110337|estExt_Genewise1.C_20183	0	No title.

437. Group probability: 0.9994. Peptides of the group

WGLPVGPITLADEVGLDVAYHVNQTLSK	44.29	51.3848	2991.57	2992.689	1	3	distinct	0	0.9074
MGLVNQVADPYALENAAISAAQQLAAGSLKPK	72.47	51.0893	3238.702	3239.997	7	3	distinct	0	0.9933

The equivalent proteins include

jgi|Physo1_1|109291|estExt_fgenesh1_pm.C_850003	0	No title.

438. Group probability: 0.9994. Peptides of the group

VYLNSDSLLLNILHDTQQSYGK	101.59	52.5588	2520.286	2521.064	3	2	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|109387|estExt_fgenesh1_pm.C_980003	0	No title.

439. Group probability: 0.9994. Peptides of the group

KIFPSALVLSPTR	78.22	55.0178	1427.85	1429.107	7	2	distinct	1	0.993
VNEVGYHGDLRPNER	50.38	54.1996	1753.85	1755.023	1	3	distinct	0	0.9088

The equivalent proteins include

jgi|Physo1_1|108834|estExt_fgenesh1_pm.C_350002	0	No title.

440. Group probability: 0.9993. Peptides of the group

MDYAVHPAALTAEAHPDLLR	74.35	53.7742	2190.089	2191.558	2	+2,+3	distinct	0	0.9993

The equivalent proteins include

jgi|Physo1_1|137242|estExt_fgenesh1_pg.C_520032	0	No title.

441. Group probability: 0.9993. Peptides of the group

YISGLGVHWYR	55.34	55.1761	1349.688	1350.819	1	2	distinct	0	0.9436
TFTLTLPGHSMQTVILPASDATK	67.25	52.763	2428.267	2428.719	2	2	distinct	0	0.9877

The equivalent proteins include

jgi|Physo1_1|108522|estExt_fgenesh1_pm.C_140002	0	No title.

442. Group probability: 0.9993. Peptides of the group

LLTAVFEHNFSTR	61.64	54.7242	1533.794	1534.763	1	2	distinct	0	0.97
VSVLPLSNNPAFEPFAAELEHVFVEEGLECK	58.53	50.2427	3470.707	3471.915	3	3	distinct	0	0.9767

The equivalent proteins include

jgi|Physo1_1|144620|estExt_fgenesh1_pg.C_2160001	0	No title.

443. Group probability: 0.9993. Peptides of the group

LAGVHVPQPK	62.1	56.2215	1044.608	1045.061	13	2	distinct	0	0.967
IAGYITHLMK	60.17	55.7971	1145.627	1146.524	4	2	distinct	0	0.9612
LTLDFDTNKR	46.67	55.1847	1221.635	1222.212	1	2	distinct	1	0.44

The equivalent proteins include

jgi|Physo1_1|138845|estExt_fgenesh1_pg.C_670047	0	No title.

444. Group probability: 0.9993. Peptides of the group

YTALTPPLSLSQGEVTNTFHR	66.53	52.9408	2331.186	2330.893	3	2	distinct	0	0.9858
MGNIEYDVPVCDPETHPGCVHTLSTR	51.77	51.3722	2983.326	2984.444	3	3	distinct	0	0.9484

The equivalent proteins include

jgi|Physo1_1|135755|estExt_fgenesh1_pg.C_400092	0	No title.

445. Group probability: 0.9993. Peptides of the group

VNRPSLMVYGGTIR	52.82	54.8527	1561.84	1562.952	6	+2,+3	distinct	0	0.9908
TLAENLENVPDLSDNHEIIHPVDRPLK	46.29	51.1841	3077.578	3078.571	1	3	distinct	0	0.9198

The equivalent proteins include

jgi|Physo1_1|109044|estExt_fgenesh1_pm.C_540018	0	No title.
jgi|Physo1_1|109043|estExt_fgenesh1_pm.C_540017	0	No title.

446. Group probability: 0.9993. Peptides of the group

RDQVSQQIAK	50.37	55.7629	1171.631	1173.033	1	2	distinct	1	0.9085
SIVAQYDAVELLAR	76.25	55.1108	1546.835	1547.88	2	2	distinct	0	0.9919

The equivalent proteins include

jgi|Physo1_1|109518|estExt_fgenesh1_pm.C_1240004	0	No title.

447. Group probability: 0.9992. Peptides of the group

VGGSEDNVIAMHAVNNYFSDNTGHAFDVSQR	97.3	50.6018	3350.501	3351.643	1	3	distinct	0	0.9992

The equivalent proteins include

jgi|Physo1_1|145391|estExt_fgenesh1_pg.C_11400001	0	No title.

jgi|Physo1_1|132225|estExt_fgenesh1_pg.C_190175	0	No title.
jgi|Physo1_1|140272|estExt_fgenesh1_pg.C_830079	0	No title.

448. Group probability: 0.9991. Peptides of the group

VAHVQALVQQHAAER	100.87	54.4562	1655.886	1656.683	7	2	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|127216|estExt_fgenesh1_pg.C_10196	0	No title.

449. Group probability: 0.9991. Peptides of the group

NMANYTNIDTFQHLLPVR	99.1	53.285	2146.063	2146.792	1	2	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|158140|C_scaffold_85000006	0	No title.

450. Group probability: 0.9991. Peptides of the group

QVHQSPAVSQGYR	51.48	54.9071	1455.722	1456.338	1	2	distinct	0	0.9267
VQKPPHADGDADYK	46.61	54.7142	1539.732	1540.406	1	2	distinct	0	0.8919
FPYPTEVGMHPSIPVQK	44.29	53.7933	1925.971	1926.49	1	2	distinct	0	0.8831

The equivalent proteins include

jgi|Physo1_1|129721|estExt_fgenesh1_pg.C_80232	0	No title.

451. Group probability: 0.9991. Peptides of the group

QPMFYAMGHFSK	51.74	54.9072	1442.647	1443.164	1	2	distinct	0	0.9257
GYPGGEYWEALALYYSK	69.6	53.816	1965.915	1966.721	2	2	distinct	0	0.9873

The equivalent proteins include

jgi|Physo1_1|130493|estExt_fgenesh1_pg.C_110162	0	No title.

452. Group probability: 0.9991. Peptides of the group

RGTTVGILGGK	46.59	56.0961	1057.624	1058.766	1	2	distinct	1	0.8761
HSQVVANNLQGK	77.72	55.1555	1293.679	1294.299	7	2	distinct	0	0.9924

The equivalent proteins include

jgi|Physo1_1|108718|estExt_fgenesh1_pm.C_270003	0	No title.

453. Group probability: 0.9990. Peptides of the group

RGEILDALSFAK	74.1	55.2642	1318.724	1319.961	1	2	distinct	1	0.9895
IVMGMPQNSVHR	49.56	55.1225	1367.68	1368.335	1	2	distinct	0	0.9097

The equivalent proteins include

jgi|Physo1_1|143156|estExt_fgenesh1_pg.C_1300033	0	No title.

454. Group probability: 0.9990. Peptides of the group

DLNPAYFHIAATNLLGK	99.34	54.6504	1856.978	1857.602	2	2	distinct	0	0.999

The equivalent proteins include

jgi|Physo1_1|142752|estExt_fgenesh1_pg.C_1210019	0	No title.
jgi|Physo1_1|142754|estExt_fgenesh1_pg.C_1210021	0	No title.

455. Group probability: 0.9990. Peptides of the group

DLNPAYFHIAAANMLGK	99.13	54.177	1844.924	1845.754	6	2	distinct	0	0.999

The equivalent proteins include

jgi|Physo1_1|142751|estExt_fgenesh1_pg.C_1210018	0	No title.

456. Group probability: 0.9990. Peptides of the group

EALQLSSNGPSSHIYHSNLAAALTYLGK	59.47	51.4925	2941.493	2942.454	1	3	distinct	0	0.9755
ALNLETGTPGEAHEAAVDEDPVVQKHPELWK	52.29	50.5348	3379.668	3380.766	1	3	distinct	1	0.9594

The equivalent proteins include

jgi|Physo1_1|127032|estExt_fgenesh1_pg.C_10012	0	No title.

457. Group probability: 0.9990. Peptides of the group

EPVGVCGIVTPWNFPLAMITR	58.85	53.156	2356.207	2357.006	4	2	distinct	0	0.9609
LGPCLAAGCTAVVKPAAETPLSALALAK	59.05	52.0138	2749.487	2750.673	4	3	distinct	0	0.9743

The equivalent proteins include

jgi|Physo1_1|108179|estExt_fgenesh1_pm.C_20011	0	No title.

458. Group probability: 0.9989. Peptides of the group

GPYESGSGHSSGLGHR	97.92	54.5994	1583.708	1584.078	4	2	distinct	0	0.9989

The equivalent proteins include

gi|88952458|ref|XP_942310.1|	197208.28	PREDICTED: similar to Hornerin [Homo sapiens]
gi|28557150|dbj|BAC57496.1|	48796.73	hornerin [Homo sapiens]
gi|55588478|ref|XP_524874.1|	126987.98	PREDICTED: hypothetical protein XP_524874 [Pan troglodytes]
gi|57546919|tpd|FAA00004.1|	283115.88	TPA: Hornerin [Homo sapiens]

gi|57864582|ref|NP_001009931.1|	283139.96	hornerin [Homo sapiens]
gi|40795897|gb|AAR91619.1|	283110.9	hornerin precursor [Homo sapiens]

459. Group probability: 0.9989. Peptides of the group

VSDKLTPLHDR	54.66	55.2656	1279.688	1280.567	2	2	distinct	1	0.94
YYLSSHSVELGR	67.45	54.9234	1409.694	1410.328	2	2	distinct	0	0.9813

The equivalent proteins include

jgi|Physo1_1|108552|estExt_fgenesh1_pm.C_150021	0	No title.

460. Group probability: 0.9989. Peptides of the group

IINEPTAAAIAYGIDKK	113.47	54.8034	1786.983	1787.369	22	2	shared(7)	1	0.9981
EVLLLDVTPLSLGIETLGGVMTK (00000000000000000000001000)	122.84	52.8653	2413.339	2413.876	45	2	distinct	0	0.9963

The equivalent proteins include

gi|76884577|gb|ABA59258.1|	70024.14	Heat shock protein Hsp70 [Nitrosococcus oceani ATCC 19707]

461. Group probability: 0.9989. Peptides of the group

KQTFNFEPDNTILHVK	69.87	53.8563	1929.995	1930.432	3	+2,+3	distinct	1	0.9989

The equivalent proteins include

jgi|Physo1_1|121940|estExt_Genewise1.C_980006	0	No title.

462. Group probability: 0.9989. Peptides of the group

LLEIGGGTNESHHK	73.07	54.8137	1490.748	1491.316	1	2	distinct	0	0.9607
EAFGRPLNNFGQIQK	61.16	54.3709	1717.89	1718.221	1	2	distinct	0	0.9711

The equivalent proteins include

jgi|Physo1_1|108282|estExt_fgenesh1_pm.C_40033	0	No title.

463. Group probability: 0.9988. Peptides of the group

EPRPFPQAPPPVLTGQTSGAQSDGSYER	94.3	51.3803	2968.431	2968.955	1	3	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|139866|estExt_fgenesh1_pg.C_790045	0	No title.

464. Group probability: 0.9988. Peptides of the group

WLGVLPQEDCFNHQVR	66.38	53.6539	1996.958	1997.38	8	2	distinct	0	0.9826
IDFGGIYYEHLPSGELYVK	49.51	53.2615	2199.089	2199.349	1	2	distinct	0	0.9319

The equivalent proteins include

jgi|Physo1_1|133321|estExt_fgenesh1_pg.C_250075	0	No title.

465. Group probability: 0.9988. Peptides of the group

GLLLPSTTTDQEMQHIR	96.17	53.8318	1938.983	1939.308	1	2	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|108957|estExt_fgenesh1_pm.C_460004	0	No title.

466. Group probability: 0.9987. Peptides of the group

AALVYGQMNEPPGAR	63.56	54.9075	1572.772	1573.149	1	2	shared(3)	0	0.926
LVLEVAQHLGEDTVR	68.18	54.8417	1677.905	1677.486	18	+2,+3	distinct	0	0.9969

The equivalent proteins include

gi|23348660|gb|AAN30694.1|	54813.6	ATP synthase F1, beta subunit [Brucella suis 1330]
gi|62196796|gb|AAX75096.1|	54813.6	AtpD, ATP synthase F1, beta subunit [Brucella abortus biovar 1 str. 9-941]

467. Group probability: 0.9987. Peptides of the group

GLEPELQWGQGADGSFASLVAHLR	61.57	52.4	2537.266	2538.726	3	+2,+3	distinct	0	0.9987

The equivalent proteins include

jgi|Physo1_1|108474|estExt_fgenesh1_pm.C_110005	0	No title.

468. Group probability: 0.9987. Peptides of the group

TVSLNHVWGNNPK	97.19	55.1424	1464.747	1466.01	9	2	distinct	0	0.9987

The equivalent proteins include

jgi|Physo1_1|109381|estExt_fgenesh1_pm.C_970004	0	No title.
jgi|Physo1_1|141345|estExt_fgenesh1_pg.C_970033	0	No title.

469. Group probability: 0.9986. Peptides of the group

HVAHMIDSTEEK	60.22	54.9289	1395.645	1396.288	1	2	distinct	0	0.9647
AEQVFWWPFTQHK	58.69	54.4175	1702.826	1703.97	1	2	distinct	0	0.9614

The equivalent proteins include

jgi|Physo1_1|134345|estExt_fgenesh1_pg.C_310055	0	No title.

470. Group probability: 0.9986. Peptides of the group

LVSVYAHWVPR	62.91	55.3215	1325.724	1326.175	4	2	distinct	0	0.9709
IYANMTKPAFFFDGR	55.46	54.1475	1776.866	1777.284	9	2	distinct	0	0.9526

The equivalent proteins include

jgi|Physo1_1|156526|C_scaffold_21000016	0	No title.

471. Group probability: 0.9986. Peptides of the group

DHSSSGIGFNTPVQVTPK	94.43	53.997	1869.922	1870.626	1	2	distinct	0	0.9986

The equivalent proteins include

jgi|Physo1_1|127337|estExt_fgenesh1_pg.C_10317	0	No title.

472. Group probability: 0.9986. Peptides of the group

VYYNSGLQPSPLHYPILGTR	58.77	53.4548	2274.18	2274.714	9	+2,+3	distinct	0	0.9986

The equivalent proteins include

jgi|Physo1_1|140785|estExt_fgenesh1_pg.C_890062	0	No title.

473. Group probability: 0.9986. Peptides of the group

ALVAFPVSYHLLCAAR	65.4	54.8113	1786.955	1787.346	2	2	distinct	0	0.9806
HSLWTYKPELINNIDGAK	49.11	53.4283	2098.085	2098.623	2	2	distinct	0	0.9266

The equivalent proteins include

jgi|Physo1_1|137936|estExt_fgenesh1_pg.C_580109	0	No title.

474. Group probability: 0.9986. Peptides of the group

VQLHPTGFINPK	47.12	55.1686	1349.746	1350.225	1	2	distinct	0	0.888
IPSIDTPMQIYAMEVAPTVHYTMGGVK	67.3	51.4042	2948.449	2949.821	1	3	distinct	0	0.9872

The equivalent proteins include

jgi|Physo1_1|115536|estExt_Genewise1.C_260177	0	No title.

475. Group probability: 0.9985. Peptides of the group

HVGLSMAGLVADGR	95.64	54.965	1381.714	1382.774	3	2	distinct	0	0.9985

The equivalent proteins include

jgi|Physo1_1|108726|estExt_fgenesh1_pm.C_270011	0	No title.

476. Group probability: 0.9985. Peptides of the group

DVNHEHLQSIEDR	54.97	54.7087	1590.739	1591.315	1	2	distinct	0	0.9462
EKPYQCTYPVDLDECGPMVLDALIK	59.31	51.5014	2953.391	2953.889	1	3	distinct	0	0.9723

The equivalent proteins include

jgi|Physo1_1|109257|estExt_fgenesh1_pm.C_810004	0	No title.

477. Group probability: 0.9985. Peptides of the group

RQDLVILTDCASPVPGFEK	93.1	53.2885	2144.094	2144.606	2	2	distinct	1	0.9985

The equivalent proteins include

jgi|Physo1_1|158850|C_scaffold_160000004	0	No title.

478. Group probability: 0.9985. Peptides of the group

ESTIHLVLR	71.03	55.1897	1066.613	1067.325	13	2	shared(3)	0	0.9848
ECPSPQCGAGVFMATHFDR	76.61	53.2998	2165.908	2165.862	3	2	distinct	0	0.9937

The equivalent proteins include

jgi|Physo1_1|109100|estExt_fgenesh1_pm.C_600006	0	No title.

479. Group probability: 0.9985. Peptides of the group

LYDSESVLALRDPTKPFPTSR	56.85	52.798	2391.243	2392.16	1	3	distinct	1	0.9594
EIPPMSAAVETVQKPEVAAAVSHDPIGAVVEEK	52.48	50.3094	3397.744	3399.116	1	3	distinct	0	0.963

The equivalent proteins include

jgi|Physo1_1|133424|estExt_fgenesh1_pg.C_260030	0	No title.

480. Group probability: 0.9985. Peptides of the group

AHIGAFATPDLIVLAPGLPK	92.57	53.8821	2000.146	2000.693	2	2	distinct	0	0.9985

The equivalent proteins include

jgi|Physo1_1|109048|estExt_fgenesh1_pm.C_550001	0	No title.

481. Group probability: 0.9984. Peptides of the group

NAVQHTGPILPITR	68.39	54.8969	1515.852	1517.18	17	+2,+3	distinct	0	0.9984

The equivalent proteins include

jgi|Physo1_1|109354|estExt_fgenesh1_pm.C_940002	0	No title.

482. Group probability: 0.9984. Peptides of the group

VGIVGIGGLGHLGIQFAK	73.97	54.2066	1735.014	1735.749	3	+2,+3	distinct	0	0.9984

The equivalent proteins include

jgi|Physo1_1|109686|estExt_fgenesh1_pm.C_2990002	0	No title.
jgi|Physo1_1|109706|estExt_fgenesh1_pm.C_5140001	0	No title.

483. Group probability: 0.9983. Peptides of the group

HLGYVGNTFPSVSVR	93.79	54.6469	1631.842	1633.336	5	2	distinct	0	0.9983

The equivalent proteins include

jgi|Physo1_1|134057|estExt_fgenesh1_pg.C_290124	0	No title.

484. Group probability: 0.9983. Peptides of the group

IGPYMSNPAHIELILTEK	92.31	53.5425	2025.06	2025.867	9	2	distinct	0	0.9983

The equivalent proteins include

jgi|Physo1_1|134218|estExt_fgenesh1_pg.C_300129	0	No title.

485. Group probability: 0.9983. Peptides of the group

ILTDYGFGEGHPLRK	68.88	54.6545	1644.862	1645.394	3	2	distinct	1	0.9847
DFPLSGFLEVFYNELK	45.53	53.8985	1916.956	1917.331	1	2	distinct	0	0.8912

The equivalent proteins include

gi|9695380|ref|NP_037602.1|	22914.22	NADH dehydrogenase subunit 9 [Phytophthora infestans]
gi|7545239|gb|AAA32025.2|	22795.14	NADH dehydrogenase [Phytophthora megasperma]
gi|56684557|gb|AAW21977.1|	22560.03	NADH dehydrogenase subunit 9 [Plasmopara viticola]

486. Group probability: 0.9983. Peptides of the group

GAGGLGHAGGKDEPTPR	92.71	54.7512	1575.775	1576.097	5	2	distinct	1	0.9983

The equivalent proteins include

jgi|Physo1_1|141112|estExt_fgenesh1_pg.C_940023	0	No title.

487. Group probability: 0.9982. Peptides of the group

KIAVNLIPFPR	70.88	55.3512	1266.781	1267.527	5	2	shared(6)	1	0.9855
EIVHIQGGQCGDQIGAK	58.29	54.34	1808.884	1808.005	5	2	distinct	0	0.8284
GHYTEGAELIDSVLDVVR	50.71	53.7106	1971.99	1972.76	1	2	shared(5)	0	0.7948
AGPYGQIFRPDNFVFGQTGAGNNWAK	79.99	52.2124	2811.352	2812.533	7	+2,+3	shared(2)	0	0.9986

The equivalent proteins include

gi|1067181|emb|CAA91942.1|	50961.07	beta-tubulin [oomycete-like MacKay2000]

488. Group probability: 0.9981. Peptides of the group

AHIGAFASPDLIVLVPGLPK	90.24	53.627	2014.161	2014.77	2	2	distinct	0	0.9981

The equivalent proteins include

jgi|Physo1_1|109049|estExt_fgenesh1_pm.C_550002	0	No title.

489. Group probability: 0.9981. Peptides of the group

HLVSPEAIDFLDGLLR	59	54.2418	1793.968	1794.747	2	+2,+3	distinct	0	0.9981

The equivalent proteins include

jgi|Physo1_1|109488|estExt_fgenesh1_pm.C_1190001	0	No title.

490. Group probability: 0.9981. Peptides of the group

RTIQFVDWCPTGFK	68.04	54.1994	1753.861	1754.812	2	2	shared(4)	1	0.9837
IHFMLSSYAPVISAEK (000010000000000000)	84.73	54.3337	1807.918	1808.932	1	2	shared(3)	0	0.9876
QIYHPEQLISGKEDAANNYAR	44.31	52.6684	2416.177	2417.298	4	+2,+3	distinct	1	0.976

The equivalent proteins include

gi|57903355|gb|AAW58089.1|	45228.32	alpha-tubulin [Apodachlya brachynema]
gi|57903369|gb|AAW58096.1|	45079.49	alpha-tubulin [Phytophthora palmivora]
gi|57903371|gb|AAW58097.1|	45063.5	alpha-tubulin [Plectospira myriandra]
gi|57903375|gb|AAW58099.1|	45054.51	alpha-tubulin [Pythium graminicola]
gi|57903377|gb|AAW58100.1|	45277.65	alpha-tubulin [Thraustotheca clavata]
gi|13649511|gb|AAK37433.1|	42984.51	alpha-tubulin [Reclinomonas americana]
jgi|Physo1_1|109111|estExt_fgenesh1_pm.C_610001	0	No title.
jgi|Physo1_1|109758|estExt_fgenesh1_pm.C_19560001	0	No title.
jgi|Physo1_1|119319|estExt_Genewise1.C_610124	0	No title.

491. Group probability: 0.9981. Peptides of the group

RLWQNNCRPAVACE	53.51	54.2877	1772.82	1773.492	1	2	distinct	1	0.9415
SSCVSGALDPVWQPAETFEFEVGHLSPNAER	54.65	50.385	3415.578	3416.917	3	3	distinct	0	0.9671

The equivalent proteins include

jgi|Physo1_1|128360|estExt_fgenesh1_pg.C_40204	0	No title.

492. Group probability: 0.9981. Peptides of the group

SIVHPSYNSNTLNNDIMLIK (00000000000000000010000)	72.88	53.0951	2272.152	2272.395	15	+2,+3	distinct	0	0.9981

The equivalent proteins include

gi|1421532|pdb|1TGB|	24658.8	Trypsinogen-Ca From Peg
gi|230765|pdb|2TLD|E	23555.36	Chain E, Bovine Trypsin (E.C.3.4.21.4) Complex With A Modified SSI (Streptomyces Subtilisin Inhibit

gi|2392803|pdb|5PTP|	23998.54	Structure Of Hydrolase (Serine Proteinase)
gi|5542503|pdb|1ZZZ|A	25388.25	Chain A, Trypsin Inhibitors With Rigid Tripeptidyl Aldehydes
gi|13096615|pdb|1G3E|A	24562.78	Chain A, Bovine Beta-Trypsin Bound To Para-Amidino Schiff-Base Copper (Ii) Chelate
gi|34811715|pdb|1HJ9|A	23972.49	Chain A, Atomic Resolution Structures Of Trypsin Provide Insight Into Structural Radiation Damage
gi|34810822|pdb|1OPH|B	26076.68	Chain B, Non-Covalent Complex Between Alpha-1-Pi-Pittsburgh And S195a Trypsin
gi|49259462|pdb|1V2P|T	23979.59	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssyi)bt.A4
gi|49259463|pdb|1V2Q|T	24002.6	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Sswi)bt.B4
gi|49259464|pdb|1V2R|T	23972.63	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssri)bt.B4
gi|49259466|pdb|1V2T|T	24005.6	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssfi.Glu)bt.B4
gi|49259469|pdb|1V2W|T	23887.56	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssai)bt.B4
gi|71042446|pdb|1ZR0|C	23960.59	Chain C, Crystal Structure Of Kunitz Domain 1 Of Tissue Factor Pathway Inhibitor-2 With Bovine Tryp
gi|88193016|pdb|2FI4|E	23971.53	Chain E, Crystal Structure Of A Bpti Variant (Cys14->ser) In Complex With Trypsin
gi|88193018|pdb|2FI5|E	24086.56	Chain E, Crystal Structure Of A Bpti Variant (Cys38->ser) In Complex With Trypsin
gi|2507249|sp|P00760|TRY1_BOVIN	26092.68	Cationic trypsin precursor (Beta-trypsin) [Contains: Alpha-trypsin chain 1; Alpha-trypsin chain 2]
gi|76615876|ref|XP_883769.1|	26246.67	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 2 [Bos taurus]
gi|76615878|ref|XP_883804.1|	26537.88	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 3 [Bos taurus]
gi|76615880|ref|XP_871686.1|	26438.81	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 1 [Bos taurus]
gi|76615882|ref|XP_883865.1|	26551.93	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 2 [Bos taurus]
gi|61873128|ref|XP_584594.1|	26452.86	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 1 [Bos taurus]
gi|67549|pir||TRBOTR	24661.84	trypsin (EC 3.4.21.4) precursor - bovine
gi|90109720|pdb|2FX6|A	23974.57	Chain A, Bovine Trypsin Complexed With 2-Aminobenzamidazole

493. Group probability: 0.9980. Peptides of the group

LMCASTACNTMITK (0010000000000000)	92.46	55.0237	1600.708	1601.274	18	2	distinct	0	0.998

The equivalent proteins include

gi|68137499|gb|AAY85678.1|	12640.04	acidic elicitin [Phytophthora alni subsp. alni]
gi|68137505|gb|AAY85681.1|	12606.05	acidic elicitin [Phytophthora alni subsp. alni]
gi|68137515|gb|AAY85686.1|	12530.02	acidic elicitin [Phytophthora fragariae var. fragariae]
gi|68137517|gb|AAY85687.1|	12564.01	acidic elicitin [Phytophthora fragariae var. fragariae]
gi|68137519|gb|AAY85688.1|	12546.02	acidic elicitin [Phytophthora fragariae var. rubi]
gi|68137521|gb|AAY85689.1|	12580	acidic elicitin [Phytophthora fragariae var. rubi]
gi|27462826|gb|AAO15602.1|	10501.94	alpha-elicitin capsicein [Phytophthora capsici]
gi|4138370|emb|CAA07710.1|	10519.91	sojein 1 protein [Phytophthora sojae]
gi|4138376|emb|CAA07713.1|	10461.91	sojein 4 protein [Phytophthora sojae]
gi|37783440|gb|AAP43023.1|	12496.96	elicitin [Phytophthora capsici]

gi|37783442|gb|AAP43024.1|	11767.76	elicitin [Phytophthora palmivora]							
494. Group probability: 0.9980. Peptides of the group									
VGNLVSDLALDAVLTVVR	90.2	54.0906	1853.062	1854.518	2	2	distinct	0	0.998
The equivalent proteins include									
jgi|Physo1_1|109716|estExt_fgenesh1_pm.C_6500001	0	No title.							
495. Group probability: 0.9980. Peptides of the group									
VIRPAKVGVVK	63.26	55.2546	1164.771	1165.228	45	2	distinct	1	0.9718
INQVGAIGDKFDPNVHDALFEYEDTTK	47.52	51.5058	3035.451	3036.49	1	3	distinct	1	0.9275
The equivalent proteins include									
jgi|Physo1_1|108704|estExt_fgenesh1_pm.C_260005	0	No title.							
496. Group probability: 0.9978. Peptides of the group									
LSINHATAR	60.6	55.0716	981.536	981.976	2	2	distinct	0	0.9622
KLSINHATAR	55.6	55.2418	1109.63	1110.45	1	2	distinct	1	0.9428
The equivalent proteins include									
jgi|Physo1_1|138394|estExt_fgenesh1_pg.C_630013	0	No title.							
497. Group probability: 0.9977. Peptides of the group									
KLTEIINSEHENVK	83.88	54.6045	1652.873	1653.119	1	2	distinct	1	0.9485
GADILIFCVPHQFLGR	55.52	54.1344	1841.961	1842.047	1	2	distinct	0	0.9545
The equivalent proteins include									
jgi|Physo1_1|108529|estExt_fgenesh1_pm.C_140009	0	No title.							
498. Group probability: 0.9976. Peptides of the group									
VLPNFALTLSAEGFPLKDDFK	86.72	53.0331	2321.231	2322.587	4	2	distinct	1	0.9976
The equivalent proteins include									
jgi|Physo1_1|108992|estExt_fgenesh1_pm.C_500005	0	No title.							
499. Group probability: 0.9976. Peptides of the group									
ILGVSPYEAVALAGRPR	58.77	54.1876	1767.999	1769.193	4	2	distinct	0	0.9669
THGACPTGPGPDPTQDPLNPWPGTCGEGAMK	45.55	50.9322	3202.391	3202.734	2	3	distinct	0	0.9261
The equivalent proteins include									
jgi|Physo1_1|109689|estExt_fgenesh1_pm.C_3170002	0	No title.							
jgi|Physo1_1|145196|estExt_fgenesh1_pg.C_6020002	0	No title.							
500. Group probability: 0.9975. Peptides of the group									
HFTESVEDAR	63.18	55.6052	1189.536	1190.488	2	2	distinct	0	0.9703
MVPLHFESWK	51.44	55.5607	1272.632	1273.176	2	2	distinct	0	0.917
The equivalent proteins include									
jgi|Physo1_1|142593|estExt_fgenesh1_pg.C_1170052	0	No title.							
501. Group probability: 0.9975. Peptides of the group									
DVSNMNTSTTLLGHNVSSPVCVAPSSTHR	85.18	51.2427	3067.445	3068.708	5	3	distinct	0	0.9975
The equivalent proteins include									
jgi|Physo1_1|143025|estExt_fgenesh1_pg.C_1270015	0	No title.							
502. Group probability: 0.9975. Peptides of the group									
SAGEAGPSYFELIVDAIK	87.85	53.9314	1865.941	1867.086	6	2	distinct	0	0.9975
The equivalent proteins include									
jgi|Physo1_1|129764|estExt_fgenesh1_pg.C_90041	0	No title.							
503. Group probability: 0.9975. Peptides of the group									
ASQVVGLHFFNPVQLMK	88.06	53.8677	1914.018	1914.69	9	2	distinct	0	0.9975
The equivalent proteins include									
jgi|Physo1_1|157244|C_scaffold_38000033	0	No title.							
504. Group probability: 0.9975. Peptides of the group									
LQAQLHQSAQDTWSYLEALK	86.58	53.025	2329.17	2329.594	2	2	distinct	0	0.9975
The equivalent proteins include									
jgi|Physo1_1|128975|estExt_fgenesh1_pg.C_60132	0	No title.							
jgi|Physo1_1|128978|estExt_fgenesh1_pg.C_60135	0	No title.							
505. Group probability: 0.9974. Peptides of the group									
GSSSSWVPSELWSFFFPSK	86.97	53.8872	2161.016	2162.091	7	2	distinct	0	0.9974
The equivalent proteins include									
jgi|Physo1_1|131384|estExt_fgenesh1_pg.C_150155	0	No title.							
506. Group probability: 0.9974. Peptides of the group									

TPGPGAQSALR	53.06	55.4048	1053.557	1054.389	1	2	distinct	0	0.9307
TKTPGPGAQSALR	59.17	55.2583	1282.699	1283.654	3	2	distinct	1	0.9624

The equivalent proteins include

gi|82623421|gb|ABB87125.1|	10677.75	hypothetical protein [Solanum tuberosum]
gi|83284009|gb|ABC01912.1|	16391.65	ribosomal protein S14-like protein [Solanum tuberosum]
gi|1762931|gb|AAC49968.1|	6995.95	ribosomal protein S14 [Nicotiana tabacum]
gi|61369149|gb|AAX43292.1|	16546.68	ribosomal protein S14 [synthetic construct]
gi|61654728|gb|AAX48890.1|	16282.67	S14 [Suberites domuncula]
gi|74268249|gb|AAI02537.1|	17050.85	Unknown (protein for MGC:127734) [Bos taurus]
gi|74226871|dbj|BAE27080.1|	16506.6	unnamed protein product [Mus musculus]
gi|91091798|ref|XP_970498.1|	16283.68	PREDICTED: similar to 40S ribosomal protein S14 [Tribolium castaneum]
gi|72015985|ref|XP_780390.1|	16159.63	PREDICTED: similar to 40S ribosomal protein S14 [Strongylocentrotus purpuratus]
gi|70909537|emb|CAJ17191.1|	16328.65	ribosomal protein S14e [Sphaerius sp. APV-2005]
gi|94468908|gb|ABF18303.1|	16302.67	40S ribosomal protein S141 [Aedes aegypti]
gi|109079317|ref|XP_001099589.1|	14487.5	PREDICTED: similar to ribosomal protein S14 [Macaca mulatta]
gi|76680427|ref|XP_584177.2|	16463.57	PREDICTED: similar to ribosomal protein S14 [Bos taurus]
gi|55625094|ref|XP_518037.1|	22706.67	PREDICTED: similar to 40S ribosomal protein S14 [Pan troglodytes]
gi|77745450|gb|ABB02624.1|	16405.67	ribosomal protein S14-like [Solanum tuberosum]
gi|71895291|ref|NP_001025790.1|	16433.6	ribosomal protein S14 [Gallus gallus]
gi|38048289|gb|AAR10047.1|	16311.71	similar to Drosophila melanogaster RpS14a [Drosophila yakuba]
gi|463857|gb|AAB60274.1|	16348.67	ribosomal protein S14
gi|730633|sp|Q08699|RS14_PODCA	16182.54	40S ribosomal protein S14
gi|5441523|emb|CAB46816.1|	8441.65	Ribosomal protein S14 [Canis familiaris]
gi|3097244|emb|CAA69615.1|	16461.6	ribosomal protein S14 [Mus musculus]
gi|458981|gb|AAC48301.1|	16352.69	Ribosomal protein, small subunit protein 14 [Caenorhabditis elegans]
gi|131772|sp|P19950|RS141_MAIZE	16304.65	40S ribosomal protein S14 (Clone MCH1)
gi|131773|sp|P19951|RS142_MAIZE	16309.64	40S ribosomal protein S14 (Clone MCH2)
gi|57129|emb|CAA33143.1|	16419.58	unnamed protein product [Rattus norvegicus]
gi|4588920|gb|AAD26263.1|	16276.64	ribosomal protein S14 [Stomoxys calcitrans]
gi|28189929|dbj|BAC56579.1|	15838.16	similar to ribosomal protein S14 [Bos taurus]
gi|15227588|ref|NP_181158.1|	16303.69	structural constituent of ribosome [Arabidopsis thaliana]
gi|15229775|ref|NP_187758.1|	16319.68	structural constituent of ribosome [Arabidopsis thaliana]
gi|15231260|ref|NP_190826.1|	16284.71	structural constituent of ribosome [Arabidopsis thaliana]
gi|55242989|gb|EAA06897.2|	16359.69	ENSANGP00000019074 [Anopheles gambiae str. PEST]
gi|55242445|gb|EAA08220.2|	16331.66	ENSANGP00000015417 [Anopheles gambiae str. PEST]
gi|62083507|gb|AAX62478.1|	16351.68	ribosomal protein S14 [Lysiphlebus testaceipes]
gi|50905421|ref|XP_464199.1|	16409.68	putative ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]
gi|54609311|gb|AAV34871.1|	16207.65	ribosomal protein S14 [Bombyx mori]
gi|50924099|ref|XP_472410.1|	16466.71	OJ000126_13.9 [Oryza sativa (japonica cultivar-group)]
gi|15213816|gb|AAK92183.1|	16264.67	ribosomal protein S14 [Spodoptera frugiperda]
gi|28436071|gb|AAO41731.1|	16361.64	cytoplasmic ribosomal protein S14 [Brassica napus]
gi|37748505|gb|AAH59561.1|	16405.59	Ribosomal protein S14 [Danio rerio]
gi|62362200|gb|AAX81537.1|	16046.47	S14e ribosomal protein-like protein [Philodina sp. NPS-2005]
gi|51011526|gb|AAT92172.1|	16166.56	ribosomal protein S14 [Ixodes pacificus]

gi|50344488|emb|CAH04330.1|	16267.68	S14e ribosomal protein [Dascillus cervinus]
gi|15294039|gb|AAK95196.1|	16376.56	40S ribosomal protein S14 [Ictalurus punctatus]
gi|94399883|ref|XP_001001619.1|	16537.67	PREDICTED: similar to ribosomal protein S14 [Mus musculus]
gi|82958328|ref|XP_913463.1|	16551.69	PREDICTED: similar to ribosomal protein S14 isoform 1 [Mus musculus]
gi|47935073|gb|AAT39883.1|	16218.46	ribosomal protein S14 [Branchiostoma belcheri tsingtaunese]
gi|51863346|gb|AAU11819.1|	16149.64	ribosomal protein S14 [Bombyx mori]
gi|51873216|gb|AAU12568.1|	12918.6	ribosomal protein S14 [Felis catus]
jgi|Physo1_1|135178|estExt_fgenesh1_pg.C_360094	0	No title.

507. Group probability: 0.9973. Peptides of the group

LGMKPVGGIIR	46.96	55.4063	1139.685	1140.551	1	2	distinct	0	0.8818
NVLFVISKPDVFK	64.93	54.7965	1504.865	1505.666	3	2	distinct	0	0.9775

The equivalent proteins include

jgi|Physo1_1|108927|estExt_fgenesh1_pm.C_430007	0	No title.

508. Group probability: 0.9973. Peptides of the group

YHEQSANFDPVHSISR	87.74	53.9221	1885.871	1886.28	4	2	distinct	0	0.9973

The equivalent proteins include

jgi|Physo1_1|131341|estExt_fgenesh1_pg.C_150112	0	No title.

509. Group probability: 0.9972. Peptides of the group

YPNEHGIVTNWDDMEK	76.88	53.8788	1946.847	1946.612	11	+2,+3	distinct	0	0.9955
VAPEEHPVLLTEAPINPK	81.4	53.7297	1953.057	1953.885	13	2	shared(10)	0	0.9887

The equivalent proteins include

gi|109507063|ref|XP_001058533.1|	42108.88	PREDICTED: similar to Actin, cytoplasmic 2 (Gamma-actin) [Rattus norvegicus]

510. Group probability: 0.9972. Peptides of the group

HVSVIAKPLATK	66.74	55.6152	1262.771	1263.206	4	2	distinct	0	0.9798
RPTSCILITPNK	44.52	55.2549	1398.765	1399.247	1	2	distinct	0	0.8591

The equivalent proteins include

jgi|Physo1_1|108290|estExt_fgenesh1_pm.C_50005	0	No title.

511. Group probability: 0.9971. Peptides of the group

QASLQEYLDGLLQVPGILDDASLQHFLELEK	82.19	50.3814	3481.798	3482.853	2	3	distinct	0	0.9971

The equivalent proteins include

jgi|Physo1_1|156141|C_scaffold_11000036	0	No title.

512. Group probability: 0.9969. Peptides of the group

YSNYYSQCKPATLPAGELCGQNDGTNVWK	82.59	50.7157	3320.487	3321.623	8	3	distinct	0	0.9969

The equivalent proteins include

jgi|Physo1_1|158550|C_scaffold_116000002	0	No title.

513. Group probability: 0.9969. Peptides of the group

ITPAHDPNDYECGKR	59.67	54.2607	1771.795	1773.17	2	3	distinct	1	0.9596
AEYGLANNVRPQFFIK	49.64	53.9314	1865.979	1866.675	1	2	distinct	0	0.9241

The equivalent proteins include

jgi|Physo1_1|108931|estExt_fgenesh1_pm.C_440004	0	No title.

514. Group probability: 0.9969. Peptides of the group

YRPAAPGAPMK	47.42	55.7963	1157.602	1158.234	2	2	distinct	0	0.8855
HEQGAGHMAQGYAR	82.64	54.7123	1511.669	1512.416	8	2	distinct	0	0.9732

The equivalent proteins include

jgi|Physo1_1|109190|estExt_fgenesh1_pm.C_700007	0	No title.

515. Group probability: 0.9969. Peptides of the group

VCAYAGDAYMHAPR	87.07	54.5581	1580.686	1581.052	5	2	distinct	0	0.9969

The equivalent proteins include

jgi|Physo1_1|135221|estExt_fgenesh1_pg.C_360137	0	No title.

516. Group probability: 0.9969. Peptides of the group

NVIHPYTPTNTNAEKGELELVVK	56.24	52.4359	2565.344	2566.442	1	3	distinct	1	0.9604
LLPGPSDESLIGVCGPPPMMDAISGNKAPDR	44.82	51.005	3190.546	3191.301	1	3	distinct	1	0.9211

The equivalent proteins include

jgi|Physo1_1|108925|estExt_fgenesh1_pm.C_430005	0	No title.

517. Group probability: 0.9968. Peptides of the group

GVEEIIEHVIGAWK	86.81	54.768	1578.841	1580.027	2	2	distinct	0	0.9968

The equivalent proteins include

jgi|Physo1_1|108161|estExt_fgenesh1_pm.C_10026	0	No title.

518. Group probability: 0.9968. Peptides of the group

FQALMPDALHWLGITK	97.8	53.9996	1839.971	1840.421	6	2	distinct	0	0.9968

The equivalent proteins include

jgi|Physo1_1|120701|estExt_Genewise1.C_810049	0	No title.

519. Group probability: 0.9968. Peptides of the group

TTGVVLDVGDGVAHVVPVYEGFTLPHAITR	81.62	51.1126	3118.645	3119.83	1	3	distinct	0	0.9968

The equivalent proteins include

jgi|Physo1_1|108184|estExt_fgenesh1_pm.C_20016	0	No title.

520. Group probability: 0.9966. Peptides of the group

EIPGLTLSEEQVNALLK	84.86	54.1243	1853.015	1854.157	2	2	distinct	0	0.9966

The equivalent proteins include

jgi|Physo1_1|139970|estExt_fgenesh1_pg.C_800054	0	No title.

521. Group probability: 0.9965. Peptides of the group

FSVLHPTK	49.91	56.7164	927.518	928.667	1	2	distinct	0	0.9001
ALPVEGLTWGEGHK	70.98	54.6429	1492.767	1493.485	4	2	shared(2)	0	0.9873
SQVVIEVKPWEAETDLEELAAK	43.79	52.584	2483.279	2483.55	1	2	shared(2)	0	0.9003

The equivalent proteins include

jgi|Physo1_1|158454|C_scaffold_106000025	0	No title.

522. Group probability: 0.9964. Peptides of the group

VGVVGIGGLGHLGIQFAK	83.69	54.2566	1720.999	1721.659	4	2	distinct	0	0.9964

The equivalent proteins include

jgi|Physo1_1|108331|estExt_fgenesh1_pm.C_60021	0	No title.
jgi|Physo1_1|109587|estExt_fgenesh1_pm.C_1500003	0	No title.
jgi|Physo1_1|109744|estExt_fgenesh1_pm.C_11770002	0	No title.
jgi|Physo1_1|109585|estExt_fgenesh1_pm.C_1500001	0	No title.

523. Group probability: 0.9963. Peptides of the group

DILLLDVTPLSLGIETLGGVMTK (0000000000000000000001000)	122.84	52.8653	2413.339	2413.876	45	2	distinct	0	0.9963

The equivalent proteins include

gi|77747092|gb|ABB02935.1|	42049.98	DnaK [Candidatus Legionella jeonii]

524. Group probability: 0.9963. Peptides of the group

HEQQHGLLGK	51.86	55.7971	1145.594	1146.402	1	2	distinct	0	0.9196
NGNHFVNTASHFMR	56.4	54.6503	1630.742	1632.12	2	2	distinct	0	0.9543

The equivalent proteins include

jgi|Physo1_1|137091|estExt_fgenesh1_pg.C_500127	0	No title.

525. Group probability: 0.9963. Peptides of the group

GIPSAVFVDSVEAFMDACGVK	81.95	53.2602	2198.039	2199.059	2	2	distinct	0	0.9963

The equivalent proteins include

jgi|Physo1_1|141993|estExt_fgenesh1_pg.C_1060052	0	No title.

526. Group probability: 0.9961. Peptides of the group

KGLTPSQIGVILR	85.08	54.9508	1380.845	1381.505	5	2	distinct	1	0.9961

The equivalent proteins include

gi|54039304|sp|P62279|RS13_PIG	12026.78	40S ribosomal protein S13
gi|4633275|gb|AAD26692.1|	17181.66	40S ribosomal protein S13 [Cricetulus griseus]
gi|61369380|gb|AAX43326.1|	17324.75	ribosomal protein S13 [synthetic construct]
gi|67764864|gb|AAY79230.1|	12287.11	ribosomal protein S13 [Siniperca chuatsi]
gi|10121613|gb|AAG13286.1|	17151.61	ribosomal protein S13 [Gillichthys mirabilis]
gi|15450535|gb|AAK96445.1|	17115.53	AT3g60770/T4C21_180 [Arabidopsis thaliana]
gi|15294037|gb|AAK95195.1|	17139.64	40S ribosomal protein S13 [Ictalurus punctatus]
gi|70909527|emb|CAJ17186.1|	17052.51	ribosomal protein S13e [Agriotes lineatus]

gi|70909529|emb|CAJ17187.1|	17146.48	ribosomal protein S13e [Curculio glandium]
gi|70909531|emb|CAJ17188.1|	17152.5	ribosomal protein S13e [Georissus sp. APV-2005]
gi|54039308|sp|O77303|RS13_LUMRU	17104.68	40S ribosomal protein S13
gi|57089981|ref|XP_537358.1|	12731.13	PREDICTED: similar to ribosomal protein S13 [Canis familiaris]
gi|94391593|ref|XP_994773.1|	14265.94	PREDICTED: similar to ribosomal protein S13 [Mus musculus]
gi|44662862|gb|AAS47510.1|	17186.52	ribosomal protein S13 [Glycine max]
gi|68449762|gb|AAY97868.1|	17077.55	cytoplasmic ribosomal protein S13 [Lycopersicon esculentum]
gi|76607499|ref|XP_581041.2|	17038.46	PREDICTED: similar to ribosomal protein S13 [Bos taurus]
gi|18411716|ref|NP_567104.1|	17141.53	structural constituent of ribosome [Arabidopsis thaliana]
gi|18411224|ref|NP_567151.1|	17131.51	ATRPS13A (RIBOSOMAL PROTEIN S13A); structural constituent of ribosome [Arabidopsis thaliana]
gi|50805893|ref|XP_424367.1|	14633.33	PREDICTED: similar to ribosomal protein S13, partial [Gallus gallus]
gi|109081167|ref|XP_001084119.1|	18100.84	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109108275|ref|XP_001083923.1|	14235.02	PREDICTED: similar to ribosomal protein S13 isoform 4 [Macaca mulatta]
gi|109110588|ref|XP_001105971.1|	10903.08	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109120657|ref|XP_001097099.1|	17234.64	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109132315|ref|XP_001095630.1|	17177.54	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109139180|ref|XP_001119129.1|	17245.61	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109476367|ref|XP_001068232.1|	17762.03	PREDICTED: similar to ribosomal protein S13 [Rattus norvegicus]
gi|55642147|ref|XP_523078.1|	17270.5	PREDICTED: similar to ribosomal protein S13 [Pan troglodytes]
gi|47211519|emb|CAF90315.1|	17169.66	unnamed protein product [Tetraodon nigroviridis]
gi|8131699|dbj|BAA96366.1|	17164.58	cytoplasmic ribosomal protein S13 [Panax ginseng]
gi|77415468|gb|AAI06138.1|	17211.67	Ribosomal protein S13 [Mus musculus]
gi|7267097|emb|CAB80768.1|	16954.4	putative ribosomal protein S13 [Arabidopsis thaliana]
gi|7329687|emb|CAB82681.1|	16964.42	ribosomal protein S13-like [Arabidopsis thaliana]
gi|699581|gb|AAA91984.1|	17156.59	ribosomal S13 protein [Ictalurus punctatus]
gi|48209913|gb|AAT40507.1|	17107.56	cytoplasmic ribosomal protein S13 [Solanum demissum]
gi|417710|sp|P33192|RS13_CANMA	16931.31	40S ribosomal protein S13 (S15)
gi|396639|emb|CAA80974.1|	17162.61	ribosomal protein S13 [Pisum sativum]
gi|553640|gb|AAC15854.1|	13312.62	ribosomal protein S13 [Homo sapiens]
gi|62860010|ref|NP_001016602.1|	17239.67	ribosomal protein S13 [Xenopus tropicalis]
gi|48735394|gb|AAH72552.1|	17183.65	Zgc:91809 [Danio rerio]
gi|67084039|gb|AAY66954.1|	17255.66	40S ribosomal protein S13 [Ixodes scapularis]
gi|50344486|emb|CAH04329.1|	17136.46	S13e ribosomal protein [Timarcha balearica]
gi|50424883|ref|XP_461031.1|	17018.25	hypothetical protein DEHA0F16698g [Debaryomyces hansenii CBS767]
gi|22758884|gb|AAN05601.1|	16995.5	ribosomal protein S13 [Argopecten irradians]
gi|15029927|gb|AAH11192.1|	16132.15	Rps13 protein [Mus musculus]
gi|33585646|gb|AAH56028.1|	17237.69	Rps13-prov protein [Xenopus laevis]
gi|94385425|ref|XP_001004217.1|	17237.72	PREDICTED: similar to ribosomal protein S13 [Mus musculus]
gi|24266981|gb|AAN52387.1|	17109.6	ribosomal protein S13 [Branchiostoma belcheri]
jgi|Physo1_1|108227|estExt_fgenesh1_pm.C_30016	0	No title.
gi|50555724|ref|XP_505270.1|	16851.25	hypothetical protein [Yarrowia lipolytica]

gi|6320269|ref|NP_010349.1|	17018.33	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 and rat S13 r
gi|44985849|gb|AAS54460.1|	16965.28	AGL030Wp [Ashbya gossypii ATCC 10895]
gi|50288301|ref|XP_446579.1|	17050.32	unnamed protein product [Candida glabrata]
gi|50311723|ref|XP_455889.1|	16758.29	unnamed protein product [Kluyveromyces lactis]

527. Group probability: 0.9961. Peptides of the group

WNTHPGYISAVANR	62.01	54.9048	1584.78	1585.476	3	2	distinct	0	0.9719
AVAFSQYPQWSCTTSGSSMNHLWR	41.4	51.9769	2800.249	2801.728	1	3	distinct	0	0.8608

The equivalent proteins include

jgi|Physo1_1|122226|estExt_Genewise1.C_1020026	0	No title.

528. Group probability: 0.9960. Peptides of the group

VFHNTNCAQEYAGEVPTKLPIDVSTCK	80.35	51.1834	3077.459	3078.673	8	3	distinct	1	0.996

The equivalent proteins include

jgi|Physo1_1|142202|estExt_fgenesh1_pg.C_1090058	0	No title.

529. Group probability: 0.9958. Peptides of the group

LGLSHMWPVR	51.33	55.2954	1194.633	1195.531	1	2	distinct	0	0.9167
EGDPISGGDIFGLVHENDILHSHK	50.66	52.4256	2585.251	2584.773	1	2	distinct	0	0.9493

The equivalent proteins include

jgi|Physo1_1|108996|estExt_fgenesh1_pm.C_500009	0	No title.

530. Group probability: 0.9957. Peptides of the group

VGFYQEYLTGLHNAIAEGADVR	79.57	52.623	2422.192	2422.883	1	2	distinct	0	0.9957

The equivalent proteins include

jgi|Physo1_1|108505|estExt_fgenesh1_pm.C_120015	0	No title.

531. Group probability: 0.9956. Peptides of the group

VLGAEGDGTSLFFQPDIVPFVLAGLAHVEK	78.04	51.1129	3125.644	3127.112	1	3	distinct	0	0.9956

The equivalent proteins include

jgi|Physo1_1|129860|estExt_fgenesh1_pg.C_90137	0	No title.

532. Group probability: 0.9955. Peptides of the group

SISAFAPISHPSQCPWGIK	80.64	53.5733	2082.036	2082.358	4	2	distinct	0	0.9955

The equivalent proteins include

jgi|Physo1_1|109641|estExt_fgenesh1_pm.C_1890003	0	No title.

533. Group probability: 0.9955. Peptides of the group

HITPEEAPWPNAEEDPEEIVGAGFHLAPR	78.4	51.3726	3207.526	3208.649	4	3	distinct	0	0.9955

The equivalent proteins include

jgi|Physo1_1|132600|estExt_fgenesh1_pg.C_210160	0	No title.

534. Group probability: 0.9955. Peptides of the group

EVLEGLPNGLGAGIYYWEPAYIK	78.66	52.4722	2551.3	2551.489	3	2	distinct	0	0.9955

The equivalent proteins include

jgi|Physo1_1|156401|C_scaffold_17000070	0	No title.

535. Group probability: 0.9955. Peptides of the group

EGVAWQTTPLDVALEISQGLADQVVVAR	76.28	51.2963	2964.556	2964.766	5	2	distinct	0	0.9955

The equivalent proteins include

jgi|Physo1_1|129616|estExt_fgenesh1_pg.C_80127	0	No title.

536. Group probability: 0.9954. Peptides of the group

TKLPGSFGDFVK	47.62	55.1535	1294.692	1295.648	1	2	distinct	1	0.8929
EKQEEWLNSFINAGAQYR	55.23	53.2645	2182.044	2182.291	2	2	distinct	1	0.9573

The equivalent proteins include

jgi|Physo1_1|108638|estExt_fgenesh1_pm.C_210012	0	No title.

537. Group probability: 0.9954. Peptides of the group

LKPNSSVALHR	52.9	55.3841	1220.699	1221.505	1	2	distinct	0	0.9298
ILLELLNQMDGFDQATNVK	50.09	53.8888	2161.109	2162.607	1	2	distinct	0	0.9344

The equivalent proteins include

jgi|Physo1_1|122821|estExt_Genewise1.C_1140049	0	No title.

538. Group probability: 0.9954. Peptides of the group

VPTVDVSVVDLTCR	67.35	54.7407	1558.802	1557.818	5	2	distinct	0	0.8676

LTGMAFRVPTVDVSVVDLTCR	58.61	52.9194	2335.203	2336.333	8	3	distinct	1	0.9651

The equivalent proteins include

gi|85860541|ref|YP_462743.1|	35966.36	glyceraldehyde 3-phosphate dehydrogenase [Syntrophus aciditrophicus SB]

539. Group probability: 0.9954. Peptides of the group

INCGQLEELIEQAEDELSVIPVYLEHK	78.75	51.121	3167.57	3168.624	1	3	distinct	0	0.9954

The equivalent proteins include

jgi|Physo1_1|141651|estExt_fgenesh1_pg.C_1010064	0	No title.

540. Group probability: 0.9952. Peptides of the group

KTATPEIHAR	49.33	55.2581	1122.615	1123.797	1	2	distinct	1	0.9008
DEFEKYDHIHK	57.11	55.0963	1459.673	1459.8	1	2	distinct	1	0.9518

The equivalent proteins include

jgi|Physo1_1|109063|estExt_fgenesh1_pm.C_560001	0	No title.

541. Group probability: 0.9951. Peptides of the group

KLNGFLTNR	56.15	55.9383	1061.598	1062.471	2	2	distinct	1	0.8643
ALPVEGLTWGEGHK	70.98	54.6429	1492.767	1493.485	4	2	shared(2)	0	0.9873
SQVVIEVKPWEAETDLEELAAK	43.79	52.584	2483.279	2483.55	1	2	shared(2)	0	0.9003

The equivalent proteins include

jgi|Physo1_1|109567|estExt_fgenesh1_pm.C_1450002	0	No title.

542. Group probability: 0.9950. Peptides of the group

VGVASGVAAGAAMAAASYWQSSQDSAFDKYAAAR	74.96	50.6401	3334.568	3335.67	1	3	distinct	1	0.995

The equivalent proteins include

jgi|Physo1_1|158693|C_scaffold_129000003	0	No title.

543. Group probability: 0.9950. Peptides of the group

EGNDLYYEMIESGVNK	75.55	54.446	1859.825	1859.155	6	2	distinct	0	0.9111
TREGNDLYYEMIESGVNK	60.23	53.3632	2116.973	2116.541	3	2	distinct	1	0.9435

The equivalent proteins include

gi|83944756|ref|ZP_00957122.1|	51401.29	ATP synthase subunit B [Oceanicaulis alexandrii HTCC2633]

544. Group probability: 0.9949. Peptides of the group

RVFGITTLDVVR	49.49	55.197	1374.798	1374.764	4	+2,+3	distinct	1	0.9517
VAVLGAAGGIGQPMSLLLK	99.61	54.2417	1794.044	1794.864	3	2	shared(2)	0	0.9894

The equivalent proteins include

gi|57228274|gb|AAW44731.1|	35807.96	malate dehydrogenase, putative [Cryptococcus neoformans var. neoformans JEC21]

545. Group probability: 0.9949. Peptides of the group

IEQNFSNYSALHHR	81.33	54.3053	1714.818	1715.286	2	2	distinct	0	0.9949

The equivalent proteins include

jgi|Physo1_1|131057|estExt_fgenesh1_pg.C_140055	0	No title.

546. Group probability: 0.9949. Peptides of the group

LGDLGVLEFTDLNPELTPFQR	78.09	52.8127	2373.222	2374.295	1	2	distinct	0	0.9949

The equivalent proteins include

gi|62147616|emb|CAI72310.1|	96727.44	vacuolar proton translocating ATPase A subunit, putative [Phytophthora infestans]
jgi|Physo1_1|132996|estExt_fgenesh1_pg.C_230139	0	No title.

547. Group probability: 0.9948. Peptides of the group

HGLAYIPLVSPTTTEDR	79.87	53.9948	1868.963	1869.882	1	2	distinct	0	0.9948

The equivalent proteins include

jgi|Physo1_1|155994|C_scaffold_10000013	0	No title.

548. Group probability: 0.9948. Peptides of the group

LVLPEVIEEGDNVTFPNRGDTMVMHYTGK	76.56	50.8963	3260.584	3262.017	3	3	distinct	1	0.9948

The equivalent proteins include

jgi|Physo1_1|138654|estExt_fgenesh1_pg.C_650073	0	No title.

549. Group probability: 0.9947. Peptides of the group

TILGGLNEILAELLEQSLHK	78.43	53.7647	2190.226	2191.391	1	2	distinct	0	0.9947

The equivalent proteins include

jgi|Physo1_1|129879|estExt_fgenesh1_pg.C_90156	0	No title.

550. Group probability: 0.9947. Peptides of the group

IRLENEIQTYR	55.92	54.8709	1433.763	1434.654	3	2	shared(2)	1	0.9467
YCVQLSQIQAQISALEEQLQEIR	48.8	52.0122	2746.396	2747.096	3	+2,+3	distinct	0	0.9771

The equivalent proteins include

gi|623409|gb|AAA60544.1|	57384.13	keratin 10

551. Group probability: 0.9944. Peptides of the group

HFALSPELGVGYVINELDNTVSVHALDAK	75.91	51.1237	3107.593	3108.807	1	3	distinct	0	0.9944

The equivalent proteins include

jgi|Physo1_1|143807|estExt_fgenesh1_pg.C_1520014	0	No title.

552. Group probability: 0.9944. Peptides of the group

LREDGSSWTQVHR	44.5	54.9771	1569.765	1570.503	1	2	distinct	1	0.8645
RGTNYTLHNEALQK	69.67	54.5884	1643.838	1644.526	5	2	distinct	1	0.959

The equivalent proteins include

jgi|Physo1_1|155728|C_scaffold_7000057	0	No title.

553. Group probability: 0.9944. Peptides of the group

LTGMAFCVPTPNVSVVDLTCR	79.39	52.9605	2336.133	2336.782	6	3	distinct	0	0.9944

The equivalent proteins include

gi|94408078|ref|XP_978778.1|	22485.22	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]
gi|94408118|ref|XP_979290.1|	31442.78	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]

554. Group probability: 0.9943. Peptides of the group

TVFAMPETAIGFFPDVGASYLLPR	75.63	52.3914	2598.319	2599.267	6	2	distinct	0	0.9943

The equivalent proteins include

jgi|Physo1_1|144060|estExt_fgenesh1_pg.C_1640015	0	No title.

555. Group probability: 0.9943. Peptides of the group

SLVGGFEFMPSPNKR	79.68	54.4285	1664.834	1665.779	5	2	distinct	1	0.9943

The equivalent proteins include

jgi|Physo1_1|108538|estExt_fgenesh1_pm.C_150007	0	No title.

556. Group probability: 0.9942. Peptides of the group

LFDPETAHQVAVQCAR	78.96	54.1376	1840.889	1841.562	3	2	distinct	0	0.9942

The equivalent proteins include

jgi|Physo1_1|109029|estExt_fgenesh1_pm.C_540003	0	No title.

557. Group probability: 0.9938. Peptides of the group

LVIIANNTPPLRK	55.82	54.9822	1447.887	1448.852	15	2	shared(2)	1	0.9498
TGVHHFTGTNNDLGTACGK	60.12	54.1271	1985.901	1985.974	3	2	distinct	0	0.9727

The equivalent proteins include

jgi|Physo1_1|108669|estExt_fgenesh1_pm.C_230019	0	No title.

558. Group probability: 0.9936. Peptides of the group

ALVHVGPCEIWLDNTK	77.79	53.9962	1850.935	1851.821	6	2	distinct	0	0.9936

The equivalent proteins include

jgi|Physo1_1|133344|estExt_fgenesh1_pg.C_250098	0	No title.

559. Group probability: 0.9935. Peptides of the group

SNYQFEKPFLWLAR	51.39	54.2815	1797.92	1798.726	4	+2,+3	distinct	0	0.9935

The equivalent proteins include

jgi|Physo1_1|108912|estExt_fgenesh1_pm.C_420006	0	No title.

560. Group probability: 0.9934. Peptides of the group

IFGVTTLDVVR	66.68	55.5937	1218.697	1219.442	1	2	shared(3)	0	0.9568
RIFGVTTLDVVR	67.93	55.1294	1374.798	1375.471	35	+2,+3	shared(2)	1	0.9958
VAVLGAAGGIGQPLSLLMK	61	54.2417	1794.044	1794.864	2	2	distinct	0	0.6858

The equivalent proteins include

gi|5929964|gb|AAD56659.1|	36347.11	malate dehydrogenase [Glycine max]

561. Group probability: 0.9933. Peptides of the group

GLVLVEIAPTTTVEEIR	46.27	54.0183	1839.035	1840.195	1	2	distinct	0	0.9013
ITIAEVEELVQPGEIHPDEVHLPGVYVQR	47.37	50.8462	3265.698	3266.671	2	3	distinct	0	0.9325

The equivalent proteins include

jgi|Physo1_1|109150|estExt_fgenesh1_pm.C_640006	0	No title.

562. Group probability: 0.9932. Peptides of the group

SIVHPSYDSNTLNNDIMLIK (00000000000000000010000)	61.13	53.3683	2273.136	2273.429	17	+2,+3	distinct	0	0.9932

The equivalent proteins include

gi|230196|pdb|1NTP|	23977.52	Modified Beta Trypsin (Monoisopropylphosphoryl Inhibited) (E.C.3.4.21.4) (Neutron Data)

563. Group probability: 0.9932. Peptides of the group

VMQGIQSGSMHAATHK	77.24	54.2539	1681.803	1682.35	1	2	distinct	0	0.9932

The equivalent proteins include

jgi|Physo1_1|135828|estExt_fgenesh1_pg.C_410019	0	No title.

564. Group probability: 0.9931. Peptides of the group

VIQHNGYGTVK	47.43	55.7524	1214.641	1215.417	1	2	distinct	0	0.8857
KVDVSNVYVVNPGNAVVTVNK	50.05	53.1716	2214.201	2214.453	1	2	distinct	1	0.9396

The equivalent proteins include

jgi|Physo1_1|132156|estExt_fgenesh1_pg.C_190106	0	No title.
jgi|Physo1_1|132157|estExt_fgenesh1_pg.C_190107	0	No title.

565. Group probability: 0.9930. Peptides of the group

LGANSLLDIVVFGR	85.27	54.9751	1472.835	1473.587	5	2	shared(2)	0	0.9963
FHSKNTVLATGGYGR	71.1	54.6092	1606.822	1607.473	7	2	distinct	1	0.8898

The equivalent proteins include

gi|66505480|ref|XP_623065.1|	73271.54	PREDICTED: similar to ENSANGP00000010243 [Apis mellifera]

566. Group probability: 0.9929. Peptides of the group

VLNALDPEAASNPFKPFHER	74.98	53.5214	2251.138	2251.68	4	2	distinct	0	0.9929

The equivalent proteins include

jgi|Physo1_1|129293|estExt_fgenesh1_pg.C_70118	0	No title.

567. Group probability: 0.9929. Peptides of the group

DSTIIMQLLR	62.92	55.7197	1188.654	1188.603	4	2	shared(5)	0	0.81
LAFDDAIAELDTLSEESYKDSTLIMQLLR	69	50.8547	3299.648	3300.563	9	3	distinct	1	0.9899

The equivalent proteins include

gi|83772732|dbj|BAE62860.1|	29229.67	unnamed protein product [Aspergillus oryzae]
gi|70989229|ref|XP_749464.1|	29197.65	hypothetical protein Afu2g03290 [Aspergillus fumigatus Af293]
gi|67534609|ref|XP_662105.1|	29211.63	hypothetical protein AN4501.2 [Aspergillus nidulans FGSC A4]
gi|13430385|gb|AAK25817.1|	29210.68	ARTA [Emericella nidulans]
gi|38490697|gb|AAR21678.1|	28585.52	14-3-3-like protein [Aspergillus flavus]

568. Group probability: 0.9928. Peptides of the group

LFFASVVPLDHLQEYPVPTR	74.74	52.983	2327.231	2327.484	3	2	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|134104|estExt_fgenesh1_pg.C_300015	0	No title.

569. Group probability: 0.9928. Peptides of the group

LFIILSPVGPYYPEGFNPVK	74.85	53.5738	2249.214	2249.69	28	2	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|109235|estExt_fgenesh1_pm.C_780004	0	No title.

570. Group probability: 0.9928. Peptides of the group

GLTFQLPTVIHGTNTMVSAAK	74.41	53.4609	2185.156	2186.254	4	2	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|108159|estExt_fgenesh1_pm.C_10024	0	No title.

571. Group probability: 0.9928. Peptides of the group

FIIAPEYGYGHEGFAPK	76.13	53.9238	1894.925	1895.571	5	2	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|141508|estExt_fgenesh1_pg.C_990053	0	No title.

572. Group probability: 0.9928. Peptides of the group

HALHESAQQAWEVTR	76.97	54.1732	1761.855	1762.574	1	2	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|129732|estExt_fgenesh1_pg.C_90009	0	No title.

573. Group probability: 0.9927. Peptides of the group

YTLAGMEVSALLGR (0000001000000000)	77.37	54.7246	1495.77	1496.39	6	2	distinct	0	0.9927

The equivalent proteins include

gi|73660119|emb|CAI82726.1|	50754.15	ATP synthase F1, beta subunit [Dehalococcoides sp. CBDB1]
gi|57225115|gb|AAW40172.1|	50764.11	ATP synthase F1, beta subunit [Dehalococcoides ethenogenes 195]

574. Group probability: 0.9927. Peptides of the group

ASFVEFINEHAGTYR	76.78	54.14	1739.827	1740.363	5	2	distinct	0	0.9927

The equivalent proteins include

jgi|Physo1_1|109255|estExt_fgenesh1_pm.C_810002	0	No title.

575. Group probability: 0.9927. Peptides of the group

ILHSTGVETDEAR	77.76	55.1014	1426.705	1427.319	5	2	distinct	0	0.9927

The equivalent proteins include

jgi|Physo1_1|127178|estExt_fgenesh1_pg.C_10158	0	No title.

576. Group probability: 0.9926. Peptides of the group

ICVLGNAVHCEMAEK	76.76	54.3248	1729.795	1730.406	3	2	distinct	0	0.9926

The equivalent proteins include

jgi|Physo1_1|109643|estExt_fgenesh1_pm.C_1910002	0	No title.

577. Group probability: 0.9926. Peptides of the group

LYHSASLVNYGCLPQTWEDPNHVDAATK	73.01	50.9248	3185.488	3186.913	5	3	distinct	0	0.9926

The equivalent proteins include

jgi|Physo1_1|135461|estExt_fgenesh1_pg.C_380095	0	No title.

578. Group probability: 0.9926. Peptides of the group

VDHYTHPDR	47.87	55.318	1138.516	1139.274	1	2	distinct	0	0.8839
FVGAAPQLSHK	54.02	55.4763	1153.624	1154.512	4	2	distinct	0	0.9362

The equivalent proteins include

jgi|Physo1_1|144183|estExt_fgenesh1_pg.C_1710013	0	No title.

579. Group probability: 0.9925. Peptides of the group

RLPLSPAEVESINSGLAFL	74.76	53.538	2012.094	2013.23	6	2	distinct	1	0.9925

The equivalent proteins include

jgi|Physo1_1|155279|C_scaffold_1000083	0	No title.

580. Group probability: 0.9925. Peptides of the group

VLVLCNLKPR	55.16	55.1485	1210.722	1211.165	5	2	distinct	0	0.9406
QIASGLVHHYSLEQMQDAR	44.83	53.4971	2182.059	2183.505	1	3	distinct	0	0.8731

The equivalent proteins include

jgi|Physo1_1|155217|C_scaffold_1000021	0	No title.

581. Group probability: 0.9923. Peptides of the group

LTLPHEYAYGER	47.52	54.9822	1447.71	1448.815	1	2	distinct	0	0.8923
AGDGVNFPKPGQTVSVHYVGTLTDGSK	47.7	51.8864	2730.361	2730.935	1	3	distinct	0	0.9281

The equivalent proteins include

jgi|Physo1_1|108555|estExt_fgenesh1_pm.C_150024	0	No title.

582. Group probability: 0.9921. Peptides of the group

YPIKHGIVTNWDDMEK	70.94	53.922	1944.94	1946.416	2	+2,+3	distinct	1	0.9873
VAPEEHPVLLTEAPINPK	81.4	53.7297	1953.057	1953.885	13	2	shared(10)	0	0.9887

The equivalent proteins include

gi|113239|sp|P27132|ACT2_NAEFO	41468.59	Actin-2 (Actin II)

583. Group probability: 0.9921. Peptides of the group

LLESFVHQGPFFLGDK	75.43	54.0579	1832.946	1833.289	4	2	distinct	0	0.9921

The equivalent proteins include

jgi|Physo1_1|129901|estExt_fgenesh1_pg.C_90178	0	No title.
jgi|Physo1_1|144900|estExt_fgenesh1_pg.C_3170004	0	No title.
jgi|Physo1_1|145195|estExt_fgenesh1_pg.C_6020001	0	No title.

584. Group probability: 0.9918. Peptides of the group

IINQPTAAAIAYGLDKK	97.09	54.8034	1785.999	1787.369	3	2	distinct	1	0.9918

The equivalent proteins include

gi|640325|pdb|1NGB|	42542.9	Heat-Shock Cognate 70kd Protein (44kd Atpase N-Terminal Fragment) (E.C.3.6.1.3) Mutant With Glu 17

585. Group probability: 0.9916. Peptides of the group

IINEPTAAALSFGLDKK	96.71	54.8034	1786.983	1787.369	4	2	distinct	1	0.9916

The equivalent proteins include

gi|15828694|ref|NP_326054.1|	65480.66	molecular chaperone DnaK [Mycoplasma pulmonis UAB CTIP]

586. Group probability: 0.9915. Peptides of the group

APFAGAMGQQLAAIDDNVLVGAPLFQIVK	68.76	51.5103	2953.573	2953.411	2	2	distinct	0	0.9915

The equivalent proteins include

jgi|Physo1_1|108495|estExt_fgenesh1_pm.C_120005	0	No title.

587. Group probability: 0.9915. Peptides of the group

SLSVERPTYTNLNR	47.15	54.6192	1648.853	1648.918	1	2	distinct	0	0.8971
RTIQFVDWCPTGFK	68.04	54.1994	1753.861	1754.812	2	2	shared(4)	1	0.9837
IHFMLSSYAPVISAEK (0000100000000000)	84.73	54.3337	1807.918	1808.932	1	2	shared(3)	0	0.9876

The equivalent proteins include

jgi|Physo1_1|119273|estExt_Genewise1.C_610078	0	No title.

588. Group probability: 0.9914. Peptides of the group

HFEINSVGPFLTTR	75.41	54.7152	1616.831	1617.821	1	2	distinct	0	0.9914

The equivalent proteins include

jgi|Physo1_1|138877|estExt_fgenesh1_pg.C_670079	0	No title.
jgi|Physo1_1|138881|estExt_fgenesh1_pg.C_670083	0	No title.

589. Group probability: 0.9905. Peptides of the group

NMSVIAHVDHGK (00100000000000)	76.73	55.4054	1306.645	1307.194	11	2	shared(2)	0	0.9916
IGSPLFSVKAHLPVLESFGFTADLR	44.88	52.0441	2700.464	2700.796	1	3	distinct	1	0.9009

The equivalent proteins include

gi|66805999|ref|XP_636721.1|	93511.92	elongation factor 2 [Dictyostelium discoideum AX4]

590. Group probability: 0.9905. Peptides of the group

VHAILDRYPENYK	74.7	54.7661	1616.831	1617.405	8	2	distinct	1	0.9905

The equivalent proteins include

jgi|Physo1_1|139617|estExt_fgenesh1_pg.C_760028	0	No title.

591. Group probability: 0.9902. Peptides of the group

MIIAGGANLPLEAVLPVFLGGLPLK	69.03	52.59	2502.465	2503.709	2	2	distinct	0	0.9902

The equivalent proteins include

jgi|Physo1_1|134803|estExt_fgenesh1_pg.C_340039	0	No title.

592. Group probability: 0.9901. Peptides of the group

AQFQHGAQLSPVYGR	73.49	54.9108	1657.832	1658.116	2	2	distinct	0	0.9901

The equivalent proteins include

jgi|Physo1_1|108995|estExt_fgenesh1_pm.C_500008	0	No title.

593. Group probability: 0.9900. Peptides of the group

VQLDTGVPVLFGVLTVLNEQQAK	69.65	52.6314	2467.369	2468.586	1	2	distinct	0	0.99

The equivalent proteins include

jgi|Physo1_1|129173|estExt_fgenesh1_pg.C_60330	0	No title.

594. Group probability: 0.9898. Peptides of the group

ATPPPSAPVALNKPAAGNK	71.44	54.4289	1799.989	1800.254	13	2	distinct	0	0.9898

The equivalent proteins include

jgi|Physo1_1|134237|estExt_fgenesh1_pg.C_300148	0	No title.

595. Group probability: 0.9898. Peptides of the group

HLLALINDILDLSKIEAGK	76.1	53.4796	2075.199	2073.811	28	3	distinct	1	0.9898

The equivalent proteins include

gi|67930180|ref|ZP_00523355.1|	87462.27	Response regulator receiver:ATP-binding region, ATPase-like:Histidine kinase, HAMP region:Histidine

596. Group probability: 0.9897. Peptides of the group

FYVQDGVTHEMPHSTFSAIK	48.19	53.0201	2293.084	2293.781	2	+2,+3	distinct	0	0.9897

The equivalent proteins include

jgi|Physo1_1|108891|estExt_fgenesh1_pm.C_400001	0	No title.

597. Group probability: 0.9895. Peptides of the group

RTIFIGPPGCGK	74.18	55.4578	1301.691	1302.775	2	2	distinct	1	0.9895

The equivalent proteins include

jgi|Physo1_1|109413|estExt_fgenesh1_pm.C_1020001	0	No title.

598. Group probability: 0.9895. Peptides of the group

QLCTGEAGVGQSGKPLHYK	70.86	53.5992	2029.005	2030.143	4	2	distinct	0	0.9895

The equivalent proteins include

jgi|Physo1_1|108195|estExt_fgenesh1_pm.C_20027	0	No title.

599. Group probability: 0.9892. Peptides of the group

VSETVKVPEHINHPDYAETGVPESEQR	69.16	51.3695	3046.463	3047.713	1	3	distinct	1	0.9892

The equivalent proteins include

jgi|Physo1_1|108381|estExt_fgenesh1_pm.C_70026	0	No title.

600. Group probability: 0.9891. Peptides of the group

LDLLKLAPGGHIGR	60.34	55.0162	1458.867	1458.974	7	+2,+3	distinct	1	0.9891

The equivalent proteins include

gi|94733357|emb|CAK04707.1|	20802.26	ribosomal protein L4 [Danio rerio]
gi|54261775|ref|NP_998272.1|	42810.18	ribosomal protein L4 [Danio rerio]

601. Group probability: 0.9889. Peptides of the group

ILHAQGVSFDSVNVLDHPEIR	69.28	52.9447	2345.213	2345.263	1	2	distinct	0	0.9889

The equivalent proteins include

jgi|Physo1_1|127728|estExt_fgenesh1_pg.C_20304	0	No title.

602. Group probability: 0.9888. Peptides of the group

KTVAVGVIK	47.89	56.6012	913.596	914.553	1	2	shared(2)	1	0.881
IGGIGTVPVGR	47.13	55.1691	1024.603	1026.063	1	2	shared(7)	0	0.8841
EHALLAFTLGVK	64.61	55.2154	1297.739	1299.156	1	2	shared(4)	0	0.9343
SVEMHHEALIEAVPGDNVGFNVK	57.63	52.5443	2491.216	2492.428	3	2	distinct	0	0.9065

The equivalent proteins include

gi|90265663|dbj|BAE91879.1|	50435.44	elongation factor 1-alpha [Athalia rosae]

603. Group probability: 0.9888. Peptides of the group

VMQGHAAANMVPVICSNR	70.63	53.7299	1953.933	1953.963	1	2	distinct	0	0.9888

The equivalent proteins include

jgi|Physo1_1|158732|C_scaffold_134000006	0	No title.

604. Group probability: 0.9887. Peptides of the group

KLFHPEQLISGK	45.03	54.9697	1395.787	1396.404	1	2	distinct	1	0.866
RTIQFVDWCPTGFK	68.04	54.1994	1753.861	1754.812	2	2	shared(4)	1	0.9837
IHFMLSSYAPVISAEK (000010000000000000)	84.73	54.3337	1807.918	1808.932	1	2	shared(3)	0	0.9876

The equivalent proteins include

gi|82400128|gb|ABB72803.1|	50580.75	alpha-tubulin-like protein [Solanum tuberosum]
gi|8928408|sp|Q9ZRB7|TBA_WHEAT	50395.6	Tubulin alpha chain
gi|1556446|gb|AAB08791.1|	50265.56	alpha tubulin [Hordeum vulgare]
gi|84105379|gb|ABC54661.1|	42854.46	alpha tubulin 1 [Trimastix marina]
gi|9965991|gb|AAG02564.1|	50293.58	alpha-tubulin [Daucus carota]
gi|3163944|emb|CAA06618.1|	50383.63	alpha-tubulin 1 [Eleusine indica]
gi|3163946|emb|CAA06619.1|	50395.67	alpha-tubulin 1 [Eleusine indica]
gi|1619297|emb|CAA69724.1|	50353.58	alpha-tubulin 2 [Hordeum vulgare subsp. vulgare]
gi|578450|emb|CAA77810.1|	50273.62	alpha-Tubulin [Oxytricha granulifera]
gi|71090024|gb|AAZ23863.1|	50082.49	alpha-tubulin [Sterkiella histriomuscorum]
gi|92896308|gb|ABE93145.1|	50206.55	Cell division protein FtsZ [Medicago truncatula]
gi|37529488|gb|AAQ92662.1|	50193.56	alpha-tubulin 2 [Gossypium hirsutum]
gi|37529490|gb|AAQ92663.1|	50223.57	alpha-tubulin 4 [Gossypium hirsutum]
gi|30683070|ref|NP_849388.1|	47889.17	TUA6 [Arabidopsis thaliana]
gi|76257841|gb|ABA41238.1|	44925.34	alpha-tubulin [Cyanophora paradoxa]
gi|76257847|gb|ABA41241.1|	44358.06	alpha-tubulin [Coleochaete scutata]
gi|76257849|gb|ABA41242.1|	44418.96	alpha-tubulin [Mantoniella squamata]
gi|76257861|gb|ABA41248.1|	44378.99	alpha-tubulin [Pterosperma cristatum]
gi|76257863|gb|ABA41249.1|	44312.96	alpha-tubulin [Pterosperma cristatum]
gi|77745465|gb|ABB02631.1|	50303.64	unknown [Solanum tuberosum]
gi|15222856|ref|NP_175423.1|	50193.56	TUA2 [Arabidopsis thaliana]
gi|15233627|ref|NP_193232.1|	50190.56	TUA6 [Arabidopsis thaliana]
gi|1174592|sp|P46259|TBA1_PEA	50305.62	Tubulin alpha-1 chain
gi|29423813|gb|AAO73546.1|	50375.6	alpha-tubulin [Ceratopteris richardii]
gi|296494|emb|CAA48927.1|	50381.68	alpha tubulin [Anemia phyllitidis]
gi|20413|emb|CAA47635.1|	50179.54	alpha-tubulin [Prunus dulcis]
gi|22147|emb|CAA33734.1|	50383.63	alpha1-tubulin [Zea mays]
gi|22148|emb|CAA33733.1|	50383.63	alpha2-tubulin [Zea mays]
gi|4165488|emb|CAA10663.1|	50381.61	alpha-tubulin 3 [Hordeum vulgare subsp. vulgare]
gi|25396550|dbj|BAC24800.1|	50222.58	alpha tubulin [Physcomitrella patens]
gi|1101025|gb|AAB36609.1|	42638.12	alpha-tubulin [Eucalyptus globulus subsp. bicostata]
gi|27819095|gb|AAO23139.1|	50261.58	alpha tubulin [Populus tremuloides]
gi|29124983|gb|AAO63781.1|	50276.59	alpha-tubulin 1 [Populus tremuloides]
gi|15029368|gb|AAK81858.1|	50379.67	alpha tubulin subunit [Rosa hybrid cultivar]
gi|16226462|gb|AAL16174.1|	50155.76	AT4g14960/dl3520c [Arabidopsis thaliana]
gi|51988174|emb|CAE52515.1|	50369.61	alpha tubulin [Setaria viridis]
gi|6723478|emb|CAB66336.1|	50227.6	alpha-tubulin [Betula pendula]
gi|17402467|emb|CAD13176.1|	50360.69	alpha-tubulin [Nicotiana tabacum]
gi|17402469|emb|CAD13177.1|	50387.7	alpha-tubulin [Nicotiana tabacum]
gi|17402471|emb|CAD13178.1|	50405.63	alpha-tubulin [Nicotiana tabacum]
gi|1743242|emb|CAA71141.1|	42363.19	alpha-tubulin [Histriculus cavicola]
gi|21632090|gb|AAL33695.1|	40779.4	alpha-tubulin [Halteria grandinella]
gi|21632086|gb|AAL33693.1|	40753.39	alpha-tubulin [Halteria grandinella]
gi|21632088|gb|AAL33694.1|	40749.42	alpha-tubulin [Halteria grandinella]

gi|21632092|gb|AAL33696.1|	40721.39	alpha-tubulin [Halteria grandinella]
gi|21632098|gb|AAL33699.1|	40837.4	alpha-tubulin [Halteria grandinella]
gi|34733239|gb|AAQ81585.1|	50089.48	putative tubulin alpha-2/alpha-4 chain [Brassica napus]
gi|22037131|gb|AAM89908.1|	40416.33	alpha-tubulin [Eutintinnus pectinis]
gi|22037135|gb|AAM89909.1|	41500.85	alpha-tubulin [Eutintinnus pectinis]
gi|23957214|gb|AAN40709.1|	40880.55	alpha-tubulin [Tintinnopsis tubulosoides]
gi|23957216|gb|AAN40710.1|	40901.59	alpha-tubulin [Tintinnopsis tubulosoides]
gi|23957221|gb|AAN40711.1|	41355.7	alpha-tubulin [Strombidium sp.]
gi|23957223|gb|AAN40712.1|	41334.81	alpha-tubulin [Strombidium sp.]
gi|23957225|gb|AAN40713.1|	40472.26	alpha-tubulin [Strombidium sp.]
gi|23957227|gb|AAN40714.1|	40634.37	alpha-tubulin [Strombidium sp.]
gi|23957263|gb|AAN40724.1|	41116.59	alpha-tubulin [Metacylis angulata]
gi|23957265|gb|AAN40725.1|	41480.9	alpha-tubulin [Metacylis angulata]
gi|23957267|gb|AAN40726.1|	40799.59	alpha-tubulin [Metacylis angulata]
gi|23957269|gb|AAN40727.1|	40730.52	alpha-tubulin [Metacylis angulata]
gi|23957275|gb|AAN40728.1|	41523.95	alpha-tubulin [Laboea strobila]
gi|23957277|gb|AAN40729.1|	41109.74	alpha-tubulin [Laboea strobila]
gi|23957281|gb|AAN40731.1|	41095.73	alpha-tubulin [Laboea strobila]
gi|23957251|gb|AAN40720.1|	40040.21	alpha-tubulin [Strombidinopsis sp.]
gi|23957257|gb|AAN40723.1|	40651.45	alpha-tubulin [Strombidinopsis sp.]
gi|23957290|gb|AAN40732.1|	40748.54	alpha-tubulin [Favella ehrenbergii]
gi|23957292|gb|AAN40733.1|	40617.43	alpha-tubulin [Favella ehrenbergii]
gi|62734655|gb|AAX96764.1|	50389.59	Tubulin/FtsZ family, GTPase domain, putative [Oryza sativa (japonica cultivar-group)]
gi|37789885|gb|AAP32191.1|	42754.39	alpha-tubulin [Trifolium repens]
gi|56481497|gb|AAV92379.1|	50294.6	alpha tubulin 1 [Pseudotsuga menziesii var. menziesii]
gi|54300498|gb|AAV32824.1|	43499.4	alpha-tubulin [Peridinium foliaceum]
gi|54300500|gb|AAV32825.1|	43469.43	alpha-tubulin [Kryptoperidinium foliaceum]

605. Group probability: 0.9887. Peptides of the group

APAAAASPAPAAAPTAAPADPVIPAPAEPEKPK	66.26	51.2711	3012.592	3013.006	3	3	distinct	0	0.9887

The equivalent proteins include

jgi|Physo1_1|140019|estExt_fgenesh1_pg.C_810008	0	No title.

606. Group probability: 0.9887. Peptides of the group

LVGLACTHQTTPGTVAFR	70.49	53.8663	1927.994	1928.369	3	2	distinct	0	0.9887

The equivalent proteins include

jgi|Physo1_1|131940|estExt_fgenesh1_pg.C_180049	0	No title.

607. Group probability: 0.9886. Peptides of the group

AVIGDQWADLLVGLLGHSAASK	68.62	53.1655	2220.19	2221.514	1	2	distinct	0	0.9886

The equivalent proteins include

jgi|Physo1_1|136952|estExt_fgenesh1_pg.C_490090	0	No title.

608. Group probability: 0.9882. Peptides of the group

FSHALVDYQYLANLIGLK	70.03	53.6366	2064.104	2065.266	2	2	distinct	0	0.9882

The equivalent proteins include

jgi|Physo1_1|139488|estExt_fgenesh1_pg.C_740059	0	No title.

609. Group probability: 0.9882. Peptides of the group

KGPAPLNLEIPPYK	71.87	54.6043	1535.871	1537.359	7	2	distinct	1	0.9882

The equivalent proteins include

jgi|Physo1_1|108628|estExt_fgenesh1_pm.C_210002	0	No title.

610. Group probability: 0.9881. Peptides of the group

NLQGIIAILGMDELSEDDKLTVAR (000000000000100000000000000)	117.63	52.4295	2613.368	2614.676	21	2	distinct	1	0.9881

The equivalent proteins include

gi|2116558|dbj|BAA20135.1|	60284.43	F1 ATPase [Pisum sativum]

611. Group probability: 0.9880. Peptides of the group

AHELVQSYADAEAQAAPPAFTHITLR	68.53	51.8241	2806.404	2807.683	1	3	distinct	0	0.988

The equivalent proteins include

jgi|Physo1_1|133601|estExt_fgenesh1_pg.C_270013	0	No title.

612. Group probability: 0.9880. Peptides of the group

NFMPFGGSFHCATCDVR	70.22	53.6546	2001.828	2002.697	10	2	distinct	0	0.988

The equivalent proteins include

jgi|Physo1_1|108613|estExt_fgenesh1_pm.C_200001	0	No title.

613. Group probability: 0.9876. Peptides of the group

ESTIHLVLR	71.03	55.1897	1066.613	1067.325	13	2	shared(3)	0	0.9848
IQEKEGIPPDQQR	55.59	54.6494	1536.79	1537.455	2	2	distinct	1	0.9491

The equivalent proteins include

gi|73945898|ref|XP_852338.1|	11035.83	PREDICTED: similar to CG5271-PA [Canis familiaris]
gi|76638698|ref|XP_869731.1|	103189.67	PREDICTED: similar to ubiquitin C isoform 3 [Bos taurus]
gi|76638702|ref|XP_879056.1|	53447.48	PREDICTED: similar to ubiquitin C isoform 5 [Bos taurus]
gi|76638704|ref|XP_879141.1|	68981.2	PREDICTED: similar to ubiquitin C isoform 6 [Bos taurus]
gi|76638708|ref|XP_879323.1|	95909.61	PREDICTED: similar to ubiquitin C isoform 8 [Bos taurus]
gi|76638716|ref|XP_879643.1|	77522.8	PREDICTED: similar to ubiquitin C isoform 12 [Bos taurus]
gi|76638724|ref|XP_879987.1|	86106.45	PREDICTED: similar to ubiquitin C isoform 16 [Bos taurus]
gi|76638728|ref|XP_586525.2|	86064.41	PREDICTED: similar to ubiquitin C isoform 1 [Bos taurus]
gi|76638730|ref|XP_880223.1|	85894.1	PREDICTED: similar to ubiquitin C isoform 18 [Bos taurus]
gi|76638736|ref|XP_880428.1|	95205.37	PREDICTED: similar to ubiquitin C isoform 21 [Bos taurus]
gi|76638740|ref|XP_880581.1|	94648.06	PREDICTED: similar to ubiquitin C isoform 23 [Bos taurus]
gi|76638744|ref|XP_880724.1|	94606.01	PREDICTED: similar to ubiquitin C isoform 25 [Bos taurus]
gi|76638746|ref|XP_880794.1|	94648.06	PREDICTED: similar to ubiquitin C isoform 26 [Bos taurus]
gi|4102845|gb|AAD01603.1|	8074.37	ubiquitin [Entamoeba invadens]
gi|67479295|ref|XP_655029.1|	8692.69	ubiquitin [Entamoeba histolytica HM-1:IMSS]
gi|9295|emb|CAA46497.1|	7845.23	ubiquitin [Entamoeba histolytica]
gi|23451860|gb|AAN32889.1|	13290.07	ubiquitin extension protein [Heterodera glycines]

614. Group probability: 0.9873. Peptides of the group

KIWEVHQGEGVDSK	70.97	54.5059	1610.805	1611.076	5	2	distinct	1	0.9873

The equivalent proteins include

jgi|Physo1_1|134434|estExt_fgenesh1_pg.C_320005	0	No title.

615. Group probability: 0.9873. Peptides of the group

VHAPPGGGSSWSFGDDPAPAPTGR	68.9	52.9974	2319.067	2320.08	3	3	distinct	0	0.9873

The equivalent proteins include

jgi|Physo1_1|132854|estExt_fgenesh1_pg.C_220202	0	No title.

616. Group probability: 0.9872. Peptides of the group

AEPSLHWIDYLGSMVK	69.96	54.1768	1844.913	1846.146	2	2	distinct	0	0.9872

The equivalent proteins include

gi|66270177|gb|AAY43418.1|	22365.38	20S proteasome subunit [Phytophthora infestans]
jgi|Physo1_1|119339|estExt_Genewise1.C_610144	0	No title.

617. Group probability: 0.9871. Peptides of the group

MSMNPFCEIAVEEAIR	85.91	53.8677	1895.858	1897.246	9	2	distinct	0	0.9871

The equivalent proteins include

gi|83859194|ref|ZP_00952715.1|	26885.32	electron transfer flavoprotein beta subunit [Oceanicaulis alexandrii HTCC2633]
gi|23394375|gb|AAN31477.1|	27072.63	electron transfer flavoprotein beta subunit [Phytophthora infestans]
jgi|Physo1_1|109126|estExt_fgenesh1_pm.C_620003	0	No title.
gi|50930317|ref|XP_474686.1|	27565.83	OSJNBb0006L01.5 [Oryza sativa (japonica cultivar-group)]

618. Group probability: 0.9870. Peptides of the group

ILINHLVESR	79.45	55.2104	1192.693	1193.567	9	2	distinct	0	0.987

The equivalent proteins include

jgi|Physo1_1|127239|estExt_fgenesh1_pg.C_10219	0	No title.

619. Group probability: 0.9870. Peptides of the group

VPTPNVSVVDLTCR	73.06	54.7391	1555.803	1557.293	3	2	distinct	0	0.8969
ITGMAFRVPTPNVSVVDLTCR	55.82	52.9126	2332.203	2333.52	1	3	distinct	1	0.8743

The equivalent proteins include

gi|229279|prf||681085A	35915.24	dehydrogenase,glyceraldehydephosphate

gi|54635963|gb|EAL25366.1|	37437.25	GA21475-PA [Drosophila pseudoobscura]
gi|40889053|pdb|1J0X|R	35849.25	Chain R, Crystal Structure Of The Rabbit Muscle Glyceraldehyde-3- Phosphate Dehydrogenase (Gapdh)
gi|1066045|gb|AAA81516.1|	11749.82	glyceraldehyde-3-phosphate dehydrogenase
gi|1218048|gb|AAA91804.1|	30745.73	glyceraldehyde-3-phosphate dehydrogenase
gi|65987|pir||DEPGG3	35914.25	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - pig
gi|1841758|gb|AAB47507.1|	33731.22	glyceraldehyde-phosphate-dehydrogenase [Bos taurus]
gi|2687661|gb|AAB88869.1|	35972.41	glyceraldehyde-3-phosphate dehydrogenase [Columba livia]
gi|2623288|gb|AAC16069.1|	19975.13	glyceraldehyde-3-phosphate dehydrogenase [Ovis aries]
gi|1730158|sp|P51640|G3P_MESAU	33739.32	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|3445501|gb|AAC32447.1|	13071.82	glyceraldehyde-3-phosphate dehydrogenase [Cavia porcellus]
gi|89272932|emb|CAJ82888.1|	36098.28	glyceraldehyde 3 phosphate dehydrogenase [Xenopus tropicalis]
gi|2506441|sp|P00355|G3P_PIG	36041.36	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|6166169|sp|Q28554|G3P_SHEEP	34937.79	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|1730164|sp|P51469|G3P_XENLA	36017.26	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|6679939|ref|NP_032111.1|	48096.38	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic [Mus musculus]
gi|62652560|ref|XP_576287.1|	22717.37	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - m
gi|50978862|ref|NP_001003142.1|	36066.26	glyceraldehyde-3-phosphate dehydrogenase [Canis familiaris]
gi|57163839|ref|NP_001009307.1|	36018.31	glyceraldehyde-3-phosphate dehydrogenase [Felis catus]
gi|4105596|gb|AAD02474.1|	35909.37	glyceraldehyde-3-phosphate dehydrogenase [Gallus gallus]
gi|1773078|gb|AAB40155.1|	16172.25	glyceraldehyde-3-phosphate dehydrogenase [Sus scrofa]
gi|55741036|gb|AAV64182.1|	35999.29	glyceraldehyde-3-phosphate dehydrogenase [Spermophilus citellus]
gi|72496432|dbj|BAE19661.1|	17001.93	glyceraldehyde 3-phosphate dehydrogenase [Oryctolagus cuniculus]
gi|74212012|dbj|BAE40174.1|	36074.21	unnamed protein product [Mus musculus]
gi|74137577|dbj|BAE35822.1|	15638.9	unnamed protein product [Mus musculus]
gi|74141423|dbj|BAE35989.1|	36044.36	unnamed protein product [Mus musculus]
gi|74194852|dbj|BAE26016.1|	36102.33	unnamed protein product [Mus musculus]
gi|74203253|dbj|BAE20812.1|	25339.9	unnamed protein product [Mus musculus]
gi|63401|emb|CAA23697.1|	14687.46	unnamed protein product [Gallus gallus]
gi|2623266|gb|AAB86435.1|	29991.26	glyceraldehyde 3-phosphate dehydrogenase [Ovis aries]
gi|73997649|ref|XP_854083.1|	17391.78	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Canis familiaris]
gi|74004878|ref|XP_852254.1|	44356.63	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Canis familiaris]
gi|84626361|gb|ABC59721.1|	7922.26	glyceraldehyde-3-phosphate dehydrogenase [Spermophilus parryii]
gi|70673311|gb|AAZ06800.1|	22296.24	glyceraldehyde-3-phosphate dehydrogenase [Oxalis stricta]
gi|37698402|gb|AAR00508.1|	35030.96	glyceraldehyde-3-phosphate dehydrogenase; GAPDH [Passer domesticus]
gi|109484558|ref|XP_001065101.1|	36045.19	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]

gi|109503243|ref|XP_001070609.1|	33300.03	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase isoform 1 [Rattus norvegicus]
gi|6978952|dbj|BAA90773.1|	36298.41	glyceraldehyde-3-phosphate dehydrogenase [Spirometra erinaceieuropaei]
gi|109476813|ref|XP_001059327.1|	36090.27	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|13702286|dbj|BAB43824.1|	34889.76	glyceraldehyde 3-phosphate dehydrogenase [Cavia porcellus]
gi|55154587|gb|AAH85275.1|	36072.32	Similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]
gi|211797|gb|AAA48774.1|	35989.41	glyceraldehyde-3-phosphate dehydrogenase
gi|1628381|emb|CAA23698.1|	35967.38	glyceraldehyde-3-phosphate dehydrogenase [Gallus gallus]
gi|2494630|sp|Q64467|G3PT_MOUSE	48367.48	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific (Spermatogenic cell-specific glyceraldehy
gi|1169794|sp|P46406|G3P_RABIT	36025.3	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|62616|emb|CAA79512.1|	35863.34	glyceraldehydephosphate dehydrogenase [Coturnix coturnix]
gi|77404273|ref|NP_001029206.1|	36073.38	glyceraldehyde-3-phosphate dehydrogenase [Bos taurus]
gi|49435|emb|CAA36368.1|	35953.3	unnamed protein product [Cricetulus griseus]
gi|62318276|dbj|BAD93764.1|	36059.28	Glyceraldehyde-3-phosphate dehydrogenase [Meriones unguiculatus]
gi|1100225|gb|AAD10214.1|	46324.43	glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
gi|1100223|gb|AAD10215.1|	46339.43	glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
gi|4966351|gb|AAD34682.1|	43648.17	Similar to gb|AJ001706 NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (GapCp1) from Pinus s
gi|5052383|gb|AAD38527.1|	20110.47	glyceraldehyde-3-phosphate dehydrogenase GAPDH [Sus scrofa]
gi|3219753|gb|AAC23533.1|	11813.23	glyceraldehyde-3-phosphate dehydrogenase [Sus scrofa]
gi|5712111|gb|AAD47370.1|	18687.6	glyceraldehyde 3-phosphate dehydrogenase [Mustela vison]
gi|3452462|gb|AAC32882.1|	14706.46	glyceraldehyde-3-phosphate dehydrogenase [Equus caballus]
gi|15219206|ref|NP_173080.1|	44988.94	NAD binding / glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphat
gi|18072805|emb|CAC80377.1|	44689.85	glyceraldehyde-3-phosphate dehydrogenase [Capsicum annuum]
gi|56188|emb|CAA26150.1|	36098.37	glyceraldehyde 3-phosphate-dehydrogenase [Rattus norvegicus]
gi|56611127|gb|AAH87743.1|	36056.29	Glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|39652292|dbj|BAD04859.1|	17342.06	glyceraldehyde-3-phosphate dehydrogenase [Laticauda semifasciata]
gi|50905605|ref|XP_464291.1|	43461.25	putative glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)]
gi|8575565|gb|AAF78051.1|	16838.72	glyceraldehyde-3-phosphate dehydrogenase; GAPDH [Taeniopygia guttata]
gi|52076528|dbj|BAD45405.1|	43752.23	putative glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)]
gi|21618027|gb|AAM67077.1|	45002.95	putative glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]
gi|1667605|gb|AAB18821.1|	7965.31	glyceraldehyde-3-phosphate dehydrogenase [Cavia porcellus]
gi|109504062|ref|XP_001073242.1|	36085.25	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]

gi|9838358|gb|AAF68961.2|	18681.56	glyceraldehyde 3-phosphate dehydrogenase GAPDH [Marmota monax]
gi|27754473|gb|AAO22684.1|	44961.93	putative glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]
gi|62201487|gb|AAH92267.1|	36100.35	Similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]
gi|49522602|gb|AAH75438.1|	31638.89	MGC89215 protein [Xenopus tropicalis]
gi|5163490|gb|AAD40684.1|	29650.02	glyceraldehyde-3-phosphate dehydrogenase [Equus caballus]
gi|56377786|dbj|BAD74117.1|	36049.37	glyceraldehyde-3-phosphate dehydrogenase (GAPDH) homologue [Pelodiscus sinensis]
gi|21070959|gb|AAK50815.2|	10679.71	glyceraldehyde-3-phosphate dehydrogenase [Capreolus capreolus]
gi|2285903|emb|CAA03875.1|	28908.03	glyceraldehyde 3-phosphate dehydrogenase [Bos taurus]
gi|3059140|emb|CAA04942.1|	39298.06	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
gi|3059122|emb|CAA06030.1|	39352.13	glyeraldehyde-3-phosphate dehydrogenase [Marsilea quadrifolia]
gi|18076096|emb|CAC80386.1|	45945.31	glyceraldehyde-3-phosphate dehydrogenase [Marchantia polymorpha]
gi|21218402|gb|AAM44068.1|	31038.79	glyceraldehyde-3-phosphate dehydrogenase [Sigmodon hispidus]
gi|13027414|ref|NP_076454.1|	47362.02	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic [Rattus norvegicus]
gi|66990025|gb|AAH98095.1|	36102.33	LOC654472 protein [Mus musculus]
gi|27882192|gb|AAH43972.1|	36097.31	Gapd-prov protein [Xenopus laevis]
gi|94397810|ref|XP_988049.1|	36074.26	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]
gi|94399312|ref|XP_978477.1|	36092.36	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]
gi|16304127|gb|AAL16930.1|	13856.15	glyceraldehyde 3-phosphate dehydrogenase 1 [Fragaria x ananassa]
gi|16226113|gb|AAL16077.1|	13870.16	glyceraldehyde 3-phosphate dehydrogenase [Fragaria x ananassa]
gi|49616580|gb|AAT67150.1|	20734.78	glyceraldehyde-3-phosphate dehydrogenase [Cervus elaphus]
gi|50086895|gb|AAT70328.1|	34343.55	glyceraldehyde 3-phosphate dehydrogenase [Petromyzon marinus]
gi|27356782|gb|AAL49972.1|	35974.29	glyceraldehyde-3-phosphate dehydrogenase [Meriones unguiculatus]
gi|55153885|gb|AAH85315.1|	36093.23	Similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]
gi|62653546|ref|XP_576394.1|	36045.19	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|62658024|ref|XP_573304.1|	36277.38	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|57232588|gb|AAW47939.1|	6830.78	GAPDH [Tupaia belangeri]
gi|56783068|gb|AAW28862.1|	29980.23	glyceraldehyde-3-phosphate dehydrogenase [Peromyscus maniculatus]

620. Group probability: 0.9870. Peptides of the group

ENIAKIMNESLMLVTALNPHIGYDK (0000000100000000000000000)	68.04	51.8712	2829.44	2829.072	4	3	distinct	1	0.987

The equivalent proteins include

gi|24640177|ref|NP_572339.1|	53826.85	lethal (1) G0255 CG4094-PA, isoform A [Drosophila melanogaster]
gi|24640179|ref|NP_727108.1|	50713.05	lethal (1) G0255 CG4094-PB, isoform B [Drosophila melanogaster]
gi|19528365|gb|AAL90297.1|	53811.88	LD46083p [Drosophila melanogaster]
gi|38047607|gb|AAR09706.1|	12956.77	similar to Drosophila melanogaster CG4094 [Drosophila yakuba]

621. Group probability: 0.9868. Peptides of the group

EAYPGDVFYIHSR	77.43	54.6655	1552.731	1553.625	13	2	shared(2)	0	0.9925
CTGRILEVPVGESLLGR	44.5	54.2928	1854.998	1855.895	1	3	distinct	1	0.8574

The equivalent proteins include

gi|78702137|ref|ZP_00866579.1|	55692.65	ATP synthase F1, alpha subunit [Alkalilimnicola ehrlichei MLHE-1]

622. Group probability: 0.9866. Peptides of the group

NPYPGQIFNKPTTK	70.43	54.6447	1603.836	1604.224	2	2	distinct	0	0.9866

The equivalent proteins include

jgi|Physo1_1|134996|estExt_fgenesh1_pg.C_350048	0	No title.

623. Group probability: 0.9866. Peptides of the group

VNTLIRPDGKK	48.33	55.2045	1239.73	1240.209	3	2	distinct	1	0.8956
VNTLIRPDGQKK	50.66	55.1171	1367.788	1368.689	3	2	distinct	1	0.8713

The equivalent proteins include

gi|61654660|gb|AAX48856.1|	17374.73	L23a [Suberites domuncula]
gi|72145683|ref|XP_792948.1|	17866.11	PREDICTED: similar to 60S ribosomal protein L23a [Strongylocentrotus purpuratus]
gi|24266954|gb|AAN52376.1|	18528.63	ribosomal protein L23a [Branchiostoma belcheri]
jgi|Physo1_1|157934|C_scaffold_70000018	0	No title.

624. Group probability: 0.9865. Peptides of the group

RLYQSNTNQAPLSLGK	69.41	54.2398	1788.948	1789.753	4	2	distinct	1	0.9865

The equivalent proteins include

jgi|Physo1_1|115505|estExt_Genewise1.C_260146	0	No title.

625. Group probability: 0.9863. Peptides of the group

GGMTSHAAVVAR (00010000000000)	91.33	55.7078	1155.582	1156.392	7	2	shared(2)	0	0.9737
SGAAISMPGMMDTVLNLGLNDETVKGLAK	45.32	51.4254	2932.471	2932.507	1	3	distinct	1	0.9183

The equivalent proteins include

gi|4980770|gb|AAD35361.1|	98387.3	pyruvate,orthophosphate dikinase [Thermotoga maritima MSB8]

626. Group probability: 0.9862. Peptides of the group

AMGIMNSFINDIFER (00100000000000000)	85.48	54.293	1772.823	1774.034	17	2	distinct	0	0.9862

The equivalent proteins include

gi|76644398|ref|XP_875437.1|	25340.43	PREDICTED: similar to Histone H2B 291B [Bos taurus]
gi|61888730|ref|XP_604423.1|	15998.07	PREDICTED: similar to H2B histone family, member C [Bos taurus]
gi|76678151|ref|XP_609308.2|	9756.19	PREDICTED: similar to Histone H2B 291B, partial [Bos taurus]
gi|109079443|ref|XP_001110898.1|	13913.59	PREDICTED: similar to H2B histone family, member T [Macaca mulatta]
gi|50261574|gb|AAT72343.1|	21971.36	H2B/t variant [Homo sapiens]
gi|49659929|gb|AAT68256.1|	18405.62	histone H2B/s [Homo sapiens]

627. Group probability: 0.9860. Peptides of the group

HFSAPYTPPYITAIPEVK	68	53.5574	2030.051	2031.29	5	2	distinct	0	0.986

The equivalent proteins include

jgi|Physo1_1|130327|estExt_fgenesh1_pg.C_100285	0	No title.

628. Group probability: 0.9857. Peptides of the group

SAYAQCIFAYAPAGAEPQVFIGQTHGK	66.09	51.6599	2881.386	2882.569	1	3	distinct	0	0.9857

The equivalent proteins include

jgi|Physo1_1|108811|estExt_fgenesh1_pm.C_340011	0	No title.

629. Group probability: 0.9856. Peptides of the group

NLRPNYVDAIWDVVNWK	67.23	53.4233	2101.074	2101.88	18	+2,+3	distinct	0	0.9856

The equivalent proteins include

gi|108879548|gb|EAT43773.1|	24617.73	superoxide dismutase, Mn [Aedes aegypti]
gi|56417578|gb|AAV90730.1|	24554.64	cytoplasmic superoxide dismutase [Aedes albopictus]

630. Group probability: 0.9855. Peptides of the group

MAMNPFCEIAVEEAIR (010000000000000000)	84.65	53.8677	1895.858	1897.246	10	2	distinct	0	0.9855

The equivalent proteins include

gi|88859195|ref|ZP_01133835.1|	25728.88	Electron transfer flavoprotein beta-subunit [Pseudoalteromonas tunicata D2]

631. Group probability: 0.9855. Peptides of the group

KIFGQVGPVVDIR	70.02	54.9895	1426.83	1428.187	6	2	distinct	1	0.9855

The equivalent proteins include

jgi|Physo1_1|108782|estExt_fgenesh1_pm.C_310006	0	No title.

632. Group probability: 0.9850. Peptides of the group

LAQGLTYHNVLGVVESIFDAAIK	67.34	52.6519	2457.327	2458.378	1	3	distinct	0	0.985

The equivalent proteins include

jgi|Physo1_1|129776|estExt_fgenesh1_pg.C_90053	0	No title.

633. Group probability: 0.9848. Peptides of the group

LIGPHSIIGR	70.89	55.9457	1061.635	1062.122	9	2	distinct	0	0.9848

The equivalent proteins include

jgi|Physo1_1|108401|estExt_fgenesh1_pm.C_80011	0	No title.

634. Group probability: 0.9845. Peptides of the group

DSTIIMQLLR	62.92	55.7197	1188.654	1188.603	4	2	shared(5)	0	0.81
TASEIATTELPPTHPIR	49.19	54.0571	1832.963	1833.15	2	2	distinct	0	0.7235
QAFDDAIAELDTLSEESYK	63.08	53.2907	2143.98	2145.265	2	2	shared(3)	0	0.9793
QAFDDAIAELDTLSEESYKDSTLIMQLLR	73.46	50.8644	3314.623	3315.694	3	3	shared(2)	1	0.9205

The equivalent proteins include

gi|6320304|ref|NP_010384.1|	31099.36	14-3-3 protein, minor isoform; binds proteins and DNA, involved in regulation of many processes inc
gi|6321025|ref|NP_011104.1|	30186.84	14-3-3 protein, major isoform; binds proteins and DNA, involved in regulation of many processes inc
gi|832919|emb|CAA50656.1|	22136.03	BMH1 [Saccharomyces cerevisiae]
gi|50293761|ref|XP_449292.1|	28405.09	unnamed protein product [Candida glabrata]
gi|671634|emb|CAA46959.1|	30271.9	BMH1 [Saccharomyces cerevisiae]
gi|683696|emb|CAA59275.1|	31262.41	BMH2 [Saccharomyces cerevisiae]

635. Group probability: 0.9844. Peptides of the group

TVTPVRPLEVPQFVTGIPAALLTDGELR	64.61	51.3921	2988.665	2990.124	2	3	distinct	0	0.9844

The equivalent proteins include

jgi|Physo1_1|133795|estExt_fgenesh1_pg.C_280016	0	No title.

636. Group probability: 0.9842. Peptides of the group

ILEWSDAPYAARPSSGHLITATTENNTTTWK	63.01	50.3737	3430.679	3431.987	2	3	distinct	0	0.9842

The equivalent proteins include

jgi|Physo1_1|134198|estExt_fgenesh1_pg.C_300109	0	No title.

637. Group probability: 0.9841. Peptides of the group

LTYTEHLNPSTR	69.35	55.0342	1430.715	1430.995	6	2	distinct	0	0.9841

The equivalent proteins include

jgi|Physo1_1|139501|estExt_fgenesh1_pg.C_740072	0	No title.

638. Group probability: 0.9840. Peptides of the group

EGDILCLLEWER	69.25	54.8916	1531.734	1532.952	7	2	distinct	0	0.984

The equivalent proteins include

jgi|Physo1_1|127339|estExt_fgenesh1_pg.C_10319	0	No title.

639. Group probability: 0.9839. Peptides of the group

TPVDDKDVLLFAPEGDKPQVVAALK	65.62	52.0907	2664.437	2664.503	1	3	distinct	1	0.9839

The equivalent proteins include

jgi|Physo1_1|108542|estExt_fgenesh1_pm.C_150011	0	No title.

640. Group probability: 0.9837. Peptides of the group

RTIQFVDWCPTGFK	68.04	54.1994	1753.861	1754.812	2	2	shared(4)	1	0.9837
ELYHPEQLISGKEDAANNYAR	55.64	52.6686	2417.161	2417.37	2	3	distinct	1	0.955

The equivalent proteins include

gi|26419422|gb|AAN78301.1|	51014.93	alpha-tubulin [Encephalitozoon intestinalis]

641. Group probability: 0.9835. Peptides of the group

TVVRPYTPTNVNEEK	67.52	54.2708	1745.895	1746.613	2	2	distinct	0	0.9835

The equivalent proteins include

jgi|Physo1_1|108379|estExt_fgenesh1_pm.C_70024	0	No title.

642. Group probability: 0.9834. Peptides of the group

KSGHIVNISSDAGR	68	54.8533	1439.748	1440.78	4	2	distinct	1	0.9834

The equivalent proteins include

jgi|Physo1_1|157895|C_scaffold_66000025	0	No title.

643. Group probability: 0.9831. Peptides of the group

LPGNLDKWEK	69.59	55.6344	1198.635	1199.17	3	2	distinct	1	0.9831

The equivalent proteins include

jgi|Physo1_1|156553|C_scaffold_22000008	0	No title.

644. Group probability: 0.9829. Peptides of the group

DFTHDSEHDVDSAEHR	45.36	53.8671	1895.767	1896.788	1	3	distinct	0	0.8642
FSENKPVPALGGDDLPIDEVYAFYDFWNK	40.22	50.5918	3345.587	3346.639	1	3	distinct	0	0.8743

The equivalent proteins include

jgi|Physo1_1|136947|estExt_fgenesh1_pg.C_490085	0	No title.

645. Group probability: 0.9826. Peptides of the group

IIIEPTAAAIAYGLDKK	88.42	54.8034	1786.024	1787.369	3	2	distinct	1	0.9826

The equivalent proteins include

gi|15620767|emb|CAC69880.1|	72796.99	heat shock protein (Hsp70) [Moneuplotes crassus]

646. Group probability: 0.9814. Peptides of the group

VVSWYDNEWGYSNR	66.58	54.2913	1773.775	1773.614	2	2	distinct	0	0.9814

The equivalent proteins include

gi|67925626|ref|ZP_00518948.1|	11174.39	similar to Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Crocosphae
gi|76797229|ref|ZP_00779563.1|	36920.09	Glyceraldehyde-3-phosphate dehydrogenase, type I [Thermoanaerobacter ethanolicus ATCC 33223]
gi|77687068|ref|ZP_00802362.1|	31226.17	Glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Alkaliphilus metalliredigenes QYMF]
gi|88946476|ref|ZP_01149554.1|	36708.19	Glyceraldehyde-3-phosphate dehydrogenase, type I [Desulfotomaculum reducens MI-1]
gi|89341241|ref|ZP_01193486.1|	38782.28	Glyceraldehyde-3-phosphate dehydrogenase, type I [Mycobacterium flavescens PYR-GCK]
gi|90204185|ref|ZP_01206829.1|	36998.22	Glyceraldehyde-3-phosphate dehydrogenase, type I [Mycobacterium vanbaalenii PYR-1]
gi|13092768|emb|CAC30078.1|	36221.9	glyceraldehyde 3-phosphate dehydrogenase [Mycobacterium leprae]
gi|13881096|gb|AAK45745.1|	36104.85	glyceraldehyde 3-phosphate dehydrogenase [Mycobacterium tuberculosis CDC1551]
gi|66965925|ref|ZP_00413489.1|	35921.58	Glyceraldehyde-3-phosphate dehydrogenase, type I [Arthrobacter sp. FB24]
gi|71677692|ref|ZP_00675427.1|	37023.86	Glyceraldehyde-3-phosphate dehydrogenase, type I [Trichodesmium erythraeum IMS101]
gi|870798|gb|AAC37245.1|	38377.72	glyceraldehyde-3-phosphate dehydrogenase
gi|3323159|gb|AAC65812.1|	38344.7	glyceraldehyde 3-phosphate dehydrogenase (gap) [Treponema pallidum subsp. pallidum str. Nichols]
gi|20516773|gb|AAM24956.1|	36775.02	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Thermoanaerobacter te
gi|51856472|dbj|BAD40630.1|	36348.86	glyceraldehyde-3-phosphate dehydrogenase [Symbiobacterium thermophilum IAM 14863]
gi|108799371|ref|YP_639568.1|	36231.88	glyceraldehyde-3-phosphate dehydrogenase, type I [Mycobacterium sp. MCS]
gi|20549|emb|CAA42902.1|	36462.75	glyceraldehyde 3-phosphate dehydrogenase [Petroselinum crispum]
gi|2749881|gb|AAB95084.1|	36186.95	glyceraldehyde-3-phosphate dehydrogenase homolog [Mycobacterium avium]
gi|520887|emb|CAA52631.1|	39455.46	glyceraldehyde-3-phosphate dehydrogenase [Trypanoplasma borreli]
gi|520888|emb|CAA52632.1|	39614.38	glyceraldehyde-3-phosphate dehydrogenase [Trypanoplasma borreli]

647. Group probability: 0.9814. Peptides of the group

HIEVHPTLPCFLTCADDMTIK	65.68	52.5365	2497.18	2497.605	1	3	distinct	0	0.9814

The equivalent proteins include

jgi|Physo1_1|117464|estExt_Genewise1.C_430005	0	No title.

648. Group probability: 0.9811. Peptides of the group

ACNALLLK	66.88	56.8713	901.505	902.794	1	2	shared(3)	0	0.9266
VPTPDVSVVDLTCR	100.87	54.7391	1556.787	1557.293	12	2	shared(4)	0	0.9926
LTGMAFRVPTPDVSVVDLTCR (000010000000000000000)	64.95	52.9126	2333.187	2333.52	9	+2,+3	shared(3)	1	0.9972

The equivalent proteins include

gi|71000249|dbj|BAE07174.1|	86477.52	polyprotein [Heterocapsa triquetra]

649. Group probability: 0.9808. Peptides of the group

WSGAVVSDIDPPAHRIR	43.71	54.463	1874.975	1874.292	2	+2,+3	distinct	1	0.9808

The equivalent proteins include

gi|76260198|ref|ZP_00767837.1|	30981	hypothetical protein CaurDRAFT_3259 [Chloroflexus aurantiacus J-10-fl]

650. Group probability: 0.9805. Peptides of the group

HYGALTGLDK	51.04	56.2074	1073.551	1074.046	2	+1,+2	shared(2)	0	0.8551
NVVIAAHGNSLR	70.88	55.2977	1249.689	1250.682	3	2	distinct	0	0.9477

The equivalent proteins include

jgi|Physo1_1|108482|estExt_fgenesh1_pm.C_110013	0	No title.

651. Group probability: 0.9801. Peptides of the group

GVNWASFHPTLPLIVSGADDR	51.78	53.5378	2251.138	2251.779	8	+2,+3	distinct	0	0.9801

The equivalent proteins include

gi|108868541|gb|EAT32766.1|	140260.25	coatomer [Aedes aegypti]
gi|108870473|gb|EAT34698.1|	140791.43	coatomer [Aedes aegypti]
gi|54641517|gb|EAL30267.1|	141311.63	GA20724-PA [Drosophila pseudoobscura]
gi|24655452|ref|NP_728648.1|	140951.6	-coatomer protein CG7961-PB, isoform B [Drosophila melanogaster]
gi|50918233|ref|XP_469513.1|	137434.92	putative alpha-coat protein [Oryza sativa]
gi|50918235|ref|XP_469514.1|	137418.94	putative alpha-coat protein [Oryza sativa]
gi|15226538|ref|NP_179734.1|	137407.07	protein transporter/ transporter [Arabidopsis thaliana]
gi|45357045|gb|AAS58474.1|	136808.66	coatomer alpha subunit [Hordeum vulgare subsp. vulgare]
jgi|Physo1_1|108346|estExt_fgenesh1_pm.C_60036	0.00	No title.

652. Group probability: 0.9800. Peptides of the group

LHPVVVLQVLDR	66.77	55.3095	1386.835	1387.944	5	+2	distinct	0	0.9800

The equivalent proteins include

jgi|Physo1_1|109294|estExt_fgenesh1_pm.C_860001	0.00	No title.

653. Group probability: 0.9796. Peptides of the group

MQAPGTTFGGGSVTIPLKVDIMEHLDELSPAAK	59.32	50.4459	3409.726	3410.919	2	+3	distinct	1	0.9796

The equivalent proteins include

jgi|Physo1_1|143339|estExt_fgenesh1_pg.C_1360011	0.00	No title.

654. Group probability: 0.9796. Peptides of the group

VVGVLLGSTFHGK	66.17	55.3349	1312.750	1313.616	2	+2	distinct	0	0.9796

The equivalent proteins include

jgi|Physo1_1|108965|estExt_fgenesh1_pm.C_470004	0.00	No title.

655. Group probability: 0.9796. Peptides of the group

LVDLVNKLNLADK	45.61	54.8330	1453.850	1453.758	2	+2,+3	distinct	1	0.9796

The equivalent proteins include

gi|15076994|gb|AAK83019.1|	42486.33	putative glycosyl transferase WbdM [Salmonella enterica]

656. Group probability: 0.9793. Peptides of the group

SGKPLHYK	48.26	56.7639	928.513	929.188	1	2	shared(2)	0	0.8844
ANPRVFFDMTVGGAPAGR	68.76	54.0312	1861.926	1860.659	5	2	distinct	1	0.9404

The equivalent proteins include

gi|829148|emb|CAA48638.1|	18565.23	cyclophilin [Zea mays]
gi|13925734|gb|AAK49427.1|	18709.18	cyclophilin A-2 [Triticum aestivum]
gi|13925737|gb|AAK49428.1|	18721.19	cyclophilin A-3 [Triticum aestivum]

657. Group probability: 0.9792. Peptides of the group

LSPSLSHLLGK	66.77	55.3227	1150.671	1151.751	2	2	distinct	0	0.9792

The equivalent proteins include

jgi|Physo1_1|156757|C_scaffold_26000041	0	No title.

658. Group probability: 0.9792. Peptides of the group

NTNSGHYVCHMK	66.29	55.0487	1446.613	1447.501	3	2	distinct	0	0.9792

The equivalent proteins include

jgi|Physo1_1|108254|estExt_fgenesh1_pm.C_40005	0	No title.

659. Group probability: 0.9788. Peptides of the group

VVHGGEAFSK	67.18	56.4228	1029.524	1029.374	5	1	distinct	0	0.9788

The equivalent proteins include

jgi|Physo1_1|108508|estExt_fgenesh1_pm.C_120018	0	No title.

660. Group probability: 0.9783. Peptides of the group

TTGCVLDSGDGVSHTVPIYEGYALPHAVIR	66.63	50.9577	3183.566	3184.421	9	+2,+3	distinct	0	0.9783

The equivalent proteins include

gi|57864662|gb|AAW56951.1|	29293.65	actin [Phaeodactylum tricornutum]
gi|54300518|gb|AAV32834.1|	27066.67	actin [Phaeodactylum tricornutum]

661. Group probability: 0.9780. Peptides of the group

KLLHFAEGGDAGNR	64.75	54.7721	1483.753	1484.214	2	2	distinct	1	0.978

The equivalent proteins include

jgi|Physo1_1|108358|estExt_fgenesh1_pm.C_70003	0	No title.

662. Group probability: 0.9779. Peptides of the group

LGADPHALEAVCAPLGLQPR	61.99	53.5548	2084.084	2084.521	2	2	distinct	0	0.9779

The equivalent proteins include

jgi|Physo1_1|132428|estExt_fgenesh1_pg.C_200200	0	No title.

663. Group probability: 0.9775. Peptides of the group

AGDVVALWLPNSAENVLTQLAAAR	59.94	52.5745	2478.323	2479.286	2	2	distinct	0	0.9775

The equivalent proteins include

jgi|Physo1_1|134331|estExt_fgenesh1_pg.C_310041	0	No title.

664. Group probability: 0.9774. Peptides of the group

FPGFSLPDNSHAVYNPLAGVLNPTLAMATMQK	58.53	50.3772	3400.695	3401.977	3	3	distinct	0	0.9774

The equivalent proteins include

jgi|Physo1_1|133544|estExt_fgenesh1_pg.C_260150	0	No title.
jgi|Physo1_1|133547|estExt_fgenesh1_pg.C_260153	0	No title.

665. Group probability: 0.9773. Peptides of the group

PEEHPVLLTEAPINPK	63.51	54.3346	1782.952	1784.318	4	2	distinct	0	0.9773

The equivalent proteins include

gi|83700630|gb|ABC41107.1|	23946.06	actin [Trichoderma koningiopsis]
gi|83700636|gb|ABC41110.1|	25557.96	actin [Trichoderma koningiopsis]
gi|84314104|gb|ABC55663.1|	22492.43	actin [Trichoderma ovalisporum]
gi|84314108|gb|ABC55665.1|	25671.05	actin [Trichoderma caribbaeum]
gi|84314110|gb|ABC55666.1|	24331.26	actin [Trichoderma ovalisporum]
gi|87133580|gb|ABD24432.1|	23815.02	actin [Trichoderma petersenii]

666. Group probability: 0.9772. Peptides of the group

THALNVIPTEAIAGFDIR	62.54	53.777	1937.037	1937.987	2	2	distinct	0	0.9772

The equivalent proteins include

jgi|Physo1_1|134969|estExt_fgenesh1_pg.C_350021	0	No title.
jgi|Physo1_1|124111|estExt_Genewise1.C_1480015	0	No title.

667. Group probability: 0.9772. Peptides of the group

HLSGFSYHDGSVDR	64.35	54.7511	1575.707	1575.653	2	2	distinct	0	0.9772

The equivalent proteins include

jgi|Physo1_1|137190|estExt_fgenesh1_pg.C_510074	0	No title.

668. Group probability: 0.9772. Peptides of the group

NQLWVGNYQNALSEGGMLNHLGEALR	61.13	51.6628	2883.408	2884.623	3	3	distinct	0	0.9772

The equivalent proteins include

jgi|Physo1_1|109221|estExt_fgenesh1_pm.C_750003	0	No title.

669. Group probability: 0.9772. Peptides of the group

LVNAATLHSQDQANHCK	62.95	53.9792	1905.911	1906.163	1	2	distinct	0	0.9772

The equivalent proteins include

jgi|Physo1_1|131774|estExt_fgenesh1_pg.C_170116	0	No title.

670. Group probability: 0.9771. Peptides of the group

HGGGGGGFGGGGFGSR	63.66	55.416	1319.575	1320.155	1	2	distinct	0	0.9771

The equivalent proteins include

gi|181402|gb|AAC83410.1|	66110.5	epidermal cytokeratin 2 [Homo sapiens]
gi|68563400|gb|AAH99643.1|	65678.32	Keratin 2A (epidermal ichthyosis bullosa of Siemens) [Homo sapiens]

671. Group probability: 0.9770. Peptides of the group

VLGAAAEHANSR	65.22	55.2953	1194.61	1195.633	1	2	distinct	0	0.977

The equivalent proteins include

jgi|Physo1_1|113945|estExt_Genewise1.C_170070	0	No title.

672. Group probability: 0.9769. Peptides of the group

QCGLALTGNHYDPLK	63.74	54.3674	1685.819	1686.139	2	2	distinct	0	0.9769

The equivalent proteins include

jgi|Physo1_1|136697|estExt_fgenesh1_pg.C_470111	0	No title.

673. Group probability: 0.9766. Peptides of the group

MFYSPWPTLALLEEFPSLK (010000000000000000000)	61.66	53.0234	2268.154	2284.847	3	2	distinct	0	0.9766

The equivalent proteins include

jgi|Physo1_1|132762|estExt_fgenesh1_pg.C_220110	0	No title.

674. Group probability: 0.9765. Peptides of the group

TLAENLEQVPDLSDNHEIIHPVDRPLK	60.26	51.132	3091.594	3092.715	4	3	distinct	0	0.9765

The equivalent proteins include

jgi|Physo1_1|145643|estExt_fgenesh1_pg.C_20470001	0	No title.

675. Group probability: 0.9760. Peptides of the group

FLLASPPGQVHEVLR	63.33	54.5309	1661.925	1662.751	2	2	distinct	0	0.976

The equivalent proteins include

jgi|Physo1_1|133005|estExt_fgenesh1_pg.C_230148	0	No title.

676. Group probability: 0.9760. Peptides of the group

AAGSGGLRPTQVAELAPFFEGPAALPALSSK	58.46	51.426	3009.592	3010.857	1	3	distinct	0	0.976

The equivalent proteins include

jgi|Physo1_1|127265|estExt_fgenesh1_pg.C_10245	0	No title.

677. Group probability: 0.9756. Peptides of the group

QAFDDAIAELDTLSEESYK	63.08	53.2907	2143.98	2145.265	2	2	shared(3)	0	0.9793
QAFDDAIAELDTLSEESYKDSTLIMQLPR (0000000000000000000000000100000)	72.53	50.8644	3314.586	3315.694	3	3	distinct	1	0.9138

The equivalent proteins include

gi|62420901|gb|AAX82172.1|	28911.23	14-3-3 1 protein [Phanerochaete chrysosporium]

678. Group probability: 0.9752. Peptides of the group

SLSFHYPGVAVQQLGLGVGK	60.71	53.5487	2056.11	2056.785	1	2	distinct	0	0.9752

The equivalent proteins include

jgi|Physo1_1|132679|estExt_fgenesh1_pg.C_220027	0	No title.

679. Group probability: 0.9737. Peptides of the group

VMAAGDFITNLLGHPTQSK	60.52	53.8676	1999.02	1999.871	1	2	distinct	0	0.9737

The equivalent proteins include

jgi|Physo1_1|109053|estExt_fgenesh1_pm.C_550006	0	No title.

680. Group probability: 0.9728. Peptides of the group

AEGADAIHPGYGFLSENAAFAR	71.58	53.1197	2263.066	2264.538	7	+2,+3	distinct	0	0.9728

The equivalent proteins include

gi|89099591|ref|ZP_01172466.1|	50699.49	acetyl-CoA carboxylase [Bacillus sp. NRRL B-14911]

681. Group probability: 0.9725. Peptides of the group

DSTIIMQLLR	62.92	55.7197	1188.654	1188.603	4	2	shared(5)	0	0.81
QAFDDAIAELDTLSEDSYKDSTLIMQLLR (0000000000000000000000000100000)	53.63	50.8106	3316.602	3317.565	3	3	distinct	1	0.9611

The equivalent proteins include

gi|34452065|gb|AAQ72489.1|	27960.81	14-3-3C1 protein [Oncorhynchus mykiss]

682. Group probability: 0.9724. Peptides of the group

LQVHTNPFTTDTIHGLR	60.74	53.8474	1949.012	1949.648	2	2	distinct	0	0.9724

The equivalent proteins include

jgi|Physo1_1|137006|estExt_fgenesh1_pg.C_500042	0	No title.

683. Group probability: 0.9721. Peptides of the group

VLITASDVLHSWAIPSLGIK	68.02	53.3001	2119.204	2119.855	1	2	distinct	0	0.9721

The equivalent proteins include

gi|7545164|gb|AAA32022.2|	30698.59	cytochrome c oxidase subunit II [Phytophthora megasperma]
gi|71063523|gb|AAZ22193.1|	21691.22	cytochrome oxidase subunit II [Pythium graminicola]

gi|71063533|gb|AAZ22198.1|	21627.22	cytochrome oxidase subunit II [Pythium irregulare]
gi|71063547|gb|AAZ22205.1|	21649.17	cytochrome oxidase subunit II [Pythium nunn]
gi|71063559|gb|AAZ22211.1|	21691.22	cytochrome oxidase subunit II [Pythium rostratum]
gi|71063565|gb|AAZ22214.1|	21675.22	cytochrome oxidase subunit II [Pythium sylvaticum]
gi|71063569|gb|AAZ22216.1|	21645.23	cytochrome oxidase subunit II [Pythium nodosum]
gi|71063571|gb|AAZ22217.1|	21661.21	cytochrome oxidase subunit II [Pythium violae]
gi|71063581|gb|AAZ22222.1|	21650.14	cytochrome oxidase subunit II [Phytophthora cactorum]
gi|71063583|gb|AAZ22223.1|	21622.07	cytochrome oxidase subunit II [Phytophthora cactorum]
gi|71063587|gb|AAZ22225.1|	21619.15	cytochrome oxidase subunit II [Phytophthora cinnamomi]
gi|71063589|gb|AAZ22226.1|	21660.23	cytochrome oxidase subunit II [Phytophthora citricola]
gi|71063593|gb|AAZ22228.1|	21517.16	cytochrome oxidase subunit II [Phytophthora citricola]
gi|71063595|gb|AAZ22229.1|	21631.2	cytochrome oxidase subunit II [Phytophthora megasperma]
gi|71063597|gb|AAZ22230.1|	21634.18	cytochrome oxidase subunit II [Phytophthora megasperma]
gi|71063599|gb|AAZ22231.1|	21634.18	cytochrome oxidase subunit II [Phytophthora megasperma]
gi|71063601|gb|AAZ22232.1|	21650.17	cytochrome oxidase subunit II [Phytophthora nicotianae]
gi|71063605|gb|AAZ22234.1|	21644.25	cytochrome oxidase subunit II [Phytophthora sojae]
gi|71063607|gb|AAZ22235.1|	21644.24	cytochrome oxidase subunit II [Phytophthora sojae]
gi|71063609|gb|AAZ22236.1|	21660.25	cytochrome oxidase subunit II [Phytophthora undulata]
gi|9695376|ref|NP_037598.1|	29827.11	cytochrome c oxidase subunit 2 [Phytophthora infestans]
gi|60203149|gb|AAX14746.1|	19484.84	cytochrome oxidase subunit II [Pythium irregulare]
gi|60203100|gb|AAX14722.1|	19355.78	cytochrome oxidase subunit II [Pythium irregulare]
gi|60203151|gb|AAX14747.1|	19512.87	cytochrome oxidase subunit II [Pythium irregulare]
gi|60203121|gb|AAX14732.1|	19466.75	cytochrome oxidase subunit II [Pythium irregulare]
gi|60203147|gb|AAX14745.1|	19494.86	cytochrome oxidase subunit II [Pythium irregulare]
gi|8885659|gb|AAF80240.1|	22174.47	cytochrome c oxidase subunit II [Peronophythora litchii]
gi|9587834|gb|AAF89404.1|	26228.38	cytochrome c oxidase subunit II [Pythium insidiosum]
gi|9587890|gb|AAF89432.1|	26214.39	cytochrome c oxidase subunit II [Pythium sylvaticum]
gi|9587846|gb|AAF89410.1|	26228.41	cytochrome c oxidase subunit II [Pythium iwagamai]
gi|9587858|gb|AAF89416.1|	26230.39	cytochrome c oxidase subunit II [Pythium nunn]
gi|9587868|gb|AAF89421.1|	26181.39	cytochrome c oxidase subunit II [Pythium pulchrum]
gi|9587870|gb|AAF89422.1|	26167.38	cytochrome c oxidase subunit II [Pythium rostratum]
gi|15428384|gb|AAK97844.1|	22170.49	cytochrome c oxidase subunit II [Lagenidium myophilum]
gi|31158504|gb|AAN01348.1|	21792.21	cytochrome c oxidase subunit II [Phytophthora palmivora]
gi|31158418|gb|AAN01305.1|	21771.35	cytochrome c oxidase subunit II [Phytophthora boehmeriae]
gi|31158424|gb|AAN01308.1|	21764.18	cytochrome c oxidase subunit II [Phytophthora cactorum]
gi|38348785|gb|AAR17798.1|	21747.21	cytochrome c oxidase subunit II [Phytophthora cinnamomi]

gi|31158432|gb|AAN01312.1|	21788.29	cytochrome c oxidase subunit II [Phytophthora citricola]
gi|31158438|gb|AAN01315.1|	21774.27	cytochrome c oxidase subunit II [Phytophthora colocasiae]
gi|31158440|gb|AAN01316.1|	21750.16	cytochrome c oxidase subunit II [Phytophthora cryptogea]
gi|38348787|gb|AAR17799.1|	21748.22	cytochrome c oxidase subunit II [Phytophthora erythroseptica]
gi|31158454|gb|AAN01323.1|	21797.38	cytochrome c oxidase subunit II [Phytophthora fragariae var. fragariae]
gi|31158456|gb|AAN01324.1|	21799.4	cytochrome c oxidase subunit II [Phytophthora fragariae var. rubi]
gi|31158458|gb|AAN01325.1|	21730.27	cytochrome c oxidase subunit II [Phytophthora gonapodyides]
gi|31158460|gb|AAN01326.1|	21748.24	cytochrome c oxidase subunit II [Phytophthora heveae]
gi|31158466|gb|AAN01329.1|	21790.27	cytochrome c oxidase subunit II [Phytophthora hibernalis]
gi|38348789|gb|AAR17800.1|	21793.21	cytochrome c oxidase subunit II [Phytophthora ilicis]
gi|31158470|gb|AAN01331.1|	21821.25	cytochrome c oxidase subunit II [Phytophthora ilicis]
gi|31158476|gb|AAN01334.1|	21790.27	cytochrome c oxidase subunit II [Phytophthora infestans]
gi|38348795|gb|AAR17803.1|	21751.16	cytochrome c oxidase subunit II [Phytophthora lateralis]
gi|31158482|gb|AAN01337.1|	21792.25	cytochrome c oxidase subunit II [Phytophthora megakarya]
gi|31158484|gb|AAN01338.1|	21702.23	cytochrome c oxidase subunit II [Phytophthora megasperma]
gi|31158486|gb|AAN01339.1|	21730.27	cytochrome c oxidase subunit II [Phytophthora megasperma]
gi|31158488|gb|AAN01340.1|	21716.25	cytochrome c oxidase subunit II [Phytophthora megasperma]
gi|38348799|gb|AAR17805.1|	21778.23	cytochrome c oxidase subunit II [Phytophthora nicotianae]
gi|31158500|gb|AAN01346.1|	21792.25	cytochrome c oxidase subunit II [Phytophthora palmivora]
gi|31158508|gb|AAN01350.1|	21763.23	cytochrome c oxidase subunit II [Phytophthora pseudotsugae]
gi|31158510|gb|AAN01351.1|	21772.31	cytochrome c oxidase subunit II [Phytophthora sojae]
gi|38348805|gb|AAR17808.1|	21795.23	cytochrome c oxidase subunit II [Phytophthora syringae]
gi|33350990|gb|AAP49016.1|	22166.57	cytochrome oxidase subunit II [Hyaloperonospora parasitica]
gi|38016575|gb|AAR07621.1|	25606.14	cytochrome c oxidase subunit II [Phytophthora nemorosa]
gi|38373703|gb|AAR19106.1|	25592.13	cytochrome c oxidase subunit II [Phytophthora pseudosyringae]
gi|38373707|gb|AAR19108.1|	25568.03	cytochrome c oxidase subunit II [Phytophthora lateralis]
gi|38373715|gb|AAR19112.1|	25593.12	cytochrome c oxidase subunit II [Phytophthora ramorum]
gi|38373717|gb|AAR19113.1|	25612.09	cytochrome c oxidase subunit II [Phytophthora syringae]
gi|38373719|gb|AAR19114.1|	25592.13	cytochrome c oxidase subunit II [Phytophthora syringae]
gi|38348779|gb|AAR17795.1|	21776.25	cytochrome c oxidase subunit II [Phytophthora ramorum]
gi|38348781|gb|AAR17796.1|	21772.31	cytochrome c oxidase subunit II [Phytophthora cambivora]
gi|38348797|gb|AAR17804.1|	21777.24	cytochrome c oxidase subunit II [Phytophthora nemorosa]
gi|38348803|gb|AAR17807.1|	21763.22	cytochrome c oxidase subunit II [Phytophthora pseudosyringae]
gi|93280090|gb|ABF06688.1|	25593.12	cytochrome c oxidase subunit II [Phytophthora capsici]
gi|93280098|gb|ABF06692.1|	25577.13	cytochrome c oxidase subunit II [Phytophthora tropicalis]
gi|71063555|gb|AAZ22209.1|	21622.3	cytochrome oxidase subunit II [Pythium periplocum]

gi|71063577|gb|AAZ22220.1|	21632.2	cytochrome oxidase subunit II [Phytophthora capsici]
gi|9587864|gb|AAF89419.1|	26201.54	cytochrome c oxidase subunit II [Pythium oligandrum]
gi|38348783|gb|AAR17797.1|	21760.26	cytochrome c oxidase subunit II [Phytophthora capsici]
gi|33350982|gb|AAP49012.1|	22166.53	cytochrome oxidase subunit II [Pythium acanthicum]

684. Group probability: 0.9718. Peptides of the group

FHVEEEGKGK	47.93	55.7704	1158.567	1159.423	2	2	shared(2)	1	0.8866
VADKIQLINNMLDK (0000000000010000)	44.36	54.6473	1629.876	1631.294	1	2	distinct	1	0.6374
LGDVYVNDAFGTAHR	79.59	54.6124	1633.785	1634.282	4	+2,+3	shared(2)	0	0.9548

The equivalent proteins include

gi|22219037|pdb|1KF0|A	44837.26	Chain A, Crystal Structure Of Pig Muscle Phosphoglycerate Kinase Ternary Complex With Amp-Pcp And 3
gi|47169449|pdb|1VJD|A	44802.18	Chain A, Structure Of Pig Muscle Pgk Complexed With Atp
gi|66893|pir||KIHOG	44865.26	phosphoglycerate kinase (EC 2.7.2.3) - horse
gi|266755|sp|P29408|PGK1_MACEU	45405.38	Phosphoglycerate kinase 1
gi|52783777|sp|P00559|PGK1_HORSE	44973.29	Phosphoglycerate kinase 1
gi|61354676|gb|AAX41039.1|	45101.31	phosphoglycerate kinase 1 [synthetic construct]
gi|74216774|dbj|BAE37790.1|	44907.12	unnamed protein product [Mus musculus]
gi|74219103|dbj|BAE26693.1|	44949.14	unnamed protein product [Mus musculus]
gi|56403927|emb|CAI29748.1|	44929.2	hypothetical protein [Pongo pygmaeus]
gi|48145549|emb|CAG32997.1|	44973.24	PGK1 [Homo sapiens]
gi|50513041|gb|AAT77773.1|	44929.23	phosphoglycerate kinase 1 [Sus scrofa]
gi|109131308|ref|XP_001100787.1|	44957.23	PREDICTED: similar to phosphoglycerate kinase 1 isoform 4 [Macaca mulatta]
gi|109131310|ref|XP_001100617.1|	40724	PREDICTED: similar to phosphoglycerate kinase 1 isoform 2 [Macaca mulatta]
gi|109131312|ref|XP_001100332.1|	41653.74	PREDICTED: similar to phosphoglycerate kinase 1 isoform 1 [Macaca mulatta]
gi|109131314|ref|XP_001100701.1|	41773.47	PREDICTED: similar to phosphoglycerate kinase 1 isoform 3 [Macaca mulatta]
gi|55663594|ref|XP_529051.1|	46230.42	PREDICTED: phosphoglycerate kinase 1 [Pan troglodytes]
gi|41350401|gb|AAS00488.1|	44985.28	migration-inducing gene 10 protein [Homo sapiens]
gi|129906|sp|P16617|PGK1_RAT	44925.09	Phosphoglycerate kinase 1
gi|129903|sp|P09411|PGK1_MOUSE	44907.08	Phosphoglycerate kinase 1
gi|987048|emb|CAA86028.1|	44933.17	phosphoglycerate kinase [Cricetulus griseus]
gi|38649310|gb|AAH63161.1|	44909.14	Phosphoglycerate kinase 1 [Rattus norvegicus]
gi|80477474|gb|AAI08373.1|	44921.14	Phosphoglycerate kinase 1 [Mus musculus]
gi|55733484|emb|CAH93420.1|	44985.26	hypothetical protein [Pongo pygmaeus]
gi|1150|emb|CAA45574.1|	45274.34	phosphoglycerate kinase [Macropus eugenii]

685. Group probability: 0.9718. Peptides of the group

ETPAGAPTCSAHPAR	61.51	54.6412	1521.699	1522.787	4	2	distinct	0	0.9718

The equivalent proteins include

jgi|Physo1_1|135987|estExt_fgenesh1_pg.C_420050	0	No title.

686. Group probability: 0.9717. Peptides of the group

QILGPLAMAGQLGGAESATR	49.51	53.7642	1940.015	1940.445	3	+2,+3	distinct	0	0.9717

The equivalent proteins include

gi|92911051|ref|ZP_01279825.1|	81636.38	ATP-dependent DNA helicase RecG [Mycobacterium sp. JLS]
gi|108798904|ref|YP_639101.1|	81658.45	ATP-dependent DNA helicase RecG [Mycobacterium sp. MCS]

687. Group probability: 0.9715. Peptides of the group

TAAEDDKDALLASGPNAPFGAWVETNLGELLLR	55.44	50.2349	3453.741	3454.906	4	3	distinct	1	0.9715

The equivalent proteins include

jgi|Physo1_1|135401|estExt_fgenesh1_pg.C_380035	0	No title.

688. Group probability: 0.9714. Peptides of the group

DPTQQTAIDNFMVHELDGTQNEWGWCK	57.97	50.8725	3219.403	3218.014	1	3	distinct	0	0.9714

The equivalent proteins include

gi|90194338|gb|ABD92697.1|	47812.23	los [Brassica rapa subsp. chinensis]
gi|15227987|ref|NP_181192.1|	47974.44	LOS2; phosphopyruvate hydratase [Arabidopsis thaliana]
gi|34597330|gb|AAQ77240.1|	47631.1	enolase [Brassica rapa]
gi|15809970|gb|AAL06912.1|	47959.47	At2g36530/F1O11.16 [Arabidopsis thaliana]
gi|16226235|gb|AAL16111.1|	35062.72	At2g36530/F1O11.16 [Arabidopsis thaliana]
gi|20260174|gb|AAM12985.1|	48032.44	enolase (2-phospho-D-glycerate hydroylase) [Arabidopsis thaliana]
gi|18175728|gb|AAL59917.1|	47983.44	putative enolase (2-phospho-D-glycerate hydroylase) [Arabidopsis thaliana]
gi|34597332|gb|AAQ77241.1|	47635.23	enolase [Brassica napus]
gi|45477377|gb|AAS66001.1|	47949.34	LOS2 [Capsella bursa-pastoris]

689. Group probability: 0.9714. Peptides of the group

NSGVVWTDETLFEYLLAPK	59.39	53.2571	2181.099	2182.527	1	2	distinct	0	0.9714

The equivalent proteins include

jgi|Physo1_1|109170|estExt_fgenesh1_pm.C_670002	0	No title.

690. Group probability: 0.9710. Peptides of the group

HYWVLDFANADGESCA	60.66	54.1243	1853.768	1854.158	1	2	distinct	0	0.971

The equivalent proteins include

jgi|Physo1_1|136645|estExt_fgenesh1_pg.C_470059	0	No title.

691. Group probability: 0.9709. Peptides of the group

GAWQRPGEGANVLIAYSDDGTHLSK	58.95	52.3616	2641.288	2642.621	3	3	distinct	0	0.9709

The equivalent proteins include

jgi|Physo1_1|137021|estExt_fgenesh1_pg.C_500057	0	No title.

692. Group probability: 0.9709. Peptides of the group

GVLIHGPPGTGK	54.48	56.2125	1131.64	1132.141	1	2	shared(2)	0	0.8714
NAPAIIFIDEIDSIAPK	82.61	54.0767	1825.982	1826.739	16	2	shared(2)	0	0.9959

The equivalent proteins include

gi|21226350|ref|NP_632272.1|	84695.37	Cell division cycle protein [Methanosarcina mazei Go1]
gi|72396736|gb|AAZ71009.1|	84500.49	cell division cycle protein [Methanosarcina barkeri str. fusaro]
gi|85375691|ref|YP_459753.1|	84366.01	Cell division cycle protein [Erythrobacter litoralis HTCC2594]

693. Group probability: 0.9706. Peptides of the group

KQNQYEFVGPFPFAR	63.28	54.11	1826.91	1827.579	2	3	distinct	1	0.9706

The equivalent proteins include

jgi|Physo1_1|130582|estExt_fgenesh1_pg.C_120014	0	No title.
jgi|Physo1_1|156179|C_scaffold_12000005	0	No title.

694. Group probability: 0.9702. Peptides of the group

VHDSLHNGELR	62.7	55.5634	1275.632	1276.444	4	2	distinct	0	0.9702

The equivalent proteins include

jgi|Physo1_1|109162|estExt_fgenesh1_pm.C_660004	0	No title.

695. Group probability: 0.9697. Peptides of the group

NRTEALASVLK	75.85	55.7009	1200.683	1201.749	2	2	distinct	1	0.9697

The equivalent proteins include

jgi|Physo1_1|142256|estExt_fgenesh1_pg.C_1100050	0	No title.

696. Group probability: 0.9696. Peptides of the group

YPIEHGIVTNWDDMEK (000000000000001000)	89.61	53.9187	1945.888	1946.177	23	+2,+3	shared(4)	0	0.9983
VAPEEHPVLLTEAPLDPK	58.57	53.717	1954.041	1953.494	4	2	distinct	0	0.8584

The equivalent proteins include

gi|62768595|gb|AAY00164.1|	21988.23	actin A1c [Haliotis iris]

697. Group probability: 0.9694. Peptides of the group

SIAPGSASHVFK	62.02	55.619	1199.63	1200.006	1	2	distinct	0	0.9694

The equivalent proteins include

jgi|Physo1_1|134025|estExt_fgenesh1_pg.C_290092	0	No title.

698. Group probability: 0.9692. Peptides of the group

AIYHATHR	45.81	55.2259	967.499	968.204	1	2	distinct	0	0.8612
KVNPINDYILATLAGGAADCQFWQR	50.27	51.7888	2820.402	2821.716	1	3	distinct	1	0.7784

The equivalent proteins include

jgi|Physo1_1|109087|estExt_fgenesh1_pm.C_580012	0	No title.

699. Group probability: 0.9678. Peptides of the group

IIALALHPGYVVTR	60.39	54.6627	1521.903	1523.239	2	2	distinct	0	0.9678

The equivalent proteins include

jgi|Physo1_1|137790|estExt_fgenesh1_pg.C_570055	0	No title.
jgi|Physo1_1|138873|estExt_fgenesh1_pg.C_670075	0	No title.

700. Group probability: 0.9670. Peptides of the group

QFAEHWQATGYK	61.04	55.1423	1464.679	1466.014	1	2	distinct	0	0.967

The equivalent proteins include

jgi|Physo1_1|137176|estExt_fgenesh1_pg.C_510060	0	No title.

701. Group probability: 0.9669. Peptides of the group

RFNFPDGAVELYAER	59.61	54.345	1782.869	1784.123	3	2	distinct	1	0.9669

The equivalent proteins include

jgi|Physo1_1|108569|estExt_fgenesh1_pm.C_160008	0	No title.

702. Group probability: 0.9667. Peptides of the group

IGPALAAGNSVILKPSEKSPLSALR	57.44	52.5282	2488.438	2489.481	5	3	distinct	1	0.9667

The equivalent proteins include

gi|91796404|gb|ABE58543.1|	54679.45	Aldehyde dehydrogenase (NAD+) [Chromohalobacter salexigens DSM 3043]
gi|83587439|ref|ZP_00926067.1|	53594.49	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli 101-1]
gi|75179045|ref|ZP_00699063.1|	53587.55	COG1012: NAD-dependent aldehyde dehydrogenases [Shigella boydii BS512]
gi|75190386|ref|ZP_00703653.1|	53601.55	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli E24377A]
gi|75212739|ref|ZP_00712737.1|	53667.64	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli B171]
gi|75240055|ref|ZP_00724016.1|	54064.73	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli E110019]
gi|75259412|ref|ZP_00730731.1|	53722.68	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli E22]
gi|74312330|ref|YP_310749.1|	48454.99	aldehyde dehydrogenase [Shigella sonnei Ss046]
gi|82544244|ref|YP_408191.1|	53631.58	aldehyde dehydrogenase [Shigella boydii Sb227]
gi|145224|gb|AAA23428.1|	53682.6	aldehyde dehydrogenase
gi|16129261|ref|NP_415816.1|	53613.53	gamma-Glu-gamma-aminobutyraldehyde dehydrogenase, NAD(P)H-dependent [Escherichia coli K12]
gi|30041068|gb|AAP16798.1|	53488.67	aldehyde dehydrogenase [Shigella flexneri 2a str. 2457T]
gi|56383426|gb|AAN42916.2|	53474.66	aldehyde dehydrogenase [Shigella flexneri 2a str. 301]

703. Group probability: 0.9665. Peptides of the group

DMVLLDVTPLSLGIETLGGVMTK (00000000000000000000001000)	55.86	52.6741	2417.28	2416.029	2	2	distinct	0	0.9665

The equivalent proteins include

gi|51573343|gb|AAU07368.1|	69363.74	heat shock protein 70 [Borrelia garinii PBi]
gi|39376|emb|CAA47888.1|	69346.75	heat-shock protein [Borrelia burgdorferi]

704. Group probability: 0.9663. Peptides of the group

TLERGAHIVVGTPGR	59.51	54.8527	1561.869	1562.893	6	2	distinct	1	0.9663

The equivalent proteins include

gi|83951704|ref|ZP_00960436.1|	83864.94	ATP-dependent RNA helicase, DEAD/DEAH box family protein [Roseovarius nubinhibens ISM]
gi|15073360|emb|CAC41868.1|	69320.08	PUTATIVE ATP-DEPENDENT RNA HELICASE PROTEIN [Sinorhizobium meliloti]
gi|56680381|gb|AAV97047.1|	76031.23	ATP-dependent RNA helicase, DEAD/DEAH box family [Silicibacter pomeroyi DSS-3]

705. Group probability: 0.9659. Peptides of the group

LEGNFKPGSTFYLYPR	58.78	53.944	1887.952	1888.505	2	2	distinct	0	0.9659

The equivalent proteins include

jgi|Physo1_1|156769|C_scaffold_27000003	0	No title.

706. Group probability: 0.9652. Peptides of the group

GAIDNVVGGGAGHDHK	58.75	54.8416	1502.723	1503.49	1	2	distinct	0	0.9652

The equivalent proteins include

jgi|Physo1_1|128251|estExt_fgenesh1_pg.C_40095	0	No title.
jgi|Physo1_1|128252|estExt_fgenesh1_pg.C_40096	0	No title.

707. Group probability: 0.9648. Peptides of the group

LWPPSTPVDEAVPYFPTAFVSFR	55.19	52.2466	2622.316	2622.589	1	2	distinct	0	0.9648

The equivalent proteins include

jgi|Physo1_1|141377|estExt_fgenesh1_pg.C_970065	0	No title.
jgi|Physo1_1|141379|estExt_fgenesh1_pg.C_970067	0	No title.
jgi|Physo1_1|141380|estExt_fgenesh1_pg.C_970068	0	No title.

708. Group probability: 0.9644. Peptides of the group

YGHVSNIWVAR	60.64	55.4357	1300.668	1301.496	4	2	distinct	0	0.9644

The equivalent proteins include

jgi|Physo1_1|136493|estExt_fgenesh1_pg.C_460039	0	No title.

709. Group probability: 0.9641. Peptides of the group

KIAVNLIPFPR	70.88	55.3512	1266.781	1267.527	5	2	shared(6)	1	0.9855
EILHVQGGQCGNQIGAK	66.3	54.3336	1807.9	1808.677	4	2	distinct	0	0.9178

The equivalent proteins include

gi|296498|emb|CAA48929.1|	50334.78	beta tubulin 1 [Anemia phyllitidis]

710. Group probability: 0.9641. Peptides of the group

TAVVQVLDRCPECAHGALDLSPTVYK	55.96	51.5837	2898.437	2899.603	1	3	distinct	1	0.9641

The equivalent proteins include

jgi|Physo1_1|134663|estExt_fgenesh1_pg.C_330053	0	No title.

711. Group probability: 0.9637. Peptides of the group

ESTIHLVLR	71.03	55.1897	1066.613	1067.325	13	2	shared(3)	0	0.9848
YPIEHGIVTNWDDMEK (000000000000001000)	89.61	53.9187	1945.888	1946.177	23	+2,+3	shared(4)	0	0.9983
VAPEEHPVLLTEAPINPK	81.4	53.7297	1953.057	1953.885	13	2	shared(10)	0	0.9887

The equivalent proteins include

gi|33346927|gb|AAP34624.1|	26433.21	ubiquitin/actin fusion protein 1 [Bigelowiella natans]
gi|33346937|gb|AAP34630.1|	26017.09	ubiquitin/actin fusion protein 3 [Lotharella amoeboformis]
gi|33346935|gb|AAP34629.1|	26031.11	ubiquitin/actin fusion protein 2 [Lotharella amoeboformis]
gi|33346941|gb|AAP34632.1|	26075.11	ubiquitin/actin fusion protein 2 [Lotharella globosa]
gi|33346943|gb|AAP34633.1|	26332.2	ubiquitin/actin fusion protein 3 [Lotharella globosa]
gi|33346945|gb|AAP34634.1|	49579.96	ubiquitin/actin fusion protein [Gymnochlora stellata]

712. Group probability: 0.9631. Peptides of the group

TVEAEAAHGTVTR	67.95	55.2417	1340.668	1341.53	1	2	shared(2)	0	0.868
FKDIFQEVYENEFK	73.99	54.1512	1834.878	1835.5	5	2	distinct	1	0.9016

The equivalent proteins include

gi|83858780|ref|ZP_00952302.1|	45770.19	isocitrate dehydrogenase [Oceanicaulis alexandrii HTCC2633]

713. Group probability: 0.9627. Peptides of the group

KYSLWDQEK	60.82	55.2954	1195.587	1195.907	7	2	distinct	1	0.9627

The equivalent proteins include

jgi|Physo1_1|141162|estExt_fgenesh1_pg.C_950010	0	No title.
jgi|Physo1_1|141164|estExt_fgenesh1_pg.C_950012	0	No title.

714. Group probability: 0.9617. Peptides of the group

KQDPKPVAVPAK	59.42	55.4681	1276.75	1277.22	2	2	distinct	1	0.9617

The equivalent proteins include

jgi|Physo1_1|138048|estExt_fgenesh1_pg.C_600007	0	No title.

715. Group probability: 0.9608. Peptides of the group

VIAWYDNEWGYSNR	85.68	54.2461	1771.795	1771.999	13	2	distinct	0	0.9608

The equivalent proteins include

gi|90585446|ref|ZP_01241155.1|	37141.23	Glyceraldehyde-3-phosphate dehydrogenase, type I [Staphylococcus aureus subsp. aureus JH9]
gi|27315825|gb|AAO04960.1|	37240.2	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus epidermidis ATCC 12228]
gi|82751275|ref|YP_417016.1|	37153.29	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus RF122]
gi|53687157|ref|ZP_00107108.2|	36947.96	COG0057: Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Nostoc punct
gi|68446963|dbj|BAE04547.1|	37303.14	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus haemolyticus JCSC1435]
gi|49483929|ref|YP_041153.1|	37151.22	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus MRSA252]
gi|73662387|ref|YP_301168.1|	37276.99	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus saprophyticus subsp. saprophyticus ATCC
gi|57637827|gb|AAW54615.1|	37256.16	glyceraldehyde 3-phosphate dehydrogenase [Staphylococcus epidermidis RP62A]
gi|77995878|gb|ABB14777.1|	36250.11	glyceraldehyde-3-phosphate dehydrogenase, type I [Carboxydothermus hydrogenoformans Z-2901]
gi|56751277|ref|YP_171978.1|	38965.41	glyceraldehyde 3-phosphate dehydrogenase [Synechococcus elongatus PCC 6301]
gi|87127690|gb|ABD22204.1|	37127.22	glyceraldehyde-3-phosphate dehydrogenase, type I [Staphylococcus aureus subsp. aureus USA300]
gi|6979050|gb|AAF34325.1|	35682.03	cytosolic glyceraldehyde-3-phosphate dehydrogenase [Phaeodactylum tricornutum]
gi|38195941|gb|AAR13671.1|	37070.2	GapB [Staphylococcus aureus]
gi|89894253|ref|YP_517740.1|	36707.21	hypothetical protein DSY1507 [Desulfitobacterium hafniense Y51]
gi|81300748|ref|YP_400956.1|	36323.85	glyceraldehyde-3-phosphate dehydrogenase, type I [Synechococcus elongatus PCC 7942]
gi|109649322|ref|ZP_01373210.1|	36579.19	glyceraldehyde-3-phosphate dehydrogenase, type I [Desulfitobacterium hafniense DCB-2]
gi|89894355|ref|YP_517842.1|	37131.45	glyceraldehyde 3-phosphate dehydrogenase [Desulfitobacterium hafniense Y51]
gi|56752164|ref|YP_172865.1|	37270.32	glyceraldehyde 3-phosphate dehydrogenase [Synechococcus elongatus PCC 6301]

716. Group probability: 0.9602. Peptides of the group

DILLLDVTPLSLGIETMGGVMTK	65.14	52.8703	2415.3	2414.453	7	2	distinct	0	0.9602

The equivalent proteins include

gi|57340176|gb|AAW50075.1|	73604.53	hypothetical protein FTT1269 [synthetic construct]
gi|3122002|sp|O32482|DNAK_LEGPN	70215.33	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70)
gi|53751737|emb|CAH13159.1|	70245.36	Chaperone protein DnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) [Legionella pneu
gi|53754755|emb|CAH16242.1|	70217.33	Chaperone protein DnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) [Legionella pneu
gi|56604821|emb|CAG45902.1|	69382.76	Chaperone protein dnaK (heat shock protein family 70 protein) [Francisella tularensis subsp. tulare
gi|52629353|gb|AAU28094.1|	70873.61	chaperone protein DnaK, heat shock protein Hsp70 [Legionella pneumophila subsp. pneumophila str. Ph

717. Group probability: 0.9602. Peptides of the group

IVYSIHGGPMAGR	58.55	55.3349	1356.697	1357.398	6	2	distinct	0	0.9602

The equivalent proteins include

jgi|Physo1_1|139819|estExt_fgenesh1_pg.C_780080	0	No title.

718. Group probability: 0.9601. Peptides of the group

LAGNHVIGTCSSPDKVEYLR	55.17	53.1686	2215.105	2215.792	1	2	distinct	1	0.9601

The equivalent proteins include

jgi|Physo1_1|108301|estExt_fgenesh1_pm.C_50016	0	No title.

719. Group probability: 0.9594. Peptides of the group

HAQGFHNVAEQK	58.65	55.0027	1364.658	1365.665	3	2	distinct	0	0.9594

The equivalent proteins include

jgi|Physo1_1|136221|estExt_fgenesh1_pg.C_440022	0	No title.

720. Group probability: 0.9593. Peptides of the group

GSSPMKPVLYLEDPYFYVR	55.4	53.2854	2260.124	2261.459	2	2	distinct	0	0.9593

The equivalent proteins include

jgi|Physo1_1|108389|estExt_fgenesh1_pm.C_70034	0	No title.

721. Group probability: 0.9593. Peptides of the group

EFGIDEKNMFGFWDWVGGR	57.73	53.2335	2289.031	2287.732	3	3	distinct	1	0.9593

The equivalent proteins include

gi|66499293|ref|XP_623552.1|	63155.85	PREDICTED: similar to glucosephosphate isomerase [Apis mellifera]

722. Group probability: 0.9588. Peptides of the group

SSMSDMEQVIDDLK (0000001000000000)	57.56	54.5472	1612.696	1614.053	2	2	distinct	0	0.9588

The equivalent proteins include

gi|56783954|dbj|BAD81391.1|	77715.32	hypothetical protein [Oryza sativa (japonica cultivar-group)]
gi|34904404|ref|NP_913549.1|	84981.03	unnamed protein product [Oryza sativa (japonica cultivar-group)]

723. Group probability: 0.9579. Peptides of the group

IEQLHQTVADHCSAR	56.84	54.1812	1763.837	1764.118	1	2	distinct	0	0.9579

The equivalent proteins include

jgi|Physo1_1|142675|estExt_fgenesh1_pg.C_1190045	0	No title.

724. Group probability: 0.9574. Peptides of the group

KLWAEDPHAPQAR	57.68	54.9508	1517.774	1518.143	1	2	distinct	1	0.9574

The equivalent proteins include

jgi|Physo1_1|128752|estExt_fgenesh1_pg.C_50249	0	No title.

725. Group probability: 0.9572. Peptides of the group

CTLESQCQAGTCNLK	76.21	54.1875	1768.754	1769.2	2	2	distinct	0	0.9572

The equivalent proteins include

jgi|Physo1_1|140877|estExt_fgenesh1_pg.C_910002	0	No title.

726. Group probability: 0.9568. Peptides of the group

ILTWVQHWTAQHADD	56.56	54.2404	1819.864	1821.234	2	2	distinct	0	0.9568

The equivalent proteins include

jgi|Physo1_1|109405|estExt_fgenesh1_pm.C_1000002	0	No title.

727. Group probability: 0.9567. Peptides of the group

NTAIVLAAK	79.15	55.8813	899.544	898.135	3	2	distinct	0	0.9567

The equivalent proteins include

gi|82738292|ref|ZP_00901128.1|	23426.53	conserved hypothetical protein [Pseudomonas putida F1]

728. Group probability: 0.9563. Peptides of the group

AEGLWAGIVIPEAGR	56.52	54.6354	1537.825	1537.225	1	2	distinct	0	0.9563

The equivalent proteins include

gi|108797038|ref|YP_637235.1|	11080.64	transcription factor WhiB [Mycobacterium sp. MCS]

729. Group probability: 0.9557. Peptides of the group

VGLTGLTVAEYFR	105.09	54.9675	1424.766	1425.451	8	2	shared(2)	0	0.9864
AALVFGQMNEPPGAR (0000000100000000)	46.86	54.9075	1572.772	1573.149	1	2	distinct	0	0.6799

The equivalent proteins include

gi|45685251|gb|AAS75379.1|	15459.04	AtpD [Mesorhizobium sp. ICMP 14330]

730. Group probability: 0.9557. Peptides of the group

FTHLAEETAPRPTQQK	55.82	54.1242	1852.943	1853.665	1	2	distinct	0	0.9557

The equivalent proteins include

jgi|Physo1_1|134242|estExt_fgenesh1_pg.C_300153	0	No title.

731. Group probability: 0.9555. Peptides of the group

NPPPPPSSSADTPPPPPSSSSSTSSSAESLR	51.42	51.3745	3004.39	3005.713	1	3	distinct	0	0.9555

The equivalent proteins include

gi|66932877|gb|AAY58271.1|	53995.63	cell cycle switch protein CCS52A [Lotus corniculatus var. japonicus]

732. Group probability: 0.9549. Peptides of the group

AAAAAAAAAPPKPAPK	55.9	55.3026	1372.783	1373.101	11	2	distinct	0	0.9549

The equivalent proteins include

jgi|Physo1_1|131865|estExt_fgenesh1_pg.C_170207	0	No title.

733. Group probability: 0.9538. Peptides of the group

MVLPSNITK (01000000000)	58.57	56.1863	1017.553	1018.433	1	2	distinct	0	0.9538

The equivalent proteins include

gi|90585996|ref|ZP_01241700.1|	67819.01	conserved hypothetical protein [Staphylococcus aureus subsp. aureus JH9]
gi|87127959|gb|ABD22473.1|	122034.25	conserved hypothetical protein [Staphylococcus aureus subsp. aureus USA300]
gi|21203232|dbj|BAB93933.1|	122052.31	MW0068 [Staphylococcus aureus subsp. aureus MW2]
gi|49243416|emb|CAG41836.1|	122053.29	hypothetical protein [Staphylococcus aureus subsp. aureus MSSA476]
gi|14245860|dbj|BAB56255.1|	122103.27	hypothetical protein [Staphylococcus aureus subsp. aureus Mu50]

734. Group probability: 0.9537. Peptides of the group

MKSYDIVVIGGGPGGYVAAIK	53.14	53.38	2094.118	2094.557	1	2	distinct	1	0.9537

The equivalent proteins include

gi|10173393|dbj|BAB04498.1|	49550.26	dihydrolipoamide dehydrogenase [Bacillus halodurans C-125]

735. Group probability: 0.9537. Peptides of the group

VVGAIMHLK	58.3	55.1167	966.568	967.148	4	2	distinct	0	0.9537

The equivalent proteins include

jgi|Physo1_1|144389|estExt_fgenesh1_pg.C_1830016	0	No title.

736. Group probability: 0.9535. Peptides of the group

YKIVLLR	50.4	56.6459	903.591	903.581	1	1	shared(2)	1	0.8337
HYGALTGLDK	51.04	56.2074	1073.551	1074.046	2	+1,+2	shared(2)	0	0.8551
VIIAAHGNSIR	55.36	55.3716	1149.662	1150.474	5	2	shared(2)	0	0.8995

The equivalent proteins include

gi|88796704|ref|ZP_01112360.1|	27940.36	phosphoglyceromutase [Alteromonas macleodii 'Deep ecotype']

737. Group probability: 0.9532. Peptides of the group

LFFRPEQAGMTK	57	54.8838	1423.728	1424.631	1	2	distinct	0	0.9532

The equivalent proteins include

jgi|Physo1_1|108205|estExt_fgenesh1_pm.C_20037	0	No title.

738. Group probability: 0.9532. Peptides of the group

SDGIFIGNFVGGDSLK	55.3	54.5388	1624.81	1625.841	1	2	distinct	0	0.9532

The equivalent proteins include

gi|3861015|emb|CAA14915.1|	25786.51	unknown [Rickettsia prowazekii]
gi|51459959|gb|AAU03922.1|	25929.56	conserved hypothetical protein [Rickettsia typhi str. Wilmington]

739. Group probability: 0.9531. Peptides of the group

MNIDTDTQWAYWDGIR	55.1	53.7869	1983.878	1984.426	2	2	distinct	0	0.9531

The equivalent proteins include

gi|21684695|gb|AAM66752.1|	44195.58	fructose-1,6-bisphosphate aldolase precursor [Odontella sinensis]

740. Group probability: 0.9528. Peptides of the group

MVQVADDHAHASNSSSDSAPFLSAAQR	52.57	52.1618	2798.268	2798.852	1	3	distinct	0	0.9528

The equivalent proteins include

jgi|Physo1_1|131406|estExt_fgenesh1_pg.C_150177	0	No title.

741. Group probability: 0.9524. Peptides of the group

IKPELAEVPSKESFPVYAGPEQR	54.17	52.5062	2570.338	2571.136	1	3	distinct	1	0.9524

The equivalent proteins include

jgi|Physo1_1|125082|estExt_Genewise1.C_1970012	0	No title.

742. Group probability: 0.9524. Peptides of the group

VGLLLEVNPDLPPAIALGLHLLEEQALGAK	51	51.0975	3102.769	3104.246	1	3	distinct	0	0.9524

The equivalent proteins include

jgi|Physo1_1|132933|estExt_fgenesh1_pg.C_230076	0	No title.

743. Group probability: 0.9521. Peptides of the group

GVKAILAAR	58.07	55.7949	897.576	898.985	3	2	distinct	1	0.9521

The equivalent proteins include

gi|19887888|gb|AAM02489.1|	49542.49	Fusion of at least two uncharacterized domain specific for M.kandleri, MK-12 family [Methanopyrus k

744. Group probability: 0.9519. Peptides of the group

LMEGFIHDKPQLWNEDIGV	53.44	53.1322	2240.094	2241.428	2	2	distinct	0	0.9519

The equivalent proteins include

jgi|Physo1_1|108743|estExt_fgenesh1_pm.C_290006	0	No title.

745. Group probability: 0.9518. Peptides of the group

LKDLHVR	59.15	55.5256	879.529	880.277	5	2	distinct	1	0.9518

The equivalent proteins include

jgi|Physo1_1|133588|estExt_fgenesh1_pg.C_260194	0	No title.

746. Group probability: 0.9516. Peptides of the group

RAYPQFAQQSPR	56.66	55.0392	1447.732	1448.114	2	2	distinct	1	0.9516

The equivalent proteins include

jgi|Physo1_1|130117|estExt_fgenesh1_pg.C_100075	0	No title.

747. Group probability: 0.9512. Peptides of the group

VKEVGSLLANLAHDQNK	56.69	54.1577	1834.99	1835.72	2	3	distinct	1	0.9512

The equivalent proteins include

gi|90962347|ref|YP_536263.1|	24674.35	ABC transporter, ATP-binding protein [Lactobacillus salivarius subsp. salivarius UCC118]

748. Group probability: 0.9510. Peptides of the group

KYDHLVYPNR	57.41	55.4566	1303.667	1304.3	2	2	distinct	1	0.951

The equivalent proteins include

jgi|Physo1_1|145595|estExt_fgenesh1_pg.C_18990001	0	No title.

749. Group probability: 0.9504. Peptides of the group

VADVYVNDAFGTAHR	78.55	54.6124	1633.785	1634.282	4	+2,+3	distinct	0	0.9504

The equivalent proteins include

gi|51860718|gb|AAU11483.1|	105253.61	chloroplast phosphoglycerate kinase precursor [Euglena gracilis]

750. Group probability: 0.9504. Peptides of the group

LSTSPFLPHMTVVSGVK	54.2	54.3787	1798.965	1800.347	1	2	distinct	0	0.9504

The equivalent proteins include

jgi|Physo1_1|135035|estExt_fgenesh1_pg.C_350087	0	No title.

751. Group probability: 0.9499. Peptides of the group

PFVHVTSNVPK	56.7	55.1416	1223.666	1224.983	1	2	distinct	0	0.9499

The equivalent proteins include

jgi|Physo1_1|157309|C_scaffold_41000011	0	No title.

752. Group probability: 0.9498. Peptides of the group

QATINIGTIGHVAHGK	54.58	54.8471	1615.879	1616.708	1	2	distinct	0	0.9498

The equivalent proteins include

gi|108872932|gb|EAT37157.1|	78606.33	histone-lysine n-methyltransferase [Aedes aegypti]
gi|54639643|gb|EAL29045.1|	72650.02	GA19622-PA [Drosophila pseudoobscura]
gi|88185753|gb|EAQ93221.1|	56170.49	hypothetical protein CHGG_01456 [Chaetomium globosum CBS 148.51]
gi|82802708|gb|ABB92405.1|	51695.4	eFI-2-gamma [Homo sapiens]
gi|82802710|gb|ABB92406.1|	51696.44	eFI-2-gamma [Pan troglodytes]
gi|82802712|gb|ABB92407.1|	51735.55	eFI-2-gamma [Gorilla gorilla]
gi|82802714|gb|ABB92408.1|	51591.42	eFI-2-gamma [Pongo pygmaeus]
gi|82802716|gb|ABB92409.1|	51701.51	eFI-2-gamma [Hylobates lar]
gi|90298719|gb|EAS28350.1|	57582.8	hypothetical protein CIMG_09554 [Coccidioides immitis RS]
gi|84310029|emb|CAJ18344.1|	68663.33	putative H3K9 methyltransferase [Bombyx mori]
gi|84310031|emb|CAJ18345.1|	67156.39	putative H3K9 methyltransferase [Cercopis vulnerata]
gi|84310033|emb|CAJ18346.1|	45956.34	putative translation initiation factor 2 gamma subunit [Drosophila nasutoides]

S4. Protein assembly of peptide sequence matches made to tag-filtered P. sojae tandem mass spectra. The NCBI NR database appended with P. sojae and P. ramorum protein sequences was searched. Protein List with probabilities. The columns are arranged as follows: peptide sequence, Mascot Ions score, Mascot Identity score, computed peptide mass, observed precursor mass, number of tandem mass spectra assigned to same peptide sequence, the charge states observed for the peptide, whether the peptide is shared between protein groups with different probabilities (number in parentheses is number of other groups peptides are shared with) or is distinct (considered a unique identifier for proteins grouped with the same probability), the number of missed tryptic cleavages in this sequence, and the probability for a particular peptide sequence.

1. Group probability: 1.0000. Peptides of the group

HYFIEVNPR	49	55.7568	1173.593	1174.399	2	2	distinct	0	0.8939
FVGPTPENLHR	58.83	55.1748	1265.652	1266.122	8	2	distinct	0	0.9584
VKDEAAGVSTVAKPK	111.39	54.7716	1498.835	1499.122	15	+2,+3	distinct	1	1
SFLTNVLNHPDFIK	77.43	54.6127	1643.867	1645.095	12	2	distinct	0	0.9928
FKDEYGSMHFLDTR (0000000010000000)	99.03	54.3095	1744.788	1745.183	6	2	distinct	1	0.9989
YLNAGTVEFLVDQQGR	57.49	54.2957	1808.906	1809.789	1	2	distinct	0	0.9615
VPVVPGTDGPVHTLEQAR	94	54.1834	1870.99	1871.743	18	+2,+3	distinct	0	1
DMAGLLKPQAAQILISAIR	70.48	54.2939	2008.15	2008.717	5	+2,+3	distinct	0	0.9995
DVDVISHAIYPDVFAGFMK	93.16	53.3963	2123.04	2123.666	3	2	distinct	0	0.9985
IAGGETFEDLGLSQDKIKPR	42.66	53.3186	2173.138	2173.425	1	2	distinct	1	0.8799
LDDGPGFVGAHITPHYDSLLVK	77.05	53.0657	2350.196	2349.203	7	+2,+3	distinct	0	0.9997
ALGATGPAPSKVDPLVPTLEAPPASTEK	49.31	52.0308	2713.454	2714.66	4	+2,+3	distinct	1	0.9968
VLPNGHEMFEGRPGAEMEPYDFEAAEK	44.72	51.4514	3049.358	3050.402	1	3	distinct	0	0.9074

The equivalent proteins include

jgi|Physo1_1|108780|estExt_fgenesh1_pm.C_310004	0	No title.

2. Group probability: 1.0000. Peptides of the group

YDAAGISYTHR	59.04	55.4801	1252.584	1253.271	4	2	distinct	0	0.9589
TVEAEAAHGTVTR	67.95	55.2657	1340.668	1341.53	1	2	shared(2)	0	0.868
AKYDAAGISYTHR	92.57	54.7622	1451.716	1452.476	10	+2,+3	distinct	1	1
KTSTNPIASIYAWTR	107.05	54.4816	1707.894	1708.844	4	2	distinct	1	0.9995
VHKPIVELDGDEMTR (00000000000001000)	74.46	54.204	1737.872	1738.472	14	+2,+3	distinct	0	0.9987
FKDIFEEVYQNEFK	96.36	54.1722	1834.878	1835.5	8	+2,+3	distinct	1	0.9986
NILNGTVFREPIVISNVPR	65.05	53.3479	2137.201	2138.382	12	+2,+3	distinct	1	0.9989
LDGNQELIDFSLGLEDAVIK	71.69	53.3054	2188.126	2188.951	1	2	distinct	0	0.9906
GKLDGNQELIDFSLGLEDAVIK	115.86	52.8366	2373.243	2374.4	13	+2,+3	distinct	1	1
DATNDQVTIDAAHAIQEHHVGIK	80.64	52.6133	2482.22	2482.751	5	+2,+3	distinct	0	0.9998
STDFIAPGPGKFEVVYTPADGSEK	81.92	52.5444	2511.217	2511.103	6	2	distinct	1	0.9967
DLAICIHGSNVTPDHYLYTEDFMDK	76.51	51.5072	2953.326	2953.969	3	3	distinct	0	0.9939

The equivalent proteins include

jgi|Physo1_1|109565|estExt_fgenesh1_pm.C_1440001	0	No title.

3. Group probability: 1.0000. Peptides of the group

FHVEEEGKGK	47.93	55.7973	1158.567	1159.423	2	2	shared(2)	1	0.8865
AHSSMVGVDLPVK (000001000000000)	80.63	55.3475	1338.697	1339.061	22	+1,+2	distinct	0	0.9998
AKDSLAPVAVAVEQK	59.62	54.6306	1524.851	1525.17	2	2	distinct	1	0.9667
GVTLHLPVDFVIADK	62.28	54.5239	1622.903	1624.366	14	+2,+3	distinct	0	0.9989
VADKIQLIMNMLDK	90.88	54.6763	1630.879	1632.087	8	2	distinct	1	0.9939
LGDVYVNDAFGTAHR	79.59	54.6361	1633.785	1634.282	4	+2,+3	shared(2)	0	0.9547
AAGFLLDKELVYFAK	63.73	54.3835	1683.923	1685.182	1	2	distinct	1	0.9769
ALDNPQRPFVSILGGAK	69.11	54.3234	1781.979	1783.172	15	+2,+3	distinct	0	0.998
IDAALPTVQYVLDQGAK	63.52	54.3363	1800.962	1802.369	2	2	distinct	0	0.9781
TVVWNGPMGVFEFEAFAHGTK (00000000100000000000000)	72.79	53.0113	2323.109	2340.277	4	2	distinct	0	0.9918
GVTLHLPVDFVIADKFAPDAAQK	94.15	52.5784	2451.316	2450.995	13	+2,+3	distinct	1	0.9999
FNTEDKVSHVSTGGGASLELLEGK	76.84	52.6073	2474.229	2474.512	7	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|109468|estExt_fgenesh1_pm.C_1120004	0	No title.

4. Group probability: 1.0000. Peptides of the group

HLTPEIYDKLK	48.96	55.3736	1355.745	1357.213	3	3	distinct	1	0.878
SKYNNYPVLTPK	84.3	54.8499	1422.751	1423.255	4	2	distinct	1	0.9957
TFLVWVNEEDHMR	51.8	54.8435	1674.782	1675.886	1	2	distinct	0	0.9287
GEHSPPGPGGVYDVSNK	101.38	54.3541	1695.785	1696.462	17	+2,+3	distinct	0	1
GSKGEHSPPGPGGVYDVSNK	93.26	53.7895	1967.934	1969.175	10	+2,+3	distinct	1	1
IGFSEVELVQTMIDGIWK	106.06	53.6598	2064.06	2064.749	28	2	distinct	0	0.9995

DLMDPVIEGWHGYKPTDTHK	82.2	53.0226	2338.105	2339.456	7	2	distinct	0	0.9963
EEEQQLIDDHFLFQKPGGGTLLTNAGAAR	81.96	51.0281	3154.568	3155.5	5	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|108967|estExt_fgenesh1_pm.C_470006	0	No title.

5. Group probability: 1.0000. Peptides of the group

KIFVGGDDFK	56	55.3757	1124.587	1125.308	6	+1,+2	distinct	1	0.9945
VIVLWSANTER	66.55	55.5379	1286.698	1287.469	1	2	distinct	0	0.9787
RAQVLDHDLQR	50.26	55.2081	1349.716	1351.185	3	+2,+3	distinct	1	0.9894
ENEHPDHVVVIK	54.16	55.1632	1414.72	1415.44	2	2	distinct	0	0.9396
ACVGLAPESHMLLENK (000000000001000000)	73.83	54.2149	1767.865	1768.785	12	2	distinct	0	0.9908
LLYKENEHPDHVVVIK	72.16	53.8514	1932.047	1932.439	2	2	distinct	1	0.9895
FSDIVEGVNDTSANLLESIK	111.59	53.258	2150.074	2151.402	1	2	distinct	0	0.9997
IKPLPSIYYPDFIAANQADR	74.8	53.1665	2291.195	2291.947	24	+2,+3	distinct	0	0.9998
TGVMIVGLGGNNGSTLLASILANK	117.8	53.0976	2299.257	2299.637	7	2	distinct	0	0.9999
SVLVDFLVSAGIKPTSIVSYNHLGNNDGK	72.96	51.2883	3043.598	3044.869	2	3	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|108192|estExt_fgenesh1_pm.C_20024	0	No title.

6. Group probability: 1.0000. Peptides of the group

KGLSPDVPPLDR	61.24	55.2636	1292.709	1294.013	1	2	distinct	1	0.9675
NMSVIAHVDHGK (00100000000000)	76.73	55.4278	1306.645	1307.194	11	2	shared(2)	0	0.9916
SGTITTSETGHTIR	75.68	55.1176	1459.727	1460.104	4	2	distinct	0	0.9915
GTVAFGSGLHQWGFTLK	98.91	54.3332	1804.926	1805.431	10	+2,+3	distinct	0	0.9999
KIWGYGPDGTGANVFVDATK	113.65	53.7404	2095.037	2095.742	17	+2,+3	distinct	1	1
ALLELHLEPEDCYQSFTR	67.32	53.1819	2220.052	2220.965	3	+2,+3	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|109259|estExt_fgenesh1_pm.C_810006	0	No title.

7. Group probability: 1.0000. Peptides of the group

IMWMLENVPGLR	60.4	55.0211	1457.752	1458.252	7	2	distinct	0	0.9651
GGIELSQLQAIGITNQR	48.27	54.3416	1796.974	1797.672	1	2	distinct	0	0.9166
ATGKPLYNAIVWHDTR	94.11	54.1066	1840.958	1841.248	8	2	distinct	0	0.9985
LSGGVHGGVHVTDVTNASR	105.43	54.1226	1861.939	1862.352	1	2	distinct	0	0.9995
AEAGDALFGNMDTWLIWK	93.63	53.7681	2036.967	2037.086	4	2	distinct	0	0.9985
QIYQQPGWCEHDADEITR	73.84	53.2891	2244.986	2245.248	5	2	distinct	0	0.9916
NTYGTGCFFMMNTGTKPTPSTK	91.5	52.7263	2440.086	2440.275	9	+2,+3	distinct	0	0.9998
AALEATAFQTQEVVAAMEGDSGVHLTK	68.65	51.9048	2773.359	2774.748	1	3	distinct	0	0.9885

The equivalent proteins include

jgi|Physo1_1|108295|estExt_fgenesh1_pm.C_50010	0	No title.

8. Group probability: 1.0000. Peptides of the group

KAGVFSAFTQGK	80.52	55.2528	1239.661	1240.284	3	2	distinct	1	0.994
AKLPGTFGNYIK	50.86	55.3697	1307.724	1308.364	6	2	distinct	1	0.919
KAAFEALAEDLR	46.48	55.4095	1332.704	1334.022	1	3	distinct	1	0.3624
EAEVFTSHHSALVK	77.54	54.7797	1553.784	1554.627	12	2	distinct	0	0.9928
SQEPGTHEEIIEFVK	67.5	54.2621	1741.852	1742.632	7	2	distinct	0	0.9834
LVYGDKFELLNLVTK	106.36	54.2255	1750.987	1751.089	13	+2,+3	distinct	1	0.9999
HDVNGSNARPIFTYLK	66.61	54.0927	1830.938	1831.582	1	2	distinct	0	0.9828
DTAVWNVVDGAIYASQLK	78.74	53.8746	1948.989	1950.089	1	2	distinct	0	0.9945
YQEEGLVVLGFPCNQFK	80.8	53.5628	2026.982	2027.709	5	2	distinct	0	0.9953
DTAVWNVVDGAIYASQLKR	78.82	53.3673	2105.09	2105.86	4	2	distinct	1	0.9948

The equivalent proteins include

jgi|Physo1_1|132609|estExt_fgenesh1_pg.C_210169	0	No title.

9. Group probability: 1.0000. Peptides of the group

YGVLVEEAGVALR	94.44	55.152	1374.751	1375.339	1	2	distinct	0	0.9983
SGKPMVADFMAPWCGK	84.95	54.3595	1780.81	1781.973	12	2	distinct	0	0.9965
ALQFVEEHGEVCPANWQPGDK	93.34	52.7428	2410.101	2410.609	8	+2,+3	distinct	0	0.9999
ALNTQLIAVSCDSPESHLAWTR	93.16	52.655	2468.212	2468.601	11	+2,+3	distinct	0	0.9999
CSQILPFVEDLAEAHPDVTFAK	104.86	52.705	2486.215	2486.63	2	2	distinct	0	0.9995
LDVSIPEIEQLKDELEVGAYPEFR	75.57	51.9213	2788.417	2789.696	8	2	distinct	1	0.9944
VQHQAPQFTAQAVLDGDITDISLDTYR	99.26	51.3538	3001.478	3002.583	8	3	distinct	0	0.9992

The equivalent proteins include

jgi|Physo1_1|141953|estExt_fgenesh1_pg.C_1060012	0	No title.

10. Group probability: 1.0000. Peptides of the group

IAELTKPGDKK	52.88	55.6521	1198.692	1199.56	2	2	distinct	1	0.9293

HTLAYHSDEGK	58.09	55.7704	1256.579	1257.953	2	2	distinct	0	0.9551
LGANSLLDIVVFGR	85.27	55.0032	1472.835	1473.587	5	2	shared(2)	0	0.9963
FHTNNTVLATGGYGR	93.88	54.6335	1606.785	1607.473	8	2	distinct	0	0.985
IYQRPFGGQSLEFGK	72.66	54.2867	1725.884	1726.233	11	+2,+3	distinct	0	0.9983
NLLACASCTMHGAEAR	45.35	54.2982	1760.776	1761.086	1	2	distinct	0	0.8885
GSDWLGDQDAIHYMCR	71.32	54.1031	1922.804	1923.786	1	2	distinct	0	0.9886
IVPGLFAAGEAACASVHGANR	114	53.6134	2067.032	2066.891	18	+2,+3	distinct	0	1
AGIPLQDPEFVQFHPTGIYGAGCLITEGSR	58.9	51.0219	3229.587	3230.987	8	3	distinct	0	0.9762

The equivalent proteins include

jgi|Physo1_1|108636|estExt_fgenesh1_pm.C_210010	0	No title.

11. Group probability: 1.0000. Peptides of the group

VTASEVNGDVVK	62.07	55.7414	1216.63	1217.854	1	2	shared(2)	0	0.9694
KQGLEFQFGTK	77.57	55.1925	1281.672	1282.3	7	+1,+2	distinct	1	0.9994
TLTGGIESLFKK	64.65	55.2619	1292.734	1293.931	1	2	distinct	1	0.9759
TQVPGIFAIGDVIK	68.39	54.9975	1456.829	1457.52	5	+1,+2	shared(2)	0	0.9995
LGGTCLNVGCIPSK	77	54.9891	1474.727	1475.148	1	2	shared(2)	0	0.9924
TCHAHPTLSEAFK	60.11	54.7891	1497.703	1497.461	5	+1,+2	shared(2)	0	0.9975
RAFTAGLGLEQMGIQTDK	122.8	53.8159	1934.988	1935.801	8	2	shared(2)	1	0.9999
AEGIEYNVGKFPMMANSR	81.68	53.5679	2012.945	2013.424	8	2	shared(2)	1	0.9958
AFTAGLGLEQMGIQTDKLGR (0000000000010000000000)	110.97	53.3656	2105.094	2105.702	9	+2,+3	shared(2)	1	1
VTVVEFQDAACPGMDKESVK	60.55	53.2658	2209.039	2210.472	1	3	distinct	1	0.8247
GAMLAHKAEEEGVACVENIAGK (000100000000000000000000)	82.86	53.0203	2283.099	2283.718	13	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|109642|estExt_fgenesh1_pm.C_1910001	0	No title.

12. Group probability: 1.0000. Peptides of the group

ILGYLNIDDLVGITK	110.28	54.5836	1645.929	1646.85	8	2	distinct	0	0.9989
VQGDAPVWHPEVGQWLSK	77.09	53.7035	2032.017	2032.627	20	+2,+3	distinct	0	0.9992
SGCGAFTWTSYNGGTCWLK	91.93	53.2808	2151.914	2151.965	5	2	distinct	0	0.9983
SGCGAFTWTNYNGGTCWLK	93.92	53.33	2178.925	2179.37	5	2	shared(2)	0	0.9986
APYPNNYWCSFPNSCAQK	57.23	53.2345	2202.925	2203.323	2	2	distinct	0	0.9641
YYENHNPLEYGDFVAMDGAK (0000000000000000100000)	76.61	52.9785	2332.011	2332.033	7	+2,+3	distinct	0	0.9999
GFEVEQSIDFWKNPGDQNANANR	85.19	52.2094	2635.205	2636.526	1	3	distinct	1	0.9969
GSATSNPGAISGVVQGSSSNNNNNNSGAWSMKPVK (0000000000000000000000000000000100000)	98.69	50.397	3417.597	3418.909	4	3	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|140695|estExt_fgenesh1_pg.C_880067	0	No title.

13. Group probability: 1.0000. Peptides of the group

IGSWVTLEYR	61.08	55.252	1222.635	1222.589	1	2	distinct	0	0.9646
LIHYVNQDAR	65.17	55.5412	1227.636	1227.479	4	1	distinct	0	0.9751
DLEFIWRPSK	47	55.4361	1289.677	1290.951	1	2	distinct	0	0.8778
SAAATVLSGDASIR	49.07	55.4013	1317.689	1318.875	1	2	distinct	0	0.9116
ELNEVLFVIGEK	57.82	55.3412	1388.755	1389.845	2	2	distinct	0	0.956
TTVQTVSIPITHK	68.3	54.9108	1423.803	1424.778	5	+2,+3	distinct	0	0.9977
QIDALYQSHHSSK	72.95	54.7345	1512.732	1512.865	4	2	distinct	0	0.9889
NKDLEFIWRPSK	81.37	54.9157	1531.815	1532.786	7	2	distinct	1	0.9945
QFMFVEQSFFQR	60.1	54.6162	1592.745	1593.401	2	2	distinct	0	0.9645
MESQFFRPLTAYR	48.95	54.6082	1644.808	1645.695	5	+2,+3	distinct	0	0.9897
AVGLVQHHDGLSGTEK	87.37	54.6227	1646.838	1647.305	14	2	distinct	0	0.9972
VQYILDTAVEELVR	81.49	54.6489	1646.888	1647.694	2	2	distinct	0	0.9949
NSVVSEVTELVLTGTK	89.52	54.8435	1674.904	1676.012	4	2	distinct	0	0.9977
DDYWSGFFTSRPTLK	64.52	54.1962	1818.858	1819.112	5	2	distinct	0	0.9785
ASQVFTGEIIDHYCPPGK	68.3	53.6862	2017.957	2018.614	2	2	distinct	0	0.9863
GNHVFIPMGCDFQFDNSR (00000000100000000000)	96.2	53.2967	2139.925	2141.339	15	+2,+3	distinct	0	1
NIQIPLSLDVAYYQAFQGDGPK	107.3	52.6295	2436.232	2436.478	3	2	distinct	0	0.9996
VPWLTVGEFPPSVGLTTVQELSK	50.73	52.607	2483.331	2483.591	1	2	distinct	0	0.9476
AKVPWLTVGEFPPSVGLTTVQELSK	69.17	52.1549	2682.463	2682.801	20	+2,+3	distinct	1	0.9996

The equivalent proteins include

jgi|Physo1_1|131780|estExt_fgenesh1_pg.C_170122	0	No title.

14. Group probability: 1.0000. Peptides of the group

MPGVNYNSR	44.68	55.5515	1036.476	1036.627	1	2	shared(2)	0	0.8456

KGPDWAPDSSK	55.08		55.8613	1186.562	1187.198	2	2	shared(2)	1	0.9414
SNFQGLTIGWKDPK	44.44		54.7031	1589.82	1590.597	1	2	distinct	1	0.8692
HLGFCLAFDNLNNK	93.19		54.5559	1661.798	1663.044	10	2	distinct	0	0.9982
HQGFCLDTDPAQNNK	68.1		54.3124	1743.763	1743.906	3	2	distinct	0	0.9843
FYTMESSKPFAQVVR (0000100000000000)	72.69		54.2656	1788.887	1789.876	11	+2,+3	distinct	0	0.9982
CLDAYQAWDGGIVHVYR	91.89		54.0985	2021.942	2022.857	2	2	distinct	0	0.9982
LQLWGCLLNNNNQVWR	82.43		53.5634	2027.016	2028.148	6	2	distinct	0	0.9957
KIVISETGWSSGGSDPAAGVASPANQAK	42.6		52.1614	2684.34	2685.048	1	3	shared(2)	1	0.8908
SGDNVAIGFGGSNVAGSQWFYDPSTHLVK	56.21		51.4498	3009.426	3010.855	2	3	distinct	0	0.9685

The equivalent proteins include

jgi|Physo1_1|128780|estExt_fgenesh1_pg.C_50277	0	No title.

15. Group probability: 1.0000. Peptides of the group

AVFPSIVGRPK	60.94		55.6675	1169.692	1170.277	8	2	distinct	0	0.8988
HLGIMVGMDQK (0000000010000)	79.27		55.6243	1227.61	1228.146	22	+1,+2	distinct	0	0.9997
TPEVLFQPSLIGK	59.88		55.0528	1427.802	1428.872	2	2	distinct	0	0.9648
AEYDESGPSIVHR	65.28		55.1212	1458.674	1459.218	3	+2,+3	shared(2)	0	0.998
AEYDESGPSIVHRK	74.83		54.9978	1586.769	1587.119	5	2	shared(2)	1	0.972
FRTPEVLFQPSLIGK	88.91		54.2984	1730.972	1731.667	11	+2,+3	distinct	1	0.9998
SYELPDGNVIVIGNER	105.1		54.3156	1773.89	1774.202	1	2	shared(2)	0	0.9923
YPIEHGIVTNWDDMEK (0000000000001000)	89.61		53.9432	1945.888	1946.177	23	+2,+3	shared(4)	0	0.9983
VAPEEHPVLLTEAPINPK	81.4		53.7548	1953.057	1953.885	13	2	shared(10)	0	0.9887
DLYCNIVLSGGTTMYPGIGER	47.6		53.1488	2315.093	2315.776	1	2	shared(2)	0	0.9251
KDLYCNIVLSGGTTMYPGIGER (0000000000000100000000)	89.96		52.8663	2443.187	2444.683	11	2	shared(2)	1	0.9982
TTGCVLDSGDGVSHTVPIYEGYALPHAIVR	72.64		50.9814	3183.566	3184.46	9	+2,+3	shared(3)	0	0.9878

The equivalent proteins include

gi|1085617|pir||S49007	41037.55	actin - Pythium irregulare (fragment)
gi|113223|sp|P22131|ACT1_PHYIN	42197.03	Actin-1
gi|9858460|gb|AAG01044.1|	42182.06	actin [Pythium splendens]
jgi|Physo1_1|108986|estExt_fgenesh1_pm.C_490003	0	No title.
jgi|Phyra1_1|71581|fgenesh1_pm.C_scaffold_28000009	0	No title.

16. Group probability: 1.0000. Peptides of the group

SHVTAGGTSLANFSFPGR	131.22		54.3043	1804.886	1805.289	4	2	distinct	0	0.9999
LDQLIFIPMPDFESR	62.59		54.2658	1819.918	1820.723	1	2	distinct	0	0.9745
NAPAIIFIDEIDSIAPK	82.61		54.0989	1825.982	1826.739	16	2	shared(2)	0	0.9959
LGDVVGIHTCGDVPYGKR	71.31		53.7344	1941.973	1942.393	5	2	distinct	1	0.9895
GAAPCVLFFDELDSIAQQR	109.54		53.2839	2136.031	2137.284	8	2	distinct	0	0.9996
ELLELVQYPVEHPEKFEK	74.77		53.1508	2226.157	2226.594	7	2	distinct	1	0.9923
VVETEPAPYCIVAPDTIIHCEGEPVR	47.84		51.4127	2950.42	2950.769	1	3	distinct	0	0.9271
VVETEPAPYCIVAPDTIIHCEGEPVRR	51.07		51.1636	3106.521	3107.843	1	3	distinct	1	0.9473

The equivalent proteins include

jgi|Physo1_1|109633|estExt_fgenesh1_pm.C_1820001	0	No title.

17. Group probability: 1.0000. Peptides of the group

ACNALLLK	66.88		56.8984	901.505	902.794	1	2	shared(3)	0	0.9265
AGWAIMASHR (000000100000)	71.83		55.8043	1098.539	1099.712	8	2	distinct	0	0.986
IGSEVYHNLK	60.26		55.7973	1158.603	1159.47	7	2	distinct	0	0.9615
IGSEVYHNLKK	47.26		55.5379	1286.698	1287.765	1	2	distinct	1	0.8845
ISADKLQEVYEGFIAK	74.71		54.2182	1809.951	1811.098	6	2	distinct	1	0.9758
VNQIGSITESIEAVTMAK	94.92		53.9668	1889.977	1890.696	2	2	distinct	0	0.9987
YMVEELDGTQNEWGWCK	111.36		53.3165	2143.898	2145.342	4	2	distinct	0	0.9997
IVSIEDPFDQDDWASWVK	121.37		53.3522	2149	2149.761	7	2	distinct	0	0.9999
LAMQEFMILPVGATSFTEAMK	55.27		53.1859	2314.141	2315.238	6	+2,+3	distinct	0	0.9889

The equivalent proteins include

jgi|Physo1_1|108827|estExt_fgenesh1_pm.C_340027	0	No title.
jgi|Physo1_1|109759|estExt_fgenesh1_pm.C_19660001	0	No title.
jgi|Physo1_1|109760|estExt_fgenesh1_pm.C_19710001	0	No title.

18. Group probability: 1.0000. Peptides of the group

IIGQEHYDVAR	74.12		55.3444	1299.657	1300.042	12	+1,+2	distinct	0	0.9988
FVPLVDTISSFK	64.81		55.1843	1351.739	1352.434	2	2	distinct	0	0.9762

IMNVIGESVDER	59.1	55.3015	1360.666	1362.105	1	2	distinct	0	0.9607
VGLTGLTVAEYFR	105.09	54.9941	1424.766	1425.451	8	2	shared(2)	0	0.9864
DNLPPILNALEIK	62.54	55.0738	1448.824	1449.583	2	2	distinct	0	0.9721
AALVYGQMNEPPGAR	63.56	54.9331	1572.772	1573.149	1	2	shared(3)	0	0.926
IVLEVAQHLGENTVR	99.26	54.5908	1676.921	1677.82	61	+2,+3	shared(2)	0	0.9998
FMSQPLHVAEVFTGK (00100000000000000)	106.28	54.8053	1689.855	1691.189	30	2	distinct	0	0.9994
QISELGIYPAVDPLDSK	70.7	54.2682	1843.957	1845.105	2	2	distinct	0	0.9884
EGNDLYYEMIESGVIK	84.54	54.4675	1858.866	1859.066	7	2	distinct	0	0.9885
DVEGQDVLLFVDNIFR	100.43	54.1126	1877.952	1879.303	48	2	distinct	0	0.9991
TREGNDLYYEMIESGVIK	85.01	53.4286	2116.015	2116.626	2	2	distinct	1	0.9843
IPSAVGYQPTLATDLGALQER	110.91	53.2356	2199.153	2200.244	2	+2,+3	distinct	0	1
GLQDIIAILGMDELSEDDKLTVAR	117.8	52.4546	2614.352	2614.676	38	+2,+3	distinct	1	1
YAPIHTSAPLLTEQGSGAEILVTGMK	90.55	52.1391	2683.389	2684.372	23	+2,+3	distinct	0	1
DIIAGNYDDLPEAAFYMVGGIEEVK	71.85	52.0555	2728.294	2728.551	2	2	distinct	0	0.9924

The equivalent proteins include

jgi|Physo1_1|109375|estExt_fgenesh1_pm.C_960005	0	No title.

19. Group probability: 1.0000. Peptides of the group

IIGSYVGNR	57.66	55.8554	977.529	978.913	2	2	shared(2)	0	0.9502
KDWPVTQQK	50.64	55.8364	1128.593	1129.379	3	2	distinct	1	0.9079
ELKPGEVLVR	45.1	55.3402	1138.671	1139.408	1	2	distinct	0	0.8559
VIAIDTGADKHK	64.31	55.3745	1266.693	1267.501	7	2	distinct	1	0.9751
VTADVFGSVLNAHR	88.03	55.0113	1484.773	1485.885	6	+2,+3	distinct	0	0.9998
WIANSCLGCEDCRK	60.07	54.228	1767.749	1767.977	7	2	shared(2)	1	0.9671
LAYSGVCHSDLHIWK	64.18	54.3434	1784.867	1785.115	3	2	distinct	0	0.9778
IIGSYVGNRQDSIEALK	45.98	54.145	1861.99	1862.754	2	2	shared(2)	1	0.8985
TQTAVIFDKLNGPLQVR	100.97	53.9061	1899.058	1899.621	4	2	distinct	1	0.9992
LPCVGGHEGAGYVAAIGDHTR	125.92	53.2875	2136.017	2136.3	7	+2,+3	distinct	0	1
VAAGGDVSTNYSIEKLDNLPSVFER	41.82	52.2049	2680.334	2681.752	1	3	distinct	1	0.8699
EINGVCGDSVVIPGAGGGLGHYACQYAR	71.37	51.6661	2876.333	2877.764	8	3	distinct	0	0.9913

The equivalent proteins include

jgi|Physo1_1|109125|estExt_fgenesh1_pm.C_620002	0	No title.

20. Group probability: 1.0000. Peptides of the group

AYEALDMLDTILAK	56.31	54.6868	1565.801	1565.994	1	1	distinct	0	0.9538
HLTEYPNVVAYLR	48.17	54.781	1573.825	1574.282	3	+2,+3	distinct	0	0.9872
YHLYVTYSCPFACR	65.75	54.1772	1835.812	1836.185	3	2	distinct	0	0.98
SDKHLTEYPNVVAYLR	66.13	53.9807	1903.979	1905.384	1	2	distinct	1	0.9821
APHVAAEGPFVDYDAAHER	108.65	53.9209	2050.95	2051.215	11	+2,+3	distinct	0	1
NLLGLEDAIGLSVAHPVFQK	118.13	53.3015	2120.163	2121.186	17	+2,+3	distinct	0	1
TKPNDPNDEHKGWTFVDPEK	51.42	52.974	2353.097	2353.574	1	2	distinct	1	0.9447

The equivalent proteins include

jgi|Physo1_1|130534|estExt_fgenesh1_pg.C_110203	0	No title.

21. Group probability: 1.0000. Peptides of the group

EHADVEHQVTMDR	66.89	54.6858	1565.689	1566.103	4	2	distinct	0	0.9811
FTNKPCNPSSPNQIFK	64.36	54.1114	1877.909	1878.644	10	2	distinct	0	0.979
FTDKPCNPDSPNQVYK	60.87	53.869	1908.868	1910.012	3	+2,+3	distinct	0	0.9987
LGLTPYDILTSGQEIMLR	73.42	54.0772	2019.071	2019.976	2	2	distinct	0	0.9912
TGPTPYDMLLSGEEIMFR	106.95	53.5761	2055.965	2056.967	8	2	distinct	0	0.9995
IAAGNTAVDILATGQEIMLR	96.28	53.5692	2056.099	2056.636	3	+2,+3	distinct	0	0.9999
NPAKPNLCFDDGGGTTAGATK	82.65	53.4264	2090.969	2090.758	6	+2,+3	distinct	0	1
NPAKPNLCFDDGGGMTPGASK (000000000000000010000000)	89.31	53.3285	2132.962	2134.11	14	+2,+3	distinct	0	1
YVMWTCDENNPNQHFEVLPR	98.55	52.5756	2548.126	2549.119	2	2	distinct	0	0.9991
FVDKTCNPSSPNQIFTYDANTR	43	52.389	2574.181	2575.326	1	3	distinct	1	0.869
FEDQPCDPTSPNQIFTYDTVTHQFK	43.31	51.3239	3014.339	3015.525	1	3	distinct	0	0.8878
AHLWYCDPNNQNQWFVMDPNTLMLK (000000000000000001000000000)	54.26	51.125	3134.42	3135.416	4	3	distinct	0	0.9572
YWLWGCDNNNPNQHFEVLSAAAMAAEK	72.36	51.1221	3135.397	3136.623	4	3	distinct	0	0.9919
YWLWTCDNANQNQHFEIVSPASMPALK (000000000000000000000100000)	51.16	50.9988	3235.485	3236.896	2	3	distinct	0	0.9479

The equivalent proteins include

jgi|Physo1_1|142672|estExt_fgenesh1_pg.C_1190042	0	No title.

22. Group probability: 1.0000. Peptides of the group

RPSFVGR	47.76	56.851	817.456	818.17	2	2	distinct	0	0.8654
IRPTGVSMNVLK	55.01	55.3688	1313.749	1314.392	2	2	distinct	0	0.9437

GTELGMEHLVIGMPHR	77.79		54.1813	1775.881	1776.481	4	+2,+3	distinct	0	0.999
APAAAPATGYNAVHQIEQDR	131.54		53.6799	2079.013	2079.351	10	+2,+3	distinct	0	1
FGHNEVDNPFFTQPLMYK	84.19		53.4842	2183.015	2183.803	9	+2,+3	distinct	0	0.9998
WVQEEPLNMGFWTYVSPR	98.16		53.1587	2238.057	2239.01	4	2	distinct	0	0.999

The equivalent proteins include

jgi|Physo1_1|109505|estExt_fgenesh1_pm.C_1210001	0	No title.

23. Group probability: 1.0000. Peptides of the group

LHPEILGDFQK	58.26		55.2414	1295.687	1296.285	5	2	shared(2)	0	0.9562
LLPWFDGMLEADEK	45.26		54.5087	1662.796	1663.888	1	2	distinct	0	0.8788
LHEAYHNLNCVNVL	62.95		54.3274	1694.82	1695.553	13	2	distinct	0	0.9744
NQNGSILGAIAAAYHVR	109.37		54.2223	1753.922	1754.905	8	+2,+3	distinct	0	1
KLLPWFDGMLEADEK (00000000010000000)	73.98		54.3457	1790.891	1792.099	20	+2,+3	distinct	1	0.9994
GYLQGQIGNPEGPDAPNKK	70.24		53.7977	1981.986	1982.802	10	+2,+3	distinct	1	0.9989
MNIDTDTQWAYWNGLR	77.83		53.8228	1982.894	1983.612	1	2	distinct	0	0.9857
MNIDTDTQWAYWNGLRK	74.4		53.4956	2110.989	2112.422	1	2	distinct	1	0.9774
YAQEHNFAIPAVNVTSSSTANAALQAAR	94.53		51.5423	2901.437	2902.552	9	+2,+3	distinct	0	1
EHGVPLWSSHMLDLSEEPMEENVAISK	55.17		51.2678	3063.432	3064.815	3	3	distinct	0	0.9631

The equivalent proteins include

jgi|Physo1_1|157135|C_scaffold_35000027	0	No title.

24. Group probability: 1.0000. Peptides of the group

EHAALEPR	45.39		55.5892	921.467	922.495	1	2	distinct	0	0.8548
TFTPGKPLTLR	47.72		55.7319	1229.713	1230.185	3	2	distinct	0	0.8886
IIYGHLDDATTK	71.53		55.3557	1345.688	1346.334	2	2	distinct	0	0.9868
KTNGNKPLTLAEK	61.19		55.1559	1412.799	1414.211	2	2	distinct	1	0.9685
CTTDHISMAGPWLK	67.23		54.7914	1615.749	1616.236	7	2	distinct	0	0.9822
FKVPYYYVTPGSEQVR	53.97		54.1656	1768.915	1769.357	2	2	distinct	1	0.9459
TAVPTTIHCDHLITAEK	101.21		54.0017	1905.962	1906.421	9	2	distinct	0	0.9992
VAMQDATAQMAVLQFISSGLPK	89.12		53.0201	2305.181	2306.117	2	2	distinct	0	0.9981
LALLSAFDEWNGEDFTDMPVLIK	66.53		52.2753	2623.288	2624.459	2	2	distinct	0	0.987
GHLDNISNNLLIGAENAETGETNSVK	73.59		52.1303	2709.32	2710.113	2	3	distinct	0	0.9923
DGILDTFLESGATVLANACGPCIGQWNR	60.05		51.366	3034.428	3035.84	2	3	distinct	0	0.9768

The equivalent proteins include

jgi|Physo1_1|109018|estExt_fgenesh1_pm.C_520011	0	No title.

25. Group probability: 1.0000. Peptides of the group

AIDQEFGSFDNFKK	52.34		54.6083	1644.778	1645.808	1	2	distinct	1	0.9347
SVGVQGSGWGWLGYSPETK	84.63		53.7903	1993.953	1995.393	2	2	distinct	0	0.9968
NVRPDYLNAIWDVVNWK	106.34		53.4432	2101.074	2102.42	34	+2,+3	distinct	0	0.9999
HHQTYVNNYNAALEQYAEAEAK	101.8		52.5367	2563.173	2563.647	22	+2,+3	distinct	0	1
LPDLAYDFGALEPSISGQIMEIHHQK (00000000000000000010000000)	97.87		51.6899	2908.443	2909.811	14	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109207|estExt_fgenesh1_pm.C_730003	0	No title.

26. Group probability: 1.0000. Peptides of the group

MLDHAAALLK	73.29		55.3167	1081.595	1082.454	11	+1,+2	distinct	0	0.9984
RMLDHAAALLK	50.73		55.1467	1237.696	1238.587	2	2	distinct	1	0.9155
IKLEDAGFDWK	58		55.3642	1320.671	1321.151	2	2	distinct	1	0.9551
YGAIKPTAIYVPLK	61.27		54.7958	1532.897	1533.739	10	+1,+2,+3	distinct	0	0.9996
KLSDLTIGPVLTVTTK	94.97		54.4065	1684.997	1685.426	3	2	distinct	1	0.9986
SFGVPGDHQGQASHGYR	71.53		54.4577	1798.813	1799.661	3	2	distinct	0	0.9891
TTGAPQNHWFGPAGDPCAGGIGTPEAIK	67.2		51.847	2806.313	2807.417	9	+2,+3	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|109579|estExt_fgenesh1_pm.C_1480002	0	No title.

27. Group probability: 1.0000. Peptides of the group

ELHNQSLR	53.69		55.353	995.515	994.391	2	2	distinct	0	0.9302
AAAHEFSGDAEK	48.11		55.6756	1231.547	1232.151	2	2	distinct	0	0.8962
YKELHNQSLR	52.09		55.5379	1286.673	1287.772	5	2	distinct	1	0.9216
LLASPLPEAEAGILR	76.33		54.7181	1548.887	1550.158	3	2	distinct	0	0.9923
LLASPLPEAEAGILRK	88.53		54.5909	1676.982	1677.577	6	2	distinct	1	0.9975
GLGTKEDLIYPIVVGR	87.53		54.3266	1728.977	1729.61	5	2	distinct	1	0.9972
MITEPLDLLAELFESAMK (000000000000000100)	133.2		53.6134	2050.037	2066.811	112	+2,+3	distinct	0	1
IAEEVSGDYGELLLSVFDAR	89.12		53.5028	2182.079	2183.549	5	2	distinct	0	0.998
MGTDEEGFVSVLVASPPEHLR	97.15		53.0901	2269.105	2269.312	8	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|140346|estExt_fgenesh1_pg.C_840073	0	No title.

28. Group probability: 1.0000. Peptides of the group

FGSGWAWLGVK	81.22	55.3563	1206.619	1206.395	29	2	distinct	0	0.9941
SILEVVQSATEAPVR	109.51	54.8067	1597.867	1598.368	16	+2,+3	distinct	0	1
RPEYISAFWNVANWDK	95.56	53.7864	1994.964	1995.412	5	+2,+3	distinct	0	1
HHQAYVNNINNYISSDK	105.99	53.6573	2015.945	2016.447	27	+2,+3	distinct	0	1

The equivalent proteins include

gi|66865886|gb|AAY57577.1|	23956.74	manganese superoxide dismutase [Phytophthora nicotianae]

29. Group probability: 1.0000. Peptides of the group

HLGAELALVAR	54.97	55.6588	1148.667	1148.529	5	+1,+2	shared(2)	0	0.9959
YYYHAVGTPR	68.16	55.4168	1225.588	1226.374	13	2	shared(2)	0	0.9809
SKDYFAGMAWK	47.88	55.4348	1302.607	1304.091	2	2	shared(2)	1	0.8908
KTQSNVSKPFPK	83.59	55.3565	1359.751	1360.299	6	+1,+2	shared(2)	1	0.9996
KLFVPYDNVIPPSAK	50.79	54.4566	1686.934	1687.763	1	2	shared(2)	1	0.9281
ILIVGGGPAGIAVAQALAADLTAK	136.7	53.7801	2189.278	2189.943	8	+2,+3	distinct	0	1
VEVVGTMLPLGPNGGVSQLPVMGGVVMGNLITK	66.41	50.9042	3262.749	3264.041	1	3	shared(2)	0	0.989
ILIVGGGPAGIAVAQALAADLTAKDDTEVLVLEK	61.75	50.7319	3330.865	3330.616	14	3	distinct	1	0.984

The equivalent proteins include

jgi|Physo1_1|142200|estExt_fgenesh1_pg.C_1090056	0	No title.

30. Group probability: 1.0000. Peptides of the group

LLADLIDYVPAR	84.07	55.4099	1357.76	1358.827	24	+1,+2	distinct	0	0.9998
SLLADAEAMDLSECILPVGDHIR (00000000010000000000000)	116.84	52.5713	2524.23	2525.574	123	+2,+3	distinct	0	1

The equivalent proteins include

gi|81159502|gb|ABB56022.1|	20174.32	elicitin-like protein SOL2A [Phytophthora sojae]
jgi|Physo1_1|108732|estExt_fgenesh1_pm.C_280002	0	No title.

31. Group probability: 1.0000. Peptides of the group

HVAALLLCVLGGNATPSVADLEK	111.1	53.0393	2347.257	2347.962	33	+2,+3	distinct	0	1
LATVSVGAAPAAGAAAGGAAPAKEEEK	95.87	52.8936	2364.228	2364.354	8	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|108694|estExt_fgenesh1_pm.C_240025	0	No title.

32. Group probability: 1.0000. Peptides of the group

NHCIMLAR	49.24	55.992	1013.49	1013.341	1	1	distinct	0	0.8956
NRDEISQMR	47.18	55.6581	1147.54	1148.265	2	2	distinct	1	0.8757
FEFASPFELHR	64.6	55.0801	1378.667	1379.471	11	+2,+3	distinct	0	0.9979
RMEITNDNEYK	44.64	55.0719	1411.64	1412.041	1	2	distinct	1	0.856
SSFNTDYYTMGNKIPGIK	75.3	54.3401	2034.972	2036.408	10	2	distinct	1	0.9925
KWCGEDNGPIFVEMNTYR	72.85	53.2022	2214.983	2215.929	2	2	distinct	1	0.9909
LPAIFCIENNHYGMGTSTAR	97.39	53.5567	2251.051	2251.562	14	+2,+3	distinct	0	0.9999
GFCHLYDGQEAVATGVEAALDR	103.78	52.806	2378.096	2379.378	8	+2,+3	distinct	0	1
KANFYGGQGIVGAQVPVGAGLAFASK	80.82	52.5042	2506.333	2506.767	8	2	distinct	1	0.9966
GFCHLYDGQEAVATGVEAALDRTDSWITSYR	61.12	50.2051	3487.61	3488.495	2	3	distinct	1	0.9814

The equivalent proteins include

jgi|Physo1_1|108775|estExt_fgenesh1_pm.C_300026	0	No title.

33. Group probability: 1.0000. Peptides of the group

AHGAQGIGLTR	68.34	55.2721	1079.584	1080.253	10	2	distinct	0	0.9819
GGMTSHAAVVAR (00010000000000)	91.33	55.7318	1155.582	1156.392	7	2	shared(2)	0	0.9737
TEHMFFSSAQR	50.12	55.2307	1339.598	1340.47	3	2	distinct	0	0.9107
LGIVHPGITEMQAK (0000000000010000)	62.94	54.7235	1492.807	1492.4	14	+1,+2	distinct	0	0.9993
IVFTAADAEAWFAR	89.72	54.6261	1566.783	1568.047	1	2	distinct	0	0.9975
HLDQLLHPSFANEK	103.93	54.649	1647.837	1648.096	13	+2,+3	distinct	0	0.9998
QLDETVHTLETHFK	58.39	54.3449	1696.842	1697.657	1	2	distinct	0	0.9618
RMEVFTNADTPEDAR	43.69	54.2214	1750.794	1751.231	1	2	distinct	1	0.8665
ALGVTFADAANPLLVSVR	57.41	54.21	1813.01	1813.874	2	2	distinct	0	0.964
IELGICGEHGGDPQSIEFFEK	87.53	52.8939	2361.095	2361.618	4	+2,+3	distinct	0	0.9997
HGVLEKDPFETLDQEGVGELVR	71.99	52.5883	2466.239	2466.788	5	+2,+3	distinct	1	0.9997

The equivalent proteins include

jgi|Physo1_1|108954|estExt_fgenesh1_pm.C_460001	0	No title.

34. Group probability: 1.0000. Peptides of the group

ATGFGVAFIQSLLK	88.38		54.9236	1450.818	1451.31	6	2	distinct	0	0.9972
DMGGAAALLGAFEAACHAK	72.12		54.0572	1859.866	1860.763	3	+2,+3	distinct	0	0.9993
GVDALHVTLHALPTQVSR	77.11		53.8508	1913.048	1913.248	9	+2,+3	distinct	0	0.9991
WLHVDMAFPSFTGDDER	92.47		54.0985	2021.894	2023.057	10	+2,+3	distinct	0	0.9999
LVDAPPNELHSDAFIAEAR	47.93		53.6249	2064.028	2064.405	1	2	distinct	0	0.9211
ANAQVSCAGQFIANHLGEFENTGK	82.28		52.5202	2562.192	2563.018	6	+2,+3	distinct	0	0.9999
LQVVYQTPLSGEQTTLVQHTADAIQLAAR	50.97		51.1934	3150.667	3151.899	2	3	distinct	0	0.9504

The equivalent proteins include

jgi|Physo1_1|140692|estExt_fgenesh1_pg.C_880064	0	No title.

35. Group probability: 1.0000. Peptides of the group

HRPSVSELEEK	45.2		55.1986	1309.663	1310.578	1	2	distinct	0	0.8625
NKTPTSTPTPPAGK	56.94		54.9935	1395.736	1396.96	1	2	distinct	1	0.9561
DHAIVHGADGVAPSLQATQEK	123.4		53.2508	2143.066	2143.234	5	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|132189|estExt_fgenesh1_pg.C_190139	0	No title.

36. Group probability: 1.0000. Peptides of the group

KPVCIMAR	48.31		56.6696	973.52	974.005	1	2	distinct	0	0.8851
AHVANWFFK	48.86		55.8441	1118.566	1119.8	1	2	distinct	0	0.8923
YAAEVEALRK	55.95		55.6328	1148.619	1149.101	4	2	distinct	1	0.944
LGAVIVAVVDPMVAK	90.3		54.8098	1480.869	1480.814	2	2	distinct	0	0.9977
IGVVKPYSETPTLK	69.49		55.275	1530.866	1531.313	20	+1,+2,+3	distinct	0	0.9999
VPVDETAIPAENRVPR	46.77		54.1813	1761.937	1762.478	2	2	distinct	1	0.9018
AGAHLFLEKPLSNAPVDEVTK	95.15		53.1353	2235.19	2236.593	11	+2,+3	distinct	0	1
VALVGAGAVNFGGAEGPWDHASR	117.07		53.1222	2237.098	2237.589	16	+2,+3	distinct	0	1
SGALGNLVHGALLQGEAYDASLEIMADGLR (000000000000000000000001000000)	52.21		51.1314	3056.524	3057.839	1	3	distinct	0	0.9571

The equivalent proteins include

jgi|Physo1_1|139835|estExt_fgenesh1_pg.C_790014	0	No title.

37. Group probability: 1.0000. Peptides of the group

RVTLEIGGK	51.91		56.3835	971.576	972.261	3	2	shared(3)	1	0.8721
HLAQHPNVDK	47.99		55.8204	1157.594	1158.743	3	2	distinct	0	0.8871
VGELIVEAGFPK	78.95		55.5194	1257.697	1258.863	1	2	shared(3)	0	0.9931
LLINNEFVPSVSGK	68.47		54.9365	1515.83	1516.785	2	2	distinct	0	0.984
VYVQEGIYDEFVK	78.44		54.8831	1587.782	1588.458	3	2	shared(2)	0	0.9931
VYVQEGIYDEFVKR	78.67		54.3331	1743.883	1744.428	22	2	shared(2)	1	0.9936
GWFIEPTVFADVTDDMTIAR (00000000000000100000)	97.86		53.0271	2283.088	2284.084	13	2	shared(3)	0	0.9991
TGTVYYVNCYDVFDGNTPFGGFK	107.51		52.7079	2457.095	2456.854	9	2	distinct	0	0.9996
LGPALAAGNTVVLKPAEQTPLSALR	85.32		52.6311	2486.422	2487.772	31	+2,+3	distinct	0	1
TGTVYYVNCYDVFDGNTPFGGFKDSGIGR	63.95		51.2163	3042.382	3043.621	1	3	distinct	1	0.9835

The equivalent proteins include

jgi|Physo1_1|120743|estExt_Genewise1.C_810091	0	No title.

38. Group probability: 1.0000. Peptides of the group

VFAHAAAR	47.15		56.5724	841.456	842.316	1	2	distinct	0	0.8731
LGGQNFVFWGGR	70.83		55.3846	1336.668	1336.88	5	2	distinct	0	0.9859
MELDHMAAFFK	76.31		55.1392	1338.61	1339.812	2	2	distinct	0	0.9809
CLWGTTNLFGHR	66.87		55.0968	1460.698	1461.211	6	2	distinct	0	0.9802
KIVEIGGLAPGGLNFDAK	51.86		54.3063	1797.999	1798.729	2	+2,+3	distinct	1	0.9919
ESTDLEDIFIAHIGSMDCFAR	47.53		52.756	2426.088	2427.271	1	3	distinct	0	0.9081
FAVCYWHTFGNTGGDPFGSETYTNR	81.26		51.6897	2883.235	2884.197	16	+2,+3	distinct	0	0.9999
LNVEPNHTTLAGHDYEHDIYYAASYK	82.29		51.5106	3020.394	3021.447	4	3	distinct	0	0.9964
MLGSVDCNTGDPLVGWDTDQFLMDEKK	61.52		51.2674	3070.372	3071.505	1	3	distinct	1	0.9789

The equivalent proteins include

jgi|Physo1_1|109314|estExt_fgenesh1_pm.C_890003	0	No title.

39. Group probability: 1.0000. Peptides of the group

QIFDFHAIKK	58.75		55.8351	1245.687	1246.433	2	2	distinct	1	0.956
FFGNLMDSHVVFGK (0000001000000000)	52.62		54.6137	1596.776	1597.069	6	+2,+3	distinct	0	0.9924
TSPFQDQKPGTSGLR	59.29		54.6705	1617.811	1618.622	7	+2,+3	distinct	0	0.9951
KLNVPFFEVPTGWK	69.72		54.5707	1660.898	1662.394	10	2	distinct	1	0.9858
EWCPPGHGDLYASLAGSGK	118.43		53.9092	2000.905	2001.097	6	+2,+3	distinct	0	1
LWIGKDGLLSTPCVSAVVR	63.87		53.6911	2070.13	2071.199	2	2	distinct	1	0.9805

EDFTFVVDAMSGVNGPYAR	77.58		53.5322	2073.947	2074.775	2	2	distinct	0	0.9942
SDAYVITEDYRPVIAPER	53.6		53.437	2093.043	2094.317	1	3	distinct	0	0.9391
TFMSDNYLQNFVASVFEALPAK (0001000000000000000000)	125.42		52.5697	2491.209	2492.633	43	2	distinct	0	0.9999
FFVTPSDSLAIIAANCTVIPFFK	108		52.4951	2557.329	2557.827	14	2	distinct	0	0.9997

The equivalent proteins include

jgi|Physo1_1|158882|C_scaffold_167000003	0	No title.

40. Group probability: 1.0000. Peptides of the group

RGVQEFELK	45.12		55.8696	1104.593	1105.548	1	2	distinct	1	0.2705
IHYDNWVSEK	47.41		55.4907	1289.604	1289.373	2	1	distinct	0	0.882
FGLSFWADFLK	66.1		55.3738	1329.676	1330.324	10	+1,+2	distinct	0	0.9975
HGEASMFSQDSGVFK (000000010000000000)	89.3		54.5407	1625.714	1626.205	5	2	distinct	0	0.9975
TKPIQGPYGTGMSGPSFGK (0000000000000100000000)	94.9		53.9399	1908.94	1909.434	28	+2,+3	distinct	0	1
WTSIASTQPVGTTTFEHWPIR	97.97		52.7964	2414.202	2414.803	8	2	distinct	0	0.9991
GHNAIIGLEPVNEPWELTPIEVLK	69.7		52.1542	2667.427	2668.76	17	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|109097|estExt_fgenesh1_pm.C_600003	0	No title.

41. Group probability: 1.0000. Peptides of the group

LGAAHFYIK	72.28		56.2525	1018.56	1019.977	10	2	distinct	0	0.9861
AKFESLNEELFK	76.63		54.8971	1453.745	1454.401	6	2	distinct	1	0.9916
SFTPEEISSMVLLR	58.33		54.5823	1607.823	1608.688	1	2	distinct	0	0.9614
ERGNAAFASGDHATAIK	73.88		54.3173	1714.839	1715.314	4	2	distinct	1	0.9912
MKPEDVTELVLVGGSTR	93.05		54.123	1829.956	1830.897	6	2	distinct	0	0.9984
EFTTAIAYEPTNVIYYSNR	70.32		53.5582	2251.08	2251.349	2	2	distinct	0	0.9889
SINPDEAVAYGAAVQGAILDGIR	93.23		53.1102	2299.181	2300.524	2	2	distinct	0	0.9987
RIINEPTAAALAYGLDTNAGTDGK	53.38		52.6309	2431.234	2432.374	1	2	distinct	1	0.9599
NDATNSLLLVDVTPLSLGIETVGK	74.06		52.7464	2468.337	2469.493	4	2	distinct	0	0.9934

The equivalent proteins include

jgi|Physo1_1|143782|estExt_fgenesh1_pg.C_1510018	0	No title.

42. Group probability: 1.0000. Peptides of the group

RPSPFAER	56.28		56.5505	958.498	959.406	3	2	distinct	0	0.943
VPAGLAQYFAMAR (000000000001000)	92.18		55.6012	1393.718	1393.523	10	2	distinct	0	0.9979
NWAVYYEKNPAK	59.1		54.7368	1481.73	1482.576	3	2	distinct	1	0.9612
EFVVAQSFTSKPVK	84.73		54.6079	1565.845	1566.662	1	2	distinct	0	0.9962
KDEYLNWAVDAFR	95.62		54.7007	1625.784	1626.84	4	2	distinct	1	0.9985
TVPIILGPLTYLALSK	53.53		54.3813	1698.033	1698.747	1	2	distinct	0	0.9455
GMLTGPVTILNWSFPR (001000000000000000)	88.68		54.7291	1787.939	1788.136	12	2	distinct	0	0.996
WFDSNYHYEVPELNAK	65.55		53.6447	2010.911	2011.234	2	2	distinct	0	0.9813
DLGPGTYDIHSPVVPPKEEIVK	50.68		52.8414	2389.253	2389.698	4	2	distinct	1	0.9452
LTSFLNLLPAEQVVVNPDCGLK	76.95		52.7548	2426.288	2427.2	1	2	distinct	0	0.9945
KLTSFLNLLPAEQVVVNPDCGLK	104.16		52.5087	2554.383	2554.986	12	2	distinct	1	0.9995

The equivalent proteins include

jgi|Physo1_1|108148|estExt_fgenesh1_pm.C_10013	0	No title.

43. Group probability: 1.0000. Peptides of the group

RMTPAEIFAR	47.69		55.4889	1190.623	1191.758	2	2	distinct	1	0.8848
LHETAFMGNGLGR	51.64		55.2844	1401.682	1402.259	2	2	distinct	0	0.9271
KSDLQDYIATHYTAPR	131.51		54.1127	1877.927	1878.565	8	+2,+3	distinct	1	1
YETTQNNGAAHFLEHMAFK	69.34		53.1772	2208.006	2208.627	3	2	distinct	0	0.988
EHALAATGPIHELPDYNFIR	84.86		53.149	2263.138	2263.509	2	+2,+3	distinct	0	0.9999
RTQQQLELEIENMGGHLNAYTSR	70.52		52.1484	2687.308	2688.653	1	3	distinct	1	0.9887
TADEVINDKEHALAATGPIHELPDYNFIR	86.07		50.9127	3248.61	3249.713	1	3	distinct	1	0.9977

The equivalent proteins include

jgi|Physo1_1|108442|estExt_fgenesh1_pm.C_100001	0	No title.

44. Group probability: 1.0000. Peptides of the group

AHAIGSGSEGALNNLK	101.2		54.6712	1537.785	1538.404	5	+2,+3	distinct	0	0.9999
RLTSPLLEPGSIEK	64.28		54.7033	1538.867	1539.617	3	2	distinct	1	0.977
VEATNHWFSYNEPVR	66.8		54.045	1847.859	1848.367	5	2	distinct	0	0.9825
HVGAAMSGITADAQTLIDHAR (0000001000000000000000)	116.68		53.3236	2134.059	2135.242	8	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108388|estExt_fgenesh1_pm.C_70033	0	No title.

jgi|Phyra1_1|71231|fgenesh1_pm.C_scaffold_9000010	0	No title.

45. Group probability: 1.0000. Peptides of the group

NLDFLLGGGR	46.89	55.9622	1060.566	1061.166	1	2	distinct	0	0.8753
GVHENTYLNK	59.6	55.7993	1173.578	1173.46	6	+1,+2	distinct	0	0.9962
NLDFLLGGGRK	55.71	55.6938	1188.661	1189.295	6	2	distinct	1	0.9448
GMVTGMIVTCR (0010000000000)	82.43	55.1677	1223.582	1224.353	9	2	distinct	0	0.9948
HGYFVMIEGSR (0000001000000)	70.97	55.1776	1294.613	1295.506	8	2	distinct	0	0.9857
VDHAGHSNDPGTMAK	62.26	54.7165	1535.679	1535.409	10	+1,+2,+3	distinct	0	0.9998
VTHATPASFASHVIDR	72.54	54.6446	1707.869	1707.289	13	+2,+3	distinct	0	0.9998
EPSLPEMVDIVLSLLR (000000010000000000)	88.18	54.218	1809.991	1810.786	91	+2,+3	distinct	0	0.9998
DLEDVMIELGHVISLR (000000100000000000)	98.54	53.9791	1837.961	1838.943	69	+2,+3	distinct	0	1
LFGLFHEDHMSYEVDR (000000000010000000)	74.87	53.7999	1993.899	1994.349	6	+2,+3	distinct	0	0.9994
SVIMMIPDGTGPNVFTLAR	91.66	53.6894	2018.033	2018.835	14	2	distinct	0	0.9946
LMTNFLGLEHQQELVTLK (00100000000000000000)	84.49	53.4152	2113.124	2114.175	39	+2,+3	distinct	0	0.9997
TYDSAIAVDTYEQPLGTVLEAAK	79.46	52.744	2454.217	2455.097	2	2	distinct	0	0.9958
VTHATPASFASHVIDRDSEDDIAAQYVANK	57.76	51.0088	3227.548	3228.269	5	3	distinct	1	0.9737

The equivalent proteins include

jgi|Physo1_1|137262|estExt_fgenesh1_pg.C_520052	0	No title.

46. Group probability: 1.0000. Peptides of the group

KIGYPVIIK	55	56.4448	1029.659	1030.666	6	2	shared(2)	1	0.9184
LGPAPAAESYLNYAK	51.06	54.7083	1563.793	1564.936	1	2	distinct	0	0.9294
ALGAVSLLLLEQLKR	69.2	54.6107	1623.008	1624.251	2	2	distinct	1	0.9856
KLQLSHDDDEAPVTVK	92.8	54.3909	1793.916	1794.136	2	2	distinct	1	0.9983
ALHEYQIVGLPTNIEFVAR	84.01	53.527	2169.158	2169.666	20	+2,+3	distinct	0	0.9999
ISGAEAVHPGYGFLSENAAFAR	84.14	53.1431	2263.102	2264.538	33	+2,+3	shared(2)	0	0.9996
IYAENPYNDFLPGSGTLQHIR	74.38	52.7481	2404.181	2404.726	19	+2,+3	shared(2)	0	0.9999
AGVPVTPGYHGEDQSFETLQSEAR	66.4	52.391	2574.199	2574.47	1	2	distinct	0	0.9873

The equivalent proteins include

jgi|Physo1_1|109683|estExt_fgenesh1_pm.C_2750001	0	No title.

47. Group probability: 1.0000. Peptides of the group

LCDLAEAAVKR	58.78	55.9269	1244.655	1245.368	1	2	distinct	1	0.9576
CLWNGWLDAHAR	89.28	54.7934	1497.694	1498.377	17	+2,+3	distinct	0	0.9999
AFHFILDPFQQEK	74.72	54.5794	1618.814	1620.082	13	2	distinct	0	0.9905
LYAASAGYFHDVADDMLDVR	90.07	53.2916	2228.021	2229.28	3	+2,+3	distinct	0	1
TFSPDYDHYNFAPQGEQSIFHAR	62.07	52.092	2726.215	2727.704	5	+2,+3	distinct	0	0.9979
DLVAYVGGVDLTNDRWDTLEHDQAELR	48.48	51.1752	3099.49	3100.85	1	3	distinct	1	0.9338

The equivalent proteins include

jgi|Physo1_1|127024|estExt_fgenesh1_pg.C_10004	0	No title.

48. Group probability: 1.0000. Peptides of the group

APGFGDNRK	48.36	56.4327	960.478	961.69	1	2	distinct	1	0.8862
NAGHEGAVVVGK	60.41	55.377	1136.594	1136.385	8	+1,+2	distinct	0	0.9979
DKFENMGAQLVR	60.33	54.965	1406.698	1407.764	2	2	distinct	1	0.965
TLYNELEVVEGMK	93.17	54.6717	1523.754	1523.955	1	2	distinct	0	0.9981
GIQMAVDHVVDGLQK	46.83	54.5341	1608.829	1610.274	1	3	distinct	0	0.8746
VSSLQSIIPMLETVVK	45.52	54.3127	1742.985	1744.109	1	2	distinct	0	0.8901
RGIQMAVDHVVDGLQK (0000010000000000)	79.91	54.1898	1764.93	1765.526	12	+2,+3	distinct	1	0.9994
KVSSLQSIIPMLETVVK	65.42	54.1836	1871.08	1871.972	6	+2,+3	distinct	1	0.9992

The equivalent proteins include

jgi|Physo1_1|109597|estExt_fgenesh1_pm.C_1550001	0	No title.

49. Group probability: 1.0000. Peptides of the group

KGVHVTYGGMGK	68.39	55.5805	1232.633	1233.641	3	+1,+2	distinct	1	0.9991
FKELISDLPAPK	66.31	55.359	1356.765	1357.762	1	2	distinct	1	0.9791
YAEFGHPLNVLK	74.63	55.3328	1386.73	1387.403	12	+2,+3	distinct	0	0.9983
EAVAVGTGSLIFHDITLK	78.86	54.0193	1870.02	1870.318	1	2	distinct	0	0.9945
IKIEDAATLAVNPATAYR	101.01	53.928	1916.037	1917.09	3	+2,+3	distinct	1	0.9998
TINIIRDDGDYDVTVQHLK	74.96	53.2003	2214.128	2214.186	2	2	distinct	1	0.9927

The equivalent proteins include

jgi|Physo1_1|136873|estExt_fgenesh1_pg.C_490011	0	No title.

50. Group probability: 1.0000. Peptides of the group

LFFTAFAQNWCEK	64.2	54.6392	1660.771	1661.582	1	2	distinct	0	0.9761
FAEAFSCPVGAPMNPEKK	83.84	53.8022	1978.928	1979.128	17	+2,+3	distinct	1	0.9999
IGMVMGHELSHGFDDQGR (00010000000000000000)	95.19	54.1509	1984.888	1985.999	13	+2,+3	distinct	0	0.9999
LFVGADPEDPSTNVLQLAQGGLTLPSR	81.98	51.9798	2794.45	2794.681	2	2	distinct	0	0.9971
NYIGGPDDVPPLPFELQADAFFNNVK	55.97	51.6513	2876.402	2876.673	1	2	distinct	0	0.9708
AIGKPVDEQAWDMFPSTVNAYYDPSANK (000000000000010000000000000000)	68.59	51.2073	3113.444	3114.447	2	3	distinct	0	0.989

The equivalent proteins include

jgi|Physo1_1|139557|estExt_fgenesh1_pg.C_750054	0	No title.

51. Group probability: 1.0000. Peptides of the group

TVAAVDHIR	54.21	55.2507	980.54	981.259	1	2	distinct	0	0.9335
LMFESHASLR	61.48	55.6294	1189.591	1190.318	2	2	distinct	0	0.9655
FGSELPKPASFLTR	55.54	54.7241	1548.83	1549.95	4	3	distinct	0	0.9392
MTGGGFGGCIVALVQQQHAQK	83.89	53.3113	2186.072	2186.685	1	2	distinct	0	0.986
VNLIGEHTDYNDGFVCPLALDK	83.48	52.5543	2489.19	2489.088	5	2	shared(2)	0	0.9969
LMDTLDAGYPADKFGSELPKPASFLTR	78.17	51.47	2939.474	2940.865	12	+2,+3	distinct	1	0.9999
AGSDNVDVVEQAVTLFYSTFSQYANLPR	104.58	51.1843	3090.493	3090.842	4	2	distinct	0	0.9983
ALLCQAAEHEYCNVPCGIMDQFISSCGK	65.64	51.4499	3257.407	3258.227	3	3	shared(2)	0	0.9857
ALLCQAAEHEYCNVPCGIMDQFISSCGKK	54.76	50.4797	3385.502	3386.878	4	3	shared(2)	1	0.965

The equivalent proteins include

jgi|Physo1_1|157829|C_scaffold_63000007	0	No title.

52. Group probability: 1.0000. Peptides of the group

HQMNNANLGR	54.11	55.2729	1153.541	1154.125	4	2	distinct	0	0.9347
LNLLKLAPGGHIGR	71.61	55.0401	1457.883	1458.974	34	+2,+3	distinct	1	0.9989
RGPLIVYANANGAEK	90.44	54.9622	1571.842	1572.18	11	2	distinct	1	0.9978
EAGHQHSAESWGTGR	52.73	54.5827	1608.703	1609.115	6	2	distinct	0	0.9392
IQGGGNQSSGQAAFGNMCR	88.09	53.8571	1938.842	1938.995	2	2	distinct	0	0.9977
RFAVASALAASAVPALVMAR	100.54	53.7465	1971.109	1972.584	5	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|121586|estExt_Genewise1.C_930071	0	No title.

53. Group probability: 1.0000. Peptides of the group

FRPALVFQPK	50.77	55.6972	1201.697	1202.728	1	2	distinct	0	0.9117
LLGCLSTTHSK	58	55.7149	1215.628	1216.255	1	2	distinct	0	0.9548
AGLHELAAEFPTLVSNVR	95.69	54.1032	1923.021	1923.719	8	+2,+3	distinct	0	0.9999
LRYPLDVHQAANEAEEAR	79.61	53.5975	2081.029	2081.729	8	2	distinct	1	0.9949
FLDVYGGQIASLPIGYNHPK	72.4	53.3282	2131.11	2131.39	13	+2,+3	distinct	0	0.9995
IAGMIIEPIQAEGGDNHASPAFFR	70.71	52.4872	2540.248	2540.779	1	2	distinct	0	0.9912
ALPSTPAPAFPDEYAHAEIVTGQVPGPK	43.9	51.7439	2859.444	2860.449	1	3	distinct	0	0.9034

The equivalent proteins include

jgi|Physo1_1|157659|C_scaffold_55000043	0	No title.

54. Group probability: 1.0000. Peptides of the group

SLQGTLMHQLK	63.91	55.6854	1254.675	1255.6	5	2	distinct	0	0.9731
ITGLTFPGDRVHSEK	62.4	54.439	1655.863	1656.158	4	2	distinct	1	0.974
LIKPGNTNLQVTEALTK	83.23	54.0433	1839.046	1839.788	2	2	distinct	0	0.9961
HDLLQAYPILEGRPGDK	69.86	53.8559	1921.006	1921.326	9	+2,+3	distinct	0	0.9995
LAAEIAQSALEGVLSQLEAGKDVVELCK	104.81	51.5027	2940.548	2942.043	3	3	distinct	1	0.9995
GVAFPTSISANEIICHFSPLQNESLVLK	66.16	51.2656	3070.58	3071.853	6	+2,+3	distinct	0	0.9989

The equivalent proteins include

jgi|Physo1_1|109304|estExt_fgenesh1_pm.C_870001	0	No title.

55. Group probability: 1.0000. Peptides of the group

TPLYDLHVALGGK	84.77	55.0639	1382.756	1383.563	1	2	distinct	0	0.996
KTPLYDLHVALGGK	64.44	54.6721	1510.851	1512.307	1	2	distinct	1	0.9774
DLEFMHGVFTPLTLK	46.15	54.2813	1746.901	1748.173	2	2	distinct	0	0.8923
REEGGFPGHAIIMDQLK	74.56	53.8633	1896.952	1897.396	4	2	distinct	1	0.9918
EQGCASLFDVSHMGQLR	57.09	53.8347	1933.877	1934.72	1	2	distinct	0	0.9619
ALVALQGPGAADVVELLKPNMNLK	105.79	52.6277	2460.377	2460.627	15	+2,+3	distinct	0	1
EGAELYDADDNVVGHVTSGTFSPSLKK	68.43	51.8046	2835.356	2836.342	1	3	distinct	1	0.9883

The equivalent proteins include

jgi|Physo1_1|155812|C_scaffold_8000018	0	No title.

56. Group probability: 1.0000. Peptides of the group

IPTLAIHLDR	75.36	55.6888	1147.671	1149.098	3	2	distinct	0	0.9898
HASVLLQLIAK	77.25	55.366	1191.734	1192.472	1	2	distinct	0	0.9917

LLLVDRPILR	47.9	55.2247	1206.781	1207.672	3	2	distinct	0	0.8875
GNGFHVIGAHTDSPCLK	71.19	54.1591	1808.863	1810.36	2	2	distinct	0	0.9889
LDNLCCSWLATQALIK	60.16	54.0037	1904.949	1905.839	1	2	distinct	0	0.9698
SFMVSADMAHGVHPNYSEK	88.02	53.3696	2105.93	2106.381	3	2	distinct	0	0.9977
LTLSPHTPQTVGAFLQFINK	76.94	53.2995	2211.205	2211.276	6	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|109605|estExt_fgenesh1_pm.C_1640002	0	No title.

57. Group probability: 1.0000. Peptides of the group

KYAEGIHK	45.86	56.5702	944.508	945.082	2	2	distinct	1	0.8579
ALGLPIERPK	48.28	55.4051	1092.665	1093.804	1	2	distinct	0	0.8908
VIPGYGHAVLR	61.31	55.1981	1180.672	1181.166	7	2	distinct	0	0.8284
AIGVLSQLFWDR	62.68	55.1631	1403.756	1405.09	1	2	distinct	0	0.9714
SVTSEWINNHFANQK	105.39	54.2634	1773.843	1774.662	5	2	distinct	0	0.9994
SLLWETSLLDAEEGIR	68.1	54.0972	1830.936	1831.818	1	2	distinct	0	0.9849
IVDTIYQVMPGVLTEHGK	70.67	53.7631	1999.045	1999.404	12	+2,+3	distinct	0	0.9998
TKNPYPNVDSHSGVLLQYYGLTQK	77.52	52.1831	2721.376	2722.503	4	3	distinct	1	0.9941

The equivalent proteins include

jgi|Physo1_1|109571|estExt_fgenesh1_pm.C_1450006	0	No title.

58. Group probability: 1.0000. Peptides of the group

KVVISAPPK	67.38	55.1779	937.596	938.69	7	+1,+2	shared(3)	1	0.9962
LEKPASMDAIK (0000000100000)	51.85	55.6621	1201.638	1218.516	5	+2,+3	shared(2)	0	0.9735
LVDLVLHMATVDK	83.6	54.8571	1452.801	1453.832	9	+2,+3	distinct	0	0.9972
VPTPDVSVVDLTCR	100.87	54.7648	1556.787	1557.293	12	2	shared(5)	0	0.9926
YDSTHGKFDGSVETK	66.7	54.3975	1669.758	1670.296	7	2	shared(2)	1	0.9822
LVAWYDNEWGYSNR	85.68	54.2699	1771.795	1771.999	7	2	shared(3)	0	0.9608
DGNLVVNGEVIHVFAAR	103.49	54.2958	1808.953	1809.9	8	+2,+3	shared(2)	0	0.999
VVAINDPFMDLEYMAYLFK (000000000000001000000)	122.87	53.0548	2278.105	2278.884	310	+2,+3	shared(3)	0	1
VVISAPPKDDTPMYVMGVNHK (00000000000000001000000)	91.26	52.9971	2297.155	2297.687	18	+2,+3	shared(3)	1	0.9999
LTGMAFRVPTPDVSVVDLTCR (00001000000000000000000)	64.95	52.937	2333.187	2333.52	9	+2,+3	shared(4)	1	0.9972
EYNGSAHVVSNASCTTNCLAPLAK	82.61	52.5282	2563.179	2563.344	2	2	distinct	0	0.9969
VINDKFGIVEGLMTTVHATTATQLPVDGPAK (000000000000010000000000000000000)	87.08	51.4019	3222.696	3224.001	116	3	shared(3)	1	0.998

The equivalent proteins include

jgi|Physo1_1|109003|estExt_fgenesh1_pm.C_510003	0	No title.

59. Group probability: 1.0000. Peptides of the group

GVLTAALNAAQYR	55.67	55.2773	1346.731	1348.029	1	2	distinct	0	0.9488
NIKPHVVNVAEDGAGVDK	74.88	54.1361	1860.969	1861.504	3	2	distinct	0	0.9922
CIQHGTPLVTASYVSPEMK	80.25	53.4606	2117.029	2117.524	7	2	distinct	0	0.9954
GLEGDDGIMMMGVDILPSELAR	97.32	52.9231	2318.096	2318.046	3	2	distinct	0	0.9991
EDANGFLQWLGAFDHSTPVVR	56.77	52.8972	2358.139	2359.099	1	2	distinct	0	0.9667
ILYGTVIDNPDYFVKPQPGFSGTPSR	84.25	51.7512	2867.449	2868.561	15	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|108801|estExt_fgenesh1_pm.C_340001	0	No title.

60. Group probability: 1.0000. Peptides of the group

EADGILFGFPTR	75.45	55.3384	1321.667	1322.724	6	2	shared(2)	0	0.9906
KDHPVATTDVLK	78.16	55.244	1322.719	1323.69	18	+1,+2	distinct	1	0.9999
QPSKLELTVATTQGK	68.19	55.1473	1599.883	1600.406	4	2	shared(2)	1	0.9841
IAIIYYSTYGHIAK	69.13	54.525	1611.866	1611.918	16	2	distinct	0	0.9851
APELFNMDEIHGGSPWGAGTLANGDGSR (000000010000000000000000000000)	94.89	51.8885	2855.293	2856.792	7	+2,+3	distinct	0	1
EGAESVEGVTAEIYQIQETLPEEVLTK	68.69	51.3948	2961.471	2961.745	4	2	distinct	0	0.9908

The equivalent proteins include

jgi|Physo1_1|156135|C_scaffold_11000030	0	No title.
jgi|Physo1_1|156136|C_scaffold_11000031	0	No title.

61. Group probability: 1.0000. Peptides of the group

EFVASLARPR	58.29	55.8165	1144.635	1145.474	7	2	distinct	0	0.9542
SPDKVDATVQR	53.45	55.777	1214.625	1215.293	1	2	distinct	1	0.9325
DFFGGHTYER	55.82	55.6633	1227.531	1228.536	1	2	distinct	0	0.9433
ERLPANLTQAQR	55.89	54.9935	1395.758	1396.461	7	2	distinct	1	0.9483
AKDEGNLPLVGYK	44.93	55.1433	1402.746	1403.533	1	2	distinct	1	0.869
ICSYAQGLNLIR	48.18	54.9651	1406.734	1408.03	1	2	distinct	0	0.8983

GIHFVGMGVSGGEEGAR	86.07	55.0292	1658.783	1659.487	7	2	distinct	0	0.9969
ILSGPSEIPAVDKQQLIDDVR	64.57	53.0869	2292.232	2292.847	2	2	distinct	1	0.9831
MVHNGIEYGDMQLIAEAYDILK	81.23	52.5252	2522.218	2523.454	3	+2,+3	distinct	0	0.9989

The equivalent proteins include

jgi|Physo1_1|108585|estExt_fgenesh1_pm.C_170009	0	No title.

62. Group probability: 1.0000. Peptides of the group

GFKDQIYEVFR	60.19	55.24	1400.709	1401.772	2	2	distinct	1	0.857
TLQQGVHIVVGTPGR	83.8	54.9043	1560.874	1561.39	7	2	distinct	0	0.9844
KGVAINFLTHNDVR	71.29	54.634	1582.858	1583.431	2	2	distinct	1	0.9876
GIYAYGFEKPSAIQKR	86.96	54.13	1826.968	1827.656	35	+2,+3	distinct	1	0.9998
VQVALFSATMPLDVLEVTR	57.32	53.4063	2088.129	2088.722	2	2	distinct	0	0.9655
AVKPILLGHDCIAQAQSGTGK	98.78	53.9517	2163.147	2164.645	12	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109443|estExt_fgenesh1_pm.C_1080002	0	No title.

63. Group probability: 1.0000. Peptides of the group

KFSDPIVQADIK	45.71	55.3534	1359.74	1360.845	1	2	distinct	1	0.8727
SQVHEVVLVGGSTR	50.59	54.9253	1466.784	1467.846	3	2	distinct	0	0.8931
ARFEDMCGDYFR	51.41	54.6867	1565.639	1565.974	3	2	distinct	1	0.9238
QKELEGVANPILQK	77.3	54.6079	1565.878	1566.538	5	2	distinct	1	0.9927
NQVAMNAHNTVFDAK	85	54.9423	1658.783	1659.309	6	2	distinct	0	0.9964
IINEPTAAAIAYGIDKK	113.47	54.8238	1786.983	1787.369	22	2	shared(7)	1	0.9981
NQVAMNAHNTVFDAKR	87.88	54.1287	1814.885	1815.33	3	2	distinct	1	0.9973
VQQLLSDFFNGKEPNK	72.42	54.1967	1862.953	1863.814	4	+2,+3	distinct	1	0.9985
SQTFSTYADNQPGVLIQVFEGER	63.02	52.4467	2585.24	2585.586	2	2	distinct	0	0.7565

The equivalent proteins include

gi|38489930|gb|AAR21576.1|	71770.42	heat shock protein 70 [Phytophthora nicotianae]
jgi|Phyra1_1|72463|fgenesh1_pm.C_scaffold_1313000001	0	No title.

64. Group probability: 1.0000. Peptides of the group

KTVAVGVIK	47.89	56.6259	913.596	914.553	1	2	shared(2)	1	0.8809
IGGIGTVPVGR	47.13	55.1937	1024.603	1026.063	1	2	shared(7)	0	0.884
EHALLAFTLGVK	64.61	55.2405	1297.739	1299.156	1	2	shared(4)	0	0.9342
FFFTVIDAPGHR	72.18	55.0761	1405.714	1406.896	27	+2,+3	distinct	0	0.9995
VETGVIKPGMVATFGPVGLSTEVK (000000000100000000000000)	112.1	52.7998	2415.308	2415.308	25	+2,+3	distinct	0	1
SVEMHHESLPEAVPGDNVGFNVK	76.04	52.5666	2491.18	2492.428	3	2	distinct	0	0.9814
SGDACMVILEPSKPMTVESFQEYPPLGR (0000010000000010000000000000)	63.79	51.0499	3137.487	3169.855	11	+2,+3	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|109384|estExt_fgenesh1_pm.C_970007	0	No title.

65. Group probability: 1.0000. Peptides of the group

RVQANLGAK	48.16	56.4525	955.556	956.8	2	2	distinct	1	0.6864
SKEWVHDIVQK	69.99	55.1434	1367.72	1368.388	7	+2,+3	distinct	1	0.9992
AISFVGGNQAGEYIHSR	102.71	54.2762	1804.886	1805.655	12	2	distinct	0	0.9993
NHAVIMPDCDKEQAVGALAGAAFGAAGQR (00000100000000000000000000000)	69.04	51.6479	2924.402	2925.636	12	+2,+3	distinct	1	0.9999
EAGLPDGVLNIIHGAHDTVNFICDAPEIK	75.46	51.165	3114.544	3115.925	6	+2,+3	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|108308|estExt_fgenesh1_pm.C_50023	0	No title.

66. Group probability: 1.0000. Peptides of the group

HCWYIPADGTQGR	53.41	54.7812	1559.694	1560.623	2	2	distinct	0	0.9382
VIIGHGDNFYWSGINSR	98.35	53.8244	1933.943	1934.531	11	2	distinct	0	0.999
SGCGAFTWTNYNGGTCWLK	93.92	53.33	2178.925	2179.37	5	2	shared(2)	0	0.9986
IVNSHYSTYNDYAEHNMK	100.95	53.4809	2184.953	2186.365	15	+2,+3	distinct	0	1
MQYHTTDNNWQFGENFQSTK	55.12	52.5036	2475.055	2474.809	1	2	distinct	0	0.9604
TIPWVNVLGNHDYGGASFICENNSR	44.4	51.7552	2819.308	2819.526	1	2	distinct	0	0.9164
SSSYSNYDVVAEDVVASLMNTQAGNQAVKPK	49.9	51.1882	3271.567	3273.007	1	3	distinct	0	0.9493

The equivalent proteins include

jgi|Physo1_1|140694|estExt_fgenesh1_pg.C_880066	0	No title.

67. Group probability: 1.0000. Peptides of the group

VVCALYEGGEAGKR	50.07	54.7277	1507.745	1508.007	2	2	distinct	1	0.9202
RNPDILGCVENELGLR	74.13	54.11	1853.942	1854.799	6	+2,+3	distinct	1	0.9997

HAMTPHYSGTTLDAQAR (0001000000000000000)	84.98	54.5357	1855.864	1856.441	15	+2,+3	distinct	0	0.9998
FFDGKPQRPEYLIAEGGK	54.25	53.933	2051.048	2051.588	2	2	distinct	0	0.9528
GHEYVVTSDKDGDQSEFVR	99.34	53.4912	2166.982	2167.961	8	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|144953|estExt_fgenesh1_pg.C_3530001	0	No title.

68. Group probability: 1.0000. Peptides of the group

HLLQLIVAGGK	68.26	55.8156	1147.708	1147.564	4	+1,+2	distinct	0	0.9956
TIITQCQQHGFQR	99.96	54.8768	1615.789	1616.433	9	2	distinct	0	0.999
FSKPVQSGEEFVIR	56.13	54.5971	1621.846	1622.698	3	2	distinct	0	0.9532
LLANPSFNPAQSSHGR	72.18	54.3267	1694.849	1695.67	11	+2,+3	distinct	0	0.9984
TIPSRDDLSHHYAEVK	48.03	53.9612	1866.922	1867.539	2	2	distinct	1	0.9124
LVIPDVAEEPDFLSFAR	51.28	53.928	1916.988	1917.155	1	2	distinct	0	0.9365
LCEAAHPGPHVEQFQER	53.05	53.6773	2003.927	2004.389	3	+2,+3	distinct	0	0.9914

The equivalent proteins include

jgi|Physo1_1|127575|estExt_fgenesh1_pg.C_20151	0	No title.

69. Group probability: 1.0000. Peptides of the group

TVVIHGMAK	45.05	55.8132	954.532	955.373	1	2	distinct	0	0.8497
LGNKPATTTTSFR	44.09	55.0854	1392.736	1393.091	1	2	distinct	0	0.8592
EHQSFATLPGMYER (0000000000010000)	63.32	54.4826	1664.762	1665.441	7	2	distinct	0	0.9751
ITSGEHNHVMDNFLR	85.53	54.1908	1768.831	1769.282	4	2	distinct	0	0.9966
TLEAVGAYQANPVTASPAVAPQEHKPVR	109.28	51.6071	2900.514	2901.557	1	3	distinct	0	0.9997
SLMLCNPSNPAGTVHSPAQLESIAAVLR (000100000000000000000000000000)	77.42	51.4531	2932.49	2932.725	11	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|129035|estExt_fgenesh1_pg.C_60192	0	No title.

70. Group probability: 1.0000. Peptides of the group

KYTFTEDFAPR	78.58	55.2219	1373.662	1374.69	1	2	distinct	1	0.9926
KAGNTNIYVTGPATSK	114.56	54.5658	1620.847	1621.439	5	2	distinct	1	0.9997
SDVLLFADQNHGWVHR	94.68	54.4004	1892.928	1893.02	16	+2,+3	distinct	0	0.9999
VPQLLMAAGDDPDFVKPDGSVHK (0000001000000000000000000)	80.33	52.6201	2435.215	2435.07	8	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|108414|estExt_fgenesh1_pm.C_90010	0	No title.

71. Group probability: 1.0000. Peptides of the group

KDIFLNSMFDK	79.97	55.2816	1356.675	1356.993	2	2	shared(3)	1	0.9935
GAHYYAYQLLHTGA	89.7	54.7086	1563.747	1564.523	19	+1,+2,+3	distinct	0	1
IISGPGLATIYEFLAK	95.06	54.6399	1691.95	1692.384	32	2	shared(3)	0	0.9986
ACPVYLVLTEELGER	64.68	54.2532	1747.881	1748.953	3	+2,+3	distinct	0	0.9993
TNELCNQTLEIFVGAYGR	96.66	53.5823	2084	2084.793	8	2	shared(3)	0	0.9989
YLNEEHASFNEVCHLFMNEAK	62.05	52.4747	2581.137	2581.619	2	2	distinct	0	0.9792

The equivalent proteins include

jgi|Physo1_1|138630|estExt_fgenesh1_pg.C_650049	0	No title.

72. Group probability: 1.0000. Peptides of the group

SERPDLASAR	45.83	55.9302	1100.557	1101.995	1	2	distinct	0	0.8632
LITVRPTGFEK	48.77	55.6904	1259.724	1260.737	1	2	distinct	0	0.8985
YDHLVAEEVAELLVAAQK	125.93	53.6403	1997.047	1998.055	4	+2,+3	distinct	0	1
VVAPELYVAAGISGAIQHLAGMK (0000000000000000000000100)	83.31	53	2294.246	2294.851	31	+2,+3	distinct	0	0.9998
VVAPELYVAAGISGAIQHLAGMKDSK	62.27	52.3158	2624.399	2625.873	1	3	distinct	1	0.9791
LDVAPISDILAVADKDTFFRPTYAGNAIAQVK	55.49	50.3701	3418.814	3419.326	5	3	distinct	1	0.9705

The equivalent proteins include

jgi|Physo1_1|108676|estExt_fgenesh1_pm.C_240007	0	No title.

73. Group probability: 1.0000. Peptides of the group

KLQITTQGR	46.45	56.2026	1043.609	1045.015	1	2	distinct	1	0.866
VSGGFTHGASGVVFK	69.8	55.0738	1448.741	1449.486	14	+1,+2	distinct	0	0.9994
VSGGFTHGASGVVFKK	60.91	54.861	1576.836	1577.424	3	2	distinct	1	0.9712
VVTEAELPNVLTQGLK	83.68	54.2645	1709.956	1710.35	1	2	distinct	0	0.9961
SAIVQHNVGASYTGADFVTSLVTK	105.91	52.6372	2464.26	2464.832	6	2	distinct	0	0.9996
SAIVQHNVGASYTGADFVTSLVTKK	66.94	52.3657	2592.355	2593.65	5	3	distinct	1	0.9856

The equivalent proteins include

jgi|Physo1_1|141609|estExt_fgenesh1_pg.C_1010022	0	No title.

74. Group probability: 1.0000. Peptides of the group

NSLMLVTALNPHIGYDK	95.39	53.949	1884.977	1886.048	5	+2,+3	distinct	0	1
THTQDATPLTLGQEFSGYR	133.31	53.336	2121.013	2121.651	10	+2,+3	distinct	0	1
LDDHFPLVVFQTGSGTQSNMNTNEVISNR	87.25	50.9574	3219.525	3220.545	1	3	distinct	0	0.998

The equivalent proteins include

jgi|Physo1_1|109373|estExt_fgenesh1_pm.C_960003	0	No title.
jgi|Phyra1_1|71712|fgenesh1_pm.C_scaffold_41000008	0	No title.

75. Group probability: 1.0000. Peptides of the group

IIGSYVGNR	57.66	55.8554	977.529	978.913	2	2	shared(2)	0	0.9502
WIANSCLGCEDCRK	60.07	54.228	1767.749	1767.977	7	2	shared(2)	1	0.9671
IIGSYVGNRQDSIEALK	45.98	54.145	1861.99	1862.754	2	2	shared(2)	1	0.8985
ELPMHAAAPILCAGVTVYK (0000100000000000000000)	76.32	53.6354	2040.054	2040.054	13	+2,+3	distinct	0	0.9994
KDWPVTQPEELKPGEVLVR	84.02	53.2063	2219.195	2219.449	10	+2,+3	distinct	1	0.9998
EIGGVCGDSVVIPGAGGGLGHLACQYAR	74.84	52.187	2769.333	2770.756	3	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|132859|estExt_fgenesh1_pg.C_230002	0	No title.
jgi|Physo1_1|138265|estExt_fgenesh1_pg.C_620001	0	No title.

76. Group probability: 1.0000. Peptides of the group

KDYPVATPDVLK	53.44	55.4629	1344.729	1345.796	2	2	distinct	1	0.9352
TNVAIIYYSTYGHIATMAESVK	86.46	52.6369	2431.209	2432.565	6	2	distinct	0	0.9976
SPLLFNMEEIHGGSPWGAGTLAGADGSR (0000000100000000000000000000000)	97.15	52.0137	2826.339	2826.773	34	+2,+3	distinct	0	1
EGVESVEGVTAEIYQVQETLSEEILGK	95.26	51.5045	2935.455	2935.692	33	2	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|130452|estExt_fgenesh1_pg.C_110121	0	No title.

77. Group probability: 1.0000. Peptides of the group

NVGAIGFELWQVK	81.48	55.1521	1459.782	1460.159	3	2	distinct	0	0.9947
WVASTWKPAAEVGK	59.44	54.813	1528.804	1529.238	8	2	distinct	0	0.9648
GKDLYLSYLVQHEQK	87.45	54.2658	1819.947	1820.73	5	2	distinct	1	0.9971
THAILNYARPGEDAVNMDHK	96.23	53.5578	2251.08	2251.117	2	2	distinct	0	0.9989
LLPADVDQANFGGESPYAVMFGPDICGSNKK (0000000000000000000001000000000000)	105.72	50.9051	3296.548	3297.458	5	3	distinct	1	0.9996

The equivalent proteins include

jgi|Physo1_1|109612|estExt_fgenesh1_pm.C_1680002	0	No title.

78. Group probability: 1.0000. Peptides of the group

HWIGYSK	47.45	56.8011	889.445	889.946	1	2	distinct	0	0.8618
VIAVLVGGRPR	67.25	55.377	1135.719	1136.627	12	2	distinct	0	0.98
ETVMLFLTQPFR	62.21	54.8538	1480.775	1481.906	2	2	distinct	0	0.9704
VYETFGEDPYLVSVIAESLIK	113.8	52.8813	2371.22	2372.058	47	+2,+3	distinct	0	1
DTLAAGTPWIFGPMLEISQNPLWPR	56.35	51.9285	2809.426	2810.345	5	2	shared(2)	0	0.9706
TPTGHDKDGVTLSDYDLLNYFLPPFK	58.8	51.478	2952.454	2952.741	8	+2,+3	distinct	1	0.9993

The equivalent proteins include

jgi|Physo1_1|131903|estExt_fgenesh1_pg.C_180012	0	No title.

79. Group probability: 1.0000. Peptides of the group

YVGSMVSDIHR	44.81	55.639	1262.608	1263.203	1	2	distinct	0	0.8565
ILDLVPTDIHQR	54.68	55.0153	1418.788	1419.159	5	+2,+3	distinct	0	0.982
KLDVLANDIFVNSLK	98.08	54.5186	1687.951	1688.937	3	2	distinct	1	0.9989
TIYSCNEGNYAHWDR	80.41	53.9408	1884.785	1885.401	7	2	distinct	0	0.9947
GVHCFTLDPTIGAFILSQK	94.88	53.4096	2103.082	2103.428	16	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109566|estExt_fgenesh1_pm.C_1450001	0	No title.
jgi|Phyra1_1|94747|C_scaffold_23000023	0	No title.

80. Group probability: 1.0000. Peptides of the group

HLVGEIIK	47.93	55.6949	907.549	908.665	5	2	distinct	0	0.6904
HLVGEIIKR	53.48	55.6033	1063.65	1064.415	3	2	distinct	1	0.927
TYIMVKPDGVQR	53.91	55.0744	1405.739	1407.063	19	2	distinct	0	0.9384
NVCHGSDSVESAEK	64.42	54.9352	1517.642	1517.955	2	2	shared(2)	0	0.9772

MLGATKPTESALGTIR (010000000000000000)	102.51	54.6429	1644.887	1661.27	23	2	distinct	0	0.9978
KMLGATKPTESALGTIR (0010000000000000000)	72.93	54.3168	1772.982	1773.647	5	2	distinct	1	0.9904
YMSSGPVTCMVWEGTNVVLEGR	120.01	52.9456	2471.128	2471.359	30	2	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|108873|estExt_fgenesh1_pm.C_370013	0	No title.

81. Group probability: 1.0000. Peptides of the group

HAWADKR	45.36	55.0111	882.446	883	1	2	shared(2)	1	0.84
HFLYHSVDYK	50.41	55.4252	1307.63	1308.106	2	2	distinct	0	0.9094
HTVFYTGVTALPISWK	123.42	54.2917	1818.967	1820.266	26	+2,+3	distinct	0	1
KPYLFGEHVVYATTEDGGK	113	53.3611	2110.037	2110.253	18	+2,+3	distinct	0	1
DINDVDSHLVGKGDWIVSDSK	68.51	53.0716	2298.113	2299.533	1	3	shared(2)	1	0.9853

The equivalent proteins include

jgi|Physo1_1|137803|estExt_fgenesh1_pg.C_570068	0	No title.

82. Group probability: 1.0000. Peptides of the group

TAAFTQVSQHHVDSK	79.89	54.3997	1654.806	1655.104	7	2	distinct	0	0.9944
VSAFKPVLDQALISLPLK	96.94	53.8563	1938.155	1938.65	6	2	distinct	0	0.9989
TFVDFFTNQTELPHTFWK	87.4	53.3359	2257.084	2258.051	5	+2,+3	distinct	0	0.9999
VSAFKPVLDQALISLPLKDQLR	90.19	52.5776	2450.426	2450.975	5	+2,+3	distinct	1	0.9993

The equivalent proteins include

jgi|Physo1_1|109348|estExt_fgenesh1_pm.C_930003	0	No title.

83. Group probability: 1.0000. Peptides of the group

IHTTIGLGSK	64.2	55.3868	1025.587	1025.524	9	+1,+2	distinct	0	0.997
LENTHSVHGAPLKPDDLSATK	93.53	53.3264	2229.139	2229.613	6	+2,+3	distinct	0	0.9999
AMPNMYVYRPADGNETVGAYIAAVENTHK	69.8	51.1789	3181.496	3182.087	4	3	distinct	0	0.9905
APGHPENFCTPGVEVSTGPLGQGISNAVGLAIAEK	97.98	50.1325	3473.725	3474.435	6	3	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|108201|estExt_fgenesh1_pm.C_20033	0	No title.

84. Group probability: 1.0000. Peptides of the group

IFGVTTLDVVR	66.68	55.6189	1218.697	1219.442	1	2	shared(3)	0	0.9568
RIFGVTTLDVVR	67.93	55.1545	1374.798	1375.471	35	+2,+3	shared(2)	1	0.9958
VAVLGAAGGIGQPMSLLLK	99.61	54.2657	1794.044	1794.864	3	2	shared(2)	0	0.9894
VIGGHAGTTILPLLSQLEGAK	122.92	53.5044	2074.179	2074.196	36	+2,+3	distinct	0	1
VTGHVGMEQAGEALEGADVVVIPAGVPR	82.16	52.0154	2757.412	2757.703	3	+2,+3	distinct	0	0.9997

The equivalent proteins include

jgi|Physo1_1|109054|estExt_fgenesh1_pm.C_550007	0	No title.

85. Group probability: 1.0000. Peptides of the group

KLAGMFVDNFK	80.1	55.3782	1268.659	1269.171	2	2	distinct	1	0.9935
KLGDIPENVLNPR	85.61	54.9808	1463.81	1464.409	7	2	distinct	1	0.9963
LSDGQAMYHFLSGYTAK	70.11	53.9829	1887.882	1889.379	4	2	distinct	0	0.9878
HNTSVYLVNTGWTSGGYGVGK	121.51	53.2993	2196.06	2196.415	3	2	distinct	0	0.9999
GVTEPTATFSACFGAAFLPLHPTK	55.79	52.6906	2519.252	2519.53	1	2	distinct	0	0.9675

The equivalent proteins include

jgi|Physo1_1|109616|estExt_fgenesh1_pm.C_1690003	0	No title.

86. Group probability: 1.0000. Peptides of the group

KAVSATSVYFESLPYR	88.61	54.2046	1816.936	1817.315	3	2	distinct	1	0.9975
EHASPFDYCDIVTTTTHK	76.3	53.3015	2120.947	2121.177	1	2	distinct	0	0.9933
YYGGNEIIDKIEILCQQR	78.36	53.2915	2211.099	2211.731	2	2	distinct	1	0.9827
LAEQAALFKPALIVCGGSAYPR	58.7	52.9785	2331.241	2331.992	6	+2,+3	distinct	0	0.9984
TLTDLGYSMCTGGTDNHLILWDLRPQK	84.59	51.1488	3104.506	3105.579	4	3	distinct	0	0.9972

The equivalent proteins include

jgi|Physo1_1|142228|estExt_fgenesh1_pg.C_1100022	0	No title.

87. Group probability: 1.0000. Peptides of the group

KLVVALGSPK	70.65	55.5147	1010.649	1011.248	10	+1,+2	distinct	1	0.9993
HNPALIAER	61.61	56.0537	1019.551	1020.495	2	2	distinct	0	0.9647
ETQLALVLNAIVNDAALAEHEAFK	91.42	52.4655	2579.359	2580.797	6	+2,+3	distinct	0	1
ETQLALVLNAIVNDAALAEHEAFKK	88.12	52.1391	2707.454	2708.363	8	3	distinct	1	0.9978

The equivalent proteins include

jgi|Physo1_1|158121|C_scaffold_82000017	0	No title.

88. Group probability: 1.0000. Peptides of the group

LQLFGLHAR	51.43	55.429	1053.608	1054.398	1	2	distinct	0	0.9148
VQIGNYFIDLSLATK	102.61	54.2964	1680.909	1682.002	1	2	distinct	0	0.9992
LLLETVVDPEILGGLK	82.19	54.4816	1708.002	1708.797	3	2	distinct	0	0.9956
EPNFASFLHDPTIAR	67.75	54.3512	1713.847	1715.094	2	2	distinct	0	0.9838
FSKPVAGLFEVLAENGR	110.57	54.0817	1832.978	1833.005	3	2	distinct	0	0.9996

The equivalent proteins include

jgi|Physo1_1|108488|estExt_fgenesh1_pm.C_110019	0	No title.
jgi|Phyra1_1|72058|fgenesh1_pm.C_scaffold_79000001	0	No title.

89. Group probability: 1.0000. Peptides of the group

IGVNQPKR	52.51	55.4152	910.535	911.453	3	2	distinct	1	0.9225
RIHEDPEFLEK	57.4	55.1195	1411.71	1412.573	3	2	distinct	1	0.7597
AYSSVGAIHAYFQK	100.69	54.7271	1540.767	1541.794	3	2	distinct	0	0.9991
FPQYGTDNGVLRPK	70.52	54.6438	1590.815	1591.835	8	2	distinct	0	0.9867
AGASWEKFEELMHVTK	59.87	54.1479	1861.903	1862.656	3	+2,+3	distinct	1	0.9981
ENEVVIPSLMFVESLDAILEDLAK (00000000001000000000000000)	76.81	52.2176	2673.382	2674.064	20	2	distinct	0	0.9949

The equivalent proteins include

jgi|Physo1_1|108461|estExt_fgenesh1_pm.C_100020	0	No title.

90. Group probability: 1.0000. Peptides of the group

GIPLIFLQNITGFMVGK	93.89	54.068	1847.038	1847.963	25	2	distinct	0	0.9985
TSGVTDHYANNDAHALDITR	76.59	53.3425	2170.004	2171.437	2	+2,+3	distinct	0	0.9999
TSGVTDHYANNDAHALDITRR	47.51	53.008	2326.105	2327.114	1	3	distinct	1	0.9074
KQPAVTQTPIEEPLYSPDELGGVIPVDSR	66.34	51.1425	3134.613	3134.558	7	+2,+3	distinct	1	0.9997

The equivalent proteins include

jgi|Physo1_1|109115|estExt_fgenesh1_pm.C_610005	0	No title.
jgi|Phyra1_1|71891|fgenesh1_pm.C_scaffold_58000008	0	No title.

91. Group probability: 1.0000. Peptides of the group

VTASEVNGDVVK	62.07	55.7414	1216.63	1217.854	1	2	shared(2)	0	0.9694
TQVPGIFAIGDVIK	68.39	54.9975	1456.829	1457.52	5	+1,+2	shared(2)	0	0.9995
LGGTCLNVGCIPSK	77	54.9891	1474.727	1475.148	1	2	shared(2)	0	0.9924
TCHAHPTLSEAFK	60.11	54.7891	1497.703	1497.461	5	+1,+2	shared(2)	0	0.9975
RAFTAGLGLEQMGIQTDK	122.8	53.8159	1934.988	1935.801	8	2	shared(2)	1	0.9999
AEGIEYNVGKFPMMANSR	81.68	53.5679	2012.945	2013.424	8	2	shared(2)	1	0.9958
AFTAGLGLEQMGIQTDKLGR (0000000000010000000000)	110.97	53.3656	2105.094	2105.702	9	+2,+3	shared(2)	1	1
VTVVEFQDAACPGMDKEAVK (0000000000000010000000)	65.85	53.2658	2209.039	2210.472	1	3	distinct	1	0.8899

The equivalent proteins include

jgi|Phyra1_1|72215|fgenesh1_pm.C_scaffold_109000002	0	No title.

92. Group probability: 1.0000. Peptides of the group

IVLSPTPARPAPTP	71.15	55.1636	1415.814	1416.084	3	2	distinct	0	0.9873
FVNLLHSMADPER	51.88	54.8201	1527.75	1529.014	3	2	shared(2)	0	0.9293
NLGNAQVDHVQGIAK	89.8	54.9217	1562.816	1563.923	11	2	distinct	0	0.9976
FVNLLHSMADPERK	58.52	54.4392	1655.845	1656.094	5	2	shared(2)	1	0.9622
DKIVLSPTPARPAPTP	62.39	54.9672	1658.936	1659.386	9	2	distinct	1	0.9746
GREFEGMGLGGTCVNFGCVPK	68.22	53.0999	2271.023	2271.363	1	2	distinct	1	0.9877
ADFDNIVAIHPTAAEELVTMAPWGMIK	70.43	51.4862	2939.456	2940.203	6	2	distinct	0	0.9921

The equivalent proteins include

jgi|Physo1_1|108729|estExt_fgenesh1_pm.C_270014	0	No title.

93. Group probability: 1.0000. Peptides of the group

FDEVYHVHFK	68.7	55.3566	1319.63	1320.273	7	2	distinct	0	0.9818
GLQDIIGLSVVHPVFQR	82.97	54.2342	1877.052	1877.826	19	+2,+3	distinct	0	1
TRPNDPEDQHMSWAFADPK	59.47	53.1615	2240.991	2241.413	4	2	distinct	0	0.9716
MFNSSFDALAPSKLDLYPAEFR	79.35	52.6238	2518.22	2517.92	5	2	distinct	1	0.9956
KTPWLPGPSGLGEYSSEGSIPDTVNNAQYVR	50.85	50.7947	3318.616	3319.967	3	3	distinct	1	0.9537

The equivalent proteins include

jgi|Physo1_1|129851|estExt_fgenesh1_pg.C_90128	0	No title.

94. Group probability: 1.0000. Peptides of the group

STSTPSPAPAPKPR	67.27	55.0824	1392.736	1393.018	7	2	distinct	0	0.9822
AVTHEYQIHEER	76.14	54.6265	1510.716	1510.782	2	2	distinct	0	0.9913

SNPASRPYPSPAAPR	51.13	54.626	1566.79	1567.637	3	2	distinct	0	0.9299
SLLQQLAEAFEMLTNR	86.92	54.145	1862.956	1862.78	6	+2,+3	distinct	0	1
LADAVHPSEQWIVELLK	75.7	53.9204	1947.046	1948.521	5	2	distinct	0	0.9925

The equivalent proteins include

jgi|Physo1_1|142023|estExt_fgenesh1_pg.C_1070014	0	No title.

95. Group probability: 1.0000. Peptides of the group

FGSHVFVGK	66.35	56.1435	976.513	977.407	4	2	distinct	0	0.9766
LRAPEVAAFDFK	70.83	55.1563	1362.73	1363.805	5	+2,+3	distinct	1	0.9977
TCQFGYAHVDTPK	73.26	54.6398	1522.687	1523.342	1	2	distinct	0	0.9892
LNPLTLITLTYPTK	61.32	54.8903	1586.928	1587.86	1	2	distinct	0	0.9701
GLTVFCQFYDNPGR	78.31	54.5854	1672.767	1673.349	2	2	distinct	0	0.9933
TPGTLFGIPDNADHISYDLWDSR	48.44	52.3837	2589.214	2590.705	1	2	distinct	0	0.9362

The equivalent proteins include

jgi|Physo1_1|140046|estExt_fgenesh1_pg.C_810035	0	No title.

96. Group probability: 1.0000. Peptides of the group

KDPIQLNHR	64.75	55.7005	1119.615	1120.319	5	2	distinct	1	0.9734
IFAQIWHTGR	57.73	55.6594	1227.651	1228.24	13	2	distinct	0	0.9521
GWQAVTEAVHAK	76.17	55.2399	1295.662	1296.731	2	2	distinct	0	0.9912
HADGVDTPVNGVAHHFR	64.14	54.0674	1827.876	1829.306	3	2	distinct	0	0.9794
VGHPLNQPDGQLPVSSSATSMDNVK (00000000000000000000100000)	78.18	52.4631	2577.249	2577.951	16	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109429|estExt_fgenesh1_pm.C_1050001	0	No title.

97. Group probability: 1.0000. Peptides of the group

LLQVLTPNLDHAR	62.06	54.9134	1488.841	1490.148	4	2	distinct	0	0.971
ALEHYTELADLKR	74.58	54.8056	1557.815	1558.329	3	2	distinct	1	0.9903
MESIELARPVLMQGR	53.75	54.3267	1728.901	1729.956	1	2	distinct	0	0.9446
AINFYLEQHPLELTR	71.42	54.1564	1842.963	1843.42	6	2	distinct	0	0.9883
LDLPGAEELYFTEFNR	75.37	53.8324	1912.921	1913.346	1	2	distinct	0	0.9921
IYITLNKDPQQFLINNQFYDSEVVGK	74.93	51.2449	3085.576	3086.849	3	3	distinct	1	0.9932

The equivalent proteins include

jgi|Physo1_1|143969|estExt_fgenesh1_pg.C_1600014	0	No title.

98. Group probability: 1.0000. Peptides of the group

QNFSALTR	59.34	55.6713	935.482	936.9	5	2	distinct	0	0.9035
AQGAAIDKYASR	49.88	55.4587	1249.641	1249.93	1	2	distinct	1	0.9115
LSSAMSAAAAIGAHLR	89.65	54.6607	1525.803	1526.381	2	2	distinct	0	0.9977
ATATELTEEKADAVEILAR	52.49	53.5798	2030.053	2030.881	1	3	distinct	1	0.935
MELQDCAFNLVDAIVPTSNLETAFK	51.69	51.9271	2825.361	2825.889	1	2	distinct	0	0.9557
VVIWGNHSSTQVPDVTYAEVQGQPLDK	73.43	51.4697	2966.477	2967.012	9	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|109232|estExt_fgenesh1_pm.C_780001	0	No title.

99. Group probability: 1.0000. Peptides of the group

RQALLAAR	51.54	55.905	897.551	898.552	1	2	distinct	1	0.56
VATLIVRPR	76.89	55.4157	1023.655	1024.259	13	2	distinct	0	0.9909
RVEITGPVDR	48.61	55.3577	1140.625	1141.063	2	2	distinct	1	0.894
KTISYTHPQTGK	46.46	55.3536	1359.715	1360.615	1	2	distinct	1	0.8808
FLAFLHEQFEPR	71.73	54.7958	1532.778	1533.76	3	2	distinct	0	0.9872
EVAAGHDGTWVAHPGLVK	89.44	54.1678	1842.938	1843.306	12	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108758|estExt_fgenesh1_pm.C_300009	0	No title.

100. Group probability: 1.0000. Peptides of the group

HSEFIGFPIK	50.2	55.7567	1173.618	1174.705	1	2	distinct	0	0.9071
TMEINPLHPIIK	69.45	55.1141	1404.78	1405.284	6	2	distinct	0	0.9842
KTMEINPLHPIIK	66.31	54.9139	1532.875	1533.139	3	+2,+3	distinct	1	0.9968
KPEDVTHEEYASFYK	106.17	54.1721	1841.847	1842.568	2	2	distinct	0	0.9994
VFIMDNCEELMPEYLSFVK	76.72	52.8671	2363.089	2363.453	1	2	distinct	0	0.9938

The equivalent proteins include

jgi|Physo1_1|108777|estExt_fgenesh1_pm.C_310001	0	No title.
jgi|Phyra1_1|71510|fgenesh1_pm.C_scaffold_24000001	0	No title.

101. Group probability: 1.0000. Peptides of the group

FHVLTPAEVK	47.44	55.3402	1139.634	1139.377	4	+1,+2	distinct	0	0.9795
YKEHAPASILVR	45.43	55.0676	1382.767	1383.361	1	2	distinct	1	0.8703
KLPTILVDEDSHK	68.79	54.6676	1493.809	1494.067	5	+2,+3	distinct	1	0.9989

KIAVLSEPAGIVYSGLGPDYR	77.68	53.2657	2204.184	2204.729	1	2	distinct	1	0.9946
YNDDLEIEDAIHTALLTLR	95.94	53.2003	2214.117	2214.158	3	2	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|109244|estExt_fgenesh1_pm.C_790006	0	No title.

102. Group probability: 1.0000. Peptides of the group

KFTPLLDVVYNDIK	91.25	54.564	1663.918	1664.905	4	2	distinct	1	0.9979
VIGLYFSGHYCPPCR	56.56	54.0689	1824.844	1825.75	1	2	distinct	0	0.957
HFVTDNSQDIDAILSHLR	115.96	53.8285	2080.034	2080.321	5	+2,+3	distinct	0	1
FTEYYEEMPWIALPYAR	61.1	53.3221	2178.013	2178.561	1	2	distinct	0	0.9735

The equivalent proteins include

jgi|Physo1_1|142576|estExt_fgenesh1_pg.C_1170035	0	No title.

103. Group probability: 1.0000. Peptides of the group

VVCMPGVQDHKR	55.68	54.8801	1424.702	1425.251	1	2	distinct	1	0.9474
AKEYLDSINHNIVVK	73.2	54.2623	1741.936	1742.915	1	2	distinct	1	0.9652
AGLINALAHITGGGLLENVPR	73.38	53.469	2085.169	2086.167	5	+2,+3	distinct	0	0.9999
FGDPETQVVLPLLHSDLFEIMR	63.35	52.4704	2555.309	2556.694	4	3	distinct	0	0.978
APSTPLVVLCGDRAPDALVQTAAALQAGGLR	75.02	51.2265	3087.65	3088.83	4	3	distinct	1	0.9944

The equivalent proteins include

jgi|Physo1_1|129332|estExt_fgenesh1_pg.C_70157	0	No title.

104. Group probability: 1.0000. Peptides of the group

VAHQLIKDELALDGNPK	117.22	54.0904	1860.01	1860.12	6	2	distinct	1	0.9998
CVTMLANLYHAPLEPGQK	78.27	53.6383	2041.012	2040.325	2	2	distinct	0	0.9943
KNYIDLDQYPQTAEIHNR	105.26	53.2021	2217.081	2217.593	3	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|109436|estExt_fgenesh1_pm.C_1070001	0	No title.

105. Group probability: 1.0000. Peptides of the group

GPIGCGVHATEK	61.42	55.2618	1224.592	1225.391	3	2	distinct	0	0.968
SPSNKPSVEVHR	65.83	55.3272	1335.689	1336.21	5	2	distinct	0	0.9782
HGIPDQTCQAYQAK	90.33	54.7951	1615.741	1616.25	7	2	distinct	0	0.9977
NSWGSFWGEDGWMR	56.24	54.3513	1713.699	1714.699	1	2	distinct	0	0.9539
NSWGTYWGENGWFR	68.08	54.3114	1758.754	1760.171	1	2	distinct	0	0.9837
NQHIPKYCGSCWAQGTTSALSDR	61.7	52.2277	2636.186	2637.502	11	3	distinct	1	0.9755

The equivalent proteins include

jgi|Physo1_1|128333|estExt_fgenesh1_pg.C_40177	0	No title.

106. Group probability: 1.0000. Peptides of the group

RALSAQAQAR	55.69	56.0199	1070.594	1071.446	3	2	distinct	1	0.8862
IINEPTAAAIAYGIDKK	113.47	54.8238	1786.983	1787.369	22	2	shared(7)	1	0.9981
LEIESLLDGEDFTESLSR	77.06	53.8815	2051.99	2052.789	2	2	distinct	0	0.9936
DVLLIDVVPLSQGIETVGGVMTK	96.73	52.9027	2382.308	2381.895	15	+2,+3	distinct	0	1
SQTFSTYQDNQPAVLIQVFEGER	81.72	52.3702	2656.277	2656.593	1	2	distinct	0	0.9966

The equivalent proteins include

gi|429116|emb|CAA53368.1|	55388.19	glucose regulated protein/BiP [Phytophthora cinnamomi]
gi|429118|emb|CAA53369.1|	72693.28	glucose regulated protein /BiP [Phytophthora cinnamomi]
jgi|Physo1_1|109481|estExt_fgenesh1_pm.C_1170002	0	No title.
jgi|Phyra1_1|71042|fgenesh1_pm.C_scaffold_1000022	0	No title.

107. Group probability: 1.0000. Peptides of the group

VLLSSPPEHLR	51.91	55.8177	1246.703	1247.741	6	+2,+3	distinct	0	0.9912
GVGTSDHLLYSVLMGR	80.17	54.4801	1703.866	1704.895	3	2	distinct	0	0.9947
ALQEPMVEYKPSFHTK (000000100000000000)	69.28	53.9948	1903.95	1904.244	10	2	distinct	0	0.9864
IQEEVGGEYQELLLQLLEAPR	80.6	52.7577	2426.269	2427.64	5	2	distinct	0	0.9959
LSLNAWPFLAEHIEGTMAGIGTDETALSAAIVR	63.34	50.2805	3453.76	3455.221	2	3	distinct	0	0.9857

The equivalent proteins include

jgi|Physo1_1|155769|C_scaffold_7000098	0	No title.

108. Group probability: 1.0000. Peptides of the group

QSLELAEHQKK	64.53	55.1693	1309.699	1310.219	4	2	distinct	1	0.9748
KQECTQSYIR	45.62	55.3322	1311.624	1312.339	1	2	distinct	1	0.8624
RQSLELAEHQK	47.09	55.3482	1337.705	1338.551	1	2	distinct	1	0.8832
DELIHHALQGVR	63.93	55.3331	1386.737	1387.455	2	2	distinct	0	0.9743
RPYGVGLLVAGVDK	63.82	55.0105	1442.824	1443.958	6	2	distinct	0	0.9704

GVHLYQTCPSGNYYEYK	81.42	53.444	2077.92	2078.457	8	2	distinct	0	0.9955
NQYDTDVTVWSPQGHLHQIDYAMEAVK (00000000000000000000000100000)	57.08	51.0597	3144.461	3145.817	8	3	distinct	0	0.9689

The equivalent proteins include

jgi|Physo1_1|109262|estExt_fgenesh1_pm.C_810009	0	No title.
jgi|Physo1_1|109746|estExt_fgenesh1_pm.C_12150001	0	No title.
jgi|Phyra1_1|71203|fgenesh1_pm.C_scaffold_8000009	0	No title.

109. Group probability: 1.0000. Peptides of the group

KVVISAPPK	67.38	55.1779	937.596	938.69	7	+1,+2	shared(3)	1	0.9962
LEKPASMDAIK (0000000100000)	51.85	55.6621	1201.638	1218.516	5	+2,+3	shared(2)	0	0.9735
LVDLVLHMATIDN	52.39	54.8572	1452.765	1453.451	7	2	distinct	0	0.7398
VPTPDVSVVDLTCR	100.87	54.7648	1556.787	1557.293	12	2	shared(5)	0	0.9926
YDSTHGKFDGSVETK	66.7	54.3975	1669.758	1670.296	7	2	shared(2)	1	0.9822
LVAWYDNEWGYSNR	85.68	54.2699	1771.795	1771.999	7	2	shared(3)	0	0.9608
DGNLVVNGEVIHVFAAR	103.49	54.2958	1808.953	1809.9	8	+2,+3	shared(2)	0	0.999
VVAINDPFMDLEYMAYLFK (000000000000001000000)	122.87	53.0548	2278.105	2278.884	310	+2,+3	shared(3)	0	1
VVISAPPKDDTPMYVMGVNHK (00000000000000001000000)	91.26	52.9971	2297.155	2297.687	18	+2,+3	shared(3)	1	0.9999
LTGMAFRVPTPDVSVVDLTCR (00001000000000000000000)	64.95	52.937	2333.187	2333.52	9	+2,+3	shared(4)	1	0.9972
VINDKFGIVEGLMTTVHATTATQLPVDGPAK (000000000000010000000000000000000)	87.08	51.4019	3222.696	3224.001	116	3	shared(3)	1	0.998

The equivalent proteins include

jgi|Physo1_1|109002|estExt_fgenesh1_pm.C_510002	0	No title.

110. Group probability: 1.0000. Peptides of the group

HGTDPLVVCAR	53.48	55.1677	1223.608	1224.546	1	2	distinct	0	0.9335
FALDQKPEQVK	66.09	55.4824	1301.698	1302.682	2	2	distinct	0	0.9347
KILTNVCQLVPSDCK	84.21	54.3126	1773.912	1774.258	4	2	distinct	1	0.9962
AIIGDLCDAMAADSMCHTFLK	82.16	53.0111	2339.042	2340.233	1	2	distinct	0	0.9964
MFDEAAADLQAGKEPHEICQALK	92.66	52.5296	2571.21	2571.487	2	2	distinct	1	0.9987

The equivalent proteins include

jgi|Physo1_1|144660|estExt_fgenesh1_pg.C_2300010	0	No title.

111. Group probability: 1.0000. Peptides of the group

LGQLVHKK	68.45	55.5892	921.576	922.745	7	2	distinct	1	0.9397
FGLNHVTSLIENK	73.84	55.0337	1470.783	1471.849	2	2	distinct	0	0.9896
NAAVVALTHVNKEDK	90.3	54.5826	1607.863	1608.502	9	2	distinct	1	0.9977
NIAAGKEEASAPPAVVK	81.02	54.7323	1650.894	1651.067	1	2	distinct	1	0.9952
LKVPPSINQFSNTLEK	69.6	54.1507	1813.994	1814.952	2	2	distinct	1	0.9867

The equivalent proteins include

jgi|Physo1_1|156835|C_scaffold_30000010	0	No title.

112. Group probability: 1.0000. Peptides of the group

SVVFKDHLR	63.38	55.9276	1099.614	1100.756	3	2	distinct	1	0.9698
AYTAAYTPCR	49.79	55.7993	1172.528	1173.727	1	2	distinct	0	0.9036
CILLGGVHGLVESLFR	96.62	54.2188	1768.966	1770.259	4	2	distinct	0	0.9988
QVGVIGWGSQGPAQAQNLR	98.03	53.8472	1965.018	1965.09	7	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|136278|estExt_fgenesh1_pg.C_440079	0	No title.

113. Group probability: 1.0000. Peptides of the group

SLPLQLLVTAEHPDTK	124.59	54.2999	1760.967	1761.312	2	2	distinct	0	0.9999
EPNVDHCFLMNHDSK	52.36	54.2113	1841.782	1842.319	3	2	distinct	0	0.9376
SYDLIANDGVNSLHGGNTWGLK	77.51	53.0056	2330.129	2330.348	5	+2,+3	distinct	0	0.9994
SYDLIANDGVNSLHGGNTWGLKDFEGPFEVK	54.01	50.5378	3378.616	3379.444	2	3	distinct	1	0.9651

The equivalent proteins include

gi|21327106|gb|AAM48174.1|	36290.12	UDP-glucose 4-epimerase-like protein [Phytophthora sojae]

114. Group probability: 1.0000. Peptides of the group

IEIVHQATR	59.9	55.3276	1065.593	1066.832	2	2	distinct	0	0.9595
LSFSWYDFPDMQLGAR	49.4	53.829	1931.888	1932.938	1	2	distinct	0	0.9226
SLAATGAPCLGETGQAPTHSLR	108.42	53.2881	2194.08	2195.498	4	2	distinct	0	0.9997
AHLPEGATFEVPDGGYFVLVR	74.17	53.3913	2273.148	2273.425	9	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|133120|estExt_fgenesh1_pg.C_240089	0	No title.

115. Group probability: 1.0000. Peptides of the group

KALIHDGLK	74.77	55.353	993.597	994.593	6	2	distinct	1	0.9548
ALIHDGLKR	56.9	55.6772	1021.603	1022.506	1	2	distinct	1	0.8091
ALCEEHGVNLILVPSGK	86.85	54.1786	1834.961	1835.603	11	+2,+3	distinct	0	0.9994
VVSTSCAVITDFGEETHALNVLLDYLK	56.35	51.3903	2993.505	2994.675	6	3	distinct	0	0.9667
KVVSTSCAVITDFGEETHALNVLLDYLK	94.97	51.1832	3121.6	3123.077	1	3	distinct	1	0.9989

The equivalent proteins include

gi|66270173|gb|AAY43416.1|	15491.87	ribosomal protein S12 [Phytophthora infestans]
jgi|Physo1_1|109491|estExt_fgenesh1_pm.C_1190004	0	No title.

116. Group probability: 1.0000. Peptides of the group

LAWHSSGSYSK	47.81	55.4085	1221.578	1221.409	1	1	distinct	0	0.8902
DIVALVGAHAIGR	85.27	55.4105	1290.741	1291.371	7	2	distinct	0	0.9946
FDPEINHGGNAGLHLAVK	58.89	53.9576	1887.959	1888.645	5	2	distinct	0	0.9685
EIVEIFDDDNYMGPTLVR	72.51	53.3533	2125.004	2125.808	2	2	distinct	0	0.9906
SGYSGPWTNAEWTFSNEFFR	95	52.9038	2382.034	2382.059	11	2	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|108469|estExt_fgenesh1_pm.C_100028	0	No title.

117. Group probability: 1.0000. Peptides of the group

SGKPLHYK	48.26	56.7889	928.513	929.188	1	2	shared(2)	0	0.8843
ITFELFADKVPK	85.33	54.9649	1406.781	1407.6	17	2	distinct	1	0.9858
NIEAVGSQSGQTKK	55.14	55.1241	1445.747	1446.405	4	2	distinct	1	0.9484
VIPNFMCQGGDFTR	50.55	54.4245	1640.744	1641.291	1	2	distinct	0	0.9239
PNPQVFFDMTVGGAPAGR	98.26	54.0905	1859.899	1859.76	6	2	distinct	0	0.999
GNGTGGESIYGEKFPDENFLLK	69.33	52.8818	2371.133	2372.324	1	3	distinct	1	0.9868

The equivalent proteins include

jgi|Physo1_1|108795|estExt_fgenesh1_pm.C_320007	0	No title.

118. Group probability: 1.0000. Peptides of the group

NVAAHLSPAFR	62.82	55.4431	1181.63	1183.049	6	2	distinct	0	0.9705
EGDVVTIGQCRPLAK	46.43	54.4786	1641.851	1642.067	1	2	distinct	0	0.8945
VKEGDVVTIGQCRPLAK	87.2	53.9559	1869.014	1869.335	7	+2,+3	distinct	1	0.9992
FNVLEVEPASETKPINVR	98.43	53.5811	2041.084	2041.623	10	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|109522|estExt_fgenesh1_pm.C_1260002	0	No title.
jgi|Physo1_1|142976|estExt_fgenesh1_pg.C_1260022	0	No title.
jgi|Phyra1_1|72111|fgenesh1_pm.C_scaffold_87000008	0	No title.
jgi|Phyra1_1|72364|fgenesh1_pm.C_scaffold_292000001	0	No title.

119. Group probability: 1.0000. Peptides of the group

KVVISAPPK	67.38	55.1779	937.596	938.69	7	+1,+2	shared(3)	1	0.9962
VPTPDVSVVDLTCR	100.87	54.7648	1556.787	1557.293	12	2	shared(5)	0	0.9926
LVAWYDNEWGYSNR	85.68	54.2699	1771.795	1771.999	7	2	shared(3)	0	0.9608
DGNLVVDGEVIHVFAAR	76.32	54.1236	1809.937	1811.335	16	+2,+3	distinct	0	0.9992
VVAINDPFMDLEYMAYLFK (0000000000000100000)	122.87	53.0548	2278.105	2278.884	310	+2,+3	shared(3)	0	1
VVISAPPKDDTPMYVMGVNHK (000000000000000100000)	91.26	52.9971	2297.155	2297.687	18	+2,+3	shared(3)	1	0.9999
LTGMAFRVPTPDVSVVDLTCR (000100000000000000000)	64.95	52.937	2333.187	2333.52	9	+2,+3	shared(4)	1	0.9972
VINDKFGIVEGLMTTVHATTATQLPVDGPAK (0000000000001000000000000000000)	87.08	51.4019	3222.696	3224.001	116	3	shared(3)	1	0.998

The equivalent proteins include

jgi|Phyra1_1|45077|gwEuk.23.110.1	0	No title.
jgi|Phyra1_1|71507|fgenesh1_pm.C_scaffold_23000017	0	No title.
jgi|Phyra1_1|71508|fgenesh1_pm.C_scaffold_23000018	0	No title.

120. Group probability: 1.0000. Peptides of the group

HMIFGPGFYEGYK	55.55	55.2391	1544.712	1546.172	3	+2,+3	distinct	0	0.9953
AYASVPHPAGSHQDYK	67.22	54.3494	1726.806	1727.632	7	+2,+3	distinct	0	0.9975
TIPHIPTLPLSYGQAR	60.11	54.2033	1762.973	1764.306	8	+2,+3	distinct	0	0.9978
AEIVEYYPLLSLPIHR	70.03	53.8495	1912.046	1913.12	6	2	distinct	0	0.9873

The equivalent proteins include

jgi|Physo1_1|143291|estExt_fgenesh1_pg.C_1340023	0	No title.

121. Group probability: 1.0000. Peptides of the group

HTHCEFTGDVLK	48.57	54.9984	1442.661	1444.118	3	+2,+3	distinct	0	0.9866
IALTTAEYLAYER	78.47	54.7822	1512.782	1513.951	3	2	distinct	0	0.9931
TISGVNGPLVILENVKLPK	47.48	53.6868	1990.183	1991.037	1	2	distinct	1	0.9179
IPIFSAAGLPHNEIAAQIVR	88.58	53.3912	2116.179	2116.455	19	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108790|estExt_fgenesh1_pm.C_320002	0	No title.
jgi|Phyra1_1|72303|fgenesh1_pm.C_scaffold_142000001	0	No title.

122. Group probability: 1.0000. Peptides of the group

LLVWIGNR	46.43	56.0189	969.576	971.004	1	2	distinct	0	0.6344
VSADLGNVAQQPFHPR	71.72	54.2339	1734.88	1735.517	8	2	distinct	0	0.989
MVHVSSLLAQPNSPSEWAASK	74.07	53.1494	2238.11	2238.579	8	+2,+3	distinct	0	0.9993
NPSLVNLPLPVAQAIGYFCEQFPDPK	77.73	51.5235	2913.473	2914.891	3	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|142305|estExt_fgenesh1_pg.C_1110046	0	No title.

123. Group probability: 1.0000. Peptides of the group

INNVNSHDAIYNK	80.71	55.0862	1500.732	1500.95	1	2	distinct	0	0.9943
LPLDVIWSDIDYMR	69.35	54.2319	1734.865	1735.677	1	2	distinct	0	0.9854
SYHDFTLDPTNFPQAK	78.11	54.0648	1879.874	1880.823	2	2	distinct	0	0.9937
YASNKLPLDVIWSDIDYMR	101.36	53.0676	2298.135	2298.86	3	2	distinct	1	0.9993

The equivalent proteins include

jgi|Physo1_1|130344|estExt_fgenesh1_pg.C_110013	0	No title.
jgi|Physo1_1|130345|estExt_fgenesh1_pg.C_110014	0	No title.

124. Group probability: 1.0000. Peptides of the group

FTHVALALPTVGR	80.64	54.9738	1380.788	1382.048	23	+1,+2,+3	distinct	0	1
YSVSVLPDQLEAAAEILAETTLAPK	66.1	52.8805	2628.39	2628.942	2	2	distinct	0	0.9872
YVNTANAALVGAGVAHNTLTDLANAYFGDLTK	89.33	50.9033	3264.641	3264.341	1	3	distinct	0	0.9985

The equivalent proteins include

jgi|Physo1_1|142149|estExt_fgenesh1_pg.C_1090005	0	No title.

125. Group probability: 1.0000. Peptides of the group

KYWATHDAQAQAK	90.68	54.9499	1516.742	1517.248	3	2	distinct	1	0.9976
LEGVDKYGNLFGSVVHPSGR	69.97	53.3346	2130.086	2130.573	2	2	distinct	1	0.989
SVLPFQKPVVDGLLNAQEIAK	62.16	53.5288	2265.273	2265.969	5	+2,+3	distinct	0	0.9972
VILKPSLQLVNFGLSGVQCPR	76.38	52.987	2324.304	2324.682	1	2	distinct	0	0.994

The equivalent proteins include

jgi|Physo1_1|141509|estExt_fgenesh1_pg.C_990054	0	No title.

126. Group probability: 1.0000. Peptides of the group

QITDKDYYGNDIK	62.09	54.9299	1571.747	1572.512	5	2	distinct	1	0.971
AYTFVNSNPGQPACYLK	71.72	53.8928	1928.909	1928.607	4	2	distinct	0	0.9894
AYTYINNNPGQPVCYLK	62.05	53.6418	2013.962	2014.14	3	2	distinct	0	0.9754
TVYVSLPSLCCDACASTAGCK	86	53.0079	2319	2319.384	1	2	distinct	0	0.9974
AYTYINNNPGQPVCYLKSAAGTPTTK	57.17	51.9025	2828.38	2829.004	1	3	distinct	1	0.9675

The equivalent proteins include

jgi|Physo1_1|108819|estExt_fgenesh1_pm.C_340019	0	No title.

127. Group probability: 1.0000. Peptides of the group

KLTPEYAAAAK	45.22	55.6147	1161.639	1162.977	1	2	distinct	1	0.8616
LLHVIMPSTEK	47.04	55.3779	1266.701	1267.294	1	2	distinct	0	0.8826
LLHVIMPSTEKR	49.76	54.9132	1422.802	1423.546	3	+2,+3	distinct	1	0.9885
GFPTLIFFPAKDK	56.85	54.8098	1479.813	1480.772	3	2	distinct	1	0.9543
IVDYFGLKDEEMPAVMLVNMAGSMK	91.42	52.0104	2787.335	2787.442	7	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|108791|estExt_fgenesh1_pm.C_320003	0	No title.

128. Group probability: 1.0000. Peptides of the group

DSTIIMQLLR	62.92	55.745	1188.654	1188.603	4	2	shared(5)	0	0.8099
AVANNHNVELTVEER	104.61	54.3483	1693.838	1694.333	3	2	distinct	0	0.9994
QASTIAMAELPPTHPIR (000000100000000000)	90.58	54.0832	1831.961	1832.424	21	+2,+3	distinct	0	0.9998
LAEQAERYDEMVDHMK	44.88	53.82	1963.877	1964.27	1	2	distinct	1	0.8849

QAFDDAIAELDTLSEESYK	63.08	53.315	2143.98	2145.265	2	2	shared(3)	0	0.9792
QAFDDAIAELDTLSEESYKDSTLIMQLLR	73.46	50.8869	3314.623	3315.694	3	3	shared(2)	1	0.9205

The equivalent proteins include

gi|23394350|gb|AAN31465.1|	28566.01	14-3-3-like protein [Phytophthora infestans]
jgi|Physo1_1|108926|estExt_fgenesh1_pm.C_430006	0	No title.
jgi|Phyra1_1|72265|fgenesh1_pm.C_scaffold_122000003	0	No title.

129. Group probability: 1.0000. Peptides of the group

YTQQHWTYELDTGR	64.72	54.1885	1796.812	1797.031	2	2	distinct	0	0.9781
EIPWQGHQGLLVDCR	80.76	54.3609	1806.883	1807.552	10	2	distinct	0	0.9948
AALDYSPSMLNSAKPIGLK	85.29	53.7061	1975.045	1975.9	2	2	distinct	0	0.997
FLLATESCNCPDVGHGDLAWFR	87.66	52.5313	2564.158	2564.748	2	2	distinct	0	0.9979

The equivalent proteins include

jgi|Physo1_1|138217|estExt_fgenesh1_pg.C_610051	0	No title.

130. Group probability: 1.0000. Peptides of the group

GKIDAIADFRPK	61.25	55.441	1329.74	1331.209	5	+2,+3	distinct	1	0.9947
KYNYGLTTWSPLASGVLTGK	104.15	53.3383	2155.131	2155.676	25	+2,+3	distinct	1	1
FDLDYVDLVFCHRPDPSTPIEETVR	41.17	51.5542	3019.439	3020.544	1	3	distinct	0	0.864

The equivalent proteins include

jgi|Physo1_1|108826|estExt_fgenesh1_pm.C_340026	0	No title.

131. Group probability: 1.0000. Peptides of the group

NLVHGSDGPDSAK	48.53	55.1104	1295.611	1296.218	1	2	distinct	0	0.9046
TFIAIKPDGVQR	46.94	55.4939	1343.756	1344.869	1	2	shared(2)	0	0.8854
ILGATNPNQAAPGTLR	72.97	54.6666	1592.863	1592.886	4	2	distinct	0	0.99
KILGATNPNQAAPGTLR	102.98	54.2864	1720.958	1721.467	16	+2,+3	distinct	1	0.9997
HEITMWFKPEEVSNYER (000001000000000000)	75.18	53.2897	2194.015	2194.313	12	2	distinct	0	0.9923

The equivalent proteins include

jgi|Physo1_1|156590|C_scaffold_22000045	0	No title.

132. Group probability: 1.0000. Peptides of the group

LTSNAIEPLHVFVPR	98.38	54.5945	1691.936	1692.419	8	2	distinct	0	0.9989
FHPTANNVLASTSSDFSVR	87.95	53.7903	2048.992	2050.213	2	2	distinct	0	0.9976
HVYVEPAKLEYCYTNVR	68.27	53.3745	2140.041	2140.371	1	2	distinct	1	0.9858
IWGIPEGGLAETCVDPLVDLTGHGR	60.08	52.2998	2661.322	2661.585	1	2	distinct	0	0.9786

The equivalent proteins include

jgi|Physo1_1|108182|estExt_fgenesh1_pm.C_20014	0	No title.

133. Group probability: 1.0000. Peptides of the group

ADGQVIHFQAPK	93.74	55.3397	1309.678	1310.03	6	2	distinct	0	0.9981
KLGVTPIPGVEEVNLFK	91.37	54.0455	1839.05	1839.616	16	+2,+3	distinct	1	0.9999
SLQELLPGIINQLGPDNLANLK	73.29	52.9087	2359.311	2360.091	4	2	distinct	0	0.9924

The equivalent proteins include

jgi|Physo1_1|108876|estExt_fgenesh1_pm.C_370016	0	No title.

134. Group probability: 1.0000. Peptides of the group

AIVIFVPFR	50.14	55.9554	1060.643	1061.495	3	2	distinct	0	0.9036
TLTHVQEQILDDLVFPTEIVGK	82.45	52.7973	2494.332	2494.614	20	+2,+3	distinct	0	0.9995
TLTHVQEQILDDLVFPTEIVGKR	87.72	52.2098	2650.433	2651.889	2	3	distinct	1	0.9975
IVKPEGQTADEFELQVAQELVNLEQSAAEIK	71.09	50.3882	3425.756	3426.532	14	3	distinct	0	0.9922

The equivalent proteins include

jgi|Physo1_1|109563|estExt_fgenesh1_pm.C_1420002	0	No title.

135. Group probability: 1.0000. Peptides of the group

APYPGNYWFSFPNSCAQK	63.42	53.354	2132.941	2133.278	7	2	distinct	0	0.9791
YYESHTPPEYGEFVAMDGAK (00000000000000100000)	73.43	53.1203	2289.989	2290.085	9	+2,+3	distinct	0	0.9999
ATNTGSGFEVDEAIDFWEKPGDEDANSER	75.63	50.9463	3185.37	3185.825	2	3	distinct	0	0.9943
TDECRAEYPGGLCPMGTSPDGVTCTFGYK	41.42	51.1207	3225.351	3226.2	1	3	distinct	1	0.8856

The equivalent proteins include

jgi|Physo1_1|131361|estExt_fgenesh1_pg.C_150132	0	No title.

136. Group probability: 1.0000. Peptides of the group

HAVIFYDDLSK	65.46	55.3439	1306.656	1306.456	12	+1,+2	distinct	0	0.9994

EAYPGDVFYIHSR	77.43		54.6898	1552.731	1553.625	13	2	shared(2)	0	0.9925
RTGSIVSVPVGPEVLGR	74.35		54.2792	1721.979	1722.923	22	2	distinct	1	0.9915
GMALNLEPDVVGVVVFSNDR (0010000000000000000000)	83.98		53.3301	2130.078	2131.325	6	2	distinct	0	0.9968

The equivalent proteins include

gi|9695382|ref|NP_037604.1|	56282.61	ATP synthase F1 subunit alpha [Phytophthora infestans]

137. Group probability: 1.0000. Peptides of the group

KPVVIYDYPK	47.16		55.4085	1220.68	1221.646	1	2	distinct	0	0.8796
YGSVPHAGFGLGFER	58.28		54.6335	1592.773	1593.442	6	2	distinct	0	0.9626
NAMAFATHEFFNQR	79.69		54.3558	1682.762	1683.883	10	2	distinct	0	0.9941
FSVKPVWGTDFGSEHER	82.9		53.7748	1976.938	1977.511	7	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108671|estExt_fgenesh1_pm.C_240002	0	No title.

138. Group probability: 1.0000. Peptides of the group

WVAFGGSYPGNLAAWVR	95.86		54.0136	1849.926	1851.096	4	2	distinct	0	0.9987
KFDDANPFAGDDSKPASGAYR	75.44		53.2916	2228.013	2229.228	1	3	distinct	1	0.992
VDVNANGWGPTALPEQFLNIPYAPFNKGDK	68.7		51.2155	3271.63	3272.486	1	3	distinct	1	0.9899
YFGGGECYHEVEQAITQLGQLMDGGKEDR	65.03		51.0401	3286.466	3287.342	1	3	distinct	1	0.9856

The equivalent proteins include

jgi|Physo1_1|141581|estExt_fgenesh1_pg.C_1000067	0	No title.

139. Group probability: 1.0000. Peptides of the group

FTIGHAWR	50.68		56.3756	986.509	987.549	4	2	distinct	0	0.9072
LFFAHGISR	56.64		55.9646	1046.566	1047.253	4	2	distinct	0	0.9455
RGDLVETLHGVQVADPYR	61.02		54.0423	2024.044	2024.553	11	+2,+3	distinct	1	0.9988
LVDNMDSAYSYILNDGDYYYFK	57.98		52.1989	2668.168	2668.642	1	2	distinct	0	0.9715
NANMIHVADLSDFDNFLKGPSDSTIPVIK	69.86		50.9836	3157.575	3158.87	1	3	distinct	1	0.9906

The equivalent proteins include

jgi|Physo1_1|108684|estExt_fgenesh1_pm.C_240015	0	No title.

140. Group probability: 1.0000. Peptides of the group

AFEASGNDVAAYVAPLFADLLAR	98.49		52.8783	2380.206	2381.697	18	+2,+3	distinct	0	1
FLAGPSAGAAPAAGAAAAGETTAKVEEK	70.17		52.6387	2513.276	2514.679	6	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|134110|estExt_fgenesh1_pg.C_300021	0	No title.

141. Group probability: 1.0000. Peptides of the group

MNAGRPFTAWLDNVK	78.93		54.4061	1718.856	1719.828	14	2	distinct	0	0.9936
KQIDGVQDHSQIFVIGDK	46.6		53.5661	2026.048	2026.282	1	2	distinct	1	0.9083
MAAMENATTNAEDLIGSLTLVYNK	131.73		52.4117	2569.24	2569.784	3	2	distinct	0	1
SLAVQPDSDAFDLYELEPDNKDELLADLK	46.88		50.9366	3262.577	3263.221	1	3	distinct	1	0.9294

The equivalent proteins include

jgi|Physo1_1|109105|estExt_fgenesh1_pm.C_600011	0	No title.

142. Group probability: 1.0000. Peptides of the group

IVGTLIHILK	66.81		55.6378	1105.722	1106.945	15	2	distinct	0	0.9784
VNVNGGAVAIGHPIGVSGAR	79.08		54.2632	1844.002	1844.568	9	2	distinct	0	0.995
TPIACFNGSFAPLSGPELGAVANAEAVRR	106.7		51.3783	2971.497	2972.3	7	3	distinct	1	0.9996
LGNGTLVDGVIHDGLWDPYNNQHMGMCGEK	51.84		50.7142	3326.491	3327.158	4	3	distinct	0	0.9561

The equivalent proteins include

jgi|Physo1_1|109674|estExt_fgenesh1_pm.C_2560001	0	No title.

143. Group probability: 1.0000. Peptides of the group

IHTFIATSDIHLK	66.27		54.765	1494.819	1495.513	7	2	shared(2)	0	0.9582
MVSHYTGMSIQPNK	71.84		54.6438	1591.749	1591.875	5	2	shared(2)	0	0.9882
SDPDFLCEVLAEVIK	75.06		54.3418	1733.855	1735.186	2	2	distinct	0	0.9915
HQATYEIMLPESVGLSENK	83.6		53.3235	2145.041	2146.257	2	2	shared(2)	0	0.9966
AIVGSNAFAHESGIHQDGVLK	80.25		53.3565	2149.092	2149.306	13	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|108956|estExt_fgenesh1_pm.C_460003	0	No title.

144. Group probability: 1.0000. Peptides of the group

KIAVNLIPFPR	70.88		55.3745	1266.781	1267.527	5	2	shared(6)	1	0.9855

EIVHIQGGQCGNQIGAK	70.47	54.3515	1807.9	1808.547	13	2	distinct	0	0.9519
GHYTEGAELIDSVLDVVR	50.71	53.7352	1971.99	1972.76	1	2	shared(5)	0	0.7947
LTTPTYGDLNHLVCAAMSGITTCLR	82.51	52.0359	2764.335	2765.271	4	2	distinct	0	0.997
AGPYGQIFRPDNFVFGQTGAGNNWAK	79.99	52.236	2811.352	2812.533	7	+2,+3	shared(2)	0	0.9986
FWEVISDEHGVDPTGSYHGDSDLQLER	57.7	51.2275	3087.385	3088.854	1	3	distinct	0	0.9705
EAESCDCIQGFQLTHSLGGGTGSGMGTLLISK	75.02	50.7561	3310.527	3311.459	11	3	shared(2)	0	0.9946

The equivalent proteins include

jgi|Physo1_1|109498|estExt_fgenesh1_pm.C_1190011	0	No title.
jgi|Phyra1_1|72114|fgenesh1_pm.C_scaffold_88000002	0	No title.

145. Group probability: 1.0000. Peptides of the group

MGHAGAIVSGGK	83.38	55.7051	1083.549	1084.128	17	+1,+2	distinct	0	0.9984
MGIMPGYIHQK (0100000000000)	60.99	55.4924	1273.631	1274.066	14	+2,+3	distinct	0	0.9944
LIGPNCPGIIKPGECK	75.63	54.1304	1751.906	1753.396	16	2	distinct	0	0.9922
QGTFHSQQAIEYGTNMVGGVTPK	57.06	52.5991	2449.17	2449.358	2	2	distinct	0	0.9699

The equivalent proteins include

jgi|Physo1_1|143975|estExt_fgenesh1_pg.C_1600020	0	No title.

146. Group probability: 1.0000. Peptides of the group

KLEELGYTLPAVAEPK	92.84	54.2368	1756.961	1758.379	2	2	distinct	1	0.9983
SGNTIYLAGHLPQPAGGELILGK	77.31	53.0203	2305.243	2305.984	10	+2,+3	distinct	0	1
DLTPEQGYDAAHYVALSLMATLK	91.85	52.5393	2506.241	2506.413	12	2	shared(2)	0	0.9986

The equivalent proteins include

jgi|Physo1_1|156147|C_scaffold_11000042	0	No title.

147. Group probability: 1.0000. Peptides of the group

AGGDRQELHEAIR	58.91	54.9673	1450.728	1451.482	1	2	distinct	1	0.9617
AVHDHMDALLDPSLFIGR (00000010000000000000)	91.85	54.1944	2006.004	2006.91	7	+2,+3	distinct	0	0.9999
CPQQVEEFISEEIAPILK	106.03	53.3396	2129.071	2130.212	1	2	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|109266|estExt_fgenesh1_pm.C_810013	0	No title.

148. Group probability: 1.0000. Peptides of the group

NMAHFAQGIR (001000000000)	54.53	55.833	1143.561	1143.422	20	+1,+2	distinct	0	0.9959
AVYGAFEPPSFDLGTIKYPR	90.18	53.2246	2227.131	2227.956	5	+2,+3	distinct	1	0.9998
MGFYTGSDDWLATSTDISQLR	87.06	52.8936	2363.074	2364.309	1	2	distinct	0	0.9977

The equivalent proteins include

jgi|Physo1_1|108318|estExt_fgenesh1_pm.C_60008	0	No title.

149. Group probability: 1.0000. Peptides of the group

IVNSHYSPSVHYAETGMK (000000000000000100)	81.92	53.6816	2018.952	2019.443	18	+2,+3	distinct	0	0.9999
AILSHGDNFYWTGINSEDGR	136.05	53.556	2251.029	2251.912	1	2	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|127847|estExt_fgenesh1_pg.C_30056	0	No title.

150. Group probability: 1.0000. Peptides of the group

MLAVDYENVKPDIVILGK	90.31	53.66	2016.096	2016.295	4	2	distinct	0	0.998
EYYDFLSAYSAVNQGHCHPK	61.95	52.8662	2385.048	2386.032	8	2	shared(2)	0	0.9781
AFYNNVLGEYQEYMTQLLGFDR	116.73	52.1733	2670.242	2670.343	31	2	distinct	0	0.9998
GLLNAIIINERPNQPDALQLCMNLAK	80.94	51.4911	2918.547	2919.912	2	3	shared(2)	0	0.996

The equivalent proteins include

jgi|Physo1_1|109298|estExt_fgenesh1_pm.C_860005	0	No title.

151. Group probability: 1.0000. Peptides of the group

FHGVSFGAK	56.88	56.1426	948.482	948.299	3	1	distinct	0	0.9464
RIYQIAQALK	55.51	55.8307	1202.713	1203.385	2	2	distinct	1	0.6742
VMGTHPTMIDSAEDR	54.1	55.0115	1658.739	1659.423	1	2	distinct	0	0.9456
SKPMLGLEPDSLFDYYKR	52.98	53.2915	2158.077	2158.849	3	2	distinct	1	0.9479
VMVGESTENDNLPPLDGPKRPEGYVGIK	62.39	51.3401	3010.507	3011.719	1	3	distinct	1	0.9811
ALELQGDNVKPIFGICLGNQLLSLAAGANTYK	80.44	50.456	3387.786	3388.727	2	3	distinct	0	0.9967

The equivalent proteins include

jgi|Physo1_1|109206|estExt_fgenesh1_pm.C_730002	0	No title.

152. Group probability: 1.0000. Peptides of the group

LCLPQVEDIIAATKR	72.64	54.3114	1725.945	1727.28	5	+2,+3	distinct	1	0.9992

GSNGPAAGVAAQHSQCYAAWYGSVPGLK	43.45	51.8223	2803.314	2804.641	2	3	distinct	0	0.8994
AAIRDPNPVVVLENELVYGVSFPVSK	90.38	52.2385	2811.517	2812.163	17	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|122568|estExt_Genewise1.C_1080034	0	No title.

153. Group probability: 1.0000. Peptides of the group

RQGVDVSPFR	51.49	55.8926	1159.61	1160.106	1	2	distinct	1	0.9168
AATFLPHTAQR	47.57	55.3975	1211.641	1212.598	3	2	distinct	0	0.8879
VNQALYLIATGAR	82.71	55.3412	1388.778	1389.838	2	2	distinct	0	0.9952
RVNQALYLIATGAR	81.13	55.2375	1544.879	1545.98	14	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|109358|estExt_fgenesh1_pm.C_950003	0	No title.
jgi|Phyra1_1|72232|fgenesh1_pm.C_scaffold_114000001	0	No title.

154. Group probability: 1.0000. Peptides of the group

HAEEFYQSLNLPYR	102.89	54.2107	1765.842	1766.938	2	2	distinct	0	0.9992
YLIATSEQPICGYHR	59.69	54.3579	1806.872	1807.543	1	2	distinct	0	0.9671
VPEVLVPFMGGVTYLPFTR	87.41	53.3361	2121.133	2122.16	3	2	distinct	0	0.9975
VHQFDKVEQFCITDPESSVAMHEEMLR	50.45	50.9429	3261.489	3262.099	1	3	distinct	1	0.9446

The equivalent proteins include

jgi|Physo1_1|108754|estExt_fgenesh1_pm.C_300005	0	No title.

155. Group probability: 1.0000. Peptides of the group

VQHIEIHGK	53.42	56.0615	1059.582	1060.719	21	+1,+2	shared(2)	0	0.9919
NTAYGATVKPR	75.48	55.63	1176.625	1177.154	8	2	shared(2)	0	0.9903
HNPNVAFVVYR	62.41	55.422	1314.683	1315.842	10	+2,+3	distinct	0	0.998
VIYLSIVDGKPVGR	82.74	54.8776	1514.882	1515.573	12	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|138074|estExt_fgenesh1_pg.C_600033	0	No title.

156. Group probability: 1.0000. Peptides of the group

SFSWTNLNGGTCWLK	89.18	54.2196	1769.819	1769.518	28	2	distinct	0	0.9975
TPGDCCGICNNWSGCR	81.58	53.8497	1912.707	1913.022	2	2	distinct	0	0.9954
AYTGCHAFSWSNYNGGTCWLK	81.59	52.5416	2479.047	2479.717	46	+2,+3	distinct	0	0.9997

The equivalent proteins include

jgi|Physo1_1|134006|estExt_fgenesh1_pg.C_290073	0	No title.

157. Group probability: 1.0000. Peptides of the group

HGDALVVNSQKPVK	79.18	54.9056	1490.82	1491.065	7	+2,+3	distinct	0	0.9994
LGGSLIPHKSDENDGIVEYK	63.61	53.5337	2170.091	2170.274	5	+2,+3	distinct	1	0.9995
FGNKYDDTFYLTGLNHADTAFR	71.07	52.4603	2565.192	2566.412	1	3	distinct	1	0.9888

The equivalent proteins include

jgi|Physo1_1|145331|estExt_fgenesh1_pg.C_10590002	0	No title.

158. Group probability: 1.0000. Peptides of the group

IHGGLLGVR	57.93	56.0187	920.556	921.119	5	2	distinct	0	0.9512
YGCNPHQNPAAILSR	72.42	54.3348	1696.81	1697.284	4	+2,+3	distinct	0	0.999
TGVVELATYLSQHGVELLSTGGTAK	79.76	52.6126	2530.328	2530.982	2	2	distinct	0	0.9962
LPFTVLNGTPGYINLLDAANAYQLVR	58.74	51.7538	2832.517	2833.63	1	2	distinct	0	0.9771

The equivalent proteins include

jgi|Physo1_1|109486|estExt_fgenesh1_pm.C_1170007	0	No title.
jgi|Phyra1_1|71046|fgenesh1_pm.C_scaffold_1000026	0	No title.

159. Group probability: 1.0000. Peptides of the group

WDYSMFVKPK	73.68	55.4038	1299.632	1300.488	5	2	distinct	0	0.9882
HWRPDMEEAEAR	49.44	54.6209	1525.673	1526.335	1	2	distinct	0	0.9096
YKGGVLMAADTLGSYGSLAR	107.13	53.6225	2029.03	2029.895	2	2	distinct	1	0.9996
LTAVHNTTLLGAGGDFSDFQFIK	70.4	52.6291	2451.243	2452.591	1	2	distinct	0	0.9907

The equivalent proteins include

jgi|Physo1_1|158871|C_scaffold_162000014	0	No title.

160. Group probability: 1.0000. Peptides of the group

NFDPGFFVEHFVK	58.47	54.5583	1581.762	1582.491	1	2	distinct	0	0.9605
KVFLDPEWGVLSSIK	74.19	54.3959	1716.945	1718.001	6	2	distinct	1	0.9781
VSDIVFGIVGYPSDVR	53.23	54.2792	1721.899	1722.725	1	2	distinct	0	0.9441
VGWIGTGVMGASMVGHILK	90.44	53.8487	1912.006	1912.791	3	2	distinct	0	0.9981
MNLSLPGLALANQLYVAVK	50.73	53.6618	2014.128	2015.623	1	2	distinct	0	0.9383

The equivalent proteins include

jgi|Physo1_1|120688|estExt_Genewise1.C_810036	0	No title.

161. Group probability: 1.0000. Peptides of the group

VGELIVEAGFPK	78.95	55.5194	1257.697	1258.863	1	2	shared(3)	0	0.9931
VYVQEGIYDEFVK	78.44	54.8831	1587.782	1588.458	3	2	shared(2)	0	0.9931
VYVQEGIYDEFVKR	78.67	54.3331	1743.883	1744.428	22	2	shared(2)	1	0.9936
GWFIEPTVFADVTDDMTIAR (0000000000000000100000)	97.86	53.0271	2283.088	2284.084	13	2	shared(3)	0	0.9991
LGPALAAGNTIVLKPAEQTPLSALR	76.71	52.6931	2500.438	2500.713	14	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Phyra1_1|71205|fgenesh1_pm.C_scaffold_8000011	0	No title.

162. Group probability: 1.0000. Peptides of the group

QYTGVGSLK	45.87	55.2697	951.502	952.559	1	2	distinct	0	0.8617
AYAEHLKR	65.71	56.3754	986.53	987.808	9	2	distinct	1	0.9677
ISSHGQQDLDR	51.24	55.2637	1254.595	1255.005	3	2	distinct	0	0.919
HILHQLEEMK (000000000100)	56.42	55.3469	1276.66	1293.137	3	2	distinct	0	0.9466
KISSHGQQDLDR	71	54.9616	1382.69	1383.156	6	2	distinct	1	0.9863
SGKIELPAWWDVVK	77.54	54.7681	1626.877	1627.787	5	2	distinct	1	0.9728

The equivalent proteins include

jgi|Physo1_1|109411|estExt_fgenesh1_pm.C_1010005	0	No title.

163. Group probability: 1.0000. Peptides of the group

IQGIGAGFVPR	62.09	55.6894	1113.629	1114.006	4	2	shared(2)	0	0.9684
IHFETTGPEVWR	61.83	55.0337	1470.726	1471.703	13	2	distinct	0	0.9692
DMTALIGNTPLVYLNR	63.91	54.234	1789.94	1791.101	1	2	shared(2)	0	0.9781
IIAVEPEESPVLSGGNPAPHK	99.6	53.3416	2140.116	2140.571	15	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109172|estExt_fgenesh1_pm.C_670004	0	No title.

164. Group probability: 1.0000. Peptides of the group

LFLHEDIHDEFLNR	88.01	54.1869	1796.885	1797.274	3	2	distinct	0	0.9972
VVAAMDNAKPQWCDLPAPAR	83.33	53.2786	2209.077	2210.289	4	+2,+3	distinct	0	0.9966
IGDPLEDGVLCGPLHNTQAVK	62.29	53.2881	2232.121	2232.879	3	+2,+3	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|108413|estExt_fgenesh1_pm.C_90009	0	No title.

165. Group probability: 1.0000. Peptides of the group

VVHDKFGIK	49.37	55.6958	1041.597	1041.469	1	1	distinct	1	0.8974
VLDLIEHMVK	57.34	55.3938	1195.663	1196.24	3	2	distinct	0	0.9507
NMHVVSNASCTTNCLAPLAK	83.89	53.3324	2187.023	2188.453	7	2	distinct	0	0.9968
FGGEISHDEQHIFVDGKPIR	81.55	52.9877	2280.129	2281.328	2	+2,+3	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|108305|estExt_fgenesh1_pm.C_50020	0	No title.

166. Group probability: 1.0000. Peptides of the group

AGKPQEVTVYVSPVVVK	62.85	54.3396	1799.019	1799.457	2	2	shared(2)	0	0.9768
HSNVIASISGATNLVNVR	65.63	54.0208	1850.996	1852.058	1	2	shared(2)	0	0.9826
LGFGGVVKPADIPTVGISR	81.6	53.9662	1882.068	1882.753	18	+2,+3	shared(2)	0	0.9999
ASVPLTMQPDYEAHFYVR	75.14	53.4103	2123.015	2123.57	1	2	distinct	0	0.9925
ALVANFMPEIVQLLEQHPDVR	83.75	52.7057	2418.273	2419.24	2	2	distinct	0	0.9577
SDNLDSSAYVGPGAGRFPTANSVMNDIIQLAR	57.3	50.7389	3335.62	3336.947	1	3	shared(2)	1	0.9747

The equivalent proteins include

jgi|Physo1_1|108556|estExt_fgenesh1_pm.C_150025	0	No title.

167. Group probability: 1.0000. Peptides of the group

HDGNLSLDQVIGVAR	100.51	54.6417	1592.827	1593.781	2	+2,+3	distinct	0	0.9999
NIKHDGNLSLDQVIGVAR	83.71	53.9866	1948.049	1948.428	6	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|108649|estExt_fgenesh1_pm.C_220010	0	No title.

168. Group probability: 1.0000. Peptides of the group

LHAASYLLPGEDILFAFESAK	82.7	53.1068	2291.184	2292.627	3	+2,+3	distinct	0	0.9999
ISAGHDLVSQATSAAEWLENAFNQR	117.74	52.0371	2714.305	2714.448	6	2	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|129572|estExt_fgenesh1_pg.C_80083	0	No title.

169. Group probability: 1.0000. Peptides of the group

RGVKPADLISGLEFACGNPDK	77.14	53.2789	2243.137	2243.741	4	+2,+3	distinct	1	0.9998
WTSIGSTQPIGTTTFEHWPLR	80.89	52.8871	2414.202	2414.591	2	2	distinct	0	0.996

YAEHPAIIGLEPVNEPWELTPIDLLK	60.32		51.3796	2956.559	2957.693	2	2	distinct	0	0.9802
The equivalent proteins include										
jgi|Physo1_1|116268|estExt_Genewise1.C_320049	0	No title.								
170. Group probability: 1.0000. Peptides of the group										
AHSYIDKVNSR	46.3		55.4908	1288.652	1289.683	1	2	distinct	1	0.8744
RPLVVMAPNPECLR	70.3		54.7319	1650.87	1651.21	2	2	distinct	0	0.9865
LSVAPMLAELIQAEHFK	70.65		53.8894	1896.018	1897.222	1	2	distinct	0	0.9884
WLPDSPAQFAMFFHGTGK	99.55		53.7684	2035.961	2036.791	2	2	distinct	0	0.9991
The equivalent proteins include										
jgi|Physo1_1|129878|estExt_fgenesh1_pg.C_90155	0	No title.								
171. Group probability: 1.0000. Peptides of the group										
FVLDKEFR	44.97		55.2927	1052.565	1053.733	1	2	distinct	1	0.8503
LRPDTGLYGK	47.03		55.8441	1118.608	1119.597	3	2	distinct	0	0.8771
AAPKEEAPKPK	54.89		55.3895	1164.65	1165.085	4	2	distinct	1	0.941
KVEHPLAVLNR	53.51		55.4538	1274.746	1275.771	2	2	distinct	1	0.9333
HMVEANPDAEYYTWTK	114.67		53.7591	1953.857	1954.586	7	2	distinct	0	0.9997
The equivalent proteins include										
jgi|Physo1_1|142260|estExt_fgenesh1_pg.C_1110001	0	No title.								
172. Group probability: 1.0000. Peptides of the group										
SSFEAPHEPR	47.32		55.4889	1155.531	1156.058	1	2	distinct	0	0.881
LHSGDSYIFLK	53.08		55.5151	1278.661	1278.982	1	2	distinct	0	0.9307
AASALLATFLDDSLGGNPVQVR	88.47		53.1832	2214.164	2214.716	3	+2,+3	distinct	0	0.9999
AASQSEEDIGVDPNGDGKHEITVWR	62.77		52.1331	2709.263	2710.376	1	3	distinct	1	0.9793
The equivalent proteins include										
jgi|Physo1_1|136639|estExt_fgenesh1_pg.C_470053	0	No title.								
173. Group probability: 1.0000. Peptides of the group										
ETHHVAGAAVR	54.14		55.8234	1146.589	1146.51	3	+1,+2	shared(2)	0	0.9946
RLTELIGAVGGK	63.93		55.6142	1212.719	1213.39	2	2	shared(2)	1	0.9741
NKPLSSLTFEELSTLHPK	99.39		53.6385	2040.089	2040.337	8	2	distinct	0	0.9991
ELIGTANQLAENNIELLMPGFTHLQPAQPLR (0000000000000000010000000000000)	90.53		50.4685	3427.792	3428.389	9	3	distinct	0	0.998
The equivalent proteins include										
jgi|Physo1_1|109558|estExt_fgenesh1_pm.C_1380002	0	No title.								
174. Group probability: 1.0000. Peptides of the group										
LLGDVTIASGGVMPNIHSVLLPK (00000000000010000000000)	96.27		52.9657	2330.303	2331.179	48	+2,+3	distinct	0	1
IGGGAPVYMAAVLEYLCAEILELAGNAAR	46.46		51.4121	2991.52	2993.001	1	3	distinct	0	0.728
NDEELNKLLGDVTIASGGVMPNIHSVLLPK	69.4		51.081	3172.68	3173.206	5	3	distinct	1	0.9905
The equivalent proteins include										
jgi|Physo1_1|158257|C_scaffold_93000012	0	No title.								
175. Group probability: 1.0000. Peptides of the group										
IPCHVLAK	51.67		55.4863	936.521	937.267	3	2	distinct	0	0.9165
HITIFSPEGR	54.99		55.7318	1155.604	1156.336	6	2	distinct	0	0.939
IDPAGHFWGYK	63.77		55.4363	1289.619	1290.383	9	2	distinct	0	0.9729
LRYEAHEFENK	62.11		54.8881	1434.689	1435.107	6	2	distinct	1	0.931
RIADVAQVYTQHASMR	55.52		54.2009	1844.932	1845.869	4	+2,+3	distinct	1	0.9974
The equivalent proteins include										
jgi|Physo1_1|108340|estExt_fgenesh1_pm.C_60030	0	No title.								
176. Group probability: 1.0000. Peptides of the group										
GAPSVLGIHPK	51.34		56.1651	1074.619	1075.066	3	2	distinct	0	0.9182
FTFGGAKPQVK	68		55.4162	1178.645	1178.989	9	2	distinct	0	0.9813
VQGMWVFHSTR	61.38		55.2764	1346.655	1347.575	5	2	distinct	0	0.9667
VWSYDNPEHTLK	45.53		54.9158	1487.704	1488.394	1	2	distinct	0	0.8719
VFMWDTGNSIGEIVGHQK	82.91		53.6602	2016.973	2018.057	2	2	distinct	0	0.9962
The equivalent proteins include										
jgi|Physo1_1|129331|estExt_fgenesh1_pg.C_70156	0	No title.								
177. Group probability: 1.0000. Peptides of the group										
AVAHHTDCTFIR	51.4		54.9757	1426.678	1427.199	2	2	distinct	0	0.9233
LLREELQLLQEPGSYVGEVVK	61.49		52.8146	2398.311	2399.497	3	+2,+3	distinct	1	0.9984
EVIELPIKHPELFDALGVAQPK	75.85		52.854	2442.352	2443.482	7	+2,+3	distinct	1	0.9997

The equivalent proteins include

jgi|Physo1_1|109338|estExt_fgenesh1_pm.C_920004	0	No title.
jgi|Phyra1_1|38740|gwEuk.1.239.1	0	No title.

178. Group probability: 1.0000. Peptides of the group

IVVHDLQPEVEEPK	48.73	54.6749	1630.857	1631.508	1	2	distinct	0	0.9103
LYSLVAGDVIHALVFSPNR	115.9	53.6944	2070.126	2070.592	4	2	distinct	0	0.9998
SLLVWQLSNDGEEYGFAR	90.91	53.5863	2083.001	2083.574	2	2	distinct	0	0.9981

The equivalent proteins include

jgi|Physo1_1|109389|estExt_fgenesh1_pm.C_980005	0	No title.

179. Group probability: 1.0000. Peptides of the group

QISQYFSSFR	46.99	55.8766	1261.609	1261.943	2	2	distinct	0	0.8766
VKECTGNAVPVGTVQR	80	54.3481	1713.883	1714.494	11	2	distinct	1	0.9947
CGVNIYPFFTQGELKPVDK	58.3	53.2912	2211.103	2211.718	9	+2,+3	distinct	0	0.9979
VAVGVQMNDLSGVDAEIQAVCDGYKR	59.59	51.9857	2793.342	2794.839	1	3	distinct	1	0.9737

The equivalent proteins include

jgi|Physo1_1|131139|estExt_fgenesh1_pg.C_140137	0	No title.

180. Group probability: 1.0000. Peptides of the group

LVQHGVTNTAGSLK	59.88	54.9122	1423.778	1424.054	5	2	distinct	0	0.9661
DYVRPGMVGNIFEK	53.01	54.5658	1623.808	1624.786	2	2	distinct	0	0.9385
HLPCFGLTGPSSGSDAANMR	96.74	53.5085	2073.936	2074.481	4	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108276|estExt_fgenesh1_pm.C_40027	0	No title.

181. Group probability: 1.0000. Peptides of the group

TACTATQQTAAYK	48.13	55.1856	1413.656	1414.142	1	2	distinct	0	0.901
LMCASTACNTMIK (000000000001000)	67.83	55.0836	1499.66	1500.494	25	2	distinct	0	0.9825
LMCASTACNTMIKK	83.1	54.7689	1627.755	1629.112	14	2	distinct	1	0.9956
TLVSILSESSFSQCSK	80.12	54.2841	1771.866	1772.861	1	2	distinct	0	0.9947

The equivalent proteins include

gi|119287|sp|P15569|ELIB_PHYCI	10629.09	Beta-elicitin cinnamomin

182. Group probability: 1.0000. Peptides of the group

TVSAPPPAPPTHSLLETK	47.6	54.1574	1841.989	1841.88	2	2	distinct	0	0.915
HLAAVLGQHENDAVVIPK	78.94	53.8445	1910.037	1910.474	10	+2,+3	distinct	0	0.9995
LMLSFYLLDPEGTGFITK	94.94	53.5636	2044.059	2045.297	4	2	distinct	0	0.9987

The equivalent proteins include

jgi|Physo1_1|156081|C_scaffold_10000100	0	No title.

183. Group probability: 1.0000. Peptides of the group

KSYMDGHNILK	50.2	55.4011	1304.655	1305.342	1	2	distinct	1	0.911
IPPLTPEQAELVESLEQVQIIAR	50.83	52.4082	2572.411	2573.623	1	2	distinct	0	0.9482
TLGSGQALIDGLFPVDGTLSLELHR	69.12	52.3308	2608.386	2608.805	3	+2,+3	distinct	0	0.9997
MIFHGEPQQLPDCHDTLCDIEEFSK	56.54	51.2915	3045.331	3046.508	1	3	distinct	0	0.9649

The equivalent proteins include

jgi|Physo1_1|158580|C_scaffold_119000001	0	No title.

184. Group probability: 1.0000. Peptides of the group

YGSANALHFK	59.83	55.4836	1106.551	1107.394	3	2	distinct	0	0.9603
ETRPTFFFGVPR	62.88	54.857	1452.751	1453.597	3	2	distinct	0	0.9721
VTESGAGARPAITAPQAFQNTLAK	85.04	52.7778	2398.26	2399.708	13	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|132768|estExt_fgenesh1_pg.C_220116	0	No title.

185. Group probability: 1.0000. Peptides of the group

HLGAELALVAR	54.97	55.6588	1148.667	1148.529	5	+1,+2	shared(2)	0	0.9959
YYYHAVGTPR	68.16	55.4168	1225.588	1226.374	13	2	shared(2)	0	0.9809
SKDYFAGMAWK	47.88	55.4348	1302.607	1304.091	2	2	shared(2)	1	0.8908
KTQSNVSKPFPK	83.59	55.3565	1359.751	1360.299	6	+1,+2	shared(2)	1	0.9996
KLFVPYDNVIPPSAK	50.79	54.4566	1686.934	1687.763	1	2	shared(2)	1	0.9281
IVPGANEVEYAPIDEAGDLLADPVK	52.22	52.4586	2594.311	2595.065	1	2	distinct	0	0.9573
VEVVGTMLPLGPNGGVSQLPVMGGVVMGNLITK	66.41	50.9042	3262.749	3264.041	1	3	shared(2)	0	0.989

The equivalent proteins include

jgi|Physo1_1|144990|estExt_fgenesh1_pg.C_3690001	0	No title.

186. Group probability: 1.0000. Peptides of the group

ESYPACGGTHQSPINIPVR	76.53	53.5426	2081.995	2082.95	8	2	distinct	0	0.9936
DLSHNDWGMFHAPLTYGGDCSK	90.78	52.5098	2507.063	2507.469	9	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|132952|estExt_fgenesh1_pg.C_230095	0	No title.

187. Group probability: 1.0000. Peptides of the group

LGDFAPVAPAIQNFHTR	72.94	54.026	1852.958	1853.431	12	+2,+3	distinct	0	0.9986
LNTWGGSLALGHPFGATGSR	85.43	53.7736	1998.007	1998.741	11	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|108326|estExt_fgenesh1_pm.C_60016	0	No title.

188. Group probability: 1.0000. Peptides of the group

LVRPFVVSAVLR	57.15	55.1925	1354.845	1355.657	2	2	distinct	0	0.9535
LGTFGVLHPQVLK	58.39	54.8723	1407.824	1408.463	6	2	distinct	0	0.96
FKPLSQDKEFEAK	45.81	54.6614	1565.809	1566.274	1	2	distinct	1	0.88
ETQGQDKDHSAHSDAVLYK	44.68	53.3871	2127.982	2128.161	1	2	distinct	1	0.8956
RICAAYTGPTDGFEVIHGLVDR	85.78	52.6549	2446.206	2447.559	1	3	distinct	1	0.9969

The equivalent proteins include

jgi|Physo1_1|108453|estExt_fgenesh1_pm.C_100012	0	No title.

189. Group probability: 1.0000. Peptides of the group

VAGLAAGAIGAAGVIGSAVSATR	110.28	53.8378	1939.085	1939.715	17	+2,+3	distinct	0	1
SVLEPVELLAELFDTTLK	56.7	53.6209	2016.103	2017.413	1	2	distinct	0	0.9621

The equivalent proteins include

jgi|Physo1_1|144346|estExt_fgenesh1_pg.C_1800007	0	No title.

190. Group probability: 1.0000. Peptides of the group

LAALVGAHK	50.61	55.7932	878.534	879.22	1	2	distinct	0	0.9078
FGSHNVYDHDASSTYK	105.31	54.1015	1826.786	1827.443	9	2	distinct	0	0.9994
FDGLFGLAFDTISVDHLK	93.05	53.7892	1994.015	1995.319	2	2	distinct	0	0.9984

The equivalent proteins include

jgi|Physo1_1|158318|C_scaffold_95000019	0	No title.

191. Group probability: 1.0000. Peptides of the group

VYADAVVNHMSGGGNDVLSHR	62.01	53.2805	2197.033	2197.983	3	+2,+3	distinct	0	0.9985
HSPYYTHSYTYGVNEYTK	92.87	53.279	2208.975	2209.873	1	2	distinct	0	0.9984
TGWAAPYIHYNSGTGWTTSPGQAITK	54.84	52.0528	2764.324	2765.768	1	3	distinct	0	0.96

The equivalent proteins include

jgi|Physo1_1|129859|estExt_fgenesh1_pg.C_90136	0	No title.

192. Group probability: 1.0000. Peptides of the group

AHHNTSQSDAAESELR	103.42	54.1806	1751.782	1751.944	5	+2,+3	distinct	0	1
ILGPESDFFANLVVDAVSSVK	82.75	53.325	2206.152	2206.484	6	2	distinct	0	0.9966

The equivalent proteins include

jgi|Physo1_1|109440|estExt_fgenesh1_pm.C_1070005	0	No title.

193. Group probability: 1.0000. Peptides of the group

ALHAQLAQLLADNQDGK	126.41	54.3085	1804.943	1805.049	2	2	distinct	0	0.9999
TQFTALLNAAAAHPVAAQSDVFK	60.95	52.9118	2370.233	2370.628	2	+2,+3	distinct	0	0.9989

The equivalent proteins include

jgi|Physo1_1|140120|estExt_fgenesh1_pg.C_820021	0	No title.

194. Group probability: 1.0000. Peptides of the group

AFTFTTHNGGTCWLK	71.93	54.2269	1739.809	1740.547	9	2	distinct	0	0.9888
MLKPLSCCSACSNFPGCR (01000000000000000000)	75.78	53.2939	2143.909	2144.284	13	+2,+3	distinct	0	0.9989
SGCNAFSWSDLNGGTCWFK	74.2	53.2504	2192.904	2193.612	2	2	distinct	0	0.9922

The equivalent proteins include

jgi|Physo1_1|135818|estExt_fgenesh1_pg.C_410009	0	No title.

195. Group probability: 1.0000. Peptides of the group

TYFVDGLHFSQK	60.43	54.9275	1440.704	1441.596	3	2	distinct	0	0.9653
WVLQHAMPIYEK (00000001000000)	74.16	54.8037	1513.775	1514.587	26	+1,+2	distinct	0	0.9987
KTYFVDGLHFSQK	66.81	54.809	1568.799	1569.437	5	+2,+3	distinct	1	0.9975

The equivalent proteins include

jgi|Physo1_1|135534|estExt_fgenesh1_pg.C_390021	0	No title.

196. Group probability: 1.0000. Peptides of the group

MYVFDGHCGVNEK	76.69	54.7798	1554.659	1555.028	2	2	distinct	0	0.992
LSAGQAQYHFLSGYTAK	91.74	54.1575	1840.911	1841.734	7	2	distinct	0	0.9982
GNHPNAVIFLTCDAYGVLPPVSK	71.84	52.7439	2468.252	2469.546	1	2	distinct	0	0.9917

The equivalent proteins include

jgi|Physo1_1|108707|estExt_fgenesh1_pm.C_260008	0	No title.

jgi|Physo1_1|108708|estExt_fgenesh1_pm.C_260009	0	No title.
jgi|Phyra1_1|71660|fgenesh1_pm.C_scaffold_35000007	0	No title.
jgi|Phyra1_1|71662|fgenesh1_pm.C_scaffold_35000009	0	No title.
jgi|Phyra1_1|71663|fgenesh1_pm.C_scaffold_35000010	0	No title.

197. Group probability: 1.0000. Peptides of the group

HEAVEVPNLQVIK	54.07	55.07	1474.814	1475.282	3	2	distinct	0	0.9413
SYLHLPAEIVPATLK	91.48	54.6425	1650.934	1652.162	4	2	distinct	0	0.998
SYLHLPAEIVPATLKK	98.28	54.1899	1779.029	1779.791	2	2	distinct	1	0.9989

The equivalent proteins include

jgi|Physo1_1|108449|estExt_fgenesh1_pm.C_100008	0	No title.

198. Group probability: 1.0000. Peptides of the group

YHGNGVVAQHGGEAKE	83.8	54.6287	1651.77	1652.662	1	2	distinct	1	0.9961
ISYSHNFLPENVETLIK	62.59	53.6891	2003.036	2004.334	2	2	distinct	0	0.9766
TILPHHATEECFPTIEK	67.35	54.0998	2021.988	2022.656	7	+2,+3	distinct	0	0.9986

The equivalent proteins include

jgi|Physo1_1|130464|estExt_fgenesh1_pg.C_110133	0	No title.

199. Group probability: 1.0000. Peptides of the group

VGQAVEIVGQAGRPK	79.26	54.6554	1507.847	1508.842	3	2	distinct	0	0.9941
SITGFQTHTTPVLLNVK	75.46	54.1052	1855.02	1855.359	9	2	distinct	0	0.9924
LLGNSTDLGSWGHEFVR	85.4	53.9998	1886.927	1888.008	2	2	distinct	0	0.9968

The equivalent proteins include

jgi|Physo1_1|109208|estExt_fgenesh1_pm.C_730004	0	No title.

200. Group probability: 1.0000. Peptides of the group

TFGHAPFTFK	56.45	55.334	1151.576	1152.031	4	2	shared(2)	0	0.9468
ITHHFGGSCYASSNTADSNR	89.04	53.2827	2180.929	2181.576	7	+2,+3	distinct	0	1
NLFDTNVVFASFSHPQMSSFQFK	55.27	52.1597	2677.263	2677.551	1	2	distinct	0	0.9651

The equivalent proteins include

jgi|Physo1_1|144141|estExt_fgenesh1_pg.C_1690006	0	No title.

201. Group probability: 1.0000. Peptides of the group

FHGIKPDQEK	53.11	55.5148	1197.614	1198.564	2	2	distinct	0	0.9284
HLSAFGLALQR	59.71	55.3975	1211.677	1212.656	1	2	distinct	0	0.9613
LVGQFPNHLPAMQAK	58.77	54.7327	1649.871	1650.987	4	2	distinct	0	0.9635
FITPPAGATWADIIFTR	94.35	54.078	1875.988	1877.247	2	2	distinct	0	0.9985

The equivalent proteins include

jgi|Physo1_1|137699|estExt_fgenesh1_pg.C_560073	0	No title.

202. Group probability: 1.0000. Peptides of the group

FQPALDLITELLYEIK	118.73	54.0038	1905.05	1905.905	12	2	distinct	0	0.9998
TYTSGLGVIENVGHIVDNLFR	97.96	53.0916	2303.191	2303.423	7	2	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|108149|estExt_fgenesh1_pm.C_10014	0	No title.

203. Group probability: 1.0000. Peptides of the group

AGMTHIMR	70.54	56.7354	915.442	915.808	7	2	distinct	0	0.9836
KSLLVHTK	65.66	55.2432	924.576	925.126	2	2	shared(2)	1	0.8739
APHLTAFMGYK	68.42	55.4349	1234.617	1234.323	4	1	distinct	0	0.982
VACIGAWHPSR	70.32	55.4274	1252.613	1253.064	9	2	shared(3)	0	0.9847
DDASKAPHLTAFMGYK	48.59	54.2254	1750.835	1750.943	1	3	distinct	1	0.7348
DITPLGGFPHYGIINEDWLMIK	54.43	52.5457	2528.277	2528.36	2	2	distinct	0	0.9608

The equivalent proteins include

jgi|Physo1_1|109017|estExt_fgenesh1_pm.C_520010	0	No title.

204. Group probability: 1.0000. Peptides of the group

RVTLEIGGK	51.91	56.3835	971.576	972.261	3	2	shared(3)	1	0.8721
VGELIVEAGFPK	78.95	55.5194	1257.697	1258.863	1	2	shared(3)	0	0.9931
IHGSVIPISGPYLCYTK	62.15	53.9742	1903.987	1905.377	4	2	distinct	0	0.9755
GWFIEPTVFADVTDDMTIAR (0000000000000000100000)	97.86	53.0271	2283.088	2284.084	13	2	shared(3)	0	0.9991
TGTVYYVNCYDVFDSNTPFGGFK	97.26	52.6314	2487.105	2488.234	1	2	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|109263|estExt_fgenesh1_pm.C_810010	0	No title.

205. Group probability: 1.0000. Peptides of the group

KALAPYLQLTNAVR	57.35	54.7655	1556.904	1558.097	1	2	distinct	1	0.9578
VGNLEDFNVVLAQHGPVFK	72.76	53.5975	2082.09	2082.195	1	2	distinct	0	0.9911
TLSVAQLQQAVEQLLPSQNASKPALLALLAK	102.29	51.1066	3242.86	3243.775	4	3	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|136709|estExt_fgenesh1_pg.C_470123	0	No title.

206. Group probability: 1.0000. Peptides of the group

KVLAVTDPMLK	66.3	55.6655	1213.71	1214.831	5	+1,+2	distinct	1	0.999
KAALENIFLVK	73.25	55.9258	1244.749	1245.954	4	2	shared(2)	1	0.9881
SLFSEANPQPIKK	67.04	55.0401	1457.788	1458.784	9	2	shared(2)	1	0.9812
TNVNLSPQTIAELNKLPNIVAIK	84.88	52.4278	2489.422	2490.89	12	+2,+3	shared(2)	1	0.9998

The equivalent proteins include

jgi|Physo1_1|108407|estExt_fgenesh1_pm.C_90003	0	No title.

207. Group probability: 1.0000. Peptides of the group

KLFNITK	53.64	56.3341	862.528	863.13	4	2	distinct	1	0.8647
VLEVDDEHKLR	84.67	55.1629	1351.71	1351.921	11	2	distinct	1	0.9957
GCIVGPDLSVLNLVVVK	110.38	54.3593	1781.012	1781.607	8	2	distinct	0	0.9996

The equivalent proteins include

jgi|Physo1_1|108459|estExt_fgenesh1_pm.C_100018	0	No title.
jgi|Phyra1_1|38589|gwEuk.1.88.1	0	No title.

208. Group probability: 1.0000. Peptides of the group

KLQVTTHGR	61.11	55.2727	1038.593	1039.622	5	2	distinct	1	0.9637
SAVVDHNVALSYR	58.69	55.0617	1429.731	1430.17	2	2	distinct	0	0.9609
LSGSFTHASSGVVFK	72.18	54.6717	1522.778	1523.848	5	2	distinct	0	0.9889
LSGSFTHASSGVVFKK	68.87	54.644	1650.873	1651.599	6	2	distinct	1	0.9857

The equivalent proteins include

jgi|Physo1_1|141610|estExt_fgenesh1_pg.C_1010023	0	No title.

209. Group probability: 1.0000. Peptides of the group

LNAVSELAPISWPEFTNVHPFVPK	45.56	52.1095	2691.406	2692.148	1	2	distinct	0	0.9212
HILENPGWYTSYTPYQAEVSQGR	59.09	52.1241	2695.267	2696.596	3	+2,+3	distinct	0	0.9992
ATSNICTAQALLANMAAAYAIYHGPEGLDK	80.06	51.1254	3134.516	3135.456	1	3	distinct	0	0.9963

The equivalent proteins include

jgi|Physo1_1|109239|estExt_fgenesh1_pm.C_790001	0	No title.

210. Group probability: 1.0000. Peptides of the group

GIQAATSHMLGQNFGK	105.14	55.0121	1658.82	1659.424	4	2	distinct	0	0.9994
EKEHLEGFAPEVAWVTK	75.72	53.7897	1968.994	1969.338	2	2	distinct	1	0.9926
ALVDAAQVNCHPLRNDQTYSLK	53.41	52.5813	2512.249	2513.569	2	3	distinct	1	0.9472

The equivalent proteins include

jgi|Physo1_1|132096|estExt_fgenesh1_pg.C_190046	0	No title.

211. Group probability: 1.0000. Peptides of the group

KVSLGVGAYR	80.5	55.7254	1048.603	1049.288	2	2	distinct	1	0.9935
ITGVQTISGTGGVR	58.48	55.4701	1344.736	1345.284	1	2	distinct	0	0.9612
EGHNIFLSQSYAK	47.08	54.6663	1492.731	1493.448	2	2	distinct	0	0.8926
HVPFFDCAYQGFASGDATR	72.92	53.3074	2144.937	2145.452	4	2	distinct	0	0.9912

The equivalent proteins include

jgi|Physo1_1|108281|estExt_fgenesh1_pm.C_40032	0	No title.

212. Group probability: 1.0000. Peptides of the group

SRDLLHPSAAEEASK	87.65	54.4781	1609.806	1610.336	5	2	distinct	1	0.9972
RLVQAPNSYFMDVK (0000000000010000)	88.99	54.4021	1666.85	1667.504	18	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|111303|estExt_Genewise1.C_50149	0	No title.

213. Group probability: 1.0000. Peptides of the group

LGGSGCQHVPIPTDNYVSDK	68.09	53.2951	2143	2144.166	5	+2,+3	distinct	0	0.999
LGGSGCQHVPIPTDNYVSDKR	49.86	53.1137	2299.101	2300.32	2	+2,+3	distinct	1	0.9922
LLATTTDFADYFPTDHNGVDATDVVFWR	56.51	50.9911	3186.493	3187.825	1	3	distinct	0	0.9685

The equivalent proteins include

jgi|Physo1_1|132826|estExt_fgenesh1_pg.C_220174	0	No title.

214. Group probability: 1.0000. Peptides of the group

FFEHYLEAK	58.96	55.8441	1182.571	1183.717	1	2	distinct	0	0.9556

ILHLVDPVDKK	55.43	55.526	1275.755	1276.179	3	2	distinct	1	0.9436
GEYDGHHVCIHIDR	45.74	54.5357	1706.758	1707.536	1	2	distinct	0	0.8837
TLPVTNDVEGVAQGFPFLVYPCRPGIAQGISR	95.01	50.2884	3457.782	3458.399	1	3	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|136340|estExt_fgenesh1_pg.C_450031	0	No title.

215. Group probability: 1.0000. Peptides of the group

VQVTPVIRPK	48.82	55.377	1135.708	1136.337	3	2	distinct	0	0.8959
MPNVGYGSNKK	44.73	55.2442	1193.586	1194.34	1	2	distinct	1	0.8566
KYCAEIAHNVSGR	106.64	54.8192	1503.725	1504.504	19	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|109525|estExt_fgenesh1_pm.C_1260005	0	No title.

216. Group probability: 1.0000. Peptides of the group

HVTQAVVTVPAYFNDSQR	105.63	53.6056	2031.017	2031.48	6	2	distinct	0	0.9946
DILLLDVTPLSLGIETLGGVFTK	122.84	52.8901	2413.372	2413.876	136	2	distinct	0	0.9963
AQQGEGAASDDSKDENVHDAEFK	65.97	52.6037	2447.047	2448.163	1	3	distinct	1	0.9831

The equivalent proteins include

jgi|Physo1_1|108503|estExt_fgenesh1_pm.C_120013	0	No title.

217. Group probability: 1.0000. Peptides of the group

NPGHPLEQFIPLLK	69.26	55.0004	1601.893	1603.234	1	2	distinct	0	0.9851
NVAAMSLELGLPTLASIPHSIANAFK (00000100000000000000000000)	78.87	52.1443	2664.431	2680.701	36	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109515|estExt_fgenesh1_pm.C_1240001	0	No title.

218. Group probability: 1.0000. Peptides of the group

HFVGYSK	48.7	55.2606	836.418	837.687	4	+1,+2	distinct	0	0.9808
TYETFGEDPYLCSVLGDAIIR	84.8	52.7054	2418.141	2419.423	3	2	distinct	0	0.9972
DTEAAGIPWIFGPILDLAQNPLWAR	73.61	52.0249	2763.438	2764.321	8	2	distinct	0	0.9935

The equivalent proteins include

jgi|Physo1_1|133710|estExt_fgenesh1_pg.C_270122	0	No title.

219. Group probability: 1.0000. Peptides of the group

HAWADKR	45.36	55.0111	882.446	883	1	2	shared(2)	1	0.84
GSNYILVAGGIHDVGPR	46.11	54.2532	1723.9	1724.968	2	2	distinct	0	0.8994
KPYLFGEHVVYATTDDGGK	97.06	53.7372	2096.021	2096.058	7	+2,+3	distinct	0	0.9999
DINDVDSHLVGKGDWIVSDSK	68.51	53.0716	2298.113	2299.533	1	3	shared(2)	1	0.9853

The equivalent proteins include

jgi|Physo1_1|137802|estExt_fgenesh1_pg.C_570067	0	No title.

220. Group probability: 1.0000. Peptides of the group

ISCHVTIR	60.18	56.4314	984.517	985.089	5	2	distinct	0	0.9596
FEGIVLDEPRK	66.67	55.4951	1301.698	1303.143	1	2	distinct	1	0.979
VLEQLTGQKPVYSK	73.63	54.7722	1588.882	1589.463	6	2	distinct	0	0.9899
LVINCCVGESGDKLTR	54.86	54.2845	1819.892	1820.108	1	2	distinct	1	0.9516

The equivalent proteins include

jgi|Physo1_1|108498|estExt_fgenesh1_pm.C_120008	0	No title.

221. Group probability: 1.0000. Peptides of the group

RTPFGNFGGK	50.97	55.2717	1079.551	1080.319	4	2	distinct	1	0.914
ELQIDPEIVNQAGGAIALGHPLGASGSR	41.51	52.2004	2769.441	2770.387	1	3	distinct	0	0.8798
VVSYQVSGVDPTIMGIGPVPAITGALKR	100.71	51.938	2824.552	2825.896	10	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|109594|estExt_fgenesh1_pm.C_1540002	0	No title.

222. Group probability: 1.0000. Peptides of the group

VGIDSPLAGAGKK	65.46	55.3316	1211.687	1211.927	18	+1,+2,+3	distinct	1	0.9999
DLNPAYFHIAAANILGK	96.39	54.1296	1826.968	1827.611	10	2	distinct	0	0.9942

The equivalent proteins include

jgi|Physo1_1|142753|estExt_fgenesh1_pg.C_1210020	0	No title.

223. Group probability: 1.0000. Peptides of the group

VAIITLNRPK	64	55.2734	1123.708	1124.61	23	2	distinct	0	0.9512
EGMAAFVEKR	69.21	55.3396	1136.565	1137.496	1	2	distinct	1	0.8594
VVPADQLLDEALK	77.34	54.9849	1409.777	1411.029	2	2	distinct	0	0.9924
VSKPVIAAVNGYALGGGCELAMLCDLIIAGDSAK	68.34	50.2688	3432.745	3433.488	9	3	distinct	0	0.9911

The equivalent proteins include

jgi|Physo1_1|108294|estExt_fgenesh1_pm.C_50009	0	No title.

224. Group probability: 1.0000. Peptides of the group

WEYMNKPAPGSWEEK	66.34	54.021	1850.83	1851.639	7	2	distinct	0	0.9818
KIGWFGGGADLTPSYLFEEDAR	104.44	52.7705	2428.17	2428.844	9	2	distinct	1	0.9995
TLDVLKNPVDWLDVPAVDLEALSTGDLLK	48.25	51.3786	3148.691	3149.923	2	3	distinct	1	0.9368

The equivalent proteins include

jgi|Physo1_1|132630|estExt_fgenesh1_pg.C_210190	0	No title.

225. Group probability: 1.0000. Peptides of the group

HYGALTGLNK	64.39	56.1141	1072.566	1073.339	9	+1,+2	shared(4)	0	0.998
IVIAAHGNSLR	56.51	55.3959	1149.662	1150.474	2	2	distinct	0	0.9091
FTGWHDVQLSEK	64	55.1264	1445.694	1446.904	2	2	distinct	0	0.9745
HYGALTGLNKQETVDK	94.29	54.2751	1772.906	1773.271	7	2	distinct	1	0.9985

The equivalent proteins include

jgi|Physo1_1|108887|estExt_fgenesh1_pm.C_390003	0	No title.

226. Group probability: 1.0000. Peptides of the group

VLVSVQEHIQR	86.9	55.3909	1306.736	1308.047	3	2	shared(2)	0	0.9964
RGMLAYVEGVQR	49.31	55.1072	1377.719	1378.413	1	2	shared(2)	1	0.9077
ISQIASHLSSHDPR	73.9	55.1267	1546.785	1547.428	3	2	distinct	0	0.99
AYGEYADLIWMETAKPGVPLAR (000000000001000000000000)	89.94	52.5642	2450.23	2451.625	3	2	shared(2)	0	0.9983
TPPTDFLRPIVADADTGHGGLTAVMK	75.09	52.1444	2679.369	2680.59	3	3	shared(2)	0	0.9932

The equivalent proteins include

jgi|Phyra1_1|71756|fgenesh1_pm.C_scaffold_44000012	0	No title.

227. Group probability: 1.0000. Peptides of the group

LFLAPWSPPAWMK (000000000000100)	68.44	54.8519	1542.806	1544.145	14	2	distinct	0	0.9775
YVDGMAFHWYEDGGER	68.26	53.8681	1930.794	1931.672	2	2	distinct	0	0.9852
VQVTNTPFCLNLVPTASEGHEVR	47.87	52.4683	2567.28	2568.595	1	3	distinct	0	0.9174
VTADKCEDEVVPHQQWTFNAEDGTLR	60.99	51.2539	3044.393	3045.428	1	3	distinct	1	0.9771

The equivalent proteins include

jgi|Physo1_1|138213|estExt_fgenesh1_pg.C_610047	0	No title.

228. Group probability: 1.0000. Peptides of the group

VLSALPGVHIR	50.83	55.6829	1160.703	1161.536	1	2	distinct	0	0.9153
EQQAGLIWQHLFVDR	72.08	53.9755	1838.943	1839.311	1	2	distinct	0	0.989
HWLGDPASNTPPPAWSR	75.23	54.0001	1887.902	1888.232	4	2	distinct	0	0.9922
VDQILLGDWASIGPTLDVFK	46.14	53.3093	2186.162	2186.787	1	2	distinct	0	0.9115

The equivalent proteins include

jgi|Physo1_1|131558|estExt_fgenesh1_pg.C_160102	0	No title.

229. Group probability: 1.0000. Peptides of the group

GVCPFHGDCIEGMVASGSIAAR	49.02	53.1769	2290.029	2291.125	1	3	distinct	0	0.9215
SPTYGYITSTPKPNWGNTDVVGVFK	70.23	52.0485	2727.354	2728.678	8	+2,+3	distinct	0	0.9995
KSPTYGYITSTPKPNWGNTDVVGVFK	64.23	51.8895	2855.449	2856.86	1	3	distinct	1	0.9825

The equivalent proteins include

jgi|Physo1_1|158834|C_scaffold_159000001	0	No title.
jgi|Physo1_1|158835|C_scaffold_159000002	0	No title.

230. Group probability: 1.0000. Peptides of the group

KIEFISFK	49.73	55.3025	1010.58	1010.471	3	1	distinct	1	0.6859
GEPGLVFTHGK	52.16	55.6519	1140.593	1141.495	2	2	distinct	0	0.9246
TAAALTLTHKPK	74.8	55.4689	1250.735	1251.19	9	2	distinct	0	0.9901
VTHVSNLFHSK	46.04	55.438	1267.667	1268.585	1	2	distinct	0	0.8717
EAFMPLVPGVHYAEFNDIESVK	59.65	52.4511	2491.209	2491.453	2	2	distinct	0	0.9752

The equivalent proteins include

jgi|Physo1_1|130851|estExt_fgenesh1_pg.C_130042	0	No title.

231. Group probability: 1.0000. Peptides of the group

VDLTPNYGSSHPWEICK	74.13	53.7754	2001.925	2002.378	3	2	distinct	0	0.9915
SLEELYADAVAEGGNLVMYHGGDFK	89.78	52.1388	2684.243	2684.492	17	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|108716|estExt_fgenesh1_pm.C_270001	0	No title.
jgi|Physo1_1|133594|estExt_fgenesh1_pg.C_270006	0	No title.

232. Group probability: 1.0000. Peptides of the group

LSQLHFLLR	62.37		55.5153	1125.666	1126.528	5	2	distinct	0	0.9213
HQHSGASTLGEPDAAAAK	99.96		54.2954	1746.828	1746.686	6	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|109023|estExt_fgenesh1_pm.C_530005	0	No title.

233. Group probability: 1.0000. Peptides of the group

IADNKDSFDWGCSHSGYER	62.6		53.2739	2242.934	2243.359	2	2	distinct	1	0.9784
VPMNDFADIYADKNGFVILGTR	74.96		52.7999	2455.22	2456.164	1	3	distinct	1	0.992
APHLAPIGNDGMLAMWEGSSSGGDLQEGGDR	77.15		51.1782	3124.398	3125.848	4	3	distinct	0	0.9954

The equivalent proteins include

jgi|Physo1_1|135613|estExt_fgenesh1_pg.C_390100	0	No title.

234. Group probability: 1.0000. Peptides of the group

RPAIETVR	66.47		56.1023	940.545	941.91	4	2	distinct	0	0.941
YGVDANTQSFMGHAMALMR	100.51		53.4605	2098.939	2099.294	3	2	distinct	0	0.9992
VLIVDRNPYYGGECASPNLTNLYK	65.07		52.0893	2755.364	2756.559	3	3	distinct	1	0.9825

The equivalent proteins include

jgi|Physo1_1|109350|estExt_fgenesh1_pm.C_930005	0	No title.

235. Group probability: 1.0000. Peptides of the group

FAVGNAEHTTK	60.67		55.858	1173.578	1174.123	1	2	distinct	0	0.9641
KHDASIDEHVK	62.4		55.5152	1277.636	1278.547	5	2	distinct	1	0.9694
TQVVHASSSTYGTVK	57.44		54.9217	1563.789	1564.03	1	2	distinct	0	0.9595
TLFDIDEAWVGPGLNALDNK	63.43		53.3357	2187.085	2187.781	2	2	distinct	0	0.9806

The equivalent proteins include

jgi|Physo1_1|156530|C_scaffold_21000020	0	No title.

236. Group probability: 1.0000. Peptides of the group

LLDLNHEELMDLVNAR (000000000010000000)	109.09		53.9457	1893.962	1895.345	15	+2,+3	distinct	0	1
NMIIVPEMIGSVVGVYNGK	60.26		53.6898	2019.053	2019.174	1	2	distinct	0	0.9732

The equivalent proteins include

jgi|Physo1_1|109596|estExt_fgenesh1_pm.C_1540004	0	No title.
jgi|Phyra1_1|71479|fgenesh1_pm.C_scaffold_22000002	0	No title.

237. Group probability: 1.0000. Peptides of the group

LLQLISRPLPEGEASILR	66.19		53.7099	2004.173	2004.931	13	+2,+3	distinct	0	0.9991
VLLAALQAPLEQFNPALHTAQR	96.32		52.8475	2400.328	2400.726	4	2	distinct	0	0.999

The equivalent proteins include

jgi|Physo1_1|108858|estExt_fgenesh1_pm.C_360012	0	No title.

238. Group probability: 1.0000. Peptides of the group

AQDVDHELPMKPITMMR	44.96		53.6358	2010.969	2011.416	2	+2,+3	distinct	0	0.9825
LNMVAITQANAHMLMSDYEAR	79.79		52.8059	2378.118	2379.35	3	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|138196|estExt_fgenesh1_pg.C_610030	0	No title.

239. Group probability: 1.0000. Peptides of the group

YTDFATAFADAGHSWSTDFCGK	119.54		52.7452	2454.022	2454.586	11	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|137332|estExt_fgenesh1_pg.C_530025	0	No title.

240. Group probability: 1.0000. Peptides of the group

FFLGTDSAPHVASK	78.12		54.9032	1475.741	1476.298	1	2	distinct	0	0.9932
KFFLGTDSAPHVASK	80.04		54.6564	1603.836	1604.521	3	+2,+3	distinct	1	0.9998

The equivalent proteins include

jgi|Physo1_1|108496|estExt_fgenesh1_pm.C_120006	0	No title.

241. Group probability: 1.0000. Peptides of the group

KIIAESGIK	50.47		56.797	957.586	958.811	1	2	distinct	1	0.7481
LNLHEFQSLEIMK	71.99		55.0459	1600.828	1602.188	1	2	distinct	0	0.9878
GGVHMCTKPEQAEDFAK	69.37		54.0184	1903.856	1904.426	11	2	distinct	0	0.987
LNLHEFQSLEIMKDFGVATPQGIPADTPAEAK	56.91		50.4278	3466.744	3467.412	1	3	distinct	1	0.9739

The equivalent proteins include

jgi|Physo1_1|108575|estExt_fgenesh1_pm.C_160014	0	No title.

242. Group probability: 1.0000. Peptides of the group

LFANALATALHVQNK	101.05		54.5313	1609.894	1610.952	6	2	distinct	0	0.9991

AMYPHDVALVYEVK	69.17	54.7589	1633.817	1634.694	1	2	distinct	0	0.985
VSEQQKLPAGQTFTLQQAIK	49.3	53.1898	2214.201	2215.116	1	3	distinct	1	0.9177

The equivalent proteins include

jgi|Physo1_1|137070|estExt_fgenesh1_pg.C_500106	0	No title.

243. Group probability: 1.0000. Peptides of the group

YLTHILTMR	45.12	55.8155	1146.622	1147.499	2	2	distinct	0	0.8506
RSELVQDVAGDTAGTTFFR	90.7	53.5154	2069.018	2069.686	6	+2,+3	distinct	1	1

The equivalent proteins include

jgi|Physo1_1|127310|estExt_fgenesh1_pg.C_10290	0	No title.

244. Group probability: 1.0000. Peptides of the group

HPEVQQEIAQLAYK	51.73	54.3769	1652.852	1653.688	1	2	distinct	0	0.9315
DYNSQVTLEEFEELIAPLLTR	71.91	52.5677	2479.248	2479.683	10	2	distinct	0	0.9912
HLAEVLGLDKEQQNYGLSTTLNADESVAR	87.58	50.9796	3170.584	3171.876	1	3	distinct	1	0.998

The equivalent proteins include

jgi|Physo1_1|144810|estExt_fgenesh1_pg.C_2700005	0	No title.

245. Group probability: 1.0000. Peptides of the group

LFQVEYAMEAINNAGSAVGILAK	83.6	52.7966	2408.241	2408.587	2	2	distinct	0	0.9971
LDDHLICAVAGLTSDANILVNYAR	104.51	52.4715	2613.322	2613.857	6	2	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|109494|estExt_fgenesh1_pm.C_1190007	0	No title.

246. Group probability: 1.0000. Peptides of the group

KLAEVWGSDLPR	65.14	55.239	1369.735	1371.209	2	2	distinct	1	0.9769
TLFVASIEDSPKPPPQR	92.26	54.0823	1881	1881.586	3	2	distinct	0	0.9982
TPPLPAANVKPTDGVVYWFIDEDAAAK	56.18	51.6963	2884.465	2885.83	3	3	distinct	0	0.9659

The equivalent proteins include

jgi|Physo1_1|132192|estExt_fgenesh1_pg.C_190142	0	No title.
jgi|Phyra1_1|54920|gwEuk.98.32.1	0	No title.

247. Group probability: 1.0000. Peptides of the group

IQHSALWENQALR	77.5	54.7083	1564.811	1564.984	2	2	distinct	0	0.9925
GGIPHDVYGMTTHSVR	77.84	54.2916	1725.826	1725.817	6	2	distinct	0	0.9935
LNTYTESQILDHILSSAEIVK	58.12	52.8752	2373.243	2373.6	1	2	distinct	0	0.9704

The equivalent proteins include

jgi|Physo1_1|143791|estExt_fgenesh1_pg.C_1510027	0	No title.

248. Group probability: 1.0000. Peptides of the group

EHIILAR	50.08	56.0207	850.502	850.484	13	+1,+2	distinct	0	0.9756
GQVLCKPGTINPHTK	71.26	54.6431	1648.872	1649.023	1	2	distinct	0	0.9276
DFEKPFLMPVEDVFSISGR	68.55	53.198	2212.087	2212.759	6	+2,+3	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|109196|estExt_fgenesh1_pm.C_720005	0	No title.
jgi|Phyra1_1|71305|fgenesh1_pm.C_scaffold_12000014	0	No title.

249. Group probability: 1.0000. Peptides of the group

HLGLLDNWLR	54.66	55.2568	1235.677	1236.454	3	2	distinct	0	0.9378
VPAEEITGLAPGEMFVHR	84.83	53.769	1951.982	1952.672	8	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|143382|estExt_fgenesh1_pg.C_1370031	0	No title.

250. Group probability: 1.0000. Peptides of the group

SDIISLHCPLFPSTK	74.74	54.3367	1713.876	1715.263	1	2	shared(2)	0	0.9912
VPAYSPYAVAEHAAALMMTLNR (0000000000000000001100000)	82.95	52.8484	2375.177	2376.169	5	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Phyra1_1|71424|fgenesh1_pm.C_scaffold_18000015	0	No title.
jgi|Phyra1_1|76504|fgenesh1_pg.C_scaffold_18000135	0	No title.

251. Group probability: 1.0000. Peptides of the group

NAIGAHGGSYCIYR	65.08	54.6706	1537.71	1538.472	4	2	distinct	0	0.9786
AHMDFPEIHEAVR	52.2	54.686	1550.73	1551.651	1	2	distinct	0	0.9314
IVTIDPFGACVVEAFPEHFQK	95.05	52.7781	2403.193	2403.928	1	2	distinct	0	0.9988

The equivalent proteins include

jgi|Phyra1_1|53364|gwEuk.8.163.1	0	No title.

252. Group probability: 1.0000. Peptides of the group

AGKPQEVTVYVSPVVVK	62.85	54.3396	1799.019	1799.457	2	2	shared(2)	0	0.9768
HSNVIASISGATNLVNVR	65.63	54.0208	1850.996	1852.058	1	2	shared(2)	0	0.9826
LGFGGVVKPADIPTVGISR	81.6	53.9662	1882.068	1882.753	18	+2,+3	shared(2)	0	0.9999
ALVANFMPEIVQLLQEHPDVR	83.75	52.7057	2418.273	2419.24	3	2	distinct	0	0.9442
SDNLDSSAYVGPGAGRFPTANSVMNDIIQLAR	57.3	50.7389	3335.62	3336.947	1	3	shared(2)	1	0.9747

The equivalent proteins include

jgi|Phyra1_1|73390|fgenesh1_pg.C_scaffold_3000147	0	No title.

253. Group probability: 1.0000. Peptides of the group

LSVGESLTNMVWAALGGR	85.34	54.0912	1859.956	1861.387	2	2	distinct	0	0.9969
MTQQVYDKPLASFWHGK	55.62	54.3176	2034.999	2036.428	2	2	distinct	0	0.9563
TLDSHLLLTAETHNFPSGVAPFPGAETGTGGR	64.45	50.8752	3249.605	3250.199	3	3	distinct	0	0.9864

The equivalent proteins include

jgi|Physo1_1|108492|estExt_fgenesh1_pm.C_120002	0	No title.

254. Group probability: 1.0000. Peptides of the group

LNVAIKPEGSEK	52.86	55.37	1283.708	1284.93	1	2	distinct	0	0.932
RPYGQLQADKTDPSK	62.39	54.4033	1702.864	1703.295	3	+2,+3	distinct	1	0.9965
NFATTISPWVVPLAALEPFR	73.84	53.2915	2228.199	2229.183	9	2	distinct	0	0.9922

The equivalent proteins include

jgi|Physo1_1|108641|estExt_fgenesh1_pm.C_220002	0	No title.

255. Group probability: 1.0000. Peptides of the group

IFAVHVAEHMK	56.79	55.2185	1280.67	1281.752	1	2	distinct	0	0.9502
VHEAIREDPSPAAK	53.35	54.9392	1518.779	1519.143	3	2	distinct	1	0.9399
GAADAGLDIPHSEKR	62.77	54.7359	1535.769	1536.139	9	+2,+3	distinct	1	0.996
TYFVEEVADEKRPFR	44.35	53.9338	1884.937	1886.351	1	3	distinct	1	0.846

The equivalent proteins include

jgi|Physo1_1|108494|estExt_fgenesh1_pm.C_120004	0	No title.

256. Group probability: 1.0000. Peptides of the group

HAGIFIAR	45.61	55.4753	883.503	883.448	1	1	distinct	0	0.514
IVALNASHFLK	71.69	55.3975	1211.703	1212.584	4	2	distinct	0	0.9865
DHAVVVGAYRVPK	58.8	54.9846	1409.778	1410.487	1	2	distinct	1	0.9613
KLQQEQFKPAEQLTLEPYER	51.94	52.611	2474.28	2474.379	4	+2,+3	distinct	1	0.9926

The equivalent proteins include

jgi|Physo1_1|111761|estExt_Genewise1.C_70003	0	No title.

257. Group probability: 1.0000. Peptides of the group

NFPSLIEHCIEWSR	57.7	54.7296	1786.846	1787.891	2	2	distinct	0	0.9591
ILQLIHNFPEDHLTNSGEK	93.24	53.2703	2204.123	2204.359	7	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|157877|C_scaffold_66000007	0	No title.

258. Group probability: 1.0000. Peptides of the group

YAQVMTATLACDHR	88.04	54.6888	1635.75	1635.956	1	2	distinct	0	0.9971
LEVPHYHLSTNLTLDK	76.27	54.2333	1878.984	1879.748	10	+2,+3	distinct	0	0.9992

The equivalent proteins include

jgi|Physo1_1|110502|estExt_Genewise1.C_30032	0	No title.
jgi|Phyra1_1|71589|fgenesh1_pm.C_scaffold_29000008	0	No title.

259. Group probability: 1.0000. Peptides of the group

KVYIEDIR	45.12	55.6972	1034.576	1035.273	3	2	distinct	1	0.851
YLLGTSLARPVIAK	69.01	55.1134	1500.903	1501.536	13	2	distinct	0	0.9847
HAHLDLEGLCMDR	46.55	54.608	1565.708	1566.965	1	3	distinct	0	0.8618
TPELTGALDLFLELNK	75.89	54.3236	1772.956	1774.37	1	2	distinct	0	0.9923

The equivalent proteins include

jgi|Physo1_1|108409|estExt_fgenesh1_pm.C_90005	0	No title.

260. Group probability: 1.0000. Peptides of the group

AVMHMALR	50.54	56.7414	927.478	928.136	4	2	shared(5)	0	0.9054
FLAGAHAMDK (000000001000)	67.37	56.0609	1059.517	1060.198	9	2	shared(4)	0	0.9477
ANIFGFWDWVGGR	81.96	54.634	1523.731	1524.464	7	2	shared(4)	0	0.9938
FAAHIQQVDMESNGER	79.62	54.1089	1830.832	1831.328	5	2	distinct	0	0.963
KLQAIASGEHVNATEDR	112.31	53.9721	1837.928	1839.353	12	+2,+3	shared(3)	1	1
HMVAASSAVPLVQQFGIDR	63.53	53.5552	2025.047	2026.423	1	2	shared(3)	0	0.9799
YSVTSAVGILPLALQYGFDITEK	71.42	52.7225	2484.315	2485.376	2	2	shared(4)	0	0.9914

The equivalent proteins include

gi|37960095|gb|AAP51072.1|	60840.39	glucose-6-phosphate isomerase [Phytophthora infestans]

261. Group probability: 1.0000. Peptides of the group

VVLQQFHATPGAKDEK	70.35	54.209	1766.931	1767.258	1	2	distinct	1	0.9876
AYVCHQSKPEIEASR	72.51	54.3044	1773.847	1774.332	4	2	distinct	0	0.9893
KQPELYSQFDAEGLPTHNAAGEELTK	62.65	51.6805	2872.388	2873.07	2	3	distinct	1	0.98

The equivalent proteins include

jgi|Physo1_1|136103|estExt_fgenesh1_pg.C_430036	0	No title.

262. Group probability: 1.0000. Peptides of the group

VLVSVQEHIQR	86.9	55.3909	1306.736	1308.047	3	2	shared(2)	0	0.9964
RGMLAYVEGVQR	49.31	55.1072	1377.719	1378.413	1	2	shared(2)	1	0.9077
GAAGIHLEDQKPGTKK	54.95	54.5729	1648.89	1649.548	2	2	distinct	1	0.9517
AYGEYADLIWMETAKPGVPLAR (000000000001000000000000)	89.94	52.5642	2450.23	2451.625	3	2	shared(2)	0	0.9983
TPPTDFLRPIVADADTGHGGLTAVMK	75.09	52.1444	2679.369	2680.59	3	3	shared(2)	0	0.9932

The equivalent proteins include

jgi|Physo1_1|109161|estExt_fgenesh1_pm.C_660003	0	No title.

263. Group probability: 1.0000. Peptides of the group

SMLDKHPEQEAR	73.44	54.8359	1439.683	1439.998	3	2	distinct	1	0.9889
YVVAIKPDTWCDVYWGGAK	82.94	53.1425	2227.077	2227.122	4	2	distinct	0	0.9964
DTEAAGIPWIFGPILDISQNTLWAR	45.52	52.0734	2783.428	2784.789	1	2	distinct	0	0.9237

The equivalent proteins include

jgi|Physo1_1|142760|estExt_fgenesh1_pg.C_1210027	0	No title.

264. Group probability: 1.0000. Peptides of the group

LVIIANNTPPLRK	55.82	55.0069	1447.887	1448.852	15	2	shared(2)	1	0.9497
TGVHHFTGNNNDLGTACGK	97.56	53.7584	1998.897	1999.496	20	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108147|estExt_fgenesh1_pm.C_10012	0	No title.

265. Group probability: 1.0000. Peptides of the group

FSHLAWINTPR	56.59	55.2664	1340.699	1341.333	3	2	shared(2)	0	0.9493
KLGCEVLGCSVDSK	81.41	54.6543	1550.743	1551.343	2	2	distinct	1	0.9949
LVEAFQFTDEHGEVCPAGWK	85.65	53.0081	2319.063	2319.419	1	2	distinct	0	0.9972

The equivalent proteins include

jgi|Physo1_1|108745|estExt_fgenesh1_pm.C_290008	0	No title.
jgi|Phyra1_1|44662|gwEuk.2169.13.1	0	No title.
jgi|Phyra1_1|71852|fgenesh1_pm.C_scaffold_55000003	0	No title.
jgi|Phyra1_1|71853|fgenesh1_pm.C_scaffold_55000004	0	No title.
jgi|Phyra1_1|71854|fgenesh1_pm.C_scaffold_55000005	0	No title.
jgi|Phyra1_1|72527|fgenesh1_pm.C_scaffold_2098000001	0	No title.
jgi|Phyra1_1|72535|fgenesh1_pm.C_scaffold_2169000003	0	No title.

266. Group probability: 1.0000. Peptides of the group

LAGTQVFGHSGK	91.58	55.8032	1200.625	1201.161	10	2	distinct	0	0.9977
LDHGVLAVGYGNDNGQK	93.55	54.2238	1755.854	1756.144	3	2	distinct	0	0.9984

The equivalent proteins include

jgi|Physo1_1|142383|estExt_fgenesh1_pg.C_1130020	0	No title.

267. Group probability: 1.0000. Peptides of the group

RWAGSAFGGFK	63.54	55.8441	1182.593	1183.381	2	2	distinct	1	0.9721
VGDHVVPCYTPQCR	50.94	54.4566	1686.761	1687.73	2	2	distinct	0	0.9264
FDLPQINEAFHAMHQGDCIR	55.63	52.8182	2398.095	2399.348	1	3	distinct	0	0.9531
SGADPEGIFPVIMGHEGAGIVESVGPDVTSLK	52.96	51.4626	3164.57	3165.533	1	3	distinct	0	0.9624

The equivalent proteins include

jgi|Physo1_1|108408|estExt_fgenesh1_pm.C_90004	0	No title.

268. Group probability: 1.0000. Peptides of the group

LIVAILPSFGER	45.66	55.3796	1313.771	1314.299	1	2	shared(2)	0	0.8721
DMTALIGNTPLVYLNR	63.91	54.234	1789.94	1791.101	1	2	shared(2)	0	0.9781
ALSLGQFDNPANPQIHFETTGPEIWR	83.39	51.5567	2937.441	2937.67	11	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|109755|estExt_fgenesh1_pm.C_17080001	0	No title.

269. Group probability: 1.0000. Peptides of the group

MPGVNYNSR	44.68	55.5515	1036.476	1036.627	1	2	shared(2)	0	0.8456
KGPDWAPDSSK	55.08	55.8613	1186.562	1187.198	2	2	shared(2)	1	0.9414
HQGFCLDTDPAQGNK	55.66	54.448	1686.742	1687.104	1	2	distinct	0	0.9531
CLDAYQPWNGGIVHVYR	87.62	53.7286	2046.973	2047.896	9	2	distinct	0	0.9974
KIVISETGWSSGGSDPAAGVASPANQAK	42.6	52.1614	2684.34	2685.048	1	3	shared(2)	1	0.8908

The equivalent proteins include

jgi|Physo1_1|128781|estExt_fgenesh1_pg.C_50278	0	No title.

270. Group probability: 1.0000. Peptides of the group

LISGKPVYVALAQR	88.73	54.8037	1513.898	1514.684	11	+2,+3	shared(2)	0	0.9996
RQDRPDADDWTNCYVK	49.6	53.6501	2037.896	2039.321	1	3	shared(2)	1	0.9067
VPGAPAPGGYPMPGYGMPMQQQR	42.77	52.8694	2386.102	2386.479	1	2	shared(2)	0	0.8941
ITGMLLEMDNGELLHLLESPEALEAK	88.95	51.7724	2865.45	2866.857	2	3	distinct	0	0.998

The equivalent proteins include

jgi|Physo1_1|108322|estExt_fgenesh1_pm.C_60012	0	No title.

271. Group probability: 1.0000. Peptides of the group

FSHLAWINTPR	56.59	55.2664	1340.699	1341.333	3	2	shared(2)	0	0.9493
GLFIIDKEGILR	55.31	55.2672	1372.808	1373.33	2	2	distinct	1	0.8323
KLNTQVIGASIDSK	86.63	55.0101	1472.82	1473.269	1	2	distinct	1	0.9967
LIEAFQFHEEHGDVCPANWK	57.1	52.756	2426.111	2427.278	3	2	distinct	0	0.9665

The equivalent proteins include

jgi|Physo1_1|108742|estExt_fgenesh1_pm.C_290005	0	No title.

272. Group probability: 1.0000. Peptides of the group

AEYDESGPSIVHR	65.28	55.1212	1458.674	1459.218	3	+2,+3	shared(2)	0	0.998
AEYDESGPSIVHRK	74.83	54.9978	1586.769	1587.119	5	2	shared(2)	1	0.972
YPIEHGIVTDWDDMEK	83.19	53.9034	1946.872	1946.691	15	+2,+3	distinct	0	0.9994

The equivalent proteins include

gi|50355625|dbj|BAD29953.1|	42035.79	actin [Ulva pertusa]

273. Group probability: 1.0000. Peptides of the group

AWGSTEAAQLAYFEEK	91.16	54.3081	1799.837	1800.666	1	2	distinct	0	0.998
IAFSPAQDIMYITNSQK	89.59	53.8506	1925.956	1927.356	1	2	distinct	0	0.9978

The equivalent proteins include

jgi|Physo1_1|142894|estExt_fgenesh1_pg.C_1240014	0	No title.

274. Group probability: 1.0000. Peptides of the group

AVGHILAK	47.93	55.6363	807.497	808.139	1	2	distinct	0	0.8837
LYGDGGVKPWSNSIATR	50.85	54.289	1819.922	1820.372	2	+2,+3	distinct	0	0.9926
VNILRDPVTGNYWQSYSEDPFLNAR	45.84	51.5123	2953.436	2954.925	1	3	distinct	1	0.9098
VSLVHGAVDEDGNQQQAGYSVPITSQGIPAIR	47.12	50.9236	3305.664	3306.357	2	3	distinct	0	0.9379

The equivalent proteins include

jgi|Physo1_1|135218|estExt_fgenesh1_pg.C_360134	0	No title.

275. Group probability: 1.0000. Peptides of the group

GVLIHGPPGTGK	54.48	56.2365	1131.64	1132.141	1	2	shared(2)	0	0.8714
KIELPHPTEEAR	65.33	55.0132	1418.752	1419.04	5	+2,+3	distinct	1	0.9981
VIAATNRPDVLDPALLR	49.97	54.1165	1833.047	1834.226	5	+2,+3	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|108207|estExt_fgenesh1_pm.C_20039	0	No title.
jgi|Phyra1_1|71146|fgenesh1_pm.C_scaffold_5000015	0	No title.

276. Group probability: 1.0000. Peptides of the group

FYINNIVGGTGAYGHSK	113.79	54.1425	1796.884	1797.44	4	2	distinct	0	0.9955
QVLALVNVPGLVDRPEIK	72.15	53.8001	1959.152	1960.13	7	+2,+3	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|108810|estExt_fgenesh1_pm.C_340010	0	No title.

277. Group probability: 1.0000. Peptides of the group

DVHPFYFATQYHPEFK	58.41	53.5677	2024.942	2025.932	3	2	distinct	0	0.965
TVQVVPHVTDAIQDWIER	91.53	53.3671	2105.09	2105.917	1	2	distinct	0	0.9982
VGPENFCLVHVSLVPVLGSVGEQK	44.53	52.5419	2563.347	2563.982	1	2	distinct	0	0.913

The equivalent proteins include

jgi|Physo1_1|109608|estExt_fgenesh1_pm.C_1650001	0	No title.

jgi|Phyra1_1|71525|fgenesh1_pm.C_scaffold_25000001	0	No title.							
278. Group probability: 1.0000. Peptides of the group									
KEYGPSQPLK	48.63	55.8234	1145.608	1146.399	2	2	distinct	1	0.8932
SKFDNIYGCR	50.4	55.6608	1258.576	1259.292	5	2	distinct	1	0.9089
CKGVSEETTTGVHR	45.84	54.7812	1559.736	1560.756	1	2	distinct	1	0.8842
WCSCNIFSTQDHAAAAIAR	79.72	53.3212	2177.973	2178.608	1	2	distinct	0	0.9952
The equivalent proteins include									
jgi|Physo1_1|109095|estExt_fgenesh1_pm.C_600001	0	No title.							
279. Group probability: 1.0000. Peptides of the group									
LYANLISQPSR	48.46	55.8759	1260.683	1261.977	1	2	shared(2)	0	0.8953
LGWTDLYPADAR	52.46	55.1468	1376.672	1377.186	1	2	distinct	0	0.9299
AVPLHDEIHEPLDQFLSSLGLK	72.03	52.6868	2457.29	2457.579	20	+2,+3	distinct	0	0.9998
The equivalent proteins include									
jgi|Physo1_1|131470|estExt_fgenesh1_pg.C_160014	0	No title.							
jgi|Physo1_1|131473|estExt_fgenesh1_pg.C_160017	0	No title.							
280. Group probability: 1.0000. Peptides of the group									
LGDAFHPK	57.12	55.4753	883.455	883.49	2	2	distinct	0	0.6818
SNLVALLEGK	47.24	56.1295	1042.602	1043.22	1	2	distinct	0	0.4752
LKQEEAATTGR	72.71	55.8308	1202.625	1203.739	3	2	distinct	1	0.9875
RYEDQLSELK	50.18	55.2958	1279.641	1281.004	1	2	distinct	1	0.9078
LVVPTDDGYVPVVVPK	60.62	54.3499	1695.945	1696.805	1	2	distinct	0	0.9707
The equivalent proteins include									
jgi|Physo1_1|139774|estExt_fgenesh1_pg.C_780035	0	No title.							
281. Group probability: 1.0000. Peptides of the group									
IIVDAHYR	55.02	56.3307	985.534	986.243	15	2	distinct	0	0.8878
EHIAAYGTGNER	55.87	55.4664	1316.611	1317.285	2	2	distinct	0	0.9477
RPASNMDPYVVTGR (0000001000000000)	67.39	54.8758	1561.767	1562.686	14	+2,+3	distinct	0	0.999
The equivalent proteins include									
gi|23394346|gb|AAN31463.1|	39801.57	glutamine synthetase [Phytophthora infestans]							
282. Group probability: 1.0000. Peptides of the group									
GNVIITYQHPDFAHSDK	56.36	53.7525	1940.938	1942.13	1	2	distinct	0	0.9595
TVAYVGSHMDVVPANPEGWQR	52.91	52.9914	2312.101	2312.675	1	2	distinct	0	0.9531
LFHSGLPNLGINGIELGMDAFTK	44.85	52.8705	2443.257	2444.212	1	3	distinct	0	0.6981
ALYSAISDVLGEAKPFSISGSLPLVR	66.87	52.0977	2689.469	2689.804	3	2	distinct	0	0.9887
The equivalent proteins include									
jgi|Physo1_1|123133|estExt_Genewise1.C_1200039	0	No title.							
283. Group probability: 1.0000. Peptides of the group									
LYANLISQPSR	48.46	55.8759	1260.683	1261.977	1	2	shared(2)	0	0.8953
LFTINIVRPEISK	71.43	55.1915	1528.898	1529.694	2	2	distinct	0	0.9872
GVDHELVPCNPGSDFFK	47.09	53.9288	1916.873	1917.297	1	2	distinct	0	0.9083
TQPFNEEIHVPLVGFIK	65.47	53.767	1967.052	1967.625	4	2	distinct	0	0.9818
The equivalent proteins include									
jgi|Physo1_1|131502|estExt_fgenesh1_pg.C_160046	0	No title.							
284. Group probability: 1.0000. Peptides of the group									
ELLQGQHVVAVR	74.97	55.2635	1347.762	1348.822	6	2	distinct	0	0.9902
VFEKPIVVDCR	58.46	55.3137	1360.717	1361.223	3	2	distinct	0	0.9569
VFAENSELKPTLAK	68.11	55.2911	1545.84	1546.271	3	2	distinct	0	0.9834
The equivalent proteins include									
jgi|Physo1_1|109046|estExt_fgenesh1_pm.C_540020	0	No title.							
285. Group probability: 1.0000. Peptides of the group									
AHALAVQK	53.75	55.9562	836.487	836.369	2	1	distinct	0	0.9297
NTYIVTHNLLR	63.48	55.4379	1342.736	1344.031	6	2	distinct	0	0.9722
MVPNPAGIAFYHDLIDEMTK	82.51	53.3077	2261.086	2261.414	16	2	distinct	0	0.9964
The equivalent proteins include									
jgi|Physo1_1|137835|estExt_fgenesh1_pg.C_580008	0	No title.							
286. Group probability: 1.0000. Peptides of the group									
GVNALQNPHDPVVIPR	82.31	54.2533	1724.932	1725.118	3	2	distinct	0	0.9956
VLVPVVPSQILGIGLNYR	58.57	53.7889	1936.151	1937.134	3	2	distinct	0	0.9678
NPPLFLAPGDMVEIEIER	53.14	53.6354	2039.04	2040.126	2	2	distinct	0	0.9482
The equivalent proteins include									

jgi|Physo1_1|135798|estExt_fgenesh1_pg.C_400135	0	No title.

287. Group probability: 1.0000. Peptides of the group

ADHSLVDKYSTR	52.14	55.1594	1390.684	1391.285	1	2	distinct	1	0.9279
LTDNIAGSLVNASKPVQAR	52.92	53.7731	1953.064	1953.358	1	2	distinct	0	0.9489
NPSNYFAEIEQIAFSPSHMVPGIEPSPDK	87.32	50.9937	3200.512	3199.973	5	3	distinct	0	0.998

The equivalent proteins include

jgi|Physo1_1|129552|estExt_fgenesh1_pg.C_80063	0	No title.

288. Group probability: 1.0000. Peptides of the group

TAPLHVSVHDR	57.97	55.6665	1230.647	1231.82	8	2	distinct	0	0.9547
GTHFQELPVSGCPK	61.5	54.8243	1555.745	1556.465	4	2	distinct	0	0.9706
RVSLDMLDWADPHAR	45.89	54.1983	1780.868	1781.239	1	2	distinct	1	0.89
LIPVSYGIWFLDSTVPLLDDR	51.46	52.7057	2418.283	2419.077	1	2	distinct	0	0.9471

The equivalent proteins include

jgi|Physo1_1|131019|estExt_fgenesh1_pg.C_140017	0	No title.

289. Group probability: 1.0000. Peptides of the group

RFMSQVWTR	52.53	55.2873	1209.608	1210.257	1	2	distinct	1	0.9229
RVEAYAGDNNQHGPR	81.15	54.2885	1682.787	1683.341	15	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|135217|estExt_fgenesh1_pg.C_360133	0	No title.

290. Group probability: 1.0000. Peptides of the group

KVVVLCNLK	49.82	56.0199	1071.647	1071.485	2	1	distinct	1	0.9007
VKSDVYSSPIVFSQLDLR	93.77	53.8811	2052.089	2052.922	3	2	distinct	1	0.9985
VDIGKGEELEMVMEHQPYFAEEELVDR (000000000000100000000000000000)	49.37	51.0371	3191.479	3192.615	3	3	distinct	1	0.9389

The equivalent proteins include

jgi|Physo1_1|144562|estExt_fgenesh1_pg.C_1980006	0	No title.
jgi|Physo1_1|144563|estExt_fgenesh1_pg.C_1980007	0	No title.

291. Group probability: 1.0000. Peptides of the group

RFFDFLPLNNK	60.06	54.9846	1409.745	1410.652	3	2	distinct	1	0.8954
DIINQIVDSFDFFEIMPDYAK	83.77	52.691	2519.193	2519.253	15	2	distinct	0	0.9969
FCDSFNIPIVTLVDVPGFLPGTDQEYGGIIR	56.34	50.2686	3438.717	3439.55	1	3	distinct	0	0.9717

The equivalent proteins include

jgi|Physo1_1|109606|estExt_fgenesh1_pm.C_1640003	0	No title.

292. Group probability: 1.0000. Peptides of the group

VHPADLKPCLTK	53.55	55.1231	1377.744	1378.016	1	2	distinct	0	0.9363
THPIAYDGFEPSGR	60.38	55.2061	1545.721	1546.764	1	2	distinct	0	0.9674
HAGAYWSQVLDGAGR	82.65	54.9862	1586.759	1587.336	2	2	distinct	0	0.9956

The equivalent proteins include

jgi|Physo1_1|136606|estExt_fgenesh1_pg.C_470020	0	No title.

293. Group probability: 1.0000. Peptides of the group

IVTGDASQAWHALCR	98.41	54.3514	1683.815	1684.212	11	+2,+3	shared(2)	0	0.9999
YKAPCVAVVQSSGFGK	80.63	54.334	1696.861	1697.291	1	2	distinct	1	0.9949
MGRPMWYSTCPNPADR	55.96	53.8021	1937.833	1937.898	1	2	shared(2)	0	0.9565

The equivalent proteins include

jgi|Physo1_1|137148|estExt_fgenesh1_pg.C_510032	0	No title.
jgi|Physo1_1|141989|estExt_fgenesh1_pg.C_1060048	0	No title.

294. Group probability: 1.0000. Peptides of the group

GMCDYGTGHCTCFPGYEGK	77.61	53.3023	2195.817	2195.839	4	2	distinct	0	0.9942
HMGCYCDQGYRGPDCSLK	47.67	53.2331	2202.87	2202.883	1	2	distinct	1	0.9171
TCPYGDAWVQVPTATNTAHSLVECSNR	62.08	51.4006	3033.371	3034.715	2	3	distinct	0	0.9798

The equivalent proteins include

jgi|Physo1_1|156623|C_scaffold_24000001	0	No title.

295. Group probability: 1.0000. Peptides of the group

AAQHLADHGAR	47.6	55.8234	1145.569	1146.503	1	2	distinct	0	0.8872
IVQLDIAPLLAQAIQNIHGK	73.79	53.3625	2154.252	2155.337	9	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Phyra1_1|72269|fgenesh1_pm.C_scaffold_123000004	0	No title.

296. Group probability: 1.0000. Peptides of the group

RPDHNNDALYFR	46.99	54.9817	1516.717	1518.184	1	3	distinct	0	0.8611
FQINLDNLEPQVALFPSPDNVKPVSEVVGMK	123.95	50.3834	3423.775	3424.897	2	3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|141550|estExt_fgenesh1_pg.C_1000036	0	No title.

297. Group probability: 1.0000. Peptides of the group

KPAALNPEHLK	54.74	55.7414	1216.693	1217.371	3	2	distinct	0	0.9398
KDYKPEGDVPTPAAPAAIK	75.49	53.7288	1967.036	1967.532	2	2	distinct	1	0.993
SSEMNVAFPAGAGSDDYVEKPIPEQFVHK	58.53	51.3892	3148.481	3149.711	1	3	distinct	0	0.9743

The equivalent proteins include

jgi|Physo1_1|158145|C_scaffold_85000011	0	No title.

298. Group probability: 1.0000. Peptides of the group

SPVILVLDEIHDPQNFGAILR	89.9	52.942	2345.274	2346.538	9	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|140510|estExt_fgenesh1_pg.C_860048	0	No title.

299. Group probability: 1.0000. Peptides of the group

AEMHAVGDHELR	53.62	55.0547	1363.63	1364.552	2	2	distinct	0	0.9368
YQAYPTYDLACPIVDSIEGVTHALR	42.66	51.7831	2851.385	2852.648	1	3	distinct	0	0.8801
AGVADESPAGAAAHAAPAAVAAATPAAAAFAGKK	89.25	51.6618	2879.489	2880.652	3	3	distinct	1	0.9985

The equivalent proteins include

jgi|Physo1_1|133964|estExt_fgenesh1_pg.C_290031	0	No title.

300. Group probability: 1.0000. Peptides of the group

ACNALLLK	66.88	56.8984	901.505	902.794	1	2	shared(3)	0	0.9265
GVPLYQHFADLIGNK	86.24	54.5861	1670.878	1671.671	15	2	distinct	0	0.9968
NLVLPVPSFNVINGGSHAGNK	83.65	53.3159	2133.133	2133.605	5	2	distinct	0	0.9914

The equivalent proteins include

jgi|Physo1_1|109144|estExt_fgenesh1_pm.C_630010	0	No title.
jgi|Phyra1_1|72151|fgenesh1_pm.C_scaffold_94000001	0	No title.

301. Group probability: 1.0000. Peptides of the group

IGGDVIIHELDTLIESLR	93.03	53.8075	1992.089	1992.831	8	2	distinct	0	0.9984
DNAYHPHVTVGGFQLDPDTGR	79	53.0436	2295.067	2295.581	3	2	distinct	0	0.9443
DTGLFPILVHGAGPQMNAELDK	62.97	53.0829	2322.168	2322.747	1	2	shared(2)	0	0.9812

The equivalent proteins include

jgi|Physo1_1|139358|estExt_fgenesh1_pg.C_730027	0	No title.

302. Group probability: 1.0000. Peptides of the group

FNANVTQKPLK	86.68	55.5166	1258.703	1258.98	5	2	distinct	0	0.996
TIIDSVHPLENVMEAFK	58.78	53.7722	1941.987	1943.368	1	2	distinct	0	0.9672
YVAPKPSSMSWNEAAGVPLAGQTSWQALVTYGK	42.63	50.7467	3493.734	3493.704	1	3	distinct	0	0.9114

The equivalent proteins include

jgi|Physo1_1|133480|estExt_fgenesh1_pg.C_260086	0	No title.

303. Group probability: 1.0000. Peptides of the group

LVNIDQVIQWLMK	91.01	54.8427	1598.885	1600.257	2	2	distinct	0	0.9977
ELNLDYIVDNPWLVIPISALR	77.8	52.6657	2452.337	2452.815	5	2	distinct	0	0.9948

The equivalent proteins include

jgi|Physo1_1|141248|estExt_fgenesh1_pg.C_960012	0	No title.
jgi|Phyra1_1|79547|fgenesh1_pg.C_scaffold_41000078	0	No title.

304. Group probability: 1.0000. Peptides of the group

KIGYPVIIK	55	56.4448	1029.659	1030.666	6	2	shared(2)	1	0.9184
ALHQYQIVGLPTNIEFVAR	51.73	53.5031	2168.174	2169.379	1	3	distinct	0	0.7367
ISGAEAVHPGYGFLSENAAFAR	84.14	53.1431	2263.102	2264.538	33	+2,+3	shared(2)	0	0.9996
IYAENPYNDFLPGSGTLQHIR	74.38	52.7481	2404.181	2404.726	19	+2,+3	shared(2)	0	0.9999

The equivalent proteins include

jgi|Phyra1_1|41181|gwEuk.131.2.1	0	No title.

305. Group probability: 1.0000. Peptides of the group

GGLDASSHNYPPHGK	61.75	54.6929	1535.712	1536.584	2	2	distinct	0	0.9724
HEYMEYLQTHQSR	80.66	54.3568	1720.763	1721.11	2	+2,+3	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|142184|estExt_fgenesh1_pg.C_1090040	0	No title.

306. Group probability: 1.0000. Peptides of the group

VVDGVIAGQFLQVFK	46.84	54.574	1618.908	1619.476	1	2	distinct	0	0.898
LKPEEFQGGSFTVSNLGSFGIDQFR	58.06	51.9756	2759.355	2760.386	1	3	distinct	0	0.9688
TQSVKPNPSVDVSVAVATPTGLITPIVPK	76.43	51.5796	2914.638	2914.781	3	2	distinct	0	0.9956

The equivalent proteins include

jgi|Physo1_1|158966|C_scaffold_188000005	0	No title.

307. Group probability: 1.0000. Peptides of the group

EADGILFGFPTR	75.45	55.3384	1321.667	1322.724	6	2	shared(2)	0	0.9906
QPSKLELTVATTQGK	68.19	55.1473	1599.883	1600.406	4	2	shared(2)	1	0.9841
APELANMEEIHGGSAWGAGTLANGDGSR	94.38	52.0576	2767.262	2768.481	1	3	distinct	0	0.9988

The equivalent proteins include

jgi|Phyra1_1|71949|fgenesh1_pm.C_scaffold_62000012	0	No title.
jgi|Phyra1_1|71950|fgenesh1_pm.C_scaffold_62000013	0	No title.

308. Group probability: 1.0000. Peptides of the group

AVEHVLLDGVR	47.63	55.2247	1206.672	1207.428	2	2	distinct	0	0.8889
DFANPIAQILSAALLLR	133.45	53.9934	1825.046	1825.424	16	2	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|109069|estExt_fgenesh1_pm.C_560007	0	No title.

309. Group probability: 1.0000. Peptides of the group

AWLGPDNQIAGYHQR	83.67	54.2515	1724.838	1725.365	2	2	distinct	0	0.996
WITEDNGLALKPASPWR	83.13	53.7546	1953.011	1953.755	6	2	distinct	0	0.9961

The equivalent proteins include

jgi|Physo1_1|141365|estExt_fgenesh1_pg.C_970053	0	No title.

310. Group probability: 1.0000. Peptides of the group

FPFGSLVPLWSR	52.51	55.1459	1404.755	1405.301	4	2	shared(2)	0	0.9302
LSHDPIHDNAYYGK	78.52	54.6613	1628.758	1629.616	2	2	distinct	0	0.9934
CMIGGILSCGLTHTGITPLDVVK	82.38	52.8755	2441.248	2441.798	5	2	distinct	0	0.9903

The equivalent proteins include

jgi|Physo1_1|109646|estExt_fgenesh1_pm.C_1930002	0	No title.
jgi|Phyra1_1|71882|fgenesh1_pm.C_scaffold_57000010	0	No title.

311. Group probability: 1.0000. Peptides of the group

LSHEQFPELK	53.66	55.5412	1226.629	1227.649	1	2	distinct	0	0.9317
VKEWYSLPHDTSK	64.94	54.776	1588.789	1589.589	3	2	distinct	1	0.9775
TGRPGTPVDIADSYEHLLQVYDQVK	69.89	52.0024	2800.403	2801.672	4	3	distinct	0	0.9889

The equivalent proteins include

jgi|Physo1_1|133628|estExt_fgenesh1_pg.C_270040	0	No title.

312. Group probability: 1.0000. Peptides of the group

AVMHMALR	50.54	56.7414	927.478	928.136	4	2	shared(5)	0	0.9054
FLAGAHAMDK (000000001000)	67.37	56.0609	1059.517	1060.198	9	2	shared(4)	0	0.9477
GVWNSSFLGHSSR	81.59	55.0707	1432.685	1433.195	3	2	distinct	0	0.9947
ANIFGFWDWVGGR	81.96	54.634	1523.731	1524.464	7	2	shared(4)	0	0.9938
FAAHIQQVDMESNGKR	69.79	54.1089	1829.884	1831.328	4	2	shared(3)	1	0.8859
HMVAASSAVPLVQQFGIDR	63.53	53.5552	2025.047	2026.423	1	2	shared(3)	0	0.9799
YSVTSAVGILPLALQYGFDITEK	71.42	52.7225	2484.315	2485.376	2	2	shared(4)	0	0.9914

The equivalent proteins include

gi|37960071|gb|AAP51060.1|	60801.41	glucose-6-phosphate isomerase [Phytophthora infestans]

313. Group probability: 1.0000. Peptides of the group

KLEPDIFHTKPDTSK	69.05	54.2237	1754.92	1755.967	2	2	distinct	1	0.9856
YLHELYGDSVKYPVLK	96.18	54.1098	1923.014	1923.434	6	2	distinct	1	0.9987

The equivalent proteins include

jgi|Physo1_1|138303|estExt_fgenesh1_pg.C_620039	0	No title.

314. Group probability: 1.0000. Peptides of the group

RFDLEDADFK	58.8	55.6854	1254.588	1255.43	1	2	distinct	1	0.9564
FGGEMIASYFDER	89.22	54.7312	1520.661	1521.396	2	2	shared(2)	0	0.9973
AAAILGEHNAVEDANLNLAK	92.09	53.6864	2033.054	2033.391	1	2	distinct	0	0.9916

The equivalent proteins include

jgi|Physo1_1|158411|C_scaffold_104000007	0	No title.

315. Group probability: 1.0000. Peptides of the group

QVMALYDKRPK	65.75	55.2635	1347.733	1348.449	4	2	distinct	1	0.9773
RIPSGQLWAGNPAK	76.36	54.6427	1493.81	1494.482	10	+2,+3	distinct	1	0.9991

The equivalent proteins include

jgi|Physo1_1|109006|estExt_fgenesh1_pm.C_510006	0	No title.

316. Group probability: 1.0000. Peptides of the group

KVHLFDIDVPGK	69.51	54.971	1366.761	1367.241	5	+2,+3	distinct	1	0.9986
ELLNEKDHPSTYALSQLAAK	67.13	53.2305	2227.148	2227.672	5	2	distinct	1	0.986

The equivalent proteins include

jgi|Physo1_1|108421|estExt_fgenesh1_pm.C_90017	0	No title.

317. Group probability: 1.0000. Peptides of the group

LLTPAQVIDYIAAHPMAK (00000000000000001000)	103.02	53.8098	1951.06	1951.264	45	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|158374|C_scaffold_101000017	0	No title.
jgi|Phyra1_1|94082|C_scaffold_11000106	0	No title.

318. Group probability: 1.0000. Peptides of the group

SRPYLFSNSLGPSVVGASLK	97.87	53.6785	2078.116	2078.725	9	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|108830|estExt_fgenesh1_pm.C_340030	0	No title.

319. Group probability: 1.0000. Peptides of the group

AHLDVVKDPK	52.56	55.5364	1120.624	1121.6	2	2	distinct	1	0.9248
AFISSKPDAGFNHK	65.52	54.9413	1517.763	1518.45	5	2	distinct	0	0.9793
IMETLEHEQHLPLASR	68.32	53.9416	1902.962	1902.894	2	2	distinct	0	0.9852

The equivalent proteins include

jgi|Physo1_1|132830|estExt_fgenesh1_pg.C_220178	0	No title.

320. Group probability: 1.0000. Peptides of the group

SLNNQFASFIDKVR	48.77	54.5323	1637.852	1638.84	1	2	distinct	1	0.7015
THNLEPYFESFINNLR	83.06	53.8059	1992.969	1993.391	17	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|109096823|ref|XP_001098292.1|	65340.78	PREDICTED: similar to keratin 1 isoform 7 [Macaca mulatta]
gi|109096825|ref|XP_001098082.1|	64503.44	PREDICTED: similar to keratin 1 isoform 5 [Macaca mulatta]
gi|109096827|ref|XP_001097902.1|	63150.85	PREDICTED: similar to keratin 1 isoform 3 [Macaca mulatta]
gi|109096829|ref|XP_001097988.1|	62009.39	PREDICTED: similar to keratin 1 isoform 4 [Macaca mulatta]
gi|109096831|ref|XP_001098182.1|	63139.76	PREDICTED: similar to keratin 1 isoform 6 [Macaca mulatta]
gi|109096833|ref|XP_001097800.1|	61737.33	PREDICTED: similar to keratin 1 isoform 2 [Macaca mulatta]
gi|109096835|ref|XP_001097706.1|	59017.2	PREDICTED: similar to keratin 1 isoform 1 [Macaca mulatta]
gi|55638143|ref|XP_522394.1|	98632.68	PREDICTED: similar to keratin 1B [Pan troglodytes]
gi|7331218|gb|AAF60327.1|	66149.05	keratin 1 [Homo sapiens]
gi|11935049|gb|AAG41947.1|	66198.07	keratin 1 [Homo sapiens]

321. Group probability: 1.0000. Peptides of the group

AQMAPWIKPK	57.87	55.7964	1168.643	1169.471	1	2	distinct	0	0.9525
LIVEKPFGHDLASFDK	106.92	54.1895	1814.957	1815.532	9	2	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|109499|estExt_fgenesh1_pm.C_1190012	0	No title.

322. Group probability: 1.0000. Peptides of the group

IKTEHDFNLEK	67.39	55.379	1372.699	1373.242	2	2	distinct	1	0.9803
LDQIYYDLKPTVR	68.76	54.6031	1622.867	1624.183	2	+2,+3	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|138060|estExt_fgenesh1_pg.C_600019	0	No title.
jgi|Phyra1_1|94247|C_scaffold_14000020	0	No title.

323. Group probability: 1.0000. Peptides of the group

KLSTELHAR	70.19	55.1679	1053.593	1053.999	8	2	distinct	1	0.9836

LCNNLALAIQMASVAEAMNLGTTLGIDPK	88.21	51.2654	3028.539	3028.547	2	2	distinct	0	0.9985

The equivalent proteins include

jgi|Physo1_1|142005|estExt_fgenesh1_pg.C_1060064	0	No title.

324. Group probability: 1.0000. Peptides of the group

KFLDGIYVSEK	77.32	55.2875	1297.692	1298.372	16	2	distinct	1	0.9918
RVALSEGVSYVR	60.59	55.3874	1334.731	1336.137	4	2	distinct	1	0.9655
FVYAHFPINVTFENNTVEIR	45.75	52.7305	2409.212	2410.666	1	2	distinct	0	0.9095

The equivalent proteins include

jgi|Physo1_1|108722|estExt_fgenesh1_pm.C_270007	0	No title.

325. Group probability: 1.0000. Peptides of the group

AVMHMALR	50.54	56.7414	927.478	928.136	4	2	shared(5)	0	0.9054
ATAGLNPEETLVVVVSK	82.55	54.3183	1725.951	1726.653	3	2	distinct	0	0.9959
KLQAIASGEHVNATEDR	112.31	53.9721	1837.928	1839.353	12	+2,+3	shared(3)	1	1

The equivalent proteins include

jgi|Physo1_1|157608|C_scaffold_54000010	0	No title.

326. Group probability: 1.0000. Peptides of the group

DYTINIHKR	54.36	55.7973	1158.615	1159.535	5	2	distinct	1	0.9336
LYTLVQHVQVASFK	110.15	54.6703	1631.903	1632.662	1	2	distinct	0	0.9996

The equivalent proteins include

jgi|Physo1_1|109268|estExt_fgenesh1_pm.C_820002	0	No title.

327. Group probability: 1.0000. Peptides of the group

CYQCGETGHWAR	70.95	54.634	1523.603	1524.466	4	2	distinct	0	0.9863
RDCPEAPSQEGFSGYGGPCFGCGK	89.88	52.2688	2619.058	2619.765	1	3	distinct	1	0.998

The equivalent proteins include

jgi|Physo1_1|109617|estExt_fgenesh1_pm.C_1690004	0	No title.

328. Group probability: 1.0000. Peptides of the group

KDIFLNSMFDK	79.97	55.2816	1356.675	1356.993	2	2	shared(3)	1	0.9935
GAHYYAYQLLQEA	47.42	54.6517	1525.72	1526.065	1	2	distinct	0	0.8958
NTVDFTNVEFGWR	45.83	54.8066	1583.737	1584.768	3	2	distinct	0	0.8798
IISGPGLATIYEFLAK	95.06	54.6399	1691.95	1692.384	32	2	shared(3)	0	0.9986
TNELCNQTLEIFVGAYGR	96.66	53.5823	2084	2084.793	8	2	shared(3)	0	0.9989

The equivalent proteins include

jgi|Physo1_1|138629|estExt_fgenesh1_pg.C_650048	0	No title.

329. Group probability: 1.0000. Peptides of the group

VVAFLHAPGAQSGLSR	70.74	54.5831	1608.874	1609.185	6	2	distinct	0	0.9879
HLYVTSLFPTSDPPLPPTR	44.52	53.3058	2137.121	2137.61	1	2	distinct	0	0.8943
IMHSGSEDPTGDAAEEDHRYPFAGAANPK	60.11	51.2402	3069.352	3070.173	2	3	distinct	1	0.9777

The equivalent proteins include

jgi|Physo1_1|140047|estExt_fgenesh1_pg.C_810036	0	No title.

330. Group probability: 1.0000. Peptides of the group

DKPITMNNHEMGITPER	86.22	53.8474	1981.935	1982.366	5	2	distinct	0	0.997
FNQYSSLTDFYTVLATNVDR	70.64	52.9576	2353.123	2353.37	2	2	distinct	0	0.9898

The equivalent proteins include

jgi|Physo1_1|108369|estExt_fgenesh1_pm.C_70014	0	No title.

331. Group probability: 1.0000. Peptides of the group

IIGADHPTLSAR	59.03	55.3236	1249.678	1250.525	2	2	distinct	0	0.9605
FAGQFGNDTHGDALQK	101.51	54.5212	1704.786	1705.393	2	2	distinct	0	0.9992

The equivalent proteins include

jgi|Physo1_1|136766|estExt_fgenesh1_pg.C_480045	0	No title.

332. Group probability: 1.0000. Peptides of the group

KGAALHALK	53.62	55.6949	907.56	908.627	1	2	distinct	1	0.9293
VLQEIQSDPSKINEHIK	56.46	53.763	1977.053	1978.335	2	3	distinct	1	0.9091
SAAYLSLDDAAHALEDAELCIETKPDWAK	76.75	50.9087	3202.513	3203.87	1	3	distinct	0	0.9949

The equivalent proteins include

jgi|Physo1_1|140327|estExt_fgenesh1_pg.C_840054	0	No title.

333. Group probability: 1.0000. Peptides of the group

AVMHMALR	50.54	56.7414	927.478	928.136	4	2	shared(5)	0	0.9054
FLAGAHAMDK (000000001000)	67.37	56.0609	1059.517	1060.198	9	2	shared(4)	0	0.9477

ANIFGFWDWVGGR	81.96	54.634	1523.731	1524.464	7	2	shared(4)	0	0.9938
FAAHIQQVDMESNGKR	69.79	54.1089	1829.884	1831.328	4	2	shared(3)	1	0.8859
KLQAIASGEHVNATEDR	112.31	53.9721	1837.928	1839.353	12	+2,+3	shared(3)	1	1
HMVAASSAVPLVQQFGIDR	63.53	53.5552	2025.047	2026.423	1	2	shared(3)	0	0.9799
YSVTSAVGILPLALQYGFDITEK	71.42	52.7225	2484.315	2485.376	2	2	shared(4)	0	0.9914

The equivalent proteins include

gi|37960107|gb|AAP51078.1|	60850.42	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960073|gb|AAP51061.1|	60861.39	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960081|gb|AAP51065.1|	60755.43	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960087|gb|AAP51068.1|	60776.38	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960091|gb|AAP51070.1|	60834.39	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960093|gb|AAP51071.1|	60842.35	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960105|gb|AAP51077.1|	60716.35	glucose-6-phosphate isomerase [Phytophthora erythroseptica]
gi|37960109|gb|AAP51079.1|	60859.42	glucose-6-phosphate isomerase [Phytophthora infestans]
gi|37960111|gb|AAP51080.1|	60792.41	glucose-6-phosphate isomerase [Phytophthora infestans]

334. Group probability: 1.0000. Peptides of the group

RPTTAEAIAHAK	61.84	55.1939	1264.689	1265.607	5	+2,+3	distinct	0	0.998
KGVNLPGLIVELPALSEK	66.04	54.1232	1876.103	1877.438	1	2	distinct	1	0.9831

The equivalent proteins include

jgi|Physo1_1|108888|estExt_fgenesh1_pm.C_390004	0	No title.

335. Group probability: 1.0000. Peptides of the group

KGGFIMIK	58.35	55.8522	892.52	893.447	2	2	distinct	1	0.8469
CNFTALDIFTNK	68.97	55.0106	1442.686	1443.695	3	2	distinct	0	0.9797
EDIKLPTFPETFADEIR	70.85	54.0633	2020.015	2020.401	1	2	distinct	1	0.9886

The equivalent proteins include

jgi|Physo1_1|155602|C_scaffold_6000033	0	No title.
jgi|Phyra1_1|71735|fgenesh1_pm.C_scaffold_43000010	0	No title.
jgi|Phyra1_1|72429|fgenesh1_pm.C_scaffold_744000001	0	No title.

336. Group probability: 1.0000. Peptides of the group

RNPYSWTER	44.92	55.2248	1207.573	1207.957	1	2	distinct	1	0.8498
QVGPFAFQQVYEAGHMVPLDQPK	74.18	52.4193	2585.274	2585.768	5	2	distinct	0	0.9933
EVGDDMFHFLQDFFQAKPEYQK	57.81	52.2174	2718.242	2719.477	2	3	distinct	0	0.9644

The equivalent proteins include

jgi|Physo1_1|109077|estExt_fgenesh1_pm.C_580002	0	No title.

337. Group probability: 1.0000. Peptides of the group

RNDGIHIINVGK	83.54	55.2222	1334.742	1335.536	9	2	distinct	1	0.9907
FAQHTGCQAIASR	60.66	55.0769	1445.683	1446.108	5	+1,+2	distinct	0	0.9961

The equivalent proteins include

jgi|Physo1_1|109027|estExt_fgenesh1_pm.C_540001	0	No title.

338. Group probability: 1.0000. Peptides of the group

IGSVVAPTPAHAAEIKR	50.06	54.3955	1715.968	1716.747	1	2	distinct	1	0.9286
SVQPGGWRPGGTLTQYK	53.69	54.0972	1830.938	1831.708	5	2	distinct	0	0.9484
SYIETHCPDDHTIIIDESMQPWVGPQWR	69.35	50.4683	3409.55	3410.542	1	3	distinct	0	0.9899

The equivalent proteins include

jgi|Physo1_1|135234|estExt_fgenesh1_pg.C_370003	0	No title.

339. Group probability: 1.0000. Peptides of the group

HLVFQGGSVLADLMK	88.74	54.7298	1613.86	1615.013	4	2	distinct	0	0.9974
NIVLSGGSSMYPGLPSRLEK	66.66	53.3514	2104.099	2104.745	1	2	distinct	1	0.9854

The equivalent proteins include

jgi|Physo1_1|109297|estExt_fgenesh1_pm.C_860004	0	No title.

340. Group probability: 1.0000. Peptides of the group

LNRPPVNSLNTALIQELDATIK	89.46	52.7309	2419.343	2419.829	10	+2,+3	distinct	0	1

The equivalent proteins include

jgi|Physo1_1|134968|estExt_fgenesh1_pg.C_350020	0	No title.

341. Group probability: 1.0000. Peptides of the group

GLVDHGLSLPK	56.18	55.7567	1134.64	1135.954	2	2	distinct	0	0.9469
RNPDFDIPLEEAIKP	56.01	54.1966	1752.905	1753.841	3	2	distinct	1	0.9547
SPESDVFVAAPIIEAAKGESAYPAINLTWDGK	62.48	50.6192	3345.677	3346.97	1	3	distinct	1	0.9839

The equivalent proteins include

jgi|Physo1_1|132215|estExt_fgenesh1_pg.C_190165	0	No title.

342. Group probability: 1.0000. Peptides of the group

AIAPFRDEDTLILCSGQATHNLR	59.9	52.4409	2597.302	2598.694	1	3	distinct	1	0.9712
ANRDPNSPIMDWAAAFQGWLDNTLTAESK (00000000000100000000000000000000)	91.5	50.8845	3218.509	3219.993	8	3	distinct	1	0.9986

The equivalent proteins include

jgi|Physo1_1|129924|estExt_fgenesh1_pg.C_90201	0	No title.

343. Group probability: 1.0000. Peptides of the group

TIRPDSSVHSFK	51.82	55.268	1372.71	1373.333	2	2	distinct	0	0.9257
IEDELPVHYFTMAHNR	59.92	53.739	1970.931	1971.568	1	2	distinct	0	0.9693
LTLGPWSHVGVDNADPFAVSK	63.79	53.2768	2209.117	2209.732	1	2	distinct	0	0.9818

The equivalent proteins include

jgi|Physo1_1|140714|estExt_fgenesh1_pg.C_880086	0	No title.

344. Group probability: 1.0000. Peptides of the group

VSRPLAQTIAAK	64.2	55.2644	1253.746	1254.823	3	2	distinct	0	0.9749
IVTGDASQAWHALCR	98.41	54.3514	1683.815	1684.212	11	+2,+3	shared(2)	0	0.9999
MGRPMWYSTCPNPADR	55.96	53.8021	1937.833	1937.898	1	2	shared(2)	0	0.9565

The equivalent proteins include

jgi|Physo1_1|138900|estExt_fgenesh1_pg.C_670102	0	No title.

345. Group probability: 1.0000. Peptides of the group

IAMQAFDITRPPVAIGAVGLAR (00010000000000000000000)	77.18	53.5279	2266.262	2265.802	5	+2,+3	distinct	0	0.9994
GITFEDVVVPEENVLGDPGYGFK	45.93	52.6024	2480.211	2481.285	2	2	distinct	0	0.9201

The equivalent proteins include

jgi|Physo1_1|114335|estExt_Genewise1.C_190173	0	No title.

346. Group probability: 1.0000. Peptides of the group

LMGINHTR	49.78	56.0297	940.491	941.059	1	2	distinct	0	0.9003
VPTPNVSLAILNLQLDPTKAEGITK	76.44	52.2801	2631.485	2632.961	6	+2,+3	distinct	1	0.9995

The equivalent proteins include

jgi|Physo1_1|108355|estExt_fgenesh1_pm.C_60045	0	No title.

347. Group probability: 0.9999. Peptides of the group

GLSGEHLTVAQLVHNAAFQK	85.9	53.3203	2119.117	2119.701	2	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|141307|estExt_fgenesh1_pg.C_960071	0	No title.

348. Group probability: 0.9999. Peptides of the group

KDIFLNSMFDK	79.97	55.2816	1356.675	1356.993	2	2	shared(3)	1	0.9935
GAHFYAYQLLHQ	63.5	55.0745	1446.704	1447.697	5	2	distinct	0	0.9734
IISGPGLATIYEFLAK	95.06	54.6399	1691.95	1692.384	32	2	shared(3)	0	0.9986
TNELCNQTLEIFVGAYGR	96.66	53.5823	2084	2084.793	8	2	shared(3)	0	0.9989

The equivalent proteins include

jgi|Physo1_1|138625|estExt_fgenesh1_pg.C_650044	0	No title.

349. Group probability: 0.9999. Peptides of the group

MTGGGFGGCIVALVQQEHAQK	52.29	53.3113	2187.056	2186.685	1	2	distinct	0	0.7768
VNLIGEHTDYNDGFVCPLALDK	83.48	52.5543	2489.19	2489.088	5	2	shared(2)	0	0.9969
AGSDDVDVVEQAVTLFYSTFKQYASVPR	49.29	51.1843	3091.514	3090.842	2	2	distinct	1	0.78
ALLCQAAEHEYCNVPCGIMDQFISSCGK	65.64	51.4499	3257.407	3258.227	3	3	shared(2)	0	0.9857
ALLCQAAEHEYCNVPCGIMDQFISSCGKK	54.76	50.4797	3385.502	3386.878	4	3	shared(2)	1	0.965

The equivalent proteins include

jgi|Phyra1_1|72155|fgenesh1_pm.C_scaffold_94000005	0	No title.
jgi|Phyra1_1|72509|fgenesh1_pm.C_scaffold_1742000001	0	No title.
jgi|Phyra1_1|83713|fgenesh1_pg.C_scaffold_94000023	0	No title.

350. Group probability: 0.9999. Peptides of the group

VFSPHVLNLTLVDLPGITK	90.72	53.4726	2062.183	2063.219	5	2	distinct	0	0.9982
LEQPGLQCVDLVFDELQR	57.84	53.2764	2158.073	2158.333	1	2	distinct	0	0.966

The equivalent proteins include

jgi|Physo1_1|109490|estExt_fgenesh1_pm.C_1190003	0	No title.

351. Group probability: 0.9999. Peptides of the group

TTPEVLAHLNANR	63.5	54.7796	1434.758	1435.296	2	2	distinct	0	0.9745
NLSAAAHLIHGSSEGR	88.71	54.5694	1618.817	1619.443	7	2	distinct	0	0.9975

The equivalent proteins include

jgi|Physo1_1|141649|estExt_fgenesh1_pg.C_1010062	0	No title.
jgi|Phyra1_1|75207|fgenesh1_pg.C_scaffold_11000219	0	No title.

352. Group probability: 0.9999. Peptides of the group

KVAGLYQK	50.12	56.4986	905.533	905.769	1	2	distinct	1	0.9023
SYLPDEIQAIQRPLEFYVSDK	44.19	52.5304	2510.269	2510.881	1	2	distinct	0	0.9003
SYLPDEIQAIQRPLEFYVSDKVVEAEK	74.55	51.2737	3165.623	3166.843	4	3	distinct	1	0.9933

The equivalent proteins include

jgi|Physo1_1|155238|C_scaffold_1000042	0	No title.

353. Group probability: 0.9999. Peptides of the group

SASNIVFSNGLLDPWSSAGVLHAPK	82.96	52.4653	2566.318	2567.758	3	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|142831|estExt_fgenesh1_pg.C_1220058	0	No title.
jgi|Phyra1_1|80328|fgenesh1_pg.C_scaffold_48000040	0	No title.

354. Group probability: 0.9999. Peptides of the group

ILSTSLPAFNLNKR	55.94	54.775	1572.899	1574.277	1	2	distinct	1	0.9522
ELNVGIIGPATVGGIKPGCLR	92.63	53.3275	2120.177	2120.53	5	2	distinct	0	0.9986

The equivalent proteins include

jgi|Physo1_1|108913|estExt_fgenesh1_pm.C_420007	0	No title.

355. Group probability: 0.9999. Peptides of the group

IVLEVAQHLGENTVR	99.26	54.5908	1676.921	1677.82	61	+2,+3	shared(2)	0	0.9998
TLQDIIAILGMDELSEDDKLTVAR	75.85	52.4213	2658.379	2657.719	20	2	distinct	1	0.9944

The equivalent proteins include

gi|46909245|gb|AAT06140.1|	45884.78	ATP synthase beta subunit [Eucidaris tribuloides]

356. Group probability: 0.9999. Peptides of the group

KVLAVTNPMLK	45.62	55.6142	1212.726	1213.479	1	1	distinct	1	0.6345
KAALENIFLVK	73.25	55.9258	1244.749	1245.954	4	2	shared(2)	1	0.9881
SLFSEANPQPIKK	67.04	55.0401	1457.788	1458.784	9	2	shared(2)	1	0.9812
TNVNLSPQTIAELNKLPNIVAIK	84.88	52.4278	2489.422	2490.89	12	+2,+3	shared(2)	1	0.9998

The equivalent proteins include

jgi|Phyra1_1|96539|C_scaffold_84000006	0	No title.

357. Group probability: 0.9999. Peptides of the group

KVPAVYETAHTR	66.91	55.3175	1370.731	1371.36	3	2	distinct	1	0.9802
YPSAININWYGVLPGNWGPR	82.68	53.4281	2273.138	2274.14	1	2	distinct	0	0.9964

The equivalent proteins include

jgi|Physo1_1|130440|estExt_fgenesh1_pg.C_110109	0	No title.

358. Group probability: 0.9999. Peptides of the group

HVNAQTGVTR	55.74	55.3167	1081.563	1082.303	4	2	distinct	0	0.9434
IHTFIATSDIHLK	66.27	54.765	1494.819	1495.513	7	2	shared(2)	0	0.9582
MVSHYTGMSIQPNK	71.84	54.6438	1591.749	1591.875	5	2	shared(2)	0	0.9882
HQATYEIMLPESVGLSENK	83.6	53.3235	2145.041	2146.257	2	2	shared(2)	0	0.9966

The equivalent proteins include

jgi|Phyra1_1|75281|fgenesh1_pg.C_scaffold_12000028	0	No title.

359. Group probability: 0.9999. Peptides of the group

VYETFGEDPYLVSTIAESLIK	74.53	52.8555	2373.199	2372.577	19	+2,+3	distinct	0	0.9995
DTLAAGTPWIFGPMLEISQNPLWPR	56.35	51.9285	2809.426	2810.345	5	2	shared(2)	0	0.9706

The equivalent proteins include

jgi|Phyra1_1|74163|fgenesh1_pg.C_scaffold_6000146	0	No title.

360. Group probability: 0.9999. Peptides of the group

TVYHLNPSGR	45.36	55.833	1142.583	1143.591	1	2	distinct	0	0.8577
NFDLRPGMIQK	49.48	55.4094	1317.686	1318.266	2	2	distinct	0	0.9042
FVIGGPHGDAGLTGR	79.38	54.8565	1452.747	1454.065	9	2	distinct	0	0.9941

The equivalent proteins include

gi|23394401|gb|AAN31489.1|	43150.8	S-adenosyl methionine synthetase [Phytophthora infestans]
jgi|Physo1_1|108486|estExt_fgenesh1_pm.C_110017	0	No title.
jgi|Phyra1_1|71941|fgenesh1_pm.C_scaffold_62000004	0	No title.

361. Group probability: 0.9999. Peptides of the group

SYELPDGNVIVIGDER	89.05	54.3156	1774.874	1774.202	1	2	distinct	0	0.9686
DLYCNIVLSGGTTMYPGIGER	47.6	53.1488	2315.093	2315.776	1	2	shared(2)	0	0.9251
KDLYCNIVLSGGTTMYPGIGER (0000000000000000100000000)	89.96	52.8663	2443.187	2444.683	11	2	shared(2)	1	0.9982
TTGCVLDSGDGVSHTVPIYEGYALPHAIVR	72.64	50.9814	3183.566	3184.46	9	+2,+3	shared(3)	0	0.9878

The equivalent proteins include

gi|57864652|gb|AAW56946.1|	29368.75	actin [Apodachlya brachynema]

362. Group probability: 0.9999. Peptides of the group

ARLECQSYR	52.09	55.4771	1181.561	1182.72	2	2	distinct	1	0.9195
AITVFSPDGHLFQVEYAMEAVK	95.64	52.6234	2451.214	2451.977	4	2	distinct	0	0.9989

The equivalent proteins include

jgi|Physo1_1|140976|estExt_fgenesh1_pg.C_920039	0	No title.
jgi|Phyra1_1|72879|fgenesh1_pg.C_scaffold_1000321	0	No title.

363. Group probability: 0.9999. Peptides of the group

LQGYGYDHLILK	49.25	54.9615	1418.756	1420.136	1	2	distinct	0	0.9074
LEWAKPSNKPANEDAGSMGTTFR	59.2	52.5093	2506.191	2507.207	4	+2,+3	distinct	0	0.999

The equivalent proteins include

jgi|Physo1_1|108333|estExt_fgenesh1_pm.C_60023	0	No title.
jgi|Phyra1_1|79758|fgenesh1_pg.C_scaffold_43000039	0	No title.

364. Group probability: 0.9999. Peptides of the group

VPPAAADCPSVAHVGPIAGSVR	52.69	53.3861	2127.089	2128.325	2	3	distinct	0	0.9428
KFAASIPDLPLYYPYLDPK	50.69	53.2995	2210.166	2211.274	1	2	distinct	1	0.9385
AAGAIILGTTNMHEVGSGVTGYNMHYGTAR	57.61	51.4999	3048.454	3049.597	1	3	distinct	0	0.9731

The equivalent proteins include

jgi|Physo1_1|139844|estExt_fgenesh1_pg.C_790023	0	No title.

365. Group probability: 0.9999. Peptides of the group

YIWLGDFYHTTR	64.84	54.9993	1570.757	1571.06	7	2	distinct	0	0.9764
KLALGSAPTIASTDYTK	81.95	54.1708	1735.936	1736.387	5	2	distinct	1	0.9957

The equivalent proteins include

jgi|Physo1_1|127729|estExt_fgenesh1_pg.C_20305	0	No title.

366. Group probability: 0.9999. Peptides of the group

NSWSTHWGEDGYVK	60.23	54.564	1664.722	1665.132	2	2	distinct	0	0.9674
NAPDYCHFNANNAIGR	85.82	54.1187	1832.801	1833.363	6	2	distinct	0	0.9968

The equivalent proteins include

jgi|Physo1_1|140951|estExt_fgenesh1_pg.C_920014	0	No title.

367. Group probability: 0.9999. Peptides of the group

HELEQHALTK	57.58	55.6683	1204.62	1206.032	2	2	distinct	0	0.9514
IRPVPFFGAPCSDAAGGQVDYADVQR	88.11	51.9192	2792.334	2793.317	2	3	distinct	0	0.9978

The equivalent proteins include

jgi|Physo1_1|128818|estExt_fgenesh1_pg.C_50315	0	No title.
jgi|Physo1_1|128819|estExt_fgenesh1_pg.C_50316	0	No title.

368. Group probability: 0.9999. Peptides of the group

YCGKDNFHMR	55.9	55.4096	1326.56	1327.638	1	2	distinct	1	0.944
ASVDAFPFVAHLVSDEKEQLSSEALEAAR	88.26	51.1239	3115.546	3116.407	2	3	distinct	1	0.9981

The equivalent proteins include

jgi|Physo1_1|109444|estExt_fgenesh1_pm.C_1080003	0	No title.

369. Group probability: 0.9999. Peptides of the group

ITMPNIHNNPIDLSR	95.57	54.3531	1733.888	1734.431	5	2	distinct	0	0.9986
RVLLETFAGPADAGVPSPAVQFTLYK	47.4	52.02	2746.469	2747.691	1	3	distinct	1	0.9233

The equivalent proteins include

jgi|Physo1_1|158534|C_scaffold_114000011	0	No title.

370. Group probability: 0.9999. Peptides of the group

RPTIQGIWQPDLDFPEFK	74.23	53.4817	2186.116	2186.345	9	+2,+3	distinct	0	0.9999

The equivalent proteins include

jgi|Physo1_1|128268|estExt_fgenesh1_pg.C_40112	0	No title.
jgi|Phyra1_1|77598|fgenesh1_pg.C_scaffold_25000119	0	No title.

371. Group probability: 0.9999. Peptides of the group

ETHHVAGAAVR	54.14	55.8234	1146.589	1146.51	3	+1,+2	shared(2)	0	0.9946
RLTELIGAVGGK	63.93	55.6142	1212.719	1213.39	2	2	shared(2)	1	0.9741
ELIGTANQLAENNIDLLMPGFTHLQPAQPLR (0000000000000000010000000000000)	68.19	50.4995	3429.771	3429.395	12	3	distinct	0	0.9899

The equivalent proteins include

gi|23394365|gb|AAN31472.1|	50896.16	argininosuccinate lyase [Phytophthora infestans]

372. Group probability: 0.9999. Peptides of the group

KILFVLGGPGAGK	60.34	55.7761	1255.765	1256.776	1	2	distinct	1	0.9657
FGFVHLSAGDLLR	86.24	55.0733	1430.767	1431.178	7	2	distinct	0	0.9965

The equivalent proteins include

jgi|Physo1_1|109056|estExt_fgenesh1_pm.C_550009	0	No title.
jgi|Phyra1_1|72044|fgenesh1_pm.C_scaffold_76000005	0	No title.

373. Group probability: 0.9999. Peptides of the group

RAQLEAQHAQQR	54.38	54.805	1434.744	1435.713	5	2	distinct	1	0.9412
LISGKPVYVALAQR	88.73	54.8037	1513.898	1514.684	11	+2,+3	shared(2)	0	0.9996
RQDRPDADDWTNCYVK	49.6	53.6501	2037.896	2039.321	1	3	shared(2)	1	0.9067
VPGAPAPGGYPMPGYGMPMQQQR	42.77	52.8694	2386.102	2386.479	1	2	shared(2)	0	0.8941

The equivalent proteins include

jgi|Phyra1_1|72316|fgenesh1_pm.C_scaffold_156000002	0	No title.

374. Group probability: 0.9999. Peptides of the group

IFSPDHPEAPVLR	52.34	54.8416	1476.772	1477.411	5	2	distinct	0	0.932
VAWTRPIFETLEPVWNEK	69.03	53.1842	2214.147	2214.631	16	+2,+3	distinct	0	0.9981

The equivalent proteins include

jgi|Physo1_1|139685|estExt_fgenesh1_pg.C_770024	0	No title.

375. Group probability: 0.9999. Peptides of the group

LTVSILDLVQQATNYK	85.92	54.2767	1804.993	1805.757	5	2	distinct	0	0.9968
ACGVSRPVISASITSNDASQLGPQIQSMR (00000000000000000000000000100)	53.21	51.2703	3029.502	3030.737	14	3	distinct	0	0.9592

The equivalent proteins include

jgi|Physo1_1|108166|estExt_fgenesh1_pm.C_10031	0	No title.

376. Group probability: 0.9999. Peptides of the group

VLGGEGGHGVIILSPR	90.86	54.7812	1559.878	1560.568	3	2	distinct	0	0.9979
QGVLVMNTPFGNTISAAELTLGLISAVSR	48.39	51.42	2958.585	2959.809	1	3	distinct	0	0.9375

The equivalent proteins include

jgi|Phyra1_1|80380|fgenesh1_pg.C_scaffold_48000092	0	No title.
jgi|Physo1_1|142688|estExt_fgenesh1_pg.C_1190058	0	No title.

377. Group probability: 0.9999. Peptides of the group

RIDAISR	51.57	57.3138	829.477	830.829	1	2	shared(2)	1	0.8258
YEPVGVVAAIIPWNYPALMALWK	44.25	52.3359	2600.386	2600.772	3	2	distinct	0	0.908
YIDVVNPATEEVIQQVAAASAADVDLAVQAAKR	76.36	50.3718	3424.784	3426.136	1	3	distinct	1	0.9954

The equivalent proteins include

jgi|Physo1_1|108817|estExt_fgenesh1_pm.C_340017	0	No title.

378. Group probability: 0.9999. Peptides of the group

IAYVHSLKEEAIK	48.94	55.0863	1499.835	1500.569	1	2	distinct	1	0.908
ESLNLSIVEAINQASEAWGIK	92.8	53.1216	2271.175	2271.854	8	2	distinct	0	0.9986

The equivalent proteins include

gi|23394406|gb|AAN31491.1|	40884.22	unknown [Phytophthora infestans]
jgi|Physo1_1|108840|estExt_fgenesh1_pm.C_350008	0	No title.

jgi|Phyra1_1|71814|fgenesh1_pm.C_scaffold_50000008	0	No title.

379. Group probability: 0.9999. Peptides of the group

GTKPAGFILNPELFMR	53.71	54.2325	1789.955	1790.475	1	2	distinct	0	0.9465
RHVDEDDNAAAEGSTQPQDEPPEAPSPAK	84.69	51.1507	3057.355	3058.052	1	3	distinct	1	0.9974

The equivalent proteins include

jgi|Physo1_1|136250|estExt_fgenesh1_pg.C_440051	0	No title.

380. Group probability: 0.9999. Peptides of the group

GPQKGEDLTHPLK	49.47	55.002	1418.752	1419.245	2	2	distinct	1	0.9123
HIAPGMVQQMQSVCPDCR	92.58	53.4152	2112.933	2114.179	5	2	distinct	0	0.9984

The equivalent proteins include

jgi|Physo1_1|109267|estExt_fgenesh1_pm.C_820001	0	No title.
jgi|Phyra1_1|71919|fgenesh1_pm.C_scaffold_60000001	0	No title.

381. Group probability: 0.9999. Peptides of the group

SHMQYWQFGIK (0001000000000)	58.35	54.8999	1423.671	1424.332	2	2	distinct	0	0.9569
KAGKPVVLEEYGIK	86.15	55.231	1529.882	1530.863	6	2	distinct	1	0.9966

The equivalent proteins include

jgi|Physo1_1|130996|estExt_fgenesh1_pg.C_130187	0	No title.

382. Group probability: 0.9999. Peptides of the group

KIWLDPNESNEIALANSR	95.33	53.7285	2069.054	2069.951	4	+2,+3	distinct	1	0.9999

The equivalent proteins include

jgi|Physo1_1|109394|estExt_fgenesh1_pm.C_980010	0	No title.
jgi|Phyra1_1|41624|gwEuk.14.157.1	0	No title.

383. Group probability: 0.9998. Peptides of the group

IAKPSVDMNSHQR	51.47	54.6409	1481.741	1482.252	1	2	distinct	0	0.927
LQIWGLSGGGNPACRPPK	89.87	54.0519	1906.984	1907.597	1	2	distinct	0	0.9979

The equivalent proteins include

jgi|Physo1_1|157072|C_scaffold_34000036	0	No title.

384. Group probability: 0.9998. Peptides of the group

VCLIGDGQVSLGHTVVKPNAK	85.11	53.7865	2191.178	2192.318	4	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|120016|estExt_Genewise1.C_700075	0	No title.

385. Group probability: 0.9998. Peptides of the group

VIMATNAIESLDPALIRPGR	84.99	53.2922	2136.172	2137.474	1	3	distinct	0	0.9964
EAVELPLTHPELYEGIGIRPPK	55.41	52.6677	2457.327	2458.578	1	3	distinct	0	0.9556

The equivalent proteins include

jgi|Physo1_1|108382|estExt_fgenesh1_pm.C_70027	0	No title.
jgi|Phyra1_1|71237|fgenesh1_pm.C_scaffold_9000016	0	No title.

386. Group probability: 0.9998. Peptides of the group

QVHPETGISKR	45.47	55.5035	1250.673	1251.306	1	2	distinct	1	0.8649
RVESYSTYIYK	45.73	54.9645	1407.703	1408.053	1	2	distinct	1	0.8694
GMSIMNSFINDIFER	91.12	54.3152	1772.823	1773.621	5	2	distinct	0	0.9908

The equivalent proteins include

jgi|Physo1_1|108804|estExt_fgenesh1_pm.C_340004	0	No title.
jgi|Physo1_1|108813|estExt_fgenesh1_pm.C_340013	0	No title.
jgi|Phyra1_1|71905|fgenesh1_pm.C_scaffold_59000006	0	No title.
jgi|Phyra1_1|71916|fgenesh1_pm.C_scaffold_59000017	0	No title.

387. Group probability: 0.9998. Peptides of the group

LTHTGFTHTGPCEVWCDDTK	78.06	52.8831	2361.015	2361.493	13	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|131638|estExt_fgenesh1_pg.C_160182	0	No title.

388. Group probability: 0.9998. Peptides of the group

AQSSHQMVLKPK	52.96	55.1245	1352.723	1353.869	1	2	distinct	0	0.9329
AYFQQLLKPESVLTDADDTEPYTVDWLKK	85.14	50.4432	3412.708	3414.135	2	3	distinct	1	0.9976

The equivalent proteins include

jgi|Physo1_1|108284|estExt_fgenesh1_pm.C_40035	0	No title.

389. Group probability: 0.9998. Peptides of the group

HIEENPEFLQPEVR	62.62	54.1884	1735.853	1736.581	1	2	distinct	0	0.9737
IAQTAEAAGVTPQQLVDKYAGIFQQLTK	74.86	51.3965	2988.592	2990.073	3	3	distinct	1	0.9937

The equivalent proteins include

jgi|Physo1_1|158682|C_scaffold_127000002	0	No title.

390. Group probability: 0.9998. Peptides of the group

RVLIVGGGDGGVLR	74.95	55.0602	1366.804	1367.928	4	2	distinct	1	0.9507
YYSAQIHEAAFVLPAFAER	82.61	53.2695	2182.085	2183.357	14	2	distinct	0	0.9963

The equivalent proteins include

jgi|Physo1_1|109524|estExt_fgenesh1_pm.C_1260004	0	No title.

391. Group probability: 0.9998. Peptides of the group

LGALPHGGGGIGLER	54.78	55.2046	1402.768	1404.245	11	+2,+3	distinct	0	0.9962
AAAAAAGPTLTDTYGELPLIQSQERPNK	51.46	51.6923	2882.477	2883.525	2	3	distinct	0	0.9503

The equivalent proteins include

jgi|Physo1_1|108386|estExt_fgenesh1_pm.C_70031	0	No title.

392. Group probability: 0.9998. Peptides of the group

SFDLVVIPGGMPGAEHLR	84.43	53.9498	1893.977	1894.831	11	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|142787|estExt_fgenesh1_pg.C_1220014	0	No title.

393. Group probability: 0.9998. Peptides of the group

GALASRPHK	51.01	55.6565	935.53	936.217	1	2	distinct	0	0.678
ANIAGKPVVTATQMLESMIK	59.63	53.4265	2101.127	2102.528	1	3	shared(3)	0	0.9666
IFCTLGPACWSQEGIGELIDAGMNVAR	69.77	51.3344	2964.393	2964.516	13	+2,+3	distinct	0	0.9979

The equivalent proteins include

jgi|Physo1_1|109368|estExt_fgenesh1_pm.C_950013	0	No title.
jgi|Phyra1_1|72241|fgenesh1_pm.C_scaffold_114000010	0	No title.

394. Group probability: 0.9998. Peptides of the group

KGGSSFLQR	73.94	55.604	978.525	979.138	4	2	distinct	1	0.9263
QIQSSVGSLKDEMIAQNAALSK	54.16	52.9507	2317.195	2318.557	2	+2,+3	distinct	1	0.9972

The equivalent proteins include

jgi|Physo1_1|155469|C_scaffold_4000037	0	No title.

395. Group probability: 0.9998. Peptides of the group

LVNSEHVGLIHVK	68.51	55.0238	1443.82	1444.229	3	2	distinct	0	0.9835
MTNPVNVEFISDKLTQFLR	68.83	53.5565	2251.167	2252.026	2	2	distinct	1	0.9874

The equivalent proteins include

jgi|Physo1_1|134211|estExt_fgenesh1_pg.C_300122	0	No title.
jgi|Phyra1_1|76157|fgenesh1_pg.C_scaffold_16000111	0	No title.

396. Group probability: 0.9998. Peptides of the group

HAVEDVKDVAAK	77.92	55.2184	1280.672	1281.49	2	2	distinct	1	0.9925
QEEHVVWNAAPKPNATTTEK	59.13	53.1907	2249.108	2249.555	3	2	distinct	0	0.9717

The equivalent proteins include

jgi|Physo1_1|129292|estExt_fgenesh1_pg.C_70117	0	No title.

397. Group probability: 0.9998. Peptides of the group

NADLKPHQQLVTSEPCVR	79.43	53.4371	2091.053	2091.497	1	2	distinct	0	0.9949
TPEVLQLSVDHKPDLEFEK	57.4	53.211	2223.142	2224.152	1	3	distinct	0	0.9581

The equivalent proteins include

jgi|Physo1_1|108204|estExt_fgenesh1_pm.C_20036	0	No title.

398. Group probability: 0.9998. Peptides of the group

KGMDVLTSHPR	80.69	55.2471	1239.639	1240.49	3	2	distinct	1	0.9939
MELSLHGQGSHR	60.3	55.1629	1350.646	1351.577	2	2	distinct	0	0.9647

The equivalent proteins include

jgi|Physo1_1|155940|C_scaffold_9000120	0	No title.

399. Group probability: 0.9998. Peptides of the group

QRPLHMSYDIDAVDPLVAPSTGTR	52.51	52.2435	2638.317	2639.345	1	3	distinct	0	0.9471
NALLSLPHAVSVIGAPMTYGQPLLGTDGGPDLLR	77.21	50.4332	3442.828	3443.719	2	3	distinct	0	0.9959

The equivalent proteins include

jgi|Physo1_1|141130|estExt_fgenesh1_pg.C_940041	0	No title.

400. Group probability: 0.9998. Peptides of the group

FAAHDVLR	48.68	56.7394	927.493	928.221	1	2	distinct	0	0.8886
SHLHDLEEK	46.67	55.4206	1106.536	1107.121	1	2	distinct	0	0.8707
LSSAGLVYNHFGR	69.47	54.9455	1419.726	1420.464	8	2	distinct	0	0.9848

The equivalent proteins include

jgi|Physo1_1|108501|estExt_fgenesh1_pm.C_120011	0	No title.

401. Group probability: 0.9998. Peptides of the group

DMVVLPGFVDAHTHPVWSGNR (00100000000000000000000)	83.76	52.8801	2333.137	2333.835	5	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|109335|estExt_fgenesh1_pm.C_920001	0	No title.
jgi|Phyra1_1|71048|fgenesh1_pm.C_scaffold_1000028	0	No title.

402. Group probability: 0.9998. Peptides of the group

LFADVNIQPLHLK	76.23	54.7713	1506.856	1506.986	8	2	distinct	0	0.9916
HCQPETCTLCPGDMATTTCCIPLKGGR	58.6	51.1386	3120.338	3121.296	1	3	distinct	1	0.9728

The equivalent proteins include

jgi|Physo1_1|156853|C_scaffold_30000028	0	No title.

403. Group probability: 0.9998. Peptides of the group

IIGHGDNIYWNGAGPDDIDYR	91.18	52.9031	2360.082	2360.561	4	+2,+3	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|130258|estExt_fgenesh1_pg.C_100216	0	No title.
jgi|Phyra1_1|72730|fgenesh1_pg.C_scaffold_1000172	0	No title.

404. Group probability: 0.9998. Peptides of the group

FNWTDLYPADVQAHAK	64.62	54.0921	1874.895	1875.782	5	+2,+3	distinct	0	0.9971
KLPHHDEIHATLDTFLASSGLK	46.08	52.7586	2429.27	2430.572	1	2	distinct	1	0.9181

The equivalent proteins include

jgi|Phyra1_1|82229|fgenesh1_pg.C_scaffold_69000053	0	No title.

405. Group probability: 0.9998. Peptides of the group

TLYTPSVSGIVDVLHVDIGADDSAK	111.16	52.5334	2571.307	2572.386	2	2	distinct	0	0.9998

The equivalent proteins include

jgi|Physo1_1|137030|estExt_fgenesh1_pg.C_500066	0	No title.
jgi|Phyra1_1|83894|fgenesh1_pg.C_scaffold_99000016	0	No title.

406. Group probability: 0.9998. Peptides of the group

YISELHANAVNAYHDK	73.26	54.2659	1843.885	1844.443	1	2	distinct	0	0.9904
YISELHANAVNAYHDKK	61.63	53.7177	1971.98	1972.306	2	2	distinct	1	0.9745

The equivalent proteins include

jgi|Physo1_1|130818|estExt_fgenesh1_pg.C_130009	0	No title.

407. Group probability: 0.9997. Peptides of the group

AVLTCKPEYAYGASGSPPK	74.69	53.7927	1994.977	1995.387	1	2	distinct	0	0.9924
AVLTCKPEYAYGASGSPPKIPANATLK	55.74	51.8206	2803.458	2804.813	3	3	distinct	1	0.9645

The equivalent proteins include

jgi|Physo1_1|121523|estExt_Genewise1.C_930008	0	No title.

408. Group probability: 0.9997. Peptides of the group

TKPFPWPESNCDLLDFDCK	69.17	52.9608	2368.05	2368.213	14	+2,+3	distinct	0	0.9997

The equivalent proteins include

jgi|Physo1_1|157932|C_scaffold_70000016	0	No title.

409. Group probability: 0.9997. Peptides of the group

FHAAPFAEFAMLESR	59.09	54.2527	1722.819	1723.621	3	3	distinct	0	0.9574
YVDEHFGGPAVLAPAANRPEIK	49.21	53.0546	2350.207	2350.567	4	+2,+3	distinct	0	0.9931

The equivalent proteins include

jgi|Physo1_1|145035|estExt_fgenesh1_pg.C_4180004	0	No title.

410. Group probability: 0.9997. Peptides of the group

SMHQGHTAAGQGETSTTQQSAGATR	111.06	52.6672	2499.116	2500.441	6	3	distinct	0	0.9997

The equivalent proteins include

jgi|Physo1_1|145389|estExt_fgenesh1_pg.C_11390001	0	No title.

411. Group probability: 0.9997. Peptides of the group

IRLENEIQTYR	55.92	54.8968	1433.763	1434.654	3	2	shared(2)	1	0.9466

YCVQLSQIQAQISALEEQLQQIR	92.55	52.0356	2745.412	2745.865	6	2	distinct	0	0.9987

The equivalent proteins include

gi|307086|gb|AAA59468.1|	46472.64	keratin-10
gi|109115260|ref|XP_001100571.1|	62234.46	PREDICTED: similar to keratin 10 isoform 2 [Macaca mulatta]
gi|109115262|ref|XP_001100664.1|	57718.17	PREDICTED: similar to keratin 10 isoform 3 [Macaca mulatta]
gi|109115264|ref|XP_001100476.1|	56875.85	PREDICTED: similar to keratin 10 isoform 1 [Macaca mulatta]
gi|547749|sp|P13645|K1C10_HUMAN	59710.96	Keratin, type I cytoskeletal 10 (Cytokeratin-10) (CK-10) (Keratin-10) (K10)
gi|55645505|ref|XP_523631.1|	94764.75	PREDICTED: similar to keratin 25D; type I inner root sheath specific keratin 25 irs4 [Pan troglodyt
gi|186629|gb|AAA59199.1|	39832.12	keratin 10
gi|40354192|ref|NP_000412.2|	59019.73	keratin 10 [Homo sapiens]

412. Group probability: 0.9997. Peptides of the group

ALGWNGHVAGTR	69.86	55.1519	1237.632	1238.288	6	2	distinct	0	0.9848
VEWLLQEGDEVKPSSVPGGKVPVAR	63.06	52.1321	2675.428	2676.475	3	3	distinct	1	0.9798

The equivalent proteins include

jgi|Physo1_1|158900|C_scaffold_173000011	0	No title.

413. Group probability: 0.9997. Peptides of the group

KIAVNLIPFPR	70.88	55.3745	1266.781	1267.527	5	2	shared(6)	1	0.9855
GHYTEGAELIDSVLDVVR	50.71	53.7352	1971.99	1972.76	1	2	shared(5)	0	0.7947
SGPFGQIFRPDNFVFGQTGAGNNWAK	79.99	52.236	2811.352	2812.533	9	+2,+3	distinct	0	0.9989

The equivalent proteins include

gi|65428041|gb|AAY42541.1|	43730.52	beta-tubulin [Micromonas pusilla]
gi|65428055|gb|AAY42548.1|	43765.39	beta-tubulin [Micromonas pusilla]
gi|65428067|gb|AAY42554.1|	43753.39	beta-tubulin [Micromonas pusilla]
gi|65428069|gb|AAY42555.1|	43749.39	beta-tubulin [Micromonas pusilla]

414. Group probability: 0.9997. Peptides of the group

VFCMHGGLSPSIDTLDHAR	77.01	53.4888	2111.988	2112.481	3	2	distinct	0	0.9939
YFTDLFDHLPMTALIENR	52.74	53.2927	2195.072	2195.136	2	2	distinct	0	0.9468

The equivalent proteins include

gi|23394371|gb|AAN31475.1|	37225.02	serine/threonine protein phosphatase [Phytophthora infestans]
jgi|Physo1_1|109080|estExt_fgenesh1_pm.C_580005	0	No title.
jgi|Phyra1_1|71426|fgenesh1_pm.C_scaffold_18000017	0	No title.

415. Group probability: 0.9997. Peptides of the group

VNFYHTGPNGER	47.65	55.3411	1389.642	1389.958	1	2	distinct	0	0.8927
WWNDDHAAANQTEAMR	86.12	53.8932	1914.807	1914.971	2	2	distinct	0	0.9969

The equivalent proteins include

jgi|Physo1_1|138692|estExt_fgenesh1_pg.C_660011	0	No title.

416. Group probability: 0.9997. Peptides of the group

VAVHEPTLHPNSEELIIGK	57.65	53.5425	2082.111	2082.786	1	2	distinct	0	0.9664
ELDTLLGYDELANVPFLVLGNK	70.07	52.574	2432.284	2433.759	2	2	distinct	0	0.99

The equivalent proteins include

gi|23394386|gb|AAN31482.1|	22024.34	GTP binding protein [Phytophthora infestans]
jgi|Physo1_1|109427|estExt_fgenesh1_pm.C_1040002	0	No title.
jgi|Phyra1_1|71111|fgenesh1_pm.C_scaffold_3000020	0	No title.

417. Group probability: 0.9997. Peptides of the group

FAADVVAPHAR	63.01	55.2254	1152.604	1154.096	1	2	distinct	0	0.9712
VDPVVGLLCDLQNTVVNNVFLVHGSQAQK	67.39	51.3584	3162.649	3164.003	5	3	distinct	0	0.9882

The equivalent proteins include

jgi|Physo1_1|109319|estExt_fgenesh1_pm.C_900005	0	No title.

418. Group probability: 0.9997. Peptides of the group

LQVLTAPHPVFTR	59.59	54.767	1477.84	1478.286	4	2	distinct	0	0.9641
RVGPGFIQQFQTTCDK	73.12	54.0626	1880.92	1881.363	1	2	distinct	1	0.9903

The equivalent proteins include

jgi|Physo1_1|140557|estExt_fgenesh1_pg.C_870004	0	No title.

419. Group probability: 0.9996. Peptides of the group

MYLHDHEQFLSTAR	73.87	54.2787	1746.815	1747.538	1	2	distinct	0	0.9902
IWHPNISSQTGAICLDILK	56.65	53.3238	2165.13	2165.992	1	2	distinct	0	0.9635

The equivalent proteins include

jgi|Physo1_1|136669|estExt_fgenesh1_pg.C_470083	0	No title.
jgi|Physo1_1|142734|estExt_fgenesh1_pg.C_1210001	0	No title.
jgi|Physo1_1|143955|estExt_fgenesh1_pg.C_1590030	0	No title.

420. Group probability: 0.9996. Peptides of the group

HGVYSWPLCGNAPDALDHGVAAAGYGVYK	107.03	51.2522	3044.424	3045.78	1	3	distinct	0	0.9996

The equivalent proteins include

gi|66270081|gb|AAY43370.1|	42024.12	cathepsin-like cysteine protease [Phytophthora infestans]
jgi|Physo1_1|108512|estExt_fgenesh1_pm.C_130003	0	No title.
jgi|Phyra1_1|46478|gwEuk.29.18.1	0	No title.

421. Group probability: 0.9996. Peptides of the group

GGHIPGSLNVPFGK	46.6	55.0802	1378.736	1379.46	1	2	distinct	0	0.891
YFGHDSVHILNGGITK	85.33	54.2477	1756.89	1757.615	5	2	distinct	0	0.9967

The equivalent proteins include

jgi|Physo1_1|144222|estExt_fgenesh1_pg.C_1730012	0	No title.

422. Group probability: 0.9996. Peptides of the group

ANIAGKPVVTATQMLESMIK	59.63	53.4265	2101.127	2102.528	1	3	shared(3)	0	0.9666
IFCTLGPACWSEEGLGELIDAGMNVAR	63.61	51.3206	2965.377	2964.766	17	+2,+3	distinct	0	0.9987

The equivalent proteins include

jgi|Phyra1_1|72242|fgenesh1_pm.C_scaffold_114000011	0	No title.
jgi|Phyra1_1|72259|fgenesh1_pm.C_scaffold_121000001	0	No title.

423. Group probability: 0.9996. Peptides of the group

GPYASMYTAKPWTVR	76.41	54.364	1726.85	1727.484	5	2	distinct	0	0.9924
TPEGIPIKPLYTQGDLEGLDVAQAPGTFPFTR	49.46	50.4789	3427.766	3428.978	4	3	distinct	0	0.9499

The equivalent proteins include

jgi|Physo1_1|108209|estExt_fgenesh1_pm.C_20041	0	No title.

424. Group probability: 0.9996. Peptides of the group

VFSSSIFKPGFK	53.04	55.4401	1342.728	1343.431	2	2	distinct	0	0.933
MLAQLLEHGTTGAPIEEDPASHPLFK (01000000000000000000000000)	76.84	51.8981	2801.406	2802.899	5	3	distinct	0	0.9942

The equivalent proteins include

jgi|Physo1_1|138999|estExt_fgenesh1_pg.C_690008	0	No title.

425. Group probability: 0.9996. Peptides of the group

HIGGCDAVMALHAK	75.35	54.9181	1478.712	1479.416	8	+2,+3	distinct	0	0.9996

The equivalent proteins include

jgi|Physo1_1|135082|estExt_fgenesh1_pg.C_350134	0	No title.
jgi|Physo1_1|139165|estExt_fgenesh1_pg.C_700100	0	No title.

426. Group probability: 0.9996. Peptides of the group

KLLGMAGIEDCYTSAR	109.69	54.3416	1783.86	1785.246	1	2	distinct	1	0.9996

The equivalent proteins include

jgi|Physo1_1|109513|estExt_fgenesh1_pm.C_1230003	0	No title.
jgi|Phyra1_1|71491|fgenesh1_pm.C_scaffold_23000001	0	No title.

427. Group probability: 0.9996. Peptides of the group

RPETSFQAADR	65.26	55.539	1276.616	1277.376	1	2	distinct	0	0.9762
SAPALAFGNSMVFKPSEETPLTALK	62.85	52.3903	2605.346	2606.745	1	2	distinct	0	0.9832

The equivalent proteins include

jgi|Physo1_1|157598|C_scaffold_53000023	0	No title.

428. Group probability: 0.9996. Peptides of the group

SPLLFNMDEIHGGSPWGAGTLAGADGSR (0000000100000000000000000000)	85.39	52.05	2828.319	2826.985	36	+2,+3	distinct	0	0.9996

The equivalent proteins include

jgi|Phyra1_1|51797|gwEuk.62.126.1	0	No title.

429. Group probability: 0.9996. Peptides of the group

IPVVASSGAGKPEHFTEVFEK	64.34	53.297	2228.148	2229.527	3	+2,+3	distinct	0	0.9996

The equivalent proteins include

jgi|Physo1_1|109060|estExt_fgenesh1_pm.C_550013	0	No title.

430. Group probability: 0.9996. Peptides of the group

FFDELPADNTIEATQYLTHVQAGTEPFQGK	44.52	50.5962	3366.604	3368.08	1	3	distinct	0	0.9168
KFFDELPADNTIEATQYLTHVQAGTEPFQGK	75.65	50.3532	3494.699	3495.464	5	3	distinct	1	0.9948

The equivalent proteins include

gi|49476326|gb|AAT66504.1|	26598.74	cell 12A endoglucanase [Phytophthora sojae]
jgi|Physo1_1|109281|estExt_fgenesh1_pm.C_840003	0	No title.

431. Group probability: 0.9995. Peptides of the group

CDDEGCHEALHSLVEDEVR	69.33	53.0466	2268.938	2270.266	4	+2,+3	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|137720|estExt_fgenesh1_pg.C_560094	0	No title.

432. Group probability: 0.9995. Peptides of the group

NNPPHILVGTPGR	69.27	55.2949	1370.742	1371.227	10	2	distinct	0	0.9845
LTLHGLQQYYIK	62.14	54.861	1475.814	1476.534	9	2	distinct	0	0.9702

The equivalent proteins include

jgi|Physo1_1|108807|estExt_fgenesh1_pm.C_340007	0	No title.
jgi|Phyra1_1|71909|fgenesh1_pm.C_scaffold_59000010	0	No title.

433. Group probability: 0.9995. Peptides of the group

TTRPPEAPGAASVQPAVIGFDMGGTSTDVSR	103.45	51.2646	3071.498	3072.567	4	3	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|108268|estExt_fgenesh1_pm.C_40019	0	No title.

434. Group probability: 0.9995. Peptides of the group

HGIVSCSQPLASEIGLR	107.41	54.0674	1822.936	1823.532	2	2	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|109055|estExt_fgenesh1_pm.C_550008	0	No title.

435. Group probability: 0.9995. Peptides of the group

HGHTDQLYPEEALELQR	79.43	54.3434	2034.976	2034.876	5	+2,+3	distinct	0	0.9995

The equivalent proteins include

jgi|Physo1_1|128423|estExt_fgenesh1_pg.C_40267	0	No title.

436. Group probability: 0.9995. Peptides of the group

WTVLHEGTCSR	57.2	55.4624	1344.624	1345.372	5	+1,+2	distinct	0	0.9956
CVFDHENCNSGNK	46.95	54.7932	1579.614	1580.257	2	2	distinct	0	0.8911

The equivalent proteins include

gi|27922927|gb|AAO24652.1|	8659	unknown protein [Phytophthora sojae]

437. Group probability: 0.9995. Peptides of the group

RLDACSSLK	52.75	55.7254	1048.533	1049.64	1	2	distinct	1	0.9236
SACQSQLVHYR	52.91	55.2767	1347.635	1347.992	2	2	distinct	0	0.93
EVLPRPDLFNHCGQGFNQGK	45.77	53.0274	2312.112	2313.27	1	2	distinct	0	0.9091

The equivalent proteins include

jgi|Physo1_1|128351|estExt_fgenesh1_pg.C_40195	0	No title.

438. Group probability: 0.9995. Peptides of the group

VAVDAAVASSQPHNFLGLNEHGLASIVR	103.9	51.6682	2871.499	2872.958	1	3	distinct	0	0.9995

The equivalent proteins include

gi|23394399|gb|AAN31488.1|	41132.38	DAHP synthase [Phytophthora infestans]
jgi|Physo1_1|108202|estExt_fgenesh1_pm.C_20034	0	No title.
jgi|Physo1_1|109603|estExt_fgenesh1_pm.C_1630002	0	No title.
jgi|Phyra1_1|71151|fgenesh1_pm.C_scaffold_5000020	0	No title.
jgi|Phyra1_1|72096|fgenesh1_pm.C_scaffold_85000004	0	No title.

439. Group probability: 0.9995. Peptides of the group

HLGIMVGMNQK (0000000010000)	58.19	55.6572	1242.621	1243.958	1	2	distinct	0	0.7893

SYELPDGNVIVIGNER	105.1	54.3156	1773.89	1774.202	1	2	shared(2)	0	0.9923
YPIEHGIVTNWDDMEK (0000000000000001000)	89.61	53.9432	1945.888	1946.177	23	+2,+3	shared(4)	0	0.9983
VAPEEHPVLLTEAPINPK	81.4	53.7548	1953.057	1953.885	13	2	shared(10)	0	0.9887
TTGCVLDSGDGVSHTVPIYEGYALPHAIVR	72.64	50.9814	3183.566	3184.46	9	+2,+3	shared(3)	0	0.9878

The equivalent proteins include

gi|3181|emb|CAA33907.1|	42303.02	unnamed protein product [Phytophthora megasperma]
jgi|Physo1_1|108972|estExt_fgenesh1_pm.C_480001	0	No title.

440. Group probability: 0.9995. Peptides of the group

VLAAQPSKPATSGGQK	50.37	54.7068	1538.842	1539.455	3	2	distinct	0	0.9276
EHNIDLHDVEGTGPQGR	76.49	54.4681	1872.871	1873.198	1	2	distinct	0	0.993

The equivalent proteins include

jgi|Physo1_1|108462|estExt_fgenesh1_pm.C_100021	0	No title.

441. Group probability: 0.9995. Peptides of the group

TYLGRPGNNVK	44.9	55.6621	1217.652	1218.494	1	2	distinct	0	0.8575
LHIPAENFPFCTIDPNDAVVPLPDQR	49.54	51.3534	2974.465	2975.956	2	3	distinct	0	0.9373
FNWLVDKYQPASVVPPVISITDIAGLVR	49.75	51.5851	3096.701	3097.932	1	3	distinct	1	0.9424

The equivalent proteins include

jgi|Physo1_1|108759|estExt_fgenesh1_pm.C_300010	0	No title.

442. Group probability: 0.9995. Peptides of the group

MYSEHHLVPSVADAVR	63.16	54.2141	1809.883	1810.525	4	2	distinct	0	0.9766
TGDLLGSMALPAGQLWYLEELTR	60.32	52.6122	2533.289	2533.614	1	2	distinct	0	0.9774

The equivalent proteins include

jgi|Physo1_1|134170|estExt_fgenesh1_pg.C_300081	0	No title.

443. Group probability: 0.9995. Peptides of the group

LLLAYESYLR	60.02	55.1716	1239.686	1239.858	1	2	distinct	0	0.9612
RLLLAYESYLR	51.23	54.9973	1395.787	1396.328	3	+2,+3	distinct	1	0.9863

The equivalent proteins include

jgi|Physo1_1|135245|estExt_fgenesh1_pg.C_370014	0	No title.
jgi|Phyra1_1|75750|fgenesh1_pg.C_scaffold_14000112	0	No title.

444. Group probability: 0.9994. Peptides of the group

LLHAPQLWAKGAK	57.81	55.0554	1431.835	1432.918	7	2	distinct	1	0.9578
YVIKPDFVAPGVGIR	70.22	54.6438	1629.924	1631.052	7	2	distinct	0	0.9869

The equivalent proteins include

jgi|Physo1_1|132390|estExt_fgenesh1_pg.C_200162	0	No title.

445. Group probability: 0.9994. Peptides of the group

VISDSPLVALFAQSLLVR	104.81	53.904	1927.114	1928.03	4	2	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|141161|estExt_fgenesh1_pg.C_950009	0	No title.

446. Group probability: 0.9994. Peptides of the group

HIITTQIEHK	49.43	55.6189	1218.672	1219.546	2	2	distinct	0	0.9009
VRLEPIISGGGQER	80.08	54.6265	1509.826	1511.012	1	2	distinct	1	0.9943

The equivalent proteins include

jgi|Physo1_1|108984|estExt_fgenesh1_pm.C_490001	0	No title.
jgi|Phyra1_1|46300|gwEuk.28.17.1	0	No title.

447. Group probability: 0.9994. Peptides of the group

IIDLHAPSDIVK	52.91	55.3741	1319.745	1320.987	2	2	distinct	0	0.9323
RIIDLHAPSDIVK	45.7	54.8579	1475.846	1476.418	2	2	distinct	1	0.8783
KSPCGEGTNTWDR	52.04	54.7714	1506.652	1506.975	1	2	distinct	1	0.9303

The equivalent proteins include

jgi|Physo1_1|108371|estExt_fgenesh1_pm.C_70016	0	No title.
jgi|Phyra1_1|72291|fgenesh1_pm.C_scaffold_132000003	0	No title.

448. Group probability: 0.9994. Peptides of the group

HAAWYATMSQMPGSR (00000000100000000)	105.79	54.3572	1692.75	1693.708	11	2	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|108424|estExt_fgenesh1_pm.C_90020	0	No title.

jgi|Phyra1_1|71081|fgenesh1_pm.C_scaffold_2000022	0	No title.

449. Group probability: 0.9994. Peptides of the group

IYKPVLPPSVTPMFDAYNDR	43.41	53.1065	2322.172	2323.527	2	+2,+3	distinct	0	0.9836
EALANAADAEPLNDADLQEVEQLVHQLLQK	53.7	50.9538	3284.652	3285.924	2	3	distinct	0	0.9625

The equivalent proteins include

jgi|Physo1_1|142328|estExt_fgenesh1_pg.C_1120012	0	No title.
jgi|Phyra1_1|84680|fgenesh1_pg.C_scaffold_121000007	0	No title.

450. Group probability: 0.9994. Peptides of the group

GFTLGTPVALFVPNENVRPK	73.51	53.2738	2155.179	2156.657	4	2	distinct	0	0.992
RGSEHNDPFCAGSEAERPEK	50.04	53.3919	2271.993	2273.342	1	3	distinct	1	0.9226

The equivalent proteins include

jgi|Physo1_1|110337|estExt_Genewise1.C_20183	0	No title.

451. Group probability: 0.9994. Peptides of the group

WGLPVGPITLADEVGLDVAYHVNQTLSK	44.29	51.4104	2991.57	2992.689	1	3	distinct	0	0.9073
MGLVNQVADPYALENAAISAAQQLAAGSLKPK	72.47	51.1119	3238.702	3239.997	7	3	distinct	0	0.9932

The equivalent proteins include

jgi|Physo1_1|109291|estExt_fgenesh1_pm.C_850003	0	No title.

452. Group probability: 0.9994. Peptides of the group

VYLNSDSLLLNILHDTQQSYGK	101.59	52.5824	2520.286	2521.064	3	2	distinct	0	0.9994

The equivalent proteins include

jgi|Physo1_1|109387|estExt_fgenesh1_pm.C_980003	0	No title.

453. Group probability: 0.9994. Peptides of the group

KIFPSALVLSPTR	78.22	55.0432	1427.85	1429.107	7	2	distinct	1	0.9929
VNEVGYHGDLRPNER	50.38	54.2225	1753.85	1755.023	1	3	distinct	0	0.9087

The equivalent proteins include

jgi|Physo1_1|108834|estExt_fgenesh1_pm.C_350002	0	No title.

454. Group probability: 0.9994. Peptides of the group

EYYDFLSAYSAVNQGHCHPK	61.95	52.8662	2385.048	2386.032	8	2	shared(2)	0	0.9781
AFYNNVLGEYQEYMTNLLGFDR (00000000000000010000000000)	48.02	52.2221	2672.222	2671.778	3	2	distinct	0	0.9316
GLLNAIIINERPNQPDALQLCMNLAK	80.94	51.4911	2918.547	2919.912	2	3	shared(2)	0	0.996

The equivalent proteins include

jgi|Phyra1_1|71772|fgenesh1_pm.C_scaffold_46000006	0	No title.
jgi|Phyra1_1|72413|fgenesh1_pm.C_scaffold_616000001	0	No title.

455. Group probability: 0.9993. Peptides of the group

MDYAVHPAALTAEAHPDLLR	74.35	53.7967	2190.089	2191.558	2	+2,+3	distinct	0	0.9993

The equivalent proteins include

jgi|Physo1_1|137242|estExt_fgenesh1_pg.C_520032	0	No title.

456. Group probability: 0.9993. Peptides of the group

YISGLGVHWYR	55.34	55.1988	1349.688	1350.819	1	2	distinct	0	0.9435
TFTLTLPGHSMQTVILPASDATK	67.25	52.7868	2428.267	2428.719	2	2	distinct	0	0.9876

The equivalent proteins include

jgi|Physo1_1|108522|estExt_fgenesh1_pm.C_140002	0	No title.

457. Group probability: 0.9993. Peptides of the group

ILTAVFEHNFSTR	61.64	54.7491	1533.794	1534.763	1	2	distinct	0	0.97
VSVLPLSNNPAFEPFAAELEHVFVEEGLECK	58.53	50.2639	3470.707	3471.915	3	3	distinct	0	0.9766

The equivalent proteins include

jgi|Phyra1_1|71152|fgenesh1_pm.C_scaffold_5000021	0	No title.
jgi|Physo1_1|144620|estExt_fgenesh1_pg.C_2160001	0	No title.

458. Group probability: 0.9993. Peptides of the group

LAGVHVPQPK	62.1	56.2474	1044.608	1045.061	13	2	distinct	0	0.9669
IAGYITHLMK	60.17	55.8234	1145.627	1146.524	4	2	distinct	0	0.9612
LTLDFDTNKR	46.67	55.21	1221.635	1222.212	1	2	distinct	1	0.4399

The equivalent proteins include

jgi|Physo1_1|138845|estExt_fgenesh1_pg.C_670047	0	No title.

459. Group probability: 0.9993. Peptides of the group

YTALTPPLSLSQGEVTNTFHR	66.53	52.968	2331.186	2330.893	3	2	distinct	0	0.9858
MGNIEYDVPVCDPETHPGCVHTLSTR	51.77	51.3987	2983.326	2984.444	3	3	distinct	0	0.9484

The equivalent proteins include

jgi|Physo1_1|135755|estExt_fgenesh1_pg.C_400092	0	No title.

460. Group probability: 0.9993. Peptides of the group

VNRPSLMVYGGTIR	52.82	54.8759	1561.84	1562.952	6	+2,+3	distinct	0	0.9908
TLAENLENVPDLSDNHEIIHPVDRPLK	46.29	51.2081	3077.578	3078.571	1	3	distinct	0	0.9197

The equivalent proteins include

jgi|Physo1_1|109044|estExt_fgenesh1_pm.C_540018	0	No title.
jgi|Physo1_1|109043|estExt_fgenesh1_pm.C_540017	0	No title.
jgi|Phyra1_1|50037|gwEuk.5.257.1	0	No title.
jgi|Phyra1_1|87317|fgenesh1_pg.C_scaffold_1819000001	0	No title.

461. Group probability: 0.9993. Peptides of the group

RDQVSQQIAK	50.37	55.788	1171.631	1173.033	1	2	distinct	1	0.9084
SIVAQYDAVELLAR	76.25	55.1327	1546.835	1547.88	2	2	distinct	0	0.9919

The equivalent proteins include

jgi|Physo1_1|109518|estExt_fgenesh1_pm.C_1240004	0	No title.
jgi|Phyra1_1|71545|fgenesh1_pm.C_scaffold_26000002	0	No title.

462. Group probability: 0.9992. Peptides of the group

VGGSEDNVIAMHAVNNYFSDNTGHAFDVSQR	97.3	50.6257	3350.501	3351.643	1	3	distinct	0	0.9992

The equivalent proteins include

jgi|Physo1_1|145391|estExt_fgenesh1_pg.C_11400001	0	No title.
jgi|Physo1_1|132225|estExt_fgenesh1_pg.C_190175	0	No title.
jgi|Physo1_1|140272|estExt_fgenesh1_pg.C_830079	0	No title.

463. Group probability: 0.9991. Peptides of the group

VAHVQALVQQHAAER	100.87	54.4826	1655.886	1656.683	7	2	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|127216|estExt_fgenesh1_pg.C_10196	0	No title.

464. Group probability: 0.9991. Peptides of the group

NMANYTNIDTFQHLLPVR	99.1	53.3088	2146.063	2146.792	1	2	distinct	0	0.9991

The equivalent proteins include

jgi|Physo1_1|158140|C_scaffold_85000006	0	No title.
jgi|Phyra1_1|97158|C_scaffold_287000007	0	No title.

465. Group probability: 0.9991. Peptides of the group

QVHQSPAVSQGYR	51.48	54.9318	1455.722	1456.338	1	2	distinct	0	0.9266
VQKPPHADGDADYK	46.61	54.7378	1539.732	1540.406	1	2	distinct	0	0.8918
FPYPTEVGMHPSIPVQK	44.29	53.8173	1925.971	1926.49	1	2	distinct	0	0.883

The equivalent proteins include

jgi|Physo1_1|129721|estExt_fgenesh1_pg.C_80232	0	No title.

466. Group probability: 0.9991. Peptides of the group

QPMFYAMGHFSK	51.74	54.9322	1442.647	1443.164	1	2	distinct	0	0.9256
GYPGGEYWEALALYYSK	69.6	53.8394	1965.915	1966.721	2	2	distinct	0	0.9873

The equivalent proteins include

jgi|Physo1_1|130493|estExt_fgenesh1_pg.C_110162	0	No title.

467. Group probability: 0.9991. Peptides of the group

RGTTVGILGGK	46.59	56.1203	1057.624	1058.766	1	2	distinct	1	0.876
HSQVVANNLQGK	77.72	55.1801	1293.679	1294.299	7	2	distinct	0	0.9923

The equivalent proteins include

jgi|Physo1_1|108718|estExt_fgenesh1_pm.C_270003	0	No title.

468. Group probability: 0.9990. Peptides of the group

RGEILDALSFAK	74.1	55.2894	1318.724	1319.961	1	2	distinct	1	0.9895
IVMGMPQNSVHR	49.56	55.1477	1367.68	1368.335	1	2	distinct	0	0.9096

The equivalent proteins include

jgi|Physo1_1|143156|estExt_fgenesh1_pg.C_1300033	0	No title.
jgi|Phyra1_1|54016|gwEuk.87.89.1	0	No title.

469. Group probability: 0.9990. Peptides of the group

DLNPAYFHIAATNLLGK	99.34	54.6715	1856.978	1857.602	2	2	distinct	0	0.999

The equivalent proteins include

jgi|Physo1_1|142752|estExt_fgenesh1_pg.C_1210019	0	No title.
jgi|Physo1_1|142754|estExt_fgenesh1_pg.C_1210021	0	No title.

470. Group probability: 0.9990. Peptides of the group

DLNPAYFHIAAANMLGK	99.13	54.2009	1844.924	1845.754	6	2	distinct	0	0.999

The equivalent proteins include

jgi|Physo1_1|142751|estExt_fgenesh1_pg.C_1210018	0	No title.

471. Group probability: 0.9990. Peptides of the group

EALQLSSNGPSSHIYHSNLAAALTYLGK	59.47	51.5175	2941.493	2942.454	1	3	distinct	0	0.9755
ALNLETGTPGEAHEAAVDEDPVVQKHPELWK	52.29	50.5583	3379.668	3380.766	1	3	distinct	1	0.9594

The equivalent proteins include

jgi|Physo1_1|127032|estExt_fgenesh1_pg.C_10012	0	No title.

472. Group probability: 0.9990. Peptides of the group

EPVGVCGIVTPWNFPLAMITR	58.85	53.1782	2356.207	2357.006	4	2	distinct	0	0.9609
LGPCLAAGCTAVVKPAAETPLSALALAK	59.05	52.0374	2749.487	2750.673	4	3	distinct	0	0.9743

The equivalent proteins include

jgi|Physo1_1|108179|estExt_fgenesh1_pm.C_20011	0	No title.
jgi|Phyra1_1|71985|fgenesh1_pm.C_scaffold_66000016	0	No title.

473. Group probability: 0.9989. Peptides of the group

SDIISLHCPLFPSTK	74.74	54.3367	1713.876	1715.263	1	2	shared(2)	0	0.9912
VPAYSPYAVAEHAATLMMTLNR	77.54	52.7202	2405.187	2406.511	3	3	distinct	0	0.9883

The equivalent proteins include

jgi|Physo1_1|109081|estExt_fgenesh1_pm.C_580006	0	No title.

474. Group probability: 0.9989. Peptides of the group

GPYESGSGHSSGLGHR	97.92	54.6253	1583.708	1584.078	4	2	distinct	0	0.9989

The equivalent proteins include

gi|88952458|ref|XP_942310.1|	197208.28	PREDICTED: similar to Hornerin [Homo sapiens]
gi|28557150|dbj|BAC57496.1|	48796.73	hornerin [Homo sapiens]
gi|55588478|ref|XP_524874.1|	126987.98	PREDICTED: hypothetical protein XP_524874 [Pan troglodytes]
gi|57546919|tpd|FAA00004.1|	283115.88	TPA: Hornerin [Homo sapiens]
gi|57864582|ref|NP_001009931.1|	283139.96	hornerin [Homo sapiens]
gi|40795897|gb|AAR91619.1|	283110.9	hornerin precursor [Homo sapiens]

475. Group probability: 0.9989. Peptides of the group

VSDKLTPLHDR	54.66	55.2919	1279.688	1280.567	2	2	distinct	1	0.9399
YYLSSHSVELGR	67.45	54.9477	1409.694	1410.328	2	2	distinct	0	0.9812

The equivalent proteins include

jgi|Physo1_1|108552|estExt_fgenesh1_pm.C_150021	0	No title.

476. Group probability: 0.9989. Peptides of the group

IINEPTAAAIAYGIDKK	113.47	54.8238	1786.983	1787.369	22	2	shared(7)	1	0.9981
EVLLLDVTPLSLGIETLGGVMTK (00000000000000000000001000)	122.84	52.8901	2413.339	2413.876	45	2	distinct	0	0.9963

The equivalent proteins include

gi|76884577|gb|ABA59258.1|	70024.14	Heat shock protein Hsp70 [Nitrosococcus oceani ATCC 19707]

477. Group probability: 0.9989. Peptides of the group

KQTFNFEPDNTILHVK	69.87	53.8816	1929.995	1930.432	3	+2,+3	distinct	1	0.9989

The equivalent proteins include

jgi|Physo1_1|121940|estExt_Genewise1.C_980006	0	No title.
jgi|Phyra1_1|50183|gwEuk.501.1.1	0	No title.

478. Group probability: 0.9989. Peptides of the group

LLEIGGGTNESHHK	73.07	54.8404	1490.748	1491.316	1	2	distinct	0	0.9607
EAFGRPLNNFGQIQK	61.16	54.3945	1717.89	1718.221	1	2	distinct	0	0.9711

The equivalent proteins include

jgi|Physo1_1|108282|estExt_fgenesh1_pm.C_40033	0	No title.

479. Group probability: 0.9988. Peptides of the group

EPRPFPQAPPPVLTGQTSGAQSDGSYER	94.3	51.4045	2968.431	2968.955	1	3	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|139866|estExt_fgenesh1_pg.C_790045	0	No title.

480. Group probability: 0.9988. Peptides of the group

WLGVLPQEDCFNHQVR	66.38	53.6776	1996.958	1997.38	8	2	distinct	0	0.9826
IDFGGIYYEHLPSGELYVK	49.51	53.2862	2199.089	2199.349	1	2	distinct	0	0.9318

The equivalent proteins include

jgi|Physo1_1|133321|estExt_fgenesh1_pg.C_250075	0	No title.

481. Group probability: 0.9988. Peptides of the group

AVMHMALR	50.54	56.7414	927.478	928.136	4	2	shared(5)	0	0.9054
HLLEAPLR	50.15	56.2213	947.555	949.049	1	2	distinct	0	0.9031
FLAGAHAMDK (000000001000)	67.37	56.0609	1059.517	1060.198	9	2	shared(4)	0	0.9477
ANIFGFWDWVGGR	81.96	54.634	1523.731	1524.464	7	2	shared(4)	0	0.9938
FAAHIQQVDMESNGKR	69.79	54.1089	1829.884	1831.328	4	2	shared(3)	1	0.8859
YSVTSAVGILPLALQYGFDITEK	71.42	52.7225	2484.315	2485.376	2	2	shared(4)	0	0.9914

The equivalent proteins include

jgi|Phyra1_1|71134|fgenesh1_pm.C_scaffold_5000003	0	No title.

482. Group probability: 0.9988. Peptides of the group

GLLLPSTTTDQEMQHIR	96.17	53.8573	1938.983	1939.308	1	2	distinct	0	0.9988

The equivalent proteins include

jgi|Physo1_1|108957|estExt_fgenesh1_pm.C_460004	0	No title.
jgi|Phyra1_1|71297|fgenesh1_pm.C_scaffold_12000006	0	No title.

483. Group probability: 0.9987. Peptides of the group

AALVYGQMNEPPGAR	63.56	54.9331	1572.772	1573.149	1	2	shared(3)	0	0.926
LVLEVAQHLGEDTVR	68.18	54.8639	1677.905	1677.486	18	+2,+3	distinct	0	0.9969

The equivalent proteins include

gi|23348660|gb|AAN30694.1|	54813.6	ATP synthase F1, beta subunit [Brucella suis 1330]
gi|62196796|gb|AAX75096.1|	54813.6	AtpD, ATP synthase F1, beta subunit [Brucella abortus biovar 1 str. 9-941]

484. Group probability: 0.9987. Peptides of the group

GLEPELQWGQGADGSFASLVAHLR	61.57	52.4233	2537.266	2538.726	3	+2,+3	distinct	0	0.9987

The equivalent proteins include

jgi|Physo1_1|108474|estExt_fgenesh1_pm.C_110005	0	No title.

485. Group probability: 0.9987. Peptides of the group

FGGEMIASYFDER	89.22	54.7312	1520.661	1521.396	2	2	shared(2)	0	0.9973
AAAILGEHNAVEDANLDLAK	56.72	53.6864	2034.038	2033.391	2	+2,+3	distinct	0	0.9747

The equivalent proteins include

jgi|Phyra1_1|93621|C_scaffold_3000060	0	No title.

486. Group probability: 0.9987. Peptides of the group

TVSLNHVWGNNPK	97.19	55.1654	1464.747	1466.01	9	2	distinct	0	0.9987

The equivalent proteins include

jgi|Physo1_1|109381|estExt_fgenesh1_pm.C_970004	0	No title.
jgi|Physo1_1|141345|estExt_fgenesh1_pg.C_970033	0	No title.

487. Group probability: 0.9986. Peptides of the group

HVAHMIDSTEEK	60.22	54.9527	1395.645	1396.288	1	2	distinct	0	0.9646
AEKVFWWPFTQHK	58.69	54.4394	1702.862	1703.97	2	2	distinct	1	0.9614

The equivalent proteins include

jgi|Physo1_1|134345|estExt_fgenesh1_pg.C_310055	0	No title.
jgi|Phyra1_1|77370|fgenesh1_pg.C_scaffold_24000039	0	No title.

488. Group probability: 0.9986. Peptides of the group

LVSVYAHWVPR	62.91	55.344	1325.724	1326.175	4	2	distinct	0	0.9708
IYANMTKPAFFFDGR	55.46	54.1733	1776.866	1777.284	9	2	distinct	0	0.9525

The equivalent proteins include

jgi|Physo1_1|156526|C_scaffold_21000016	0	No title.

489. Group probability: 0.9986. Peptides of the group

DHSSSGIGFNTPVQVTPK	94.43	54.0207	1869.922	1870.626	1	2	distinct	0	0.9986

The equivalent proteins include

jgi|Physo1_1|127337|estExt_fgenesh1_pg.C_10317	0	No title.

490. Group probability: 0.9986. Peptides of the group

DALSGWGAVVHIITPK	95.24	54.5087	1662.909	1663.596	4	2	distinct	0	0.9986

The equivalent proteins include

jgi|Phyra1_1|71646|fgenesh1_pm.C_scaffold_33000007	0	No title.

491. Group probability: 0.9986. Peptides of the group

VYYNSGLQPSPLHYPILGTR	58.77	53.4761	2274.18	2274.714	9	+2,+3	distinct	0	0.9986

The equivalent proteins include

jgi|Physo1_1|140785|estExt_fgenesh1_pg.C_890062	0	No title.

492. Group probability: 0.9986. Peptides of the group

ALVAFPVSYHLLCAAR	65.4	54.8315	1786.955	1787.346	2	2	distinct	0	0.9806
HSLWTYKPELINNIDGAK	49.11	53.4539	2098.085	2098.623	2	2	distinct	0	0.9266

The equivalent proteins include

jgi|Physo1_1|137936|estExt_fgenesh1_pg.C_580109	0	No title.

493. Group probability: 0.9986. Peptides of the group

VQLHPTGFINPK	47.12	55.1915	1349.746	1350.225	1	2	distinct	0	0.8879
IPSIDTPMQIYAMEVAPTVHYTMGGVK	67.3	51.4291	2948.449	2949.821	1	3	distinct	0	0.9872

The equivalent proteins include

jgi|Physo1_1|115536|estExt_Genewise1.C_260177	0	No title.

494. Group probability: 0.9985. Peptides of the group

YGAHSATDVTGFGILAHAR	88.25	53.8233	1942.965	1944.266	3	+2,+3	shared(2)	0	0.9999
LLGYLDNLANDLKPNETPGMDSSVVK	64.03	51.834	2802.411	2803.412	1	3	distinct	0	0.8771

The equivalent proteins include

jgi|Physo1_1|127317|estExt_fgenesh1_pg.C_10297	0	No title.

495. Group probability: 0.9985. Peptides of the group

HVGLSMAGLVADGR	95.64	54.9907	1381.714	1382.774	3	2	distinct	0	0.9985

The equivalent proteins include

jgi|Physo1_1|108726|estExt_fgenesh1_pm.C_270011	0	No title.
jgi|Phyra1_1|71595|fgenesh1_pm.C_scaffold_30000006	0	No title.

496. Group probability: 0.9985. Peptides of the group

DVNHEHLQSIEDR	54.97	54.7338	1590.739	1591.315	1	2	distinct	0	0.9462
EKPYQCTYPVDLDECGPMVLDALIK	59.31	51.5241	2953.391	2953.889	1	3	distinct	0	0.9723

The equivalent proteins include

jgi|Physo1_1|109257|estExt_fgenesh1_pm.C_810004	0	No title.

497. Group probability: 0.9985. Peptides of the group

RQDLVILTDCASPVPGFEK	93.1	53.313	2144.094	2144.606	2	2	distinct	1	0.9985

The equivalent proteins include

jgi|Physo1_1|158850|C_scaffold_160000004	0	No title.

498. Group probability: 0.9985. Peptides of the group

ESTIHLVLR	71.03	55.2163	1066.613	1067.325	13	2	shared(3)	0	0.9848
ECPSPQCGAGVFMATHFDR	76.61	53.3237	2165.908	2165.862	3	2	distinct	0	0.9937

The equivalent proteins include

jgi|Physo1_1|109100|estExt_fgenesh1_pm.C_600006	0	No title.
jgi|Phyra1_1|71343|fgenesh1_pm.C_scaffold_14000008	0	No title.

499. Group probability: 0.9985. Peptides of the group

LYDSESVLALRDPTKPFPTSR	56.85	52.821	2391.243	2392.16	1	3	distinct	1	0.9593
EIPPMSAAVETVQKPEVAAAVSHDPIGAVVEEK	52.48	50.3331	3397.744	3399.116	1	3	distinct	0	0.963

The equivalent proteins include

jgi|Physo1_1|133424|estExt_fgenesh1_pg.C_260030	0	No title.

500. Group probability: 0.9985. Peptides of the group

AHIGAFATPDLIVLAPGLPK	92.57	53.908	2000.146	2000.693	2	2	distinct	0	0.9985

The equivalent proteins include

jgi|Physo1_1|109048|estExt_fgenesh1_pm.C_550001	0	No title.

501. Group probability: 0.9984. Peptides of the group

NAVQHTGPILPITR	68.39	54.9228	1515.852	1517.18	17	+2,+3	distinct	0	0.9984

The equivalent proteins include

jgi|Physo1_1|109354|estExt_fgenesh1_pm.C_940002	0	No title.

502. Group probability: 0.9984. Peptides of the group

VGIVGIGGLGHLGIQFAK	73.97	54.2319	1735.014	1735.749	3	+2,+3	distinct	0	0.9984

The equivalent proteins include

jgi|Physo1_1|109686|estExt_fgenesh1_pm.C_2990002	0	No title.
jgi|Physo1_1|109706|estExt_fgenesh1_pm.C_5140001	0	No title.
jgi|Phyra1_1|46413|gwEuk.285.1.1	0	No title.

503. Group probability: 0.9984. Peptides of the group

VVAAMDDAKPQWCDLPAPAR	70.88	53.2994	2210.061	2210.722	7	+2,+3	distinct	0	0.9984

The equivalent proteins include

jgi|Phyra1_1|71090|fgenesh1_pm.C_scaffold_2000031	0	No title.

504. Group probability: 0.9983. Peptides of the group

HLGYVGNTFPSVSVR	93.79	54.6702	1631.842	1633.336	5	2	distinct	0	0.9983

The equivalent proteins include

jgi|Physo1_1|134057|estExt_fgenesh1_pg.C_290124	0	No title.
jgi|Phyra1_1|80991|fgenesh1_pg.C_scaffold_55000019	0	No title.

505. Group probability: 0.9983. Peptides of the group

IGPYMSNPAHIELILTEK	92.31	53.5677	2025.06	2025.867	9	2	distinct	0	0.9983

The equivalent proteins include

jgi|Physo1_1|134218|estExt_fgenesh1_pg.C_300129	0	No title.
jgi|Phyra1_1|71395|fgenesh1_pm.C_scaffold_16000015	0	No title.

506. Group probability: 0.9983. Peptides of the group

ILTDYGFEGHPLRK	68.88	54.6779	1644.862	1645.394	3	2	distinct	1	0.9847
DFPLSGFLEVFYNELK	45.53	53.9245	1916.956	1917.331	1	2	distinct	0	0.8911

The equivalent proteins include

gi|9695380|ref|NP_037602.1|	22914.22	NADH dehydrogenase subunit 9 [Phytophthora infestans]
gi|7545239|gb|AAA32025.2|	22795.14	NADH dehydrogenase [Phytophthora megasperma]
gi|56684557|gb|AAW21977.1|	22560.03	NADH dehydrogenase subunit 9 [Plasmopara viticola]

507. Group probability: 0.9983. Peptides of the group

GAGGLGHAGGKDEPTPR	92.71	54.7745	1575.775	1576.097	5	2	distinct	1	0.9983

The equivalent proteins include

jgi|Physo1_1|141112|estExt_fgenesh1_pg.C_940023	0	No title.
jgi|Phyra1_1|75480|fgenesh1_pg.C_scaffold_13000046	0	No title.

508. Group probability: 0.9982. Peptides of the group

YGAHSATDVTGFGILAHAR	88.25	53.8233	1942.965	1944.266	3	+2,+3	shared(2)	0	0.9999
LLGYLDDLANDLKPNETPGMDSSVVK	62.18	51.834	2803.395	2803.412	1	3	distinct	0	0.8554

The equivalent proteins include

jgi|Phyra1_1|72185|fgenesh1_pm.C_scaffold_102000004	0	No title.

509. Group probability: 0.9982. Peptides of the group

IALLPFLQAEADVEYLEQEK	90.78	53.0247	2318.204	2319.651	3	2	distinct	0	0.9982

The equivalent proteins include

jgi|Phyra1_1|81219|fgenesh1_pg.C_scaffold_57000071	0	No title.

510. Group probability: 0.9982. Peptides of the group

IFITNTGAHQPSYIYR	92.5	54.2332	1879.958	1880.104	3	2	distinct	0	0.9982

The equivalent proteins include

jgi|Phyra1_1|52278|gwEuk.67.33.1	0	No title.

511. Group probability: 0.9982. Peptides of the group

KIAVNLIPFPR	70.88	55.3745	1266.781	1267.527	5	2	shared(6)	1	0.9855
EIVHIQGGQCGDQIGAK	58.29	54.3637	1808.884	1808.005	5	2	distinct	0	0.8284
GHYTEGAELIDSVLDVVR	50.71	53.7352	1971.99	1972.76	1	2	shared(5)	0	0.7947
AGPYGQIFRPDNFVFGQTGAGNNWAK	79.99	52.236	2811.352	2812.533	7	+2,+3	shared(2)	0	0.9986

The equivalent proteins include

gi|1067181|emb|CAA91942.1|	50961.07	beta-tubulin [oomycete-like MacKay2000]

512. Group probability: 0.9981. Peptides of the group

AHIGAFASPDLIVLVPGLPK	90.24	53.6526	2014.161	2014.77	2	2	distinct	0	0.9981

The equivalent proteins include

jgi|Physo1_1|109049|estExt_fgenesh1_pm.C_550002	0	No title.
jgi|Phyra1_1|72194|fgenesh1_pm.C_scaffold_104000005	0	No title.

513. Group probability: 0.9981. Peptides of the group

HLVSPEAIDFLDGLLR	59	54.2658	1793.968	1794.747	2	+2,+3	distinct	0	0.9981

The equivalent proteins include

jgi|Physo1_1|109488|estExt_fgenesh1_pm.C_1190001	0	No title.
jgi|Phyra1_1|72121|fgenesh1_pm.C_scaffold_88000009	0	No title.

514. Group probability: 0.9981. Peptides of the group

RTIQFVDWCPTGFK	68.04	54.2223	1753.861	1754.812	2	2	shared(4)	1	0.9837
IHFMLSSYAPVISAEK (000010000000000000)	84.73	54.3555	1807.918	1808.932	1	2	shared(3)	0	0.9876
QIYHPEQLISGKEDAANNYAR	44.31	52.6909	2416.177	2417.298	4	+2,+3	distinct	1	0.976

The equivalent proteins include

gi|57903355|gb|AAW58089.1|	45228.32	alpha-tubulin [Apodachlya brachynema]
gi|57903369|gb|AAW58096.1|	45079.49	alpha-tubulin [Phytophthora palmivora]
gi|57903371|gb|AAW58097.1|	45063.5	alpha-tubulin [Plectospira myriandra]
gi|57903375|gb|AAW58099.1|	45054.51	alpha-tubulin [Pythium graminicola]
gi|57903377|gb|AAW58100.1|	45277.65	alpha-tubulin [Thraustotheca clavata]
gi|13649511|gb|AAK37433.1|	42984.51	alpha-tubulin [Reclinomonas americana]
jgi|Physo1_1|109111|estExt_fgenesh1_pm.C_610001	0	No title.
jgi|Physo1_1|109758|estExt_fgenesh1_pm.C_19560001	0	No title.
jgi|Physo1_1|119319|estExt_Genewise1.C_610124	0	No title.
jgi|Phyra1_1|51050|gwEuk.58.65.1	0	No title.
jgi|Phyra1_1|51154|gwEuk.58.169.1	0	No title.
jgi|Phyra1_1|71889|fgenesh1_pm.C_scaffold_58000006	0	No title.
jgi|Phyra1_1|71890|fgenesh1_pm.C_scaffold_58000007	0	No title.
jgi|Phyra1_1|71894|fgenesh1_pm.C_scaffold_58000011	0	No title.

515. Group probability: 0.9981. Peptides of the group

RLWQNNCRPAVACE	53.51	54.312	1772.82	1773.492	1	2	distinct	1	0.9414
SSCVSGALDPVWQPAETFEFEVGHLSPNAER	54.65	50.4095	3415.578	3416.917	3	3	distinct	0	0.9671

The equivalent proteins include

jgi|Physo1_1|128360|estExt_fgenesh1_pg.C_40204	0	No title.

516. Group probability: 0.9980. Peptides of the group

SIVHPSYNSNTLNNDIMLIK (0000000000000000010000)	72.88	53.1203	2272.152	2272.395	15	+2,+3	distinct	0	0.998

The equivalent proteins include

gi|1421532|pdb|1TGB|	24658.8	Trypsinogen-Ca From Peg
gi|230765|pdb|2TLD|E	23555.36	Chain E, Bovine Trypsin (E.C.3.4.21.4) Complex With A Modified SSI (Streptomyces Subtilisin Inhibit
gi|2392803|pdb|5PTP|	23998.54	Structure Of Hydrolase (Serine Proteinase)
gi|5542503|pdb|1ZZZ|A	25388.25	Chain A, Trypsin Inhibitors With Rigid Tripeptidyl Aldehydes
gi|13096615|pdb|1G3E|A	24562.78	Chain A, Bovine Beta-Trypsin Bound To Para-Amidino Schiff-Base Copper (Ii) Chelate
gi|34811715|pdb|1HJ9|A	23972.49	Chain A, Atomic Resolution Structures Of Trypsin Provide Insight Into Structural Radiation Damage
gi|34810822|pdb|1OPH|B	26076.68	Chain B, Non-Covalent Complex Between Alpha-1-Pi-Pittsburgh And S195a Trypsin
gi|49259462|pdb|1V2P|T	23979.59	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssyi)bt.A4
gi|49259463|pdb|1V2Q|T	24002.6	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Sswi)bt.B4

gi|49259464|pdb|1V2R|T	23972.63	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssri)bt.B4
gi|49259466|pdb|1V2T|T	24005.6	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssfi.Glu)bt.B4
gi|49259469|pdb|1V2W|T	23887.56	Chain T, Trypsin Inhibitor In Complex With Bovine Trypsin Variant X(Ssai)bt.B4
gi|71042446|pdb|1ZR0|C	23960.59	Chain C, Crystal Structure Of Kunitz Domain 1 Of Tissue Factor Pathway Inhibitor-2 With Bovine Tryp
gi|88193016|pdb|2FI4|E	23971.53	Chain E, Crystal Structure Of A Bpti Variant (Cys14->ser) In Complex With Trypsin
gi|88193018|pdb|2FI5|E	24086.56	Chain E, Crystal Structure Of A Bpti Variant (Cys38->ser) In Complex With Trypsin
gi|2507249|sp|P00760|TRY1_BOVIN	26092.68	Cationic trypsin precursor (Beta-trypsin) [Contains: Alpha-trypsin chain 1; Alpha-trypsin chain 2]
gi|76615876|ref|XP_883769.1|	26246.67	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 2 [Bos taurus]
gi|76615878|ref|XP_883804.1|	26537.88	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 3 [Bos taurus]
gi|76615880|ref|XP_871686.1|	26438.81	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 1 [Bos taurus]
gi|76615882|ref|XP_883865.1|	26551.93	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 2 [Bos taurus]
gi|61873128|ref|XP_584594.1|	26452.86	PREDICTED: similar to Cationic trypsin III precursor (Pretrypsinogen III) isoform 1 [Bos taurus]
gi|67549|pir||TRBOTR	24661.84	trypsin (EC 3.4.21.4) precursor - bovine
gi|90109720|pdb|2FX6|A	23974.57	Chain A, Bovine Trypsin Complexed With 2-Aminobenzamidazole

517. Group probability: 0.9980. Peptides of the group

LMCASTACNTMITK (0010000000000000)	92.46	55.0456	1600.708	1601.274	18	2	distinct	0	0.998

The equivalent proteins include

gi|68137499|gb|AAY85678.1|	12640.04	acidic elicitin [Phytophthora alni subsp. alni]
gi|68137505|gb|AAY85681.1|	12606.05	acidic elicitin [Phytophthora alni subsp. alni]
gi|68137515|gb|AAY85686.1|	12530.02	acidic elicitin [Phytophthora fragariae var. fragariae]
gi|68137517|gb|AAY85687.1|	12564.01	acidic elicitin [Phytophthora fragariae var. fragariae]
gi|68137519|gb|AAY85688.1|	12546.02	acidic elicitin [Phytophthora fragariae var. rubi]
gi|68137521|gb|AAY85689.1|	12580	acidic elicitin [Phytophthora fragariae var. rubi]
gi|27462826|gb|AAO15602.1|	10501.94	alpha-elicitin capsicein [Phytophthora capsici]
gi|4138370|emb|CAA07710.1|	10519.91	sojein 1 protein [Phytophthora sojae]
gi|4138376|emb|CAA07713.1|	10461.91	sojein 4 protein [Phytophthora sojae]
gi|37783440|gb|AAP43023.1|	12496.96	elicitin [Phytophthora capsici]
gi|37783442|gb|AAP43024.1|	11767.76	elicitin [Phytophthora palmivora]

518. Group probability: 0.9980. Peptides of the group

EKEYNYSCPSTMKPTR	64.31	53.658	1989.892	1989.877	1	2	distinct	1	0.9791
LFHSGLPNLGINGLELAMDGMTK (0000000000000000001000000)	54.34	52.8705	2443.224	2444.212	7	3	distinct	0	0.9045

The equivalent proteins include

jgi|Phyra1_1|81858|fgenesh1_pg.C_scaffold_64000060	0	No title.

519. Group probability: 0.9980. Peptides of the group

VGNLVSDLALDAVLTVVR	90.2	54.114	1853.062	1854.518	2	2	distinct	0	0.998

The equivalent proteins include

jgi|Physo1_1|109716|estExt_fgenesh1_pm.C_6500001	0	No title.

jgi|Phyra1_1|72416|fgenesh1_pm.C_scaffold_633000001	0	No title.

520. Group probability: 0.9980. Peptides of the group

VIRPAKVGVVK	63.26	55.2804	1164.771	1165.228	45	2	distinct	1	0.9717
INQVGAIGDKFDPNVHDALFEYEDTTK	47.52	51.5312	3035.451	3036.49	1	3	distinct	1	0.9275

The equivalent proteins include

jgi|Physo1_1|108704|estExt_fgenesh1_pm.C_260005	0	No title.

521. Group probability: 0.9978. Peptides of the group

LSINHATAR	60.6	55.0965	981.536	981.976	2	2	distinct	0	0.9621
KLSINHATAR	55.6	55.2661	1109.63	1110.45	1	2	distinct	1	0.9427

The equivalent proteins include

jgi|Physo1_1|138394|estExt_fgenesh1_pg.C_630013	0	No title.
jgi|Phyra1_1|83725|fgenesh1_pg.C_scaffold_94000035	0	No title.

522. Group probability: 0.9977. Peptides of the group

KLTEIINSEHENVK	83.88	54.6294	1652.873	1653.119	1	2	distinct	1	0.9485
GADILIFCVPHQFLGR	55.52	54.1574	1841.961	1842.047	1	2	distinct	0	0.9544

The equivalent proteins include

jgi|Physo1_1|108529|estExt_fgenesh1_pm.C_140009	0	No title.

523. Group probability: 0.9976. Peptides of the group

VLPNFALTLSAEGFPLKDDFK	86.72	53.0566	2321.231	2322.587	4	2	distinct	1	0.9976

The equivalent proteins include

jgi|Physo1_1|108992|estExt_fgenesh1_pm.C_500005	0	No title.

524. Group probability: 0.9976. Peptides of the group

ILGVSPYEAVALAGRPR	58.77	54.2146	1767.999	1769.193	4	2	distinct	0	0.9669
THGACPTGPGPDPTQDPLNPWPGTCGEGAMK	45.55	50.9589	3202.391	3202.734	2	3	distinct	0	0.9261

The equivalent proteins include

jgi|Physo1_1|109689|estExt_fgenesh1_pm.C_3170002	0	No title.
jgi|Physo1_1|145196|estExt_fgenesh1_pg.C_6020002	0	No title.

525. Group probability: 0.9975. Peptides of the group

HFTESVEDAR	63.18	55.6295	1189.536	1190.488	2	2	distinct	0	0.9703
MVPLHFESWK	51.44	55.5864	1272.632	1273.176	2	2	distinct	0	0.9169

The equivalent proteins include

jgi|Physo1_1|142593|estExt_fgenesh1_pg.C_1170052	0	No title.

526. Group probability: 0.9975. Peptides of the group

DVSNMNTSTTLLGHNVSSPVCVAPSSTHR	85.18	51.2672	3067.445	3068.708	5	3	distinct	0	0.9975

The equivalent proteins include

jgi|Physo1_1|143025|estExt_fgenesh1_pg.C_1270015	0	No title.

527. Group probability: 0.9975. Peptides of the group

SAGEAGPSYFELIVDAIK	87.85	53.9571	1865.941	1867.086	6	2	distinct	0	0.9975

The equivalent proteins include

jgi|Physo1_1|129764|estExt_fgenesh1_pg.C_90041	0	No title.

528. Group probability: 0.9975. Peptides of the group

ASQVVGLHFFNPVQLMK	88.06	53.8931	1914.018	1914.69	9	2	distinct	0	0.9975

The equivalent proteins include

jgi|Physo1_1|157244|C_scaffold_38000033	0	No title.
jgi|Phyra1_1|71640|fgenesh1_pm.C_scaffold_33000001	0	No title.

529. Group probability: 0.9975. Peptides of the group

LQAQLHQSAQDTWSYLEALK	86.58	53.0501	2329.17	2329.594	2	2	distinct	0	0.9975

The equivalent proteins include

jgi|Physo1_1|128975|estExt_fgenesh1_pg.C_60132	0	No title.
jgi|Physo1_1|128978|estExt_fgenesh1_pg.C_60135	0	No title.

530. Group probability: 0.9974. Peptides of the group

GSSSSWVPSELWSFFFPSK	86.97	53.9093	2161.016	2162.091	7	2	distinct	0	0.9974

The equivalent proteins include

jgi|Physo1_1|131384|estExt_fgenesh1_pg.C_150155	0	No title.

531. Group probability: 0.9974. Peptides of the group

TPGPGAQSALR	53.06	55.429	1053.557	1054.389	1	2	distinct	0	0.9307
TKTPGPGAQSALR	59.17	55.2824	1282.699	1283.654	2	2	distinct	1	0.9623

The equivalent proteins include

gi|82623421|gb|ABB87125.1|	10677.75	hypothetical protein [Solanum tuberosum]
gi|83284009|gb|ABC01912.1|	16391.65	ribosomal protein S14-like protein [Solanum tuberosum]
gi|1762931|gb|AAC49968.1|	6995.95	ribosomal protein S14 [Nicotiana tabacum]
gi|61369149|gb|AAX43292.1|	16546.68	ribosomal protein S14 [synthetic construct]
gi|61654728|gb|AAX48890.1|	16282.67	S14 [Suberites domuncula]
gi|74268249|gb|AAI02537.1|	17050.85	Unknown (protein for MGC:127734) [Bos taurus]
gi|74226871|dbj|BAE27080.1|	16506.6	unnamed protein product [Mus musculus]
gi|91091798|ref|XP_970498.1|	16283.68	PREDICTED: similar to 40S ribosomal protein S14 [Tribolium castaneum]
gi|72015985|ref|XP_780390.1|	16159.63	PREDICTED: similar to 40S ribosomal protein S14 [Strongylocentrotus purpuratus]
gi|70909537|emb|CAJ17191.1|	16328.65	ribosomal protein S14e [Sphaerius sp. APV-2005]
gi|94468908|gb|ABF18303.1|	16302.67	40S ribosomal protein S141 [Aedes aegypti]
gi|109079317|ref|XP_001099589.1|	14487.5	PREDICTED: similar to ribosomal protein S14 [Macaca mulatta]
gi|76680427|ref|XP_584177.2|	16463.57	PREDICTED: similar to ribosomal protein S14 [Bos taurus]
gi|55625094|ref|XP_518037.1|	22706.67	PREDICTED: similar to 40S ribosomal protein S14 [Pan troglodytes]
gi|77745450|gb|ABB02624.1|	16405.67	ribosomal protein S14-like [Solanum tuberosum]
gi|71895291|ref|NP_001025790.1|	16433.6	ribosomal protein S14 [Gallus gallus]
gi|38048289|gb|AAR10047.1|	16311.71	similar to Drosophila melanogaster RpS14a [Drosophila yakuba]
gi|463857|gb|AAB60274.1|	16348.67	ribosomal protein S14
gi|730633|sp|Q08699|RS14_PODCA	16182.54	40S ribosomal protein S14
gi|5441523|emb|CAB46816.1|	8441.65	Ribosomal protein S14 [Canis familiaris]
gi|3097244|emb|CAA69615.1|	16461.6	ribosomal protein S14 [Mus musculus]
gi|458981|gb|AAC48301.1|	16352.69	Ribosomal protein, small subunit protein 14 [Caenorhabditis elegans]
gi|131772|sp|P19950|RS141_MAIZE	16304.65	40S ribosomal protein S14 (Clone MCH1)
gi|131773|sp|P19951|RS142_MAIZE	16309.64	40S ribosomal protein S14 (Clone MCH2)
gi|57129|emb|CAA33143.1|	16419.58	unnamed protein product [Rattus norvegicus]
gi|4588920|gb|AAD26263.1|	16276.64	ribosomal protein S14 [Stomoxys calcitrans]
gi|28189929|dbj|BAC56579.1|	15838.16	similar to ribosomal protein S14 [Bos taurus]
gi|15227588|ref|NP_181158.1|	16303.69	structural constituent of ribosome [Arabidopsis thaliana]
gi|15229775|ref|NP_187758.1|	16319.68	structural constituent of ribosome [Arabidopsis thaliana]
gi|15231260|ref|NP_190826.1|	16284.71	structural constituent of ribosome [Arabidopsis thaliana]
gi|55242989|gb|EAA06897.2|	16359.69	ENSANGP00000019074 [Anopheles gambiae str. PEST]
gi|55242445|gb|EAA08220.2|	16331.66	ENSANGP00000015417 [Anopheles gambiae str. PEST]
gi|62083507|gb|AAX62478.1|	16351.68	ribosomal protein S14 [Lysiphlebus testaceipes]
gi|50905421|ref|XP_464199.1|	16409.68	putative ribosomal protein S14 [Oryza sativa (japonica cultivar-group)]
gi|54609311|gb|AAV34871.1|	16207.65	ribosomal protein S14 [Bombyx mori]
gi|50924099|ref|XP_472410.1|	16466.71	OJ000126_13.9 [Oryza sativa (japonica cultivar-group)]
gi|15213816|gb|AAK92183.1|	16264.67	ribosomal protein S14 [Spodoptera frugiperda]

gi|28436071|gb|AAO41731.1|	16361.64	cytoplasmic ribosomal protein S14 [Brassica napus]							
gi|37748505|gb|AAH59561.1|	16405.59	Ribosomal protein S14 [Danio rerio]							
gi|62362200|gb|AAX81537.1|	16046.47	S14e ribosomal protein-like protein [Philodina sp. NPS-2005]							
gi|51011526|gb|AAT92172.1|	16166.56	ribosomal protein S14 [Ixodes pacificus]							
gi|50344488|emb|CAH04330.1|	16267.68	S14e ribosomal protein [Dascillus cervinus]							
gi|15294039|gb|AAK95196.1|	16376.56	40S ribosomal protein S14 [Ictalurus punctatus]							
gi|94399883|ref|XP_001001619.1|	16537.67	PREDICTED: similar to ribosomal protein S14 [Mus musculus]							
gi|82958328|ref|XP_913463.1|	16551.69	PREDICTED: similar to ribosomal protein S14 isoform 1 [Mus musculus]							
gi|47935073|gb|AAT39883.1|	16218.46	ribosomal protein S14 [Branchiostoma belcheri tsingtaunese]							
gi|51863346|gb|AAU11819.1|	16149.64	ribosomal protein S14 [Bombyx mori]							
gi|51873216|gb|AAU12568.1|	12918.6	ribosomal protein S14 [Felis catus]							
jgi|Physo1_1|135178|estExt_fgenesh1_pg.C_360094	0	No title.							
jgi|Phyra1_1|53078|gwEuk.77.61.1	0	No title.							
532. Group probability: 0.9973. Peptides of the group									
LGMKPVGGIIR	46.96	55.431	1139.685	1140.551	1	2	distinct	0	0.8816
NVLFVISKPDVFK	64.93	54.8205	1504.865	1505.666	3	2	distinct	0	0.9775
The equivalent proteins include									
jgi|Physo1_1|108927|estExt_fgenesh1_pm.C_430007	0	No title.							
533. Group probability: 0.9973. Peptides of the group									
YHEQSANFDPVHSISR	87.74	53.9458	1885.871	1886.28	4	2	distinct	0	0.9973
The equivalent proteins include									
jgi|Physo1_1|131341|estExt_fgenesh1_pg.C_150112	0	No title.							
jgi|Phyra1_1|73325|fgenesh1_pg.C_scaffold_3000082	0	No title.							
534. Group probability: 0.9972. Peptides of the group									
YPNEHGIVTNWDDMEK	76.88	53.9027	1946.847	1946.612	11	+2,+3	distinct	0	0.9955
VAPEEHPVLLTEAPINPK	81.4	53.7548	1953.057	1953.885	13	2	shared(10)	0	0.9887
The equivalent proteins include									
gi|109507063|ref|XP_001058533.1|	42108.88	PREDICTED: similar to Actin, cytoplasmic 2 (Gamma-actin) [Rattus norvegicus]							
535. Group probability: 0.9971. Peptides of the group									
HVSVIAKPLATK	66.74	55.6391	1262.771	1263.206	4	2	distinct	0	0.9798
RPTSCILITPNK	44.52	55.28	1398.765	1399.247	1	2	distinct	0	0.859
The equivalent proteins include									
jgi|Physo1_1|108290|estExt_fgenesh1_pm.C_50005	0	No title.							
536. Group probability: 0.9971. Peptides of the group									
QASLQEYLDGLLQVPGILDDASLQHFLELEK	82.19	50.4032	3481.798	3482.853	2	3	distinct	0	0.9971
The equivalent proteins include									
jgi|Physo1_1|156141|C_scaffold_11000036	0	No title.							
jgi|Phyra1_1|96093|C_scaffold_62000023	0	No title.							
537. Group probability: 0.9969. Peptides of the group									
YSNYYSQCKPATLPAGELCGQNDGTNVWK	82.59	50.7395	3320.487	3321.623	8	3	distinct	0	0.9969
The equivalent proteins include									
jgi|Physo1_1|158550|C_scaffold_116000002	0	No title.							
538. Group probability: 0.9969. Peptides of the group									
ITPAHDPNDYECGKR	59.67	54.2847	1771.795	1773.17	2	3	distinct	1	0.9595
AEYGLANNVRPKFFIK	49.64	53.9571	1866.015	1866.675	1	2	distinct	1	0.924
The equivalent proteins include									
jgi|Physo1_1|108931|estExt_fgenesh1_pm.C_440004	0	No title.							
jgi|Phyra1_1|72256|fgenesh1_pm.C_scaffold_118000004	0	No title.							
539. Group probability: 0.9969. Peptides of the group									
LIVEKPFGHDLASFNK	64.32	54.1497	1813.973	1815.234	2	2	distinct	0	0.8549
GSTTPTFATAIMYVNNPR	63.36	53.8455	1939.946	1939.579	1	2	distinct	0	0.9788

The equivalent proteins include

jgi|Phyra1_1|49578|gwEuk.48.73.1	0	No title.

540. Group probability: 0.9969. Peptides of the group

YRPAAPGAPMK	47.42	55.8228	1157.602	1158.234	2	2	distinct	0	0.8854
HEQGAGHMAQGYAR	82.64	54.7387	1511.669	1512.416	8	2	distinct	0	0.9731

The equivalent proteins include

jgi|Physo1_1|109190|estExt_fgenesh1_pm.C_700007	0	No title.

541. Group probability: 0.9969. Peptides of the group

VCAYAGDAYMHAPR	87.07	54.5832	1580.686	1581.052	5	2	distinct	0	0.9969

The equivalent proteins include

jgi|Physo1_1|135221|estExt_fgenesh1_pg.C_360137	0	No title.
jgi|Phyra1_1|82759|fgenesh1_pg.C_scaffold_77000009	0	No title.

542. Group probability: 0.9969. Peptides of the group

NVIHPYTPTNTNAEKGELELVVK	56.24	52.4604	2565.344	2566.442	1	3	distinct	1	0.9603
LLPGPSDESLIGVCGPPPMMDAISGNKAPDR	44.82	51.03	3190.546	3191.301	1	3	distinct	1	0.9211

The equivalent proteins include

jgi|Physo1_1|108925|estExt_fgenesh1_pm.C_430005	0	No title.

543. Group probability: 0.9968. Peptides of the group

GVEEIIEHVIGAWK	86.81	54.7929	1578.841	1580.027	2	2	distinct	0	0.9968

The equivalent proteins include

jgi|Physo1_1|108161|estExt_fgenesh1_pm.C_10026	0	No title.

544. Group probability: 0.9968. Peptides of the group

FQALMPDALHWLGITK	97.8	54.0233	1839.971	1840.421	6	2	distinct	0	0.9968

The equivalent proteins include

jgi|Physo1_1|120701|estExt_Genewise1.C_810049	0	No title.

545. Group probability: 0.9967. Peptides of the group

TTGVVLDVGDGVAHVVPVYEGFTLPHAITR	81.62	51.1353	3118.645	3119.83	1	3	distinct	0	0.9967

The equivalent proteins include

jgi|Physo1_1|108184|estExt_fgenesh1_pm.C_20016	0	No title.
jgi|Phyra1_1|71165|fgenesh1_pm.C_scaffold_5000034	0	No title.

546. Group probability: 0.9966. Peptides of the group

EIPGLTLSEEQVNALLK	84.86	54.1478	1853.015	1854.157	2	2	distinct	0	0.9966

The equivalent proteins include

jgi|Physo1_1|139970|estExt_fgenesh1_pg.C_800054	0	No title.

547. Group probability: 0.9966. Peptides of the group

VQHIEIHGK	53.42	56.0615	1059.582	1060.719	21	+1,+2	shared(2)	0	0.9919
NTAYGATVKPR	75.48	55.63	1176.625	1177.154	8	2	shared(2)	0	0.9903
VIYLSIVDGKVVGR	43.88	54.8776	1516.898	1515.573	1	2	distinct	1	0.6288

The equivalent proteins include

jgi|Phyra1_1|75704|fgenesh1_pg.C_scaffold_14000066	0	No title.

548. Group probability: 0.9965. Peptides of the group

FVNLLHSMADPER	51.88	54.8201	1527.75	1529.014	3	2	shared(2)	0	0.9293
FVNLLHSMADPERK	58.52	54.4392	1655.845	1656.094	5	2	shared(2)	1	0.9622
GREFDGMGLGGTCVNFGCVPK (0000000010000000000000000)	51.2	53.4282	2273.003	2274.256	1	3	distinct	1	0.9324

The equivalent proteins include

jgi|Phyra1_1|72037|fgenesh1_pm.C_scaffold_75000002	0	No title.

549. Group probability: 0.9965. Peptides of the group

FSVLHPTK	49.91	56.7394	927.518	928.667	1	2	distinct	0	0.9
ALPVEGLTWGEGHK	70.98	54.667	1492.767	1493.485	4	2	shared(2)	0	0.9873
SQVVIEVKPWEAETDLEELAAK	43.79	52.6082	2483.279	2483.55	1	2	shared(2)	0	0.9002

The equivalent proteins include

jgi|Physo1_1|158454|C_scaffold_106000025	0	No title.

550. Group probability: 0.9964. Peptides of the group

VGVVGIGGLGHLGIQFAK	83.69	54.2809	1720.999	1721.659	4	2	distinct	0	0.9964

The equivalent proteins include

jgi|Physo1_1|108331|estExt_fgenesh1_pm.C_60021	0	No title.
jgi|Physo1_1|109587|estExt_fgenesh1_pm.C_1500003	0	No title.
jgi|Physo1_1|109744|estExt_fgenesh1_pm.C_11770002	0	No title.
jgi|Physo1_1|109585|estExt_fgenesh1_pm.C_1500001	0	No title.

551. Group probability: 0.9964. Peptides of the group

LHPEILGDFQK	58.26	55.2414	1295.687	1296.285	5	2	shared(2)	0	0.9562
MNIDTDTQWAYWDGIR	55.1	53.8121	1983.878	1984.426	3	2	distinct	0	0.953
MNIDTDTQWAYWDGLRK	42.64	53.4956	2111.973	2112.422	1	2	distinct	1	0.6335

The equivalent proteins include

jgi|Phyra1_1|71696|fgenesh1_pm.C_scaffold_38000010	0	No title.
jgi|Phyra1_1|71816|fgenesh1_pm.C_scaffold_50000010	0	No title.
jgi|Phyra1_1|71817|fgenesh1_pm.C_scaffold_50000011	0	No title.

552. Group probability: 0.9963. Peptides of the group

DILLLDVTPLSLGIETLGGVMTK (000000000000000000000001000)	122.84	52.8901	2413.339	2413.876	45	2	distinct	0	0.9963

The equivalent proteins include

gi|77747092|gb|ABB02935.1|	42049.98	DnaK [Candidatus Legionella jeonii]

553. Group probability: 0.9963. Peptides of the group

HEQQHGLLGK	51.86	55.8234	1145.594	1146.402	1	2	distinct	0	0.9196
NGNHFVNTASHFMR	56.4	54.6755	1630.742	1632.12	2	2	distinct	0	0.9542

The equivalent proteins include

jgi|Physo1_1|137091|estExt_fgenesh1_pg.C_500127	0	No title.

554. Group probability: 0.9963. Peptides of the group

GIPSAVFVDSVEAFMDACGVK	81.95	53.2849	2198.039	2199.059	2	2	distinct	0	0.9963

The equivalent proteins include

jgi|Physo1_1|141993|estExt_fgenesh1_pg.C_1060052	0	No title.

555. Group probability: 0.9963. Peptides of the group

SHVIVLPGGK	67.64	56.145	1005.597	1005.447	9	+1,+2	shared(2)	0	0.9971
VGQIEHNISPQDSVSK	62.31	54.1879	1736.869	1737.222	3	2	distinct	0	0.922

The equivalent proteins include

jgi|Physo1_1|140949|estExt_fgenesh1_pg.C_920012	0	No title.

556. Group probability: 0.9963. Peptides of the group

HEVGDLDKIK	49.91	55.3688	1152.614	1153.492	3	2	distinct	1	0.9054
DLTPEQGYDAAHYVALSLMATLK	91.85	52.5393	2506.241	2506.413	12	2	shared(2)	0	0.9986

The equivalent proteins include

jgi|Phyra1_1|96088|C_scaffold_62000018	0	No title.

557. Group probability: 0.9961. Peptides of the group

KGLTPSQIGVILR	85.08	54.9754	1380.845	1381.505	5	2	distinct	1	0.9961

The equivalent proteins include

gi|54039304|sp|P62279|RS13_PIG	12026.78	40S ribosomal protein S13
gi|4633275|gb|AAD26692.1|	17181.66	40S ribosomal protein S13 [Cricetulus griseus]
gi|61369380|gb|AAX43326.1|	17324.75	ribosomal protein S13 [synthetic construct]
gi|67764864|gb|AAY79230.1|	12287.11	ribosomal protein S13 [Siniperca chuatsi]
gi|10121613|gb|AAG13286.1|	17151.61	ribosomal protein S13 [Gillichthys mirabilis]
gi|15450535|gb|AAK96445.1|	17115.53	AT3g60770/T4C21_180 [Arabidopsis thaliana]
gi|15294037|gb|AAK95195.1|	17139.64	40S ribosomal protein S13 [Ictalurus punctatus]
gi|70909527|emb|CAJ17186.1|	17052.51	ribosomal protein S13e [Agriotes lineatus]
gi|70909529|emb|CAJ17187.1|	17146.48	ribosomal protein S13e [Curculio glandium]
gi|70909531|emb|CAJ17188.1|	17152.5	ribosomal protein S13e [Georissus sp. APV-2005]
gi|54039308|sp|O77303|RS13_LUMRU	17104.68	40S ribosomal protein S13
gi|57089981|ref|XP_537358.1|	12731.13	PREDICTED: similar to ribosomal protein S13 [Canis familiaris]
gi|94391593|ref|XP_994773.1|	14265.94	PREDICTED: similar to ribosomal protein S13 [Mus musculus]

gi|44662862|gb|AAS47510.1|	17186.52	ribosomal protein S13 [Glycine max]
gi|68449762|gb|AAY97868.1|	17077.55	cytoplasmic ribosomal protein S13 [Lycopersicon esculentum]
gi|76607499|ref|XP_581041.2|	17038.46	PREDICTED: similar to ribosomal protein S13 [Bos taurus]
gi|18411716|ref|NP_567104.1|	17141.53	structural constituent of ribosome [Arabidopsis thaliana]
gi|18411224|ref|NP_567151.1|	17131.51	ATRPS13A (RIBOSOMAL PROTEIN S13A); structural constituent of ribosome [Arabidopsis thaliana]
gi|50805893|ref|XP_424367.1|	14633.33	PREDICTED: similar to ribosomal protein S13, partial [Gallus gallus]
gi|109081167|ref|XP_001084119.1|	18100.84	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109108275|ref|XP_001083923.1|	14235.02	PREDICTED: similar to ribosomal protein S13 isoform 4 [Macaca mulatta]
gi|109110588|ref|XP_001105971.1|	10903.08	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109120657|ref|XP_001097099.1|	17234.64	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109132315|ref|XP_001095630.1|	17177.54	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109139180|ref|XP_001119129.1|	17245.61	PREDICTED: similar to ribosomal protein S13 [Macaca mulatta]
gi|109476367|ref|XP_001068232.1|	17762.03	PREDICTED: similar to ribosomal protein S13 [Rattus norvegicus]
gi|55642147|ref|XP_523078.1|	17270.5	PREDICTED: similar to ribosomal protein S13 [Pan troglodytes]
gi|47211519|emb|CAF90315.1|	17169.66	unnamed protein product [Tetraodon nigroviridis]
gi|8131699|dbj|BAA96366.1|	17164.58	cytoplasmic ribosomal protein S13 [Panax ginseng]
gi|77415468|gb|AAI06138.1|	17211.67	Ribosomal protein S13 [Mus musculus]
gi|7267097|emb|CAB80768.1|	16954.4	putative ribosomal protein S13 [Arabidopsis thaliana]
gi|7329687|emb|CAB82681.1|	16964.42	ribosomal protein S13-like [Arabidopsis thaliana]
gi|699581|gb|AAA91984.1|	17156.59	ribosomal S13 protein [Ictalurus punctatus]
gi|48209913|gb|AAT40507.1|	17107.56	cytoplasmic ribosomal protein S13 [Solanum demissum]
gi|417710|sp|P33192|RS13_CANMA	16931.31	40S ribosomal protein S13 (S15)
gi|396639|emb|CAA80974.1|	17162.61	ribosomal protein S13 [Pisum sativum]
gi|553640|gb|AAC15854.1|	13312.62	ribosomal protein S13 [Homo sapiens]
gi|62860010|ref|NP_001016602.1|	17239.67	ribosomal protein S13 [Xenopus tropicalis]
gi|48735394|gb|AAH72552.1|	17183.65	Zgc:91809 [Danio rerio]
gi|67084039|gb|AAY66954.1|	17255.66	40S ribosomal protein S13 [Ixodes scapularis]
gi|50344486|emb|CAH04329.1|	17136.46	S13e ribosomal protein [Timarcha balearica]
gi|50424883|ref|XP_461031.1|	17018.25	hypothetical protein DEHA0F16698g [Debaryomyces hansenii CBS767]
gi|22758884|gb|AAN05601.1|	16995.5	ribosomal protein S13 [Argopecten irradians]
gi|15029927|gb|AAH11192.1|	16132.15	Rps13 protein [Mus musculus]
gi|33585646|gb|AAH56028.1|	17237.69	Rps13-prov protein [Xenopus laevis]
gi|94385425|ref|XP_001004217.1|	17237.72	PREDICTED: similar to ribosomal protein S13 [Mus musculus]
gi|24266981|gb|AAN52387.1|	17109.6	ribosomal protein S13 [Branchiostoma belcheri]
jgi|Physo1_1|108227|estExt_fgenesh1_pm.C_30016	0	No title.
jgi|Phyra1_1|71627|fgenesh1_pm.C_scaffold_32000009	0	No title.
gi|50555724|ref|XP_505270.1|	16851.25	hypothetical protein [Yarrowia lipolytica]
gi|6320269|ref|NP_010349.1|	17018.33	Protein component of the small (40S) ribosomal subunit; has similarity to E. coli S15 and rat S13 r
gi|44985849|gb|AAS54460.1|	16965.28	AGL030Wp [Ashbya gossypii ATCC 10895]

gi|50288301|ref|XP_446579.1|	17050.32	unnamed protein product [Candida glabrata]
gi|50311723|ref|XP_455889.1|	16758.29	unnamed protein product [Kluyveromyces lactis]

558. Group probability: 0.9961. Peptides of the group

WNTHPGYISAVANR	62.01	54.9285	1584.78	1585.476	3	2	distinct	0	0.9719
AVAFSQYPQWSCTTSGSSMNHLWR	41.4	52.0008	2800.249	2801.728	1	3	distinct	0	0.8607

The equivalent proteins include

jgi|Physo1_1|122226|estExt_Genewise1.C_1020026	0	No title.
jgi|Phyra1_1|71876|fgenesh1_pm.C_scaffold_57000004	0	No title.

559. Group probability: 0.9960. Peptides of the group

FPFGSLVPLWSR	52.51	55.1459	1404.755	1405.301	4	2	shared(2)	0	0.9302
CMVGGILSCGITHTGITPLDVVK (0010000000000000000000000)	65.41	52.8704	2427.232	2441.863	7	+2,+3	distinct	0	0.985

The equivalent proteins include

jgi|Phyra1_1|81225|fgenesh1_pg.C_scaffold_57000077	0	No title.

560. Group probability: 0.9960. Peptides of the group

VFHNTNCAQEYAGEVPTKLPIDVSTCK	80.35	51.2075	3077.459	3078.673	8	3	distinct	1	0.996

The equivalent proteins include

jgi|Physo1_1|142202|estExt_fgenesh1_pg.C_1090058	0	No title.

561. Group probability: 0.9958. Peptides of the group

LGLSHMWPVR	51.33	55.3211	1194.633	1195.531	1	2	distinct	0	0.9166
EGDPISGGDIFGLVHENDILHSHK	50.66	52.4494	2585.251	2584.773	1	2	distinct	0	0.9493

The equivalent proteins include

jgi|Physo1_1|108996|estExt_fgenesh1_pm.C_500009	0	No title.
jgi|Phyra1_1|72398|fgenesh1_pm.C_scaffold_433000001	0	No title.

562. Group probability: 0.9957. Peptides of the group

VGFYQEYLTGLHNAIAEGADVR	79.57	52.6474	2422.192	2422.883	1	2	distinct	0	0.9957

The equivalent proteins include

jgi|Physo1_1|108505|estExt_fgenesh1_pm.C_120015	0	No title.

563. Group probability: 0.9955. Peptides of the group

SISAFAPISHPSQCPWGIK	80.64	53.5982	2082.036	2082.358	4	2	distinct	0	0.9955

The equivalent proteins include

jgi|Physo1_1|109641|estExt_fgenesh1_pm.C_1890003	0	No title.
jgi|Phyra1_1|71745|fgenesh1_pm.C_scaffold_44000001	0	No title.

564. Group probability: 0.9955. Peptides of the group

HITPEEAPWPNAEEDPEEIVGAGFHLAPR	78.4	51.3946	3207.526	3208.649	4	3	distinct	0	0.9955

The equivalent proteins include

jgi|Physo1_1|132600|estExt_fgenesh1_pg.C_210160	0	No title.

565. Group probability: 0.9955. Peptides of the group

EVLEGLPNGLGAGIYYWEPAYIK	78.66	52.4975	2551.3	2551.489	3	2	distinct	0	0.9955

The equivalent proteins include

jgi|Physo1_1|156401|C_scaffold_17000070	0	No title.

566. Group probability: 0.9955. Peptides of the group

EGVAWQTTPLDVALEISQGLADQVVVAR	76.28	51.3206	2964.556	2964.766	5	2	distinct	0	0.9955

The equivalent proteins include

jgi|Physo1_1|129616|estExt_fgenesh1_pg.C_80127	0	No title.
jgi|Phyra1_1|79358|fgenesh1_pg.C_scaffold_39000056	0	No title.

567. Group probability: 0.9954. Peptides of the group

TKLPGSFGDFVK	47.62	55.1776	1294.692	1295.648	1	2	distinct	1	0.8928
EKQEEWLNSFINAGAQYR	55.23	53.2891	2182.044	2182.291	2	2	distinct	1	0.9572

The equivalent proteins include

jgi|Physo1_1|108638|estExt_fgenesh1_pm.C_210012	0	No title.

568. Group probability: 0.9954. Peptides of the group

LKPNSSVALHR	52.9	55.4085	1220.699	1221.505	1	2	distinct	0	0.9297

ILLELLNQMDGFDQATNVK	50.09	53.9117	2161.109	2162.607	1	2	distinct	0	0.9344

The equivalent proteins include

jgi|Physo1_1|122821|estExt_Genewise1.C_1140049	0	No title.
jgi|Phyra1_1|95904|C_scaffold_56000022	0	No title.

569. Group probability: 0.9954. Peptides of the group

VPTVDVSVVDLTCR	67.35	54.7657	1558.802	1557.818	5	2	distinct	0	0.8675
LTGMAFRVPTVDVSVVDLTCR	58.61	52.9436	2335.203	2336.333	8	3	distinct	1	0.9651

The equivalent proteins include

gi|85860541|ref|YP_462743.1|	35966.36	glyceraldehyde 3-phosphate dehydrogenase [Syntrophus aciditrophicus SB]

570. Group probability: 0.9953. Peptides of the group

INCGQLEELIEQAEDELSVIPVYLEHK	78.75	51.1439	3167.57	3168.624	1	3	distinct	0	0.9953

The equivalent proteins include

jgi|Physo1_1|141651|estExt_fgenesh1_pg.C_1010064	0	No title.

571. Group probability: 0.9952. Peptides of the group

KTATPEIHAR	49.33	55.2856	1122.615	1123.797	1	2	distinct	1	0.9007
DEFEKYDHIHK	57.11	55.1198	1459.673	1459.8	1	2	distinct	1	0.9517

The equivalent proteins include

jgi|Physo1_1|109063|estExt_fgenesh1_pm.C_560001	0	No title.

572. Group probability: 0.9951. Peptides of the group

KLNGFLTNR	56.15	55.9637	1061.598	1062.471	2	2	distinct	1	0.8642
ALPVEGLTWGEGHK	70.98	54.667	1492.767	1493.485	4	2	shared(2)	0	0.9873
SQVVIEVKPWEAETDLEELAAK	43.79	52.6082	2483.279	2483.55	1	2	shared(2)	0	0.9002

The equivalent proteins include

jgi|Physo1_1|109567|estExt_fgenesh1_pm.C_1450002	0	No title.

573. Group probability: 0.9950. Peptides of the group

VGVASGVAAGAAMAAASYWQSSQDSAFDKYAAAR	74.96	50.664	3334.568	3335.67	1	3	distinct	1	0.995

The equivalent proteins include

jgi|Physo1_1|158693|C_scaffold_129000003	0	No title.

574. Group probability: 0.9950. Peptides of the group

EGNDLYYEMIESGVNK	75.55	54.4676	1859.825	1859.155	6	2	distinct	0	0.911
TREGNDLYYEMIESGVNK	60.23	53.3873	2116.973	2116.541	3	2	distinct	1	0.9434

The equivalent proteins include

gi|83944756|ref|ZP_00957122.1|	51401.29	ATP synthase subunit B [Oceanicaulis alexandrii HTCC2633]

575. Group probability: 0.9949. Peptides of the group

RVFGITTLDVVR	49.49	55.2219	1374.798	1374.764	4	+2,+3	distinct	1	0.9517
VAVLGAAGGIGQPMSLLLK	99.61	54.2657	1794.044	1794.864	3	2	shared(2)	0	0.9894

The equivalent proteins include

gi|57228274|gb|AAW44731.1|	35807.96	malate dehydrogenase, putative [Cryptococcus neoformans var. neoformans JEC21]

576. Group probability: 0.9949. Peptides of the group

IEQNFSNYSALHHR	81.33	54.3297	1714.818	1715.286	2	2	distinct	0	0.9949

The equivalent proteins include

jgi|Physo1_1|131057|estExt_fgenesh1_pg.C_140055	0	No title.
jgi|Phyra1_1|74295|fgenesh1_pg.C_scaffold_7000066	0	No title.

577. Group probability: 0.9949. Peptides of the group

LGDLGVLEFTDLNPELTPFQR	78.09	52.8363	2373.222	2374.295	1	2	distinct	0	0.9949

The equivalent proteins include

gi|62147616|emb|CAI72310.1|	96727.44	vacuolar proton translocating ATPase A subunit, putative [Phytophthora infestans]
jgi|Physo1_1|132996|estExt_fgenesh1_pg.C_230139	0	No title.
jgi|Phyra1_1|80897|fgenesh1_pg.C_scaffold_54000023	0	No title.

578. Group probability: 0.9948. Peptides of the group

HGLAYIPLVSPTTTEDR	79.87	54.0186	1868.963	1869.882	1	2	distinct	0	0.9948

The equivalent proteins include

jgi|Physo1_1|155994|C_scaffold_10000013	0	No title.

579. Group probability: 0.9948. Peptides of the group

LVLPEVIEEGDNVTFPNRGDTMVMHYTGK	76.56	50.921	3260.584	3262.017	3	3	distinct	1	0.9948

The equivalent proteins include

jgi|Physo1_1|138654|estExt_fgenesh1_pg.C_650073	0	No title.

580. Group probability: 0.9947. Peptides of the group

TILGGLNEILAELLEQSLHK	78.43	53.7871	2190.226	2191.391	1	2	distinct	0	0.9947

The equivalent proteins include

jgi|Physo1_1|129879|estExt_fgenesh1_pg.C_90156	0	No title.

581. Group probability: 0.9947. Peptides of the group

IRLENEIQTYR	55.92	54.8968	1433.763	1434.654	3	2	shared(2)	1	0.9466
YCVQLSQIQAQISALEEQLQEIR	48.8	52.036	2746.396	2747.096	3	+2,+3	distinct	0	0.977

The equivalent proteins include

gi|623409|gb|AAA60544.1|	57384.13	keratin 10

582. Group probability: 0.9944. Peptides of the group

HFALSPELGVGYVINELDNTVSVHALDAK	75.91	51.1475	3107.593	3108.807	1	3	distinct	0	0.9944

The equivalent proteins include

jgi|Physo1_1|143807|estExt_fgenesh1_pg.C_1520014	0	No title.

583. Group probability: 0.9944. Peptides of the group

LREDGSSWTQVHR	44.5	54.9995	1569.765	1570.503	1	2	distinct	1	0.8644
RGTNYTLHNEALQK	69.67	54.6119	1643.838	1644.526	5	2	distinct	1	0.959

The equivalent proteins include

jgi|Physo1_1|155728|C_scaffold_7000057	0	No title.

584. Group probability: 0.9943. Peptides of the group

LTGMAFCVPTPNVSVVDLTCR	79.39	52.9849	2336.133	2336.782	6	3	distinct	0	0.9943

The equivalent proteins include

gi|94408078|ref|XP_978778.1|	22485.22	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]
gi|94408118|ref|XP_979290.1|	31442.78	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]

585. Group probability: 0.9943. Peptides of the group

TVFAMPETAIGFFPDVGASYLLPR	75.63	52.4159	2598.319	2599.267	6	2	distinct	0	0.9943

The equivalent proteins include

jgi|Physo1_1|144060|estExt_fgenesh1_pg.C_1640015	0	No title.
jgi|Phyra1_1|73427|fgenesh1_pg.C_scaffold_3000184	0	No title.

586. Group probability: 0.9943. Peptides of the group

SLVGGFEFMPSPNKR	79.68	54.4538	1664.834	1665.779	5	2	distinct	1	0.9943

The equivalent proteins include

jgi|Physo1_1|108538|estExt_fgenesh1_pm.C_150007	0	No title.

587. Group probability: 0.9942. Peptides of the group

LFDPETAHQVAVQCAR	78.96	54.1606	1840.889	1841.562	3	2	distinct	0	0.9942

The equivalent proteins include

jgi|Physo1_1|109029|estExt_fgenesh1_pm.C_540003	0	No title.

588. Group probability: 0.9938. Peptides of the group

LVIIANNTPPLRK	55.82	55.0069	1447.887	1448.852	15	2	shared(2)	1	0.9497
TGVHHFTGTNNDLGTACGK	60.12	54.1509	1985.901	1985.974	3	2	distinct	0	0.9726

The equivalent proteins include

jgi|Physo1_1|108669|estExt_fgenesh1_pm.C_230019	0	No title.

589. Group probability: 0.9935. Peptides of the group

SNYQFEKPFLWLAR	51.39	54.3063	1797.92	1798.726	4	+2,+3	distinct	0	0.9935

The equivalent proteins include

jgi|Physo1_1|108912|estExt_fgenesh1_pm.C_420006	0	No title.
jgi|Phyra1_1|51857|gwEuk.63.30.1	0	No title.

590. Group probability: 0.9934. Peptides of the group

IFGVTTLDVVR	66.68	55.6189	1218.697	1219.442	1	2	shared(3)	0	0.9568
RIFGVTTLDVVR	67.93	55.1545	1374.798	1375.471	35	+2,+3	shared(2)	1	0.9958
VAVLGAAGGIGQPLSLLMK	61	54.2657	1794.044	1794.864	2	2	distinct	0	0.6857

The equivalent proteins include

gi|5929964|gb|AAD56659.1|	36347.11	malate dehydrogenase [Glycine max]

591. Group probability: 0.9933. Peptides of the group

GLVLVEIAPTTTVEEIR	46.27	54.0424	1839.035	1840.195	1	2	distinct	0	0.9012
ITIAEVEELVQPGEIHPDEVHLPGVYVQR	47.37	50.8699	3265.698	3266.671	2	3	distinct	0	0.9325

The equivalent proteins include

jgi|Physo1_1|109150|estExt_fgenesh1_pm.C_640006	0	No title.

592. Group probability: 0.9932. Peptides of the group

SIVHPSYDSNTLNNDIMLIK (000000000000000010000)	61.13	53.3918	2273.136	2273.429	16	+2,+3	distinct	0	0.9932

The equivalent proteins include

gi|230196|pdb|1NTP|	23977.52	Modified Beta Trypsin (Monoisopropylphosphoryl Inhibited) (E.C.3.4.21.4) (Neutron Data)

593. Group probability: 0.9932. Peptides of the group

VMQGIQSGSMHAATHK	77.24	54.2799	1681.803	1682.35	1	2	distinct	0	0.9932

The equivalent proteins include

jgi|Physo1_1|135828|estExt_fgenesh1_pg.C_410019	0	No title.

594. Group probability: 0.9931. Peptides of the group

VIQHNGYGTVK	47.43	55.777	1214.641	1215.417	1	2	distinct	0	0.8856
KVDVSNVYVVNPGNAVVTVNK	50.05	53.1984	2214.201	2214.453	1	2	distinct	1	0.9395

The equivalent proteins include

jgi|Physo1_1|132156|estExt_fgenesh1_pg.C_190106	0	No title.
jgi|Physo1_1|132157|estExt_fgenesh1_pg.C_190107	0	No title.

595. Group probability: 0.9930. Peptides of the group

LFHSGLPNLGINGIELGMDAMTK (000000000000000000001000000)	56.79	52.8455	2443.224	2442.953	10	+2,+3	distinct	0	0.993

The equivalent proteins include

jgi|Phyra1_1|81859|fgenesh1_pg.C_scaffold_64000061	0	No title.

596. Group probability: 0.9929. Peptides of the group

LGANSLLDIVVFGR	85.27	55.0032	1472.835	1473.587	5	2	shared(2)	0	0.9963
FHSKNTVLATGGYGR	71.1	54.6335	1606.822	1607.473	7	2	distinct	1	0.8897

The equivalent proteins include

gi|66505480|ref|XP_623065.1|	73271.54	PREDICTED: similar to ENSANGP00000010243 [Apis mellifera]

597. Group probability: 0.9929. Peptides of the group

VLNALDPEAASNPFKPFHER	74.98	53.5418	2251.138	2251.68	4	2	distinct	0	0.9929

The equivalent proteins include

jgi|Physo1_1|129293|estExt_fgenesh1_pg.C_70118	0	No title.

598. Group probability: 0.9929. Peptides of the group

DSTIIMQLLR	62.92	55.745	1188.654	1188.603	4	2	shared(5)	0	0.8099
LAFDDAIAELDTLSEESYKDSTLIMQLLR	69	50.879	3299.648	3300.563	9	3	distinct	1	0.9899

The equivalent proteins include

gi|83772732|dbj|BAE62860.1|	29229.67	unnamed protein product [Aspergillus oryzae]
gi|70989229|ref|XP_749464.1|	29197.65	hypothetical protein Afu2g03290 [Aspergillus fumigatus Af293]
gi|67534609|ref|XP_662105.1|	29211.63	hypothetical protein AN4501.2 [Aspergillus nidulans FGSC A4]
gi|13430385|gb|AAK25817.1|	29210.68	ARTA [Emericella nidulans]
gi|38490697|gb|AAR21678.1|	28585.52	14-3-3-like protein [Aspergillus flavus]

599. Group probability: 0.9928. Peptides of the group

LFFASVVPLDHLQEYPVPTR	74.74	53.006	2327.231	2327.484	3	2	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|134104|estExt_fgenesh1_pg.C_300015	0	No title.
jgi|Phyra1_1|81342|fgenesh1_pg.C_scaffold_59000006	0	No title.

600. Group probability: 0.9928. Peptides of the group

LFIILSPVGPYYPEGFNPVK	74.85	53.5957	2249.214	2249.69	28	2	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|109235|estExt_fgenesh1_pm.C_780004	0	No title.
jgi|Phyra1_1|71857|fgenesh1_pm.C_scaffold_55000008	0	No title.

601. Group probability: 0.9928. Peptides of the group

GLTFQLPTVIHGTNTMVSAAK	74.41	53.4827	2185.156	2186.254	4	2	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|108159|estExt_fgenesh1_pm.C_10024	0	No title.
jgi|Phyra1_1|40693|gwEuk.123.30.1	0	No title.

602. Group probability: 0.9928. Peptides of the group

FIIAPEYGYGHEGFAPK	76.13	53.9469	1894.925	1895.571	5	2	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|141508|estExt_fgenesh1_pg.C_990053	0	No title.

603. Group probability: 0.9928. Peptides of the group

HALHESAQQAWEVTR	76.97	54.1965	1761.855	1762.574	1	2	distinct	0	0.9928

The equivalent proteins include

jgi|Physo1_1|129732|estExt_fgenesh1_pg.C_90009	0	No title.

604. Group probability: 0.9927. Peptides of the group

YTLAGMEVSALLGR (0000001000000000)	77.37	54.7505	1495.77	1496.39	6	2	distinct	0	0.9927

The equivalent proteins include

gi|73660119|emb|CAI82726.1|	50754.15	ATP synthase F1, beta subunit [Dehalococcoides sp. CBDB1]
gi|57225115|gb|AAW40172.1|	50764.11	ATP synthase F1, beta subunit [Dehalococcoides ethenogenes 195]

605. Group probability: 0.9927. Peptides of the group

ASFVEFINEHAGTYR	76.78	54.1647	1739.827	1740.363	5	2	distinct	0	0.9927

The equivalent proteins include

jgi|Physo1_1|109255|estExt_fgenesh1_pm.C_810002	0	No title.

606. Group probability: 0.9926. Peptides of the group

ILHSTGVETDEAR	77.76	55.1256	1426.705	1427.319	5	2	distinct	0	0.9926

The equivalent proteins include

jgi|Physo1_1|127178|estExt_fgenesh1_pg.C_10158	0	No title.

607. Group probability: 0.9926. Peptides of the group

ICVLGNAVHCEMAEK	76.76	54.3488	1729.795	1730.406	3	2	distinct	0	0.9926

The equivalent proteins include

jgi|Physo1_1|109643|estExt_fgenesh1_pm.C_1910002	0	No title.

608. Group probability: 0.9926. Peptides of the group

LYHSASLVNYGCLPQTWEDPNHVDAATK	73.01	50.9494	3185.488	3186.913	5	3	distinct	0	0.9926

The equivalent proteins include

jgi|Physo1_1|135461|estExt_fgenesh1_pg.C_380095	0	No title.

609. Group probability: 0.9926. Peptides of the group

VDHYTHPDR	47.87	55.3406	1138.516	1139.274	1	2	distinct	0	0.8838
FVGAAPQLSHK	54.02	55.4997	1153.624	1154.512	4	2	distinct	0	0.9362

The equivalent proteins include

jgi|Physo1_1|144183|estExt_fgenesh1_pg.C_1710013	0	No title.

610. Group probability: 0.9925. Peptides of the group

RLPLSPAEVESINSGLAFL	74.76	53.5619	2012.094	2013.23	6	2	distinct	1	0.9925

The equivalent proteins include

jgi|Physo1_1|155279|C_scaffold_1000083	0	No title.

611. Group probability: 0.9924. Peptides of the group

VLVLCNLKPR	55.16	55.1714	1210.722	1211.165	5	2	distinct	0	0.9406
QIASGLVHHYSLEQMQDAR	44.83	53.52	2182.059	2183.505	1	3	distinct	0	0.873

The equivalent proteins include

jgi|Physo1_1|155217|C_scaffold_1000021	0	No title.

612. Group probability: 0.9922. Peptides of the group

LTLPHEYAYGER	47.52	55.0069	1447.71	1448.815	1	2	distinct	0	0.8922
AGDGVNFPKPGQTVSVHYVGTLTDGSK	47.7	51.9117	2730.361	2730.935	1	3	distinct	0	0.928

The equivalent proteins include

jgi|Physo1_1|108555|estExt_fgenesh1_pm.C_150024	0	No title.

613. Group probability: 0.9922. Peptides of the group

DPAQYSEYFGEMPFLALPFEER	72.79	52.2311	2635.194	2635.489	2	2	distinct	0	0.9922

The equivalent proteins include

jgi|Phyra1_1|72800|fgenesh1_pg.C_scaffold_1000242	0	No title.

614. Group probability: 0.9921. Peptides of the group

YPIKHGIVTNWDDMEK	70.94	53.9465	1944.94	1946.416	2	+2,+3	distinct	1	0.9872
VAPEEHPVLLTEAPINPK	81.4	53.7548	1953.057	1953.885	13	2	shared(10)	0	0.9887

The equivalent proteins include

gi|113239|sp|P27132|ACT2_NAEFO	41468.59	Actin-2 (Actin II)

615. Group probability: 0.9921. Peptides of the group

LLESFVHQGPFFLGDK	75.43	54.0825	1832.946	1833.289	4	2	distinct	0	0.9921

The equivalent proteins include

jgi|Physo1_1|129901|estExt_fgenesh1_pg.C_90178	0	No title.
jgi|Physo1_1|144900|estExt_fgenesh1_pg.C_3170004	0	No title.
jgi|Physo1_1|145195|estExt_fgenesh1_pg.C_6020001	0	No title.

616. Group probability: 0.9918. Peptides of the group

IINQPTAAAIAYGLDKK	97.09	54.8238	1785.999	1787.369	3	2	distinct	1	0.9918

The equivalent proteins include

gi|640325|pdb|1NGB|	42542.9	Heat-Shock Cognate 70kd Protein (44kd Atpase N-Terminal Fragment) (E.C.3.6.1.3) Mutant With Glu 17

617. Group probability: 0.9918. Peptides of the group

AEGADAIHPGYGFLSENAAFAR	71.58	53.1431	2263.066	2264.538	7	+2,+3	distinct	0	0.9918

The equivalent proteins include

gi|89099591|ref|ZP_01172466.1|	50699.49	acetyl-CoA carboxylase [Bacillus sp. NRRL B-14911]

618. Group probability: 0.9916. Peptides of the group

IINEPTAAALSFGLDKK	96.71	54.8238	1786.983	1787.369	4	2	distinct	1	0.9916

The equivalent proteins include

gi|15828694|ref|NP_326054.1|	65480.66	molecular chaperone DnaK [Mycoplasma pulmonis UAB CTIP]

619. Group probability: 0.9915. Peptides of the group

APFAGAMGQQLAAIDDNVLVGAPLFQIVK	68.76	51.5341	2953.573	2953.411	2	2	distinct	0	0.9915

The equivalent proteins include

jgi|Physo1_1|108495|estExt_fgenesh1_pm.C_120005	0	No title.

620. Group probability: 0.9915. Peptides of the group

SLSVERPTYTNLNR	47.15	54.6426	1648.853	1648.918	1	2	distinct	0	0.897
RTIQFVDWCPTGFK	68.04	54.2223	1753.861	1754.812	2	2	shared(4)	1	0.9837
IHFMLSSYAPVISAEK (000010000000000000)	84.73	54.3555	1807.918	1808.932	1	2	shared(3)	0	0.9876

The equivalent proteins include

jgi|Physo1_1|119273|estExt_Genewise1.C_610078	0	No title.

621. Group probability: 0.9913. Peptides of the group

HFEINSVGPFLTTR	75.41	54.7404	1616.831	1617.821	1	2	distinct	0	0.9913

The equivalent proteins include

jgi|Physo1_1|138877|estExt_fgenesh1_pg.C_670079	0	No title.
jgi|Physo1_1|138881|estExt_fgenesh1_pg.C_670083	0	No title.
jgi|Phyra1_1|84520|fgenesh1_pg.C_scaffold_115000017	0	No title.

622. Group probability: 0.9909. Peptides of the group

QSVITMMGQHAVR	75.26	54.9975	1456.728	1457.709	4	2	distinct	0	0.9909

The equivalent proteins include

jgi|Phyra1_1|84089|fgenesh1_pg.C_scaffold_103000020	0	No title.

623. Group probability: 0.9905. Peptides of the group

NMSVIAHVDHGK (00100000000000)	76.73	55.4278	1306.645	1307.194	11	2	shared(2)	0	0.9916
IGSPLFSVKAHLPVLESFGFTADLR	44.88	52.0679	2700.464	2700.796	1	3	distinct	1	0.9008

The equivalent proteins include

gi|66805999|ref|XP_636721.1|	93511.92	elongation factor 2 [Dictyostelium discoideum AX4]

624. Group probability: 0.9904. Peptides of the group

VHAILDRYPENYK	74.7	54.7902	1616.831	1617.405	8	2	distinct	1	0.9904

The equivalent proteins include

jgi|Physo1_1|139617|estExt_fgenesh1_pg.C_760028	0	No title.
jgi|Phyra1_1|85108|fgenesh1_pg.C_scaffold_141000017	0	No title.

625. Group probability: 0.9902. Peptides of the group

MIIAGGANLPLEAVLPVFLGGLPLK	69.03	52.6131	2502.465	2503.709	2	2	distinct	0	0.9902

The equivalent proteins include

jgi|Physo1_1|134803|estExt_fgenesh1_pg.C_340039	0	No title.							
626. Group probability: 0.9901. Peptides of the group									
AQFQHGAQLSPVYGR	73.49	54.9336	1657.832	1658.116	2	2	distinct	0	0.9901
The equivalent proteins include									
jgi|Physo1_1|108995|estExt_fgenesh1_pm.C_500008	0	No title.							
627. Group probability: 0.9900. Peptides of the group									
VQLDTGVPVLFGVLTVLNEQQAK	69.65	52.657	2467.369	2468.586	1	2	distinct	0	0.99
The equivalent proteins include									
jgi|Physo1_1|129173|estExt_fgenesh1_pg.C_60330	0	No title.							
jgi|Phyra1_1|86002|fgenesh1_pg.C_scaffold_413000002	0	No title.							
628. Group probability: 0.9898. Peptides of the group									
ATPPPSAPVALNKPAAGNK	71.44	54.4529	1799.989	1800.254	13	2	distinct	0	0.9898
The equivalent proteins include									
jgi|Physo1_1|134237|estExt_fgenesh1_pg.C_300148	0	No title.							
jgi|Phyra1_1|76182|fgenesh1_pg.C_scaffold_16000136	0	No title.							
629. Group probability: 0.9898. Peptides of the group									
HLLALINDILDLSKIEAGK	76.1	53.5046	2075.199	2073.811	28	3	distinct	1	0.9898
The equivalent proteins include									
gi|67930180|ref|ZP_00523355.1|	87462.27	Response regulator receiver:ATP-binding region, ATPase-like:Histidine kinase, HAMP region:Histidine							
630. Group probability: 0.9897. Peptides of the group									
FYVQDGVTHEMPHSTFSAIK	48.19	53.0433	2293.084	2293.781	2	+2,+3	distinct	0	0.9897
The equivalent proteins include									
jgi|Physo1_1|108891|estExt_fgenesh1_pm.C_400001	0	No title.							
631. Group probability: 0.9895. Peptides of the group									
RTIFIGPPGCGK	74.18	55.4824	1301.691	1302.775	2	2	distinct	1	0.9895
The equivalent proteins include									
jgi|Physo1_1|109413|estExt_fgenesh1_pm.C_1020001	0	No title.							
jgi|Phyra1_1|71875|fgenesh1_pm.C_scaffold_57000003	0	No title.							
632. Group probability: 0.9894. Peptides of the group									
QLCTGEAGVGQSGKPLHYK	70.86	53.6224	2029.005	2030.143	4	2	distinct	0	0.9894
The equivalent proteins include									
jgi|Physo1_1|108195|estExt_fgenesh1_pm.C_20027	0	No title.							
jgi|Phyra1_1|49920|gwEuk.5.140.1	0	No title.							
633. Group probability: 0.9892. Peptides of the group									
VSETVKVPEHINHPDYAETGVPESEQR	69.16	51.3942	3046.463	3047.713	1	3	distinct	1	0.9892
The equivalent proteins include									
jgi|Physo1_1|108381|estExt_fgenesh1_pm.C_70026	0	No title.							
634. Group probability: 0.9891. Peptides of the group									
LDLLKLAPGGHIGR	60.34	55.0401	1458.867	1458.974	7	+2,+3	distinct	1	0.9891
The equivalent proteins include									
gi|94733357|emb|CAK04707.1|	20802.26	ribosomal protein L4 [Danio rerio]							
gi|54261775|ref|NP_998272.1|	42810.18	ribosomal protein L4 [Danio rerio]							
635. Group probability: 0.9889. Peptides of the group									
IFSPDHPESPVLR	49.14	54.6671	1492.767	1493.561	3	+2,+3	distinct	0	0.9889
The equivalent proteins include									
jgi|Phyra1_1|82132|fgenesh1_pg.C_scaffold_68000022	0	No title.							
636. Group probability: 0.9889. Peptides of the group									
ILHAQGVSFDSVNVLDHPEIR	69.28	52.9684	2345.213	2345.263	1	2	distinct	0	0.9889
The equivalent proteins include									
jgi|Physo1_1|127728|estExt_fgenesh1_pg.C_20304	0	No title.							
jgi|Phyra1_1|49838|gwEuk.5.58.1	0	No title.							
637. Group probability: 0.9888. Peptides of the group									
KTVAVGVIK	47.89	56.6259	913.596	914.553	1	2	shared(2)	1	0.8809
IGGIGTVPVGR	47.13	55.1937	1024.603	1026.063	1	2	shared(7)	0	0.884
EHALLAFTLGVK	64.61	55.2405	1297.739	1299.156	1	2	shared(4)	0	0.9342
SVEMHHEALIEAVPGDNVGFNVK	57.63	52.5666	2491.216	2492.428	3	2	distinct	0	0.9065

The equivalent proteins include

gi|90265663|dbj|BAE91879.1|	50435.44	elongation factor 1-alpha [Athalia rosae]

638. Group probability: 0.9888. Peptides of the group

VMQGHAAANMVPVICSNR	70.63	53.7549	1953.933	1953.963	1	2	distinct	0	0.9888

The equivalent proteins include

jgi|Physo1_1|158732|C_scaffold_134000006	0	No title.

639. Group probability: 0.9887. Peptides of the group

KLFHPEQLISGK	45.03	54.9936	1395.787	1396.404	1	2	distinct	1	0.8659
RTIQFVDWCPTGFK	68.04	54.2223	1753.861	1754.812	2	2	shared(4)	1	0.9837
IHFMLSSYAPVISAEK (000010000000000000)	84.73	54.3555	1807.918	1808.932	1	2	shared(3)	0	0.9876

The equivalent proteins include

gi|82400128|gb|ABB72803.1|	50580.75	alpha-tubulin-like protein [Solanum tuberosum]
gi|8928408|sp|Q9ZRB7|TBA_WHEAT	50395.6	Tubulin alpha chain
gi|1556446|gb|AAB08791.1|	50265.56	alpha tubulin [Hordeum vulgare]
gi|84105379|gb|ABC54661.1|	42854.46	alpha tubulin 1 [Trimastix marina]
gi|9965991|gb|AAG02564.1|	50293.58	alpha-tubulin [Daucus carota]
gi|3163944|emb|CAA06618.1|	50383.63	alpha-tubulin 1 [Eleusine indica]
gi|3163946|emb|CAA06619.1|	50395.67	alpha-tubulin 1 [Eleusine indica]
gi|1619297|emb|CAA69724.1|	50353.58	alpha-tubulin 2 [Hordeum vulgare subsp. vulgare]
gi|578450|emb|CAA77810.1|	50273.62	alpha-Tubulin [Oxytricha granulifera]
gi|71090024|gb|AAZ23863.1|	50082.49	alpha-tubulin [Sterkiella histriomuscorum]
gi|92896308|gb|ABE93145.1|	50206.55	Cell division protein FtsZ [Medicago truncatula]
gi|37529488|gb|AAQ92662.1|	50193.56	alpha-tubulin 2 [Gossypium hirsutum]
gi|37529490|gb|AAQ92663.1|	50223.57	alpha-tubulin 4 [Gossypium hirsutum]
gi|30683070|ref|NP_849388.1|	47889.17	TUA6 [Arabidopsis thaliana]
gi|76257841|gb|ABA41238.1|	44925.34	alpha-tubulin [Cyanophora paradoxa]
gi|76257847|gb|ABA41241.1|	44358.06	alpha-tubulin [Coleochaete scutata]
gi|76257849|gb|ABA41242.1|	44418.96	alpha-tubulin [Mantoniella squamata]
gi|76257861|gb|ABA41248.1|	44378.99	alpha-tubulin [Pterosperma cristatum]
gi|76257863|gb|ABA41249.1|	44312.96	alpha-tubulin [Pterosperma cristatum]
gi|77745465|gb|ABB02631.1|	50303.64	unknown [Solanum tuberosum]
gi|15222856|ref|NP_175423.1|	50193.56	TUA2 [Arabidopsis thaliana]
gi|15233627|ref|NP_193232.1|	50190.56	TUA6 [Arabidopsis thaliana]
gi|1174592|sp|P46259|TBA1_PEA	50305.62	Tubulin alpha-1 chain
gi|29423813|gb|AAO73546.1|	50375.6	alpha-tubulin [Ceratopteris richardii]
gi|296494|emb|CAA48927.1|	50381.68	alpha tubulin [Anemia phyllitidis]
gi|20413|emb|CAA47635.1|	50179.54	alpha-tubulin [Prunus dulcis]
gi|22147|emb|CAA33734.1|	50383.63	alpha1-tubulin [Zea mays]
gi|22148|emb|CAA33733.1|	50383.63	alpha2-tubulin [Zea mays]
gi|4165488|emb|CAA10663.1|	50381.61	alpha-tubulin 3 [Hordeum vulgare subsp. vulgare]
gi|25396550|dbj|BAC24800.1|	50222.58	alpha tubulin [Physcomitrella patens]
gi|1101025|gb|AAB36609.1|	42638.12	alpha-tubulin [Eucalyptus globulus subsp. bicostata]
gi|27819095|gb|AAO23139.1|	50261.58	alpha tubulin [Populus tremuloides]
gi|29124983|gb|AAO63781.1|	50276.59	alpha-tubulin 1 [Populus tremuloides]
gi|15029368|gb|AAK81858.1|	50379.67	alpha tubulin subunit [Rosa hybrid cultivar]
gi|16226462|gb|AAL16174.1|	50155.76	AT4g14960/dl3520c [Arabidopsis thaliana]
gi|51988174|emb|CAE52515.1|	50369.61	alpha tubulin [Setaria viridis]
gi|6723478|emb|CAB66336.1|	50227.6	alpha-tubulin [Betula pendula]
gi|17402467|emb|CAD13176.1|	50360.69	alpha-tubulin [Nicotiana tabacum]
gi|17402469|emb|CAD13177.1|	50387.7	alpha-tubulin [Nicotiana tabacum]
gi|17402471|emb|CAD13178.1|	50405.63	alpha-tubulin [Nicotiana tabacum]
gi|1743242|emb|CAA71141.1|	42363.19	alpha-tubulin [Histriculus cavicola]
gi|21632090|gb|AAL33695.1|	40779.4	alpha-tubulin [Halteria grandinella]
gi|21632086|gb|AAL33693.1|	40753.39	alpha-tubulin [Halteria grandinella]
gi|21632088|gb|AAL33694.1|	40749.42	alpha-tubulin [Halteria grandinella]
gi|21632092|gb|AAL33696.1|	40721.39	alpha-tubulin [Halteria grandinella]
gi|21632098|gb|AAL33699.1|	40837.4	alpha-tubulin [Halteria grandinella]
gi|34733239|gb|AAQ81585.1|	50089.48	putative tubulin alpha-2/alpha-4 chain [Brassica napus]
gi|22037131|gb|AAM89908.1|	40416.33	alpha-tubulin [Eutintinnus pectinis]
gi|22037135|gb|AAM89909.1|	41500.85	alpha-tubulin [Eutintinnus pectinis]
gi|23957214|gb|AAN40709.1|	40880.55	alpha-tubulin [Tintinnopsis tubulosoides]

gi|23957216|gb|AAN40710.1|	40901.59	alpha-tubulin [Tintinnopsis tubulosoides]
gi|23957221|gb|AAN40711.1|	41355.7	alpha-tubulin [Strombidium sp.]
gi|23957223|gb|AAN40712.1|	41334.81	alpha-tubulin [Strombidium sp.]
gi|23957225|gb|AAN40713.1|	40472.26	alpha-tubulin [Strombidium sp.]
gi|23957227|gb|AAN40714.1|	40634.37	alpha-tubulin [Strombidium sp.]
gi|23957263|gb|AAN40724.1|	41116.59	alpha-tubulin [Metacylis angulata]
gi|23957265|gb|AAN40725.1|	41480.9	alpha-tubulin [Metacylis angulata]
gi|23957267|gb|AAN40726.1|	40799.59	alpha-tubulin [Metacylis angulata]
gi|23957269|gb|AAN40727.1|	40730.52	alpha-tubulin [Metacylis angulata]
gi|23957275|gb|AAN40728.1|	41523.95	alpha-tubulin [Laboea strobila]
gi|23957277|gb|AAN40729.1|	41109.74	alpha-tubulin [Laboea strobila]
gi|23957281|gb|AAN40731.1|	41095.73	alpha-tubulin [Laboea strobila]
gi|23957251|gb|AAN40720.1|	40040.21	alpha-tubulin [Strombidinopsis sp.]
gi|23957257|gb|AAN40723.1|	40651.45	alpha-tubulin [Strombidinopsis sp.]
gi|23957290|gb|AAN40732.1|	40748.54	alpha-tubulin [Favella ehrenbergii]
gi|23957292|gb|AAN40733.1|	40617.43	alpha-tubulin [Favella ehrenbergii]
gi|62734655|gb|AAX96764.1|	50389.59	Tubulin/FtsZ family, GTPase domain, putative [Oryza sativa (japonica cultivar-group)]
gi|37789885|gb|AAP32191.1|	42754.39	alpha-tubulin [Trifolium repens]
gi|56481497|gb|AAV92379.1|	50294.6	alpha tubulin 1 [Pseudotsuga menziesii var. menziesii]
gi|54300498|gb|AAV32824.1|	43499.4	alpha-tubulin [Peridinium foliaceum]
gi|54300500|gb|AAV32825.1|	43469.43	alpha-tubulin [Kryptoperidinium foliaceum]

640. Group probability: 0.9887. Peptides of the group

APAAAASPAPAAAPTAAPADPVIPAPAEPEKPK	66.26	51.2961	3012.592	3013.006	3	3	distinct	0	0.9887

The equivalent proteins include

jgi|Physo1_1|140019|estExt_fgenesh1_pg.C_810008	0	No title.

641. Group probability: 0.9887. Peptides of the group

VCVLDYVKPSPQGTSWGLGGTCVNVGCIPK	67.39	50.966	3247.583	3248.792	4	3	distinct	0	0.9887

The equivalent proteins include

jgi|Phyra1_1|50855|gwEuk.56.99.1	0	No title.

642. Group probability: 0.9886. Peptides of the group

LVGLACTHQTTPGTVAFR	70.49	53.8897	1927.994	1928.369	3	2	distinct	0	0.9886

The equivalent proteins include

jgi|Physo1_1|131940|estExt_fgenesh1_pg.C_180049	0	No title.
jgi|Phyra1_1|81928|fgenesh1_pg.C_scaffold_66000005	0	No title.

643. Group probability: 0.9886. Peptides of the group

AVIGDQWADLLVGLLGHSAASK	68.62	53.1892	2220.19	2221.514	1	2	distinct	0	0.9886

The equivalent proteins include

jgi|Physo1_1|136952|estExt_fgenesh1_pg.C_490090	0	No title.

644. Group probability: 0.9882. Peptides of the group

FSHALVDYQYLANLIGLK	70.03	53.6604	2064.104	2065.266	2	2	distinct	0	0.9882

The equivalent proteins include

jgi|Physo1_1|139488|estExt_fgenesh1_pg.C_740059	0	No title.

645. Group probability: 0.9882. Peptides of the group

KGPAPLNLEIPPYK	71.87	54.6284	1535.871	1537.359	7	2	distinct	1	0.9882

The equivalent proteins include

jgi|Physo1_1|108628|estExt_fgenesh1_pm.C_210002	0	No title.

646. Group probability: 0.9880. Peptides of the group

NLQGIIAILGMDELSEDDKLTVAR (000000000000100000000000000)	117.63	52.4546	2613.368	2614.676	21	2	distinct	1	0.988

The equivalent proteins include

gi|2116558|dbj|BAA20135.1|	60284.43	F1 ATPase [Pisum sativum]

647. Group probability: 0.9880. Peptides of the group

AHELVQSYADAEAQAAPPAFTHITLR	68.53	51.8495	2806.404	2807.683	1	3	distinct	0	0.988

The equivalent proteins include

jgi|Physo1_1|133601|estExt_fgenesh1_pg.C_270013	0	No title.

648. Group probability: 0.9880. Peptides of the group

NFMPFGGSFHCATCDVR	70.22	53.6805	2001.828	2002.697	10	2	distinct	0	0.988

The equivalent proteins include

jgi|Physo1_1|108613|estExt_fgenesh1_pm.C_200001	0	No title.
jgi|Phyra1_1|53110|gwEuk.78.27.1	0	No title.

649. Group probability: 0.9878. Peptides of the group

NNAYHPHVTVGGFQLDPDTGR	74.12	53.0436	2294.083	2295.581	2	2	distinct	0	0.9146
DTGLFPILVHGAGPQMNAELDK	62.97	53.0829	2322.168	2322.747	1	2	shared(2)	0	0.9812

The equivalent proteins include

jgi|Phyra1_1|78196|fgenesh1_pg.C_scaffold_30000001	0	No title.

650. Group probability: 0.9875. Peptides of the group

ESTIHLVLR	71.03	55.2163	1066.613	1067.325	13	2	shared(3)	0	0.9848
IQEKEGIPPDQQR	55.59	54.6732	1536.79	1537.455	2	2	distinct	1	0.9491

The equivalent proteins include

gi|73945898|ref|XP_852338.1|	11035.83	PREDICTED: similar to CG5271-PA [Canis familiaris]
gi|76638698|ref|XP_869731.1|	103189.67	PREDICTED: similar to ubiquitin C isoform 3 [Bos taurus]
gi|76638702|ref|XP_879056.1|	53447.48	PREDICTED: similar to ubiquitin C isoform 5 [Bos taurus]
gi|76638704|ref|XP_879141.1|	68981.2	PREDICTED: similar to ubiquitin C isoform 6 [Bos taurus]
gi|76638708|ref|XP_879323.1|	95909.61	PREDICTED: similar to ubiquitin C isoform 8 [Bos taurus]
gi|76638716|ref|XP_879643.1|	77522.8	PREDICTED: similar to ubiquitin C isoform 12 [Bos taurus]
gi|76638724|ref|XP_879987.1|	86106.45	PREDICTED: similar to ubiquitin C isoform 16 [Bos taurus]
gi|76638728|ref|XP_586525.2|	86064.41	PREDICTED: similar to ubiquitin C isoform 1 [Bos taurus]
gi|76638730|ref|XP_880223.1|	85894.1	PREDICTED: similar to ubiquitin C isoform 18 [Bos taurus]
gi|76638736|ref|XP_880428.1|	95205.37	PREDICTED: similar to ubiquitin C isoform 21 [Bos taurus]
gi|76638740|ref|XP_880581.1|	94648.06	PREDICTED: similar to ubiquitin C isoform 23 [Bos taurus]
gi|76638744|ref|XP_880724.1|	94606.01	PREDICTED: similar to ubiquitin C isoform 25 [Bos taurus]
gi|76638746|ref|XP_880794.1|	94648.06	PREDICTED: similar to ubiquitin C isoform 26 [Bos taurus]
gi|4102845|gb|AAD01603.1|	8074.37	ubiquitin [Entamoeba invadens]
gi|67479295|ref|XP_655029.1|	8692.69	ubiquitin [Entamoeba histolytica HM-1:IMSS]
gi|9295|emb|CAA46497.1|	7845.23	ubiquitin [Entamoeba histolytica]
gi|23451860|gb|AAN32889.1|	13290.07	ubiquitin extension protein [Heterodera glycines]

651. Group probability: 0.9873. Peptides of the group

KIWEVHQGEGVDSK	70.97	54.5315	1610.805	1611.076	5	2	distinct	1	0.9873

The equivalent proteins include

jgi|Physo1_1|134434|estExt_fgenesh1_pg.C_320005	0	No title.
jgi|Phyra1_1|85111|fgenesh1_pg.C_scaffold_142000001	0	No title.
jgi|Phyra1_1|85391|fgenesh1_pg.C_scaffold_175000003	0	No title.

652. Group probability: 0.9872. Peptides of the group

VHAPPGGGSSWSFGDDPAPAPTGR	68.9	53.0212	2319.067	2320.08	3	3	distinct	0	0.9872

The equivalent proteins include

jgi|Physo1_1|132854|estExt_fgenesh1_pg.C_220202	0	No title.

653. Group probability: 0.9871. Peptides of the group

MSMNPFCEIAVEEAIR	85.91	53.8905	1895.858	1897.246	9	2	distinct	0	0.9871

The equivalent proteins include

gi|83859194|ref|ZP_00952715.1|	26885.32	electron transfer flavoprotein beta subunit [Oceanicaulis alexandrii HTCC2633]
gi|23394375|gb|AAN31477.1|	27072.63	electron transfer flavoprotein beta subunit [Phytophthora infestans]
jgi|Physo1_1|109126|estExt_fgenesh1_pm.C_620003	0	No title.
jgi|Phyra1_1|72212|fgenesh1_pm.C_scaffold_108000004	0	No title.

gi|50930317|ref|XP_474686.1|	27565.83	OSJNBb0006L01.5 [Oryza sativa (japonica cultivar-group)]

654. Group probability: 0.9870. Peptides of the group

ILINHLVESR	79.45	55.2375	1192.693	1193.567	9	2	distinct	0	0.987

The equivalent proteins include

jgi|Physo1_1|127239|estExt_fgenesh1_pg.C_10219	0	No title.

655. Group probability: 0.9870. Peptides of the group

VPTPNVSVVDLTCR	73.06	54.7648	1555.803	1557.293	3	2	distinct	0	0.8968
ITGMAFRVPTPNVSVVDLTCR	55.82	52.937	2332.203	2333.52	1	3	distinct	1	0.8742

The equivalent proteins include

gi|229279|prf||681085A	35915.24	dehydrogenase,glyceraldehydephosphate
gi|54635963|gb|EAL25366.1|	37437.25	GA21475-PA [Drosophila pseudoobscura]
gi|40889053|pdb|1J0X|R	35849.25	Chain R, Crystal Structure Of The Rabbit Muscle Glyceraldehyde-3- Phosphate Dehydrogenase (Gapdh)
gi|1066045|gb|AAA81516.1|	11749.82	glyceraldehyde-3-phosphate dehydrogenase
gi|1218048|gb|AAA91804.1|	30745.73	glyceraldehyde-3-phosphate dehydrogenase
gi|65987|pir||DEPGG3	35914.25	glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - pig
gi|1841758|gb|AAB47507.1|	33731.22	glyceraldehyde-phosphate-dehydrogenase [Bos taurus]
gi|2687661|gb|AAB88869.1|	35972.41	glyceraldehyde-3-phosphate dehydrogenase [Columba livia]
gi|2623288|gb|AAC16069.1|	19975.13	glyceraldehyde-3-phosphate dehydrogenase [Ovis aries]
gi|1730158|sp|P51640|G3P_MESAU	33739.32	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|3445501|gb|AAC32447.1|	13071.82	glyceraldehyde-3-phosphate dehydrogenase [Cavia porcellus]
gi|89272932|emb|CAJ82888.1|	36098.28	glyceraldehyde 3 phosphate dehydrogenase [Xenopus tropicalis]
gi|2506441|sp|P00355|G3P_PIG	36041.36	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|6166169|sp|Q28554|G3P_SHEEP	34937.79	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|1730164|sp|P51469|G3P_XENLA	36017.26	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|6679939|ref|NP_032111.1|	48096.38	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic [Mus musculus]
gi|62652560|ref|XP_576287.1|	22717.37	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase (phosphorylating) (EC 1.2.1.12) - m
gi|50978862|ref|NP_001003142.1|	36066.26	glyceraldehyde-3-phosphate dehydrogenase [Canis familiaris]
gi|57163839|ref|NP_001009307.1|	36018.31	glyceraldehyde-3-phosphate dehydrogenase [Felis catus]
gi|4105596|gb|AAD02474.1|	35909.37	glyceraldehyde-3-phosphate dehydrogenase [Gallus gallus]
gi|1773078|gb|AAB40155.1|	16172.25	glyceraldehyde-3-phosphate dehydrogenase [Sus scrofa]
gi|55741036|gb|AAV64182.1|	35999.29	glyceraldehyde-3-phosphate dehydrogenase [Spermophilus citellus]
gi|72496432|dbj|BAE19661.1|	17001.93	glyceraldehyde 3-phosphate dehydrogenase [Oryctolagus cuniculus]
gi|74212012|dbj|BAE40174.1|	36074.21	unnamed protein product [Mus musculus]
gi|74137577|dbj|BAE35822.1|	15638.9	unnamed protein product [Mus musculus]
gi|74141423|dbj|BAE35989.1|	36044.36	unnamed protein product [Mus musculus]
gi|74194852|dbj|BAE26016.1|	36102.33	unnamed protein product [Mus musculus]
gi|74203253|dbj|BAE20812.1|	25339.9	unnamed protein product [Mus musculus]
gi|63401|emb|CAA23697.1|	14687.46	unnamed protein product [Gallus gallus]
gi|2623266|gb|AAB86435.1|	29991.26	glyceraldehyde 3-phosphate dehydrogenase [Ovis aries]
gi|73997649|ref|XP_854083.1|	17391.78	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Canis familiaris]

gi|74004878|ref|XP_852254.1|	44356.63	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Canis familiaris]
gi|84626361|gb|ABC59721.1|	7922.26	glyceraldehyde-3-phosphate dehydrogenase [Spermophilus parryii]
gi|70673311|gb|AAZ06800.1|	22296.24	glyceraldehyde-3-phosphate dehydrogenase [Oxalis stricta]
gi|37698402|gb|AAR00508.1|	35030.96	glyceraldehyde-3-phosphate dehydrogenase; GAPDH [Passer domesticus]
gi|109484558|ref|XP_001065101.1|	36045.19	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|109503243|ref|XP_001070609.1|	33300.03	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase isoform 1 [Rattus norvegicus]
gi|6978952|dbj|BAA90773.1|	36298.41	glyceraldehyde-3-phosphate dehydrogenase [Spirometra erinaceieuropaei]
gi|109476813|ref|XP_001059327.1|	36090.27	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|13702286|dbj|BAB43824.1|	34889.76	glyceraldehyde 3-phosphate dehydrogenase [Cavia porcellus]
gi|55154587|gb|AAH85275.1|	36072.32	Similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]
gi|211797|gb|AAA48774.1|	35989.41	glyceraldehyde-3-phosphate dehydrogenase
gi|1628381|emb|CAA23698.1|	35967.38	glyceraldehyde-3-phosphate dehydrogenase [Gallus gallus]
gi|2494630|sp|Q64467|G3PT_MOUSE	48367.48	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific (Spermatogenic cell-specific glyceraldehy
gi|1169794|sp|P46406|G3P_RABIT	36025.3	Glyceraldehyde-3-phosphate dehydrogenase (GAPDH)
gi|62616|emb|CAA79512.1|	35863.34	glyceraldehydephosphate dehydrogenase [Coturnix coturnix]
gi|77404273|ref|NP_001029206.1|	36073.38	glyceraldehyde-3-phosphate dehydrogenase [Bos taurus]
gi|49435|emb|CAA36368.1|	35953.3	unnamed protein product [Cricetulus griseus]
gi|62318276|dbj|BAD93764.1|	36059.28	Glyceraldehyde-3-phosphate dehydrogenase [Meriones unguiculatus]
gi|1100225|gb|AAD10214.1|	46324.43	glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
gi|1100223|gb|AAD10215.1|	46339.43	glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
gi|4966351|gb|AAD34682.1|	43648.17	Similar to gb|AJ001706 NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (GapCp1) from Pinus s
gi|5052383|gb|AAD38527.1|	20110.47	glyceraldehyde-3-phosphate dehydrogenase GAPDH [Sus scrofa]
gi|3219753|gb|AAC23533.1|	11813.23	glyceraldehyde-3-phosphate dehydrogenase [Sus scrofa]
gi|5712111|gb|AAD47370.1|	18687.6	glyceraldehyde 3-phosphate dehydrogenase [Mustela vison]
gi|3452462|gb|AAC32882.1|	14706.46	glyceraldehyde-3-phosphate dehydrogenase [Equus caballus]
gi|15219206|ref|NP_173080.1|	44988.94	NAD binding / glyceraldehyde-3-phosphate dehydrogenase (phosphorylating)/ glyceraldehyde-3-phosphat
gi|18072805|emb|CAC80377.1|	44689.85	glyceraldehyde-3-phosphate dehydrogenase [Capsicum annuum]
gi|56188|emb|CAA26150.1|	36098.37	glyceraldehyde 3-phosphate-dehydrogenase [Rattus norvegicus]
gi|56611127|gb|AAH87743.1|	36056.29	Glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|39652292|dbj|BAD04859.1|	17342.06	glyceraldehyde-3-phosphate dehydrogenase [Laticauda semifasciata]

gi|50905605|ref|XP_464291.1|	43461.25	putative glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)]
gi|8575565|gb|AAF78051.1|	16838.72	glyceraldehyde-3-phosphate dehydrogenase; GAPDH [Taeniopygia guttata]
gi|52076528|dbj|BAD45405.1|	43752.23	putative glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)]
gi|21618027|gb|AAM67077.1|	45002.95	putative glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]
gi|1667605|gb|AAB18821.1|	7965.31	glyceraldehyde-3-phosphate dehydrogenase [Cavia porcellus]
gi|109504062|ref|XP_001073242.1|	36085.25	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|9838358|gb|AAF68961.2|	18681.56	glyceraldehyde 3-phosphate dehydrogenase GAPDH [Marmota monax]
gi|27754473|gb|AAO22684.1|	44961.93	putative glyceraldehyde-3-phosphate dehydrogenase [Arabidopsis thaliana]
gi|62201487|gb|AAH92267.1|	36100.35	Similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]
gi|49522602|gb|AAH75438.1|	31638.89	MGC89215 protein [Xenopus tropicalis]
gi|5163490|gb|AAD40684.1|	29650.02	glyceraldehyde-3-phosphate dehydrogenase [Equus caballus]
gi|56377786|dbj|BAD74117.1|	36049.37	glyceraldehyde-3-phosphate dehydrogenase (GAPDH) homologue [Pelodiscus sinensis]
gi|21070959|gb|AAK50815.2|	10679.71	glyceraldehyde-3-phosphate dehydrogenase [Capreolus capreolus]
gi|2285903|emb|CAA03875.1|	28908.03	glyceraldehyde 3-phosphate dehydrogenase [Bos taurus]
gi|3059140|emb|CAA04942.1|	39298.06	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase [Pinus sylvestris]
gi|3059122|emb|CAA06030.1|	39352.13	glyeraldehyde-3-phosphate dehydrogenase [Marsilea quadrifolia]
gi|18076096|emb|CAC80386.1|	45945.31	glyceraldehyde-3-phosphate dehydrogenase [Marchantia polymorpha]
gi|21218402|gb|AAM44068.1|	31038.79	glyceraldehyde-3-phosphate dehydrogenase [Sigmodon hispidus]
gi|13027414|ref|NP_076454.1|	47362.02	glyceraldehyde-3-phosphate dehydrogenase, spermatogenic [Rattus norvegicus]
gi|66990025|gb|AAH98095.1|	36102.33	LOC654472 protein [Mus musculus]
gi|27882192|gb|AAH43972.1|	36097.31	Gapd-prov protein [Xenopus laevis]
gi|94397810|ref|XP_988049.1|	36074.26	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]
gi|94399312|ref|XP_978477.1|	36092.36	PREDICTED: similar to Glyceraldehyde-3-phosphate dehydrogenase (GAPDH) [Mus musculus]
gi|16304127|gb|AAL16930.1|	13856.15	glyceraldehyde 3-phosphate dehydrogenase 1 [Fragaria x ananassa]
gi|16226113|gb|AAL16077.1|	13870.16	glyceraldehyde 3-phosphate dehydrogenase [Fragaria x ananassa]
gi|49616580|gb|AAT67150.1|	20734.78	glyceraldehyde-3-phosphate dehydrogenase [Cervus elaphus]
gi|50086895|gb|AAT70328.1|	34343.55	glyceraldehyde 3-phosphate dehydrogenase [Petromyzon marinus]
gi|27356782|gb|AAL49972.1|	35974.29	glyceraldehyde-3-phosphate dehydrogenase [Meriones unguiculatus]
gi|55153885|gb|AAH85315.1|	36093.23	Similar to glyceraldehyde-3-phosphate dehydrogenase [Mus musculus]
gi|62653546|ref|XP_576394.1|	36045.19	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]
gi|62658024|ref|XP_573304.1|	36277.38	PREDICTED: similar to glyceraldehyde-3-phosphate dehydrogenase [Rattus norvegicus]

gi|57232588|gb|AAW47939.1|	6830.78	GAPDH [Tupaia belangeri]
gi|56783068|gb|AAW28862.1|	29980.23	glyceraldehyde-3-phosphate dehydrogenase [Peromyscus maniculatus]

656. Group probability: 0.9870. Peptides of the group

ENIAKIMNESLMLVTALNPHIGYDK (0000000100000000000000000)	68.04	51.8973	2829.44	2829.072	4	3	distinct	1	0.987

The equivalent proteins include

gi|24640177|ref|NP_572339.1|	53826.85	lethal (1) G0255 CG4094-PA, isoform A [Drosophila melanogaster]
gi|24640179|ref|NP_727108.1|	50713.05	lethal (1) G0255 CG4094-PB, isoform B [Drosophila melanogaster]
gi|19528365|gb|AAL90297.1|	53811.88	LD46083p [Drosophila melanogaster]
gi|38047607|gb|AAR09706.1|	12956.77	similar to Drosophila melanogaster CG4094 [Drosophila yakuba]

657. Group probability: 0.9867. Peptides of the group

EAYPGDVFYIHSR	77.43	54.6898	1552.731	1553.625	13	2	shared(2)	0	0.9925
CTGRILEVPVGESLLGR	44.5	54.3156	1854.998	1855.895	1	3	distinct	1	0.8573

The equivalent proteins include

gi|78702137|ref|ZP_00866579.1|	55692.65	ATP synthase F1, alpha subunit [Alkalilimnicola ehrlichei MLHE-1]

658. Group probability: 0.9866. Peptides of the group

NPYPGQIFNKPTTK	70.43	54.669	1603.836	1604.224	2	2	distinct	0	0.9866

The equivalent proteins include

jgi|Physo1_1|134996|estExt_fgenesh1_pg.C_350048	0	No title.

659. Group probability: 0.9865. Peptides of the group

VNTLIRPDGKK	48.33	55.2298	1239.73	1240.209	3	2	distinct	1	0.8955
VNTLIRPDGQKK	50.66	55.1424	1367.788	1368.689	3	2	distinct	1	0.8712

The equivalent proteins include

gi|61654660|gb|AAX48856.1|	17374.73	L23a [Suberites domuncula]
gi|72145683|ref|XP_792948.1|	17866.11	PREDICTED: similar to 60S ribosomal protein L23a [Strongylocentrotus purpuratus]
gi|24266954|gb|AAN52376.1|	18528.63	ribosomal protein L23a [Branchiostoma belcheri]
jgi|Physo1_1|157934|C_scaffold_70000018	0	No title.
jgi|Phyra1_1|79226|fgenesh1_pg.C_scaffold_38000044	0	No title.
jgi|Phyra1_1|95330|C_scaffold_38000019	0	No title.

660. Group probability: 0.9865. Peptides of the group

RLYQSNTNQAPLSLGK	69.41	54.2656	1788.948	1789.753	4	2	distinct	1	0.9865

The equivalent proteins include

jgi|Physo1_1|115505|estExt_Genewise1.C_260146	0	No title.
jgi|Phyra1_1|74564|fgenesh1_pg.C_scaffold_8000165	0	No title.

661. Group probability: 0.9862. Peptides of the group

GGMTSHAAVVAR (00010000000000)	91.33	55.7318	1155.582	1156.392	7	2	shared(2)	0	0.9737
SGAAISMPGMMDTVLNLGLNDETVKGLAK	45.32	51.4516	2932.471	2932.507	1	3	distinct	1	0.9182

The equivalent proteins include

gi|4980770|gb|AAD35361.1|	98387.3	pyruvate,orthophosphate dikinase [Thermotoga maritima MSB8]

662. Group probability: 0.9862. Peptides of the group

AMGIMNSFINDIFER (00100000000000000)	85.48	54.3171	1772.823	1774.034	17	2	distinct	0	0.9862

The equivalent proteins include

gi|76644398|ref|XP_875437.1|	25340.43	PREDICTED: similar to Histone H2B 291B [Bos taurus]
gi|61888730|ref|XP_604423.1|	15998.07	PREDICTED: similar to H2B histone family, member C [Bos taurus]
gi|76678151|ref|XP_609308.2|	9756.19	PREDICTED: similar to Histone H2B 291B, partial [Bos taurus]
gi|109079443|ref|XP_001110898.1|	13913.59	PREDICTED: similar to H2B histone family, member T [Macaca mulatta]
gi|50261574|gb|AAT72343.1|	21971.36	H2B/t variant [Homo sapiens]
gi|49659929|gb|AAT68256.1|	18405.62	histone H2B/s [Homo sapiens]

663. Group probability: 0.9860. Peptides of the group

SDIVGRPLAAMLANDGADVYSADIDSLYLFR	64.44	50.7102	3327.644	3328.102	1	3	distinct	0	0.986

The equivalent proteins include

jgi|Phyra1_1|50564|gwEuk.54.35.1	0	No title.

664. Group probability: 0.9860. Peptides of the group

HFSAPYTPPYITAIPEVK	68	53.5828	2030.051	2031.29	5	2	distinct	0	0.986

The equivalent proteins include

jgi|Physo1_1|130327|estExt_fgenesh1_pg.C_100285	0	No title.

665. Group probability: 0.9857. Peptides of the group

SAYAQCIFAYAPAGAEPQVFIGQTHGK	66.09	51.6843	2881.386	2882.569	1	3	distinct	0	0.9857

The equivalent proteins include

jgi|Physo1_1|108811|estExt_fgenesh1_pm.C_340011	0	No title.
jgi|Phyra1_1|71914|fgenesh1_pm.C_scaffold_59000015	0	No title.

666. Group probability: 0.9856. Peptides of the group

NLRPNYVDAIWDVVNWK	67.23	53.4479	2101.074	2101.88	18	+2,+3	distinct	0	0.9856

The equivalent proteins include

gi|108879548|gb|EAT43773.1|	24617.73	superoxide dismutase, Mn [Aedes aegypti]
gi|56417578|gb|AAV90730.1|	24554.64	cytoplasmic superoxide dismutase [Aedes albopictus]

667. Group probability: 0.9855. Peptides of the group

MAMNPFCEIAVEEAIR (010000000000000000)	84.65	53.8905	1895.858	1897.246	10	2	distinct	0	0.9855

The equivalent proteins include

gi|88859195|ref|ZP_01133835.1|	25728.88	Electron transfer flavoprotein beta-subunit [Pseudoalteromonas tunicata D2]

668. Group probability: 0.9855. Peptides of the group

KIFGQVGPVVDIR	70.02	55.0141	1426.83	1428.187	6	2	distinct	1	0.9855

The equivalent proteins include

jgi|Physo1_1|108782|estExt_fgenesh1_pm.C_310006	0	No title.

669. Group probability: 0.9850. Peptides of the group

LAQGLTYHNVLGVVESIFDAAIK	67.34	52.6767	2457.327	2458.378	1	3	distinct	0	0.985

The equivalent proteins include

jgi|Physo1_1|129776|estExt_fgenesh1_pg.C_90053	0	No title.

670. Group probability: 0.9848. Peptides of the group

LIGPHSIIGR	70.89	55.9714	1061.635	1062.122	9	2	distinct	0	0.9848

The equivalent proteins include

jgi|Physo1_1|108401|estExt_fgenesh1_pm.C_80011	0	No title.

671. Group probability: 0.9845. Peptides of the group

DSTIIMQLLR	62.92	55.745	1188.654	1188.603	4	2	shared(5)	0	0.8099
TASEIATTELPPTHPIR	49.19	54.0818	1832.963	1833.15	2	2	distinct	0	0.7234
QAFDDAIAELDTLSEESYK	63.08	53.315	2143.98	2145.265	2	2	shared(3)	0	0.9792
QAFDDAIAELDTLSEESYKDSTLIMQLLR	73.46	50.8869	3314.623	3315.694	3	3	shared(2)	1	0.9205

The equivalent proteins include

gi|6320304|ref|NP_010384.1|	31099.36	14-3-3 protein, minor isoform; binds proteins and DNA, involved in regulation of many processes inc
gi|6321025|ref|NP_011104.1|	30186.84	14-3-3 protein, major isoform; binds proteins and DNA, involved in regulation of many processes inc
gi|832919|emb|CAA50656.1|	22136.03	BMH1 [Saccharomyces cerevisiae]
gi|50293761|ref|XP_449292.1|	28405.09	unnamed protein product [Candida glabrata]
gi|671634|emb|CAA46959.1|	30271.9	BMH1 [Saccharomyces cerevisiae]
gi|683696|emb|CAA59275.1|	31262.41	BMH2 [Saccharomyces cerevisiae]

672. Group probability: 0.9844. Peptides of the group

TVTPVRPLEVPQFVTGIPAALLTDGELR	64.61	51.4168	2988.665	2990.124	2	3	distinct	0	0.9844

The equivalent proteins include

jgi|Physo1_1|133795|estExt_fgenesh1_pg.C_280016	0	No title.

673. Group probability: 0.9842. Peptides of the group

ILEWSDAPYAARPSSGHLITATTENNTTTWK	63.01	50.3963	3430.679	3431.987	2	3	distinct	0	0.9842

The equivalent proteins include

jgi|Physo1_1|134198|estExt_fgenesh1_pg.C_300109	0	No title.							
674. Group probability: 0.9841. Peptides of the group									
LTYTEHLNPSTR	69.35	55.0597	1430.715	1430.995	6	2	distinct	0	0.9841
The equivalent proteins include									
jgi|Physo1_1|139501|estExt_fgenesh1_pg.C_740072	0	No title.							
jgi|Phyra1_1|81871|fgenesh1_pg.C_scaffold_65000007	0	No title.							
675. Group probability: 0.9840. Peptides of the group									
EGDILCLLEWER	69.25	54.9157	1531.734	1532.952	7	2	distinct	0	0.984
The equivalent proteins include									
jgi|Physo1_1|127339|estExt_fgenesh1_pg.C_10319	0	No title.							
jgi|Phyra1_1|40681|gwEuk.123.18.1	0	No title.							
676. Group probability: 0.9839. Peptides of the group									
TPVDDKDVLLFAPEGDKPQVVAALK	65.62	52.1153	2664.437	2664.503	1	3	distinct	1	0.9839
The equivalent proteins include									
jgi|Physo1_1|108542|estExt_fgenesh1_pm.C_150011	0	No title.							
677. Group probability: 0.9837. Peptides of the group									
RTIQFVDWCPTGFK	68.04	54.2223	1753.861	1754.812	2	2	shared(4)	1	0.9837
ELYHPEQLISGKEDAANNYAR	55.64	52.6912	2417.161	2417.37	2	3	distinct	1	0.9549
The equivalent proteins include									
gi|26419422|gb|AAN78301.1|	51014.93	alpha-tubulin [Encephalitozoon intestinalis]							
678. Group probability: 0.9835. Peptides of the group									
TVVRPYTPTNVNEEK	67.52	54.2947	1745.895	1746.613	2	2	distinct	0	0.9835
The equivalent proteins include									
jgi|Physo1_1|108379|estExt_fgenesh1_pm.C_70024	0	No title.							
679. Group probability: 0.9834. Peptides of the group									
KSGHIVNISSDAGR	68	54.8778	1439.748	1440.78	4	2	distinct	1	0.9834
The equivalent proteins include									
jgi|Physo1_1|157895|C_scaffold_66000025	0	No title.							
jgi|Phyra1_1|95562|C_scaffold_44000020	0	No title.							
680. Group probability: 0.9831. Peptides of the group									
LPGNLDKWEK	69.59	55.6589	1198.635	1199.17	3	2	distinct	1	0.9831
The equivalent proteins include									
jgi|Physo1_1|156553|C_scaffold_22000008	0	No title.							
681. Group probability: 0.9830. Peptides of the group									
SHVIVLPGGK	67.64	56.145	1005.597	1005.447	9	+1,+2	shared(2)	0	0.9971
VGQIEHNVTPQDSVSK	49.17	54.1881	1736.869	1737.063	3	2	distinct	0	0.7179
The equivalent proteins include									
jgi|Phyra1_1|72857|fgenesh1_pg.C_scaffold_1000299	0	No title.							
682. Group probability: 0.9829. Peptides of the group									
DFTHDSEHDVDSAEHR	45.36	53.8899	1895.767	1896.788	1	3	distinct	0	0.8641
FSENKPVPALGGDDLPIDEVYAFYDFWNK	40.22	50.6158	3345.587	3346.639	1	3	distinct	0	0.8742
The equivalent proteins include									
jgi|Physo1_1|136947|estExt_fgenesh1_pg.C_490085	0	No title.							
683. Group probability: 0.9825. Peptides of the group									
IIIEPTAAAIAYGLDKK	88.42	54.8238	1786.024	1787.369	3	2	distinct	1	0.9825
The equivalent proteins include									
gi|15620767|emb|CAC69880.1|	72796.99	heat shock protein (Hsp70) [Moneuplotes crassus]							
684. Group probability: 0.9814. Peptides of the group									
VVSWYDNEWGYSNR	66.58	54.3154	1773.775	1773.614	2	2	distinct	0	0.9814
The equivalent proteins include									
gi|67925626|ref|ZP_00518948.1|	11174.39	similar to Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Crocosphae							
gi|76797229|ref|ZP_00779563.1|	36920.09	Glyceraldehyde-3-phosphate dehydrogenase, type I [Thermoanaerobacter ethanolicus ATCC 33223]							

gi|77687068|ref|ZP_00802362.1|	31226.17	Glyceraldehyde 3-phosphate dehydrogenase (phosphorylating) [Alkaliphilus metalliredigenes QYMF]
gi|88946476|ref|ZP_01149554.1|	36708.19	Glyceraldehyde-3-phosphate dehydrogenase, type I [Desulfotomaculum reducens MI-1]
gi|89341241|ref|ZP_01193486.1|	38782.28	Glyceraldehyde-3-phosphate dehydrogenase, type I [Mycobacterium flavescens PYR-GCK]
gi|90204185|ref|ZP_01206829.1|	36998.22	Glyceraldehyde-3-phosphate dehydrogenase, type I [Mycobacterium vanbaalenii PYR-1]
gi|13092768|emb|CAC30078.1|	36221.9	glyceraldehyde 3-phosphate dehydrogenase [Mycobacterium leprae]
gi|13881096|gb|AAK45745.1|	36104.85	glyceraldehyde 3-phosphate dehydrogenase [Mycobacterium tuberculosis CDC1551]
gi|66965925|ref|ZP_00413489.1|	35921.58	Glyceraldehyde-3-phosphate dehydrogenase, type I [Arthrobacter sp. FB24]
gi|71677692|ref|ZP_00675427.1|	37023.86	Glyceraldehyde-3-phosphate dehydrogenase, type I [Trichodesmium erythraeum IMS101]
gi|870798|gb|AAC37245.1|	38377.72	glyceraldehyde-3-phosphate dehydrogenase
gi|3323159|gb|AAC65812.1|	38344.7	glyceraldehyde 3-phosphate dehydrogenase (gap) [Treponema pallidum subsp. pallidum str. Nichols]
gi|20516773|gb|AAM24956.1|	36775.02	Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Thermoanaerobacter te
gi|51856472|dbj|BAD40630.1|	36348.86	glyceraldehyde-3-phosphate dehydrogenase [Symbiobacterium thermophilum IAM 14863]
gi|108799371|ref|YP_639568.1|	36231.88	glyceraldehyde-3-phosphate dehydrogenase, type I [Mycobacterium sp. MCS]
gi|20549|emb|CAA42902.1|	36462.75	glyceraldehyde 3-phosphate dehydrogenase [Petroselinum crispum]
gi|2749881|gb|AAB95084.1|	36186.95	glyceraldehyde-3-phosphate dehydrogenase homolog [Mycobacterium avium]
gi|520887|emb|CAA52631.1|	39455.46	glyceraldehyde-3-phosphate dehydrogenase [Trypanoplasma borreli]
gi|520888|emb|CAA52632.1|	39614.38	glyceraldehyde-3-phosphate dehydrogenase [Trypanoplasma borreli]

685. Group probability: 0.9814. Peptides of the group

HIEVHPTLPCFLTCADDMTIK	65.68	52.559	2497.18	2497.605	1	3	distinct	0	0.9814

The equivalent proteins include

jgi|Physo1_1|117464|estExt_Genewise1.C_430005	0	No title.
jgi|Phyra1_1|48363|gwEuk.4.2.1	0	No title.

686. Group probability: 0.9807. Peptides of the group

WSGAVVSDIDPPAHRIR	43.71	54.4843	1874.975	1874.292	2	+2,+3	distinct	1	0.9807

The equivalent proteins include

gi|76260198|ref|ZP_00767837.1|	30981	hypothetical protein CaurDRAFT_3259 [Chloroflexus aurantiacus J-10-fl]

687. Group probability: 0.9807. Peptides of the group

IKPGDTLIEPTSGNTGIGLALAAALYGFR	61.83	51.5284	2915.576	2916.614	4	3	distinct	0	0.9807

The equivalent proteins include

jgi|Phyra1_1|72167|fgenesh1_pm.C_scaffold_99000001	0	No title.

688. Group probability: 0.9805. Peptides of the group

HYGALTGLDK	51.04	56.2324	1073.551	1074.046	2	+1,+2	shared(2)	0	0.855
NVVIAAHGNSLR	70.88	55.3236	1249.689	1250.682	3	2	distinct	0	0.9477

The equivalent proteins include

jgi|Physo1_1|108482|estExt_fgenesh1_pm.C_110013	0	No title.

689. Group probability: 0.9801. Peptides of the group

GVNWASFHPTLPLIVSGADDR	51.78	53.558	2251.138	2251.779	8	+2,+3	distinct	0	0.9801

The equivalent proteins include

gi|108868541|gb|EAT32766.1|	140260.25	coatomer [Aedes aegypti]
gi|108870473|gb|EAT34698.1|	140791.43	coatomer [Aedes aegypti]
gi|54641517|gb|EAL30267.1|	141311.63	GA20724-PA [Drosophila pseudoobscura]
gi|24655452|ref|NP_728648.1|	140951.6	-coatomer protein CG7961-PB, isoform B [Drosophila melanogaster]
gi|50918233|ref|XP_469513.1|	137434.92	putative alpha-coat protein [Oryza sativa]
gi|50918235|ref|XP_469514.1|	137418.94	putative alpha-coat protein [Oryza sativa]
gi|15226538|ref|NP_179734.1|	137407.07	protein transporter/ transporter [Arabidopsis thaliana]
gi|45357045|gb|AAS58474.1|	136808.66	coatomer alpha subunit [Hordeum vulgare subsp. vulgare]
jgi|Physo1_1|108346|estExt_fgenesh1_pm.C_60036	0.00	No title.
jgi|Phyra1_1|71742|fgenesh1_pm.C_scaffold_43000017	0.00	No title.

690. Group probability: 0.9799. Peptides of the group

LHPVVVLQVLDR	66.77	55.3331	1386.835	1387.944	5	+2	distinct	0	0.9799

The equivalent proteins include

jgi|Physo1_1|109294|estExt_fgenesh1_pm.C_860001	0.00	No title.

691. Group probability: 0.9796. Peptides of the group

MQAPGTTFGGGSVTIPLKVDIMEHLDELSPAAK	59.32	50.4681	3409.726	3410.919	2	+3	distinct	1	0.9796

The equivalent proteins include

jgi|Physo1_1|143339|estExt_fgenesh1_pg.C_1360011	0.00	No title.

692. Group probability: 0.9796. Peptides of the group

VVGVLLGSTFHGK	66.17	55.3611	1312.750	1313.616	2	+2	distinct	0	0.9796

The equivalent proteins include

jgi|Physo1_1|108965|estExt_fgenesh1_pm.C_470004	0.00	No title.
jgi|Phyra1_1|53287|gwEuk.8.86.1	0.00	No title.

693. Group probability: 0.9796. Peptides of the group

LVDLVNKLNLADK	45.61	54.8571	1453.850	1453.758	2	+2,+3	distinct	1	0.9796

The equivalent proteins include

gi|15076994|gb|AAK83019.1|	42486.33	putative glycosyl transferase WbdM [Salmonella enterica]

694. Group probability: 0.9793. Peptides of the group

SGKPLHYK	48.26	56.7889	928.513	929.188	1	2	shared(2)	0	0.8843
ANPRVFFDMTVGGAPAGR	68.76	54.0555	1861.926	1860.659	5	2	distinct	1	0.9403

The equivalent proteins include

gi|829148|emb|CAA48638.1|	18565.23	cyclophilin [Zea mays]
gi|13925734|gb|AAK49427.1|	18709.18	cyclophilin A-2 [Triticum aestivum]
gi|13925737|gb|AAK49428.1|	18721.19	cyclophilin A-3 [Triticum aestivum]

695. Group probability: 0.9792. Peptides of the group

LSPSLSHLLGK	66.77	55.3467	1150.671	1151.751	2	2	distinct	0	0.9792

The equivalent proteins include

jgi|Physo1_1|156757|C_scaffold_26000041	0	No title.
jgi|Phyra1_1|95232|C_scaffold_35000016	0	No title.

696. Group probability: 0.9792. Peptides of the group

NTNSGHYVCHMK	66.29	55.0745	1446.613	1447.501	3	2	distinct	0	0.9792

The equivalent proteins include

jgi|Physo1_1|108254|estExt_fgenesh1_pm.C_40005	0	No title.
jgi|Phyra1_1|77563|fgenesh1_pg.C_scaffold_25000084	0	No title.

697. Group probability: 0.9787. Peptides of the group

VVHGGEAFSK	67.18	56.4452	1029.524	1029.374	5	1	distinct	0	0.9787

The equivalent proteins include

jgi|Physo1_1|108508|estExt_fgenesh1_pm.C_120018	0	No title.
jgi|Phyra1_1|71117|fgenesh1_pm.C_scaffold_4000004	0	No title.

698. Group probability: 0.9783. Peptides of the group

TTGCVLDSGDGVSHTVPIYEGYALPHAVIR	66.63	50.9816	3183.566	3184.421	9	+2,+3	distinct	0	0.9783

The equivalent proteins include

gi|57864662|gb|AAW56951.1|	29293.65	actin [Phaeodactylum tricornutum]
gi|54300518|gb|AAV32834.1|	27066.67	actin [Phaeodactylum tricornutum]

699. Group probability: 0.9779. Peptides of the group

KLLHFAEGGDAGNR	64.75	54.7972	1483.753	1484.214	2	2	distinct	1	0.9779

The equivalent proteins include

jgi|Physo1_1|108358|estExt_fgenesh1_pm.C_70003	0	No title.
jgi|Phyra1_1|77112|fgenesh1_pg.C_scaffold_22000083	0	No title.

700. Group probability: 0.9778. Peptides of the group

LGADPHALEAVCAPLGLQPR	61.99	53.5802	2084.084	2084.521	2	2	distinct	0	0.9778

The equivalent proteins include

jgi|Physo1_1|132428|estExt_fgenesh1_pg.C_200200	0	No title.

701. Group probability: 0.9774. Peptides of the group

AGDVVALWLPNSAENVLTQLAAAR	59.94	52.5976	2478.323	2479.286	2	2	distinct	0	0.9774

The equivalent proteins include

jgi|Physo1_1|134331|estExt_fgenesh1_pg.C_310041	0	No title.

702. Group probability: 0.9774. Peptides of the group

FPGFSLPDNSHAVYNPLAGVLNPTLAMATMQK	58.53	50.4006	3400.695	3401.977	3	3	distinct	0	0.9774

The equivalent proteins include

jgi|Physo1_1|133544|estExt_fgenesh1_pg.C_260150	0	No title.
jgi|Physo1_1|133547|estExt_fgenesh1_pg.C_260153	0	No title.

703. Group probability: 0.9773. Peptides of the group

PEEHPVLLTEAPINPK	63.51	54.3583	1782.952	1784.318	4	2	distinct	0	0.9773

The equivalent proteins include

gi|83700630|gb|ABC41107.1|	23946.06	actin [Trichoderma koningiopsis]
gi|83700636|gb|ABC41110.1|	25557.96	actin [Trichoderma koningiopsis]
gi|84314104|gb|ABC55663.1|	22492.43	actin [Trichoderma ovalisporum]
gi|84314108|gb|ABC55665.1|	25671.05	actin [Trichoderma caribbaeum]
gi|84314110|gb|ABC55666.1|	24331.26	actin [Trichoderma ovalisporum]
gi|87133580|gb|ABD24432.1|	23815.02	actin [Trichoderma petersenii]

704. Group probability: 0.9772. Peptides of the group

THALNVIPTEAIAGFDIR	62.54	53.8021	1937.037	1937.987	2	2	distinct	0	0.9772

The equivalent proteins include

jgi|Physo1_1|134969|estExt_fgenesh1_pg.C_350021	0	No title.
jgi|Physo1_1|124111|estExt_Genewise1.C_1480015	0	No title.
jgi|Phyra1_1|80568|fgenesh1_pg.C_scaffold_50000076	0	No title.

705. Group probability: 0.9772. Peptides of the group

HLSGFSYHDGSVDR	64.35	54.7743	1575.707	1575.653	2	2	distinct	0	0.9772

The equivalent proteins include

jgi|Physo1_1|137190|estExt_fgenesh1_pg.C_510074	0	No title.

706. Group probability: 0.9771. Peptides of the group

NQLWVGNYQNALSEGGMLNHLGEALR	61.13	51.6883	2883.408	2884.623	3	3	distinct	0	0.9771

The equivalent proteins include

jgi|Physo1_1|109221|estExt_fgenesh1_pm.C_750003	0	No title.

707. Group probability: 0.9771. Peptides of the group

LVNAATLHSQDQANHCK	62.95	54.004	1905.911	1906.163	1	2	distinct	0	0.9771

The equivalent proteins include

jgi|Physo1_1|131774|estExt_fgenesh1_pg.C_170116	0	No title.

708. Group probability: 0.9771. Peptides of the group

HGGGGGGFGGGGFGSR	63.66	55.4405	1319.575	1320.155	1	2	distinct	0	0.9771

The equivalent proteins include

gi|181402|gb|AAC83410.1|	66110.5	epidermal cytokeratin 2 [Homo sapiens]
gi|68563400|gb|AAH99643.1|	65678.32	Keratin 2A (epidermal ichthyosis bullosa of Siemens) [Homo sapiens]

709. Group probability: 0.9770. Peptides of the group

VLGAAAEHANSR	65.22	55.321	1194.61	1195.633	1	2	distinct	0	0.977

The equivalent proteins include

jgi|Physo1_1|113945|estExt_Genewise1.C_170070	0	No title.
jgi|Phyra1_1|71467|fgenesh1_pm.C_scaffold_21000008	0	No title.

710. Group probability: 0.9769. Peptides of the group

QCGLALTGNHYDPLK	63.74	54.3908	1685.819	1686.139	2	2	distinct	0	0.9769

The equivalent proteins include

jgi|Physo1_1|136697|estExt_fgenesh1_pg.C_470111	0	No title.

711. Group probability: 0.9766. Peptides of the group

MFYSPWPTLALLEEFPSLK (01000000000000000000)	61.66	53.0502	2268.154	2284.847	3	2	distinct	0	0.9766

The equivalent proteins include

jgi|Physo1_1|132762|estExt_fgenesh1_pg.C_220110	0	No title.

712. Group probability: 0.9765. Peptides of the group

AFVQHYYTTFDTNR	63.9	54.2186	1761.811	1762.398	2	2	distinct	0	0.9765

The equivalent proteins include

jgi|Phyra1_1|75123|fgenesh1_pg.C_scaffold_11000135	0	No title.

713. Group probability: 0.9764. Peptides of the group

TLAENLEQVPDLSDNHEIIHPVDRPLK	60.26	51.1598	3091.594	3092.715	4	3	distinct	0	0.9764

The equivalent proteins include

jgi|Physo1_1|145643|estExt_fgenesh1_pg.C_20470001	0	No title.

714. Group probability: 0.9760. Peptides of the group

FLLASPPGQVHEVLR	63.33	54.5556	1661.925	1662.751	2	2	distinct	0	0.976

The equivalent proteins include

jgi|Physo1_1|133005|estExt_fgenesh1_pg.C_230148	0	No title.

715. Group probability: 0.9759. Peptides of the group

AAGSGGLRPTQVAELAPFFEGPAALPALSSK	58.46	51.4497	3009.592	3010.857	1	3	distinct	0	0.9759

The equivalent proteins include

jgi|Physo1_1|127265|estExt_fgenesh1_pg.C_10245	0	No title.

716. Group probability: 0.9756. Peptides of the group

QAFDDAIAELDTLSEESYK	63.08	53.315	2143.98	2145.265	2	2	shared(3)	0	0.9792
QAFDDAIAELDTLSEESYKDSTLIMQLPR (00000000000000000000000100000)	72.53	50.8869	3314.586	3315.694	3	3	distinct	1	0.9138

The equivalent proteins include

gi|62420901|gb|AAX82172.1|	28911.23	14-3-3 1 protein [Phanerochaete chrysosporium]

717. Group probability: 0.9752. Peptides of the group

SLSFHYPGVAVQQLGLGVGK	60.71	53.5743	2056.11	2056.785	1	2	distinct	0	0.9752

The equivalent proteins include

jgi|Physo1_1|132679|estExt_fgenesh1_pg.C_220027	0	No title.
jgi|Phyra1_1|79591|fgenesh1_pg.C_scaffold_42000001	0	No title.

718. Group probability: 0.9737. Peptides of the group

VMAAGDFITNLLGHPTQSK	60.52	53.8944	1999.02	1999.871	1	2	distinct	0	0.9737

The equivalent proteins include

jgi|Physo1_1|109053|estExt_fgenesh1_pm.C_550006	0	No title.

719. Group probability: 0.9735. Peptides of the group

TFLHPDSPAYLPVQR	62.13	54.2237	1739.899	1740.966	12	2	distinct	0	0.9735

The equivalent proteins include

jgi|Phyra1_1|77509|fgenesh1_pg.C_scaffold_25000030	0	No title.

720. Group probability: 0.9724. Peptides of the group

DSTIIMQLLR	62.92	55.745	1188.654	1188.603	4	2	shared(5)	0	0.8099
QAFDDAIAELDTLSEDSYKDSTLIMQLLR (00000000000000000000000100000)	53.63	50.8379	3316.602	3317.565	3	3	distinct	1	0.961

The equivalent proteins include

gi|34452065|gb|AAQ72489.1|	27960.81	14-3-3C1 protein [Oncorhynchus mykiss]

721. Group probability: 0.9723. Peptides of the group

LQVHTNPFTTDTIHGLR	60.74	53.8727	1949.012	1949.648	2	2	distinct	0	0.9723

The equivalent proteins include

jgi|Physo1_1|137006|estExt_fgenesh1_pg.C_500042	0	No title.
jgi|Phyra1_1|85609|fgenesh1_pg.C_scaffold_265000008	0	No title.

722. Group probability: 0.9721. Peptides of the group

KSLLVHTK	65.66	55.2432	924.576	925.126	2	2	shared(2)	1	0.8739
VACIGAWHPSR	70.32	55.4274	1252.613	1253.064	9	2	shared(3)	0	0.9847

DDASKAPHLTAFMGFK (000000000000010000)	44.23	54.2254	1750.835	1750.943	1	3	distinct	1	0.6113

The equivalent proteins include

jgi|Phyra1_1|71555|fgenesh1_pm.C_scaffold_27000001	0	No title.

723. Group probability: 0.9720. Peptides of the group

VLITASDVLHSWAIPSLGIK	68.02	53.325	2119.204	2119.855	1	2	distinct	0	0.972

The equivalent proteins include

gi|7545164|gb|AAA32022.2|	30698.59	cytochrome c oxidase subunit II [Phytophthora megasperma]
gi|71063523|gb|AAZ22193.1|	21691.22	cytochrome oxidase subunit II [Pythium graminicola]
gi|71063533|gb|AAZ22198.1|	21627.22	cytochrome oxidase subunit II [Pythium irregulare]
gi|71063547|gb|AAZ22205.1|	21649.17	cytochrome oxidase subunit II [Pythium nunn]
gi|71063559|gb|AAZ22211.1|	21691.22	cytochrome oxidase subunit II [Pythium rostratum]
gi|71063565|gb|AAZ22214.1|	21675.22	cytochrome oxidase subunit II [Pythium sylvaticum]
gi|71063569|gb|AAZ22216.1|	21645.23	cytochrome oxidase subunit II [Pythium nodosum]
gi|71063571|gb|AAZ22217.1|	21661.21	cytochrome oxidase subunit II [Pythium violae]
gi|71063581|gb|AAZ22222.1|	21650.14	cytochrome oxidase subunit II [Phytophthora cactorum]
gi|71063583|gb|AAZ22223.1|	21622.07	cytochrome oxidase subunit II [Phytophthora cactorum]
gi|71063587|gb|AAZ22225.1|	21619.15	cytochrome oxidase subunit II [Phytophthora cinnamomi]
gi|71063589|gb|AAZ22226.1|	21660.23	cytochrome oxidase subunit II [Phytophthora citricola]
gi|71063593|gb|AAZ22228.1|	21517.16	cytochrome oxidase subunit II [Phytophthora citricola]
gi|71063595|gb|AAZ22229.1|	21631.2	cytochrome oxidase subunit II [Phytophthora megasperma]
gi|71063597|gb|AAZ22230.1|	21634.18	cytochrome oxidase subunit II [Phytophthora megasperma]
gi|71063599|gb|AAZ22231.1|	21634.18	cytochrome oxidase subunit II [Phytophthora megasperma]
gi|71063601|gb|AAZ22232.1|	21650.17	cytochrome oxidase subunit II [Phytophthora nicotianae]
gi|71063605|gb|AAZ22234.1|	21644.25	cytochrome oxidase subunit II [Phytophthora sojae]
gi|71063607|gb|AAZ22235.1|	21644.24	cytochrome oxidase subunit II [Phytophthora sojae]
gi|71063609|gb|AAZ22236.1|	21660.25	cytochrome oxidase subunit II [Phytophthora undulata]
gi|9695376|ref|NP_037598.1|	29827.11	cytochrome c oxidase subunit 2 [Phytophthora infestans]
gi|60203149|gb|AAX14746.1|	19484.84	cytochrome oxidase subunit II [Pythium irregulare]
gi|60203100|gb|AAX14722.1|	19355.78	cytochrome oxidase subunit II [Pythium irregulare]
gi|60203151|gb|AAX14747.1|	19512.87	cytochrome oxidase subunit II [Pythium irregulare]
gi|60203121|gb|AAX14732.1|	19466.75	cytochrome oxidase subunit II [Pythium irregulare]
gi|60203147|gb|AAX14745.1|	19494.86	cytochrome oxidase subunit II [Pythium irregulare]
gi|8885659|gb|AAF80240.1|	22174.47	cytochrome c oxidase subunit II [Peronophythora litchii]
gi|9587834|gb|AAF89404.1|	26228.38	cytochrome c oxidase subunit II [Pythium insidiosum]
gi|9587890|gb|AAF89432.1|	26214.39	cytochrome c oxidase subunit II [Pythium sylvaticum]
gi|9587846|gb|AAF89410.1|	26228.41	cytochrome c oxidase subunit II [Pythium iwagamai]
gi|9587858|gb|AAF89416.1|	26230.39	cytochrome c oxidase subunit II [Pythium nunn]

gi|9587868|gb|AAF89421.1|	26181.39	cytochrome c oxidase subunit II [Pythium pulchrum]
gi|9587870|gb|AAF89422.1|	26167.38	cytochrome c oxidase subunit II [Pythium rostratum]
gi|15428384|gb|AAK97844.1|	22170.49	cytochrome c oxidase subunit II [Lagenidium myophilum]
gi|31158504|gb|AAN01348.1|	21792.21	cytochrome c oxidase subunit II [Phytophthora palmivora]
gi|31158418|gb|AAN01305.1|	21771.35	cytochrome c oxidase subunit II [Phytophthora boehmeriae]
gi|31158424|gb|AAN01308.1|	21764.18	cytochrome c oxidase subunit II [Phytophthora cactorum]
gi|38348785|gb|AAR17798.1|	21747.21	cytochrome c oxidase subunit II [Phytophthora cinnamomi]
gi|31158432|gb|AAN01312.1|	21788.29	cytochrome c oxidase subunit II [Phytophthora citricola]
gi|31158438|gb|AAN01315.1|	21774.27	cytochrome c oxidase subunit II [Phytophthora colocasiae]
gi|31158440|gb|AAN01316.1|	21750.16	cytochrome c oxidase subunit II [Phytophthora cryptogea]
gi|38348787|gb|AAR17799.1|	21748.22	cytochrome c oxidase subunit II [Phytophthora erythroseptica]
gi|31158454|gb|AAN01323.1|	21797.38	cytochrome c oxidase subunit II [Phytophthora fragariae var. fragariae]
gi|31158456|gb|AAN01324.1|	21799.4	cytochrome c oxidase subunit II [Phytophthora fragariae var. rubi]
gi|31158458|gb|AAN01325.1|	21730.27	cytochrome c oxidase subunit II [Phytophthora gonapodyides]
gi|31158460|gb|AAN01326.1|	21748.24	cytochrome c oxidase subunit II [Phytophthora heveae]
gi|31158466|gb|AAN01329.1|	21790.27	cytochrome c oxidase subunit II [Phytophthora hibernalis]
gi|38348789|gb|AAR17800.1|	21793.21	cytochrome c oxidase subunit II [Phytophthora ilicis]
gi|31158470|gb|AAN01331.1|	21821.25	cytochrome c oxidase subunit II [Phytophthora ilicis]
gi|31158476|gb|AAN01334.1|	21790.27	cytochrome c oxidase subunit II [Phytophthora infestans]
gi|38348795|gb|AAR17803.1|	21751.16	cytochrome c oxidase subunit II [Phytophthora lateralis]
gi|31158482|gb|AAN01337.1|	21792.25	cytochrome c oxidase subunit II [Phytophthora megakarya]
gi|31158484|gb|AAN01338.1|	21702.23	cytochrome c oxidase subunit II [Phytophthora megasperma]
gi|31158486|gb|AAN01339.1|	21730.27	cytochrome c oxidase subunit II [Phytophthora megasperma]
gi|31158488|gb|AAN01340.1|	21716.25	cytochrome c oxidase subunit II [Phytophthora megasperma]
gi|38348799|gb|AAR17805.1|	21778.23	cytochrome c oxidase subunit II [Phytophthora nicotianae]
gi|31158500|gb|AAN01346.1|	21792.25	cytochrome c oxidase subunit II [Phytophthora palmivora]
gi|31158508|gb|AAN01350.1|	21763.23	cytochrome c oxidase subunit II [Phytophthora pseudotsugae]
gi|31158510|gb|AAN01351.1|	21772.31	cytochrome c oxidase subunit II [Phytophthora sojae]
gi|38348805|gb|AAR17808.1|	21795.23	cytochrome c oxidase subunit II [Phytophthora syringae]
gi|33350990|gb|AAP49016.1|	22166.57	cytochrome oxidase subunit II [Hyaloperonospora parasitica]
gi|38016575|gb|AAR07621.1|	25606.14	cytochrome c oxidase subunit II [Phytophthora nemorosa]
gi|38373703|gb|AAR19106.1|	25592.13	cytochrome c oxidase subunit II [Phytophthora pseudosyringae]
gi|38373707|gb|AAR19108.1|	25568.03	cytochrome c oxidase subunit II [Phytophthora lateralis]
gi|38373715|gb|AAR19112.1|	25593.12	cytochrome c oxidase subunit II [Phytophthora ramorum]
gi|38373717|gb|AAR19113.1|	25612.09	cytochrome c oxidase subunit II [Phytophthora syringae]

gi|38373719|gb|AAR19114.1|	25592.13	cytochrome c oxidase subunit II [Phytophthora syringae]
gi|38348779|gb|AAR17795.1|	21776.25	cytochrome c oxidase subunit II [Phytophthora ramorum]
gi|38348781|gb|AAR17796.1|	21772.31	cytochrome c oxidase subunit II [Phytophthora cambivora]
gi|38348797|gb|AAR17804.1|	21777.24	cytochrome c oxidase subunit II [Phytophthora nemorosa]
gi|38348803|gb|AAR17807.1|	21763.22	cytochrome c oxidase subunit II [Phytophthora pseudosyringae]
gi|93280090|gb|ABF06688.1|	25593.12	cytochrome c oxidase subunit II [Phytophthora capsici]
gi|93280098|gb|ABF06692.1|	25577.13	cytochrome c oxidase subunit II [Phytophthora tropicalis]
gi|71063555|gb|AAZ22209.1|	21622.3	cytochrome oxidase subunit II [Pythium periplocum]
gi|71063577|gb|AAZ22220.1|	21632.2	cytochrome oxidase subunit II [Phytophthora capsici]
gi|9587864|gb|AAF89419.1|	26201.54	cytochrome c oxidase subunit II [Pythium oligandrum]
gi|38348783|gb|AAR17797.1|	21760.26	cytochrome c oxidase subunit II [Phytophthora capsici]
gi|33350982|gb|AAP49012.1|	22166.53	cytochrome oxidase subunit II [Pythium acanthicum]

724. Group probability: 0.9718. Peptides of the group

FHVEEEGKGK	47.93	55.7973	1158.567	1159.423	2	2	shared(2)	1	0.8865
VADKIQLINNMLDK (0000000000010000)	44.36	54.6734	1629.876	1631.294	1	2	distinct	1	0.6372
LGDVYVNDAFGTAHR	79.59	54.6361	1633.785	1634.282	4	+2,+3	shared(2)	0	0.9547

The equivalent proteins include

gi|22219037|pdb|1KF0|A	44837.26	Chain A, Crystal Structure Of Pig Muscle Phosphoglycerate Kinase Ternary Complex With Amp-Pcp And 3
gi|47169449|pdb|1VJD|A	44802.18	Chain A, Structure Of Pig Muscle Pgk Complexed With Atp
gi|66893|pir||KIHOG	44865.26	phosphoglycerate kinase (EC 2.7.2.3) - horse
gi|266755|sp|P29408|PGK1_MACEU	45405.38	Phosphoglycerate kinase 1
gi|52783777|sp|P00559|PGK1_HORSE	44973.29	Phosphoglycerate kinase 1
gi|61354676|gb|AAX41039.1|	45101.31	phosphoglycerate kinase 1 [synthetic construct]
gi|74216774|dbj|BAE37790.1|	44907.12	unnamed protein product [Mus musculus]
gi|74219103|dbj|BAE26693.1|	44949.14	unnamed protein product [Mus musculus]
gi|56403927|emb|CAI29748.1|	44929.2	hypothetical protein [Pongo pygmaeus]
gi|48145549|emb|CAG32997.1|	44973.24	PGK1 [Homo sapiens]
gi|50513041|gb|AAT77773.1|	44929.23	phosphoglycerate kinase 1 [Sus scrofa]
gi|109131308|ref|XP_001100787.1|	44957.23	PREDICTED: similar to phosphoglycerate kinase 1 isoform 4 [Macaca mulatta]
gi|109131310|ref|XP_001100617.1|	40724	PREDICTED: similar to phosphoglycerate kinase 1 isoform 2 [Macaca mulatta]
gi|109131312|ref|XP_001100332.1|	41653.74	PREDICTED: similar to phosphoglycerate kinase 1 isoform 1 [Macaca mulatta]
gi|109131314|ref|XP_001100701.1|	41773.47	PREDICTED: similar to phosphoglycerate kinase 1 isoform 3 [Macaca mulatta]
gi|55663594|ref|XP_529051.1|	46230.42	PREDICTED: phosphoglycerate kinase 1 [Pan troglodytes]
gi|41350401|gb|AAS00488.1|	44985.28	migration-inducing gene 10 protein [Homo sapiens]
gi|129906|sp|P16617|PGK1_RAT	44925.09	Phosphoglycerate kinase 1
gi|129903|sp|P09411|PGK1_MOUSE	44907.08	Phosphoglycerate kinase 1
gi|987048|emb|CAA86028.1|	44933.17	phosphoglycerate kinase [Cricetulus griseus]
gi|38649310|gb|AAH63161.1|	44909.14	Phosphoglycerate kinase 1 [Rattus norvegicus]
gi|80477474|gb|AAI08373.1|	44921.14	Phosphoglycerate kinase 1 [Mus musculus]
gi|55733484|emb|CAH93420.1|	44985.26	hypothetical protein [Pongo pygmaeus]
gi|1150|emb|CAA45574.1|	45274.34	phosphoglycerate kinase [Macropus eugenii]

725. Group probability: 0.9718. Peptides of the group

ETPAGAPTCSAHPAR	61.51	54.6648	1521.699	1522.787	4	2	distinct	0	0.9718

The equivalent proteins include

jgi|Physo1_1|135987|estExt_fgenesh1_pg.C_420050	0	No title.

726. Group probability: 0.9717. Peptides of the group

QILGPLAMAGQLGGAESATR	49.51	53.7901	1940.015	1940.445	3	+2,+3	distinct	0	0.9717

The equivalent proteins include

gi|92911051|ref|ZP_01279825.1|	81636.38	ATP-dependent DNA helicase RecG [Mycobacterium sp. JLS]
gi|108798904|ref|YP_639101.1|	81658.45	ATP-dependent DNA helicase RecG [Mycobacterium sp. MCS]

727. Group probability: 0.9715. Peptides of the group

TAAEDDKDALLASGPNAPFGAWVETNLGELLLR	55.44	50.2602	3453.741	3454.906	4	3	distinct	1	0.9715

The equivalent proteins include

jgi|Physo1_1|135401|estExt_fgenesh1_pg.C_380035	0	No title.
jgi|Phyra1_1|78676|fgenesh1_pg.C_scaffold_33000086	0	No title.

728. Group probability: 0.9714. Peptides of the group

DPTQQTAIDNFMVHELDGTQNEWGWCK	57.97	50.8974	3219.403	3218.014	1	3	distinct	0	0.9714

The equivalent proteins include

gi|90194338|gb|ABD92697.1|	47812.23	los [Brassica rapa subsp. chinensis]
gi|15227987|ref|NP_181192.1|	47974.44	LOS2; phosphopyruvate hydratase [Arabidopsis thaliana]
gi|34597330|gb|AAQ77240.1|	47631.1	enolase [Brassica rapa]
gi|15809970|gb|AAL06912.1|	47959.47	At2g36530/F1O11.16 [Arabidopsis thaliana]
gi|16226235|gb|AAL16111.1|	35062.72	At2g36530/F1O11.16 [Arabidopsis thaliana]
gi|20260174|gb|AAM12985.1|	48032.44	enolase (2-phospho-D-glycerate hydroylase) [Arabidopsis thaliana]
gi|18175728|gb|AAL59917.1|	47983.44	putative enolase (2-phospho-D-glycerate hydroylase) [Arabidopsis thaliana]
gi|34597332|gb|AAQ77241.1|	47635.23	enolase [Brassica napus]
gi|45477377|gb|AAS66001.1|	47949.34	LOS2 [Capsella bursa-pastoris]

729. Group probability: 0.9713. Peptides of the group

NSGVVWTDETLFEYLLAPK	59.39	53.282	2181.099	2182.527	1	2	distinct	0	0.9713

The equivalent proteins include

jgi|Physo1_1|109170|estExt_fgenesh1_pm.C_670002	0	No title.

730. Group probability: 0.9710. Peptides of the group

HYWVLDFANADGESCA	60.66	54.1478	1853.768	1854.158	1	2	distinct	0	0.971

The equivalent proteins include

jgi|Physo1_1|136645|estExt_fgenesh1_pg.C_470059	0	No title.

731. Group probability: 0.9709. Peptides of the group

GAWQRPGEGANVLIAYSDDGTHLSK	58.95	52.3851	2641.288	2642.621	3	3	distinct	0	0.9709

The equivalent proteins include

jgi|Physo1_1|137021|estExt_fgenesh1_pg.C_500057	0	No title.

732. Group probability: 0.9708. Peptides of the group

WEPAETFQFQVDRPK	61.01	54.1217	1876.911	1877.41	2	2	distinct	0	0.9708

The equivalent proteins include

jgi|Phyra1_1|80454|fgenesh1_pg.C_scaffold_49000060	0	No title.

733. Group probability: 0.9708. Peptides of the group

GVLIHGPPGTGK	54.48	56.2365	1131.64	1132.141	1	2	shared(2)	0	0.8714
NAPAIIFIDEIDSIAPK	82.61	54.0989	1825.982	1826.739	16	2	shared(2)	0	0.9959

The equivalent proteins include

gi|21226350|ref|NP_632272.1|	84695.37	Cell division cycle protein [Methanosarcina mazei Go1]
gi|72396736|gb|AAZ71009.1|	84500.49	cell division cycle protein [Methanosarcina barkeri str. fusaro]
gi|85375691|ref|YP_459753.1|	84366.01	Cell division cycle protein [Erythrobacter litoralis HTCC2594]

734. Group probability: 0.9706. Peptides of the group

KQNQYEFVGPFPFAR	63.28	54.1329	1826.91	1827.579	2	3	distinct	1	0.9706

The equivalent proteins include

jgi|Physo1_1|130582|estExt_fgenesh1_pg.C_120014	0	No title.

jgi|Physo1_1|156179|C_scaffold_12000005	0	No title.
jgi|Phyra1_1|73788|fgenesh1_pg.C_scaffold_4000274	0	No title.
jgi|Phyra1_1|93705|C_scaffold_4000069	0	No title.

735. Group probability: 0.9704. Peptides of the group

TFGHAPFTFK	56.45	55.334	1151.576	1152.031	4	2	shared(2)	0	0.9468
NLFDTNVVFASFSHPQMSSFLYK (00000000000000000010000000)	43.35	52.1686	2694.279	2695.692	1	3	distinct	0	0.8779

The equivalent proteins include

jgi|Phyra1_1|78970|fgenesh1_pg.C_scaffold_36000013	0	No title.

736. Group probability: 0.9701. Peptides of the group

VHDSLHNGELR	62.7	55.587	1275.632	1276.444	4	2	distinct	0	0.9701

The equivalent proteins include

jgi|Physo1_1|109162|estExt_fgenesh1_pm.C_660004	0	No title.

737. Group probability: 0.9697. Peptides of the group

NRTEALASVLK	75.85	55.726	1200.683	1201.749	2	2	distinct	1	0.9697

The equivalent proteins include

jgi|Physo1_1|142256|estExt_fgenesh1_pg.C_1100050	0	No title.
jgi|Phyra1_1|78034|fgenesh1_pg.C_scaffold_28000082	0	No title.
jgi|Phyra1_1|78037|fgenesh1_pg.C_scaffold_28000085	0	No title.

738. Group probability: 0.9696. Peptides of the group

YPIEHGIVTNWDDMEK (0000000000000001000)	89.61	53.9432	1945.888	1946.177	23	+2,+3	shared(4)	0	0.9983
VAPEEHPVLLTEAPLDPK	58.57	53.7419	1954.041	1953.494	4	2	distinct	0	0.8583

The equivalent proteins include

gi|62768595|gb|AAY00164.1|	21988.23	actin A1c [Haliotis iris]

739. Group probability: 0.9694. Peptides of the group

SIAPGSASHVFK	62.02	55.6428	1199.63	1200.006	1	2	distinct	0	0.9694

The equivalent proteins include

jgi|Physo1_1|134025|estExt_fgenesh1_pg.C_290092	0	No title.

740. Group probability: 0.9692. Peptides of the group

AIYHATHR	45.81	55.2514	967.499	968.204	1	2	distinct	0	0.861
KVNPINDYILATLAGGAADCQFWQR	50.27	51.8145	2820.402	2821.716	1	3	distinct	1	0.7783

The equivalent proteins include

jgi|Physo1_1|109087|estExt_fgenesh1_pm.C_580012	0	No title.
jgi|Phyra1_1|43059|gwEuk.18.22.1	0	No title.

741. Group probability: 0.9677. Peptides of the group

IIALALHPGYVVTR	60.39	54.6857	1521.903	1523.239	2	2	distinct	0	0.9677

The equivalent proteins include

jgi|Physo1_1|137790|estExt_fgenesh1_pg.C_570055	0	No title.
jgi|Physo1_1|138873|estExt_fgenesh1_pg.C_670075	0	No title.
jgi|Phyra1_1|72246|fgenesh1_pm.C_scaffold_115000004	0	No title.
jgi|Phyra1_1|82598|fgenesh1_pg.C_scaffold_74000043	0	No title.

742. Group probability: 0.9670. Peptides of the group

QFAEHWQATGYK	61.04	55.1654	1464.679	1466.014	1	2	distinct	0	0.967

The equivalent proteins include

jgi|Physo1_1|137176|estExt_fgenesh1_pg.C_510060	0	No title.

743. Group probability: 0.9669. Peptides of the group

RFNFPDGAVELYAER	59.61	54.3687	1782.869	1784.123	3	2	distinct	1	0.9669

The equivalent proteins include

jgi|Physo1_1|108569|estExt_fgenesh1_pm.C_160008	0	No title.
jgi|Phyra1_1|71822|fgenesh1_pm.C_scaffold_51000005	0	No title.

744. Group probability: 0.9667. Peptides of the group

IGPALAAGNSVILKPSEKSPLSALR	57.44	52.5544	2488.438	2489.481	5	3	distinct	1	0.9667

The equivalent proteins include

gi|91796404|gb|ABE58543.1|	54679.45	Aldehyde dehydrogenase (NAD+) [Chromohalobacter salexigens DSM 3043]
gi|83587439|ref|ZP_00926067.1|	53594.49	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli 101-1]
gi|75179045|ref|ZP_00699063.1|	53587.55	COG1012: NAD-dependent aldehyde dehydrogenases [Shigella boydii BS512]
gi|75190386|ref|ZP_00703653.1|	53601.55	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli E24377A]
gi|75212739|ref|ZP_00712737.1|	53667.64	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli B171]
gi|75240055|ref|ZP_00724016.1|	54064.73	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli E110019]
gi|75259412|ref|ZP_00730731.1|	53722.68	COG1012: NAD-dependent aldehyde dehydrogenases [Escherichia coli E22]
gi|74312330|ref|YP_310749.1|	48454.99	aldehyde dehydrogenase [Shigella sonnei Ss046]
gi|82544244|ref|YP_408191.1|	53631.58	aldehyde dehydrogenase [Shigella boydii Sb227]
gi|145224|gb|AAA23428.1|	53682.6	aldehyde dehydrogenase
gi|16129261|ref|NP_415816.1|	53613.53	gamma-Glu-gamma-aminobutyraldehyde dehydrogenase, NAD(P)H-dependent [Escherichia coli K12]
gi|30041068|gb|AAP16798.1|	53488.67	aldehyde dehydrogenase [Shigella flexneri 2a str. 2457T]
gi|56383426|gb|AAN42916.2|	53474.66	aldehyde dehydrogenase [Shigella flexneri 2a str. 301]

745. Group probability: 0.9665. Peptides of the group

DMVLLDVTPLSLGIETLGGVMTK (00000000000000000000001000)	55.86	52.6974	2417.28	2416.029	2	2	distinct	0	0.9665

The equivalent proteins include

gi|51573343|gb|AAU07368.1|	69363.74	heat shock protein 70 [Borrelia garinii PBi]
gi|39376|emb|CAA47888.1|	69346.75	heat-shock protein [Borrelia burgdorferi]

746. Group probability: 0.9662. Peptides of the group

TLERGAHIVVGTPGR	59.51	54.8759	1561.869	1562.893	6	2	distinct	1	0.9662

The equivalent proteins include

gi|83951704|ref|ZP_00960436.1|	83864.94	ATP-dependent RNA helicase, DEAD/DEAH box family protein [Roseovarius nubinhibens ISM]
gi|15073360|emb|CAC41868.1|	69320.08	PUTATIVE ATP-DEPENDENT RNA HELICASE PROTEIN [Sinorhizobium meliloti]
gi|56680381|gb|AAV97047.1|	76031.23	ATP-dependent RNA helicase, DEAD/DEAH box family [Silicibacter pomeroyi DSS-3]

747. Group probability: 0.9659. Peptides of the group

LEGNFKPGSTFYLYPR	58.78	53.9685	1887.952	1888.505	2	2	distinct	0	0.9659

The equivalent proteins include

jgi|Physo1_1|156769|C_scaffold_27000003	0	No title.

748. Group probability: 0.9652. Peptides of the group

GAIDNVVGGGAGHDHK	58.75	54.8657	1502.723	1503.49	1	2	distinct	0	0.9652

The equivalent proteins include

jgi|Physo1_1|128251|estExt_fgenesh1_pg.C_40095	0	No title.
jgi|Physo1_1|128252|estExt_fgenesh1_pg.C_40096	0	No title.

749. Group probability: 0.9648. Peptides of the group

LWPPSTPVDEAVPYFPTAFVSFR	55.19	52.2723	2622.316	2622.589	1	2	distinct	0	0.9648

The equivalent proteins include

jgi|Physo1_1|141377|estExt_fgenesh1_pg.C_970065	0	No title.
jgi|Physo1_1|141379|estExt_fgenesh1_pg.C_970067	0	No title.
jgi|Physo1_1|141380|estExt_fgenesh1_pg.C_970068	0	No title.

750. Group probability: 0.9643. Peptides of the group

YGHVSNIWVAR	60.64	55.4606	1300.668	1301.496	4	2	distinct	0	0.9643

The equivalent proteins include

jgi|Physo1_1|136493|estExt_fgenesh1_pg.C_460039	0	No title.
jgi|Phyra1_1|75301|fgenesh1_pg.C_scaffold_12000048	0	No title.

751. Group probability: 0.9641. Peptides of the group

SVPCLYRAPAEGYQVPGEVYR	58.27	52.786	2410.174	2409.619	1	3	distinct	1	0.9641

The equivalent proteins include

jgi|Phyra1_1|80303|fgenesh1_pg.C_scaffold_48000015	0	No title.

752. Group probability: 0.9641. Peptides of the group

KIAVNLIPFPR	70.88	55.3745	1266.781	1267.527	5	2	shared(6)	1	0.9855
EILHVQGGQCGNQIGAK	66.3	54.3555	1807.9	1808.677	4	2	distinct	0	0.9178

The equivalent proteins include

gi|296498|emb|CAA48929.1|	50334.78	beta tubulin 1 [Anemia phyllitidis]

753. Group probability: 0.9641. Peptides of the group

TAVVQVLDRCPECAHGALDLSPTVYK	55.96	51.6094	2898.437	2899.603	1	3	distinct	1	0.9641

The equivalent proteins include

jgi|Physo1_1|134663|estExt_fgenesh1_pg.C_330053	0	No title.
jgi|Phyra1_1|76346|fgenesh1_pg.C_scaffold_17000108	0	No title.

754. Group probability: 0.9637. Peptides of the group

ESTIHLVLR	71.03	55.2163	1066.613	1067.325	13	2	shared(3)	0	0.9848
YPIEHGIVTNWDDMEK (0000000000000001000)	89.61	53.9432	1945.888	1946.177	23	+2,+3	shared(4)	0	0.9983
VAPEEHPVLLTEAPINPK	81.4	53.7548	1953.057	1953.885	13	2	shared(10)	0	0.9887

The equivalent proteins include

gi|33346927|gb|AAP34624.1|	26433.21	ubiquitin/actin fusion protein 1 [Bigelowiella natans]
gi|33346937|gb|AAP34630.1|	26017.09	ubiquitin/actin fusion protein 3 [Lotharella amoeboformis]
gi|33346935|gb|AAP34629.1|	26031.11	ubiquitin/actin fusion protein 2 [Lotharella amoeboformis]
gi|33346941|gb|AAP34632.1|	26075.11	ubiquitin/actin fusion protein 2 [Lotharella globosa]
gi|33346943|gb|AAP34633.1|	26332.2	ubiquitin/actin fusion protein 3 [Lotharella globosa]
gi|33346945|gb|AAP34634.1|	49579.96	ubiquitin/actin fusion protein [Gymnochlora stellata]

755. Group probability: 0.9630. Peptides of the group

TVEAEAAHGTVTR	67.95	55.2657	1340.668	1341.53	1	2	shared(2)	0	0.868
FKDIFQEVYENEFK	73.99	54.1722	1834.878	1835.5	5	2	distinct	1	0.9016

The equivalent proteins include

gi|83858780|ref|ZP_00952302.1|	45770.19	isocitrate dehydrogenase [Oceanicaulis alexandrii HTCC2633]

756. Group probability: 0.9627. Peptides of the group

KYSLWDQEK	60.82	55.3211	1195.587	1195.907	7	2	distinct	1	0.9627

The equivalent proteins include

jgi|Physo1_1|141162|estExt_fgenesh1_pg.C_950010	0	No title.
jgi|Physo1_1|141164|estExt_fgenesh1_pg.C_950012	0	No title.

757. Group probability: 0.9627. Peptides of the group

FHAAPLPEFTLR	59.67	55.2268	1397.746	1398.703	1	2	distinct	0	0.9627

The equivalent proteins include

jgi|Phyra1_1|71774|fgenesh1_pm.C_scaffold_46000008	0	No title.

758. Group probability: 0.9624. Peptides of the group

VLGAEGDGTSLFFQPDIVPFALAGLTHVEK	72.23	51.1371	3127.623	3127.112	5	3	distinct	0	0.9624

The equivalent proteins include

jgi|Phyra1_1|73176|fgenesh1_pg.C_scaffold_2000241	0	No title.
jgi|Phyra1_1|87857|fgenesh1_pg.C_scaffold_2779000001	0	No title.

759. Group probability: 0.9617. Peptides of the group

KQDPKPVAVPAK	59.42	55.4915	1276.75	1277.22	2	2	distinct	1	0.9617

The equivalent proteins include

jgi|Physo1_1|138048|estExt_fgenesh1_pg.C_600007	0	No title.

760. Group probability: 0.9608. Peptides of the group

VIAWYDNEWGYSNR	85.68	54.2699	1771.795	1771.999	13	2	distinct	0	0.9608

The equivalent proteins include

gi|90585446|ref|ZP_01241155.1|	37141.23	Glyceraldehyde-3-phosphate dehydrogenase, type I [Staphylococcus aureus subsp. aureus JH9]
gi|27315825|gb|AAO04960.1|	37240.2	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus epidermidis ATCC 12228]
gi|82751275|ref|YP_417016.1|	37153.29	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus RF122]
gi|53687157|ref|ZP_00107108.2|	36947.96	COG0057: Glyceraldehyde-3-phosphate dehydrogenase/erythrose-4-phosphate dehydrogenase [Nostoc punct
gi|68446963|dbj|BAE04547.1|	37303.14	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus haemolyticus JCSC1435]
gi|49483929|ref|YP_041153.1|	37151.22	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus aureus subsp. aureus MRSA252]
gi|73662387|ref|YP_301168.1|	37276.99	glyceraldehyde 3-phosphate dehydrogenase 2 [Staphylococcus saprophyticus subsp. saprophyticus ATCC
gi|57637827|gb|AAW54615.1|	37256.16	glyceraldehyde 3-phosphate dehydrogenase [Staphylococcus epidermidis RP62A]
gi|77995878|gb|ABB14777.1|	36250.11	glyceraldehyde-3-phosphate dehydrogenase, type I [Carboxydothermus hydrogenoformans Z-2901]
gi|56751277|ref|YP_171978.1|	38965.41	glyceraldehyde 3-phosphate dehydrogenase [Synechococcus elongatus PCC 6301]
gi|87127690|gb|ABD22204.1|	37127.22	glyceraldehyde-3-phosphate dehydrogenase, type I [Staphylococcus aureus subsp. aureus USA300]
gi|6979050|gb|AAF34325.1|	35682.03	cytosolic glyceraldehyde-3-phosphate dehydrogenase [Phaeodactylum tricornutum]
gi|38195941|gb|AAR13671.1|	37070.2	GapB [Staphylococcus aureus]
gi|89894253|ref|YP_517740.1|	36707.21	hypothetical protein DSY1507 [Desulfitobacterium hafniense Y51]
gi|81300748|ref|YP_400956.1|	36323.85	glyceraldehyde-3-phosphate dehydrogenase, type I [Synechococcus elongatus PCC 7942]
gi|109649322|ref|ZP_01373210.1|	36579.19	glyceraldehyde-3-phosphate dehydrogenase, type I [Desulfitobacterium hafniense DCB-2]
gi|89894355|ref|YP_517842.1|	37131.45	glyceraldehyde 3-phosphate dehydrogenase [Desulfitobacterium hafniense Y51]
gi|56752164|ref|YP_172865.1|	37270.32	glyceraldehyde 3-phosphate dehydrogenase [Synechococcus elongatus PCC 6301]

761. Group probability: 0.9602. Peptides of the group

DILLLDVTPLSLGIETMGGVMTK	65.14	52.8951	2415.3	2414.453	7	2	distinct	0	0.9602

The equivalent proteins include

gi|57340176|gb|AAW50075.1|	73604.53	hypothetical protein FTT1269 [synthetic construct]
gi|3122002|sp|O32482|DNAK_LEGPN	70215.33	Chaperone protein dnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70)
gi|53751737|emb|CAH13159.1|	70245.36	Chaperone protein DnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) [Legionella pneu
gi|53754755|emb|CAH16242.1|	70217.33	Chaperone protein DnaK (Heat shock protein 70) (Heat shock 70 kDa protein) (HSP70) [Legionella pneu

gi|56604821|emb|CAG45902.1|	69382.76	Chaperone protein dnaK (heat shock protein family 70 protein) [Francisella tularensis subsp. tulare
gi|52629353|gb|AAU28094.1|	70873.61	chaperone protein DnaK, heat shock protein Hsp70 [Legionella pneumophila subsp. pneumophila str. Ph

762. Group probability: 0.9602. Peptides of the group

IVYSIHGGPMAGR	58.55	55.3588	1356.697	1357.398	6	2	distinct	0	0.9602

The equivalent proteins include

jgi|Physo1_1|139819|estExt_fgenesh1_pg.C_780080	0	No title.
jgi|Phyra1_1|85165|fgenesh1_pg.C_scaffold_149000001	0	No title.

763. Group probability: 0.9600. Peptides of the group

LAGNHVIGTCSSPDKVEYLR	55.17	53.1945	2215.105	2215.792	1	2	distinct	1	0.96

The equivalent proteins include

jgi|Physo1_1|108301|estExt_fgenesh1_pm.C_50016	0	No title.
jgi|Phyra1_1|71065|fgenesh1_pm.C_scaffold_2000006	0	No title.

764. Group probability: 0.9594. Peptides of the group

HAQGFHNVAEQK	58.65	55.0274	1364.658	1365.665	3	2	distinct	0	0.9594

The equivalent proteins include

jgi|Physo1_1|136221|estExt_fgenesh1_pg.C_440022	0	No title.

765. Group probability: 0.9593. Peptides of the group

GSSPMKPVLYLEDPYFYVR	55.4	53.3074	2260.124	2261.459	2	2	distinct	0	0.9593

The equivalent proteins include

jgi|Physo1_1|108389|estExt_fgenesh1_pm.C_70034	0	No title.

766. Group probability: 0.9592. Peptides of the group

EFGIDEKNMFGFWDWVGGR	57.73	53.2573	2289.031	2287.732	3	3	distinct	1	0.9592

The equivalent proteins include

gi|66499293|ref|XP_623552.1|	63155.85	PREDICTED: similar to glucosephosphate isomerase [Apis mellifera]

767. Group probability: 0.9587. Peptides of the group

SSMSDMEQVIDDLK (0000001000000000)	57.56	54.5711	1612.696	1614.053	2	2	distinct	0	0.9587

The equivalent proteins include

gi|56783954|dbj|BAD81391.1|	77715.32	hypothetical protein [Oryza sativa (japonica cultivar-group)]
gi|34904404|ref|NP_913549.1|	84981.03	unnamed protein product [Oryza sativa (japonica cultivar-group)]

768. Group probability: 0.9579. Peptides of the group

IEQLHQTVADHCSAR	56.84	54.2044	1763.837	1764.118	1	2	distinct	0	0.9579

The equivalent proteins include

jgi|Physo1_1|142675|estExt_fgenesh1_pg.C_1190045	0	No title.

769. Group probability: 0.9573. Peptides of the group

KLWAEDPHAPQAR	57.68	54.9759	1517.774	1518.143	1	2	distinct	1	0.9573

The equivalent proteins include

jgi|Physo1_1|128752|estExt_fgenesh1_pg.C_50249	0	No title.

770. Group probability: 0.9572. Peptides of the group

CTLESQCQAGTCNLK	76.21	54.2145	1768.754	1769.2	2	2	distinct	0	0.9572

The equivalent proteins include

jgi|Physo1_1|140877|estExt_fgenesh1_pg.C_910002	0	No title.
jgi|Phyra1_1|80861|fgenesh1_pg.C_scaffold_53000054	0	No title.

771. Group probability: 0.9569. Peptides of the group

ACNALLLK	66.88	56.8984	901.505	902.794	1	2	shared(3)	0	0.9265
VPTPDVSVVDLTCR	100.87	54.7648	1556.787	1557.293	12	2	shared(5)	0	0.9926
LTGMAFRVPTPDVSVVDLTCR (000010000000000000000)	64.95	52.937	2333.187	2333.52	9	+2,+3	shared(4)	1	0.9972

The equivalent proteins include

gi|71000249|dbj|BAE07174.1|	86477.52	polyprotein [Heterocapsa triquetra]

772. Group probability: 0.9568. Peptides of the group

ILTWVQHWTAQHADD	56.56	54.2652	1819.864	1821.234	2	2	distinct	0	0.9568

The equivalent proteins include

jgi|Physo1_1|109405|estExt_fgenesh1_pm.C_1000002	0	No title.

773. Group probability: 0.9566. Peptides of the group

NTAIVLAAK	79.15	55.9067	899.544	898.135	3	2	distinct	0	0.9566

The equivalent proteins include

gi|82738292|ref|ZP_00901128.1|	23426.53	conserved hypothetical protein [Pseudomonas putida F1]

774. Group probability: 0.9563. Peptides of the group

AEGLWAGIVIPEAGR	56.52	54.6587	1537.825	1537.225	1	2	distinct	0	0.9563

The equivalent proteins include

gi|108797038|ref|YP_637235.1|	11080.64	transcription factor WhiB [Mycobacterium sp. MCS]

775. Group probability: 0.9557. Peptides of the group

VGLTGLTVAEYFR	105.09	54.9941	1424.766	1425.451	8	2	shared(2)	0	0.9864
AALVFGQMNEPPGAR (000000000100000000)	46.86	54.9331	1572.772	1573.149	1	2	distinct	0	0.6798

The equivalent proteins include

gi|45685251|gb|AAS75379.1|	15459.04	AtpD [Mesorhizobium sp. ICMP 14330]

776. Group probability: 0.9556. Peptides of the group

FTHLAEETAPRPTQQK	55.82	54.1477	1852.943	1853.665	1	2	distinct	0	0.9556

The equivalent proteins include

jgi|Physo1_1|134242|estExt_fgenesh1_pg.C_300153	0	No title.

777. Group probability: 0.9555. Peptides of the group

FYIDNIVGGTGAYGHSK	84.54	54.1425	1797.869	1797.44	5	2	distinct	0	0.9555

The equivalent proteins include

jgi|Phyra1_1|71911|fgenesh1_pm.C_scaffold_59000012	0	No title.
jgi|Phyra1_1|71912|fgenesh1_pm.C_scaffold_59000013	0	No title.

778. Group probability: 0.9554. Peptides of the group

NPPPPPSSSADTPPPPPSSSSSTSSSAESLR	51.42	51.3983	3004.39	3005.713	1	3	distinct	0	0.9554

The equivalent proteins include

gi|66932877|gb|AAY58271.1|	53995.63	cell cycle switch protein CCS52A [Lotus corniculatus var. japonicus]

779. Group probability: 0.9548. Peptides of the group

AAAAAAAAAPPKPAPK	55.9	55.3256	1372.783	1373.101	11	2	distinct	0	0.9548

The equivalent proteins include

jgi|Physo1_1|131865|estExt_fgenesh1_pg.C_170207	0	No title.

780. Group probability: 0.9537. Peptides of the group

MVLPSNITK (01000000000)	58.57	56.2117	1017.553	1018.433	1	2	distinct	0	0.9537

The equivalent proteins include

gi|90585996|ref|ZP_01241700.1|	67819.01	conserved hypothetical protein [Staphylococcus aureus subsp. aureus JH9]
gi|87127959|gb|ABD22473.1|	122034.25	conserved hypothetical protein [Staphylococcus aureus subsp. aureus USA300]
gi|21203232|dbj|BAB93933.1|	122052.31	MW0068 [Staphylococcus aureus subsp. aureus MW2]
gi|49243416|emb|CAG41836.1|	122053.29	hypothetical protein [Staphylococcus aureus subsp. aureus MSSA476]
gi|14245860|dbj|BAB56255.1|	122103.27	hypothetical protein [Staphylococcus aureus subsp. aureus Mu50]

781. Group probability: 0.9537. Peptides of the group

MKSYDIVVIGGGPGGYVAAIK	53.14	53.4055	2094.118	2094.557	1	2	distinct	1	0.9537

The equivalent proteins include

gi|10173393|dbj|BAB04498.1|	49550.26	dihydrolipoamide dehydrogenase [Bacillus halodurans C-125]

782. Group probability: 0.9537. Peptides of the group

QMSLKDVVAQEPK (001000000000000)	56.73	54.9192	1487.765	1488.506	2	2	distinct	1	0.9537

The equivalent proteins include

jgi|Phyra1_1|93883|C_scaffold_9000037	0	No title.

783. Group probability: 0.9536. Peptides of the group

VVGAIMHLK	58.3	55.1427	966.568	967.148	4	2	distinct	0	0.9536

The equivalent proteins include

jgi|Physo1_1|144389|estExt_fgenesh1_pg.C_1830016	0	No title.

784. Group probability: 0.9535. Peptides of the group

YKIVLLR	50.4	56.672	903.591	903.581	1	1	shared(2)	1	0.8334
HYGALTGLDK	51.04	56.2324	1073.551	1074.046	2	+1,+2	shared(2)	0	0.855
VIIAAHGNSIR	55.36	55.3959	1149.662	1150.474	5	2	shared(2)	0	0.8995

The equivalent proteins include

gi|88796704|ref|ZP_01112360.1|	27940.36	phosphoglyceromutase [Alteromonas macleodii 'Deep ecotype']

785. Group probability: 0.9531. Peptides of the group

SDGIFIGNFVGGDSLK	55.3	54.5645	1624.81	1625.841	1	2	distinct	0	0.9531

The equivalent proteins include

gi|3861015|emb|CAA14915.1|	25786.51	unknown [Rickettsia prowazekii]
gi|51459959|gb|AAU03922.1|	25929.56	conserved hypothetical protein [Rickettsia typhi str. Wilmington]

786. Group probability: 0.9531. Peptides of the group

LFFRPEQAGMTK	57	54.9108	1423.728	1424.631	1	2	distinct	0	0.9531

The equivalent proteins include

jgi|Physo1_1|108205|estExt_fgenesh1_pm.C_20037	0	No title.
jgi|Phyra1_1|71148|fgenesh1_pm.C_scaffold_5000017	0	No title.

787. Group probability: 0.9528. Peptides of the group

MVQVADDHAHASNSSSDSAPFLSAAQR	52.57	52.1844	2798.268	2798.852	1	3	distinct	0	0.9528

The equivalent proteins include

jgi|Physo1_1|131406|estExt_fgenesh1_pg.C_150177	0	No title.

788. Group probability: 0.9524. Peptides of the group

IKPELAEVPSKESFPVYAGPEQR	54.17	52.5299	2570.338	2571.136	1	3	distinct	1	0.9524

The equivalent proteins include

jgi|Physo1_1|125082|estExt_Genewise1.C_1970012	0	No title.

789. Group probability: 0.9523. Peptides of the group

VGLLLEVNPDLPPAIALGLHLLEEQALGAK	51	51.1216	3102.769	3104.246	1	3	distinct	0	0.9523

The equivalent proteins include

jgi|Physo1_1|132933|estExt_fgenesh1_pg.C_230076	0	No title.

790. Group probability: 0.9520. Peptides of the group

GVKAILAAR	58.07	55.8218	897.576	898.985	3	2	distinct	1	0.952

The equivalent proteins include

gi|19887888|gb|AAM02489.1|	49542.49	Fusion of at least two uncharacterized domain specific for M.kandleri, MK-12 family [Methanopyrus k

791. Group probability: 0.9518. Peptides of the group

LMEGFIHDKPQLWNEDIGV	53.44	53.1595	2240.094	2241.428	2	2	distinct	0	0.9518

The equivalent proteins include

jgi|Physo1_1|108743|estExt_fgenesh1_pm.C_290006	0	No title.

792. Group probability: 0.9517. Peptides of the group

LKDLHVR	59.15	55.5514	879.529	880.277	5	2	distinct	1	0.9517

The equivalent proteins include

jgi|Physo1_1|133588|estExt_fgenesh1_pg.C_260194	0	No title.
jgi|Phyra1_1|95221|C_scaffold_35000005	0	No title.

793. Group probability: 0.9516. Peptides of the group

RAYPQFAQQSPR	56.66	55.065	1447.732	1448.114	2	2	distinct	1	0.9516

The equivalent proteins include

jgi|Physo1_1|130117|estExt_fgenesh1_pg.C_100075	0	No title.
jgi|Phyra1_1|72623|fgenesh1_pg.C_scaffold_1000065	0	No title.

794. Group probability: 0.9511. Peptides of the group

VKEVGSLLANLAHDQNK	56.69	54.1787	1834.99	1835.72	2	3	distinct	1	0.9511

The equivalent proteins include

gi|90962347|ref|YP_536263.1|	24674.35	ABC transporter, ATP-binding protein [Lactobacillus salivarius subsp. salivarius UCC118]

795. Group probability: 0.9509. Peptides of the group

KYDHLVYPNR	57.41	55.4793	1303.667	1304.3	2	2	distinct	1	0.9509

The equivalent proteins include

jgi|Physo1_1|145595|estExt_fgenesh1_pg.C_18990001	0	No title.

jgi|Phyra1_1|74442|fgenesh1_pg.C_scaffold_8000043	0	No title.
jgi|Phyra1_1|86209|fgenesh1_pg.C_scaffold_537000001	0	No title.

796. Group probability: 0.9509. Peptides of the group

ALVHVGPCEIWLDNTK	77.79	54.0207	1850.935	1851.821	6	2	distinct	0	0.9509

The equivalent proteins include

jgi|Physo1_1|133344|estExt_fgenesh1_pg.C_250098	0	No title.

797. Group probability: 0.9504. Peptides of the group

VADVYVNDAFGTAHR	78.55	54.6361	1633.785	1634.282	4	+2,+3	distinct	0	0.9504

The equivalent proteins include

gi|51860718|gb|AAU11483.1|	105253.61	chloroplast phosphoglycerate kinase precursor [Euglena gracilis]

798. Group probability: 0.9504. Peptides of the group

LSTSPFLPHMTVVSGVK	54.2	54.4027	1798.965	1800.347	1	2	distinct	0	0.9504

The equivalent proteins include

jgi|Physo1_1|135035|estExt_fgenesh1_pg.C_350087	0	No title.

799. Group probability: 0.9499. Peptides of the group

PFVHVTSNVPK	56.7	55.1669	1223.666	1224.983	1	2	distinct	0	0.9499

The equivalent proteins include

jgi|Physo1_1|157309|C_scaffold_41000011	0	No title.

800. Group probability: 0.9498. Peptides of the group

QATINIGTIGHVAHGK	54.58	54.8701	1615.879	1616.708	1	2	distinct	0	0.9498

The equivalent proteins include

gi|108872932|gb|EAT37157.1|	78606.33	histone-lysine n-methyltransferase [Aedes aegypti]
gi|54639643|gb|EAL29045.1|	72650.02	GA19622-PA [Drosophila pseudoobscura]
gi|88185753|gb|EAQ93221.1|	56170.49	hypothetical protein CHGG_01456 [Chaetomium globosum CBS 148.51]
gi|82802708|gb|ABB92405.1|	51695.4	eFI-2-gamma [Homo sapiens]
gi|82802710|gb|ABB92406.1|	51696.44	eFI-2-gamma [Pan troglodytes]
gi|82802712|gb|ABB92407.1|	51735.55	eFI-2-gamma [Gorilla gorilla]
gi|82802714|gb|ABB92408.1|	51591.42	eFI-2-gamma [Pongo pygmaeus]
gi|82802716|gb|ABB92409.1|	51701.51	eFI-2-gamma [Hylobates lar]
gi|90298719|gb|EAS28350.1|	57582.8	hypothetical protein CIMG_09554 [Coccidioides immitis RS]
gi|84310029|emb|CAJ18344.1|	68663.33	putative H3K9 methyltransferase [Bombyx mori]
gi|84310031|emb|CAJ18345.1|	67156.39	putative H3K9 methyltransferase [Cercopis vulnerata]
gi|84310033|emb|CAJ18346.1|	45956.34	putative translation initiation factor 2 gamma subunit [Drosophila nasutoides]
gi|84310034|emb|CAJ18347.1|	73704.71	putative H3K9 methyltransferase [Drosophila nasutoides]
gi|84310038|emb|CAJ18349.1|	64986.86	putative H3K9 methyltransferase [Forficula auricularia]
gi|84310040|emb|CAJ18350.1|	70097.84	putative H3K9 methyltransferase [Lepisma saccharina]
gi|66526442|ref|XP_393032.2|	52172.87	PREDICTED: similar to eukaryotic translation initiation factor 2 gamma [Apis mellifera]
gi|74147228|dbj|BAE27514.1|	51643.41	unnamed protein product [Mus musculus]
gi|74211920|dbj|BAE29303.1|	48647.81	unnamed protein product [Mus musculus]
gi|83769182|dbj|BAE59319.1|	56448.4	unnamed protein product [Aspergillus oryzae]
gi|31071349|emb|CAB93768.2|	72998.77	histone-lysine N-methyltransferase, H3 lysine-9 specific [Drosophila melanogaster]
gi|91077468|ref|XP_966493.1|	106697.7	PREDICTED: similar to CG6476-PB, isoform B isoform 1 [Tribolium castaneum]
gi|91077470|ref|XP_975868.1|	107489.99	PREDICTED: similar to CG6476-PB, isoform B isoform 2 [Tribolium castaneum]
gi|91077472|ref|XP_975907.1|	51662.7	PREDICTED: similar to eukaryotic translation initiation factor 2, subunit 3, structural gene X-link

S5. Protein assembly of peptide sequence matches made to tag-filtered F. graminearum tandem mass spectra. The NCBI NR database was searched. Protein List with probabilities. The columns are arranged as follows: peptide sequence, Mascot Ions score, Mascot Identity score, computed peptide mass, observed precursor mass, number of tandem mass spectra assigned to same peptide sequence, the charge states observed for the peptide, whether the peptide is shared between protein groups with different probabilities (number in parentheses is number of other groups peptides are shared with) or is distinct (considered a unique identifier for proteins grouped with the same probability), the number of missed tryptic cleavages in this sequence, and the probability for a particular peptide sequence.

1. Group probability: 1.0000. Peptides of the group

VDELKPEFPAAGKK	64.97	54.7546	1527.83	1529.233	4	+2,+3	distinct	1	0.9993
SKVDELKPEFPAAGK	85.48	54.7521	1614.862	1615.473	7	+2,+3	distinct	1	0.9998

The equivalent proteins include

gi|46136709|ref|XP_390046.1|	35379.6	GBLP_NEUCR Guanine nucleotide-binding protein beta subunit-like protein (Cross-pathway control WD-r

2. Group probability: 1.0000. Peptides of the group

IKDADNEVITKPDFYK	77.67	53.8964	1894.968	1895.253	1	2	distinct	1	0.9935
DPYDSPVDSVGDKLDPLPWR	98.79	52.9879	2270.085	2269.883	3	2	distinct	1	0.9991
IPFTPGDRDPYDSPVDSVGDK	55.12	53.1577	2276.06	2276.923	1	2	distinct	1	0.9613

The equivalent proteins include

gi|46139197|ref|XP_391289.1|	54443.44	hypothetical protein FG11113.1 [Gibberella zeae PH-1]

3. Group probability: 1.0000. Peptides of the group

GGVGVQPDALVDFIDDFR	95.76	53.8426	1918.942	1919.753	1	2	distinct	0	0.9988
NKGGVGVQPDALVDFIDDFR	104.59	53.2232	2161.08	2161.043	5	2	distinct	1	0.9995

The equivalent proteins include

gi|46135701|ref|XP_389542.1|	47729.96	hypothetical protein FG09366.1 [Gibberella zeae PH-1]

4. Group probability: 1.0000. Peptides of the group

SAKPADEEQSNADAEEGAKPR	113.86	53.2551	2199.004	2199.523	2	+2,+3	distinct	0	1

The equivalent proteins include

gi|46135951|ref|XP_389667.1|	133537.38	hypothetical protein FG09491.1 [Gibberella zeae PH-1]

5. Group probability: 1.0000. Peptides of the group

DAASDKIDESTHGAK	99.7	54.8798	1543.711	1544.523	13	+1,+2,+3	distinct	1	1

The equivalent proteins include

gi|46125549|ref|XP_387328.1|	7176.51	hypothetical protein FG07152.1 [Gibberella zeae PH-1]

6. Group probability: 1.0000. Peptides of the group

SLENFHGALPEGIDK	80.96	54.595	1625.805	1626.343	2	2	distinct	0	0.9949
SLENFHGALPEGIDKK	68.42	54.1689	1753.9	1754.833	6	+2,+3	distinct	1	0.9986

The equivalent proteins include

gi|46105144|ref|XP_380376.1|	62768.47	hypothetical protein FG00200.1 [Gibberella zeae PH-1]

7. Group probability: 1.0000. Peptides of the group

KLDGVDLSPGMLDEAR (000000000001000000)	116.07	54.3034	1714.856	1715.803	14	+2,+3	distinct	1	1

The equivalent proteins include

gi|46128493|ref|XP_388800.1|	27433.75	hypothetical protein FG08624.1 [Gibberella zeae PH-1]

8. Group probability: 1.0000. Peptides of the group

KTSQKPVSPEEGEEIR	70.72	54.1544	1812.922	1813.533	3	+2,+3	distinct	1	0.9981
TSQKPVSPEEGEEIRK	48.99	54.2088	1812.922	1813.253	3	+2,+3	distinct	1	0.9906

The equivalent proteins include

gi|46117116|ref|XP_384576.1|	22473.59	hypothetical protein FG04400.1 [Gibberella zeae PH-1]

9. Group probability: 1.0000. Peptides of the group

HGYIGEFEEIDDHR	99.77	54.3346	1715.754	1716.423	19	+2,+3	distinct	0	1

The equivalent proteins include

gi|46125827|ref|XP_387467.1|	14806.04	RS22_KLUMA 40S RIBOSOMAL PROTEIN S22 (S15A) (YS24) [Gibberella zeae PH-1]
gi|39977153|ref|XP_369964.1|	14730.98	hypothetical protein MG06479.4 [Magnaporthe grisea 70-15]

10. Group probability: 0.9999. Peptides of the group

FEVNEPEPVFEESLHGPEEEDHEDLTK	49.6	51.1948	3180.405	3181.433	2	+2,+3	distinct	0	0.9956
TKFEVNEPEPVFEESLHGPEEEDHEDLTK	64.7	50.4152	3409.547	3410.954	2	3	distinct	1	0.9854

The equivalent proteins include

gi|46136781|ref|XP_390082.1|	11925.64	hypothetical protein FG09906.1 [Gibberella zeae PH-1]

11. Group probability: 0.9999. Peptides of the group

APFTVEAPGYEKIPGETIPR	92.73	53.2817	2171.126	2171.493	9	+2,+3	distinct	1	0.9999

The equivalent proteins include

gi|46128331|ref|XP_388719.1|	76165.99	hypothetical protein FG08543.1 [Gibberella zeae PH-1]

12. Group probability: 0.9999. Peptides of the group

HSPSPEDQLRPPVSGK	46.28	54.2873	1729.875	1730.423	1	2	distinct	0	0.8973
EGQFHPIGGSWVEHDTNLPSGESLVR	63.56	51.7199	2847.358	2848.824	2	+2,+3	distinct	0	0.9993

The equivalent proteins include

gi|46124907|ref|XP_387007.1|	129696.58	hypothetical protein FG06831.1 [Gibberella zeae PH-1]

13. Group probability: 0.9999. Peptides of the group

IPGDSPLEFCPGDHAADLIK	80.52	53.2358	2151.031	2152.523	7	+2,+3	distinct	0	0.9999

The equivalent proteins include

gi|46136141|ref|XP_389762.1|	19394.14	hypothetical protein FG09586.1 [Gibberella zeae PH-1]

14. Group probability: 0.9999. Peptides of the group

KQEYDESGPSIVHR	82.99	54.5732	1643.79	1644.103	5	+2,+3	distinct	1	0.9999

The equivalent proteins include

gi|38017227|gb|AAR07975.1|	2078.98	beta-actin [Macaca mulatta]
gi|77744596|gb|ABB02262.1|	2078.95	beta-actin [Ovis aries]

15. Group probability: 0.9998. Peptides of the group

SFANLEPPKVEDGKPPPK	66.22	53.8157	1949.026	1949.953	4	+2,+3	distinct	1	0.9975
VIEEIVEEVIEESEEVLA	51.26	53.5052	2057.03	2057.623	1	2	distinct	0	0.9392

The equivalent proteins include

gi|46122799|ref|XP_385953.1|	85364.78	conserved hypothetical protein [Gibberella zeae PH-1]

16. Group probability: 0.9998. Peptides of the group

MAQGAKPGEGGELPGHK	54.42	54.5012	1662.815	1663.303	3	2	distinct	0	0.9355
ASIGPPGLPESGEYHWR	88.59	53.9618	1851.89	1852.233	3	2	distinct	0	0.9976

The equivalent proteins include

gi|46109102|ref|XP_381609.1|	235590.71	hypothetical protein FG01433.1 [Gibberella zeae PH-1]

17. Group probability: 0.9998. Peptides of the group

APTGLNDETAEEVHDIIHR	118.28	53.4364	2116.018	2117.043	3	2	distinct	0	0.9998

The equivalent proteins include

gi|46116256|ref|XP_384146.1|	11963.92	hypothetical protein FG03970.1 [Gibberella zeae PH-1]

18. Group probability: 0.9997. Peptides of the group

SPPDPVNDTGHFTDR	85.8	54.3166	1653.738	1653.923	4	+2,+3	distinct	0	0.9997

The equivalent proteins include

gi|46138415|ref|XP_390898.1|	124803.32	conserved hypothetical protein [Gibberella zeae PH-1]

19. Group probability: 0.9996. Peptides of the group

VPGHEIIGDVVEVGEDVDNFK	107.17	53.4409	2266.112	2266.513	1	2	distinct	0	0.9996

The equivalent proteins include

gi|46135697|ref|XP_389540.1|	36843.86	hypothetical protein FG09364.1 [Gibberella zeae PH-1]

20. Group probability: 0.9996. Peptides of the group

SVEMHHEQLTEGKPGDNVGFNVK (00001000000000000000000)	82.06	52.4421	2551.212	2551.474	9	+2,+3	distinct	0	0.9996

The equivalent proteins include

gi|58531922|gb|AAW78673.1|	34223.68	translation elongation factor 1-alpha [Cortinarius iodes]
gi|45645231|gb|AAS73253.1|	34226.65	translation elongation factor 1 alpha [Melanopsamma pomiformis]
gi|66274349|gb|AAY43937.1|	32645.94	translation elongation factor 1-alpha [Aschersonia andropogonis]
gi|66274351|gb|AAY43938.1|	32628.89	translation elongation factor 1-alpha [Aschersonia basicystis]
gi|66274353|gb|AAY43939.1|	33619.3	translation elongation factor 1-alpha [Aschersonia basicystis]
gi|66274355|gb|AAY43940.1|	33497.22	translation elongation factor 1-alpha [Aschersonia basicystis]
gi|66274357|gb|AAY43941.1|	33760.44	translation elongation factor 1-alpha [Aschersonia blumenaviensis]
gi|66274359|gb|AAY43942.1|	33025.03	translation elongation factor 1-alpha [Aschersonia cubensis]
gi|66274361|gb|AAY43943.1|	33620.26	translation elongation factor 1-alpha [Aschersonia cubensis]
gi|66274363|gb|AAY43944.1|	33503.33	translation elongation factor 1-alpha [Aschersonia rhombispora]

gi|66274365|gb|AAY43945.1|	33627.42	translation elongation factor 1-alpha [Aschersonia incrassata]
gi|66274375|gb|AAY43950.1|	32712.95	translation elongation factor 1-alpha [Aschersonia viridans]
gi|66274379|gb|AAY43952.1|	33654.3	translation elongation factor 1-alpha [Aschersonia sp. P.C. 569]
gi|66274385|gb|AAY43955.1|	33541.24	translation elongation factor 1-alpha [Hypocrella castanea]
gi|66274387|gb|AAY43956.1|	33306.22	translation elongation factor 1-alpha [Hypocrella discoidea]
gi|66274389|gb|AAY43957.1|	33611.27	translation elongation factor 1-alpha [Hypocrella macrostroma]
gi|66274391|gb|AAY43958.1|	32770.85	translation elongation factor 1-alpha [Hypocrella macrostroma]
gi|66274393|gb|AAY43959.1|	33227.12	translation elongation factor 1-alpha [Hypocrella schizostachyi]
gi|66274395|gb|AAY43960.1|	33185.1	translation elongation factor 1-alpha [Hypocrella sp. P.C. 436.2]
gi|46129252|ref|XP_388987.1|	50182.16	EF1A_TRIRE ELONGATION FACTOR 1-ALPHA (EF-1-ALPHA) [Gibberella zeae PH-1]
gi|71067985|gb|AAZ22973.1|	29790.08	elongation factor 1-alpha [Aschersonia andropogonis]
gi|71067987|gb|AAZ22974.1|	29789.15	elongation factor 1-alpha [Aschersonia andropogonis]
gi|71067991|gb|AAZ22976.1|	29844.36	elongation factor 1-alpha [Aschersonia andropogonis]
gi|71067993|gb|AAZ22977.1|	30212.61	elongation factor 1-alpha [Aschersonia andropogonis]
gi|71067995|gb|AAZ22978.1|	30546.65	elongation factor 1-alpha [Aschersonia andropogonis]
gi|71067998|gb|AAZ22979.1|	30746.77	elongation factor 1-alpha [Aschersonia andropogonis]
gi|71068000|gb|AAZ22980.1|	25153.96	elongation factor 1-alpha [Aschersonia turbinata]
gi|71068004|gb|AAZ22982.1|	30402.7	elongation factor 1-alpha [Aschersonia viridans]
gi|71068006|gb|AAZ22983.1|	30453.85	elongation factor 1-alpha [Aschersonia incrassata]
gi|71068009|gb|AAZ22984.1|	30145.61	elongation factor 1-alpha [Aschersonia rhombispora]
gi|45645255|gb|AAS73265.1|	36268.92	translation elongation factor 1 alpha [Cordyceps gunnii]
gi|33330203|gb|AAQ10467.1|	25296.98	translation elongation factor 1-alpha [Hypocrea semiorbis]
gi|46362229|gb|AAS89583.1|	25279.02	translation elongation factor 1-alpha [Hypocrea minutispora]
gi|33330193|gb|AAQ10462.1|	25321.05	translation elongation factor 1-alpha [Hypocrea pilulifera]
gi|33330263|gb|AAQ10497.1|	25269.98	translation elongation factor 1-alpha [Trichoderma fertile]
gi|33330273|gb|AAQ10502.1|	25358.03	translation elongation factor 1-alpha [Trichoderma oblongisporum]

21. Group probability: 0.9994. Peptides of the group

FPVLPDPYKDTK	59.12	54.8956	1418.745	1419.353	9	+1,+2	distinct	1	0.9952
QFYVPFHPEYNGGR	45.27	54.2927	1709.795	1710.773	2	2	distinct	0	0.8796

The equivalent proteins include

gi|46122839|ref|XP_385973.1|	63567.33	hypothetical protein FG05797.1 [Gibberella zeae PH-1]

22. Group probability: 0.9994. Peptides of the group

NVLDGINEFDGTDHQYFHGGGK	78.54	52.6864	2419.083	2420.113	11	+2,+3	distinct	0	0.9994

The equivalent proteins include

gi|46116942|ref|XP_384489.1|	80139.39	conserved hypothetical protein [Gibberella zeae PH-1]

23. Group probability: 0.9994. Peptides of the group

KALDGGIVILPNINPDGVK	102.92	53.7704	1932.104	1933.363	6	2	distinct	1	0.9994

The equivalent proteins include

gi|46126977|ref|XP_388042.1|	48709.6	hypothetical protein FG07866.1 [Gibberella zeae PH-1]

24. Group probability: 0.9993. Peptides of the group

FPTPVSHADDLTGR	79.21	54.6497	1511.737	1513.193	6	+2,+3	distinct	0	0.9993

The equivalent proteins include

gi|46125093|ref|XP_387100.1|	24230.09	conserved hypothetical protein [Gibberella zeae PH-1]

25. Group probability: 0.9992. Peptides of the group

YWNKPIEDLSPINPDLDNLADLPK	62	52.0592	2779.407	2780.023	4	+2,+3	distinct	0	0.9992

The equivalent proteins include

gi|46126151|ref|XP_387629.1|	108740.27	hypothetical protein FG07453.1 [Gibberella zeae PH-1]

26. Group probability: 0.9991. Peptides of the group

GGKPIVICNPDDEEFK	75.92	54.1791	1816.866	1817.773	4	+2,+3	distinct	0	0.9991

The equivalent proteins include

gi|53987051|tpg|DAA05488.1|	78203.4	TPA: TPA_inf: glutamine:fructose-6-phosphate amidotransferase [Gibberella zeae]
gi|46108634|ref|XP_381375.1|	77002.83	conserved hypothetical protein [Gibberella zeae PH-1]

27. Group probability: 0.9989. Peptides of the group

HFIDTGAGVIDADYR	98.67	54.5183	1648.784	1649.813	2	2	distinct	0	0.9989

The equivalent proteins include

gi|88185215|gb|EAQ92683.1|	18504.58	dUTP pyrophosphatase [Chaetomium globosum CBS 148.51]
gi|83765657|dbj|BAE55800.1|	20709.79	unnamed protein product [Aspergillus oryzae]
gi|46108044|ref|XP_381080.1|	17998.22	hypothetical protein FG00904.1 [Gibberella zeae PH-1]
gi|70990380|ref|XP_750039.1|	26543.94	dUTPase [Aspergillus fumigatus Af293]
gi|39974675|ref|XP_368728.1|	29426.27	hypothetical protein MG00516.4 [Magnaporthe grisea 70-15]

28. Group probability: 0.9989. Peptides of the group

GTTKPGATDSDQTEHK	48.36	54.5294	1671.77	1672.123	1	2	distinct	0	0.914
RFLENPQEFNDAFAK	70.22	54.0158	1824.879	1826.223	1	2	distinct	1	0.987

The equivalent proteins include

gi|46114264|ref|XP_383150.1|	81289.62	hypothetical protein FG02974.1 [Gibberella zeae PH-1]

29. Group probability: 0.9989. Peptides of the group

SKDAVIIDPANPPEVAPILK	95.78	53.3475	2086.167	2087.033	8	2	distinct	1	0.9989

The equivalent proteins include

gi|46125539|ref|XP_387323.1|	87294.7	hypothetical protein FG07147.1 [Gibberella zeae PH-1]

30. Group probability: 0.9989. Peptides of the group

HELSPELGFTR	45.43	55.3925	1284.646	1285.523	2	2	distinct	0	0.8649
KVFGSDDDTHPGVK	75.69	55.0568	1500.721	1501.623	2	2	distinct	1	0.9915

The equivalent proteins include

gi|46129380|ref|XP_389051.1|	68821.67	hypothetical protein FG08875.1 [Gibberella zeae PH-1]

31. Group probability: 0.9988. Peptides of the group

KLPDMPGQINNPLTGR	97.31	54.1687	1749.92	1750.673	4	2	distinct	1	0.9988

The equivalent proteins include

gi|46139165|ref|XP_391273.1|	98449.77	hypothetical protein FG11097.1 [Gibberella zeae PH-1]

32. Group probability: 0.9985. Peptides of the group

LKEEYGAHPVFIDDELADR	93	53.1478	2216.075	2216.323	3	2	distinct	1	0.9985

The equivalent proteins include

gi|46123347|ref|XP_386227.1|	67928.9	hypothetical protein FG06051.1 [Gibberella zeae PH-1]

33. Group probability: 0.9983. Peptides of the group

SGSPNPTMGELPEAHHK	92.78	54.6795	1787.826	1788.093	4	2	distinct	0	0.9983

The equivalent proteins include

gi|46121289|ref|XP_385199.1|	45633.04	hypothetical protein FG05023.1 [Gibberella zeae PH-1]

34. Group probability: 0.9982. Peptides of the group

NQPPPPPAPQPTVQPK	69.81	54.677	1691.899	1692.303	14	+2,+3	distinct	0	0.9982

The equivalent proteins include

gi|46116780|ref|XP_384408.1|	66919.07	hypothetical protein FG04232.1 [Gibberella zeae PH-1]

35. Group probability: 0.9981. Peptides of the group

KEEQQQQQPPQQQPQDGNR	58.01	53.0634	2290.069	2290.043	3	+2,+3	distinct	1	0.9981

The equivalent proteins include

gi|46134131|ref|XP_389381.1|	43876.97	hypothetical protein FG09205.1 [Gibberella zeae PH-1]

36. Group probability: 0.9979. Peptides of the group

DRLDDDLAYGQPGVPPRPK	58.96	53.2889	2108.065	2108.253	2	2	distinct	1	0.9703
SSHDRVDSNLPGAFPGAFPDDSR	49.85	52.8172	2443.115	2444.404	1	3	distinct	1	0.9301

The equivalent proteins include

gi|46128723|ref|XP_388915.1|	90867.62	hypothetical protein FG08739.1 [Gibberella zeae PH-1]

37. Group probability: 0.9978. Peptides of the group

WEGVPIGQEDVTKR	62.33	54.5192	1612.821	1613.463	1	2	distinct	1	0.9729
DIQHAPGSNPSSGFSTPK	48.12	54.0447	1825.859	1826.873	2	2	distinct	0	0.919

The equivalent proteins include

gi|46136039|ref|XP_389711.1|	36315.35	hypothetical protein FG09535.1 [Gibberella zeae PH-1]

38. Group probability: 0.9976. Peptides of the group

HYFGDIDAPPVPVTYPIPNTPR	86.2	52.5905	2465.238	2465.653	1	2	distinct	0	0.9976

The equivalent proteins include

gi|46105124|ref|XP_380366.1|	8590.44	hypothetical protein FG00190.1 [Gibberella zeae PH-1]

39. Group probability: 0.9975. Peptides of the group

FSHSAPSDGDPLSEMPEYK (000000000000000100000)	48.28	53.3069	2108.9	2109.773	1	2	distinct	0	0.9241
AEHLPALPLEPLPEIPSGLR	57.56	53.3016	2148.194	2148.983	1	2	distinct	0	0.9675

The equivalent proteins include

gi|46139355|ref|XP_391368.1|	68802.96	hypothetical protein FG11192.1 [Gibberella zeae PH-1]

40. Group probability: 0.9975. Peptides of the group

LPLVGGHEGAGVVVAR	88.73	55.1793	1529.868	1530.633	8	2	distinct	0	0.9975

The equivalent proteins include

gi|86278351|gb|ABC88428.1|	38180.68	alcohol dehydrogenase [Cochliobolus lunatus]
gi|88766407|gb|ABD49723.1|	37795.37	alcohol dehydrogenase I [Metarhizium anisopliae]
gi|46138681|ref|XP_391031.1|	42020.57	hypothetical protein FG10855.1 [Gibberella zeae PH-1]

41. Group probability: 0.9974. Peptides of the group

RFEVALPEFPK	49.47	55.4272	1331.724	1332.993	1	2	distinct	1	0.9051
KFMQNPTEHYVDEDTK	61.38	53.7395	1980.889	1981.623	1	2	distinct	1	0.973

The equivalent proteins include

gi|88182398|gb|EAQ89866.1|	49629.14	ATP-dependent RNA helicase [Chaetomium globosum CBS 148.51]
gi|46128571|ref|XP_388839.1|	62549.72	hypothetical protein FG08663.1 [Gibberella zeae PH-1]

42. Group probability: 0.9973. Peptides of the group

ALGAPIERPK	48.98	55.297	1050.619	1051.423	2	2	distinct	0	0.8977
FAELLPEKIEQVK	63.06	54.7244	1542.866	1543.233	1	2	distinct	1	0.9735

The equivalent proteins include

gi|46109080|ref|XP_381598.1|	51994.98	CISY_NEUCR Citrate synthase, mitochondrial precursor [Gibberella zeae PH-1]

43. Group probability: 0.9970. Peptides of the group

FGFGGSKPDPSTLGPR	58.46	54.5207	1618.81	1619.844	2	+2,+3	distinct	0	0.997

The equivalent proteins include

gi|46124731|ref|XP_386919.1|	153782.71	hypothetical protein FG06743.1 [Gibberella zeae PH-1]

44. Group probability: 0.9970. Peptides of the group

EVDVILCPPYFGAASPHEQSR	84.26	52.9156	2371.127	2371.463	6	2	distinct	0	0.997

The equivalent proteins include

gi|46115124|ref|XP_383580.1|	103207.76	hypothetical protein FG03404.1 [Gibberella zeae PH-1]

45. Group probability: 0.9963. Peptides of the group

GGPGLGEHR	54.29	55.7335	878.436	879.343	1	2	distinct	0	0.9333
GMDARPPPGVWGER	56.48	54.5775	1523.73	1524.814	1	3	distinct	0	0.9442

The equivalent proteins include

gi|46107454|ref|XP_380786.1|	39690.8	conserved hypothetical protein [Gibberella zeae PH-1]

46. Group probability: 0.9962. Peptides of the group

VIGINPLPASEGAGNPIKLEPGEK	80.4	52.7499	2399.306	2400.243	5	2	distinct	1	0.9962

The equivalent proteins include

gi|46136743|ref|XP_390063.1|	71473.3	hypothetical protein FG09887.1 [Gibberella zeae PH-1]

47. Group probability: 0.9960. Peptides of the group

SHNPVSDNLHQK	48.42	55.0941	1374.664	1375.733	2	2	distinct	0	0.9003
AEGAPEELVPHKR	58.26	54.9953	1431.747	1432.953	7	2	distinct	1	0.9595

The equivalent proteins include

gi|46122931|ref|XP_386019.1|	61460.83	conserved hypothetical protein [Gibberella zeae PH-1]

48. Group probability: 0.9954. Peptides of the group

HGLDVPLGENR	47.48	55.3153	1205.615	1207.033	1	2	distinct	0	0.8873

HGLDVPLGENREEK	57.62	54.6126	1591.795	1592.743	1	2	distinct	1	0.959

The equivalent proteins include

gi|46117426|ref|XP_384731.1|	34281.18	conserved hypothetical protein [Gibberella zeae PH-1]

49. Group probability: 0.9947. Peptides of the group

AGAVDNGKPGPR	59.86	55.1548	1137.589	1138.673	2	+1,+2	distinct	0	0.9947

The equivalent proteins include

gi|46137761|ref|XP_390572.1|	15285.23	hypothetical protein FG10396.1 [Gibberella zeae PH-1]

50. Group probability: 0.9946. Peptides of the group

EEAFEIIKEHEQK	81.1	54.6137	1628.805	1629.433	1	2	distinct	1	0.9946

The equivalent proteins include

gi|46124309|ref|XP_386708.1|	19724.84	hypothetical protein FG06532.1 [Gibberella zeae PH-1]

51. Group probability: 0.9945. Peptides of the group

EQVPQAPDGLHQYR	80.55	54.4554	1636.796	1637.603	6	2	distinct	0	0.9945

The equivalent proteins include

gi|46111573|ref|XP_382844.1|	129452.33	hypothetical protein FG02668.1 [Gibberella zeae PH-1]

52. Group probability: 0.9943. Peptides of the group

HGDMITIHPCPDIK (0000100000000000)	80.07	54.5934	1632.775	1633.653	7	2	distinct	0	0.9943

The equivalent proteins include

gi|46122305|ref|XP_385706.1|	90533.81	hypothetical protein FG05530.1 [Gibberella zeae PH-1]

53. Group probability: 0.9938. Peptides of the group

HGTYPIPNDDAEQNR	78.71	54.2605	1725.771	1726.683	2	2	distinct	0	0.9938

The equivalent proteins include

gi|46115988|ref|XP_384012.1|	38393.77	hypothetical protein FG03836.1 [Gibberella zeae PH-1]

54. Group probability: 0.9938. Peptides of the group

EALEDILPIVEQYKDELLAR	76.34	53.129	2356.253	2357.153	1	2	distinct	1	0.9938

The equivalent proteins include

gi|46124405|ref|XP_386756.1|	255320.03	hypothetical protein FG06580.1 [Gibberella zeae PH-1]

55. Group probability: 0.9932. Peptides of the group

EDLGKAINEILAP	56.09	54.9183	1381.745	1381.523	4	+1,+2	distinct	1	0.9932

The equivalent proteins include

gi|93453881|gb|EAT04239.1|	13191.83	Response regulator receiver [delta proteobacterium MLMS-1]

56. Group probability: 0.9929. Peptides of the group

AHPGSGAPIVGTGPGGTVTESDR	73.59	53.267	2119.029	2120.183	4	2	distinct	0	0.9929

The equivalent proteins include

gi|46125135|ref|XP_387121.1|	160777.12	hypothetical protein FG06945.1 [Gibberella zeae PH-1]

57. Group probability: 0.9928. Peptides of the group

VKNPVVEIDGDEMTR (0000000000001000)	68.93	54.3397	1716.835	1717.483	7	+2,+3	distinct	1	0.9928

The equivalent proteins include

gi|94496948|ref|ZP_01303522.1|	46146.36	isocitrate dehydrogenase, NADP-dependent [Sphingomonas sp. SKA58]
gi|1052977|gb|AAC43640.1|	45625.07	isocitrate dehydrogenase
gi|58264156|ref|XP_569234.1|	50829.82	isocitrate dehydrogenase (NADP+) [Cryptococcus neoformans var. neoformans JEC21]
gi|58264154|ref|XP_569233.1|	50457.64	isocitrate dehydrogenase (NADP+) [Cryptococcus neoformans var. neoformans JEC21]
gi|87199303|ref|YP_496560.1|	46116.3	isocitrate dehydrogenase, NADP-dependent [Novosphingobium aromaticivorans DSM 12444]
gi|88177211|gb|EAQ84679.1|	52490.09	conserved hypothetical protein [Chaetomium globosum CBS 148.51]
gi|90299296|gb|EAS28927.1|	57179.41	isocitrate dehydrogenase NADP, mitochondrial precursor [Coccidioides immitis RS]
gi|1778638|dbj|BAA19074.1|	55695.63	NADP-dependent isocitrate dehydrogenase precursor [Aspergillus niger]
gi|71062461|gb|AAZ21464.1|	46230.39	isocitrate dehydrogenase (NADP) [Candidatus Pelagibacter ubique HTCC1062]
gi|83766186|dbj|BAE56329.1|	56200.66	unnamed protein product [Aspergillus oryzae]

gi|46137663|ref|XP_390523.1|	50195.93	hypothetical protein FG10347.1 [Gibberella zeae PH-1]
gi|85074555|ref|XP_955850.1|	51986.72	hypothetical protein NCU03857.1 [Neurospora crassa OR74A]
gi|71000064|ref|XP_754749.1|	55967.66	isocitrate dehydrogenase, NADP-dependent [Aspergillus fumigatus Af293]
gi|67525083|ref|XP_660603.1|	55039.37	isocitrate dehydrogenase [Aspergillus nidulans FGSC A4]
gi|15027826|gb|AAK76730.1|	55317.61	mitochondrial NADP-dependent isocitrate dehydrogenase [Aspergillus nidulans]
gi|15027827|gb|AAK76731.1|	46910.29	peroxisomal NADP-dependent isocitrate dehydrogenase [Aspergillus nidulans]
gi|39936895|ref|NP_949171.1|	45609.13	isocitrate dehydrogenase [Rhodopseudomonas palustris CGA009]
gi|39971905|ref|XP_367343.1|	50823.09	hypothetical protein MG07268.4 [Magnaporthe grisea 70-15]
gi|109456038|gb|ABG32243.1|	45231.83	isocitrate dehydrogenase [Roseobacter denitrificans OCh 114]

58. Group probability: 0.9922. Peptides of the group

VKTDDEAPYELIYWPTIPGR	73.77	52.8383	2362.184	2362.313	2	2	distinct	1	0.9922

The equivalent proteins include

gi|46116630|ref|XP_384333.1|	29895.1	hypothetical protein FG04157.1 [Gibberella zeae PH-1]

59. Group probability: 0.9922. Peptides of the group

APSDFADYPKPVEAPAATYNPHVENNPVFR	71.5	50.6774	3312.584	3314.054	1	3	distinct	0	0.9922

The equivalent proteins include

gi|46107650|ref|XP_380884.1|	64439.35	hypothetical protein FG00708.1 [Gibberella zeae PH-1]

60. Group probability: 0.9910. Peptides of the group

LPTPPPVDGLWVPR	74.94	54.7967	1542.856	1543.783	2	2	distinct	0	0.991

The equivalent proteins include

gi|46127097|ref|XP_388102.1|	100281.27	hypothetical protein FG07926.1 [Gibberella zeae PH-1]

61. Group probability: 0.9907. Peptides of the group

AFQAHPEPYPESDQDLVPR	72.21	53.2309	2195.028	2195.053	2	2	distinct	0	0.9907

The equivalent proteins include

gi|46110106|ref|XP_382111.1|	108433.35	hypothetical protein FG01935.1 [Gibberella zeae PH-1]

62. Group probability: 0.9904. Peptides of the group

RFDLSPIQTPENAPR	73.71	54.1673	1739.895	1740.933	3	2	distinct	1	0.9904

The equivalent proteins include

gi|46138859|ref|XP_391120.1|	167957.17	hypothetical protein FG10944.1 [Gibberella zeae PH-1]

63. Group probability: 0.9904. Peptides of the group

VPMNPHLGDVQAPSPGPGSEEYK	70.09	52.6736	2405.132	2405.223	1	2	distinct	0	0.9904

The equivalent proteins include

gi|46135983|ref|XP_389683.1|	108030.84	hypothetical protein FG09507.1 [Gibberella zeae PH-1]

64. Group probability: 0.9897. Peptides of the group

LGIDKTNPDELTEDEIHR	71.48	53.3819	2094.023	2093.953	1	2	distinct	1	0.9897

The equivalent proteins include

gi|46137503|ref|XP_390443.1|	109887.31	hypothetical protein FG10267.1 [Gibberella zeae PH-1]

65. Group probability: 0.9896. Peptides of the group

TYKEYPHQELGVPTEK	72.31	53.8308	1917.947	1918.623	1	2	distinct	1	0.9896

The equivalent proteins include

gi|46125283|ref|XP_387195.1|	53694.37	hypothetical protein FG07019.1 [Gibberella zeae PH-1]

66. Group probability: 0.9894. Peptides of the group

RLGGDGEEGGVSR	47.77	55.4877	1287.617	1288.383	1	2	distinct	1	0.8973
EIPARPLPFGSGDGK	46.73	54.6754	1539.804	1540.733	1	2	distinct	0	0.8969

The equivalent proteins include

gi|46110000|ref|XP_382058.1|	78455.02	hypothetical protein FG01882.1 [Gibberella zeae PH-1]

67. Group probability: 0.9891. Peptides of the group

DFGPDKYDTIPPHGR	72.29	54.2853	1713.811	1714.473	3	2	distinct	1	0.9891

The equivalent proteins include

gi|46114612|ref|XP_383324.1|	46475.49	hypothetical protein FG03148.1 [Gibberella zeae PH-1]

68. Group probability: 0.9885. Peptides of the group

VENPVVELDGDEMTR (0000000000001000)	55.88	54.3262	1701.788	1702.513	4	+2,+3	distinct	0	0.9885

The equivalent proteins include

gi|69938744|ref|ZP_00633145.1|	45430.05	Isocitrate dehydrogenase NADP-dependent, eukaryotic [Paracoccus denitrificans PD1222]
gi|89070004|ref|ZP_01157336.1|	45553.96	isocitrate dehydrogenase [Oceanicola granulosus HTCC2516]
gi|71916699|gb|AAZ56601.1|	45782.3	isocitrate dehydrogenase NADP-dependent, eukaryotic [Thermobifida fusca YX]

69. Group probability: 0.9882. Peptides of the group

ENVREENPGISFGQVGK	70.47	54.0341	1858.917	1860.133	1	2	distinct	1	0.9882

The equivalent proteins include

gi|90303012|gb|EAS32643.1|	11796.92	hypothetical protein CIMG_03667 [Coccidioides immitis RS]
gi|46105649|ref|XP_380561.1|	11480.82	conserved hypothetical protein [Gibberella zeae PH-1]

70. Group probability: 0.9882. Peptides of the group

IPQEWLDALEPVKNDDVAVR	69.01	52.9979	2306.191	2307.653	1	2	distinct	1	0.9882

The equivalent proteins include

gi|46136113|ref|XP_389748.1|	70213.11	hypothetical protein FG09572.1 [Gibberella zeae PH-1]

71. Group probability: 0.9875. Peptides of the group

EGAPSFEDQHEHLR	71.2	54.6794	1650.739	1651.173	5	2	distinct	0	0.9875

The equivalent proteins include

gi|46128767|ref|XP_388937.1|	70282.27	hypothetical protein FG08761.1 [Gibberella zeae PH-1]

72. Group probability: 0.9874. Peptides of the group

FKGEIQVPEFINSAGEK	69.79	54.3504	1891.968	1892.963	3	2	distinct	1	0.9874

The equivalent proteins include

gi|46125395|ref|XP_387251.1|	173995.39	hypothetical protein FG07075.1 [Gibberella zeae PH-1]

73. Group probability: 0.9872. Peptides of the group

HPDPYTPPTAPGGSK	70.55	54.6616	1520.726	1521.333	7	2	distinct	0	0.9872

The equivalent proteins include

gi|46140227|ref|XP_391804.1|	13576.14	hypothetical protein FG11628.1 [Gibberella zeae PH-1]

74. Group probability: 0.9870. Peptides of the group

HWDNKPAENETPEER	70.21	53.9434	1850.818	1851.513	2	2	distinct	0	0.987

The equivalent proteins include

gi|46111803|ref|XP_382959.1|	42679.9	hypothetical protein FG02783.1 [Gibberella zeae PH-1]

75. Group probability: 0.9848. Peptides of the group

QLGGPIKDVEDMLELIDR (00000000000010000000)	67.11	53.5206	2040.056	2041.453	5	2	distinct	1	0.9848

The equivalent proteins include

gi|46136033|ref|XP_389708.1|	37957.47	hypothetical protein FG09532.1 [Gibberella zeae PH-1]

76. Group probability: 0.9848. Peptides of the group

LPLDHLQPPTAVQPDGPR	67.15	53.7503	1950.032	1951.013	3	2	distinct	0	0.9848

The equivalent proteins include

gi|46138325|ref|XP_390853.1|	89780.75	hypothetical protein FG10677.1 [Gibberella zeae PH-1]

77. Group probability: 0.9839. Peptides of the group

KIEFSLPDLEGR	69.23	55.0875	1402.746	1403.713	1	2	distinct	1	0.9839

The equivalent proteins include

gi|90307353|gb|EAS36984.1|	26783.93	hypothetical protein CIMG_02338 [Coccidioides immitis RS]
gi|74354958|gb|AAI02392.1|	51460.57	PSMC2 protein [Bos taurus]
gi|74142439|dbj|BAE31973.1|	49053.19	unnamed protein product [Mus musculus]
gi|76879893|dbj|BAE45763.1|	48986.31	putative protein product of Nbla10058 [Homo sapiens]
gi|46107352|ref|XP_380735.1|	49448.38	conserved hypothetical protein [Gibberella zeae PH-1]
gi|73981961|ref|XP_533103.2|	99122.71	PREDICTED: similar to proteasome (prosome, macropain) 26S subunit, ATPase 2 [Canis familiaris]
gi|109069308|ref|XP_001118310.1|	18078.27	PREDICTED: similar to proteasome (prosome, macropain) 26S subunit, ATPase 2, partial [Macaca mulatt
gi|55621138|ref|XP_526309.1|	45681.4	PREDICTED: similar to proteasome (prosome, macropain) 26S subunit, ATPase 2; Proteasome (prosome, m

gi|55629168|ref|XP_519288.1|	48892.21	PREDICTED: similar to proteasome 26S ATPase subunit 2; proteasome 26S subunit, ATPase, 2; mammalian
gi|47208144|emb|CAF93400.1|	49119.27	unnamed protein product [Tetraodon nigroviridis]
gi|68076831|ref|XP_680335.1|	47357.37	26S proteasome regulatory subunit 7 [Plasmodium berghei strain ANKA]
gi|70941981|ref|XP_741212.1|	33299.31	26S proteasome regulatory subunit 7 [Plasmodium chabaudi chabaudi]
gi|4506209|ref|NP_002794.1|	49002.27	proteasome 26S ATPase subunit 2 [Homo sapiens]
gi|38494277|gb|AAH61627.1|	49032.28	26S protease regulatory subunit 7 [Xenopus tropicalis]
gi|15100181|ref|NP_150239.1|	48943.22	proteasome (prosome, macropain) 26S subunit, ATPase 2 [Rattus norvegicus]
gi|83315300|ref|XP_730734.1|	54291.03	26S proteasome subunit P45 [Plasmodium yoelii yoelii str. 17XNL]
gi|85111842|ref|XP_964130.1|	49227.41	probable 26S proteasome regulatory particle chain RPT1 [MIPS] [Neurospora crassa OR74A]
gi|11265294|pir||T49507	49371.48	probable 26S proteasome regulatory particle chain RPT1 [imported] - Neurospora crassa
gi|13529470|gb|AAH05462.1|	49016.28	Psmc2 protein [Mus musculus]
gi|51262008|gb|AAH80137.1|	49006.26	26S protease regulatory subunit 7 [Xenopus tropicalis]
gi|31419198|gb|AAH53187.1|	49072.35	Similar to proteasome (prosome, macropain) 26S subunit, ATPase 2 [Danio rerio]
gi|33859604|ref|NP_035318.1|	53289.39	proteasome (prosome, macropain) 26S subunit, ATPase 2 [Mus musculus]
gi|55730503|emb|CAH91973.1|	48955.29	hypothetical protein [Pongo pygmaeus]
gi|57525333|ref|NP_001006225.1|	49030.3	proteasome (prosome, macropain) 26S subunit, ATPase, 2 [Gallus gallus]
gi|27735425|gb|AAH41186.1|	50326.74	Unknown (protein for IMAGE:4681581) [Xenopus laevis]
gi|41472112|gb|AAS07429.1|	46201.89	unknown [Homo sapiens]
gi|39951877|ref|XP_363655.1|	49387.47	hypothetical protein MG01581.4 [Magnaporthe grisea 70-15]
gi|38181888|gb|AAH61542.1|	48986.27	Proteasome (prosome, macropain) 26S subunit, ATPase 2 [Rattus norvegicus]

78. Group probability: 0.9834. Peptides of the group

FVEKPVEFVGNR	68.83	54.8848	1419.751	1421.083	6	2	distinct	0	0.9834

The equivalent proteins include

gi|88177632|gb|EAQ85100.1|	39957.87	hypothetical protein CHGG_09114 [Chaetomium globosum CBS 148.51]
gi|90306591|gb|EAS36222.1|	40400.24	hypothetical protein CIMG_01576 [Coccidioides immitis RS]
gi|3777501|gb|AAC64911.1|	40102.13	putative GDP-mannose pyrophosphorylase [Candida albicans]
gi|3777503|gb|AAC64912.1|	40130.18	putative GDP-mannose pyrophosphorylase [Candida albicans]
gi|83768031|dbj|BAE58170.1|	40390.13	unnamed protein product [Aspergillus oryzae]
gi|71063814|gb|AAZ22401.1|	38928.11	putative GDP-mannose pyrophosphorylase enzyme [Cryptococcus neoformans var. neoformans]
gi|46128791|ref|XP_388949.1|	40262.13	hypothetical protein FG08773.1 [Gibberella zeae PH-1]
gi|50308377|ref|XP_454190.1|	39352.03	unnamed protein product [Kluyveromyces lactis]
gi|68490504|ref|XP_710946.1|	40121.13	GDP-mannose pyrophosphorylase [Candida albicans SC5314]
gi|70993664|ref|XP_751679.1|	47163.71	mannose-1-phosphate guanylyltransferase [Aspergillus fumigatus Af293]
gi|50548099|ref|XP_501519.1|	39970.05	hypothetical protein [Yarrowia lipolytica]
gi|3323397|gb|AAC39498.1|	40544.17	mannose-1-phosphate guanylyltransferase [Hypocrea jecorina]
gi|44985257|gb|AAS53970.1|	39674.05	AFR599Wp [Ashbya gossypii ATCC 10895]

gi|50259609|gb|EAL22282.1|	36728.92	hypothetical protein CNBC4190 [Cryptococcus neoformans var. neoformans B-3501A]
gi|67538832|ref|XP_663190.1|	39177.41	hypothetical protein AN5586.2 [Aspergillus nidulans FGSC A4]
gi|63259386|gb|AAY40351.1|	40384.25	GDP-mannose pyrophosphorylase [Aspergillus fumigatus]
gi|7331158|gb|AAF60300.1|	40325.23	GDP-mannose pyrophosphorylase [Pichia angusta]
gi|50423647|ref|XP_460408.1|	39987.23	hypothetical protein DEHA0F01265g [Debaryomyces hansenii CBS767]
gi|57225832|gb|AAW42293.1|	40322.93	mannose-1-phosphate guanylyltransferase, putative [Cryptococcus neoformans var. neoformans JEC21]
gi|40362538|gb|AAR84601.1|	43370.39	Psa1p [Cryptococcus neoformans var. neoformans]

79. Group probability: 0.9816. Peptides of the group

TEEHGYKPYPEGPAR	66.28	54.2705	1729.806	1730.923	4	2	distinct	0	0.9816

The equivalent proteins include

gi|46108086|ref|XP_381101.1|	87713.11	hypothetical protein FG00925.1 [Gibberella zeae PH-1]

80. Group probability: 0.9808. Peptides of the group

GTKPEDGEFSPIFYR	65.78	54.1445	1741.831	1742.323	1	2	distinct	0	0.9808

The equivalent proteins include

gi|46109934|ref|XP_382025.1|	33898.34	hypothetical protein FG01849.1 [Gibberella zeae PH-1]

81. Group probability: 0.9796. Peptides of the group

TPESFKLPTPKPEEK	65.1	54.2534	1726.914	1727.273	5	2	distinct	1	0.9796

The equivalent proteins include

gi|46134189|ref|XP_389410.1|	33241.85	hypothetical protein FG09234.1 [Gibberella zeae PH-1]

82. Group probability: 0.9788. Peptides of the group

HADGTMEPIMPDGSR (00000010001000000)	64.75	54.6109	1644.687	1645.333	1	2	distinct	0	0.9788

The equivalent proteins include

gi|46107516|ref|XP_380817.1|	53780.55	hypothetical protein FG00641.1 [Gibberella zeae PH-1]

83. Group probability: 0.9763. Peptides of the group

FLDLVKPFVPFLPEVQQPETK	60.68	52.9477	2470.351	2470.373	2	2	distinct	0	0.9763

The equivalent proteins include

gi|88178854|gb|EAQ86322.1|	52412.42	protein transport protein SEC61 alpha subunit [Chaetomium globosum CBS 148.51]
gi|85091301|ref|XP_958835.1|	52448.38	hypothetical protein [Neurospora crassa OR74A]
gi|39940768|ref|XP_359921.1|	52696.36	hypothetical protein MG04856.4 [Magnaporthe grisea 70-15]

84. Group probability: 0.9762. Peptides of the group

TKNNPVIIGEPGVGK	63.45	54.6085	1521.851	1522.993	1	2	distinct	1	0.9762

The equivalent proteins include

gi|106881592|ref|ZP_01348996.1|	95814.54	AAA ATPase, central region:Clp, N terminal:ATPase associated with various cellular activities, AAA_
gi|84393598|ref|ZP_00992351.1|	96006.2	ClpB protein [Vibrio splendidus 12B01]
gi|75813710|ref|ZP_00744479.1|	29766.98	COG0542: ATPases with chaperone activity, ATP-binding subunit [Vibrio cholerae V52]
gi|75824073|ref|ZP_00753540.1|	95903.39	COG0542: ATPases with chaperone activity, ATP-binding subunit [Vibrio cholerae RC385]
gi|75826068|ref|ZP_00755503.1|	95952.41	COG0542: ATPases with chaperone activity, ATP-binding subunit [Vibrio cholerae O395]
gi|75853631|ref|ZP_00761428.1|	96117.21	COG0542: ATPases with chaperone activity, ATP-binding subunit [Vibrio sp. Ex25]
gi|89075037|ref|ZP_01161478.1|	96015.07	putative clpB, ATPase with chaperone activity [Photobacterium sp. SKA34]
gi|90408475|ref|ZP_01216634.1|	96134.92	putative clpB, ATPase with chaperone activity [Psychromonas sp. CNPT3]
gi|90580379|ref|ZP_01236186.1|	95980.11	putative clpB, ATPase with chaperone activity [Vibrio angustum S14]

gi|91227643|ref|ZP_01261920.1|	96080.07	ClpB protein [Vibrio alginolyticus 12G01]
gi|28805544|dbj|BAC58824.1|	95984.12	ClpB protein [Vibrio parahaemolyticus RIMD 2210633]
gi|37678899|ref|NP_933508.1|	96208.25	clpB protein [Vibrio vulnificus YJ016]
gi|27360063|gb|AAO09001.1|	96147.23	ClpB protein [Vibrio vulnificus CMCP6]
gi|66963185|ref|ZP_00410757.1|	95281.82	AAA ATPase, central region:Clp, N terminal [Arthrobacter sp. FB24]
gi|9655153|gb|AAF93876.1|	95939.4	clpB protein [Vibrio cholerae O1 biovar eltor str. N16961]
gi|18400735|ref|NP_565586.1|	108936.65	ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding [Arabidopsis
gi|9651530|gb|AAF91178.1|	109564.54	ClpB [Phaseolus lunatus]
gi|108804998|ref|YP_644935.1|	93792.39	ATPase AAA-2 [Rubrobacter xylanophilus DSM 9941]
gi|98662201|dbj|GAA00752.1|	95712.89	unnamed protein product [Pelotomaculum thermopropionicum SI]
gi|98663188|dbj|GAA00063.1|	90445.03	unnamed protein product [Pelotomaculum thermopropionicum SI]
gi|81177485|ref|ZP_00876287.1|	72751.28	UvrB/UvrC protein:AAA ATPase, central region [Streptococcus suis 89/1591]
gi|81255750|ref|ZP_00880219.1|	66217.69	COG0542: ATPases with chaperone activity, ATP-binding subunit [Mycobacterium tuberculosis C]
gi|82500780|ref|ZP_00886178.1|	99098.95	ATPas [Caldicellulosiruptor saccharolyticus DSM 8903]
gi|94416168|ref|ZP_01295998.1|	94464.85	hypothetical protein PaerP_01002011 [Pseudomonas aeruginosa PA7]
gi|94492493|ref|ZP_01299700.1|	96735.98	hypothetical protein CburD_01000070 [Coxiella burnetii Dugway 7E9-12]
gi|94493469|ref|ZP_01300673.1|	97575.71	hypothetical protein Rgryl_01001304 [Rickettsiella grylli]
gi|99034310|ref|ZP_01314351.1|	41594.99	hypothetical protein Wendoof_01000850 [Wolbachia endosymbiont of Drosophila willistoni TSC#14030-08
gi|82739080|ref|ZP_00901896.1|	94918.18	ATPas [Pseudomonas putida F1]
gi|82748788|ref|ZP_00911265.1|	97684.89	ATPas [Clostridium beijerincki NCIMB 8052]
gi|62423737|ref|ZP_00378894.1|	93317.8	COG0542: ATPases with chaperone activity, ATP-binding subunit [Brevibacterium linens BL2]
gi|62426046|ref|ZP_00381176.1|	94468.04	COG0542: ATPases with chaperone activity, ATP-binding subunit [Brevibacterium linens BL2]
gi|62462120|ref|ZP_00381592.1|	84280.48	COG0542: ATPases with chaperone activity, ATP-binding subunit [Lactococcus lactis subsp. cremoris S
gi|62462742|ref|ZP_00382121.1|	83370.6	COG0542: ATPases with chaperone activity, ATP-binding subunit [Lactococcus lactis subsp. cremoris S
gi|83616914|ref|ZP_00927476.1|	26497.17	COG0542: ATPases with chaperone activity, ATP-binding subunit [Burkholderia mallei FMH]
gi|62513420|ref|ZP_00384970.1|	91677.15	COG0542: ATPases with chaperone activity, ATP-binding subunit [Lactobacillus casei ATCC 334]
gi|62526947|ref|ZP_00388255.1|	83922.15	COG0542: ATPases with chaperone activity, ATP-binding subunit [Streptococcus thermophilus LMD-9]
gi|69935649|ref|ZP_00630585.1|	96243	AAA ATPase, central region:Clp, N terminal [Paracoccus denitrificans PD1222]
gi|83371212|ref|ZP_00916031.1|	95796.38	ATPas [Rhodobacter sphaeroides ATCC 17025]
gi|83372165|ref|ZP_00916945.1|	95655.31	ATPas [Rhodobacter sphaeroides ATCC 17029]
gi|106884685|ref|ZP_01352054.1|	97571.21	AAA ATPase, central region:Clp, N terminal:ATPase associated with various cellular activities, AAA_
gi|69954129|ref|ZP_00640937.1|	96682.39	AAA ATPase, central region:Clp, N terminal [Shewanella frigidimarina NCIMB 400]

gi|83748548|ref|ZP_00945568.1|	95688.67	ClpB protein [Ralstonia solanacearum UW551]
gi|83750605|ref|ZP_00947022.1|	97278.22	COG0542: ATPases with chaperone activity, ATP-binding subunit [Bartonella bacilliformis KC583]
gi|106891444|ref|ZP_01358630.1|	98020.07	AAA ATPase, central region:Clp, N terminal:ATPase associated with various cellular activities, AAA_
gi|107099795|ref|ZP_01363713.1|	94421.83	hypothetical protein PaerPA_01000813 [Pseudomonas aeruginosa PACS2]
gi|83855155|ref|ZP_00948685.1|	95232.95	ATP-dependent Clp protease, ATP-binding subunit ClpB [Sulfitobacter sp. NAS-14.1]
gi|83859253|ref|ZP_00952774.1|	96304.7	endopeptidase Clp: ATP-binding subunit B, clpB [Oceanicaulis alexandrii HTCC2633]
gi|83941677|ref|ZP_00954139.1|	95258.96	ATP-dependent Clp protease, ATP-binding subunit ClpB [Sulfitobacter sp. EE-36]
gi|83950866|ref|ZP_00959599.1|	95752.07	ATP-dependent Clp protease, ATP-binding subunit ClpB [Roseovarius nubinhibens ISM]
gi|84323213|ref|ZP_00971289.1|	91729.41	COG0542: ATPases with chaperone activity, ATP-binding subunit [Pseudomonas aeruginosa 2192]
gi|84354867|ref|ZP_00979764.1|	95948.5	COG0542: ATPases with chaperone activity, ATP-binding subunit [Burkholderia cenocepacia PC184]
gi|84362042|ref|ZP_00986679.1|	96042.58	COG0542: ATPases with chaperone activity, ATP-binding subunit [Burkholderia dolosa AUO158]
gi|21465699|pdb|1JBK|A	21544.46	Chain A, Crystal Structure Of The First Nucelotide Binding Domain Of Clpb
gi|71367651|ref|ZP_00658171.1|	95054.71	UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal [Nocardioides sp. JS614]
gi|71368674|ref|ZP_00659163.1|	93903.02	AAA ATPase, central region:Clp, N terminal [Nocardioides sp. JS614]
gi|71482382|ref|ZP_00662075.1|	48787.87	AAA ATPase, central region:Clp, N terminal [Prosthecochloris vibrioformis DSM 265]
gi|67734571|ref|ZP_00485689.1|	96020.59	COG0542: ATPases with chaperone activity, ATP-binding subunit [Burkholderia pseudomallei 668]
gi|84497246|ref|ZP_00996068.1|	93071.18	putative ATP-dependent Clp protease [Janibacter sp. HTCC2649]
gi|84497608|ref|ZP_00996430.1|	92625.35	ATP-dependent protease ATP-binding subunit [Janibacter sp. HTCC2649]
gi|84501333|ref|ZP_00999538.1|	95514.08	ATP-dependent Clp protease, ATP-binding subunit ClpB [Oceanicola batsensis HTCC2597]
gi|71547803|ref|ZP_00668357.1|	98151.25	AAA ATPase, central region:Clp, N terminal [Syntrophobacter fumaroxidans MPOB]
gi|84514618|ref|ZP_01001982.1|	96724.93	Chaperone ClpB [Loktanella vestfoldensis SKA53]
gi|71550106|ref|ZP_00670254.1|	96560.48	AAA ATPase, central region:Clp, N terminal [Nitrosomonas eutropha C71]
gi|84517835|ref|ZP_01005184.1|	95032.51	ATPase with chaperone activity ATP-binding subunit [Prochlorococcus marinus str. MIT 9211]
gi|84517860|ref|ZP_01005209.1|	98331.74	ATPase with chaperone activity ATP-binding subunit [Prochlorococcus marinus str. MIT 9211]
gi|84701533|ref|ZP_01016108.1|	97002.83	endopeptidase Clp: ATP-binding subunit B, clpB [Parvularcula bermudensis HTCC2503]
gi|71837201|ref|ZP_00676967.1|	98376.01	AAA ATPase, central region:Clp, N terminal [Pelobacter propionicus DSM 2379]
gi|84713092|ref|ZP_01020878.1|	95936.58	ATPas [Polaromonas naphthalenivorans CJ2]

gi|85666674|ref|ZP_01028898.1|	95348.58	hypothetical protein Badol_01001521 [Bifidobacterium adolescentis]
gi|85666911|ref|ZP_01029134.1|	99310.57	hypothetical protein Badol_01000881 [Bifidobacterium adolescentis]
gi|67931722|ref|ZP_00524879.1|	92773.7	AAA ATPase, central region:Clp, N terminal [Solibacter usitatus Ellin6076]
gi|67931988|ref|ZP_00525140.1|	97309.44	AAA ATPase, central region:Clp, N terminal [Solibacter usitatus Ellin6076]
gi|67934490|ref|ZP_00527533.1|	98470.88	AAA ATPase, central region:Clp, N terminal [Solibacter usitatus Ellin6076]
gi|85706748|ref|ZP_01037840.1|	95624.09	ATP-dependent Clp protease, ATP-binding subunit ClpB [Roseovarius sp. 217]
gi|67939123|ref|ZP_00531634.1|	48792.78	AAA ATPase, central region:Clp, N terminal [Chlorobium phaeobacteroides BS1]
gi|74019149|ref|ZP_00689767.1|	96041.49	AAA ATPase, central region:Clp, N terminal [Burkholderia ambifaria AMMD]
gi|85713565|ref|ZP_01044555.1|	96483.49	AAA ATPase [Nitrobacter sp. Nb-311A]
gi|75178201|ref|ZP_00698260.1|	95723	COG0542: ATPases with chaperone activity, ATP-binding subunit [Shigella boydii BS512]
gi|109644799|ref|ZP_01368719.1|	97074.59	ATPase AAA-2 [Desulfitobacterium hafniense DCB-2]
gi|68229264|ref|ZP_00568461.1|	94627.74	AAA ATPase, central region:Clp, N terminal [Frankia sp. EAN1pec]
gi|68229492|ref|ZP_00568686.1|	92213.9	UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal [Frankia sp. EAN1pec]
gi|86139320|ref|ZP_01057889.1|	95620.62	ATP-dependent Clp protease, ATP-binding subunit ClpB [Roseobacter sp. MED193]
gi|75760630|ref|ZP_00740659.1|	90627.9	Negative regulator of genetic competence clpC/mecB [Bacillus thuringiensis serovar israelensis ATCC
gi|75763427|ref|ZP_00743154.1|	79778.74	ClpB protein [Bacillus thuringiensis serovar israelensis ATCC 35646]
gi|71490495|gb|EAO22879.1|	96904.03	AAA ATPase, central region:Clp, N terminal [Syntrophomonas wolfei subsp. wolfei str. Goettingen]
gi|87124024|ref|ZP_01079874.1|	95461.91	ATP-dependent Clp protease, Hsp 100, ATP-binding subunit ClpB [Synechococcus sp. RS9917]
gi|87124752|ref|ZP_01080600.1|	94530.81	endopeptidase Clp ATP-binding chain C [Synechococcus sp. RS9917]
gi|68551190|ref|ZP_00590613.1|	48927.94	AAA ATPase, central region:Clp, N terminal [Pelodictyon phaeoclathratiforme BU-1]
gi|68553506|ref|ZP_00592879.1|	48501.75	AAA ATPase, central region:Clp, N terminal [Prosthecochloris aestuarii DSM 271]
gi|87303275|ref|ZP_01086068.1|	96620.6	ATPase [Synechococcus sp. WH 5701]
gi|87303420|ref|ZP_01086208.1|	94089.89	endopeptidase Clp ATP-binding chain C [Synechococcus sp. WH 5701]
gi|87311811|ref|ZP_01093925.1|	105894.49	ClpB protein [Blastopirellula marina DSM 3645]
gi|76260724|ref|ZP_00768354.1|	96228.08	AAA ATPase, central region:Clp, N terminal:Clp, N terminal [Chloroflexus aurantiacus J-10-fl]
gi|88183938|gb|EAQ91406.1|	103157.94	heat shock protein HSP98 [Chaetomium globosum CBS 148.51]
gi|76796592|ref|ZP_00778950.1|	91946.17	UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal [Thermoanaerobacter ethanolicus ATCC 3
gi|88707050|ref|ZP_01104746.1|	94789.34	Chaperone clpB [gamma proteobacterium KT 71]
gi|77408376|ref|ZP_00785116.1|	83951.19	ATP-dependent Clp protease, ATP-binding subunit [Streptococcus agalactiae COH1]
gi|77414691|ref|ZP_00790824.1|	76765.81	ATP-dependent Clp protease, ATP-binding subunit [Streptococcus agalactiae 515]

gi|88796221|ref|ZP_01111900.1|	95550.92	ClpB protein [Alteromonas macleodii 'Deep ecotype']
gi|82408817|gb|ABB73202.1|	101516.35	heat shock protein 101 [Funaria hygrometrica]
gi|88809567|ref|ZP_01125074.1|	96339.13	ATP-dependent Clp protease, Hsp 100, ATP-binding subunit ClpB [Synechococcus sp. WH 7805]
gi|88811113|ref|ZP_01126369.1|	97006.59	ClpB protein [Nitrococcus mobilis Nb-231]
gi|88808913|ref|ZP_01124422.1|	94491.85	ATPase [Synechococcus sp. WH 7805]
gi|77743042|ref|ZP_00811514.1|	97125.74	IMP dehydrogenase/GMP reductase:AAA ATPase, central region:Clp, N terminal [Rhodopseudomonas palust
gi|88854942|ref|ZP_01129608.1|	79149.82	ATP-dependent Clp protease, ATP-binding subunit [marine actinobacterium PHSC20C1]
gi|88857985|ref|ZP_01132627.1|	96018.34	ATP-dependent protease, Hsp 100 [Pseudoalteromonas tunicata D2]
gi|77956726|ref|ZP_00820808.1|	95693.08	COG0542: ATPases with chaperone activity, ATP-binding subunit [Yersinia bercovieri ATCC 43970]
gi|77960423|ref|ZP_00824294.1|	95727.09	COG0542: ATPases with chaperone activity, ATP-binding subunit [Yersinia mollaretii ATCC 43969]
gi|88931632|ref|ZP_01137326.1|	94998.95	ATPase [Acidothermus cellulolyticus 11B]
gi|77972196|ref|ZP_00827770.1|	95851.24	COG0542: ATPases with chaperone activity, ATP-binding subunit [Yersinia frederiksenii ATCC 33641]
gi|77976237|ref|ZP_00831746.1|	95805.17	COG0542: ATPases with chaperone activity, ATP-binding subunit [Yersinia intermedia ATCC 29909]
gi|88938987|ref|ZP_01144439.1|	94446.71	ATPase [Acidiphilium cryptum JF-5]
gi|88947328|ref|ZP_01150327.1|	90260.73	ATPas [Desulfotomaculum reducens MI-1]
gi|89071046|ref|ZP_01158260.1|	95791.08	ATP-dependent Clp protease, ATP-binding subunit ClpB [Oceanicola granulosus HTCC2516]
gi|89091375|ref|ZP_01164384.1|	92870.63	ATPas [Lactobacillus reuteri JCM 1112]
gi|89093544|ref|ZP_01166492.1|	95817.8	ClpB protein [Oceanospirillum sp. MED92]
gi|78694065|ref|ZP_00858578.1|	95577.61	ATPas [Bradyrhizobium sp. BTAi1]
gi|89098078|ref|ZP_01170964.1|	97029.85	ClpB protein [Bacillus sp. NRRL B-14911]
gi|78699747|ref|ZP_00864236.1|	96849.8	ATPas [Bradyrhizobium sp. BTAi1]
gi|89100727|ref|ZP_01173582.1|	90797.91	class III stress response-related ATPase [Bacillus sp. NRRL B-14911]
gi|78702749|ref|ZP_00867175.1|	96206.04	ATPas [Alkalilimnicola ehrlichei MLHE-1]
gi|89200617|ref|ZP_01179369.1|	97756.57	AAA ATPase, central region:Clp, N terminal [Bacillus cereus subsp. cytotoxis NVH 391-98]
gi|89203265|ref|ZP_01181951.1|	90890.19	UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal [Bacillus cereus subsp. cytotoxis NVH
gi|89204605|ref|ZP_01183182.1|	97579.45	AAA ATPase, central region:Clp, N terminal [Bacillus weihenstephanensis KBAB4]
gi|89208529|ref|ZP_01187031.1|	90628.93	UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal [Bacillus weihenstephanensis KBAB4]
gi|89211788|ref|ZP_01190129.1|	36959.05	Clp, N terminal [Halothermothrix orenii H 168]
gi|89338857|ref|ZP_01191622.1|	92469.39	AAA ATPase, central region:Clp, N terminal [Mycobacterium flavescens PYR-GCK]
gi|89340537|ref|ZP_01192794.1|	93323.98	UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal [Mycobacterium flavescens PYR-GCK]
gi|89360542|ref|ZP_01198360.1|	96766.78	ATPas [Xanthobacter autotrophicus Py2]
gi|54035876|sp|Q8YM56|CLPB2_ANASP	98620.41	Chaperone clpB 2
gi|54035747|sp|O68185|CLPB_LACLC	97270.94	Chaperone clpB
gi|90205850|ref|ZP_01208488.1|	92274.31	AAA ATPase, central region:Clp, N terminal [Mycobacterium vanbaalenii PYR-1]

gi|90206346|ref|ZP_01208981.1|	93507.16	UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal [Mycobacterium vanbaalenii PYR-1]
gi|90417179|ref|ZP_01225106.1|	94787.67	ClpB protein [marine gamma proteobacterium HTCC2207]
gi|90420190|ref|ZP_01228098.1|	96237.22	chaperone clpB [Aurantimonas sp. SI85-9A1]
gi|54035803|sp|Q7U637|CLPB1_SYNPX	95667.94	Chaperone clpB 1
gi|54035749|sp|O87444|CLPB_PLEBO	99300.65	Chaperone clpB
gi|54035866|sp|Q8PHQ4|CLPB_XANAC	95630.05	Chaperone clpB
gi|90585866|ref|ZP_01241572.1|	98399.74	AAA ATPase, central region:Clp, N terminal [Staphylococcus aureus subsp. aureus JH9]
gi|91770187|ref|ZP_01272015.1|	95711.51	AAA ATPase, central region:Clp, N terminal [Psychrobacter sp. PRwf-1]
gi|92090120|ref|ZP_01275022.1|	92820.74	UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal:ATPase associated with various cellula
gi|90302568|gb|EAS32199.1|	102020.44	hypothetical protein CIMG_03223 [Coccidioides immitis RS]
gi|92906854|ref|ZP_01275634.1|	93572.01	UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal [Mycobacterium sp. JLS]
gi|93453739|gb|EAT04115.1|	97584.35	AAA ATPase, central region:Clp, N terminal [delta proteobacterium MLMS-1]
gi|3150046|gb|AAC16900.1|	97281.03	ClpB chaperone homolog [Lactococcus lactis subsp. cremoris]
gi|82173987|emb|CAI94864.1|	52047.85	heat shock protein 101 [Triticum turgidum subsp. durum]
gi|82173989|emb|CAI94865.1|	52116.88	heat shock protein 101 [Triticum turgidum subsp. durum]
gi|82173992|emb|CAI94866.1|	68873.63	heat shock protein 101 [Triticum turgidum subsp. durum]
gi|82173995|emb|CAI94867.1|	69022.75	heat shock protein 101 [Triticum turgidum subsp. durum]
gi|54035774|sp|Q73IE4|CLPB_WOLPM	94971.29	Chaperone clpB
gi|54035819|sp|Q81GM5|CLPB_BACCR	97436.26	Chaperone clpB
gi|27315136|gb|AAO04271.1|	98240.58	clpB protein [Staphylococcus epidermidis ATCC 12228]
gi|3360502|gb|AAC62621.1|	100561.25	heat shock protein [Plectonema boryanum]
gi|83999833|emb|CAH60133.1|	93064.25	putative Clp-family ATP-binding protease [Streptomyces tenjimariensis]
gi|54035875|sp|Q8YJ91|CLPB_BRUME	96905.58	Chaperone clpB
gi|54035809|sp|Q7VBL0|CLPB_PROMA	98224.1	Chaperone clpB
gi|4098131|gb|AAD00218.1|	95767.41	clpB [Mycobacterium bovis]
gi|4322269|gb|AAD15989.1|	94206.42	heat shock protein ClpB [Streptomyces albus G]
gi|26987361|ref|NP_742786.1|	94917.16	ATP-dependent Clp protease, ATP-binding subunit ClpB [Pseudomonas putida KT2440]
gi|4103470|gb|AAD01782.1|	83442.67	ClpE [Lactococcus lactis]
gi|23465812|ref|NP_696415.1|	96254.39	protease of ClpA/ClpB type [Bifidobacterium longum NCC2705]
gi|24375079|ref|NP_719122.1|	95759.03	clpB protein [Shewanella oneidensis MR-1]
gi|41409951|ref|NP_962787.1|	92574.61	ClpB [Mycobacterium avium subsp. paratuberculosis K-10]
gi|83719137|ref|YP_442726.1|	96104.71	ATP-dependent Clp protease, ATP-binding subunit ClpB [Burkholderia thailandensis E264]
gi|82750232|ref|YP_415973.1|	91068.5	endopeptidase [Staphylococcus aureus RF122]
gi|82750590|ref|YP_416331.1|	98358.61	putative ATP-dependent protease protein [Staphylococcus aureus RF122]
gi|54035773|sp|Q73BY1|CLPB_BACC1	97536.26	Chaperone clpB
gi|54035825|sp|Q831Y7|CLPB_ENTFA	98010.02	Chaperone clpB
gi|91204090|emb|CAJ71743.1|	97930.82	strongly similar to ATP-dependent protease Clp (chain B) [Candidatus Kuenenia stuttgartiensis]
gi|47568371|ref|ZP_00239072.1|	97566.27	ATP-dependent Clp protease, ATP-binding subunit ClpB [Bacillus cereus G9241]

gi|48870729|ref|ZP_00323448.1|	97064.77	COG0542: ATPases with chaperone activity, ATP-binding subunit [Pediococcus pentosaceus ATCC 25745]
gi|48871265|ref|ZP_00323981.1|	91373.18	COG0542: ATPases with chaperone activity, ATP-binding subunit [Pediococcus pentosaceus ATCC 25745]
gi|46202513|ref|ZP_00053096.2|	76418.28	COG0542: ATPases with chaperone activity, ATP-binding subunit [Magnetospirillum magnetotacticum MS-
gi|46204054|ref|ZP_00209236.1|	28866.26	COG0542: ATPases with chaperone activity, ATP-binding subunit [Magnetospirillum magnetotacticum MS-
gi|23123825|ref|ZP_00105864.1|	98514.66	COG0542: ATPases with chaperone activity, ATP-binding subunit [Nostoc punctiforme PCC 73102]
gi|23126880|ref|ZP_00108763.1|	92510.75	COG0542: ATPases with chaperone activity, ATP-binding subunit [Nostoc punctiforme PCC 73102]
gi|23128455|ref|ZP_00110302.1|	100330.04	COG0542: ATPases with chaperone activity, ATP-binding subunit [Nostoc punctiforme PCC 73102]
gi|23128552|ref|ZP_00110397.1|	91177.28	COG0542: ATPases with chaperone activity, ATP-binding subunit [Nostoc punctiforme PCC 73102]
gi|23025097|ref|ZP_00064272.1|	91438.13	COG0542: ATPases with chaperone activity, ATP-binding subunit [Leuconostoc mesenteroides subsp. mes
gi|23024482|ref|ZP_00063692.1|	76732.25	COG0542: ATPases with chaperone activity, ATP-binding subunit [Leuconostoc mesenteroides subsp. mes
gi|23336357|ref|ZP_00121578.1|	95313.55	COG0542: ATPases with chaperone activity, ATP-binding subunit [Bifidobacterium longum DJO10A]
gi|23335984|ref|ZP_00121214.1|	96921.61	COG0542: ATPases with chaperone activity, ATP-binding subunit [Bifidobacterium longum DJO10A]
gi|46165006|ref|ZP_00138099.2|	94407.82	COG0542: ATPases with chaperone activity, ATP-binding subunit [Pseudomonas aeruginosa UCBPP-PA14]
gi|46156241|ref|ZP_00133175.2|	97524.15	COG0542: ATPases with chaperone activity, ATP-binding subunit [Haemophilus somnus 2336]
gi|32035169|ref|ZP_00135209.1|	95884.22	COG0542: ATPases with chaperone activity, ATP-binding subunit [Actinobacillus pleuropneumoniae sero
gi|42631176|ref|ZP_00156714.1|	95842.11	COG0542: ATPases with chaperone activity, ATP-binding subunit [Haemophilus influenzae R2866]
gi|57637163|gb|AAW53951.1|	98265.65	ATP-dependent Clp protease, ATP-binding subunit ClpB [Staphylococcus epidermidis RP62A]
gi|17428350|emb|CAD15037.1|	95614.69	probable chaperone clpb protein [Ralstonia solanacearum]
gi|56807845|ref|ZP_00365685.1|	78050.25	COG0542: ATPases with chaperone activity, ATP-binding subunit [Streptococcus pyogenes M49 591]
gi|58696668|ref|ZP_00372220.1|	90817.98	ATP-dependent Clp protease, ATP-binding subunit ClpB [Wolbachia endosymbiont of Drosophila simulans
gi|58698222|ref|ZP_00373142.1|	96317.83	ATP-dependent Clp protease, ATP-binding subunit ClpB [Wolbachia endosymbiont of Drosophila ananassa
gi|46908440|ref|YP_014829.1|	97580.06	clpB protein [Listeria monocytogenes str. 4b F2365]
gi|30042249|gb|AAP17974.1|	95727.01	heat shock protein [Shigella flexneri 2a str. 2457T]
gi|14023715|dbj|BAB50320.1|	95976.53	endopeptidase Clp ATP-binding chain B; ClpB [Mesorhizobium loti MAFF303099]
gi|23494457|dbj|BAC19423.1|	93387.71	putative endopeptidase Clp ATP-binding chain B [Corynebacterium efficiens YS-314]
gi|35214149|dbj|BAC91518.1|	98195.54	clpB [Gloeobacter violaceus PCC 7421]

gi|55772869|dbj|BAD71310.1|	96194.93	ATP-dependent Clp protease, ATP-binding subunit ClpB [Thermus thermophilus HB8]
gi|21204024|dbj|BAB94722.1|	98355.75	clpB [Staphylococcus aureus subsp. aureus MW2]
gi|22775771|dbj|BAC12049.1|	90504.74	ATP-dependent Clp protease (ATP-binding subunit) [Oceanobacillus iheyensis HTE831]
gi|21648328|gb|AAM73494.1|	49070.04	ATP-dependent Clp protease, ATP-binding subunit ClpB [Chlorobium tepidum TLS]
gi|83033300|gb|ABB97103.1|	17779.46	ClpC [Bacillus cereus]
gi|83033322|gb|ABB97114.1|	17770.46	ClpC [Bacillus cereus]
gi|83033342|gb|ABB97124.1|	17709.44	ClpC [Bacillus thuringiensis]
gi|83033360|gb|ABB97133.1|	17743.46	ClpC [Bacillus thuringiensis]
gi|83033388|gb|ABB97147.1|	17773.47	ClpC [Bacillus thuringiensis]
gi|83033438|gb|ABB97172.1|	17759.46	ClpC [Bacillus thuringiensis]
gi|83316459|gb|ABC02403.1|	36522.52	ClpC [Bacillus weihenstephanensis]
gi|83316475|gb|ABC02412.1|	36058.28	ClpC [Bacillus weihenstephanensis]
gi|82778016|ref|YP_404365.1|	95725.03	heat shock protein [Shigella dysenteriae Sd197]
gi|81428651|ref|YP_395651.1|	96937.45	Chaperone ClpB [Lactobacillus sakei subsp. sakei 23K]
gi|68989120|dbj|BAE06227.1|	110564.3	heat shock protein [Lycopersicon esculentum]
gi|17065040|gb|AAL32674.1|	50815.98	heat shock protein 101 [Arabidopsis thaliana]
gi|68447700|dbj|BAE05284.1|	98339.37	unnamed protein product [Staphylococcus haemolyticus JCSC1435]
gi|68448209|dbj|BAE05793.1|	91669.46	endopeptidas Clp ATP-binding chain C [Staphylococcus haemolyticus JCSC1435]
gi|83766016|dbj|BAE56159.1|	103106.83	unnamed protein product [Aspergillus oryzae]
gi|86359337|ref|YP_471229.1|	95854.19	ATP-dependent Clp protease, ATP-binding subunit protein [Rhizobium etli CFN 42]
gi|27376515|ref|NP_768044.1|	96619.51	ATP-dependent protease ATP-binding subunit [Bradyrhizobium japonicum USDA 110]
gi|83319920|ref|YP_424350.1|	80681.71	ATP-dependent Clp protease, ATP-binding subunit ClpB, putative [Mycoplasma capricolum subsp. capric
gi|84622886|ref|YP_450258.1|	95537.1	ATP-dependent Clp protease subunit [Xanthomonas oryzae pv. oryzae MAFF 311018]
gi|85058562|ref|YP_454264.1|	96534.12	heat shock protein [Sodalis glossinidius str. 'morsitans']
gi|85859726|ref|YP_461928.1|	98834.28	clpB protein [Syntrophus aciditrophicus SB]
gi|86604906|ref|YP_473669.1|	99745.72	ATP-dependent chaperone protein ClpB [Synechococcus sp. JA-3-3Ab]
gi|86605369|ref|YP_474132.1|	91831.91	Clp protease, ATP-binding subunit ClpC [Synechococcus sp. JA-3-3Ab]
gi|86608097|ref|YP_476859.1|	91651.85	Clp protease, ATP-binding subunit ClpC [Synechococcus sp. JA-2-3B'a(2-13)]
gi|86609958|ref|YP_478720.1|	99701.67	ATP-dependent chaperone protein ClpB [Synechococcus sp. JA-2-3B'a(2-13)]
gi|88194669|ref|YP_499465.1|	98384.73	ATP-dependent Clp protease, ATP-binding subunit ClpB [Staphylococcus aureus subsp. aureus NCTC 8325
gi|88658213|ref|YP_507187.1|	95829.82	ATP-dependent Clp protease, ATP-binding subunit ClpB [Ehrlichia chaffeensis str. Arkansas]
gi|89255534|ref|YP_512895.1|	96101.17	ClpB protein [Francisella tularensis subsp. holarctica]
gi|22535406|emb|CAC87117.1|	100945.34	heat shock protein 101 [Oryza sativa (japonica cultivar-group)]
gi|21109529|gb|AAM38039.1|	96731.5	ATP-dependent Clp protease subunit [Xanthomonas axonopodis pv. citri str. 306]

gi|28271389|emb|CAD64294.1|	96511.02	ATP-dependent Clp protease, ATP-binding subunit ClpB [Lactobacillus plantarum WCFS1]
gi|82702670|ref|YP_412236.1|	96914.98	ATPase with chaperone activity [Nitrosospira multiformis ATCC 25196]
gi|38200917|emb|CAE50634.1|	92845.63	Putative ATP-dependent protease regulatory subunit, ClpB [Corynebacterium diphtheriae]
gi|77917974|ref|YP_355789.1|	97691.66	putative ATPase with chaperone activity, two ATP-binding domains [Pelobacter carbinolicus DSM 2380]
gi|36784664|emb|CAE13564.1|	95774.3	heat shock protein F84.1 [Photorhabdus luminescens subsp. laumondii TTO1]
gi|33571973|emb|CAE41494.1|	96331.59	ATP-dependent protease, ATPase subunit [Bordetella pertussis Tohama I]
gi|33566210|emb|CAE37116.1|	96359.63	ATP-dependent protease, ATPase subunit [Bordetella parapertussis]
gi|33151758|ref|NP_873111.1|	95857.38	ATP-dependant Clp protease chain B [Haemophilus ducreyi 35000HP]
gi|33576707|emb|CAE33785.1|	96373.64	ATP-dependent protease, ATPase subunit [Bordetella bronchiseptica RB50]
gi|49483136|ref|YP_040360.1|	98342.68	putative ATPase subunit of an ATP-dependent protease [Staphylococcus aureus subsp. aureus MRSA252]
gi|42527829|ref|NP_972927.1|	96812.19	ATP-dependent Clp protease, ATP-binding subunit ClpB [Treponema denticola ATCC 35405]
gi|39576649|emb|CAE80813.1|	95237.46	ATPase with chaperone activity, two ATP-binding domains [Bdellovibrio bacteriovorus HD100]
gi|41326957|emb|CAF20801.1|	93174.39	PROBABLE ATP-DEPENDENT PROTEASE (HEAT SHOCK PROTEIN) [Corynebacterium glutamicum ATCC 13032]
gi|32141212|ref|NP_733613.1|	94380.42	ATP-dependent protease ATP-binding subunit [Streptomyces coelicolor A3(2)]
gi|24214579|ref|NP_712060.1|	96309.19	ATPase with chaperone activity, two ATP-binding domains [Leptospira interrogans serovar Lai str. 56
gi|28199560|ref|NP_779874.1|	95703.4	ATP-dependent Clp protease subunit [Xylella fastidiosa Temecula1]
gi|34497399|ref|NP_901614.1|	94808.03	ATP-dependent Clp protease subunit; heat-shock protein [Chromobacterium violaceum ATCC 12472]
gi|45657869|ref|YP_001955.1|	96323.21	ATP-dependent protease [Leptospira interrogans serovar Copenhageni str. Fiocruz L1-130]
gi|5305170|emb|CAA69163.2|	57018.77	ClpB-homologue [Thermus thermophilus]
gi|83310659|ref|YP_420923.1|	86399.38	ATPase with chaperone activity [Magnetospirillum magneticum AMB-1]
gi|89894414|ref|YP_517901.1|	97018.48	hypothetical protein DSY1668 [Desulfitobacterium hafniense Y51]
gi|68346908|gb|AAY94514.1|	95104.94	ClpB protein PA4542 [Pseudomonas fluorescens Pf-5]
gi|46199425|ref|YP_005092.1|	96081.84	endopeptidase clp ATP-binding chain B, clpB [Thermus thermophilus HB27]
gi|90994524|ref|YP_537014.1|	91042.08	Clp protease ATP binding subunit [Porphyra yezoensis]
gi|29540716|gb|AAO89660.1|	96822.93	clpB protein [Coxiella burnetii RSA 493]
gi|71842249|ref|YP_277337.1|	90634.03	Clp protease ATP binding subunit [Emiliania huxleyi]
gi|16421207|gb|AAL21550.1|	95548.88	ATP-dependent protease [Salmonella typhimurium LT2]
gi|83316491|gb|ABC02421.1|	37661.07	ClpC [Bacillus weihenstephanensis]
gi|29831057|ref|NP_825691.1|	94985.76	ATP-dependent Clp protease [Streptomyces avermitilis MA-4680]
gi|11465497|ref|NP_045112.1|	95687.79	Clp protease ATP binding subunit [Cyanidium caldarium]
gi|71466871|emb|CAH41011.1|	79274.79	clpL2 protein [Oenococcus oeni]
gi|41114|emb|CAA40846.1|	65972.55	analogue of ATP-dependent protease regulatory subunit [Escherichia coli]
gi|31872394|gb|AAP59445.1|	94812.43	ClpB-like protein [Meiothermus ruber]

gi|91211926|ref|YP_541912.1|	96069.18	heat shock protein [Escherichia coli UTI89]
gi|15075632|emb|CAC47187.1|	95669.14	PROBABLE ATP-DEPENDENT PROTEASE (HEAT SHOCK PROTEIN) [Sinorhizobium meliloti]
gi|68262865|emb|CAI36353.1|	94767.05	ATP-dependent Clp protease, ATP-binding subunit ClpB [Corynebacterium jeikeium K411]
gi|68262963|emb|CAI36451.1|	97524.77	ATP-dependent Clp protease [Corynebacterium jeikeium K411]
gi|76874793|emb|CAI86014.1|	95740.03	ATP-dependent protease, Hsp 100, part of multi-chaperone system with DnaK, DnaJ, and GrpE [Pseudoal
gi|78032595|emb|CAI65391.1|	91479.82	ATP-dependent Clp protease, ATP binding subunit ClpC [Oenococcus oeni]
gi|72384775|gb|AAZ67679.1|	76661.05	chaperone putative [Haemophilus parasuis]
gi|78048880|ref|YP_365055.1|	95623.08	ATP-dependent Clp protease subunit [Xanthomonas campestris pv. vesicatoria str. 85-10]
gi|71401304|ref|XP_803323.1|	67777.78	ATP-dependent Clp protease subunit, heat shock protein 100 (HSP100) [Trypanosoma cruzi strain CL Br
gi|71661302|ref|XP_817674.1|	90460.27	ATP-dependent Clp protease subunit [Trypanosoma cruzi strain CL Brener]
gi|73663109|ref|YP_301890.1|	98365.78	putative ATPase subunit of an ATP-dependent protease [Staphylococcus saprophyticus subsp. saprophyt
gi|73663540|ref|YP_302321.1|	91435.49	putative stress response-related Clp ATPase [Staphylococcus saprophyticus subsp. saprophyticus ATCC
gi|28851292|gb|AAO54370.1|	95243.25	clpB protein [Pseudomonas syringae pv. tomato str. DC3000]
gi|94676876|ref|YP_588651.1|	97601.65	ATP-dependent chaperone protein ClpB [Baumannia cicadellinicola str. Hc (Homalodisca coagulata)]
gi|94990765|ref|YP_598865.1|	84894.41	ATP-dependent endopeptidase clp ATP-binding subunit clpE [Streptococcus pyogenes MGAS10270]
gi|94992755|ref|YP_600854.1|	84849.39	ATP-dependent endopeptidase clp ATP-binding subunit clpE [Streptococcus pyogenes MGAS2096]
gi|94994743|ref|YP_602841.1|	84907.48	ATP-dependent endopeptidase clp ATP-binding subunit clpE [Streptococcus pyogenes MGAS10750]
gi|94970600|ref|YP_592648.1|	93086.83	ATPase AAA-2 [Acidobacteria bacterium Ellin345]
gi|94971790|ref|YP_593838.1|	97883.93	ATPase AAA-2 [Acidobacteria bacterium Ellin345]
gi|74419657|gb|ABA03856.1|	97963.14	AAA ATPase [Nitrobacter winogradskyi Nb-255]
gi|61679301|gb|AAX52929.1|	97060.68	ClpB [Bifidobacterium breve]
gi|61679305|gb|AAX52932.1|	98574.46	ClpB [Bifidobacterium animalis subsp. animalis]
gi|70799667|gb|AAZ09583.1|	97091.95	Serine peptidase, putative [Leishmania major strain Friedlin]
gi|99079971|ref|YP_612125.1|	95487.95	ATPase AAA-2 [Silicibacter sp. TM1040]
gi|104783632|ref|YP_610130.1|	94733.98	ATP-dependent Clp protease, ATP-binding subunit ClpB [Pseudomonas entomophila L48]
gi|12722113|gb|AAK03788.1|	95621.96	ClpB [Pasteurella multocida subsp. multocida str. Pm70]
gi|108708929|gb|ABF96724.1|	91671.76	Chaperone clpB 1, putative, expressed [Oryza sativa (japonica cultivar-group)]
gi|15803116|ref|NP_289147.1|	96041.15	heat shock protein [Escherichia coli O157:H7 EDL933]
gi|39982528|gb|AAR33988.1|	96568.06	ClpB protein [Geobacter sulfurreducens PCA]
gi|108761289|ref|YP_632993.1|	98501.36	ATP-dependent Clp protease, ATP-binding subunit ClpC [Myxococcus xanthus DK 1622]
gi|108763122|ref|YP_633246.1|	97073.32	ATP-dependent chaperone protein ClpB [Myxococcus xanthus DK 1622]

gi|13883563|gb|AAK48060.1|	93467.18	ATP-dependent Clp protease, ATP-binding subunit ClpC [Mycobacterium tuberculosis CDC1551]
gi|59805048|gb|AAX08108.1|	101437.44	heat shock protein 101 [Vitis vinifera]
gi|52353699|gb|AAU44265.1|	101062.36	heat shock protein HSP101 [Oryza sativa (japonica cultivar-group)]
gi|72382499|ref|YP_291854.1|	94964.41	ATPase [Prochlorococcus marinus str. NATL2A]
gi|22298932|ref|NP_682179.1|	98442.78	ClpB protein [Thermosynechococcus elongatus BP-1]
gi|22299995|ref|NP_683242.1|	99949.61	endopeptidase Clp ATP-binding chain B [Thermosynechococcus elongatus BP-1]
gi|75910545|ref|YP_324841.1|	89771.33	UvrB/UvrC protein [Anabaena variabilis ATCC 29413]
gi|23348732|gb|AAN30759.1|	96903.63	ATP-dependent Clp protease, ATP-binding subunit ClpB [Brucella suis 1330]
gi|76884158|gb|ABA58839.1|	96577.62	ATP-dependent Clp protease [Nitrosococcus oceani ATCC 19707]
gi|71853835|gb|AAZ51858.1|	84942.41	ATP-dependent clp protease ATP-binding subunit [Streptococcus pyogenes MGAS5005]
gi|57339190|gb|AAW49584.1|	95377.53	ClpC [Bifidobacterium breve]
gi|61679297|gb|AAX52926.1|	94168.2	ClpC [Bifidobacterium animalis subsp. animalis]
gi|71556762|gb|AAZ35973.1|	95245.24	clpB protein [Pseudomonas syringae pv. phaseolicola 1448A]
gi|109454207|gb|ABG30412.1|	95303.52	ATP-dependent Clp protease, ATP-binding subunit ClpB [Roseobacter denitrificans OCh 114]
gi|45435364|gb|AAS60923.1|	96429.5	Clp ATPase [Yersinia pestis biovar Medievalis str. 91001]
gi|70800165|gb|AAZ10006.1|	91356.6	serine peptidase, putative [Leishmania major strain Friedlin]
gi|87126055|gb|ABD20569.1|	98356.7	Chaperone clpB [Staphylococcus aureus subsp. aureus USA300]
gi|77995993|gb|ABB14892.1|	90799.91	negative regulator of genetic competence clpC/mecB [Carboxydothermus hydrogenoformans Z-2901]
gi|78165953|gb|ABB23051.1|	48665.77	ATPase [Pelodictyon luteolum DSM 273]
gi|78168780|gb|ABB25877.1|	95708.69	ATPase [Synechococcus sp. CC9902]
gi|78169256|gb|ABB26353.1|	93034.06	ATPase [Synechococcus sp. CC9902]
gi|78172030|gb|ABB29126.1|	49685.42	ATPase [Chlorobium chlorochromatii CaD3]
gi|78197000|gb|ABB34765.1|	95303.69	ATPase [Synechococcus sp. CC9605]
gi|78197611|gb|ABB35376.1|	93134.2	ATPase [Synechococcus sp. CC9605]
gi|56383701|gb|AAN44151.2|	95672.04	heat shock protein [Shigella flexneri 2a str. 301]
gi|78363045|gb|ABB41010.1|	94685.38	AAA ATPase [Thiomicrospira crunogena XCL-2]
gi|78712464|gb|ABB49641.1|	97180.63	ATPase [Prochlorococcus marinus str. MIT 9312]
gi|78712981|gb|ABB50158.1|	93572.53	ATPase [Prochlorococcus marinus str. MIT 9312]
gi|38492939|pdb|1QVR|C	96180.92	Chain C, Crystal Structure Analysis Of Clpb
gi|2632353|emb|CAB11862.1|	90120.41	class III stress response-related ATPase [Bacillus subtilis subsp. subtilis str. 168]
gi|81299071|ref|YP_399279.1|	91271.4	ATPase [Synechococcus elongatus PCC 7942]
gi|81299898|ref|YP_400106.1|	99654.39	ATPase [Synechococcus elongatus PCC 7942]
gi|82533469|ref|ZP_00892537.1|	96058.62	hypothetical protein Bpse110_02005250 [Burkholderia pseudomallei 1106b]
gi|16130513|ref|NP_417083.1|	95697	protein disaggregation chaperone [Escherichia coli K12]
gi|95931190|ref|ZP_01313912.1|	97086.74	ATPase AAA-2 [Desulfuromonas acetoxidans DSM 684]
gi|76581578|gb|ABA51053.1|	96048.6	ClpB heat-shock protein [Burkholderia pseudomallei 1710b]
gi|68195609|gb|EAN10049.1|	83571.72	UvrB/UvrC protein:AAA ATPase, central region [Enterococcus faecium DO]

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<tr><td>gi|52427027|gb|AAU47620.1|</td><td>96082.58</td><td>ATP-dependent Clp protease, ATP-binding subunit ClpB [Burkholderia mallei ATCC 23344]</td></tr>
<tr><td>gi|85083984|ref|XP_957228.1|</td><td>103346.11</td><td>hypothetical protein [Neurospora crassa OR74A]</td></tr>
<tr><td>gi|68195152|gb|EAN09610.1|</td><td>97873.23</td><td>AAA ATPase, central region:Clp, N terminal [Enterococcus faecium DO]</td></tr>
<tr><td>gi|68189537|gb|EAN04203.1|</td><td>98925.03</td><td>AAA ATPase, central region:Clp, N terminal [Mesorhizobium sp. BNC1]</td></tr>
<tr><td>gi|67985293|gb|EAM73247.1|</td><td>95017.6</td><td>AAA ATPase, central region:Clp, N terminal:Clp, N terminal [Kineococcus radiotolerans SRS30216]</td></tr>
<tr><td>gi|69300937|ref|ZP_00622398.1|</td><td>98812.61</td><td>AAA ATPase, central region:Clp, N terminal [Silicibacter sp. TM1040]</td></tr>
<tr><td>gi|49333108|gb|AAT63754.1|</td><td>90531.81</td><td>negative regulator of genetic competence clpC/mecB (ATP-dependent Clp protease) [Bacillus thuringie</td></tr>
<tr><td>gi|65318547|ref|ZP_00391506.1|</td><td>81240.68</td><td>COG0542: ATPases with chaperone activity, ATP-binding subunit [Bacillus anthracis str. A2012]</td></tr>
<tr><td>gi|70996282|ref|XP_752896.1|</td><td>111484.04</td><td>ATP-dependent Clp protease [Aspergillus fumigatus Af293]</td></tr>
<tr><td>gi|66963733|ref|ZP_00411304.1|</td><td>91796.38</td><td>UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal [Arthrobacter sp. FB24]</td></tr>
<tr><td>gi|14972293|gb|AAK74952.1|</td><td>83990.24</td><td>ATP-dependent Clp protease, ATP-binding subunit ClpE [Streptococcus pneumoniae TIGR4]</td></tr>
<tr><td>gi|67153835|ref|ZP_00415580.1|</td><td>105117.35</td><td>AAA ATPase, central region:Clp, N terminal [Azotobacter vinelandii AvOP]</td></tr>
<tr><td>gi|107028974|ref|YP_626069.1|</td><td>95934.47</td><td>ATPase AAA-2 [Burkholderia cenocepacia AU 1054]</td></tr>
<tr><td>gi|67543764|ref|ZP_00421695.1|</td><td>95874.57</td><td>AAA ATPase, central region:Clp, N terminal:Clp, N terminal [Burkholderia vietnamiensis G4]</td></tr>
<tr><td>gi|71901099|ref|ZP_00683207.1|</td><td>95657.36</td><td>AAA ATPase, central region:Clp, N terminal [Xylella fastidiosa Ann-1]</td></tr>
<tr><td>gi|68246595|gb|EAN28691.1|</td><td>101191.44</td><td>AAA ATPase, central region:Clp, N terminal [Magnetococcus sp. MC-1]</td></tr>
<tr><td>gi|6899376|gb|AAF30801.1|</td><td>80509.23</td><td>ATP-dependent serine proteinase - heat shock protein [Ureaplasma parvum serovar 3 str. ATCC 700970]</td></tr>
<tr><td>gi|71677561|ref|ZP_00675297.1|</td><td>101278.37</td><td>AAA ATPase, central region:Clp, N terminal [Trichodesmium erythraeum IMS101]</td></tr>
<tr><td>gi|67923982|ref|ZP_00517435.1|</td><td>99351.02</td><td>AAA ATPase, central region:Clp, N terminal:Clp, N terminal [Crocosphaera watsonii WH 8501]</td></tr>
<tr><td>gi|71675746|ref|ZP_00673490.1|</td><td>92017.61</td><td>UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal [Trichodesmium erythraeum IMS101]</td></tr>
<tr><td>gi|71675495|ref|ZP_00673240.1|</td><td>98333.87</td><td>AAA ATPase, central region:Clp, N terminal [Trichodesmium erythraeum IMS101]</td></tr>
<tr><td>gi|71675077|ref|ZP_00672823.1|</td><td>91707.47</td><td>UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal [Trichodesmium erythraeum IMS101]</td></tr>
<tr><td>gi|67920889|ref|ZP_00514408.1|</td><td>91391.44</td><td>UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal:Clp, N terminal [Crocosphaera watsonii</td></tr>
<tr><td>gi|71900191|ref|ZP_00682330.1|</td><td>95677.35</td><td>AAA ATPase, central region:Clp, N terminal [Xylella fastidiosa Ann-1]</td></tr>
<tr><td>gi|537446|gb|AAA67927.1|</td><td>101434.23</td><td>AtHSP101</td></tr>
<tr><td>gi|89893184|ref|YP_516671.1|</td><td>91352.38</td><td>hypothetical protein DSY0438 [Desulfitobacterium hafniense Y51]</td></tr>
<tr><td>gi|55820681|ref|YP_139123.1|</td><td>83933.16</td><td>ATP-dependent Clp protease [Streptococcus thermophilus LMG 18311]</td></tr>
<tr><td>gi|23464638|ref|NP_695241.1|</td><td>95412.65</td><td>protease [Bifidobacterium longum NCC2705]</td></tr>
<tr><td>gi|7435720|pir||D71409</td><td>92883.79</td><td>probable endopeptidase Clp ATP-binding chain - Arabidopsis thaliana</td></tr>
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<tr><td>gi|76562675|gb|ABA45259.1|</td><td>83943.15</td><td>ATP-dependent Clp protease, ATP-binding subunit ClpE [Streptococcus agalactiae A909]</td></tr>
<tr><td>gi|31794773|ref|NP_857266.1|</td><td>93495.19</td><td>PROBABLE ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPC [Mycobacterium bovis AF2122/97]</td></tr>
<tr><td>gi|68054833|ref|ZP_00538983.1|</td><td>96315.25</td><td>AAA ATPase, central region:Clp, N terminal:DNA-directed DNA polymerase B [Exiguobacterium sibiricum</td></tr>
<tr><td>gi|13879896|gb|AAK44619.1|</td><td>92511.73</td><td>ATP-dependent Clp protease, ATP-binding subunit ClpB [Mycobacterium tuberculosis CDC1551]</td></tr>
<tr><td>gi|68056364|ref|ZP_00540488.1|</td><td>90773.89</td><td>UvrB/UvrC protein:AAA ATPase, central region:Clp, N terminal [Exiguobacterium sibiricum 255-15]</td></tr>
<tr><td>gi|108810986|ref|YP_646753.1|</td><td>95757.17</td><td>Clp ATPase [Yersinia pestis Nepal516]</td></tr>
<tr><td>gi|91978556|ref|YP_571215.1|</td><td>96681.5</td><td>ATPase AAA-2 [Rhodopseudomonas palustris BisB5]</td></tr>
<tr><td>gi|56908137|dbj|BAD62664.1|</td><td>91352.19</td><td>ATP-dependent Clp protease ATP-binding subunit ClpC [Bacillus clausii KSM-K16]</td></tr>
<tr><td>gi|1705925|sp|P51332|CLPC_PORPU</td><td>91062.18</td><td>ATP-dependent Clp protease ATP-binding subunit clpA homolog</td></tr>
<tr><td>gi|9105213|gb|AAF83191.1|</td><td>95805.33</td><td>ATP-dependent Clp protease subunit [Xylella fastidiosa 9a5c]</td></tr>
<tr><td>gi|33238085|gb|AAQ00152.1|</td><td>95053.25</td><td>ATPase with chaperone activity ATP-binding subunit [Prochlorococcus marinus subsp. marinus str. CCM</td></tr>
<tr><td>gi|885934|gb|AAB09631.1|</td><td>99590.34</td><td>ClpB</td></tr>
<tr><td>gi|16409597|emb|CAD00759.1|</td><td>91166.36</td><td>endopeptidase Clp ATP-binding chain C [Listeria monocytogenes]</td></tr>
<tr><td>gi|16411676|emb|CAD00284.1|</td><td>97617.08</td><td>clpB [Listeria monocytogenes]</td></tr>
<tr><td>gi|21114288|gb|AAM42341.1|</td><td>95544</td><td>ATP-dependent Clp protease subunit [Xanthomonas campestris pv. campestris str. ATCC 33913]</td></tr>
<tr><td>gi|23494372|dbj|BAC19339.1|</td><td>101597.73</td><td>putative endopeptidase Clp ATP-binding chain C [Corynebacterium efficiens YS-314]</td></tr>
<tr><td>gi|21203645|dbj|BAB94345.1|</td><td>91054.52</td><td>endopeptidase [Staphylococcus aureus subsp. aureus MW2]</td></tr>
<tr><td>gi|47501589|gb|AAT30265.1|</td><td>97598.37</td><td>ATP-dependent Clp protease, ATP-binding subunit ClpB [Bacillus anthracis str. 'Ames Ancestor']</td></tr>
<tr><td>gi|49612793|emb|CAG76243.1|</td><td>95750.21</td><td>ClpB protein (heat shock protein f84.1) [Erwinia carotovora subsp. atroseptica SCRI1043]</td></tr>
<tr><td>gi|52307890|gb|AAU38390.1|</td><td>95440.85</td><td>ClpA protein [Mannheimia succiniciproducens MBEL55E]</td></tr>
<tr><td>gi|17982078|gb|AAL51377.1|</td><td>103438.78</td><td>ATP-DEPENDENT CLP PROTEASE, ATP-BINDING SUBUNIT CLPB [Brucella melitensis 16M]</td></tr>
<tr><td>gi|29342763|gb|AAO80527.1|</td><td>83158.44</td><td>ATP-dependent Clp protease, ATP-binding subunit ClpE [Enterococcus faecalis V583]</td></tr>
<tr><td>gi|29893892|gb|AAP07184.1|</td><td>90573.85</td><td>Negative regulator of genetic competence clpC/mecB [Bacillus cereus ATCC 14579]</td></tr>
<tr><td>gi|90425750|ref|YP_534120.1|</td><td>96893.68</td><td>ATPase AAA-2 [Rhodopseudomonas palustris BisB18]</td></tr>
<tr><td>gi|3322325|gb|AAC65062.1|</td><td>99547.19</td><td>ATP-dependent Clp protease subunit B (clpB) [Treponema pallidum subsp. pallidum str. Nichols]</td></tr>
<tr><td>gi|54013887|dbj|BAD55257.1|</td><td>94104.63</td><td>putative Clp protease [Nocardia farcinica IFM 10152]</td></tr>
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<tr><td>gi|35212107|dbj|BAC89483.1|</td><td>84920.86</td><td>endopeptidase Clp ATP-binding chain [Gloeobacter violaceus PCC 7421]</td></tr>
<tr><td>gi|35212631|dbj|BAC90005.1|</td><td>91138.26</td><td>endopeptidase Clp ATP-binding chain [Gloeobacter violaceus PCC 7421]</td></tr>
<tr><td>gi|57161447|emb|CAH58372.1|</td><td>96404.15</td><td>heat shock protein ClpB [Ehrlichia ruminantium str. Welgevonden]</td></tr>
<tr><td>gi|38200810|emb|CAE50514.1|</td><td>97511.81</td><td>ATP-dependent Clp protease ATP-binding subunit [Corynebacterium diphtheriae]</td></tr>
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gi|56543894|gb|AAV90048.1|	95720.18	ATP-dependent Clp protease [Zymomonas mobilis subsp. mobilis ZM4]
gi|50363792|gb|AAT75777.1|	80058.43	ATPase subunit of ATP-dependant protease [Mesoplasma florum L1]
gi|10172715|dbj|BAB03822.1|	90558.81	class III stress response-related ATPase [Bacillus halodurans C-125]
gi|52209532|emb|CAH35485.1|	97332.34	ClpB heat-shock protein [Burkholderia pseudomallei K96243]
gi|16412693|emb|CAC95497.1|	91067.42	endopeptidase Clp ATP-binding chain C [Listeria innocua]
gi|16414821|emb|CAC97537.1|	97614.18	clpB [Listeria innocua]
gi|13092579|emb|CAC29743.1|	93944.39	putative ATP-dependent Clp protease [Mycobacterium leprae]
gi|13094038|emb|CAC32007.1|	93206.69	heat shock protein [Mycobacterium leprae]
gi|20517331|gb|AAM25468.1|	91982.2	ATPases with chaperone activity, ATP-binding subunit [Thermoanaerobacter tengcongensis MB4]
gi|87126998|gb|ABD21512.1|	91038.49	endopeptidase [Staphylococcus aureus subsp. aureus USA300]
gi|49240131|emb|CAF26578.1|	98464.01	ATP-dependent clp protease, ATP-binding subunit clpB [Bartonella quintana str. Toulouse]
gi|52001792|gb|AAU21734.1|	90167.47	class III stress response-related ATPase [Bacillus licheniformis ATCC 14580]
gi|49238883|emb|CAF28176.1|	96057.66	ATP-dependent clp protease, ATP-binding subunit clpB [Bartonella henselae str. Houston-1]
gi|51977631|gb|AAU19181.1|	97598.3	ATP-dependent Clp protease, ATP-binding subunit ClpB [Bacillus cereus E33L]
gi|51978604|gb|AAU20154.1|	90550.84	negative regulator of genetic competence clpC/mecB (ATP-dependent Clp protease) [Bacillus cereus E3
gi|51857957|dbj|BAD42115.1|	92937.32	class III stress response-related ATPase [Symbiobacterium thermophilum IAM 14863]
gi|58418757|gb|AAW70772.1|	95317.49	ATP-binding subunit of Clp protease and DnaK/DnaJ chaperones [Wolbachia endosymbiont strain TRS of
gi|56128884|gb|AAV78390.1|	95532.89	ClpB protein (heat shock protein f84.1) [Salmonella enterica subsp. enterica serovar Paratyphi A st
gi|53751448|emb|CAH12866.1|	95906.06	endopeptidase Clp ATP-binding chain B (ClpB) [Legionella pneumophila str. Paris]
gi|53754469|emb|CAH15953.1|	95890.09	endopeptidase Clp ATP-binding chain B (ClpB) [Legionella pneumophila str. Lens]
gi|16331048|ref|NP_441776.1|	98119.29	ClpB protein [Synechocystis sp. PCC 6803]
gi|7380324|emb|CAB84911.1|	95149.01	ClpB protein [Neisseria meningitidis Z2491]
gi|7226713|gb|AAF41829.1|	95250.02	clpB protein [Neisseria meningitidis MC58]
gi|14246744|dbj|BAB57137.1|	98383.71	ClpB chaperone homologue [Staphylococcus aureus subsp. aureus Mu50]
gi|15981209|emb|CAC92509.1|	95756.23	Clp ATPase [Yersinia pestis CO92]
gi|46906465|ref|YP_012854.1|	91206.43	ClpC ATPase [Listeria monocytogenes str. 4b F2365]
gi|30250327|ref|NP_842397.1|	96400.51	ClpB ATPase dependent protease, chaperonin [Nitrosomonas europaea ATCC 19718]
gi|33862722|ref|NP_894282.1|	95891.1	ATP-dependent Clp protease, Hsp 100, ATP-binding subunit ClpB [Prochlorococcus marinus str. MIT 931
gi|33861137|ref|NP_892698.1|	97589.08	ATP-dependent Clp protease, Hsp 100, ATP-binding subunit ClpB [Prochlorococcus marinus subsp. pasto
gi|90574409|ref|ZP_01230909.1|	97708.18	hypothetical protein CdifQ_02002161 [Clostridium difficile QCD-32g58]
gi|66802530|ref|XP_635137.1|	99550.51	hypothetical protein DDB0183816 [Dictyostelium discoideum]

gi|66805423|ref|XP_636444.1|	88973.12	hypothetical protein DDB0188234 [Dictyostelium discoideum]
gi|755163|gb|AAB67745.1|	92884.21	ClpC
gi|108797458|ref|YP_637655.1|	92558.34	ATPase AAA-2 [Mycobacterium sp. MCS]
gi|108801719|ref|YP_641916.1|	93368.97	ATPase AAA-2 [Mycobacterium sp. MCS]
gi|41326857|emb|CAF20701.1|	101450.54	PROBABLE ATP-DEPENDENT PROTEASE (HEAT SHOCK PROTEIN) [Corynebacterium glutamicum ATCC 13032]
gi|1573874|gb|AAC22518.1|	96006.14	ATP-dependent Clp protease, ATPase subunit (clpB) [Haemophilus influenzae Rd KW20]
gi|16331384|ref|NP_442112.1|	91175.46	ATP-dependent Clp protease regulatory subunit [Synechocystis sp. PCC 6803]
gi|93141242|sp|P53533|CLPB1_SYNP7	98722.92	Chaperone clpB 1
gi|57636760|gb|AAW53548.1|	91013.46	ATP-dependent Clp protease, ATP-binding subunit ClpC [Staphylococcus epidermidis RP62A]
gi|62196857|gb|AAX75157.1|	96866.59	ClpB, ATP-dependent Clp protease, ATP-binding subunit ClpB [Brucella abortus biovar 1 str. 9-941]
gi|17742634|gb|AAL44977.1|	96337.32	ATP-dependent Clp protease, ATP-binding subunit [Agrobacterium tumefaciens str. C58]
gi|1314297|gb|AAC44446.1|	91822.76	ClpC ATPase
gi|41406559|ref|NP_959395.1|	93279.94	ClpC [Mycobacterium avium subsp. paratuberculosis K-10]
gi|12724524|gb|AAK05623.1|	97275.03	ClpB protein [Lactococcus lactis subsp. lactis Il1403]
gi|12723443|gb|AAK04655.1|	83321.55	ATP-dependent protease ATP-binding subunit [Lactococcus lactis subsp. lactis Il1403]
gi|28270656|emb|CAD63562.1|	92585.36	ATP-dependent Clp protease, ATP-binding subunit ClpC [Lactobacillus plantarum WCFS1]
gi|17131053|dbj|BAB73662.1|	89928.29	endopeptidase Clp ATP-binding chain [Nostoc sp. PCC 7120]
gi|17132093|dbj|BAB74698.1|	93140.13	endopeptidase Clp ATP-binding chain [Nostoc sp. PCC 7120]
gi|17134222|dbj|BAB76783.1|	94301.33	endopeptidase Clp ATP-binding chain B [Nostoc sp. PCC 7120]
gi|23094957|emb|CAD46179.1|	83979.22	Unknown [Streptococcus agalactiae NEM316]
gi|32423740|gb|AAP81264.1|	95061.21	ClpB [Pseudomonas aeruginosa]
gi|13422139|gb|AAK22863.1|	94059.24	ATP-dependent Clp protease, ATP-binding subunit ClpB [Caulobacter crescentus CB15]
gi|15023863|gb|AAK78935.1|	97988.64	ATPase with chaperone activity, two ATP-binding domains [Clostridium acetobutylicum ATCC 824]
gi|58580960|ref|YP_199976.1|	99468.02	ATP-dependent Clp protease subunit [Xanthomonas oryzae pv. oryzae KACC10331]
gi|18410584|ref|NP_565083.1|	101460.25	ATHSP101 (HEAT SHOCK PROTEIN 101); ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide bind
gi|59801418|ref|YP_208130.1|	95152.99	putative ClpB protein [Neisseria gonorrhoeae FA 1090]
gi|49530427|emb|CAG68139.1|	95348.02	ATP-dependent protease, Hsp 100, part of multi-chaperone system with DnaK, DnaJ, and GrpE [Acinetob
gi|56315289|emb|CAI09934.1|	95885.4	ClpB protein [Azoarcus sp. EbN1]
gi|13622598|gb|AAK34306.1|	84908.42	putative ATP-dependent protease [Streptococcus pyogenes M1 GAS]
gi|15458317|gb|AAK99529.1|	84016.29	ATP dependent protease [Streptococcus pneumoniae R6]
gi|56605256|emb|CAG46402.1|	95983.18	ClpB protein [Francisella tularensis subsp. tularensis SCHU S4]
gi|19748664|gb|AAL98096.1|	84908.42	putative ATP-dependent protease [Streptococcus pyogenes MGAS8232]

gi|28810860|dbj|BAC63794.1|	84893.43	putative ATP-dependent protease [Streptococcus pyogenes SSI-1]
gi|56378455|dbj|BAD74363.1|	90338.95	ATP-dependent Clp protease ATPase subunit [Geobacillus kaustophilus HTA426]
gi|56379176|dbj|BAD75084.1|	97305.33	ATP-dependent Clp protease ATP-binding subunit [Geobacillus kaustophilus HTA426]
gi|56679839|gb|AAV96505.1|	95880.23	ATP-dependent Clp protease, ATP-binding subunit ClpB [Silicibacter pomeroyi DSS-3]
gi|71038368|gb|AAZ18676.1|	95962.81	putative chaperonin clpA/B [Psychrobacter arcticus 273-4]
gi|77967362|gb|ABB08742.1|	96053.59	AAA ATPase, ClpB [Burkholderia sp. 383]
gi|39937493|ref|NP_949769.1|	96668.55	endopeptidase Clp: ATP-binding subunit B, clpB [Rhodopseudomonas palustris CGA009]
gi|68057652|gb|AAX87905.1|	95843.1	ClpB [Haemophilus influenzae 86-028NP]
gi|55738557|gb|AAV62198.1|	83914.12	ATP-dependent Clp protease [Streptococcus thermophilus CNRZ1066]
gi|30468134|ref|NP_849021.1|	92112.77	Clp protease ATP binding subunit [Cyanidioschyzon merolae strain 10D]
gi|33863332|ref|NP_894892.1|	94782.06	ClpC [Prochlorococcus marinus str. MIT 9313]
gi|48864938|ref|ZP_00318807.1|	91422.77	COG0542: ATPases with chaperone activity, ATP-binding subunit [Oenococcus oeni PSU-1]
gi|48864977|ref|ZP_00318845.1|	81242.7	COG0542: ATPases with chaperone activity, ATP-binding subunit [Oenococcus oeni PSU-1]
gi|67517159|ref|XP_658462.1|	103805.9	hypothetical protein AN0858.2 [Aspergillus nidulans FGSC A4]
gi|67463040|ref|XP_648177.1|	56501.31	heat shock protein 101 [Entamoeba histolytica HM-1:IMSS]
gi|67463114|ref|XP_648214.1|	95043.64	HSP101-related protein [Entamoeba histolytica HM-1:IMSS]
gi|67463218|ref|XP_648266.1|	97173.89	AAA family ATPase [Entamoeba histolytica HM-1:IMSS]
gi|67465519|ref|XP_648944.1|	97766.07	AAA family ATPase [Entamoeba histolytica HM-1:IMSS]
gi|67469889|ref|XP_650916.1|	96109.2	heat shock protein 101 [Entamoeba histolytica HM-1:IMSS]
gi|67470328|ref|XP_651132.1|	35238.39	hsp101-related protein [Entamoeba histolytica HM-1:IMSS]
gi|67473761|ref|XP_652630.1|	97734.09	AAA family ATPase [Entamoeba histolytica HM-1:IMSS]
gi|67475516|ref|XP_653452.1|	97744.06	AAA family ATPase [Entamoeba histolytica HM-1:IMSS]
gi|67477107|ref|XP_654067.1|	52270.08	heat shock protein 101 [Entamoeba histolytica HM-1:IMSS]
gi|67482746|ref|XP_656674.1|	21277.16	heat shock protein 101 [Entamoeba histolytica HM-1:IMSS]
gi|24379042|ref|NP_720997.1|	83910.07	ATP-dependent protease ClpE [Streptococcus mutans UA159]
gi|147365|gb|AAA24422.1|	95654.91	ATP-dependent protease binding subunit [Escherichia coli]
gi|22297851|ref|NP_681098.1|	91908.96	ATP-dependent Clp protease regulatory subunit [Thermosynechococcus elongatus BP-1]
gi|22255857|gb|AAM94782.1|	88270.85	CalR4 [Micromonospora echinospora]
gi|62998570|gb|AAF01451.2|	99393.98	HSP100 [Pleurotus sajor-caju]
gi|11561806|gb|AAC83688.2|	101276.18	101 kDa heat shock protein; HSP101 [Nicotiana tabacum]
gi|11561808|gb|AAC83689.2|	101281.21	101 kDa heat shock protein; HSP101 [Triticum aestivum]
gi|53802726|ref|YP_115493.1|	95277.11	ATP-dependent Clp protease, ATP-binding subunit ClpB [Methylococcus capsulatus str. Bath]
gi|74316833|ref|YP_314573.1|	94792.92	ClpB protein [Thiobacillus denitrificans ATCC 25259]
gi|37904167|gb|AAP68612.1|	17789.47	ClpC [Bacillus weihenstephanensis]
gi|37904163|gb|AAP68610.1|	17819.48	ClpC [Bacillus weihenstephanensis]

gi|37904149|gb|AAP68603.1|	17773.47	ClpC [Bacillus thuringiensis serovar israelensis]
gi|86751350|ref|YP_487846.1|	96549.34	AAA_5 ATPase [Rhodopseudomonas palustris HaA2]
gi|83592092|ref|YP_425844.1|	95555.31	Chaperone clpB [Rhodospirillum rubrum ATCC 11170]
gi|4481954|emb|CAB38512.1|	100616.57	SPBC16D10.08c [Schizosaccharomyces pombe]
gi|4928488|gb|AAD33606.1|	101297.44	heat shock protein HSP101 [Zea mays]
gi|8575704|gb|AAF78058.1|	96056.24	ClpB protease [secondary endosymbiont of Glycaspis brimblecombei]
gi|86743031|ref|YP_483431.1|	94497.99	ATPase AAA-2 [Frankia sp. CcI3]
gi|86743058|ref|YP_483458.1|	92007.84	ATPase AAA-2 [Frankia sp. CcI3]
gi|29829142|ref|NP_823776.1|	93228.24	ATP-dependent Clp protease [Streptomyces avermitilis MA-4680]
gi|29831240|ref|NP_825874.1|	92967.32	ATP-dependent Clp protease [Streptomyces avermitilis MA-4680]
gi|89056478|ref|YP_511929.1|	95575.63	ATPase AAA-2 [Jannaschia sp. CCS1]
gi|56750469|ref|YP_171170.1|	99600.32	ClpB protein [Synechococcus elongatus PCC 6301]
gi|56751262|ref|YP_171963.1|	92882.12	ATP-dependent Clp protease regulatory subunit ClpC [Synechococcus elongatus PCC 6301]
gi|18447672|gb|AAL67969.1|	12528.92	ClpB [Paracoccidioides brasiliensis]
gi|89900705|ref|YP_523176.1|	96306.98	ATPase AAA-2 [Rhodoferax ferrireducens T118]
gi|90022193|ref|YP_528020.1|	97510.85	ClpB protein [Saccharophagus degradans 2-40]
gi|4558484|gb|AAD22629.1|	101288.31	heat shock protein 101 [Triticum aestivum]
gi|6013196|gb|AAF01280.1|	100949.14	heat shock protein 101 [Triticum aestivum]
gi|57898943|emb|CAI44947.1|	101022.78	putative HSP100 protein [Phycomyces blakesleeanus]
gi|5302773|emb|CAB46061.1|	74168.87	heat shock protein like [Arabidopsis thaliana]
gi|18417676|ref|NP_568314.1|	109046.73	ATP binding / ATPase/ nucleoside-triphosphatase/ nucleotide binding / protein binding [Arabidopsis
gi|21221802|ref|NP_627581.1|	92957.19	Clp-family ATP-binding protease [Streptomyces coelicolor A3(2)]
gi|33866037|ref|NP_897596.1|	97262.72	endopeptidase Clp ATP-binding chain B [Synechococcus sp. WH 8102]
gi|33865472|ref|NP_897031.1|	92984.04	endopeptidase Clp ATP-binding chain C [Synechococcus sp. WH 8102]
gi|33861644|ref|NP_893205.1|	93426.58	ClpC [Prochlorococcus marinus subsp. pastoris str. CCMP1986]
gi|52629088|gb|AAU27829.1|	95966.12	ClpB protein [Legionella pneumophila subsp. pneumophila str. Philadelphia 1]
gi|42561142|ref|NP_975593.1|	80789.62	ATP dependant protease ClpB [Mycoplasma mycoides subsp. mycoides SC str. PG1]
gi|15159084|gb|AAK89256.1|	97539.9	AGR_L_1346p [Agrobacterium tumefaciens str. C58]
gi|58617389|ref|YP_196588.1|	96866.4	ClpB protein [Ehrlichia ruminantium str. Gardel]
gi|58579335|ref|YP_197547.1|	96875.44	ClpB protein [Ehrlichia ruminantium str. Welgevonden]
gi|44417|emb|CAA37573.1|	71803.87	unnamed protein product [Mycobacterium leprae]
gi|49333257|gb|AAT63903.1|	97654.4	ATP-dependent Clp protease, ATP-binding subunit ClpB [Bacillus thuringiensis serovar konkukian str.
gi|50839369|gb|AAT82036.1|	93366.68	putative Clp-family ATP-binding protease [Propionibacterium acnes KPA171202]
gi|50841068|gb|AAT83735.1|	93620.18	ATP-dependent protease (Clp chaperone) [Propionibacterium acnes KPA171202]
gi|1946209|emb|CAA86116.1|	97086.03	100 kDa heat shock protein (Hsp100) [Leishmania major]
gi|71914336|gb|AAZ54238.1|	95335.96	ATPase [Thermobifida fusca YX]
gi|2058336|emb|CAB08073.1|	97231.07	heat shock protein 100 [Leishmania donovani]

gi|72119081|gb|AAZ61344.1|	95381.54	AAA ATPase, central region:Clp, N terminal [Ralstonia eutropha JMP134]
gi|77389402|gb|ABA80587.1|	95645.29	Chaperone ClpB [Rhodobacter sphaeroides 2.4.1]
gi|50952303|gb|AAT90004.1|	81008.59	ATP-dependent Clp protease, ATP-binding subunit [Leifsonia xyli subsp. xyli str. CTCB07]
gi|71847961|gb|AAZ47457.1|	95708.29	AAA ATPase, central region:Clp, N terminal [Dechloromonas aromatica RCB]
gi|77385058|gb|ABA76571.1|	95606.91	Chaperone clpB [Pseudomonas fluorescens PfO-1]
gi|75705548|gb|ABA25220.1|	99661.61	ATPase [Anabaena variabilis ATCC 29413]
gi|17864015|gb|AAL47016.1|	87929.45	ClpB ATP protease [Paracoccidioides brasiliensis]
gi|50903681|gb|AAT87396.1|	84907.48	ATP-dependent clp protease ATP-binding subunit [Streptococcus pyogenes MGAS10394]
gi|91783442|ref|YP_558648.1|	96111.68	Heat-shock protein, chaperone ClpB [Burkholderia xenovorans LB400]
gi|91788074|ref|YP_549026.1|	96045.73	ATPase AAA-2 [Polaromonas sp. JS666]
gi|91776550|ref|YP_546306.1|	95538.33	ATPase AAA-2 [Methylobacillus flagellatus KT]
gi|92116299|ref|YP_576028.1|	96646.7	ATPase AAA-2 [Nitrobacter hamburgensis X14]
gi|78195302|gb|ABB33069.1|	96300.99	AAA ATPase [Geobacter metallireducens GS-15]
gi|91795722|gb|ABE57861.1|	94784.14	ATPase AAA-2 [Chromohalobacter salexigens DSM 3043]
gi|93005671|ref|YP_580108.1|	96034.88	ATPase AAA-2 [Psychrobacter cryohalolentis K5]
gi|29570852|gb|AAO73810.2|	103091.83	heat shock protein CLPA [Paracoccidioides brasiliensis]
gi|37718900|gb|AAR01771.1|	82645.06	putative heat shock protein, 5'-partial [Oryza sativa (japonica cultivar-group)]
gi|62358440|gb|AAX78903.1|	90951.48	ATP-dependent Clp protease subunit, heat shock protein 78 (HSP78), putative [Trypanosoma brucei]
gi|94310897|ref|YP_584107.1|	95997.78	ATPase AAA-2 [Ralstonia metallidurans CH34]
gi|50916753|ref|XP_468773.1|	109145.9	putative heat shock protein [Oryza sativa (japonica cultivar-group)]
gi|63254700|gb|AAY35796.1|	95252.15	AAA ATPase, central region:Clp, N terminal:Clp, N terminal [Pseudomonas syringae pv. syringae B728a
gi|94985312|ref|YP_604676.1|	95692.63	ATPase AAA-2 [Deinococcus geothermalis DSM 11300]
gi|37904161|gb|AAP68609.1|	17788.47	ClpC [Bacillus weihenstephanensis]
gi|37904169|gb|AAP68613.1|	17804.5	ClpC [Bacillus cereus]
gi|75907133|ref|YP_321429.1|	91369.25	UvrB/UvrC protein [Anabaena variabilis ATCC 29413]
gi|75908552|ref|YP_322848.1|	98473.41	ATPase [Anabaena variabilis ATCC 29413]
gi|39977113|ref|XP_369944.1|	103081.78	hypothetical protein MG06459.4 [Magnaporthe grisea 70-15]
gi|103487872|ref|YP_617433.1|	93169.76	ATPase AAA-2 [Sphingopyxis alaskensis RB2256]
gi|18414279|ref|NP_567437.1|	68969.2	ATP binding / nucleoside-triphosphatase/ nucleotide binding / protein binding [Arabidopsis thaliana
gi|51209900|ref|YP_063564.1|	91778.64	Clp protease ATP binding subunit [Gracilaria tenuistipitata var. liui]
gi|51572403|gb|AAU07694.1|	35797.04	plastid clpB [Helicosporidium sp. ex Simulium jonesii]
gi|90961178|ref|YP_535094.1|	92790.21	Negative regulator of genetic competence [Lactobacillus salivarius subsp. salivarius UCC118]

85. Group probability: 0.9752. Peptides of the group

EQRIEVTIQGPK	64.27	54.9594	1396.767	1398.163	1	2	distinct	1	0.9752

The equivalent proteins include

gi|67469507|ref|XP_650732.1|	53642.22	hypothetical protein 202.t00015 [Entamoeba histolytica HM-1:IMSS]

86. Group probability: 0.9747. Peptides of the group

FHDHIFPDINNSGGDPQK	61.27	53.6023	2036.934	2038.063	1	2	distinct	0	0.9747

The equivalent proteins include

gi|46123049|ref|XP_386078.1|	112137.76	hypothetical protein FG05902.1 [Gibberella zeae PH-1]

87. Group probability: 0.9744. Peptides of the group

VGQAVDVVGQAGRPK	84.06	54.7507	1479.816	1480.383	2	2	distinct	0	0.9744

The equivalent proteins include

gi|88180570|gb|EAQ88038.1|	100873.99	hypothetical protein CHGG_04657 [Chaetomium globosum CBS 148.51]
gi|90298340|gb|EAS27971.1|	101420.11	hypothetical protein CIMG_09175 [Coccidioides immitis RS]
gi|83772758|dbj|BAE62886.1|	101198.42	unnamed protein product [Aspergillus oryzae]
gi|12044480|emb|CAC19753.1|	98392.99	mts4 [Schizosaccharomyces pombe]
gi|92887682|gb|ABE89010.1|	97855.87	Proteasome/cyclosome, regulatory subunit [Medicago truncatula]
gi|46136535|ref|XP_389959.1|	97075.99	hypothetical protein FG09783.1 [Gibberella zeae PH-1]
gi|76157471|gb|AAX28383.2|	18945.89	SJCHGC08055 protein [Schistosoma japonicum]
gi|17298151|dbj|BAB78497.1|	26225.99	26S proteasome regulatory particle non-ATPase subunit1b [Oryza sativa (japonica cultivar-group)]
gi|85105477|ref|XP_961971.1|	98370.78	hypothetical protein [Neurospora crassa OR74A]
gi|70997461|ref|XP_753478.1|	100825.53	26s proteasome regulatory subunit mts4 [Aspergillus fumigatus Af293]
gi|2072122|emb|CAA70948.1|	98280.76	19S regulatory cap region of 26S protease subunit 2 [Schizosaccharomyces pombe]
gi|67515687|ref|XP_657729.1|	177787.66	hypothetical protein AN0125.2 [Aspergillus nidulans FGSC A4]
gi|50905317|ref|XP_464147.1|	98608.63	putative 26S proteasome regulatory subunit S2 [Oryza sativa (japonica cultivar-group)]
gi|53791880|dbj|BAD54002.1|	90632.62	putative 26S proteasome regulatory subunit S2 [Oryza sativa (japonica cultivar-group)]
gi|62319162|dbj|BAD94334.1|	26622.09	putative 26S proteasome regulatory subunit S2 [Arabidopsis thaliana]
gi|32700010|gb|AAP86655.1|	98766.05	26S proteasome subunit RPN1a [Arabidopsis thaliana]
gi|7269701|emb|CAB79649.1|	123811.57	putative protein [Arabidopsis thaliana]
gi|32700012|gb|AAP86656.1|	98576.1	26S proteasome subunit RPN1b [Arabidopsis thaliana]

88. Group probability: 0.9733. Peptides of the group

SILPDVLEHQLPEELPFPFK	59.67	52.8407	2347.246	2347.633	1	2	distinct	0	0.9733

The equivalent proteins include

gi|46123863|ref|XP_386485.1|	73665.27	hypothetical protein FG06309.1 [Gibberella zeae PH-1]

89. Group probability: 0.9713. Peptides of the group

KEEAPSFGCGPGSK	61.8	55.0526	1449.656	1449.263	1	2	distinct	1	0.9713

The equivalent proteins include

gi|46129318|ref|XP_389020.1|	89732.26	hypothetical protein FG08844.1 [Gibberella zeae PH-1]

90. Group probability: 0.9708. Peptides of the group

AHPWEESDAPSLPK	61.55	54.8684	1562.736	1564.113	3	2	distinct	0	0.9708

The equivalent proteins include

gi|46115716|ref|XP_383876.1|	60175.88	hypothetical protein FG03700.1 [Gibberella zeae PH-1]

91. Group probability: 0.9686. Peptides of the group

AEQERPGSQYGDLIK	60.27	54.5608	1689.832	1689.733	1	2	distinct	0	0.9686

The equivalent proteins include

gi|46125493|ref|XP_387300.1|	81969.13	hypothetical protein FG07124.1 [Gibberella zeae PH-1]

92. Group probability: 0.9680. Peptides of the group

KPTDELYQDTR	61.74	54.9733	1364.657	1365.823	4	2	distinct	0	0.968

The equivalent proteins include

gi|46121597|ref|XP_385353.1|	20378.47	hypothetical protein FG05177.1 [Gibberella zeae PH-1]

93. Group probability: 0.9664. Peptides of the group

DGYKHPDVDGEFVDSEEDR	57.51	53.0819	2207.924	2208.863	1	2	distinct	1	0.9664

The equivalent proteins include

gi|46125435|ref|XP_387271.1|	34736.22	hypothetical protein FG07095.1 [Gibberella zeae PH-1]								
94. Group probability: 0.9650. Peptides of the group										
VDKPNLPFPDIAEQTEDATEEDLKR	56.71		51.8774	2869.398	2870.714	1	3	distinct	1	0.965
The equivalent proteins include										
gi|46123327|ref|XP_386217.1|	115826.94	hypothetical protein FG06041.1 [Gibberella zeae PH-1]								
95. Group probability: 0.9637. Peptides of the group										
TGIIIIDFPGKK	60.01		55.4046	1300.775	1301.903	1	2	distinct	1	0.9637
The equivalent proteins include										
gi|46122555|ref|XP_385831.1|	39703.75	hypothetical protein FG05655.1 [Gibberella zeae PH-1]								
96. Group probability: 0.9621. Peptides of the group										
SVEMHHEQLESAEPGDNVGFNVK	61.38		52.4421	2552.16	2551.474	2	+2,+3	distinct	0	0.9621
The equivalent proteins include										
gi|53829548|gb|AAU94653.1|	46265.75	ef1a [Corallochytrium limacisporum]								
97. Group probability: 0.9612. Peptides of the group										
MLIAPIENSPKPPPK (01000000000000000)	57.83		54.5536	1646.907	1645.803	5	2	distinct	0	0.9612
The equivalent proteins include										
gi|55244449|gb|EAA05555.2|	25267.87	ENSANGP00000018993 [Anopheles gambiae str. PEST]								
98. Group probability: 0.9609. Peptides of the group										
VPAEGPAALKR	59.52		55.236	1107.64	1108.843	3	2	distinct	1	0.9609
The equivalent proteins include										
gi|46127921|ref|XP_388514.1|	39495.49	hypothetical protein FG08338.1 [Gibberella zeae PH-1]								
99. Group probability: 0.9595. Peptides of the group										
MSVAHDKPFLLQTYR (01000000000000000)	57.26		54.1967	1820.924	1821.473	1	2	distinct	0	0.9595
The equivalent proteins include										
gi|84352650|ref|ZP_00977599.1|	50905.78	COG0840: Methyl-accepting chemotaxis protein [Burkholderia cenocepacia PC184]								
gi|107025593|ref|YP_623104.1|	51838.26	methyl-accepting chemotaxis sensory transducer [Burkholderia cenocepacia AU 1054]								
gi|67662996|ref|ZP_00460281.1|	60627.76	chemotaxis sensory transducer [Burkholderia cenocepacia HI2424]								
100. Group probability: 0.9584. Peptides of the group										
DADDAYHEMHNK (00000000010000)	58.37		55.041	1460.563	1461.713	1	2	distinct	0	0.9584
The equivalent proteins include										
gi|90303584|gb|EAS33215.1|	24308.92	hypothetical protein CIMG_04239 [Coccidioides immitis RS]								
gi|83775253|dbj|BAE65376.1|	24969.05	unnamed protein product [Aspergillus oryzae]								
gi|46136697|ref|XP_390040.1|	32709.37	hypothetical protein FG09864.1 [Gibberella zeae PH-1]								
gi|71000792|ref|XP_755077.1|	26581.93	pre-mRNA splicing factor Srp1 [Aspergillus fumigatus Af293]								
gi|67539264|ref|XP_663406.1|	26849.04	hypothetical protein AN5802.2 [Aspergillus nidulans FGSC A4]								
101. Group probability: 0.9577. Peptides of the group										
QLIEGPGPKPGQR	57.79		55.0505	1375.757	1376.453	1	2	distinct	0	0.9577
The equivalent proteins include										
gi|46117458|ref|XP_384747.1|	47017.29	hypothetical protein FG04571.1 [Gibberella zeae PH-1]								
102. Group probability: 0.9549. Peptides of the group										
HPYEPVGDAVK	57.91		55.237	1210.598	1210.313	3	2	distinct	0	0.9549
The equivalent proteins include										
gi|46114454|ref|XP_383245.1|	36836.98	hypothetical protein FG03069.1 [Gibberella zeae PH-1]								
103. Group probability: 0.9533. Peptides of the group										
SDDNTLKPDSPCHK	56.12		54.5155	1612.715	1613.863	2	2	distinct	0	0.9533
The equivalent proteins include										
gi|46114284|ref|XP_383160.1|	44646.3	hypothetical protein FG02984.1 [Gibberella zeae PH-1]								
104. Group probability: 0.9520. Peptides of the group										
RDDGYLDEEEFDDLIELR	53.87		53.136	2241.007	2241.833	1	2	distinct	1	0.952
The equivalent proteins include										
gi|46105342|ref|XP_380475.1|	118477.89	hypothetical protein FG00299.1 [Gibberella zeae PH-1]								
105. Group probability: 0.9518. Peptides of the group										
GGPCPIEIYPPDNDDKK	54.37		53.7501	1913.883	1914.413	2	2	distinct	1	0.9518

The equivalent proteins include

gi|46128834|ref|XP_388956.1|	28551.14	hypothetical protein FG08780.1 [Gibberella zeae PH-1]

106. Group probability: 0.9514. Peptides of the group

MLLSILYK	65.54	55.5248	979.578	979.953	5	1	distinct	0	0.9514

The equivalent proteins include

gi|1591430|gb|AAB98708.1|	88518.79	hydrogenase expression regulatory protein (hypF) [Methanocaldococcus jannaschii DSM 2661]
gi|50556066|ref|XP_505441.1|	36614.75	hypothetical protein [Yarrowia lipolytica]

107. Group probability: 0.9513. Peptides of the group

SVEMHHETLEEGKPGDNVGFNVK (000010000000000000000000)	67.21	52.4421	2552.196	2551.474	5	+2,+3	distinct	0	0.9513

The equivalent proteins include

gi|66473251|gb|AAY46267.1|	45279.33	translation elongation factor 1-alpha [Polyporus squamosus]

108. Group probability: 0.9505. Peptides of the group

RGFGSPIAPER	56.98	55.8124	1185.625	1186.553	5	2	distinct	1	0.9505

The equivalent proteins include

gi|46108678|ref|XP_381397.1|	30487.52	hypothetical protein FG01221.1 [Gibberella zeae PH-1]

109. Group probability: 0.9503. Peptides of the group

TWWEQPGHWGEESEFK	54.4	53.6246	2031.875	2032.233	2	2	distinct	0	0.9503

The equivalent proteins include

gi|46127923|ref|XP_388515.1|	42964.83	hypothetical protein FG08339.1 [Gibberella zeae PH-1]

110. Group probability: 0.9500. Peptides of the group

VPPKGEPAPPR	56.85	55.7666	1143.64	1144.483	1	2	distinct	1	0.95

The equivalent proteins include

gi|46135967|ref|XP_389675.1|	57444.34	hypothetical protein FG09499.1 [Gibberella zeae PH-1]

111. Group probability: 0.9496. Peptides of the group

EGEVDDHKGPVELVTPPEGSK	52.11	53.1844	2218.075	2218.283	3	2	distinct	1	0.9496

The equivalent proteins include

gi|46121267|ref|XP_385188.1|	42464.04	hypothetical protein FG05012.1 [Gibberella zeae PH-1]

112. Group probability: 0.9491. Peptides of the group

TPSLPIHAGPPSEAPK	54.4	54.7659	1597.846	1598.623	3	2	distinct	0	0.9491

The equivalent proteins include

gi|46122529|ref|XP_385818.1|	130972.27	hypothetical protein FG05642.1 [Gibberella zeae PH-1]

113. Group probability: 0.9487. Peptides of the group

HGTTEPIQTPK	56.43	55.1895	1207.62	1208.513	1	2	distinct	0	0.9487

The equivalent proteins include

gi|46115140|ref|XP_383588.1|	62090.91	hypothetical protein FG03412.1 [Gibberella zeae PH-1]

114. Group probability: 0.9461. Peptides of the group

LPHEFHYDDVSNR	54.94	54.7135	1627.738	1628.803	2	2	distinct	0	0.9461

The equivalent proteins include

gi|46121349|ref|XP_385229.1|	42425.96	hypothetical protein FG05053.1 [Gibberella zeae PH-1]

115. Group probability: 0.9438. Peptides of the group

YREPEPLPDLHVDR	53.94	54.2413	1734.869	1735.393	2	2	distinct	1	0.9438

The equivalent proteins include

gi|46136295|ref|XP_389839.1|	90255.59	hypothetical protein FG09663.1 [Gibberella zeae PH-1]

116. Group probability: 0.9423. Peptides of the group

KAEDDVNTPQKPESVK	52.86	54.2907	1783.895	1784.613	1	2	distinct	1	0.9423

The equivalent proteins include

gi|46108658|ref|XP_381387.1|	63388.97	hypothetical protein FG01211.1 [Gibberella zeae PH-1]

117. Group probability: 0.9409. Peptides of the group

QIPLADVAGLIAR	53.99	55.164	1335.787	1335.593	3	2	distinct	0	0.9409

The equivalent proteins include

gi|67989111|gb|EAM76886.1|	66528.46	Drug resistance transporter EmrB/QacA subfamily [Kineococcus radiotolerans SRS30216]

118. Group probability: 0.9375. Peptides of the group

KIEIPLPNEVGR	53.72	55.0016	1363.782	1364.873	3	2	distinct	1	0.9375

The equivalent proteins include

gi|88181908|gb|EAQ89376.1|	43828.23	hypothetical protein CHGG_05995 [Chaetomium globosum CBS 148.51]

S6. Protein assembly of peptide sequence matches made to tag-filtered R. solani tandem mass spectra. The NCBI NR database was searched. Protein List with probabilities. The columns are arranged as follows: peptide sequence, Mascot Ions score, Mascot Identity score, computed peptide mass, observed precursor mass, number of tandem mass spectra assigned to same peptide sequence, the charge states observed for the peptide, whether the peptide is shared between protein groups with different probabilities (number in parentheses is number of other groups peptides are shared with) or is distinct (considered a unique identifier for proteins grouped with the same probability), the number of missed tryptic cleavages in this sequence, and the probability for a particular peptide sequence.

1. Group probability: 1.0000. Peptides of the group

KNGHVVIK	45.74	55.6048	893.545	894.657	1	2	shared(2)	1	0.8593
VHIVALDIFTGK	74.93	55.2502	1311.755	1313.093	31	+1,+2	shared(2)	0	0.9997
KLEDLSPSTHNMDVPNVTR	105.09	53.2373	2152.058	2152.618	4	+2,+3	distinct	1	0.9997

The equivalent proteins include

gi|70990614|ref|XP_750156.1|	21492.39	eukaryotic initiation factor 5A [Aspergillus fumigatus Af293]

2. Group probability: 1.0000. Peptides of the group

IPIFSAAGLPHNEIAAQICR	101.96	53.2806	2177.141	2177.09	19	+2,+3	distinct	0	1

The equivalent proteins include

gi|522193|gb|AAA58661.1|	56792.03	vacuolar H+-ATPase 56,000 subunit
gi|54637522|gb|EAL26924.1|	54795.03	GA14484-PA [Drosophila pseudoobscura]
gi|88176297|gb|EAQ83765.1|	44000.26	hypothetical protein CHGG_10169 [Chaetomium globosum CBS 148.51]
gi|90304422|gb|EAS34053.1|	56351.84	hypothetical protein CIMG_05077 [Coccidioides immitis RS]
gi|13938355|gb|AAH07309.1|	55708.39	ATP6V1B2 protein [Homo sapiens]
gi|21040528|gb|AAH30640.1|	56734.98	ATPase, H+ transporting, lysosomal 56/58kD, V1 subunit B, isoform 2 [Homo sapiens]
gi|66531434|ref|XP_624112.1|	55394.35	PREDICTED: similar to H(+)-transporting ATPase [Apis mellifera]
gi|19913428|ref|NP_001684.2|	56807	vacuolar H+ATPase B2 [Homo sapiens]
gi|74198052|dbj|BAE35206.1|	56823.93	unnamed protein product [Mus musculus]
gi|74223066|dbj|BAE40674.1|	56874.93	unnamed protein product [Mus musculus]
gi|74185453|dbj|BAE30197.1|	56885.01	unnamed protein product [Mus musculus]
gi|74177659|dbj|BAE38930.1|	56725.93	unnamed protein product [Mus musculus]
gi|74213615|dbj|BAE35612.1|	56896.03	unnamed protein product [Mus musculus]
gi|74195936|dbj|BAE30526.1|	57843.44	unnamed protein product [Mus musculus]
gi|74220440|dbj|BAE31441.1|	57831.4	unnamed protein product [Mus musculus]
gi|55732316|emb|CAH92861.1|	56837.01	hypothetical protein [Pongo pygmaeus]
gi|91090031|ref|XP_967844.1|	55441.22	PREDICTED: similar to CG17369-PB, isoform B [Tribolium castaneum]
gi|30584483|gb|AAP36494.1|	56920.09	Homo sapiens ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2 [synthetic constr
gi|72017502|ref|XP_794151.1|	40908.66	PREDICTED: similar to CG17369-PB, isoform B [Strongylocentrotus purpuratus]
gi|72141200|ref|XP_791610.1|	50604.57	PREDICTED: similar to CG17369-PB, isoform B [Strongylocentrotus purpuratus]
gi|73970277|ref|XP_531858.2|	58254.41	PREDICTED: similar to ATPase, H+ transporting, lysosomal 56/58kD, V1 subunit B, isoform 1 [Canis fa
gi|73993818|ref|XP_543263.2|	56885	PREDICTED: similar to ATPase, H+ transporting, V1 subunit B, isoform 2 isoform 1 [Canis familiaris]
gi|73993820|ref|XP_859600.1|	56142.64	PREDICTED: similar to ATPase, H+ transporting, V1 subunit B, isoform 2 isoform 2 [Canis familiaris]
gi|104530891|gb|ABF72864.1|	22817.38	vacuolar H(+)-ATPase B subunit-like [Belgica antarctica]
gi|50806920|ref|XP_424534.1|	55044.93	PREDICTED: similar to adenosinetriphosphatase (EC 3.6.1.3) B chain - chicken [Gallus gallus]
gi|109085770|ref|XP_001100869.1|	59852.51	PREDICTED: vacuolar H+ATPase B2 [Macaca mulatta]
gi|109103298|ref|XP_001100824.1|	57195.99	PREDICTED: similar to ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1 isoform 3 [Macaca
gi|109103300|ref|XP_001100745.1|	58188.48	PREDICTED: similar to ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1 isoform 2 [Macaca

gi|109103302|ref|XP_001100657.1|	55445.09	PREDICTED: similar to ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1 isoform 1 [Macaca
gi|55596846|ref|XP_525782.1|	78337.08	PREDICTED: similar to ATPase, H+ transporting, lysosomal 56/58kD, V1 subunit B, isoform 1; ATPase,
gi|109473792|ref|XP_001073086.1|	57213.81	PREDICTED: similar to ATPase, H+ transporting, V1 subunit B, isoform 1 [Rattus norvegicus]
gi|55630310|ref|XP_519638.1|	59821.17	PREDICTED: ATPase, H+ transporting, lysosomal 56/58kD, V1 subunit B, isoform 2 [Pan troglodytes]
gi|47211598|emb|CAF94534.1|	61044.99	unnamed protein product [Tetraodon nigroviridis]
gi|47228596|emb|CAG05416.1|	66602.25	unnamed protein product [Tetraodon nigroviridis]
gi|28603810|ref|NP_788844.1|	56832.96	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B, isoform 2 [Bos taurus]
gi|28603772|ref|NP_788827.1|	57052.98	ATPase, H+ transporting, V1 subunit B, isoform 1 [Bos taurus]
gi|47564046|ref|NP_001001146.1|	56784.01	vacuolar H+-ATPase [Bos taurus]
gi|85109951|ref|XP_963165.1|	56887.22	VACUOLAR ATP SYNTHASE SUBUNIT B (V-ATPASE B SUBUNIT) (VACUOLAR PROTON PUMP B SUBUNIT) (V-ATPASE 57
gi|179563|gb|AAA35610.1|	45724.08	H+-ATPase B subunit
gi|190460|gb|AAA36498.1|	57140.96	proton pump 58 kDa subunit
gi|71001950|ref|XP_755656.1|	56497	V-type ATPase, subunit B [Aspergillus fumigatus Af293]
gi|4680480|gb|AAD27666.1|	55466.33	vacuolar ATPase B subunit [Aedes aegypti]
gi|1718088|sp|P49712|VATB_CHICK	50535.52	Vacuolar ATP synthase subunit B (V-ATPase B subunit) (Vacuolar proton pump B subunit)
gi|283083|pir||S25335	55877.45	H+-exporting ATPase (EC 3.6.3.6) chain B, vacuolar - fission yeast (Schizosaccharomyces pombe)
gi|18874534|gb|AAL79837.1|	56222.51	vacuolar-type H+ transporting ATPase subunit B1 [Danio rerio]
gi|37794|emb|CAA44721.1|	56823	vacuolar isoform 2 of H+ATPase Mr 56,000 subunit [Homo sapiens]
gi|24646341|ref|NP_731726.1|	54800.02	Vacuolar H+-ATPase 55kD B subunit CG17369-PA, isoform A [Drosophila melanogaster]
gi|19705578|ref|NP_031535.2|	56856.98	vacuolar H+ATPase B2 [Mus musculus]
gi|66817510|ref|XP_642608.1|	55012.95	vacuolar H+ ATPase B subunit [Dictyostelium discoideum]
gi|37748736|gb|AAH59455.1|	56292.59	ATPase, H+ transporting, lysosomal, V1 subunit B, member a [Danio rerio]
gi|9714|emb|CAA45706.1|	55155.22	H(+)-transporting ATPase [Manduca sexta]
gi|237459|gb|AAB20098.1|	55144.28	vacuolar (V-type) H(+)-ATPase B subunit [Heliothis virescens]
gi|62087192|dbj|BAD92043.1|	34924.76	ATPase, H+ transporting, lysosomal 56/58kD, V1 subunit B, isoform 2 variant [Homo sapiens]
gi|1184661|gb|AAC52411.1|	56948.04	vacuolar adenosine triphosphatase subunit B
gi|4093211|gb|AAD11943.1|	47388.05	H+-ATPase beta 1 subunit [Homo sapiens]
gi|19913426|ref|NP_001683.2|	57195.99	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B1 [Homo sapiens]
gi|23271177|gb|AAH35978.1|	28540.29	ATP6V1B1 protein [Homo sapiens]
gi|418175|sp|P15313|VATB1_HUMAN	57343.04	Vacuolar ATP synthase subunit B, kidney isoform (V-ATPase B1 subunit) (Vacuolar proton pump B isofo
gi|297129|emb|CAA41275.1|	56882.04	H+-ATPase non-catalytic subunit B [Bos taurus]
gi|5140|emb|CAA49339.1|	55863.43	vacuolar H+-ATPase subunit B [Schizosaccharomyces pombe]
gi|71006198|ref|XP_757765.1|	47497.92	hypothetical protein UM01618.1 [Ustilago maydis 521]

gi|30177356|gb|EAA08175.2|	54820.05	ENSANGP00000018716 [Anopheles gambiae str. PEST]
gi|57229095|gb|AAW45529.1|	56711.88	vacuolar ATP synthase, putative [Cryptococcus neoformans var. neoformans JEC21]
gi|67481369|ref|XP_656034.1|	55480	V-type ATPase, B subunit [Entamoeba histolytica HM-1:IMSS]
gi|3901366|gb|AAC78641.1|	56965.86	vacuolar-type H+ transporting ATPase B2 subunit [Anguilla anguilla]
gi|5881241|gb|AAD55091.1|	56212.44	vacuolar-type H+ transporting ATPase B1 subunit [Anguilla anguilla]
gi|6425061|gb|AAF08281.1|	54880.85	vacuolar ATP synthase subunit B K form; v-ATPase subunit B; v-type H+-ATPase subunit B [Carcinus ma
gi|4929105|gb|AAD33861.1|	56045.38	V-type ATPase B subunit [Oncorhynchus mykiss]
gi|8163560|gb|AAF73735.1|	55357.13	vacuolar H-ATPase B subunit osteoclast isozyme [Gallus gallus]
gi|24078511|gb|AAN45856.1|	57153.7	vacuolar proton translocating ATPase B1 isoform [Mus musculus]
gi|27372077|gb|AAN87887.1|	30129.14	H(+)-ATPase B subunit [Spodoptera littoralis]
gi|13435885|gb|AAH04789.1|	44877.65	Atp6v1b1 protein [Mus musculus]
gi|38566117|gb|AAH62202.1|	57066.66	ATPase, H+ transporting, V1 subunit B, isoform 1 [Mus musculus]
gi|18874536|gb|AAL79838.1|	56830.99	vacuolar-type H+ transporting ATPase subunit B2 [Danio rerio]
gi|2921502|gb|AAC04806.1|	55029.13	B subunit V-ATPase [Culex pipiens quinquefasciatus]
gi|62897863|dbj|BAD96871.1|	57208.03	ATPase, H+ transporting, lysosomal 56/58kD, V1 subunit B, isoform 1 variant [Homo sapiens]
gi|26351667|dbj|BAC39470.1|	57195.74	unnamed protein product [Mus musculus]
gi|67971164|dbj|BAE01924.1|	45840.06	unnamed protein product [Macaca fascicularis]
gi|37781636|gb|AAP37188.1|	55786.45	vacuolar proton-ATPase B-subunit [Artemia franciscana]
gi|28436920|gb|AAH46738.1|	56753.79	Vha55-prov protein [Xenopus laevis]
gi|38196215|gb|AAR13795.1|	25855.01	vacuolar ATPase [Anopheles gambiae]
gi|51705457|gb|AAU09450.1|	21720.73	vacuolar H+-ATPase B1 [Dasyatis sabina]
gi|2493131|sp|Q40078|VATB1_HORVU	54106.59	Vacuolar ATP synthase subunit B isoform 1 (V-ATPase B subunit 1) (Vacuolar proton pump B subunit 1)
gi|6721109|gb|AAF26763.1|	58357.72	T4O12.24 [Arabidopsis thaliana]
gi|22329688|ref|NP_173451.2|	36449.68	ATP binding / hydrogen-transporting ATP synthase, rotational mechanism / hydrogen-transporting ATPa
gi|15222929|ref|NP_177729.1|	54187.64	ATP binding / hydrogen-exporting ATPase, phosphorylative mechanism / hydrogen-transporting ATP synt
gi|6721533|dbj|BAA89597.1|	40412.44	vacuolar H+-ATPase B subunit [Citrus unshiu]
gi|14150751|gb|AAK54617.1|	54138.59	vacuolar ATPase B subunit [Oryza sativa]
gi|4519264|dbj|BAA75517.1|	54442.68	vacuolar H+-ATPase B subunit [Citrus unshiu]
gi|2493129|sp|Q43432|VATB1_GOSHI	54285.57	Vacuolar ATP synthase subunit B isoform 1 (V-ATPase B subunit 1) (Vacuolar proton pump B subunit 1)
gi|2493132|sp|Q40079|VATB2_HORVU	53806.42	Vacuolar ATP synthase subunit B isoform 2 (V-ATPase B subunit 2) (Vacuolar proton pump B subunit 2)
gi|166627|gb|AAC36485.1|	54818.94	nucleotide-binding subunit of vacuolar ATPase [Arabidopsis thaliana]
gi|15233891|ref|NP_195563.1|	54384.71	ATP binding / hydrogen-exporting ATPase, phosphorylative mechanism / hydrogen-transporting ATP synt
gi|6715512|gb|AAF26445.1|	53975.46	vacuolar H+-ATPase B subunit [Nicotiana tabacum]
gi|34787350|dbj|BAC87784.1|	14628.22	vacuolar ATPase B-subunit [Hordeum vulgare]

gi|26986106|emb|CAD27443.1|	54206.53	vacuolar ATPase subunit B [Mesembryanthemum crystallinum]
gi|23197884|gb|AAN15469.1|	54391.7	Unknown protein [Arabidopsis thaliana]
gi|42571561|ref|NP_973871.1|	54447.68	ATP binding / hydrogen-exporting ATPase, phosphorylative mechanism / hydrogen-transporting ATP synt
gi|34910488|ref|NP_916591.1|	54359.69	putative H+-transporting ATP synthase [Oryza sativa (japonica cultivar-group)]
gi|1336804|gb|AAB36110.1|	19163.54	vacuolar H(+)-ATPase subunit B [Mesembryanthemum crystallinum, leaf, Peptide Partial, 170 aa]
gi|19699258|gb|AAL90995.1|	43722.21	AT4g38510/F20M13_70 [Arabidopsis thaliana]

3. Group probability: 1.0000. Peptides of the group

AAVPSGASTGIHEAVELR	43.79	54.1341	1763.917	1764.793	1	2	distinct	0	0.8814
LGANAILGVSIAVAKAGAGEK	91.16	53.7937	1909.1	1910.591	7	+2,+3	distinct	1	0.9999

The equivalent proteins include

gi|71018545|ref|XP_759503.1|	47609.67	hypothetical protein UM03356.1 [Ustilago maydis 521]

4. Group probability: 1.0000. Peptides of the group

RVVDLIAHIAK	83.78	55.3717	1233.756	1235.109	10	+1,+2,+3	distinct	1	1
IVSWYDNEWGYSR	69.34	54.5751	1673.747	1674.283	3	2	shared(3)	0	0.9848

The equivalent proteins include

gi|13194756|gb|AAK15540.1|	36175.68	glyceraldehyde-3-phosphate dehydrogenase [Thanatephorus cucumeris]

5. Group probability: 1.0000. Peptides of the group

VVDLIAPYAR	45.27	55.9175	1115.634	1115.645	3	2	shared(2)	0	0.8565
TVLIQELINNVAK	83.96	54.8486	1453.85	1454.364	12	+1,+2	shared(2)	0	0.9996
DEEGQDVLLFIDNIFR	45.37	53.7927	1921.942	1922.397	1	2	shared(2)	0	0.6713
SLQDIIAILGMDELSEEDKLTVER	80.26	52.0652	2716.384	2716.944	13	+2,+3	shared(2)	1	1

The equivalent proteins include

gi|71018215|ref|XP_759338.1|	55695.02	hypothetical protein UM03191.1 [Ustilago maydis 521]

6. Group probability: 1.0000. Peptides of the group

VGAGAPVYLAAVLEYLAAEILELAGNAAR	86.24	51.6454	2884.57	2885.967	2	+2,+3	distinct	0	1

The equivalent proteins include

gi|90307147|gb|EAS36778.1|	14210.76	histone H2A [Coccidioides immitis RS]
gi|83773130|dbj|BAE63257.1|	14083.76	unnamed protein product [Aspergillus oryzae]
gi|3242067|emb|CAA07351.1|	14493.01	histone H2A [Botryotinia fuckeliana]
gi|27802990|emb|CAD60693.1|	14242.83	unnamed protein product [Podospora anserina]
gi|2632155|emb|CAA75581.1|	14140.79	histone H2A [Aspergillus niger]
gi|72076496|ref|XP_797553.1|	14408.99	PREDICTED: similar to CG31618-PA [Strongylocentrotus purpuratus]
gi|72080034|ref|XP_790517.1|	13345.52	PREDICTED: similar to CG31618-PA [Strongylocentrotus purpuratus]
gi|72156532|ref|XP_790098.1|	13371.55	PREDICTED: similar to CG31618-PA [Strongylocentrotus purpuratus]
gi|46140225|ref|XP_391803.1|	14151.76	H2A_NEUCR Histone H2A [Gibberella zeae PH-1]
gi|59799574|sp|P69140|H2A_PARAN	13402.54	Histone H2A, gonadal
gi|121980|sp|P09590|H2A3_STRPU	9784.51	Histone H2A-beta, sperm
gi|67526021|ref|XP_661072.1|	13970.72	histone H2A [Aspergillus nidulans FGSC A4]
gi|4959|emb|CAA28848.1|	13869.67	unnamed protein product [Schizosaccharomyces pombe]
gi|2239199|emb|CAB10117.1|	13767.63	hta2 [Schizosaccharomyces pombe]
gi|173404|gb|AAA35311.1|	13770.59	histone H2A-alpha
gi|85092526|ref|XP_959442.1|	14145.78	hypothetical protein [Neurospora crassa OR74A]
gi|71000767|ref|XP_755065.1|	30009.74	histone H2A [Aspergillus fumigatus Af293]
gi|10237|emb|CAA29851.1|	13442.58	histone L3 H2a [Strongylocentrotus purpuratus]
gi|39942994|ref|XP_361034.1|	14291.79	hypothetical protein MG03577.4 [Magnaporthe grisea 70-15]
gi|71005970|ref|XP_757651.1|	14190.76	histone H2A [Ustilago maydis 521]

7. Group probability: 0.9999. Peptides of the group

AVFPSIVGRPR	59.43	55.4844	1197.698	1198.218	11	2	distinct	0	0.9007

TTGIVLDSGDGVTHTVPIYEGFALPHAILR	56.63	51.3407	3148.656	3149.706	10	+2,+3	distinct	0	0.9987

The equivalent proteins include

gi|14194431|sp|Q9UVX4|ACT_COPCI	41928.08	Actin
gi|5053107|gb|AAD38853.1|	41876.11	actin 1 [Schizophyllum commune]
gi|48527433|gb|AAT45848.1|	41948.06	actine [Elaeis guineensis]

8. Group probability: 0.9999. Peptides of the group

VVDLIAPYAR	45.27	55.9175	1115.634	1115.645	3	2	shared(2)	0	0.8565
FTQAGSEVSALLGR	98.4	54.8356	1434.747	1434.927	1	2	shared(3)	0	0.9988
DEEGQDVLLFIDNIFR	45.37	53.7927	1921.942	1922.397	1	2	shared(2)	0	0.6713
SLQDIIAILGMDELSEEDKLTVER	80.26	52.0652	2716.384	2716.944	13	+2,+3	shared(2)	1	1

The equivalent proteins include

gi|57227707|gb|AAW44165.1|	58581.62	conserved hypothetical protein [Cryptococcus neoformans var. neoformans JEC21]

9. Group probability: 0.9998. Peptides of the group

TNHYGHTGYINTVSVSPDGSLAASGGK	66.39	52.0941	2689.273	2689.657	5	+2,+3	distinct	0	0.9998

The equivalent proteins include

gi|30024660|gb|AAP13580.1|	34877.29	guanine nucleotide binding protein beta subunit [Lentinula edodes]

10. Group probability: 0.9998. Peptides of the group

NALESYAYNLR	67.73	55.323	1312.641	1313.281	3	2	distinct	0	0.9809
ARFEELCQDLFR	46.01	54.575	1582.756	1583.431	4	2	distinct	1	0.8781
IINEPTAAAIAYGIDKK	91.3	54.7937	1786.983	1787.496	8	2	shared(5)	1	0.9914
KSEIFSTYSDNQPGVLIQVYEGER	56.7	51.9529	2758.345	2759.097	1	3	distinct	1	0.7441

The equivalent proteins include

gi|2495359|sp|Q01877|HSP71_PUCGR	70709.09	Heat shock protein HSS1

11. Group probability: 0.9995. Peptides of the group

YMVTVIDAPGHR	56.78	55.2973	1357.681	1358.102	1	2	shared(2)	0	0.7807
TLLDAIDAIEPPVRPSDKPLR	51.26	53.0911	2315.285	2315.851	7	3	shared(4)	0	0.9333
SVEMHHEQLVEGVPGDNVGFNVK (0000100000000000000000000)	73.04	52.5935	2520.207	2520.486	6	+2,+3	distinct	0	0.9964
TLLDAIDAIEPPVRPSDKPLRLPLQDVYK	68.09	51.1634	3271.818	3272.676	1	3	shared(4)	1	0.893

The equivalent proteins include

gi|58415160|gb|AAW73153.1|	46347.05	translation elongation factor 1-alpha [Boletellus projectellus]
gi|66731352|gb|AAY51889.1|	45557.63	translation elongation factor 1-alpha [Aureoboletus thibetanus]

12. Group probability: 0.9993. Peptides of the group

VIHDEFGIVEGLMTTVHATTATQK	99.04	52.4236	2597.316	2597.828	7	+2,+3	distinct	0	0.9993

The equivalent proteins include

gi|72256532|gb|AAZ67148.1|	36215.62	glyceraldehyde-3-phosphate dehydrogenase [Volvariella volvacea]

13. Group probability: 0.9990. Peptides of the group

KNGHVVIK	45.74	55.6048	893.545	894.657	1	2	shared(2)	1	0.8593
VHIVALDIFTGK	74.93	55.2502	1311.755	1313.093	31	+1,+2	shared(2)	0	0.9997
KLEDLSPSTHNMEVPNVSR	63.69	53.2373	2152.058	2152.618	2	2	distinct	1	0.8599

The equivalent proteins include

gi|4204352|gb|AAD10697.1|	17098.45	eIF-5A [Candida albicans]
gi|68478463|ref|XP_716733.1|	15130.6	hypothetical protein CaO19_3426 [Candida albicans SC5314]

14. Group probability: 0.9989. Peptides of the group

RADGIHLLNIGK	69.04	55.2898	1305.752	1306.807	2	+2,+3	distinct	1	0.9989

The equivalent proteins include

gi|71022107|ref|XP_761284.1|	30046.26	hypothetical protein UM05137.1 [Ustilago maydis 521]

15. Group probability: 0.9989. Peptides of the group

DSTLIMKILR	46.39	55.6349	1188.69	1189.928	1	2	shared(3)	1	0.8707
ICEDILDVLDK	49.24	55.3396	1331.664	1331.961	1	1	distinct	0	0.5848
QAFDDAIAELDTLSEESYK	46.9	53.257	2143.98	2144.621	1	2	shared(2)	0	0.9144
QAFDDAIAELDTLSEESYKDSTLIMQLLR (0000000000000000000000000100000)	88.07	50.839	3314.623	3315.961	8	3	distinct	1	0.9823

The equivalent proteins include

gi|61676645|gb|AAX51846.1|	28817.18	14-3-3 protein [Paxillus involutus]
gi|38569374|gb|AAR24348.1|	29737.84	14-3-3-like protein 2 [Paracoccidioides brasiliensis]

16. Group probability: 0.9988. Peptides of the group

SGPIGGIFRPDNFVFGQSGAGNNWAK	88.97	52.0567	2692.314	2692.51	31	+2,+3	distinct	0	0.9988

The equivalent proteins include

gi|50917473|ref|XP_469133.1|	50228.84	tubulin beta subunit [Oryza sativa (japonica cultivar-group)]
gi|63333595|gb|AAY40453.1|	43417.61	beta-tubulin [Piriformospora indica]

gi|71023491|ref|XP_761975.1|	50585.44	tubulin subunit beta-2 [Ustilago maydis 521]
gi|4683|emb|CAA44972.1|	50225.37	betatubulin [Schizophyllum commune]
gi|20429150|emb|CAD30548.1|	30703.18	putative beta-tubulin [Piriformospora indica]

17. Group probability: 0.9980. Peptides of the group

FTQAGSEVSALLGR	98.4	54.8356	1434.747	1434.927	1	2	shared(3)	0	0.9988
TVLIQELINNVAK	83.96	54.8486	1453.85	1454.364	12	+1,+2	shared(2)	0	0.9996

The equivalent proteins include

gi|85713719|ref|ZP_01044709.1|	50857.21	ATP synthase subunit B [Nitrobacter sp. Nb-311A]
gi|77739661|ref|ZP_00808151.1|	50924.26	ATP synthase F1, beta subunit [Rhodopseudomonas palustris BisA53]
gi|78694506|ref|ZP_00859019.1|	51284.63	ATP synthase F1, beta subunit [Bradyrhizobium sp. BTAi1]
gi|90418835|ref|ZP_01226746.1|	51918.48	ATP synthase, beta subunit [Aurantimonas sp. SI85-9A1]
gi|74419501|gb|ABA03700.1|	50905.27	ATP synthase F1, beta subunit [Nitrobacter winogradskyi Nb-255]
gi|68193203|gb|EAN07855.1|	55025.59	ATP synthase F1, beta subunit [Mesorhizobium sp. BNC1]
gi|91975039|ref|YP_567698.1|	50882.24	ATP synthase F1, beta subunit [Rhodopseudomonas palustris BisB5]
gi|90421698|ref|YP_530068.1|	50898.21	ATP synthase F1, beta subunit [Rhodopseudomonas palustris BisB18]
gi|83592562|ref|YP_426314.1|	50821.35	ATP synthase F1, beta subunit [Rhodospirillum rubrum ATCC 11170]
gi|27375551|ref|NP_767080.1|	50987.42	ATP synthase subunit B [Bradyrhizobium japonicum USDA 110]
gi|86747391|ref|YP_483887.1|	50883.2	ATP synthase F1, beta subunit [Rhodopseudomonas palustris HaA2]
gi|92116150|ref|YP_575879.1|	51019.32	ATP synthase F1, beta subunit [Nitrobacter hamburgensis X14]

18. Group probability: 0.9977. Peptides of the group

LNLLKLAPGGHIGR	69.9	54.9861	1457.883	1459.074	22	+2,+3	distinct	1	0.9977

The equivalent proteins include

gi|15293869|gb|AAK95127.1|	44099.05	ribosomal protein L4 [Ictalurus punctatus]
gi|4887131|gb|AAD32206.1|	44898.05	60S ribosomal protein L1 [Prunus armeniaca]
gi|84468330|dbj|BAE71248.1|	44765.09	putative 60S ribosomal protein L1 [Trifolium pratense]
gi|84468414|dbj|BAE71290.1|	44778.09	putative 60S ribosomal protein L1 [Trifolium pratense]
gi|92894088|gb|ABE92091.1|	44992.22	Ribosomal protein L4/L1e [Medicago truncatula]
gi|79313167|ref|NP_001030663.1|	44659.02	structural constituent of ribosome [Arabidopsis thaliana]
gi|15232723|ref|NP_187574.1|	44788.06	structural constituent of ribosome [Arabidopsis thaliana]
gi|77999245|gb|ABB16969.1|	45060.16	unknown [Solanum tuberosum]
gi|39589455|emb|CAE74484.1|	38657.2	Hypothetical protein CBG22235 [Caenorhabditis briggsae]
gi|66817212|ref|XP_642484.1|	40278.16	60S ribosomal protein L4 [Dictyostelium discoideum]
gi|17508669|ref|NP_491416.1|	38749.21	Ribosomal Protein, Large subunit family member (rpl-4) [Caenorhabditis elegans]
gi|15242558|ref|NP_195907.1|	44807.92	structural constituent of ribosome [Arabidopsis thaliana]
gi|26450328|dbj|BAC42280.1|	44810.87	putative 60S ribosomal protein [Arabidopsis thaliana]
gi|21593543|gb|AAM65510.1|	44744.06	60S ribosomal protein L4-B (L1) [Arabidopsis thaliana]
gi|28828239|gb|AAO50916.1|	40203.12	similar to Arabidopsis thaliana (Mouse-ear cress). AT3g09630/F11F8_22 [Dictyostelium discoideum]
gi|22137186|gb|AAM91438.1|	34448.7	AT5g02870/F9G14_180 [Arabidopsis thaliana]
gi|54609195|gb|AAV34813.1|	48195.24	ribosomal protein L4 [Bombyx mori]
gi|7630164|emb|CAB88236.1|	39942.81	rpl4 [Schizosaccharomyces pombe]
gi|3810827|emb|CAA21788.1|	39799.75	SPBP8B7.03c [Schizosaccharomyces pombe]
gi|71017629|ref|XP_759045.1|	36494.8	hypothetical protein UM02898.1 [Ustilago maydis 521]

gi|312177|emb|CAA51666.1|	38901.11	ribosomal protein L2 [Schizosaccharomyces pombe]

19. Group probability: 0.9972. Peptides of the group

LGANSLLDIVVFGR	55.16	54.9406	1472.835	1473.762	1	2	distinct	0	0.9487
AGLPNQDLEFVQFHPTGIYGAGCLITEGSR	49.42	50.8921	3246.577	3248.026	2	3	distinct	0	0.9456

The equivalent proteins include

gi|83773477|dbj|BAE63604.1|	71678.48	unnamed protein product [Aspergillus oryzae]
gi|46125967|ref|XP_387537.1|	197878.4	hypothetical protein FG07361.1 [Gibberella zeae PH-1]
gi|39975371|ref|XP_369076.1|	71125.99	hypothetical protein MG00168.4 [Magnaporthe grisea 70-15]

20. Group probability: 0.9967. Peptides of the group

VVIIGSGPAGHTAAIYLAR	102.66	54.0113	1865.052	1866.214	10	2	distinct	0	0.9967

The equivalent proteins include

gi|22536156|gb|AAN01228.1|	34767.71	thioredoxin reductase [Schizosaccharomyces pombe]
gi|71019359|ref|XP_759910.1|	37731.21	hypothetical protein UM03763.1 [Ustilago maydis 521]

21. Group probability: 0.9964. Peptides of the group

VVHEEFGIVEGLMTTVHATTATQK	97.68	52.4236	2597.316	2597.828	6	+2,+3	distinct	0	0.9964

The equivalent proteins include

gi|70673311|gb|AAZ06800.1|	22296.24	glyceraldehyde-3-phosphate dehydrogenase [Oxalis stricta]
gi|18072805|emb|CAC80377.1|	44689.85	glyceraldehyde-3-phosphate dehydrogenase [Capsicum annuum]
gi|50905605|ref|XP_464291.1|	43461.25	putative glyceraldehyde-3-phosphate dehydrogenase [Oryza sativa (japonica cultivar-group)]

22. Group probability: 0.9960. Peptides of the group

FVVTVIDAPGHR	73.42	55.1409	1309.714	1310.737	1	3	distinct	0	0.9863
TLLDAIDAIEPPVRPSDKPLR	51.26	53.0911	2315.285	2315.851	7	3	shared(4)	0	0.9333
TLLDAIDAIEPPVRPSDKPLRLPLQDVYK	68.09	51.1634	3271.818	3272.676	1	3	shared(4)	1	0.893

The equivalent proteins include

gi|86451396|gb|ABC96911.1|	27273.5	elongation factor 1 alpha [Tricholoma myomyces]

23. Group probability: 0.9954. Peptides of the group

IFGVTTLDVVR	60.95	55.6221	1218.697	1219.164	3	2	shared(4)	0	0.9301
RIFGVTTLDVVR	48.62	55.0941	1374.798	1375.47	3	2	shared(3)	1	0.8823
VAVLGAAGGIGQPLSLILK	64.17	54.1671	1776.087	1776.09	1	2	distinct	0	0.9808

The equivalent proteins include

gi|83765359|dbj|BAE55502.1|	35728.87	unnamed protein product [Aspergillus oryzae]
gi|70986899|ref|XP_748936.1|	35876.09	malate dehydrogenase, NAD-dependent [Aspergillus fumigatus Af293]

24. Group probability: 0.9951. Peptides of the group

TLLDAIDAIEPPTRPSDKPLR	52.73	52.8658	2317.264	2317.96	5	3	distinct	0	0.8545
TLLDAIDAIEPPTRPSDKPLRLPLQDVYK	72.4	51.1634	3273.797	3272.676	6	3	distinct	1	0.9664

The equivalent proteins include

gi|58758735|gb|AAW81766.1|	34557.89	translation elongation factor EF1-alpha [Echinodontium tinctorium]

25. Group probability: 0.9949. Peptides of the group

DSTLIMKILR	46.39	55.6349	1188.69	1189.928	1	2	shared(3)	1	0.8707
LAFDDAIAELDTLSEESYKDSTLIMQLLR	69.1	50.8344	3299.648	3298.591	13	3	distinct	1	0.99

The equivalent proteins include

gi|83772732|dbj|BAE62860.1|	29229.67	unnamed protein product [Aspergillus oryzae]
gi|70989229|ref|XP_749464.1|	29197.65	hypothetical protein Afu2g03290 [Aspergillus fumigatus Af293]
gi|67534609|ref|XP_662105.1|	29211.63	hypothetical protein AN4501.2 [Aspergillus nidulans FGSC A4]
gi|13430385|gb|AAK25817.1|	29210.68	ARTA [Emericella nidulans]
gi|38490697|gb|AAR21678.1|	28585.52	14-3-3-like protein [Aspergillus flavus]

26. Group probability: 0.9946. Peptides of the group

SCSDLLLITSDLYSLEHGK	78.43	53.2978	2150.056	2150.574	2	2	distinct	0	0.9946

The equivalent proteins include

gi|71023003|ref|XP_761731.1|	56490.35	hypothetical protein UM05584.1 [Ustilago maydis 521]

27. Group probability: 0.9940. Peptides of the group

AAYFVAFGPHGPR	80.18	55.3876	1388.699	1388.89	10	2	distinct	0	0.994

The equivalent proteins include

gi|57229832|gb|AAW46234.1|	18283.31	cytochrome c oxidase subunit V, putative [Cryptococcus neoformans var. neoformans JEC21]

28. Group probability: 0.9938. Peptides of the group

IVIAYEPVWAIGTGK	64.67	54.8192	1615.897	1616.858	4	2	distinct	0	0.944
ELFANPDVDGGLIGGAALK	44.27	54.2628	1855.968	1856.214	1	2	distinct	0	0.89

The equivalent proteins include

gi|60494608|emb|CAH09409.1|	26861.77	putative triosephosphate isomerase [Bacteroides fragilis NCTC 9343]

29. Group probability: 0.9930. Peptides of the group

TCHAHPTLSEAFK	56.06	54.6497	1497.703	1498.26	3	+2,+3	distinct	0	0.993

The equivalent proteins include

gi|83774859|dbj|BAE64982.1|	54922.59	unnamed protein product [Aspergillus oryzae]
gi|50551225|ref|XP_503086.1|	53449.59	hypothetical protein [Yarrowia lipolytica]
gi|44985105|gb|AAS53883.1|	53811.88	AFR512Wp [Ashbya gossypii ATCC 10895]
gi|71013524|ref|XP_758608.1|	53946.24	hypothetical protein UM02461.1 [Ustilago maydis 521]
gi|25956306|gb|AAN75720.1|	54817.68	LPD1 [Cryptococcus neoformans var. neoformans]
gi|68487498|ref|XP_712370.1|	53051.83	putative mitochondrial matrix dihydrolipoamide dehydrogenase Lpd1p [Candida albicans SC5314]
gi|25777812|gb|AAN75618.1|	54757.68	LPD1 [Cryptococcus neoformans var. neoformans]
gi|27803033|emb|CAD60736.1|	52628.44	unnamed protein product [Podospora anserina]
gi|50418005|ref|XP_457740.1|	53386.76	hypothetical protein DEHA0C01463g [Debaryomyces hansenii CBS767]
gi|54112143|gb|AAV28746.1|	54786.73	LPD1p [Cryptococcus gattii]
gi|54112177|gb|AAV28779.1|	54790.73	LPD1p [Cryptococcus gattii]
gi|25573183|gb|AAN75159.1|	54784.7	LPD1 [Cryptococcus neoformans var. grubii]
gi|25573215|gb|AAN75183.1|	54935.66	LPD1 [Cryptococcus neoformans var. grubii]

30. Group probability: 0.9927. Peptides of the group

VPTSDVSVVDLVAR	74.39	54.8778	1455.793	1455.426	9	2	distinct	0	0.9905
VIHDKFGIVEGLMSTIHATTATQK	65.08	52.4236	2596.368	2597.828	1	2	distinct	1	0.2344

The equivalent proteins include

gi|45421755|emb|CAF74786.1|	36369.82	glyceraldehyde 3-phosphate dehydrogenase [Armillariella tabescens]
gi|34765757|gb|AAQ82456.1|	22655.68	glyceraldehyde 3-phosphate dehydrogenase [Armillariella tabescens]

31. Group probability: 0.9921. Peptides of the group

LDLLKLAPGGHIGR	69.73	55.0646	1458.867	1459.422	9	+2,+3	distinct	1	0.9921

The equivalent proteins include

gi|94733357|emb|CAK04707.1|	20802.26	ribosomal protein L4 [Danio rerio]
gi|54261775|ref|NP_998272.1|	42810.18	ribosomal protein L4 [Danio rerio]

32. Group probability: 0.9919. Peptides of the group

ILLSNFFAQPEALAFGK	74.72	54.0123	1865.009	1865.901	2	2	distinct	0	0.9919

The equivalent proteins include

gi|40713647|emb|CAC87889.1|	61578.33	putative glucose-6-phosphate isomerase [Agaricus bisporus]
gi|50980810|gb|AAT91251.1|	61670.38	Glc-6-P isomerase [Paxillus involutus]
gi|50980838|gb|AAT91265.1|	55372.19	Glc-6-P isomerase [Paxillus filamentosus]
gi|50980944|gb|AAT91318.1|	55293.06	putative Glc-6-P isomerase [Paxillus involutus]
gi|50980946|gb|AAT91319.1|	55295.14	Glc-6-P isomerase [Paxillus involutus]
gi|50980948|gb|AAT91320.1|	55291.08	Glc-6-P isomerase [Paxillus involutus]
gi|50980950|gb|AAT91321.1|	55261.09	Glc-6-P isomerase [Paxillus involutus]
gi|50980952|gb|AAT91322.1|	55213.09	Glc-6-P isomerase [Paxillus involutus]

33. Group probability: 0.9918. Peptides of the group

VAVLGAGGGIGQPLSLLLK	98.85	54.1402	1762.072	1763.03	3	2	distinct	0	0.9918

The equivalent proteins include

gi|68466091|ref|XP_722820.1|	34821.09	putative mitochondrial malate dehydrogenase [Candida albicans SC5314]

34. Group probability: 0.9918. Peptides of the group

SPYIYPLYGLGELPQAFAR	73.61	53.2994	2154.115	2154.155	1	2	distinct	0	0.9918

The equivalent proteins include

gi|66828303|ref|XP_647506.1|	51313.16	hypothetical protein DDB0189731 [Dictyostelium discoideum]
gi|71004474|ref|XP_756903.1|	50895.96	hypothetical protein UM00756.1 [Ustilago maydis 521]
gi|50256793|gb|EAL19513.1|	50506.87	hypothetical protein CNBG4600 [Cryptococcus neoformans var. neoformans B-3501A]
gi|57227968|gb|AAW44425.1|	61710.53	RAB GDP-dissociation inhibitor, putative [Cryptococcus neoformans var. neoformans JEC21]

35. Group probability: 0.9903. Peptides of the group

GGPLGSLFRPDNFVFGQSGAGNNWAK	65.07	52.0742	2692.314	2693.392	13	+2,+3	distinct	0	0.9903

The equivalent proteins include

gi|57225882|gb|AAW42343.1|	50176.23	beta1-tubulin, putative [Cryptococcus neoformans var. neoformans JEC21]

36. Group probability: 0.9901. Peptides of the group

DSTLIMKILR	46.39	55.6349	1188.69	1189.928	1	2	shared(3)	1	0.8707
QAFDDAIAELDTLSEDSYKDSTLIMQLLR (00000000000000000000000000100000)	61.49	50.8432	3316.602	3316.312	8	3	distinct	1	0.9805

The equivalent proteins include

gi|34452065|gb|AAQ72489.1|	27960.81	14-3-3C1 protein [Oncorhynchus mykiss]

37. Group probability: 0.9890. Peptides of the group

ELLKPSSSVALHR	48.88	54.7734	1435.815	1436.395	4	+2,+3	distinct	0	0.989

The equivalent proteins include

gi|88175769|gb|EAQ83237.1|	47041.54	hypothetical protein CHGG_09641 [Chaetomium globosum CBS 148.51]
gi|85094546|ref|XP_959904.1|	46902.53	26S PROTEASE REGULATORY SUBUNIT 6B HOMOLOG [Neurospora crassa OR74A]
gi|50550483|ref|XP_502714.1|	45559.04	hypothetical protein [Yarrowia lipolytica]
gi|58264340|ref|XP_569326.1|	46919.54	endopeptidase [Cryptococcus neoformans var. neoformans JEC21]
gi|50426259|ref|XP_461726.1|	46677.37	hypothetical protein DEHA0G04763g [Debaryomyces hansenii CBS767]
gi|39973891|ref|XP_368336.1|	46961.43	hypothetical protein MG00908.4 [Magnaporthe grisea 70-15]

38. Group probability: 0.9885. Peptides of the group

IINEPTAAAIAYGIDKK	91.3	54.7937	1786.983	1787.496	8	2	shared(5)	1	0.9914
LDKSVIHDIVLVGGSTR	58.37	54.2529	1808.016	1809.38	2	2	distinct	1	0.9657

The equivalent proteins include

gi|77403899|gb|ABA81828.1|	71372.48	LP19893p [Drosophila melanogaster]
gi|157665|gb|AAA28627.1|	71300.38	heat shock cognate 4
gi|19527633|gb|AAL89931.1|	71345.43	RH04426p [Drosophila melanogaster]

39. Group probability: 0.9863. Peptides of the group

QAFDDAIAELDTLSEESYK	46.9	53.257	2143.98	2144.621	1	2	shared(2)	0	0.9144
QAFDDAIAELDTLSEESYKDSTLIMQLPR (00000000000000000000000000100000)	86.85	50.839	3314.586	3315.961	5	3	distinct	1	0.954

The equivalent proteins include

gi|62420901|gb|AAX82172.1|	28911.23	14-3-3 1 protein [Phanerochaete chrysosporium]

40. Group probability: 0.9861. Peptides of the group

TLLDAIDAIEPPVRPSDKPLR	51.26	53.0911	2315.285	2315.851	7	3	shared(4)	0	0.9333
LVPSKPMCVETYNEYPPLGR	53.21	53.0198	2349.15	2349.754	3	2	distinct	0	0.9527
TLLDAIDAIEPPVRPSDKPLRLPLQDVYK	68.09	51.1634	3271.818	3272.676	1	3	shared(4)	1	0.893

The equivalent proteins include

gi|66969459|gb|AAY59903.1|	35860.57	translation elongation factor 1-alpha [Bourdotia sp. GEL5065]
gi|66473221|gb|AAY46252.1|	36073.67	translation elongation factor 1-alpha [Anthracophyllum archeri]

41. Group probability: 0.9857. Peptides of the group

YMVTVIDAPGHR	56.78	55.2973	1357.681	1358.102	1	2	shared(2)	0	0.7807
TLLDAIDAIEPPSRPTDKPLR	52.95	52.9367	2317.264	2316.747	4	3	distinct	0	0.754
TLLDAIDAIEPPSRPTDKPLRLPLQDVYK	59.43	51.1634	3273.797	3272.676	5	3	distinct	1	0.8766

The equivalent proteins include

gi|71004810|ref|XP_757071.1|	50311.08	elongation factor 1-alpha [Ustilago maydis 521]

42. Group probability: 0.9854. Peptides of the group

DYGEESEGLNVLLEYFK	67.94	53.6221	2003.936	2003.38	4	2	distinct	0	0.9854

The equivalent proteins include

gi|71005598|ref|XP_757465.1|	16438.33	hypothetical protein UM01318.1 [Ustilago maydis 521]

43. Group probability: 0.9848. Peptides of the group

TIYLPTPSWGNHTPIFR	67.51	53.7123	1999.032	1999.389	6	2	distinct	0	0.9848

The equivalent proteins include

gi|71004152|ref|XP_756742.1|	47738.55	hypothetical protein UM00595.1 [Ustilago maydis 521]

44. Group probability: 0.9848. Peptides of the group

FMVTVIDAPGHR (00100000000000)	73.24	55.2973	1357.681	1358.102	1	2	distinct	0	0.9482
TLLDAIDAIEPPVRPSDKPLR	51.26	53.0911	2315.285	2315.851	7	3	shared(4)	0	0.9333
TLLDAIDAIEPPVRPSDKPLRLPLQDVYK	68.09	51.1634	3271.818	3272.676	1	3	shared(4)	1	0.893

The equivalent proteins include

gi|67005747|gb|AAY62530.1|	41737.8	translation elongation factor 1-alpha [Ganoderma tsugae]
gi|67005749|gb|AAY62531.1|	44414.96	translation elongation factor 1-alpha [Albatrellus higanensis]
gi|58618691|gb|AAW80840.1|	45785.78	translation elongation factor EF1-alpha [Hygrophoropsis aurantiaca]
gi|58618693|gb|AAW80841.1|	46058.88	translation elongation factor EF1-alpha [Strobilomyces floccopus]
gi|58758727|gb|AAW81762.1|	44499.15	translation elongation factor EF1-alpha [Grifola frondosa]
gi|66775566|gb|AAY56358.1|	44443.15	translation elongation factor 1-alpha [Sparassis crispa]

45. Group probability: 0.9844. Peptides of the group

EEVKEGLKPK	48.63	55.5335	1155.65	1155.849	2	+1,+2	distinct	1	0.9844

The equivalent proteins include

gi|88713604|ref|ZP_01107686.1|	26008.12	hypothetical protein FB2170_13061 [Flavobacteriales bacterium HTCC2170]

46. Group probability: 0.9839. Peptides of the group

SNYNFEEPFLWLAR	50.91	54.2915	1784.852	1785.162	6	+2,+3	distinct	0	0.9839

The equivalent proteins include

gi|61366565|gb|AAX42876.1|	24692.71	RAN member RAS oncogene family [synthetic construct]
gi|74229915|gb|ABA00476.1|	24366.34	GTP-binding protein [Trichophyton rubrum]

47. Group probability: 0.9835. Peptides of the group

IVSWYDNEWGYSR	69.34	54.5751	1673.747	1674.283	3	2	shared(3)	0	0.9848
VIHDKFGIVEGLMTTVHATTATQK	77.73	52.4236	2596.368	2597.828	2	+2,+3	distinct	1	0.9284

The equivalent proteins include

gi|13194752|gb|AAK15538.1|	37280.18	glyceraldehyde-3-phosphate dehydrogenase [Thanatephorus cucumeris]

48. Group probability: 0.9831. Peptides of the group

THNLEPYFESFINNLR	69.1	53.7434	1992.969	1994.315	3	3	distinct	0	0.9831

The equivalent proteins include

gi|109096823|ref|XP_001098292.1|	65340.78	PREDICTED: similar to keratin 1 isoform 7 [Macaca mulatta]
gi|109096825|ref|XP_001098082.1|	64503.44	PREDICTED: similar to keratin 1 isoform 5 [Macaca mulatta]
gi|109096827|ref|XP_001097902.1|	63150.85	PREDICTED: similar to keratin 1 isoform 3 [Macaca mulatta]
gi|109096829|ref|XP_001097988.1|	62009.39	PREDICTED: similar to keratin 1 isoform 4 [Macaca mulatta]
gi|109096831|ref|XP_001098182.1|	63139.76	PREDICTED: similar to keratin 1 isoform 6 [Macaca mulatta]
gi|109096833|ref|XP_001097800.1|	61737.33	PREDICTED: similar to keratin 1 isoform 2 [Macaca mulatta]
gi|109096835|ref|XP_001097706.1|	59017.2	PREDICTED: similar to keratin 1 isoform 1 [Macaca mulatta]
gi|55638143|ref|XP_522394.1|	98632.68	PREDICTED: similar to keratin 1B [Pan troglodytes]
gi|7428712|pir||KRHU2	65568.53	keratin 1, type II, cytoskeletal - human
gi|7331218|gb|AAF60327.1|	66149.05	keratin 1 [Homo sapiens]
gi|11935049|gb|AAG41947.1|	66198.07	keratin 1 [Homo sapiens]

49. Group probability: 0.9817. Peptides of the group

SGPLGNLFRPDNFVFGQSGAGNNWAK	63.72	51.9749	2749.336	2750.256	1	3	distinct	0	0.9817

The equivalent proteins include

gi|63333597|gb|AAY40454.1|	43345.56	beta-tubulin [Polyporus lepideus]
gi|63333599|gb|AAY40455.1|	43474.59	beta-tubulin [Trametes versicolor]
gi|63333601|gb|AAY40456.1|	43356.54	beta-tubulin [Trametes versicolor]
gi|60477737|gb|AAM92170.2|	43375.54	beta tubulin 3 [Trametes versicolor]
gi|38230100|emb|CAD88276.1|	13977.85	putative beta-tubulin [Funalia trogii]

50. Group probability: 0.9807. Peptides of the group

SNYNFEKPFLWLAR	67.47	54.2778	1783.905	1785.269	9	+2,+3	distinct	0	0.9807

The equivalent proteins include

gi|5107637|pdb|1QBK|C	24518.56	Chain C, Structure Of The Karyopherin Beta2-Ran Gppnhp Nuclear Transport Complex
gi|5107684|pdb|1RRP|C	23307.18	Chain C, Structure Of The Ran-Gppnhp-Ranbd1 Complex
gi|5542357|pdb|1QG4|B	24594.68	Chain B, Canine Gdp-Ran F72y Mutant
gi|5542355|pdb|1QG2|A	24551.62	Chain A, Canine Gdp-Ran R76e Mutant
gi|4139787|pdb|3RAN|D	24563.71	Chain D, Canine Gdp-Ran Q69l Mutant
gi|108874624|gb|EAT38849.1|	24681.58	ran [Aedes aegypti]
gi|54643004|gb|EAL31748.1|	24934.75	GA12719-PA [Drosophila pseudoobscura]
gi|58177141|pdb|1WA5|A	20336.68	Chain A, Crystal Structure Of The Exportin Cse1p Complexed With Its Cargo (Kap60p) And Rangtp
gi|67464643|pdb|2BKU|C	20461.76	Chain C, Kap95p:rangtp Complex
gi|90298007|gb|EAS27638.1|	24843.75	GTP-binding nuclear protein GSP1/Ran [Coccidioides immitis RS]
gi|83306033|emb|CAE00803.1|	22609.62	putative small G-protein [Sordaria macrospora]
gi|89266827|emb|CAJ83821.1|	24576.68	RAN, member RAS oncogene family [Xenopus tropicalis]
gi|51338726|sp|P52301|RAN_XENLA	24553.66	GTP-binding nuclear protein Ran (GTPase Ran) (Ras-like protein TC4)
gi|8698689|gb|AAF78478.1|	24446.52	small G-protein Gsp1p [Candida albicans]
gi|48097366|ref|XP_393761.1|	24856.75	PREDICTED: similar to GTP-binding nuclear protein RAN1 [Apis mellifera]
gi|44986324|gb|AAS54784.1|	24523.54	AGR294Cp [Ashbya gossypii ATCC 10895]
gi|4092054|gb|AAC99400.1|	24667.68	GTP binding protein [Homo sapiens]
gi|29893187|gb|AAP03080.1|	24617.63	GTP-binding protein [Carassius auratus]
gi|87248587|gb|ABD36346.1|	24549.51	GTP-binding nuclear protein Ran [Bombyx mori]
gi|12846283|dbj|BAB27105.1|	24520.6	unnamed protein product [Mus musculus]
gi|74208259|dbj|BAE26338.1|	24506.66	unnamed protein product [Mus musculus]
gi|83767492|dbj|BAE57631.1|	24106.49	unnamed protein product [Aspergillus oryzae]
gi|24641219|ref|NP_727499.1|	24920.73	ran CG1404-PB, isoform B [Drosophila melanogaster]
gi|3850120|emb|CAA10040.1|	24528.65	Ran protein [Salmo salar]
gi|68349615|gb|AAY96645.1|	24772.77	Ras-related nuclear protein [Marsupenaeus japonicus]
gi|91091116|ref|XP_975893.1|	24928.73	PREDICTED: similar to CG1404-PA, isoform A isoform 2 [Tribolium castaneum]
gi|72006189|ref|XP_786730.1|	25802.1	PREDICTED: similar to RAN, member RAS oncogene family [Strongylocentrotus purpuratus]
gi|50555191|ref|XP_505004.1|	24382.25	hypothetical protein [Yarrowia lipolytica]
gi|50289695|ref|XP_447279.1|	24499.51	hypothetical protein CAGL0I00594g [Candida glabrata CBS138]
gi|46108434|ref|XP_381275.1|	24637.59	RAN_BRUMA GTP-binding nuclear protein RAN/TC4 [Gibberella zeae PH-1]
gi|27735390|gb|AAH41293.1|	24496.64	Ran-1-prov protein [Xenopus laevis]
gi|82884526|ref|XP_899694.1|	24856.81	PREDICTED: similar to RAN, member RAS oncogene family isoform 1 [Mus musculus]
gi|94368195|ref|XP_999944.1|	24884.85	PREDICTED: similar to RAN, member RAS oncogene family [Mus musculus]
gi|74004288|ref|XP_854554.1|	25894.19	PREDICTED: similar to RAN, member RAS oncogene family [Canis familiaris]
gi|82619320|gb|ABB85359.1|	25226.91	Ran [Branchiostoma belcheri tsingtaunese]
gi|32425497|gb|AAH04272.2|	25378.04	RAN protein [Homo sapiens]
gi|37046693|gb|AAH58047.1|	24615.65	Ras-related nuclear protein [Danio rerio]
gi|48734884|gb|AAH72000.1|	24608.69	Ras-related nuclear protein [Homo sapiens]
gi|49257810|gb|AAH74619.1|	24610.66	MGC69330 protein [Xenopus tropicalis]
gi|54697198|gb|AAV38971.1|	24691.77	RAN, member RAS oncogene family [synthetic construct]
gi|55626142|ref|XP_518329.1|	18396.37	PREDICTED: similar to RAN, member RAS oncogene family [Pan troglodytes]
gi|55639371|ref|XP_509522.1|	26677.75	PREDICTED: similar to RAN protein [Pan troglodytes]
gi|55731873|emb|CAH92646.1|	14835.63	hypothetical protein [Pongo pygmaeus]

gi|3924787|emb|CAB07240.1|	24409.47	Hypothetical protein K01G5.4 [Caenorhabditis elegans]
gi|23508374|ref|NP_701043.1|	24973.81	GTP-binding nuclear protein ran/tc4 [Plasmodium falciparum 3D7]
gi|47215705|emb|CAG04789.1|	23785.27	unnamed protein product [Tetraodon nigroviridis]
gi|70953024|ref|XP_745640.1|	24984.83	GTP-binding nuclear protein ran/tc4 [Plasmodium chabaudi chabaudi]
gi|6323324|ref|NP_013396.1|	24965.71	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, R
gi|6324759|ref|NP_014828.1|	25145.78	GTP binding protein (mammalian Ranp homolog) involved in the maintenance of nuclear organization, R
gi|45383966|ref|NP_990589.1|	24582.71	RAN, member RAS oncogene family [Gallus gallus]
gi|50979248|ref|NP_001003375.1|	24578.68	ras-related nuclear protein [Canis familiaris]
gi|82540395|ref|XP_724519.1|	28532.52	GTP-binding nuclear protein RAN/TC4 [Plasmodium yoelii yoelii str. 17XNL]
gi|85114464|ref|XP_964704.1|	24431.36	GTP-BINDING NUCLEAR PROTEIN SPI1 [Neurospora crassa OR74A]
gi|70992715|ref|XP_751206.1|	24233.43	GTP-binding nuclear protein Ran [Aspergillus fumigatus Af293]
gi|6730007|pdb|1BYU|B	24604.7	Chain B, Canine Gdp-Ran
gi|1518129|gb|AAB07465.1|	14891.65	RAN/Tc4
gi|58568774|gb|AAW79002.1|	9367.7	GekBS156P [Gekko japonicus]
gi|71005690|ref|XP_757511.1|	24484.51	GTP-binding nuclear protein RAN [Ustilago maydis 521]
gi|55245201|gb|EAA04041.3|	26820.9	ENSANGP00000021540 [Anopheles gambiae str. PEST]
gi|4490658|emb|CAB38683.1|	24767.64	spi1 [Schizosaccharomyces pombe]
gi|57227234|gb|AAW43693.1|	24110.19	RAN small monomeric GTPase, putative [Cryptococcus neoformans var. neoformans JEC21]
gi|68489336|ref|XP_711509.1|	24469.53	RAN-like GTP binding protein [Candida albicans SC5314]
gi|55245200|gb|EAL41718.1|	24683.58	ENSANGP00000028287 [Anopheles gambiae str. PEST]
gi|67538624|ref|XP_663086.1|	25089.85	GTP-binding nuclear protein RAN/TC4 [Aspergillus nidulans FGSC A4]
gi|67624139|ref|XP_668352.1|	24208.59	GTP-binding nuclear protein ran/tc4 [Cryptosporidium hominis TU502]
gi|56236508|gb|AAV84610.1|	7186.56	RAN/TC4-like monomeric G-protein [Setosphaeria turcica]
gi|38141524|emb|CAE53394.1|	13286.98	Ran Protein [Platichthys flesus]
gi|40641623|emb|CAE55862.1|	24882.69	GTP-binding nuclear protein RAN1 [Chironomus tentans]
gi|50302525|ref|XP_451197.1|	24511.5	unnamed protein product [Kluyveromyces lactis]
gi|50423731|ref|XP_460450.1|	24497.54	hypothetical protein DEHA0F02244g [Debaryomyces hansenii CBS767]
gi|436408|emb|CAA52140.1|	24875.77	ras-related nuclear protein [Plasmodium falciparum]
gi|22023144|gb|AAM88935.1|	25007.8	ras-like nuclear protein [Plasmodium chabaudi]
gi|38018012|gb|AAR08135.1|	24332.47	small GTPase RanA [Emericella nidulans]

51. Group probability: 0.9799. Peptides of the group

NMSVIAHVDHGK	66.73	55.3411	1306.645	1307.459	1	2	distinct	0	0.9799

The equivalent proteins include

gi|39590460|emb|CAE66200.1|	95725.85	Hypothetical protein CBG11440 [Caenorhabditis briggsae]
gi|737058|prf||1921319A	18776.68	elongation factor 2
gi|108879886|gb|EAT44111.1|	95301.25	eukaryotic translation elongation factor [Aedes aegypti]
gi|54644076|gb|EAL32818.1|	192989.47	GA15316-PA [Drosophila pseudoobscura]
gi|67464018|pdb|1ZM9|E	93660.34	Chain E, Structure Of Eef2-Eta In Complex With Pj34
gi|89285379|gb|EAR83394.1|	92833.8	Elongation factor G, domain IV family protein [Tetrahymena thermophila SB210]
gi|89292737|gb|EAR90725.1|	94988.54	Elongation factor G, domain IV family protein [Tetrahymena thermophila SB210]

gi|89301992|gb|EAR99980.1|	94965.56	Elongation factor G, domain IV family protein [Tetrahymena thermophila SB210]
gi|89301994|gb|EAR99982.1|	95961.02	Elongation factor G, domain IV family protein [Tetrahymena thermophila SB210]
gi|89302115|gb|EAS00103.1|	107079.21	Elongation factor G, domain IV family protein [Tetrahymena thermophila SB210]
gi|90304379|gb|EAS34010.1|	93987.84	elongation factor 2 [Coccidioides immitis RS]
gi|706975|gb|AAC46607.1|	93614.8	elongation factor-2 [Cryptosporidium parvum]
gi|8927038|gb|AAF81924.1|	90436.75	elongation factor 2 [Candida albicans]
gi|28564217|gb|AAO32487.1|	93626.11	EFT [Saccharomyces castellii]
gi|28564956|gb|AAO32562.1|	93816.32	EFT2 [Saccharomyces kluyveri]
gi|66508439|ref|XP_392691.2|	95547.34	PREDICTED: similar to translation elongation factor 2 [Apis mellifera]
gi|86161656|gb|ABC86958.1|	95060.91	elongation factor 2 [Leishmania braziliensis]
gi|74353984|gb|AAI03386.1|	96276.32	Unknown (protein for MGC:127305) [Bos taurus]
gi|44984670|gb|AAS53513.1|	93943.5	AFR142Cp [Ashbya gossypii ATCC 10895]
gi|84105365|gb|ABC54654.1|	94686.64	translation elongation factor 2 [Naegleria gruberi]
gi|68361350|ref|XP_697966.1|	96849.6	PREDICTED: wu:fj53d02 [Danio rerio]
gi|74189143|dbj|BAE39328.1|	96123.17	unnamed protein product [Mus musculus]
gi|74197201|dbj|BAE35145.1|	96188.3	unnamed protein product [Mus musculus]
gi|74191026|dbj|BAE39354.1|	96164.24	unnamed protein product [Mus musculus]
gi|74204678|dbj|BAE35408.1|	96138.21	unnamed protein product [Mus musculus]
gi|74151550|dbj|BAE38881.1|	96192.25	unnamed protein product [Mus musculus]
gi|74213791|dbj|BAE29333.1|	96119.24	unnamed protein product [Mus musculus]
gi|74197032|dbj|BAE35069.1|	96194.22	unnamed protein product [Mus musculus]
gi|74201313|dbj|BAE26111.1|	96235.28	unnamed protein product [Mus musculus]
gi|74181334|dbj|BAE29945.1|	96231.21	unnamed protein product [Mus musculus]
gi|74140876|dbj|BAE22047.1|	96221.34	unnamed protein product [Mus musculus]
gi|83769606|dbj|BAE59741.1|	94612.81	unnamed protein product [Aspergillus oryzae]
gi|18447458|gb|AAL68292.1|	95424.48	RE38659p [Drosophila melanogaster]
gi|4585664|emb|CAA70857.2|	93865.45	translation elongation factor 2 [Candida albicans]
gi|45382453|ref|NP_990699.1|	96343.28	eukaryotic translation elongation factor 2 [Gallus gallus]
gi|91087369|ref|XP_975635.1|	95712.64	PREDICTED: similar to Elongation factor 2 (EF-2) [Tribolium castaneum]
gi|72081276|ref|XP_797399.1|	100783.26	PREDICTED: similar to eukaryotic translation elongation factor 2, like [Strongylocentrotus purpurat
gi|92887256|gb|ABE88774.1|	95050.75	Translation factor; Elongation factor G, III and V [Medicago truncatula]
gi|92887257|gb|ABE88775.1|	94978.18	Elongation factor Tu, domain 2; Translation elongation factor G [Medicago truncatula]
gi|71032815|ref|XP_766049.1|	93186.9	elongation factor 2 [Theileria parva strain Muguga]
gi|72256098|gb|AAR01295.2|	82298	elongation factor-2 [Metajapyx subterraneus]
gi|71415412|ref|XP_809774.1|	22678.57	elongation factor 2 [Trypanosoma cruzi strain CL Brener]
gi|71401612|ref|XP_803516.1|	19215.83	elongation factor 2 [Trypanosoma cruzi strain CL Brener]
gi|71415388|ref|XP_809762.1|	95099.12	elongation factor 2 [Trypanosoma cruzi strain CL Brener]
gi|71413833|ref|XP_809041.1|	95098.14	elongation factor 2 [Trypanosoma cruzi strain CL Brener]
gi|50284959|ref|XP_444908.1|	93783.19	hypothetical protein CAGL0A03234g [Candida glabrata CBS138]
gi|46136117|ref|XP_389750.1|	91848.9	EF2_NEUCR Elongation factor 2 (EF-2) (Colonial temperature-sensitive 3) [Gibberella zeae PH-1]
gi|71747298|ref|XP_822704.1|	95300.11	elongation factor 2 [Trypanosoma brucei TREU927]
gi|849206|gb|AAB64821.1|	57232.98	Etf1p: Elongation factor 2 (Swiss Prot. accession number P32324). Note that the entire gene is not

gi|73987435|ref|XP_533949.2|	78574.99	PREDICTED: similar to Elongation factor 2 (EF-2) [Canis familiaris]
gi|28629446|gb|AAO39212.1|	93866.57	elongation factor 2 [Pichia pastoris]
gi|50426399|ref|XP_461796.1|	93705.37	hypothetical protein DEHA0G06380g [Debaryomyces hansenii CBS767]
gi|95103088|gb|ABF51485.1|	95749.55	translation elongation factor 2 [Bombyx mori]
gi|103058022|gb|ABF71565.1|	98231.85	translation elongation factor 2 [Bombyx mori]
gi|50308159|ref|XP_454080.1|	93814.55	unnamed protein product [Kluyveromyces lactis]
gi|109122950|ref|XP_001118006.1|	157373.37	PREDICTED: eukaryotic translation elongation factor 2 [Macaca mulatta]
gi|39580704|emb|CAE70384.1|	95542.73	Hypothetical protein CBG16945 [Caenorhabditis briggsae]
gi|47180786|emb|CAG06203.1|	8000.15	unnamed protein product [Tetraodon nigroviridis]
gi|6324707|ref|NP_014776.1|	93686.4	Elongation factor 2 (EF-2), also encoded by EFT2; catalyzes ribosomal translocation during protein
gi|68060335|ref|XP_672146.1|	7209.73	hypothetical protein PB301482.00.0 [Plasmodium berghei strain ANKA]
gi|82595325|ref|XP_725803.1|	94455.66	elongation factor 2 [Plasmodium yoelii yoelii str. 17XNL]
gi|2641946|dbj|BAA23591.1|	93713.74	elongation factor 2 [Schizosaccharomyces pombe]
gi|119167|sp|P28996|EF2_CHLKE	94853.06	Elongation factor 2 (EF-2)
gi|119169|sp|P15112|EF2_DICDI	92497.58	Elongation factor 2 (EF-2)
gi|70943098|ref|XP_741636.1|	42223.35	elongation factor 2 [Plasmodium chabaudi chabaudi]
gi|8393296|ref|NP_058941.1|	96192.24	eukaryotic translation elongation factor 2 [Rattus norvegicus]
gi|85106981|ref|XP_962286.1|	93556.39	ELONGATION FACTOR 2 (EF-2) [Neurospora crassa OR74A]
gi|71076808|ref|XP_770921.1|	100588.78	elongation factor 2 [Giardia lamblia ATCC 50803]
gi|71002010|ref|XP_755686.1|	93595.53	translation elongation factor EF-2 subunit [Aspergillus fumigatus Af293]
gi|119168|sp|P09445|EF2_CRIGR	96304.27	Elongation factor 2 (EF-2)
gi|119173|sp|P05086|EF2_MESAU	96232.27	Elongation factor 2 (EF-2)
gi|66805999|ref|XP_636721.1|	93511.92	elongation factor 2 [Dictyostelium discoideum AX4]
gi|66806657|ref|XP_637051.1|	95477.41	elongation factor 2 [Dictyostelium discoideum]
gi|600159|gb|AAB60497.1|	96218.25	elongation factor 2
gi|56474887|gb|AAN04123.2|	94963.71	elongation factor-related protein 1 [Tetrahymena thermophila]
gi|2369714|emb|CAB09900.1|	94707.65	elongation factor 2 [Beta vulgaris subsp. vulgaris]
gi|3876400|emb|CAB02985.1|	95476.66	Hypothetical protein F25H5.4 [Caenorhabditis elegans]
gi|13938072|gb|AAH07152.1|	96222.25	Eukaryotic translation elongation factor 2 [Mus musculus]
gi|50542892|ref|XP_499612.1|	94027.3	hypothetical protein [Yarrowia lipolytica]
gi|50545473|ref|XP_500274.1|	94064.97	hypothetical protein [Yarrowia lipolytica]
gi|3642665|gb|AAC36522.1|	28866.59	elongation factor 2 [Mus musculus]
gi|4503483|ref|NP_001952.1|	96246.31	eukaryotic translation elongation factor 2 [Homo sapiens]
gi|50921395|ref|XP_471058.1|	94938.94	OSJNBa0020P07.3 [Oryza sativa (japonica cultivar-group)]
gi|24585713|ref|NP_724358.1|	94049.78	Elongation factor 2b CG2238-PC, isoform C [Drosophila melanogaster]
gi|156279|gb|AAD03339.1|	95326.51	elongation factor [Caenorhabditis elegans]
gi|29539334|dbj|BAC67668.1|	94958.54	elongation factor-2 [Cyanidioschyzon merolae]
gi|6066758|emb|CAB58373.1|	93798.81	SPCP31B10.07 [Schizosaccharomyces pombe]
gi|66360030|ref|XP_627193.1|	94127.1	Eft2p GTpase; translation elongation factor 2 (EF-2) [Cryptosporidium parvum Iowa II]
gi|30179014|gb|EAA03632.2|	94070.64	ENSANGP00000018623 [Anopheles gambiae str. PEST]

<table>
<tr><td>gi|55246389|gb|EAL42047.1|</td><td>22679.5</td><td>ENSANGP00000029149 [Anopheles gambiae str. PEST]</td></tr>
<tr><td>gi|9963972|gb|AAG09782.1|</td><td>93360.49</td><td>translation elongation factor 2 [Filobasidiella neoformans]</td></tr>
<tr><td>gi|68481380|ref|XP_715329.1|</td><td>92506.72</td><td>translation elongation factor EF-2 [Candida albicans SC5314]</td></tr>
<tr><td>gi|67540320|ref|XP_663934.1|</td><td>94085.97</td><td>elongation factor 2 [Aspergillus nidulans FGSC A4]</td></tr>
<tr><td>gi|67623439|ref|XP_668002.1|</td><td>93586.79</td><td>elongation factor 2 (EF-2) [Cryptosporidium hominis TU502]</td></tr>
<tr><td>gi|50909007|ref|XP_465992.1|</td><td>94986.92</td><td>putative elongation factor 2 [Oryza sativa (japonica cultivar-group)]</td></tr>
<tr><td>gi|23497558|gb|AAN37099.1|</td><td>94545.79</td><td>elongation factor 2 [Plasmodium falciparum 3D7]</td></tr>
<tr><td>gi|30696056|ref|NP_849818.1|</td><td>94742.58</td><td>LOS1; GTP binding / translation elongation factor/ translation factor, nucleic acid binding [Arabid</td></tr>
<tr><td>gi|8927040|gb|AAF81925.1|</td><td>90393.61</td><td>elongation factor 2 [Candida glabrata]</td></tr>
<tr><td>gi|8927044|gb|AAF81927.1|</td><td>90176.7</td><td>elongation factor 2 [Candida tropicalis]</td></tr>
<tr><td>gi|8927048|gb|AAF81929.1|</td><td>90304.9</td><td>elongation factor 2 [Candida parapsilosis]</td></tr>
<tr><td>gi|62752006|ref|NP_001015785.1|</td><td>96342.61</td><td>MGC108369 protein [Xenopus tropicalis]</td></tr>
<tr><td>gi|28564005|gb|AAO32381.1|</td><td>46361.15</td><td>EFT2 [Saccharomyces bayanus]</td></tr>
<tr><td>gi|28564219|gb|AAO32488.1|</td><td>50852.23</td><td>EFT [Saccharomyces castellii]</td></tr>
<tr><td>gi|12667408|gb|AAK01430.1|</td><td>95313.29</td><td>elongation factor 2 [Aedes aegypti]</td></tr>
<tr><td>gi|34910726|ref|NP_916710.1|</td><td>96021.51</td><td>putative elongation factor 2 [Oryza sativa (japonica cultivar-group)]</td></tr>
<tr><td>gi|15028587|gb|AAK77225.1|</td><td>95287.24</td><td>elongation factor 2 [Aedes aegypti]</td></tr>
<tr><td>gi|26324898|dbj|BAC26203.1|</td><td>96223.23</td><td>unnamed protein product [Mus musculus]</td></tr>
<tr><td>gi|26328763|dbj|BAC28120.1|</td><td>96165.16</td><td>unnamed protein product [Mus musculus]</td></tr>
<tr><td>gi|16554298|gb|AAK27414.1|</td><td>94356.67</td><td>elongation factor 2 [Monosiga brevicollis]</td></tr>
<tr><td>gi|13925370|gb|AAK49353.1|</td><td>93509.28</td><td>elongation factor 2 [Neurospora crassa]</td></tr>
<tr><td>gi|19335670|gb|AAL85604.1|</td><td>95306.15</td><td>elongation factor 2 [Aedes aegypti]</td></tr>
<tr><td>gi|19335672|gb|AAL85605.1|</td><td>95359.26</td><td>elongation factor 2 [Aedes aegypti]</td></tr>
<tr><td>gi|55728420|emb|CAH90954.1|</td><td>96218.28</td><td>hypothetical protein [Pongo pygmaeus]</td></tr>
<tr><td>gi|55730085|emb|CAH91767.1|</td><td>96186.31</td><td>hypothetical protein [Pongo pygmaeus]</td></tr>
<tr><td>gi|6090545|emb|CAB58724.1|</td><td>6782.42</td><td>SPAC513.01c [Schizosaccharomyces pombe]</td></tr>
<tr><td>gi|54035090|gb|AAH84061.1|</td><td>96603.38</td><td>Eukaryotic translation elongation factor 2 [Xenopus tropicalis]</td></tr>
<tr><td>gi|7919|emb|CAA33804.1|</td><td>95438.49</td><td>unnamed protein product [Drosophila melanogaster]</td></tr>
<tr><td>gi|37362212|gb|AAQ91234.1|</td><td>96463.16</td><td>eukaryotic translation elongation factor 2 [Danio rerio]</td></tr>
<tr><td>gi|13111488|gb|AAK12341.1|</td><td>81882.68</td><td>elongation factor-2 [Armadillidium vulgare]</td></tr>
<tr><td>gi|13111492|gb|AAK12343.1|</td><td>82284.64</td><td>elongation factor-2 [Eumesocampa frigilis]</td></tr>
<tr><td>gi|13111496|gb|AAK12345.1|</td><td>74472.81</td><td>elongation factor-2 [Hutchinsoniella macracantha]</td></tr>
<tr><td>gi|13111498|gb|AAK12346.1|</td><td>74233.13</td><td>elongation factor-2 [Limulus polyphemus]</td></tr>
<tr><td>gi|13111502|gb|AAK12348.1|</td><td>82376.04</td><td>elongation factor-2 [Mastigoproctus giganteus]</td></tr>
<tr><td>gi|13111504|gb|AAK12349.1|</td><td>81730.77</td><td>elongation factor-2 [Nipponopsalis abei]</td></tr>
<tr><td>gi|13111506|gb|AAK12350.1|</td><td>81963.23</td><td>elongation factor-2 [Cypridopsis vidua]</td></tr>
<tr><td>gi|13111508|gb|AAK12351.1|</td><td>74765.07</td><td>elongation factor-2 [Polyxenus fasciculatus]</td></tr>
<tr><td>gi|13111510|gb|AAK12352.1|</td><td>82226.03</td><td>elongation factor-2 [Scutigerella sp. 'Scu2']</td></tr>
<tr><td>gi|13111512|gb|AAK12353.1|</td><td>82681.09</td><td>elongation factor-2 [Scolopendra polymorpha]</td></tr>
<tr><td>gi|13111516|gb|AAK12355.1|</td><td>74213.62</td><td>elongation factor-2 [Tomocerus sp. jcrjws1]</td></tr>
<tr><td>gi|13111518|gb|AAK12356.1|</td><td>82185.53</td><td>elongation factor-2 [Tanystylum orbiculare]</td></tr>
<tr><td>gi|13111520|gb|AAK12357.1|</td><td>82218.76</td><td>elongation factor-2 [Chaetopleura apiculata]</td></tr>
<tr><td>gi|13111524|gb|AAK12359.1|</td><td>74215.84</td><td>elongation factor-2 [Nereis virens]</td></tr>
<tr><td>gi|13111526|gb|AAK12360.1|</td><td>82254.17</td><td>elongation factor-2 [Peripatus sp. Per2]</td></tr>
<tr><td>gi|84999038|ref|XP_954240.1|</td><td>93136.86</td><td>elongation factor 2 [Theileria annulata strain Ankara]</td></tr>
<tr><td>gi|68129664|emb|CAJ08970.1|</td><td>94927.93</td><td>elongation factor 2 [Leishmania major]</td></tr>
<tr><td>gi|34597146|gb|AAQ77148.1|</td><td>82709.21</td><td>elongation factor 2 [Australobius scabrior]</td></tr>
<tr><td>gi|34597148|gb|AAQ77149.1|</td><td>82235.12</td><td>elongation factor 2 [Ballophilus australiae]</td></tr>
</table>

gi|34597166|gb|AAQ77158.1|	82361.06	elongation factor 2 [Globotherium sp. 'Glo2']
gi|34597168|gb|AAQ77159.1|	82531.13	elongation factor 2 [Glomeris marginata]
gi|34597170|gb|AAQ77160.1|	82524.2	elongation factor 2 [Glomeridesmus trinidadensis]
gi|34597172|gb|AAQ77161.1|	82349.93	elongation factor 2 [Geophilus vittatus]
gi|34597178|gb|AAQ77164.1|	23897.24	elongation factor 2 [Hiltonius sp. 'Hil']
gi|34597182|gb|AAQ77166.1|	82498.38	elongation factor 2 [Ophyiulus pilosus]
gi|34597184|gb|AAQ77167.1|	82191.86	elongation factor 2 [Phryssonotus sp. 'jump']
gi|34597186|gb|AAQ77168.1|	82115.82	elongation factor 2 [Lamyctes fulvicornis]
gi|34597188|gb|AAQ77169.1|	-48453.86	elongation factor 2 [Lithobius forficatus]
gi|34597190|gb|AAQ77170.1|	82435.8	elongation factor 2 [Plesioproctus comans]
gi|34597192|gb|AAQ77171.1|	82644.14	elongation factor 2 [Narceus americanus]
gi|34597194|gb|AAQ77172.1|	23795.24	elongation factor 2 [Nemasoma varicorne]
gi|34597198|gb|AAQ77174.1|	82245.02	elongation factor 2 [Oxidus gracilus]
gi|34597204|gb|AAQ77177.1|	82588.47	elongation factor 2 [Uroblaniulus canadensis]
gi|34597206|gb|AAQ77178.1|	82503.12	elongation factor 2 [Pokabius bilabiatus]
gi|34597208|gb|AAQ77179.1|	82633.38	elongation factor 2 [Proteroiulus fuscus]
gi|34597214|gb|AAQ77182.1|	82277.03	elongation factor 2 [Platydesmus sp. 'Pla']
gi|34597216|gb|AAQ77183.1|	82493.97	elongation factor 2 [Pachymerium ferrugineum]
gi|34597224|gb|AAQ77187.1|	74705.11	elongation factor 2 [Scutigera coleoptrata]
gi|34597226|gb|AAQ77188.1|	82024.73	elongation factor 2 [Siphonocybe sp. 'Siph']
gi|34597232|gb|AAQ77191.1|	82550.19	elongation factor 2 [Orthocricus sp. 'Spi1']
gi|34597234|gb|AAQ77192.1|	82299.01	elongation factor 2 [Scolopocryptops sexspinosus]
gi|34597236|gb|AAQ77193.1|	82556.11	elongation factor 2 [Stemmiulus insulanus]
gi|34597238|gb|AAQ77194.1|	82125.89	elongation factor 2 [Striaria columbiana]
gi|34597240|gb|AAQ77195.1|	82680.07	elongation factor 2 [Scolopendra viridis]
gi|34597246|gb|AAQ77198.1|	82414.03	elongation factor 2 [Theatops posticus]
gi|37703915|gb|AAR01279.1|	82079.91	elongation factor-2 [Acanthocyclops vernalis]
gi|37703917|gb|AAR01280.1|	82157.17	elongation factor-2 [Abacion magnum]
gi|37703919|gb|AAR01281.1|	82381.87	elongation factor-2 [Anopsobius neozelandicus]
gi|37703925|gb|AAR01284.1|	82583.1	elongation factor-2 [Bothropolys multidentatus]
gi|37703929|gb|AAR01286.1|	82526.82	elongation factor-2 [Ctenolepisma lineata]
gi|37703933|gb|AAR01288.1|	74175.05	elongation factor-2 [Carcinoscorpius rotundicauda]
gi|37703937|gb|AAR01290.1|	81886.74	elongation factor-2 [Eurypauropus spinosus]
gi|37703939|gb|AAR01291.1|	23810.12	elongation factor-2 [Forficula auricularia]
gi|37703953|gb|AAR01298.1|	81917.42	elongation factor-2 [Libinia emarginata]
gi|37703959|gb|AAR01301.1|	82421.78	elongation factor-2 [Lynceus sp. JCR-2003]
gi|37703963|gb|AAR01303.1|	82383.76	elongation factor-2 [Mesocyclops edax]
gi|37703965|gb|AAR01304.1|	82008.43	elongation factor-2 [Neogonodactylus oerstedii]
gi|37703967|gb|AAR01305.1|	81972.77	elongation factor-2 [Nebalia hessleri]
gi|37703969|gb|AAR01306.1|	82464.8	elongation factor-2 [Nicoletia meinerti]
gi|37703971|gb|AAR01307.1|	23704.04	elongation factor-2 [Orchesella imitari]
gi|37703975|gb|AAR01309.1|	82316.81	elongation factor-2 [Periplaneta americana]
gi|37703979|gb|AAR01311.1|	82312.96	elongation factor-2 [Paralamyctes sp. JCR-2003]
gi|37703983|gb|AAR01313.1|	82191.03	elongation factor-2 [Rhinotus purpureus]
gi|37703991|gb|AAR01317.1|	82503.24	elongation factor-2 [Trachyiulus nordquisti]
gi|37703993|gb|AAR01318.1|	82330.78	elongation factor-2 [Streptocephalus seali]
gi|37704003|gb|AAR01323.1|	74479.19	elongation factor-2 [Ooperipatellus nanus]
gi|37704005|gb|AAR01324.1|	82058.09	elongation factor-2 [Richtersius coronifer]
gi|33869643|gb|AAH06547.1|	65366.05	EEF2 protein [Homo sapiens]
gi|57226782|gb|AAW43242.1|	91971.78	translation elongation factor 2 [Cryptococcus neoformans var. neoformans JEC21]

gi|27882475|gb|AAH44327.1|	96449.29	Eef2-prov protein [Xenopus laevis]
gi|38511951|gb|AAH60707.1|	94464.35	Eef2 protein [Mus musculus]
gi|28627569|gb|AAL83698.1|	95586.4	translation elongation factor 2 [Spodoptera exigua]
gi|6056373|gb|AAF02837.1|	95097.76	elongation factor EF-2 [Arabidopsis thaliana]
gi|37748712|gb|AAH60025.1|	39351.35	MGC68699 protein [Xenopus laevis]
gi|37590856|gb|AAH59523.1|	37893.47	Wu:fj53d02 protein [Danio rerio]
gi|39952199|ref|XP_363816.1|	96722.3	hypothetical protein MG01742.4 [Magnaporthe grisea 70-15]
gi|47559179|gb|AAT35592.1|	95084.16	elongation factor 2 [Trypanosoma cruzi]
gi|28278942|gb|AAH45488.1|	96415.15	Eukaryotic translation elongation factor 2, like [Danio rerio]
gi|52630939|gb|AAU84933.1|	95726.43	putative translation elongation factor 2 [Toxoptera citricida]
gi|50603727|gb|AAH77595.1|	95661.16	Eft-2-prov protein [Xenopus laevis]
gi|56474885|gb|AAN04122.2|	94292.56	elongation factor 2 [Tetrahymena thermophila]

52. Group probability: 0.9796. Peptides of the group

ILTDYGFEGHPLRK	65.59	54.5749	1644.862	1646.337	7	2	distinct	1	0.9796

The equivalent proteins include

gi|1020087|dbj|BAA07214.1|	23052.53	NADH dehydrogenase subunit 9 [Beta trigyna]
gi|1020088|dbj|BAA07215.1|	23121.6	NADH dehydrogenase subunit 9 [Beta webbiana]
gi|83751387|ref|ZP_00947800.1|	23895.02	COG0852: NADH:ubiquinone oxidoreductase 27 kD subunit [Bartonella bacilliformis KC583]
gi|91219863|ref|ZP_01256390.1|	24151.28	NADH Dehydrogenase I Chain C [Psychroflexus torquis ATCC 700755]
gi|2828209|sp|P34944|NUGM_MARPO	23509.71	NADH-ubiquinone oxidoreductase 27 kDa subunit (Complex I-27KD) (CI-27KD) (NADH dehydrogenase subuni
gi|2499319|sp|Q33994|NUGM_BETTR	23208.6	NADH-ubiquinone oxidoreductase 27 kDa subunit (Complex I-27KD) (CI-27KD) (NADH dehydrogenase subuni
gi|2499321|sp|Q34011|NUGM_BETWE	23277.67	NADH-ubiquinone oxidoreductase 27 kDa subunit (Complex I-27KD) (CI-27KD) (NADH dehydrogenase subuni
gi|38605724|sp|P80261|NUGM_SOLTU	22982.4	NADH-ubiquinone oxidoreductase 27 kDa subunit (Complex I-27KD) (CI-27KD) (NADH dehydrogenase subuni
gi|84508538|ref|YP_448702.1|	23037.62	NADH dehydrogenase subunit 9 [Dictyota dichotoma]
gi|27753503|dbj|BAA07213.2|	23307.65	NADH dehydrogenase subunit 9 [Beta vulgaris subsp. vulgaris]
gi|23013442|ref|ZP_00053336.1|	22803.35	COG0852: NADH:ubiquinone oxidoreductase 27 kD subunit [Magnetospirillum magnetotacticum MS-1]
gi|71062697|gb|AAZ21700.1|	24188.33	NADH Dehydrogenase I Chain C [Candidatus Pelagibacter ubique HTCC1062]
gi|48099278|ref|XP_394885.1|	30752.81	PREDICTED: similar to ENSANGP00000014099 [Apis mellifera]
gi|86357238|ref|YP_469130.1|	22996.49	NADH-ubiquinone oxidoreductase chain C protein [Rhizobium etli CFN 42]
gi|83311884|ref|YP_422148.1|	22848.35	NADH:ubiquinone oxidoreductase 27 kD subunit [Magnetospirillum magneticum AMB-1]
gi|84508616|ref|YP_448663.1|	22564.39	NADH dehydrogenase subunit 9 [Desmarestia viridis]
gi|72037413|ref|XP_790261.1|	16730.36	PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reduct
gi|72088811|ref|XP_796382.1|	30118.25	PREDICTED: similar to NADH dehydrogenase (ubiquinone) Fe-S protein 3, 30kDa (NADH-coenzyme Q reduct
gi|91208867|ref|YP_539028.1|	23467.69	NADH dehydrogenase subunit 9 [Physcomitrella patens]
gi|74325198|ref|YP_316618.1|	22522.47	NADH dehydrogenase subunit 9 [Thalassiosira pseudonana]

gi|9838362|ref|NP_063974.1|	23125.53	NADH dehydrogenase subunit 9 [Beta vulgaris subsp. vulgaris]
gi|68191689|gb|EAN06345.1|	23593.87	NADH (or F420H2) dehydrogenase, subunit C [Mesorhizobium sp. BNC1]
gi|37591060|dbj|BAC98862.1|	22980.45	NADH dehydrogenase subunit 9 [Brassica napus]
gi|60498753|dbj|BAC19900.2|	23029.47	NADH dehydrogenase subunit 9 [Oryza sativa (japonica cultivar-group)]
gi|15147749|emb|CAC50850.1|	22390.29	NADH dehydrogenase subunit 9 [Pylaiella littoralis]
gi|786229|gb|AAC09443.1|	25608.89	ORF212 [Marchantia polymorpha]
gi|17935170|ref|NP_531960.1|	23210.72	NADH dehydrogenase subunit C [Agrobacterium tumefaciens str. C58]
gi|23347613|gb|AAN29733.1|	23442.79	NADH dehydrogenase I, C subunit [Brucella suis 1330]
gi|49239683|emb|CAF26058.1|	23603.82	NADH dehydrogenase I, C subunit [Bartonella quintana str. Toulouse]
gi|49238463|emb|CAF27691.1|	23835.97	NADH dehydrogenase I, C subunit [Bartonella henselae str. Houston-1]
gi|32966601|gb|AAP92184.1|	22623.41	NADH dehydrogenase subunit 9 [Chara vulgaris]
gi|21425338|emb|CAC87971.1|	22478.37	NADH dehydrogenase subunit 9 [Laminaria digitata]
gi|22417013|gb|AAM96612.1|	22189.26	NADH dehydrogenase subunit 9 [Chaetosphaeridium globosum]
gi|54606793|dbj|BAD66816.1|	23111.55	NADH dehydrogenase subunit 9 [Beta vulgaris subsp. vulgaris]
gi|9695380|ref|NP_037602.1|	22914.22	NADH dehydrogenase subunit 9 [Phytophthora infestans]
gi|62195885|gb|AAX74185.1|	23408.8	NuoC, NADH dehydrogenase I, C subunit [Brucella abortus biovar 1 str. 9-941]
gi|41019517|sp|Q95748|NUGM_ARATH	22979.47	NADH-ubiquinone oxidoreductase 27 kDa subunit (Complex I-27KD) (CI-27KD) (NADH dehydrogenase subuni
gi|71006324|ref|XP_757828.1|	44332.49	hypothetical protein UM01681.1 [Ustilago maydis 521]
gi|68468682|ref|XP_721660.1|	32589.63	putative mitochondrial complex I, NUGM_30kd subunit [Candida albicans SC5314]
gi|7545239|gb|AAA32025.2|	22795.14	NADH dehydrogenase [Phytophthora megasperma]
gi|56684557|gb|AAW21977.1|	22560.03	NADH dehydrogenase subunit 9 [Plasmopara viticola]
gi|6066174|gb|AAF03192.1|	22444.33	NADH dehydrogenase subunit 9 [Nephroselmis olivacea]
gi|27380028|ref|NP_771557.1|	23200.61	NADH dehydrogenase subunit C [Bradyrhizobium japonicum USDA 110]
gi|10802934|gb|AAG23682.1|	23274.16	NADH dehydrogenase subunit 9 [Thraustochytrium aureum]
gi|67043755|gb|AAY63976.1|	31085	NADH dehydrogenase [Lysiphlebus testaceipes]
gi|15054572|gb|AAK82657.1|	24556.26	NADH dehydrogenase subunit 9 [Beta vulgaris subsp. maritima]
gi|57337517|emb|CAI23792.1|	23030.49	NADH dehydrogenase, subunit 9 [Zea mays]
gi|9280614|gb|AAF86495.1|	22966.4	NADH dehydrogenase subunit 9 [Lupinus angustifolius]
gi|9280616|gb|AAF86496.1|	22976.42	NADH dehydrogenase subunit 9 [Lupinus angustifolius]
gi|84508576|ref|YP_448624.1|	22735.66	NADH dehydrogenase subunit 9 [Fucus vesiculosus]
gi|14022147|dbj|BAB48757.1|	23346.75	NADH-ubiquinone dehydrogenase chain C 1 [Mesorhizobium loti MAFF303099]

53. Group probability: 0.9780. Peptides of the group

IINQPTAAAIAYGLDKK	80.57	54.7937	1785.999	1787.496	1	2	distinct	1	0.978

The equivalent proteins include

gi|640325|pdb|1NGB|	42542.9	Heat-Shock Cognate 70kd Protein (44kd Atpase N-Terminal Fragment) (E.C.3.6.1.3) Mutant With Glu 17

54. Group probability: 0.9747. Peptides of the group

LQILKPFKPWDGK	63.57	54.7515	1568.908	1569.479	5	2	distinct	0	0.9747

The equivalent proteins include

gi|51012446|gb|AAT92542.1|	81777.25	mitochondrial aconitate hydratase [Yarrowia lipolytica]
gi|50550287|ref|XP_502616.1|	84209.71	hypothetical protein [Yarrowia lipolytica]
gi|170982|gb|AAA34389.1|	86094.39	aconitase (ACO1) (EC 4.2.1.3)
gi|6323335|ref|NP_013407.1|	85713.93	Aconitase, required for the tricarboxylic acid (TCA) cycle and also independently required for mito
gi|57226478|gb|AAW42938.1|	86700.44	aconitase, putative [Cryptococcus neoformans var. neoformans JEC21]

55. Group probability: 0.9728. Peptides of the group

QIFEDAQKSAPSIIFIDEIDSIAPK	59.57	51.8169	2774.438	2775.458	1	3	distinct	1	0.9728

The equivalent proteins include

gi|88951313|ref|ZP_01153827.1|	80507.39	AAA ATPase, CDC48 [Methanosaeta thermophila PT]

56. Group probability: 0.9718. Peptides of the group

IINEPTAAALSFGLDKK	77.73	54.7937	1786.983	1787.496	2	2	distinct	1	0.9718

The equivalent proteins include

gi|15828694|ref|NP_326054.1|	65480.66	molecular chaperone DnaK [Mycoplasma pulmonis UAB CTIP]

57. Group probability: 0.9716. Peptides of the group

IFGVTTLDVVR	60.95	55.6221	1218.697	1219.164	3	2	shared(4)	0	0.9301
RIFGVTTLDVVR	48.62	55.0941	1374.798	1375.47	3	2	shared(3)	1	0.8823
VAVVGAAGGIGQPLSLLLK	68.94	54.1402	1762.072	1763.03	3	2	distinct	0	0.8877

The equivalent proteins include

gi|54642260|gb|EAL31009.1|	33842.04	GA10541-PA [Drosophila pseudoobscura]

58. Group probability: 0.9701. Peptides of the group

RPDCTLATTDHNVPTSSR	61.71	53.5101	2026.949	2025.863	1	3	distinct	0	0.9701

The equivalent proteins include

gi|46136147|ref|XP_389765.1|	85355.85	conserved hypothetical protein [Gibberella zeae PH-1]

59. Group probability: 0.9698. Peptides of the group

KIENVATGPNNRPK	61.14	54.6365	1536.837	1536.971	2	2	distinct	1	0.9698

The equivalent proteins include

gi|92879371|gb|ABE85500.1|	20604.18	Peptidyl-prolyl cis-trans isomerase, cyclophilin type [Medicago truncatula]
gi|50919309|ref|XP_470051.1|	22174.83	putative cyclophilin [Oryza sativa (japonica cultivar-group)]

60. Group probability: 0.9688. Peptides of the group

HTGPGILSMANAGR	60.82	54.9183	1380.693	1381.709	1	2	distinct	0	0.9688

The equivalent proteins include

gi|83779024|gb|ABC47329.1|	22006.4	cyclophilin B precursor [Orpinomyces sp. PC-2]
gi|849081|gb|AAD04195.1|	22012.37	cyclophilin B precursor [Orpinomyces sp. PC-2]
gi|53792607|dbj|BAD53622.1|	23591.23	putative cyclophilin [Oryza sativa (japonica cultivar-group)]
gi|53792606|dbj|BAD53621.1|	24166.6	putative cyclophilin [Oryza sativa (japonica cultivar-group)]

61. Group probability: 0.9674. Peptides of the group

ELVELPLRHPELFK	60.19	54.4048	1718.972	1718.967	1	2	distinct	1	0.9674

The equivalent proteins include

gi|18159541|gb|AAL62959.1|	81676.01	AAA family ATPase, possible cell division control protein cdc48 [Pyrobaculum aerophilum str. IM2]
gi|18161441|gb|AAL64724.1|	82229.07	AAA family ATPase, possible cell division control protein cdc48 [Pyrobaculum aerophilum str. IM2]
gi|13813310|gb|AAK40524.1|	85982.62	AAA family ATPase [Sulfolobus solfataricus P2]
gi|68567217|gb|AAY80146.1|	86575.06	SAV protein-like [Sulfolobus acidocaldarius DSM 639]

62. Group probability: 0.9657. Peptides of the group

TTGLVLDSGDGVTHTVPIYEGYSVSHGCMR	54.79	51.3062	3207.496	3207.192	3	3	distinct	0	0.9657

The equivalent proteins include

gi|54637211|gb|EAL26614.1|	42820.5	GA18861-PA [Drosophila pseudoobscura]

63. Group probability: 0.9656. Peptides of the group

IFGVTTLDVVR	60.95	55.6221	1218.697	1219.164	3	2	shared(4)	0	0.9301
RIFGVTTLDVVR	48.62	55.0941	1374.798	1375.47	3	2	shared(3)	1	0.8823
VTVLGAAGGIGQPLSLLLK	64.86	54.1504	1806.098	1806.624	2	2	distinct	0	0.8657

The equivalent proteins include

gi|88181085|gb|EAQ88553.1|	35504.65	malate dehydrogenase, mitochondrial precursor [Chaetomium globosum CBS 148.51]
gi|39960255|ref|XP_364559.1|	35397.53	hypothetical protein MG09367.4 [Magnaporthe grisea 70-15]

64. Group probability: 0.9613. Peptides of the group

AFVLIISNPVNSTVPIVAETLK	54.7	53.0528	2324.335	2323.249	2	2	distinct	0	0.9613

The equivalent proteins include

gi|50411825|ref|XP_457081.1|	36218.17	hypothetical protein DEHA0B02651g [Debaryomyces hansenii CBS767]

65. Group probability: 0.9594. Peptides of the group

SINPDEAVAYGAAVQAAILSGDKSSR	74.34	52.3464	2589.303	2590.757	1	2	distinct	1	0.9594

The equivalent proteins include

gi|66800327|ref|XP_629089.1|	70246.02	hypothetical protein DDB0192086 [Dictyostelium discoideum]

66. Group probability: 0.9560. Peptides of the group

AVAHHTTASFIR	57.76	55.141	1309.689	1310.529	1	2	distinct	0	0.956

The equivalent proteins include

gi|54643817|gb|EAL32560.1|	47114.13	GA14216-PA [Drosophila pseudoobscura]
gi|18860063|ref|NP_572686.1|	47083.22	Rpt3 CG16916-PA [Drosophila melanogaster]
gi|28573127|ref|NP_731401.2|	44014.83	Rpt3R CG9475-PB, isoform B [Drosophila melanogaster]
gi|24645494|ref|NP_649938.1|	47769.71	Rpt3R CG9475-PA, isoform A [Drosophila melanogaster]
gi|21064189|gb|AAM29324.1|	29990.57	AT28212p [Drosophila melanogaster]
gi|54650682|gb|AAV36920.1|	46044.88	RE01104p [Drosophila melanogaster]

67. Group probability: 0.9557. Peptides of the group

NEKIAVLASPK	58.2	55.6373	1168.682	1169.035	1	2	distinct	1	0.9557

The equivalent proteins include

gi|77382950|gb|ABA74463.1|	34090.76	Transcriptional Regulator, LysR family [Pseudomonas fluorescens PfO-1]

68. Group probability: 0.9556. Peptides of the group

FTQAGSEVSALLGR	98.4	54.8356	1434.747	1434.927	1	2	shared(3)	0	0.9988
DVESQDVLLFIDNIFR	45.16	53.7927	1921.978	1922.397	1	2	distinct	0	0.6652

The equivalent proteins include

gi|56808123|ref|ZP_00365911.1|	43843.55	COG0055: F0F1-type ATP synthase, beta subunit [Streptococcus pyogenes M49 591]

69. Group probability: 0.9537. Peptides of the group

LMKNMGSLGGIMK (001000000000100)	64.58	55.0187	1410.703	1411.615	3	3	distinct	1	0.9537

The equivalent proteins include

gi|71674984|ref|ZP_00672730.1|	52598.65	Signal recognition particle protein [Trichodesmium erythraeum IMS101]

70. Group probability: 0.9536. Peptides of the group

SLKHIITPALK	57.63	55.4056	1219.765	1220.751	1	2	distinct	1	0.9536

The equivalent proteins include

gi|89208433|ref|ZP_01186941.1|	20804.81	BioY protein [Bacillus weihenstephanensis KBAB4]
gi|47567911|ref|ZP_00238618.1|	20090.43	BioY family protein [Bacillus cereus G9241]
gi|49329857|gb|AAT60503.1|	20019.3	bioY family protein [Bacillus thuringiensis serovar konkukian str. 97-27]
gi|29897282|gb|AAP10559.1|	20062.37	BioY protein [Bacillus cereus ATCC 14579]
gi|51975381|gb|AAU16931.1|	20010.31	bioY family protein [Bacillus cereus E33L]
gi|42782698|ref|NP_979945.1|	20034.37	bioY family protein [Bacillus cereus ATCC 10987]

71. Group probability: 0.9522. Peptides of the group

IIIEPTAAAIAYGLDKK	71.7	54.7937	1786.024	1787.496	1	2	distinct	1	0.9522

The equivalent proteins include

gi|15620767|emb|CAC69880.1|	72796.99	heat shock protein (Hsp70) [Moneuplotes crassus]

72. Group probability: 0.9489. Peptides of the group

YIHSANVIHR	61.86	55.1896	1208.641	1208.482	1	2	distinct	0	0.9489

The equivalent proteins include

gi|89285975|gb|EAR83980.1|	64054.1	Protein kinase domain containing protein [Tetrahymena thermophila SB210]
gi|68420287|ref|XP_692716.1|	94925.93	PREDICTED: similar to mitogen-activated protein kinase 7 isoform 1 [Danio rerio]
gi|70569435|dbj|BAE06412.1|	40825.77	mitogen-activated protein kinase [Ciona intestinalis]

Supporting Information S1. Protein assembly of peptide sequence matches made to tag-filtered *U. maydis* tandem mass spectra. The NCBI NR database was searched.

Supporting Information S2. Protein assembly of peptide sequence matches made to tag-filtered *P. sojae* tandem mass spectra. The NCBI NR database was searched.

Supporting Information S3. Protein assembly of peptide sequence matches made to tag-filtered *P. sojae* tandem mass spectra. The NCBI NR database appended with *P. sojae* protein sequences was searched.

Supporting Information S4. Protein assembly of peptide sequence matches made to tag-filtered *P. sojae* tandem mass spectra. The NCBI NR database appended with *P. sojae* and *P. ramorum* protein sequences was searched.

Supporting Information S5. Protein assembly of peptide sequence matches made to tag-filtered *F. graminearum* tandem mass spectra. The NCBI NR database was searched.

Supporting Information S6. Protein assembly of peptide sequence matches made to tag-filtered *R. solani* tandem mass spectra. The NCBI NR database was searched.