

# PROTEOMICS

## Supporting Information for Proteomics

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**Proteomic and bioinformatic analysis of iron- and sulfur-oxidizing  
*Acidithiobacillus ferrooxidans* using immobilized pH gradients  
and mass spectrometry**

SSP	Mr	pI	Growth on iron		Growth on sulfur		Qty ratios		Induced by growth mode	ID status	Protein name	ORF	Theoretical Mr/pI	Physiological significance in <i>At.ferrooxidans</i>
			Avg Qty	Norm C.V.	Avg Qty	Norm C.V.	Fe/S	S/Fe						
0202	28.6	4.6	0.0	0.0	526.4	8.8	0.0	417.1	S	c				
0406	38.4	4.5	485.1	56.1	4307.5	8.1	0.1	8.9	S	b	Omp 40	359835:361127	45122/5.2	not definitely clear*
1101	22.2	4.6	2221.9	33.2	164.8	15.4	13.5	0.1	Fe	c				
1102	25.8	4.6	1522.5	28.5	654.8	6.4	2.3	0.4	Fe	h				
1105	21.4	4.7	503.2	81.5	1994.7	24.6	0.3	4.0	S	h				
1107	22.6	4.9	858.1	30.2	361.1	42.4	2.4	0.4	Fe	h				
1109	26.6	4.8	977.0	13.5	281.2	29.5	3.5	0.3	Fe	h				
1111	27.1	5.0	613.4	36.0	0.0	0.0	619.1	0.0	Fe	c				
1218	32.2	4.7	0.0	0.0	442.8	4.5	0.0	350.8	S	b	phage shock protein A	1037494:1038228	26454/4.9	not clear
1308	33.7	4.8	50.4	169.2	837.7	19.8	0.1	16.6	S	c				
1415	39.3	4.9	860.0	18.2	2191.8	11.2	0.4	2.5	S	h				
1513	41.2	4.9	256.9	77.7	859.3	7.2	0.3	3.3	S	h				
1710	55.9	4.7	0.0	0.0	569.9	24.1	0.0	451.6	S	c				
1718	62.2	4.9	341.0	9.0	99.9	17.9	3.4	0.3	Fe	h				
1807	67.9	4.9	3082.2	18.9	3730.5	15.2	0.8	1.2	ns	d	chaperone protein dnaK (Heat shock protein 70)	432157:434061	68180/5.0	identical with DnaK protein*
2107	24.5	5.2	993.8	10.0	2227.3	0.6	0.4	2.2	S	h				
2209	31.7	5.2	1428.2	16.4	331.7	7.2	4.3	0.2	Fe	h				
2218	32.2	5.0	623.8	5.3	292.7	32.9	2.1	0.5	Fe	h				
2313	34.9	5.1	518.4	31.8	141.5	3.3	3.7	0.3	Fe	h				
2416	39.9	5.2	587.3	25.0	1357.5	10.3	0.4	2.3	S	h				
2419	37.9	5.3	981.7	3.2	0.0	0.0	990.8	0.0	Fe	c				
2424	36.7	5.3	1432.6	31.0	545.2	30.1	2.6	0.4	Fe	h				
2719	53.9	5.1	368.5	31.7	441.2	17.6	0.8	1.2	ns	e	pyruvate dehydrogenase alfa chain/ 3-dehydroquinase synthase/ pyruvate dehydrogenase beta chain/ fructose-1,6-bisphosphatase	40695:41678/ 2137971:2139065/ 41581:42651/ 2632599:2633618	37122/5.3/ 38899/5.4/ 39279/6.5/ 37347/5.5	oxidative decarboxylation/ not clear/ oxidative decarboxylation/ glycolysis
2731	59.3	5.1	1051.5	25.0	1189.3	27.5	0.9	1.1	ns	d	60 kDa chaperonin	2325118:2326773	58594/5.1	identical with GroEL protein*
3009	17.1	5.4	4262.6	49.1	833.0	35.9	4.9	0.2	Fe	h				
3408	39.5	5.4	345.9	36.6	1110.4	9.8	0.3	3.2	S	h				
3509	46.0	5.4	468.9	21.2	166.5	19.5	2.8	0.4	Fe	h				
3514	45.0	5.4	283.6	5.4	122.7	34.4	2.3	0.4	Fe	h				

3718	65.1	5.5	136.1	8.3	332.6	24.2	0.4	2.4	S	h				
4322	32.8	5.6	195.5	84.5	568.5	19.2	0.3	2.9	S	h				
4334	34.4	5.6	336.4	25.5	0.0	0.0	339.5	0.0	Fe	c				
4410	35.6	5.6	87.5	33.6	300.0	6.5	0.3	3.4	S	h				
4412	38.1	5.6	287.1	33.1	791.2	44.3	0.4	2.8	S	h				
4430	39.1	5.5	300.6	10.6	0.0	0.0	303.4	0.0	Fe	c				
5218	29.5	5.8	146.9	80.0	949.1	13.8	0.2	6.5	S	b	pteridine reductase 1	2682788:2683561	27066/6.2	not clear
5219	28.0	5.8	2458.5	23.9	565.2	54.4	4.3	0.2	Fe	h				
5314	32.5	5.8	791.3	16.5	1802.7	37.8	0.4	2.3	S	h				
5316	33.2	5.8	104.3	32.9	310.3	28.9	0.3	3.0	S	h				
5405	37.8	5.7	215.8	41.6	456.0	32.2	0.5	2.1	S	h				
5415	39.5	5.8	272.4	43.3	543.8	31.6	0.5	2.0	S	h				
5503	44.8	5.7	164.8	10.9	363.9	14.1	0.5	2.2	S	h				
5510	46.6	5.8	70.4	48.9	473.8	50.6	0.1	6.7	S	c				
5515	46.4	5.8	0.0	0.0	664.4	20.5	0.0	526.4	S	a	seryl-tRNA synthetase	2469610:2470875	46529/5.8	proteosynthesis
5612	46.6	5.7	0.0	0.0	844.6	33.7	0.0	669.2	S	c				
5614	50.5	5.8	141.7	19.5	319.1	19.7	0.4	2.3	S	h				
5616	53.1	5.8	139.3	31.8	409.7	16.2	0.3	2.9	S	h				
5617	47.9	5.8	208.1	30.1	757.6	20.9	0.3	3.6	S	h				
5716	59.3	5.8	57.1	86.3	376.1	19.1	0.2	6.6	S	c				
6222	31.2	5.9	59.8	87.4	755.8	26.0	0.1	12.6	S	a	probable ABC transport system ATP-binding protein	2660251:2661075	29392/6.1	transport
6224	28.3	5.9	231.9	8.4	682.6	25.5	0.3	2.9	S	h				
6230	29.7	5.9	230.1	66.0	1504.3	9.2	0.2	6.5	S	b	hypothetical protein	2660251:2661075	29683/6.4	unknown function
6307	33.1	5.9	408.2	4.4	182.9	52.4	2.2	0.4	Fe	h				
6411	36.3	5.9	576.8	33.5	1357.1	10.1	0.4	2.4	S	h				
6418	36.6	5.9	347.9	12.9	0.0	0.0	351.1	0.0	Fe	c				
6524	44.7	5.9	0.0	0.0	1036.3	72.5	0.0	821.1	S	b	phosphoserine aminotransferase/ putative long-chain fatty acid transport protein	1989075:1990163/ 539767:541110	39721/5.9 46973/8.6	amino acid modification substrate sorption
6525	41.6	5.9	0.0	0.0	1057.4	51.5	0.0	837.8	S	c				
6603	47.7	5.8	91.1	36.1	387.4	1.0	0.2	4.3	S	h				
6612	50.1	5.9	116.5	61.9	306.8	37.7	0.4	2.6	S	h				
6623	53.4	6.0	0.0	0.0	1089.0	18.8	0.0	862.8	S	b	serine protease/ sulfide dehydrogenase SQR2	265012:266532/ 1243084:1244388	53366/7.3 47375/6.3	protease/ sulfur metabolism
6702	56.4	5.8	94.4	22.4	352.4	33.0	0.3	3.7	S	h				
6707	59.6	5.9	149.3	15.6	351.2	28.4	0.4	2.4	S	h				

6721	65.0	5.9	35.8	26.3	312.4	43.2	0.1	8.7	S	a	transketolase 1	2852840:2854837	72535/6.0	not clear
7120	24.4	6.1	634.1	10.0	94.1	72.1	6.7	0.1	Fe	a	ribosome recycling factor	1551985:1552545	20743/6.2	proteosynthesis
7123	26.6	6.0	3363.4	10.9	5621.5	12.7	0.6	1.7	ns	d	Fe superoxidismutase	1142739:1143359	23090/6.2	superoxide scavenger
7220	32.2	6.4	0.0	0.0	296.6	8.1	0.0	235.0	S	c				
7225	30.8	6.2	1913.6	6.6	7029.3	19.7	0.3	3.7	S	h				
7227	29.2	6.4	663.6	19.0	2722.8	2.1	0.2	4.1	S	h				
7327	35.2	6.3	299.6	14.1	0.0	0.0	302.4	0.0	Fe	b	sulfate adenylyltransferase subunit 2 (CysH)	2971057:2971995	35597/6.3	sulfate assimilation
7424	36.4	6.2	632.5	12.1	0.0	0.0	638.4	0.0	Fe	c				
7429	36.7	6.0	582.9	4.2	0.0	0.0	588.3	0.0	Fe	a	ketol-acid reductoisomerase	2125436:2126452	36565/6.0	not clear
7530	41.9	6.2	76.9	29.3	448.8	53.0	0.2	5.8	S	c				
7531	41.9	6.1	135.9	18.9	475.7	21.6	0.3	3.5	S	h				
7532	42.1	6.0	241.8	23.2	2226.5	36.7	0.1	9.2	S	c				
7626	52.2	6.2	670.2	38.2	2347.6	19.4	0.3	3.5	S	h				
8006	19.7	7.0	7552.6	14.5	541.6	51.3	13.9	0.1	Fe	a	rusticyanin	2954144:2954707	19844/8.8	electron transport*
8014	20.2	7.8	0.0	0.0	1423.1	29.1	0.0	1127.6	S	f				
8016	19.6	6.6	4131.0	17.6	83.8	89.2	49.3	0.0	Fe	c				
8018	20.2	7.3	5700.6	4.2	416.6	30.5	13.7	0.1	Fe	f				
8201	28.8	6.6	1652.2	23.3	463.1	33.8	3.6	0.3	Fe	h				
8209	31.9	6.8	103.1	75.1	433.1	16.8	0.2	4.2	S	h				
8213	31.9	7.0	644.6	79.8	2126.2	29.2	0.3	3.3	S	h				
8215	27.9	7.2	0.0	0.0	456.6	15.6	0.0	361.8	S	f				
8218	30.7	7.6	2180.2	9.1	3620.3	15.0	0.6	1.7	ns	d	peptidyl-prolyl cis-trans isomerase D	2346852:2347643	28005/9.2	substrate attachment
8222	30.7	6.6	216.3	100.0	1926.2	15.6	0.1	8.9	S	c				
8223	31.5	6.6	229.2	76.1	481.4	10.4	0.5	2.1	S	h				
8225	32.0	6.6	101.6	64.2	1102.9	17.1	0.1	10.9	S	c				
8231	29.6	7.0	1329.5	31.4	281.5	111.9	4.7	0.2	Fe	h				
8303	34.7	6.6	159.1	18.8	1020.4	17.1	0.2	6.4	S	f				
8305	34.7	6.8	0.0	0.0	3008.7	7.1	0.0	2383.9	S	f				
8307	33.2	7.4	0.0	0.0	281.6	18.1	0.0	223.1	S	f				
8316	33.1	6.6	95.7	77.0	732.7	17.8	0.1	7.7	S	f				
8319	33.9	7.5	1207.6	28.7	2762.8	7.8	0.4	2.3	S	h				
8323	33.8	7.0	500.2	21.5	1279.2	25.7	0.4	2.6	S	h				
8324	34.8	7.0	545.0	51.8	6036.3	7.6	0.1	11.1	S	f				

8327	33.8	6.8	0.0	0.0	626.1	44.1	0.0	496.0	S	f				
8402	37.0	6.7	0.0	0.0	589.0	26.4	0.0	466.7	S	f				
8405	36.5	6.8	0.0	0.0	1734.6	25.1	0.0	1374.4	S	f				
8407	36.4	7.0	0.0	0.0	1424.3	14.5	0.0	1128.5	S	f				
8409	36.6	7.5	0.0	0.0	1517.2	13.9	0.0	1202.1	S	f				
8517	42.4	7.5	1042.9	16.6	0.0	0.0	1052.6	0.0	Fe	f				
8612	47.8	6.9	287.0	21.9	140.4	8.2	2.0	0.5	Fe	h				
8614	50.7	7.0	129.3	6.4	415.3	9.0	0.3	3.2	S	h				
8616	50.7	7.3	134.4	9.5	828.5	27.8	0.2	6.2	S	f				
8620	47.0	6.4	0.0	0.0	296.6	57.0	0.0	235.0	S	a	Serine hydroxymethyltransferase 3	2534669:2535913	44470/6.7	-OH group modification
8622	52.8	6.4	994.6	16.7	2127.8	32.6	0.5	2.1	S	h				
8627	51.0	7.8	148.3	59.0	778.4	22.6	0.2	5.2	S	f				
8628	52.6	7.3	0.0	0.0	323.8	10.2	0.0	256.6	S	f				
9023	20.1	8.2	33204.7	10.9	1644.9	26.6	20.2	0.0	Fe	a	rusticyanin	2954144:2954707	19844/8.8	electron transport*
9125	24.2	8.1	0.0	0.0	317.8	33.1	0.0	251.8	S	f				
9203	31.7	8.1	0.0	0.0	1800.7	37.8	0.0	1426.7	S	f				
9217	29.9	7.6	3360.0	11.1	0.0	0.0	3391.2	0.0	Fe	f				
9306	35.0	7.9	2006.3	31.7	4411.7	18.2	0.5	2.2	S	a	ABC-type phosphate transport system	1109541:1110659	39351/9.3	phosphate transport*
9309	34.2	8.2	296.0	172.5	4232.3	5.8	0.1	14.3	S	f				
9602	50.8	8.2	0.0	0.0	1142.6	36.4	0.0	905.3	S	f				

Supplementary Table 1. Review of protein spots detected on IPG 3-10 NL/12% SDS-PAGE gels with significant differences in quantity between growth on iron and sulfur (several most abundant protein spots analyzed with MS are also included).

SSP	Mr	pI	Growth on iron		Growth on sulfur		Qty ratios		Induced by growth mode	ID status	Protein name	ORF	Theoretical Mr/Pi	Physiological significance in <i>At.ferrooxidans</i>
			Avg Qty	Norm C.V.	Avg Qty	Norm C.V.	Fe/S	S/Fe						
B2213	26.1	~6.5	1441.6	11.7	515.2	38.6	2.8	0.4	Fe	h				
B2514	38.8	~6.5	693.5	19.4	0.0	0.0	586.4	0.0	Fe	c				
B2617	46.2	~6.6	4867.2	8.8	0.0	0.0	4115.3	0.0	Fe	b	hypothetical sulfide dehydrogenase	491338:492477	28005/9.2	sulfide oxidation
B3206	21.4	~6.7	1169.1	7.8	285.8	41.9	4.1	0.2	Fe	h				
B3209	19.2	6.5	498.5	48.1	33.7	67.2	14.8	0.1	Fe	c				
B3311	32.6	7.1	0.0	0.0	951.6	17.7	0.0	415.6	S	c				
B3312	31.9	7.1	0.0	0.0	3863.2	13.5	0.0	1687.1	S	b	peptidyl-prolyl cis-trans isomerase D (rotamase)	2346867:2347643	28005/9.2	substrate attachment
B3406	35.8	~6.7	3361.3	11.3	1053.2	20.3	3.2	0.3	Fe	h				
B3408	37.3	~6.7	575.0	30.2	0.0	0.0	486.2	0.0	Fe	c				
B3412	37.5	~6.9	351.4	13.3	0.0	0.0	297.1	0.0	Fe	c				
B3414	36.1	~6.9	6295.4	7.3	1957.2	18.3	3.2	0.3	Fe	h				
B3416	35.5	7.0	0.0	0.0	3787.9	13.8	0.0	1654.2	S	b	ABC-type phosphate transport system	1109541:1110629	38379/9.3	phosphate transport
B3515	38.6	~6.8	0.0	0.0	746.0	38.4	0.0	325.8	S	c				
B3612	42.7	~6.8	1343.5	5.9	368.4	61.8	3.6	0.3	Fe	h				
B3730	53.8	6.7	521.8	16.8	257.1	14.4	2.0	0.5	Fe	h				
B4315	32.2	7.8	731.4	2.8	124.6	44.8	5.9	0.2	Fe	b	serine protease	1589447:1590886	49642/7.1	protease
B4402	33.4	7.2	393.7	18.6	0.0	0.0	332.9	0.0	Fe	c				
B4406	33.1	7.1	522.5	26.6	1684.2	11.8	0.3	3.2	S	h				
B4410	33.7	7.1	761.0	16.4	0.0	0.0	643.4	0.0	Fe	c				
B4412	33.2	7.1	719.5	12.2	0.0	0.0	608.4	0.0	Fe	c				
B4415	36.6	7.1	135.0	100.7	1634.9	36.8	0.1	12.1	S	b	sulfate/molybdate binding protein	2752341:2753351	36650/9.1	sulfate transport
B4501	42.3	7.0	457.2	12.8	0.0	0.0	386.6	0.0	Fe	c				
B4506	38.7	7.8	130.0	12.4	2028.0	9.5	0.1	15.6	S	c				
B4617	43.4	7.5	404.7	47.3	0.0	0.0	342.2	0.0	Fe	c				
B4708	57.9	7.1	364.1	25.3	149.4	35.5	2.4	0.4	Fe	h				
B4710	51.4	7.3	3145.2	2.5	1456.1	1.8	2.2	0.5	Fe	h				
B4714	51.8	7.9	589.0	10.7	48.3	24.6	12.2	0.1	Fe	b	UDP-N-acetylmuramoylalanyl-D-glutamate-2,6-diaminopimelate ligase	2611391:2612842	51372/6.7	substrate attachment
B5110	18.2	7.1	339.7	24.4	0.0	0.0	287.2	0.0	Fe	c				
B5202	27.2	7.3	306.7	32.8	0.0	0.0	259.3	0.0	Fe	c				

B5214	20.1	7.0	6846.4	22.2	1436.7	36.2	4.8	0.2	Fe	h				
B5215	21.8	7.4	47.0	14.7	595.4	25.6	0.1	12.7	S	c				
B5312	31.1	7.2	316.4	27.5	0.0	0.0	267.5	0.0	Fe	c				
B5313	32.1	7.2	915.2	9.4	2731.9	18.3	0.3	3.0	S	h				
B5405	33.3	7.4	495.1	26.2	1669.3	22.4	0.3	3.4	S	h				
B5409	35.2	7.3	165.3	52.0	3607.3	3.3	0.0	21.8	S	b	ABC-type phosphate transport system	1109541:1110629	38379/9.3	phosphate transport
B5410	34.5	7.2	79.5	26.2	1523.9	21.7	0.1	19.2	S	b	sulfate/molybdate binding protein	2752341:2753351	36650/9.1	sulfate transport
B5411	38.0	7.6	0.0	0.0	2423.8	15.9	0.0	1058.5	S	b	sulfate/molybdate binding protein	2752341:2753351	36650/9.1	sulfate transport
B5412	36.5	7.4	0.0	0.0	1963.6	18.3	0.0	857.5	S	b	sulfate/molybdate binding protein	2752341:2753351	36650/9.1	sulfate transport
B5413	34.0	7.0	0.0	0.0	489.5	29.2	0.0	213.8	S	c				
B5415	35.4	7.7	0.0	0.0	4127.0	10.2	0.0	1802.3	S	b	sulfate/molybdate binding protein/ABC-type phosphate transport system	2752341:2753351/ 1109541:1110629	36650/9.1/ 38379/9.3	sulfate transport / phosphate transport
B5416	33.7	7.3	696.5	46.3	0.0	0.0	588.9	0.0	Fe	c				
B5504	40.7	7.5	343.6	13.2	0.0	0.0	290.5	0.0	Fe	c				
B5510	38.5	7.2	214.5	11.2	2886.4	6.8	0.1	13.5	S	b	sulfate/molybdate binding protein	2752341:2753351	36650/9.1	sulfate transport
B5604	46.2	7.8	512.2	22.7	204.8	34.5	2.5	0.4	Fe	h				
B5605	42.7	7.9	1037.1	21.5	198.8	27.4	5.2	0.2	Fe	b	tyrosyl-tRNA synthetase	28367:29590	45738/7.2	proteosynthesis
B5607	47.9	7.0	1495.3	23.5	609.6	15.0	2.5	0.4	Fe	h				
B5609	45.9	7.6	380.1	45.5	102.5	8.9	3.7	0.3	Fe	h				
B5703	57.6	7.3	465.4	26.7	100.7	22.7	4.6	0.2	Fe	h				
B5705	50.5	7.9	787.9	24.2	199.6	62.6	3.9	0.3	Fe	h				
B5706	51.0	7.4	414.5	13.9	102.3	58.0	4.1	0.2	Fe	h				
B6210	27.8	8.1	316.3	54.7	0.0	0.0	267.4	0.0	Fe	c				
B6212	27.0	8.6	1414.6	30.1	35.8	95.5	39.6	0.0	Fe	b	hypothetical protein/ (cyt c-552 precursor)	934750:935427/ 2948903:2949595	24136/8.9/ 25163/9.2	unknown function/ electron transport
B6216	25.2	8.2	2038.9	4.8	209.9	46.2	9.7	0.1	Fe	g	not identified			
B6226	21.5	8.8	416.2	86.3	3690.8	16.2	0.1	8.9	S	c				
B6227	20.0	8.4	52482.8	7.0	3592.4	7.8	14.6	0.1	Fe		rusticyanin (according to spot matching with pH 3-10 NL gel; the most abundant protein in the proteome)			electron transport*
B6310	29.6	8.3	984.2	22.7	0.0	0.0	832.2	0.0	Fe	c				
B6313	31.1	8.7	1801.9	11.1	0.0	0.0	1523.5	0.0	Fe	c				
B6317	31.1	8.9	417.4	56.7	0.0	0.0	352.9	0.0	Fe	c				
B6404	34.9	8.6	2164.9	10.2	7545.6	4.6	0.3	3.5	S	h				

B6407	35.6	8.6	722.5	31.9	5445.1	31.0	0.1	7.5	S	b	ABC-type phosphate transport system / sulfate/molybdate binding protein	1109541:1110629/ 2752341:2753351	38379/9.3/ 36650/9.1	phosphate transport / sulfate transport
B6416	35.9	8.2	811.3	9.6	0.0	0.0	686.0	0.0	Fe	c				
B6417	37.4	8.1	802.8	12.4	326.8	29.2	2.5	0.4	Fe	h				
B6419	35.5	8.6	2485.5	5.2	5783.8	17.9	0.4	2.3	S	h				
B6421	33.8	9.0	642.5	24.3	0.0	0.0	543.3	0.0	Fe	c				
B6423	37.5	8.0	75.7	65.1	2211.4	12.3	0.0	29.2	S	b	ABC-type phosphate transport system / sulfate/molybdate binding protein	1109541:1110629/ 2752341:2753351	38379/9.3/ 36650/9.1	phosphate transport / sulfate transport
B6425	35.8	7.7	139.8	35.5	9184.1	4.6	0.0	65.7	S	b	sulfate/molybdate binding protein / ABC-type phosphate transport system	2752341:2753351/ 1109541:1110629	36650/9.1/ 38379/9.3	sulfate transport / phosphate transport
B6426	34.6	7.1	96.9	37.9	2647.5	4.3	0.0	27.3	S	a	sulfate/molybdate binding protein	2752341:2753351	36650/9.1	sulfate transport
B6502	37.7	8.1	408.5	14.4	142.3	21.0	2.9	0.3	Fe	h				
B6614	48.3	8.5	280.5	9.2	0.0	0.0	237.1	0.0	Fe	c				
B7206	20.8	8.4	2505.6	20.5	1082.4	13.6	2.3	0.4	Fe	h				
B7215	24.4	9.0	1055.0	14.8	0.0	0.0	892.1	0.0	Fe	c				
B7218	26.4	9.9	1330.9	34.2	150.9	84.7	8.8	0.1	Fe	a	hypothetical protein	2658338:2658976	23455/9.3	unknown function
B7220	25.6	9.7	909.8	9.4	133.0	62.6	6.8	0.1	Fe	c				
B7222	21.6	9.1	1074.6	4.8	6537.2	42.7	0.2	6.1	S	b	hypothetical protein	939543:940118	20536/9.4	unknown function
B7224	22.8	9.2	70.3	24.1	435.5	15.6	0.2	6.2	S	c				
B7227	26.2	9.1	320.2	46.8	0.0	0.0	270.7	0.0	Fe	c				
B7301	32.8	8.5	1687.1	8.5	512.3	25.7	3.3	0.3	Fe	h				
B7307	31.4	9.5	713.3	9.2	0.0	0.0	603.1	0.0	Fe	c				
B7308	31.0	9.3	286.2	53.4	0.0	0.0	242.0	0.0	Fe	c				
B7313	31.9	9.1	0.0	0.0	4646.2	7.8	0.0	2029.1	S	b	hypothetical protein	1500959:1501984	37308/9.2	unknown function
B7405	33.9	9.5	297.3	18.5	96.9	33.4	3.1	0.3	Fe	h				
B7418	33.0	9.5	1107.3	29.1	0.0	0.0	936.3	0.0	Fe	a	HflC protein	1154652:1155524	32139/9.3	not clear
B7421	37.2	8.2	0.0	0.0	413.1	3.5	0.0	180.4	S	c				
B7512	39.1	9.2	2275.6	29.5	0.0	0.0	1924.1	0.0	Fe	c				
B7515	40.5	9.7	999.6	23.3	154.6	19.9	6.5	0.2	Fe	b	D-Ala-D-Ala-carboxypeptidase	517755:518921	41975/9.3	substrate attachment
B7517	39.0	9.2	3419.4	44.1	0.0	0.0	2891.2	0.0	Fe	c				
B7706	50.5	9.2	178.2	14.8	3092.7	17.4	0.1	17.4	S	b	outer membrane protein	2768128:2769672	55015/8.9	probable dehydrogenase activity



B7708	50.4	9.3	162.4	15.5	2302.1	5.7	0.1	14.2	S	b	outer membrane protein	2768128:2769672	55015/8.9	probable dehydrogenase activity
B7714	52.4	9.8	717.3	19.2	0.0	0.0	606.5	0.0	Fe	c				
B7715	50.3	8.5	0.0	0.0	4158.5	20.4	0.0	1816.1	S	b	outer membrane protein	2768128:2769672	55015/8.9	probable dehydrogenase activity
B7801	69.7	8.7	436.4	17.9	205.4	56.0	2.1	0.5	Fe	h				
B7811	88.9	9.3	737.3	31.6	0.0	0.0	623.4	0.0	Fe	c				
B8134	19.3	9.2	501.9	13.4	0.0	0.0	424.4	0.0	Fe	c				
B8210	21.4	10.2	3123.1	14.2	444.0	135.2	7.0	0.1	Fe	c				
B8211	20.9	10.2	370.0	62.1	0.0	0.0	312.9	0.0	Fe	c				
B8212	21.3	10.1	2738.3	39.9	396.3	107.4	6.9	0.1	Fe	c				
B8216	29.0	10.2	0.0	0.0	590.9	44.0	0.0	258.1	S	c				
B8302	29.3	10.0	3364.9	27.0	0.0	0.0	2845.1	0.0	Fe	b	putative ubiquinol-cytochrome c reductase iron-sulfur Rieske protein	6285:6905	22605/8.8	electron transport
B8403	33.6	9.5	1213.6	14.7	157.3	45.1	7.7	0.1	Fe	b	ATP synthase gamma chain	2894672:2895538	31975/9.3	ATP production
B8406	35.8	9.8	290.9	27.4	0.0	0.0	246.0	0.0	Fe	c				
B8504	38.6	9.1	331.4	24.1	0.0	0.0	280.2	0.0	Fe	c				
B8505	41.8	9.2	282.5	6.7	0.0	0.0	238.9	0.0	Fe	c				
B8605	42.9	10.8	1155.5	11.4	385.3	24.5	3.0	0.3	Fe	h				
B8701	52.4	9.8	572.2	22.2	0.0	0.0	483.8	0.0	Fe	c				
B8815	71.3	9.4	831.5	25.5	0.0	0.0	703.1	0.0	Fe	c				
B9809	83.8	10.8	744.7	8.6	97.9	57.5	7.6	0.1	Fe	c				
B9810	79.2	10.7	436.4	42.4	40.5	94.1	10.8	0.1	Fe	c				

Supplementary Table 2. Review of protein spots detected on IPG 6-11/12% SDS-PAGE gels with significant differences in quantity between growth on iron and sulfur.

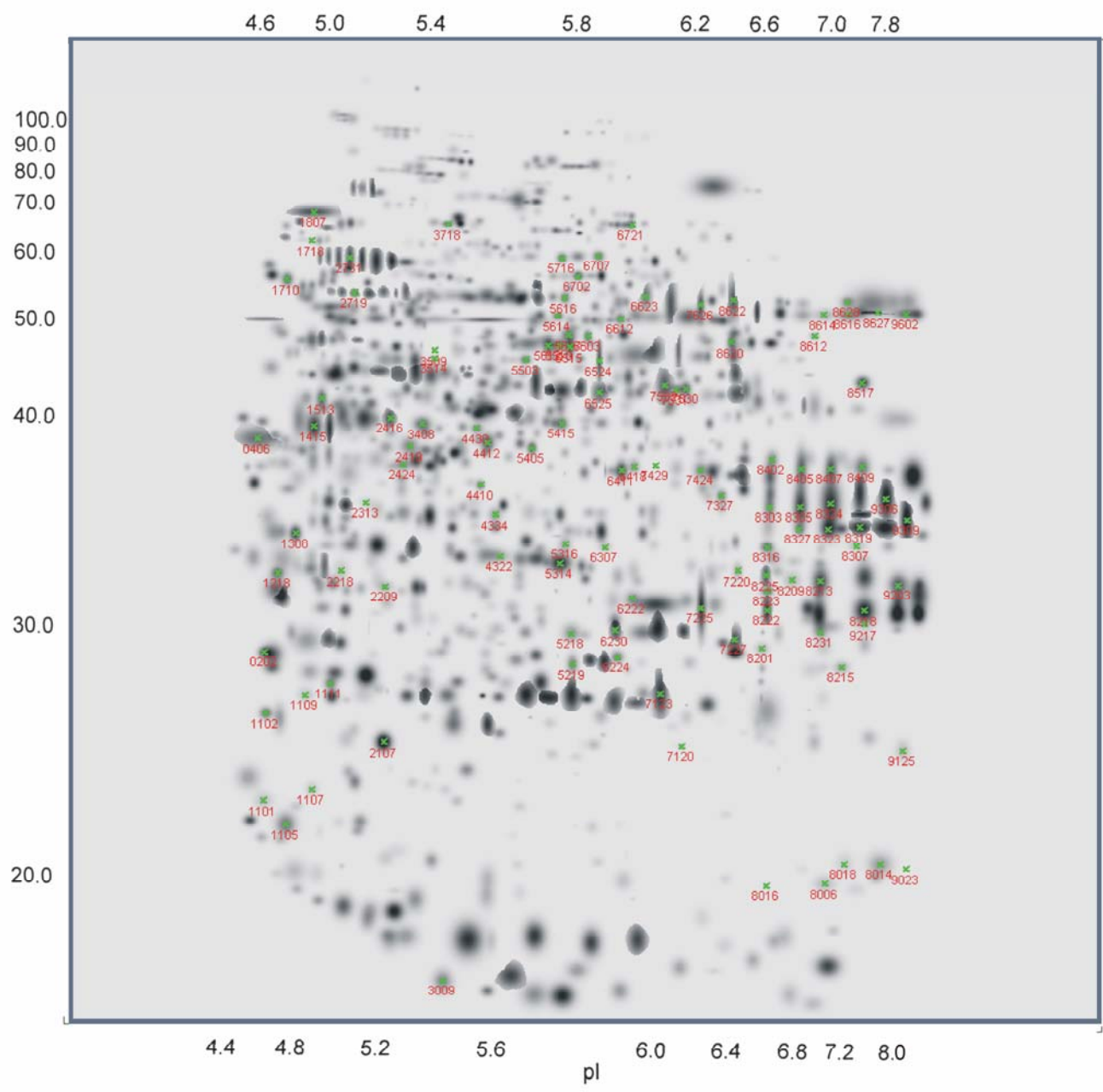
## Legend for Supplementary Table 1 and 2

### *Column ID status:*

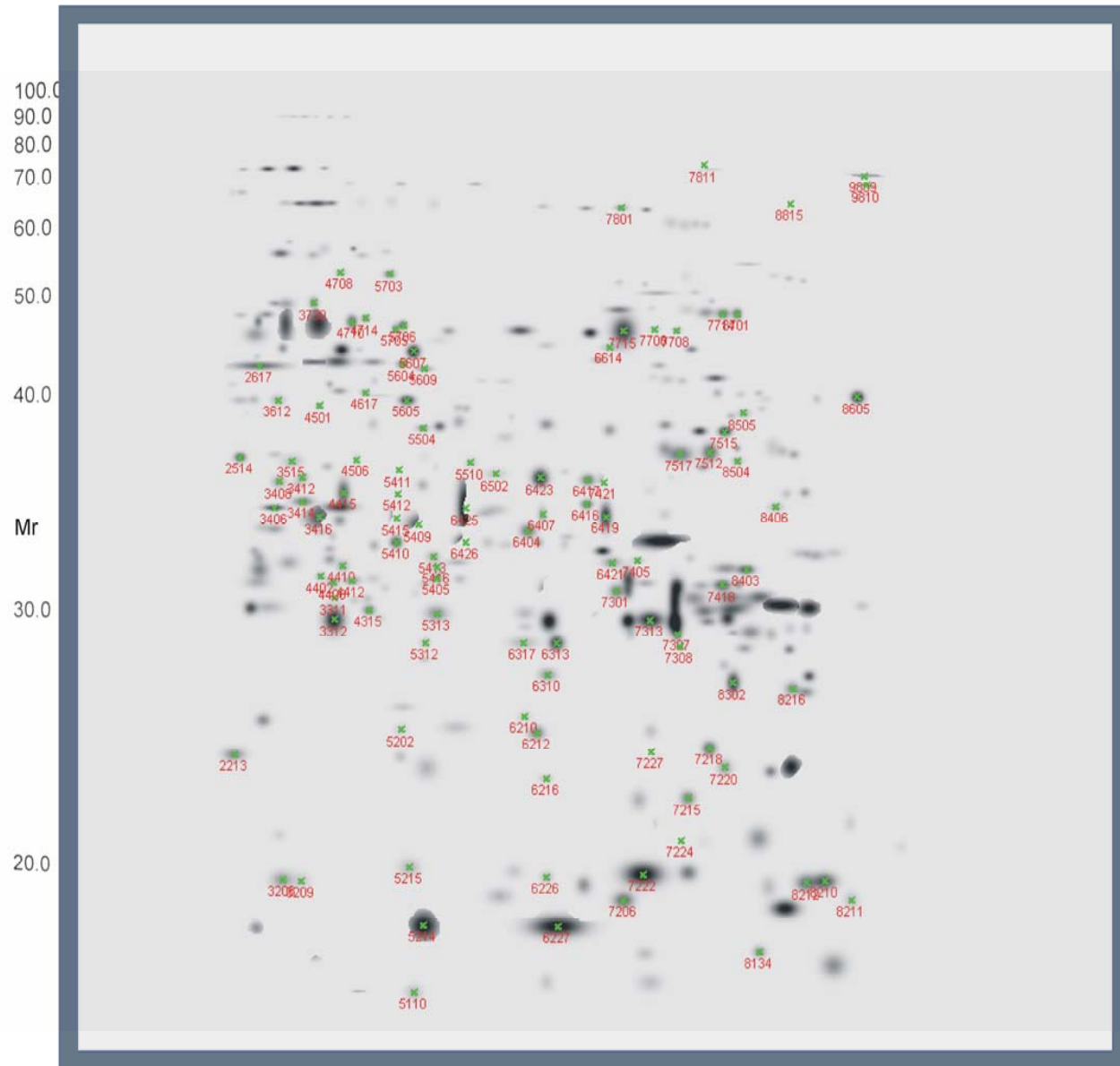
- a This spot matched identification criteria (statistical significance of the change - Student *t*-test at 0.05 confidence level), more than 5-fold change, spot quantity and quality on silver stained gels more than 280 and 20, respectively). The spot was analyzed with peptide mass fingerprinting. Successful protein identification.
- b This spot matched identification criteria (statistical significance of the change - Student *t*-test at 0.05 confidence level), more than 5-fold change, spot quantity and quality on silver stained gels more than 280 and 20, respectively). The spot was analyzed with peptide mass fingerprinting. The PMF MASCOT score was insufficient; it was further analyzed by LC-MS/MS. Successful protein identification.
- c This spot matched identification criteria (statistical significance of the change - Student *t*-test at 0.05 confidence level, more than 5-fold change, spot quantity and quality on silver stained gels more than 280 and 20, respectively). However, the spot quantity or spot quality on Coomassie Brilliant blue – stained gels was insufficient to excise from gel and submit for MS identification.
- d This spot did not matched identification criteria (statistical significance of the change - Student *t*-test at 0.05 confidence level, more than 5-fold change, spot quantity and quality on silver stained gels more than 280 and 20, respectively). However, it is one of several most abundant proteins in the gel (or member of abundant spot train, respectively). For this reason, it was analyzed with peptide mass fingerprinting. Successful protein identification.
- e This spot did not matched identification criteria (statistical significance of the change - Student *t*-test at 0.05 confidence level, more than 5-fold change, spot quantity and quality on silver stained gels more than 280 and 20, respectively). However, it is one of several most abundant proteins in the gel (or member of abundant spot train, respectively). For this reason, it was analyzed with peptide mass fingerprinting. The PMF MASCOT score was insufficient; it was further analyzed by LC-MS/MS. Successful protein identification.
- f This spot matched identification criteria (statistical significance of the change - Student *t*-test at 0.05 confidence level, more than 5-fold change, spot quantity and quality on silver stained gels more than 280 and 20, respectively). However, the spot is situated in the basic part of proteome. These spots were analyzed preferably from the basic range (pI 6-11) gels.
- g This spot matched identification criteria (statistical significance of the change - Student *t*-test at 0.05 confidence level), more than 5-fold change, spot quantity and quality on silver stained gels more than 280 and 20, respectively). The spot was analyzed with peptide mass fingerprinting and LC-MS/MS. Protein was not identified.
- h This spot did not matched identification criteria.

### *Other columns:*

- ns not significantly changed quantity
- \* proteins identified previously [6,8,9]



Supplementary Figure 1.  
 Master gel image, IPG 3-10  
 NL / 12% SDS-PAGE.  
 Positions of protein spots  
 mentioned in Supplementary  
 Table 1 can be viewed in this  
 cyber gel. These spots are  
 marked with spot number  
 (SSP).



Supplementary Figure 2.  
Master gel image, IPG 6-11 /  
12% SDS-PAGE. Positions of  
protein spots mentioned in  
Supplementary Table 2 can  
be viewed in this cyber gel.  
These spots are marked with  
spot number (SSP, without  
“B” at the beginning).