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Supporting Information

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High content peptide microarrays for deciphering kinase specificity and biology

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Identification of phosphorylation sites in kinase substrate proteins. In a first set of experiments we detected individual phosphorylation sites in substrate proteins. We generated a peptide microarray containing 79 peptides derived from bovine myelin basic protein (MBP; Swiss-Prot: P02687), a promiscuous protein substrate for kinases. The 13meric sequences on that microarray represent a complete overlapping peptide scan (MBP scan) through the primary structure of the protein. The entire list of peptide sequences can be found below. For a proof of concept we selected the catalytic subunit of bovine heart cAMP-dependent protein kinase (PKA) because this enzyme phosphorylates one threonine and seven serine residues in full-length bovine MBP[24]. Figure S1 shows the MBP scan after incubation with PKA in the presence of ^{32}P-ATP. All phosphorylation sites detected on the MBP protein were also identified on the microarray (Fig. S1). They share an arginine residue N-terminal to the phosphorylation site. The immobilised positive control peptide Kemptide[25] allows an estimation of the substrate quality. Serine 110 seems to be the major phosphorylation site for PKA on bovine MBP which is consistent with published kinetic measurements with soluble peptides[24]. This experiment demonstrates that microarrays containing overlapping protein-derived peptide scans represent an efficient tool for detection or prediction of potential phosphorylation sites in substrate proteins.

Autophosphorylation is an important principle regulating kinase activities in vivo. In the case of the angiopoietin 1 receptor (Tie-2) several autophosphorylation sites were identified or predicted to serve as a docking module for SH2 domains[26]. In order to find out whether these arrays could be applied for the prediction of autophosphorylation sites we prepared an array containing an overlapping peptide scan through the predicted cytoplasmic domain of Tie-2 (residues 771-1224; Swiss-Prot: Q02763) to detect autophosphorylation site-derived substrate peptides. Figure S1C shows a phosphorimage of the Tie-2 scan after incubation with the kinase domain of Tie-2 in the presence of ^{32}P-ATP. Similar results were obtained using a fluoresceine labelled anti-phosphotyrosine-antibody for the detection of phosphorylated peptides (data not shown).

We identified 11 from a total of 19 tyrosine residues in Tie-2 as substrates for Tie-2 (Y^{816}, Y^{860}, Y^{897}, Y^{954}, Y^{992}, Y^{1015}, Y^{1048}, Y^{1068}, Y^{1080}, Y^{1102} and Y^{1108}). Figure 2 demonstrates the identification of distinct tyrosine autophosphorylation sites in peptides containing more than one tyrosine residue. Peptides L1 to L8 (corresponding to residues 1035 to 1062) allow the identification of Y^{1048} as the only phosphorylation site in these peptides. Inspection of the Tie-2 crystal structure (pdb1FVR)[27] shows that all detected tyrosine residues are well exposed at the surface of the Tie-2 kinase domain. While residues Y^{992}, Y^{1048} and Y^{1108} were shown to be autophosphorylation sites, residues Y^{860} and Y^{897} are found to be phosphorylated in baculovirus-expressed Tie-2 and discussed to be additional autophosporylation sites[28]. For residues Y^{816}, Y^{1068} and Y^{1102} interactions with SH2 domains of Grb14/Shp2, p85-N-terminal domain and Grb2/Grb7/p85-C-terminal domain, respectively, could be demonstrated if these tyrosine residues are phosphorylated in respective peptides[26]. As a control for the selectivity of this

approach we incubated the Tie-2 scan with Abelson tyrosine kinase (Abl, data not shown) and detected incorporated phosphate at residues Y^{904}, Y^{1012}, Y^{1048}, Y^{1068}, Y^{1080} and Y^{1108}.

The catalytic activity of Tie-2 is negatively regulated by phosphorylation at the very C-terminal serine residue (S^{1119}) with acidic residues in -2, +2 and +3 position[27]. To search for upstream kinases phosphorylating S^{1119} we incubated the Tie-2 scan with casein kinase 1 (data not shown) and casein kinase 2 (CK2) an enzyme claimed to be responsible for phosphorylation of about 10-20 % of the eukaryotic phosphoproteome[29] through phosphoryl transfer to serine or threonine residues surrounded by acidic amino acids[30]. The data shown in Figure S2 indicate that CK2 indeed could phosphorylate Tie-2-derived peptides containing the T^{1017} (and Ser^{1019}) residue but not the C-terminal S^{1119} residue. An identical picture was obtained using casein kinase 1.

In summary, we provide clear evidence that overlapping peptide scans on microarrays enable the detection of both autophosphorylation sites and phosphorylation sites of potential upstream kinases.

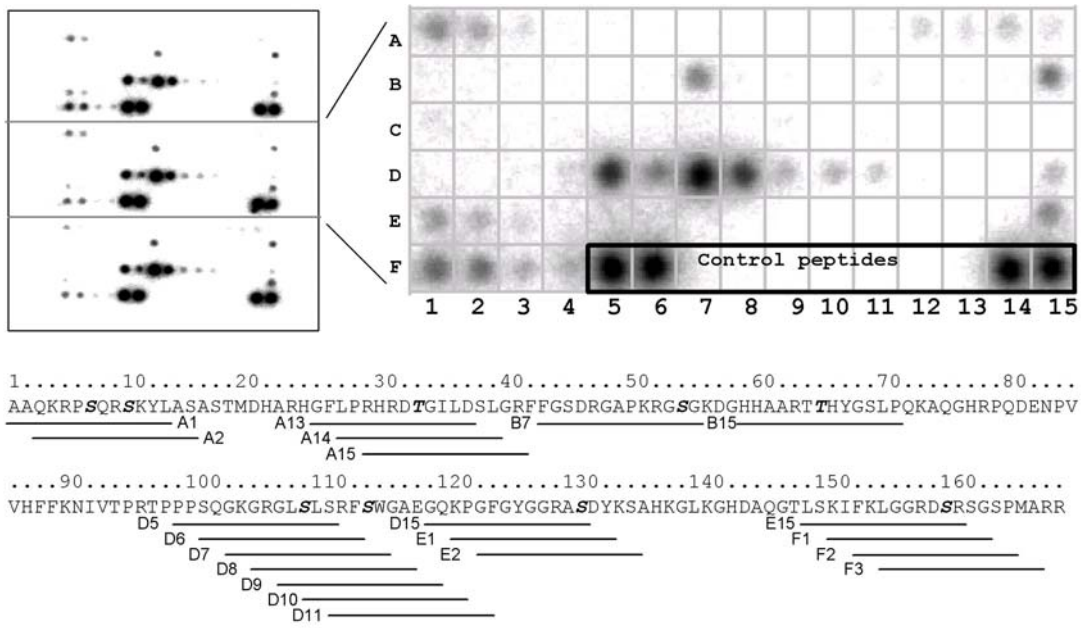


Figure S1: Peptide microarray displaying a myelin basic protein (MBP) overlapping peptide scan in triplicates (13mers, 11 amino acids overlap, A1-F4) and control peptides (F5, F6, F14, F15 are identical and correspond to Kemptide[25]) after incubation with PKA and ^{32}P-ATP. The complete area of the array is shown in the upper left panel. A magnification of one subarray completed with a grid is shown in the upper right panel. The sequence of MBP is shown in the lower panel. Peptides which are phosphorylated in the microarray experiment are underlined and labeled with the respective coordinates.

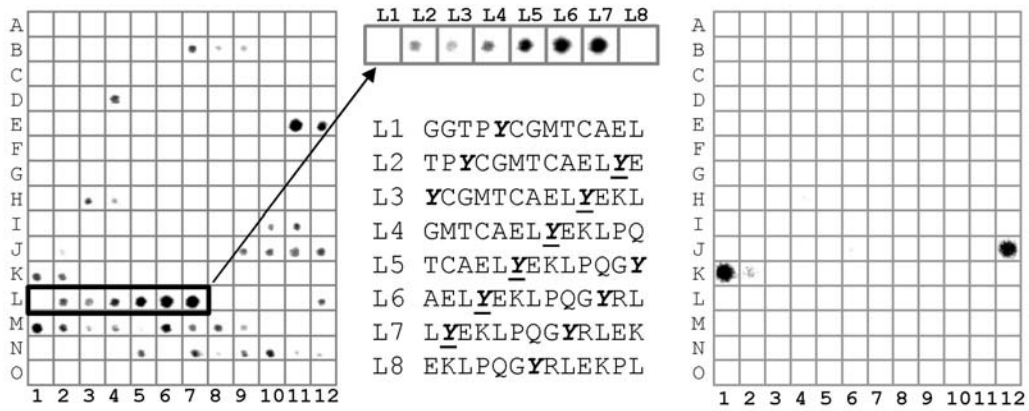


Figure S2: Microarray displaying overlapping peptide scan (13mers, 11 amino acids overlap) through the cytoplasmic domain of the receptor tyrosine kinase Tie-2. The left panel shows the phosphorimage after incubation with Tie-2 and ^{32}P-ATP. Magnification of an area of this image showing the signals for peptides L1-L8 and the respective peptide sequences is shown in the middle panel. In the right panel the microarray displaying Tie-2 scan is shown after incubation with CK2 kinase. The common peptide sequence of spots J12 (SLNYSVYTTNSDV) and K1 (NYSVYTTNSDVWS) is NYSVYTTNSDV.

Materials and Methods

Reagents. Aldehyde modified glass slides were obtained from Quantifoil (Jena, Germany). ^{32}P-ATP was purchased from Amersham Biosciences (Freiburg, Germany). Abl, GSK3ß, CK1 and CK2 were from New England BioLabs (Beverly, Massachusetts), PKA was from Sigma (Taufkirchen, Germany) and Tie-2 was from Proqinase (Freiburg, Germany). PDK1 was cloned and expressed as described earlier.[20] Amino-oxy-acetylated peptides were synthesized by SPOT synthesis.[3] Biotinylated peptides were synthesized on Fmoc-Rink MBHA resin using standard protocols. Biotinylated peptides were purified by RP-HPLC (>95% purity at 220 nm) and identity of peptides was analysed using ESI-mass spectrometry.

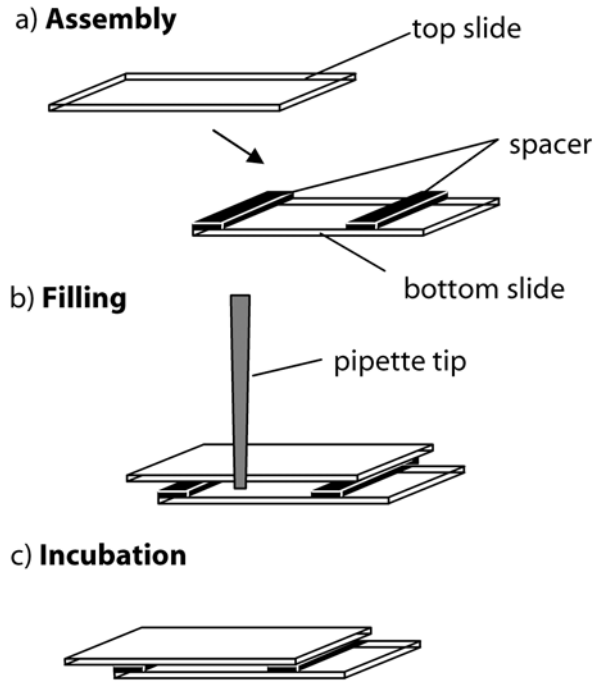
Preparation of micro-arrays. Amino-oxy-acetylated peptides were dissolved in printing solution (70% DMSO, 25% 0.2 M sodium acetate pH 4.5, 5 % glycerol; by vol.). Two droplets of 0.5 nL peptide solution were deposited per spot on aldehyde functionalized glass slides using the non-contact printer Nanoplotter of GESIM (Großerkmannsdorf, Germany) equipped with 8 piezoelectric NanoTips (GESIM, Großerkmannsdorf, Germany). Dot size of the microarrays was 250 µm with a pitch of 380 µm. Peptide microarrays were kept at room temperature for 5 hours, washed with deionised water, quenched with 50% aqueous hydroxylamine, washed extensively with water and ethanol, and dried under a stream of nitrogen. The spotted microarrays were stored at 4 °C and maintained reactivity for more than 15 months.

Solution-phase kinase assay. PDK1 was assayed with peptide and protein substrates as described previously.[20] CK2 assays were done according to the following protocol. Briefly, 25 µL of peptide solution (2 µM-4 mM, Fig. 2) containing 300 µM ATP, 1 µCi ^{32}P-ATP and kinase were incubated in BSA coated 96-well microtiter plates for 5 min at 30 °C (for details see Supplemental Methods online). Reactions were stopped by addition of 25 µL 7.5 M guanidinium hydrochloride. Aliquots of each well were transferred to a Streptavidin Flashplate Plus (PerkinElmer Life Sciences, Belgium). Subsequent to incubation for 1h plates were washed according to the manufacturer´s protocol and radioactivity was counted on a Topcount NXT Microplate Scintillation and Luminescence Counter (PerkinElmer Life Sciences, Belgium). Kinetic data were analysed according to the Michaelis-Menten equation.

Probing and scanning peptide microarrays. Kinase assay solutions including ^{32}P-ATP were prepared and added to the surfaces of the appropriate peptide microarrays (300 µL per experiment) in a humidified chamber. For conditions of all kinase assays see Supplementary Table 2 and Supplementary Methods. Subsequent to incubation for the specified time at given temperature the reaction was stopped by washing 5 times with 0.1 M phosphoric acid followed by washings with deionised water. Finally, microarrays were washed with methanol and dried. Microarrays were exposed to an imaging plate for 8 hours. Data analysis was done using a FLA-3000 Phosphor Imager (Fuji, Japan). Data evaluation was carried out using ArrayPro software package (Media Cybernetics, Silver Spring, MD).

Assay Procedures:

Microarray Assays. Two microarray slides are positioned face to face separated by two plastic spacers (0.3 mm thickness) as shown in the drawing (a). 300 µL of kinase solution in assay buffer (see Supplementary Table 2 online) containing 100 µM ATP and 80µCi/mL γ–^{32}P ATP are applied to the resulting space between the two slides. Microarrays were incubated for 1 hour at 30°C. Then the slides were washed 5 times for 3 minutes with 25 mL of 0.1 M phosphoric acid followed by washing steps with 25 mL deionised water. Finally, microarrays were washed with 25 mL methanol for 2 minutes and dried at room temperature.



Detection Methods:

A) Phosphorimaging. Peptide microarrays were exposed for 8 hours to a BAS-MS imaging plate (Fuji Photo Film Co., Ltd., Japan). Phosphorylation of peptides in the presence of ^{32}P ATP was detected using a FLA-3000 Phosphor Imager (Fuji, Japan).

B) Fluorescence scanning. Peptide microarrays were incubated with anti-phospho-tyrosine monoclonal antibody (Pt66, fluoresceine-labelled, Sigma, Product No. F3145) according to manufacturers protocols. Readout was performed with a resolution of 5 µM (excitation: 488 nm; emission: 530 nm) using a Array-WoRx Biochip Reader (Applied Precision, LLC, Issaquah, USA).

Microarrays employed in this study:

MBP-Scan array. This microarray displays 79 peptides derived from bovine myelin basic protein (MBP; Swiss-Prot: P02687). The 13meric sequences represent a complete overlapping peptide scan through the primary structure of the protein (11 amino acids overlap).

710 kinase substrates array. This microarray displays 710 annotated human phosphorylation sites as 13meric peptides extracted from Swiss-Prot rel. 4.0 and Phosphobase vers. 2.0.

Phosphopeptide array. All peptides containing at least two potential phosphoacceptor sites in the 710 kinase substrates were extracted (694 peptides). All possible monophosphorylated derivatives resulting in 2234 phosphopeptides were immobilised together with the 694 wild type peptides on microarrays.

Tie2 scan array. This microarray displays 171 peptides derived from protein tyrosine kinase Tie2 (Swiss-Prot: Q02763; amino acid residues 771-1124). The 13meric sequences represent a complete overlapping peptide scan through the primary structure of the protein (11 amino acids overlap).

Human kinase activation loop array. Sequences of activation loops of human kinases were extracted from primary structure data using an alignment from the literature (Kostich,M., English,J., Madison,V., Gheyas,F., Wang,L., Qiu,P., Greene,J. and Laz,T.M. (2002) Human members of the eukaryotic protein kinase family. *Genome Biol.,* **3,** RESEARCH0043). The sequences were dissected into 13-meric peptides with an overlap of three amino acids resulting in 1228 sequences. Additionally we included 166 hydrophobic motifs derived from C-terminal tails of human kinases.

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Supplementary Table 1

Complete list of all peptides represented on the Myelin Basic Protein Scan. The peptide sequences are numbered according to the arrangement in Figure 1 A.

A1	AAQKRPSQRSKYL	C1	AARTTHYGSLPQK	E1	KPGFGYGGRASDY
A2	QKRPSQRSKYLAS	C2	RTTHYGSLPQKAQ	E2	GFGYGGRASDYKS
A3	RPSQRSKYLASAS	C3	THYGSLPQKAQGH	E3	GYGGRASDYKSAH
A4	SQRSKYLASASTM	C4	YGSLPQKAQGHRP	E4	GGRASDYKSAHKG
A5	RSKYLASASTMDH	C5	SLPQKAQGHRPQD	E5	RASDYKSAHKGLK
A6	KYLASASTMDHAR	C6	PQKAQGHRPQDEN	E6	SDYKSAHKGLKGH
A7	LASASTMDHARHG	C7	KAQGHRPQDENPV	E7	YKSAHKGLKGHDA
A8	SASTMDHARHGFL	C8	QGHRPQDENPVVH	E8	SAHKGLKGHDAQG
A9	STMDHARHGFLPR	C9	HRPQDENPVVHFF	E9	HKGLKGHDAQGTL
A10	MDHARHGFLPRHR	C10	PQDENPVVHFFKN	E10	GLKGHDAQGTLSK
A11	HARHGFLPRHRDT	C11	DENPVVHFFKNIV	E11	KGHDAQGTLSKIF
A12	RHGFLPRHRDTGI	C12	NPVVHFFKNIVTP	E12	HDAQGTLSKIFKL
A13	GFLPRHRDTGILD	C13	VVHFFKNIVTPRT	E13	AQGTLSKIFKLGG
A14	LPRHRDTGILDSL	C14	HFFKNIVTPRTPP	E14	GTLSKIFKLGGRD
A15	RHRDTGILDSLGR	C15	FKNIVTPRTPPPS	E15	LSKIFKLGGRDSR
B1	RDTGILDSLGRFF	D1	NIVTPRTPPPSQG	F1	KIFKLGGRDSRSG
B2	TGILDSLGRFFGS	D2	VTPRTPPPSQGKG	F2	FKLGGRDSRSGSP
B3	ILDSLGRFFGSDR	D3	PRTPPPSQGKGRG	F3	LGGRDSRSGSPMA
B4	DSLGRFFGSDRGA	D4	TPPPSQGKGRGLS	F4	GRDSRSGSPMARR
B5	LGRFFGSDRGAPK	D5	PPSQGKGRGLSLS	F5	LRRASLG
B6	RFFGSDRGAPKRG	D6	SQGKGRGLSLSRF	F6	LRRASLG
B7	FGSDRGAPKRGSG	D7	GKGRGLSLSRFSW	F7	VVSHFND
B8	SDRGAPKRGSGKD	D8	GRGLSLSRFSWGA	F8	Blank
B9	RGAPKRGSGKDGH	D9	GLSLSRFSWGAEG	F9	Blank
B10	APKRGSGKDGHHA	D10	SLSRFSWGAEGQK	F10	Blank
B11	KRGSGKDGHHAAR	D11	SRFSWGAEGQKPG	F11	Blank
B12	GSGKDGHHAARTT	D12	FSWGAEGQKPGFG	F12	Blank
B13	GKDGHHAARTTHY	D13	WGAEGQKPGFGYG	F13	VVSHFND
B14	DGHHAARTTHYGS	D14	AEGQKPGFGYGGR	F14	LRRASLG
B15	HHAARTTHYGSLP	D15	GQKPGFGYGGRAS	F15	LRRASLG

Supplementary Table 2

Buffers, microarray types, kinase activities and detection methods used in this study for each kinase.

Kinase	Buffer	Micorarray	Units/mL	Detection Method
PKA	1)	MBP-Scan	30	A)
PKA	1)	710 Kinase Substrates	30	A)
CK2	2)	Primed 710 Kinase Subtrates	400	A)
CK2	2)	710	400	A)
CK2	2)	Tie2 Scan	400	A)
Tie2	3)	Tie2 Scan	30µg/mL	A), B)
ABL	4)	Tie2 Scan	400	A)
PDK1	5)	Activation Loop	40µg/mL	A)
GSK3	6)	710 Kinase Substrates	500	A)

Buffers

1) 50 mM Tris-HCl, 150 mM NaCl, 30 mM $MgCl_2$, 4 mM DTT, 2 mM EGTA, pH 7.5 at 25°C
2) 20 mM Tris-HCl, 50 mM KCl, 10 mM $MgCl_2$, pH 7.5 at 25°C
3) 60 mM HEPES-NaOH, 3 mM $MgCl_2$, 3$MnCl_2$, 3µM Na-orthovanadate, 1.2 mM DTT, pH 7.5 at 25°C
4) 50 mM Tris-HCl, 10 mM $MgCl_2$, 1 mM EGTA, 2 mM DTT, 0.01% Brij 35, pH 7.5 at 25°C
5) 50 mM Tris-HCl, 10 mM magnesium acetate, 0.1 mM EDTA, 0.1 mM EGTA, 0.1 % (v/v) beta-mercaptoethanole, 1 µM microcystin-LR (Sigma M2912), 50 µM PIFtide, pH 7.5 at 25°C
6) 20 mM Tris-HCl, 10 mM $MgCl_2$, 5 mM DTT, pH 7.5 at 25°C

Supplementary Table 3

Complete list of all peptides represented on the overlapping peptide scan through the cytoplasmatic domain of Tie2. The peptide sequences are numbered according to the arrangement in Figures 1C and 1E.

A1	QLKRANVQRRMAQ	E10	IINLLGACEHRGY	J7	RLPVRWMAIESLN
A2	KRANVQRRMAQAF	E11	NLLGACEHRGYLY	J8	PVRWMAIESLNYS
A3	ANVQRRMAQAFQN	E12	LGACEHRGYLYLA	J9	RWMAIESLNYSVY
A4	VQRRMAQAFQNVR	F1	ACEHRGYLYLAIE	J10	MAIESLNYSVYTT
A5	RRMAQAFQNVREE	F2	EHRGYLYLAIEYA	J11	IESLNYSVYTTNS
A6	MAQAFQNVREEPA	F3	RGYLYLAIEYAPH	J12	SLNYSVYTTNSDV
A7	QAFQNVREEPAVQ	F4	YLYLAIEYAPHGN	K1	NYSVYTTNSDVWS
A8	FQNVREEPAVQFN	F5	YLAIEYAPHGNLL	K2	SVYTTNSDVWSYG
A9	NVREEPAVQFNSG	F6	AIEYAPHGNLLDF	K3	YTTNSDVWSYGVL
A10	REEPAVQFNSGTL	F7	EYAPHGNLLDFLR	K4	TNSDVWSYGVLLW
A11	EPAVQFNSGTLAL	F8	APHGNLLDFLRKS	K5	SDVWSYGVLLWEI
A12	AVQFNSGTLALNR	F9	HGNLLDFLRKSRV	K6	VWSYGVLLWEIVS
B1	QFNSGTLALNRKV	F10	NLLDFLRKSRVLE	K7	SYGVLLWEIVSLG
B2	NSGTLALNRKVKN	F11	LDFLRKSRVLETD	K8	GVLLWEIVSLGGT
B3	GTLALNRKVKNNP	F12	FLRKSRVLETDPA	K9	LLWEIVSLGGTPY
B4	LALNRKVKNNPDP	G1	RKSRVLETDPAFA	K10	WEIVSLGGTPYCG
B5	LNRKVKNNPDPTI	G2	SRVLETDPAFAIA	K11	IVSLGGTPYCGMT
B6	RKVKNNPDPTIYP	G3	VLETDPAFAIANS	K12	SLGGTPYCGMTCA
B7	VKNNPDPTIYPVL	G4	ETDPAFAIANSTA	L1	GGTPYCGMTCAEL
B8	NNPDPTIYPVLDW	G5	DPAFAIANSTAST	L2	TPYCGMTCAELYE
B9	PDPTIYPVLDWND	G6	AFAIANSTASTLS	L3	YCGMTCAELYEKL
B10	PTIYPVLDWNDIK	G7	AIANSTASTLSSQ	L4	GMTCAELYEKLPQ
B11	IYPVLDWNDIKFQ	G8	ANSTASTLSSQQL	L5	TCAELYEKLPQGY
B12	PVLDWNDIKFQDV	G9	STASTLSSQQLLH	L6	AELYEKLPQGYRL
C1	LDWNDIKFQDVIG	G10	ASTLSSQQLLHFA	L7	LYEKLPQGYRLEK
C2	WNDIKFQDVIGEG	G11	TLSSQQLLHFAAD	L8	EKLPQGYRLEKPL
C3	DIKFQDVIGEGNF	G12	SSQQLLHFAADVA	L9	LPQGYRLEKPLNC
C4	KFQDVIGEGNFGQ	H1	QQLLHFAADVARG	L10	QGYRLEKPLNCDD
C5	QDVIGEGNFGQVL	H2	LLHFAADVARGMD	L11	YRLEKPLNCDDEV
C6	VIGEGNFGQVLKA	H3	HFAADVARGMDYL	L12	LEKPLNCDDEVYD
C7	GEGNFGQVLKARI	H4	AADVARGMDYLSQ	M1	KPLNCDDEVYDLM
C8	GNFGQVLKARIKK	H5	DVARGMDYLSQKQ	M2	LNCDDEVYDLMRQ
C9	FGQVLKARIKKDG	H6	ARGMDYLSQKQFI	M3	CDDEVYDLMRQCW
C10	QVLKARIKKDGLR	H7	GMDYLSQKQFIHR	M4	DEVYDLMRQCWRE
C11	LKARIKKDGLRMD	H8	DYLSQKQFIHRDL	M5	VYDLMRQCWREKP
C12	ARIKKDGLRMDAA	H9	LSQKQFIHRDLAA	M6	DLMRQCWREKPYE
D1	IKKDGLRMDAAIK	H10	QKQFIHRDLAARN	M7	MRQCWREKPYERP
D2	KDGLRMDAAIKRM	H11	QFIHRDLAARNIL	M8	QCWREKPYERPSF
D3	GLRMDAAIKRMKE	H12	IHRDLAARNILVG	M9	WREKPYERPSFAQ
D4	RMDAAIKRMKEYA	I1	RDLAARNILVGEN	M10	EKPYERPSFAQIL
D5	DAAIKRMKEYASK	I2	LAARNILVGENYV	M11	PYERPSFAQILVS
D6	AIKRMKEYASKDD	I3	ARNILVGENYVAK	M12	ERPSFAQILVSLN
D7	KRMKEYASKDDHR	I4	NILVGENYVAKIA	N1	PSFAQILVSLNRM
D8	MKEYASKDDHRDF	I5	LVGENYVAKIADF	N2	FAQILVSLNRMLE
D9	EYASKDDHRDFAG	I6	GENYVAKIADFGL	N3	QILVSLNRMLEER
D10	ASKDDHRDFAGEL	I7	NYVAKIADFGLSR	N4	LVSLNRMLEERKT
D11	KDDHRDFAGELEV	I8	VAKIADFGLSRGQ	N5	SLNRMLEERKTYV
D12	DHRDFAGELEVLC	I9	KIADFGLSRGQEV	N6	NRMLEERKTYVNT
E1	RDFAGELEVLCKL	I10	ADFGLSRGQEVYV	N7	MLEERKTYVNTTL
E2	FAGELEVLCKLGH	I11	FGLSRGQEVYVKK	N8	EERKTYVNTTLYE
E3	GELEVLCKLGHHP	I12	LSRGQEVYVKKTM	N9	RKTYVNTTLYEKF
E4	LEVLCKLGHHPNI	J1	RGQEVYVKKTMGR	N10	TYVNTTLYEKFTY
E5	VLCKLGHHPNIIN	J2	QEVYVKKTMGRLP	N11	VNTTLYEKFTYAG
E6	CKLGHHPNIINLL	J3	VYVKKTMGRLPVR	N12	TTLYEKFTYAGID
E7	LGHHPNIINLLGA	J4	VKKTMGRLPVRWM	O1	LYEKFTYAGIDCS
E8	HHPNIINLLGACE	J5	KTMGRLPVRWMAI	O2	EKFTYAGIDCSAE
E9	PNIINLLGACEHR	J6	MGRLPVRWMAIES	O3	FTYAGIDCSAEEA

Supplementary Table 4

Complete list of all peptides represented on the peptide microarray with 710 annotated phosphorylation sites from the human proteome. The peptide sequences are numbered according to the arrangement in Figure 2A.

A1	FSLHDALSGSGNP	**B26**	STAENAEYLRVAP	**D21**	FQDIQQLSSEEND
A2	ISLDNPDYQQDFF	**B27**	ISMISADSHEKRH	**D22**	MGKDGRGYVPATI
A3	GSPNRAYTHQVVT	**B28**	TERGDKGYVPSVF	**D23**	SPVFTSRSAAFSG
A4	ELFDDPSYVNVQN	**B29**	SSPGSPGTPGSRS	**D24**	YDPAKRISGKMAL
A5	CNATFKKTFRHLL	**B30**	**Blank**	**D25**	ELLCLRRSSLKAY
A6	NRTLSMSSLPGLE	**C1**	LSRGEEVYVKKTM	**D26**	DSRSHQNSPTELN
A7	SEKRKQISVRGLA	**C2**	SKSKDVLSAAEVM	**D27**	YFLGSSFSPVRCG
A8	STSIEYVTQRNCN	**C3**	GLSLSRFSWGAEG	**D28**	LNTSYPLSPLSDF
A9	RQEDGGVYSSSGL	**C4**	RVQSKIGSLDNIT	**D29**	VPSSRGDYMTMQM
A10	CQLGQRIYQYIQS	**C5**	TPGSRSRTPSLPT	**D30**	EEKKKKTTTIAVE
A11	QCKPVSVTPQGND	**C6**	TRAAPALTPPDRL	**E1**	RKRSRKESYSVYV
A12	PSVEPPLSQETFS	**C7**	KGAKPDVSNGQPE	**E2**	IAKRRRLSSLRAS
A13	LDIEQFSTVKGVN	**C8**	RNLYSGDYYRIQG	**E3**	FVSNRKPSKDKDK
A14	GPMRRSKSPADSA	**C9**	YEEKKKKTTTIAV	**E4**	QGKGRGLSLSRFS
A15	CADVPLLTPSSKE	**C10**	ESSISSSSEEMSL	**E5**	IPTLNRMSFSSNL
A16	PQKSHGRTQDENP	**C11**	TSGEDTLSDSDDE	**E6**	ARAAARLSLTDPL
A17	RLSSLRASTSKSE	**C12**	GVRLLQDSVDFSL	**E7**	TFRPRTSSNASTI
A18	**Blank**	**C13**	KEVHKSGYLSSER	**E8**	SVIVADQTPTPTR
A19	CMDKYRLSCLEEE	**C14**	RDVYSTDYYRVGG	**E9**	KWTKRTLSETSSS
A20	GQDGVRQSRASDK	**C15**	DQARKAVSMHEVN	**E10**	KEFGVERSVRPTD
A21	IGTAEPDYGALYE	**C16**	INSIRKFSIVQKT	**E11**	ILVSTVKSKRREH
A22	EHIERRVSNAGGP	**C17**	KHDTEMKYYIVHL	**E12**	AAELVNNYGKGWS
A23	IQDVGAFSTVKGV	**C18**	TQNVPKDTMDHVN	**E13**	ALGADDSYYTARS
A24	NVLSPLPSQAMDD	**C19**	KEEEEGISQESSE	**E14**	ISGYLVDSVAKTI
A25	EELRKARSNSTLS	**C20**	LARRRKATQVGEK	**E15**	LNQGVRTYVDPFT
A26	TVDGKEIYNTIRR	**C21**	MKIDEPSTPYHSM	**E16**	EAQKVIYTLMEKD
A27	DRMSLVNSRCQEA	**C22**	YGSLPQKSHGRTQ	**E17**	DPGSAAPYLKTKF
A28	ASARAGETRFTDT	**C23**	PINGSPRTPRRGQ	**E18**	SFGLSAMSPTKAA
A29	ERVSRKMSIQEYE	**C24**	STPTSPGSLRKHK	**E19**	SMSDPGVSYRTRE
A30	TKREIMLTPVTVA	**C25**	GRRGRLPSKPKQP	**E20**	KDGATMKTFCGTP
B1	GFIDQNLSPTKGN	**C26**	GIVYAVSSDRFRS	**E21**	TYRIGHHSTSDDS
B2	DRIDEKLSEILGM	**C27**	EILSRRPSYRKIL	**E22**	PPTETGESSQAEE
B3	GLVEVASYCEESR	**C28**	MARKMKDTDSEEE	**E23**	RAKISQGTKVPEE
B4	ISVDGLSTPVVLS	**C29**	AGTSFMMTPYVVT	**E24**	LRPDSEASQSPQY
B5	KKRPQRATSNVFA	**C30**	TSGSKRNSVDTAT	**E25**	AVIPINGSPRTPR
B6	RDIYRASYYRRGD	**D1**	SDRKGGSYSQAAS	**E26**	GSGLLCVSPWPFV
B7	TPVTVAYSPKRSP	**D2**	GVRQSRASDKQTL	**E27**	GGTDEGIYDVPLL
B8	NLNGREFSGRALR	**D3**	DRTSRDSSPVMRS	**E28**	QRSRKRLSQDAYR
B9	LQNLAKASPVYLD	**D4**	CSDSTNEYMDMKP	**E29**	LVDSVAKTIDAGC
B10	FSLLRGPSWDPFR	**D5**	YEDDDYVSKKSKH	**E30**	Kemptide*
B11	PLGPLAGSPVIAA	**D6**	GDDEDACSDTEAT	**F1**	ARIIDSEYTAQEG
B12	EQGKRNFSKAMSV	**D7**	LSTPVVLSPGPQK	**F2**	KFEEAERSLKDME
B13	DMKGDVKYADIES	**D8**	PFKLSGLSFKRNR	**F3**	PKLGRRHSMENME
B14	RSRVVGGSLRGAQ	**D9**	KKFELLPTPPLSP	**F4**	RLIEDNEYTAREG
B15	SLLKKRDSFRTPR	**D10**	LLPTHTLTPVLLT	**F5**	WTASSPYSTVPPY
B16	LTLWTSDSAGEEC	**D11**	QKRREILSRRPSY	**F6**	YRDVRFESIRLPG
B17	EITQDENTVSTSL	**D12**	DVHNLDYYKKTTN	**F7**	AGLTAEVSWKVLE
B18	LARETIESLSSSE	**D13**	SSNDSRSSLIRKR	**F8**	VFLRCINYVFFPS
B19	YISKAEEYFLLKS	**D14**	TQDENTVSTSLGH	**F9**	LPVPQPSSAPPTP
B20	NYLRRRLSDSNFM	**D15**	QASSPQSSDVEDE	**F10**	LIEDNEYTARQGA
B21	RLQRRRGSSIPQF	**D16**	LHALGKATPIYLD	**F11**	FGPARNDSVIVAD
B22	VASVMQEYTQSGG	**D17**	ERNRAAASRCRQK	**F12**	SNDSTSVSAVASN
B23	SRFNRRVSVCAET	**D18**	EPKSPGEYINIDF	**F13**	LLPTPPLSPSRRS
B24	DTATKSGSTTKNR	**D19**	EGEEDTEYMTPSS	**F14**	VLKEQTGSDDEDE
B25	LHTLVVASAGPTS	**D20**	ICRHVRYSTNNGN	**F15**	AILRRPTSPVSRE

F16	RELVEPLTPSGEA	H20	VKSRWSGSQQVEQ	J24	RHIVRKRTLRRLL
F17	IAEPMRRSVSEAA	H21	TLTPVLLTPSSLP	J25	NVKSKIGSTENLK
F18	RLDGENIYIRHSN	H22	KGVDAQGTLSKIF	J26	MPLNRTLSMSSLP
F19	AVEEDAESEDEEE	H23	ADIESSNYMAPYD	J27	GEEELSNYICMGG
F20	KEVVRTDSLKGRR	H24	IVAILVSTVKSKR	J28	MNMLMERYRVESD
F21	AALSRMPSPGGRI	H25	LMLRLQDYEEKTK	J29	LQKKQLCSFEIYE
F22	RGKEGPGTPTRSS	H26	ECNSSTDSCDSGP	J30	P4*
F23	SKRKGHEYTNIKY	H27	RDLELPLSPSLLG	K1	SGAQASSTPLSPT
F24	SKVKRQSSTPSAP	H28	PRSSSNASSVSTR	K2	EKMWAFMSSRQQT
F25	YMAPYDNYVPSAP	H29	FAKTFVGTPYYMS	K3	DMKVRKSSTPEEV
F26	TKLTRIPSAKKYK	H30	Tab2*	K4	LLSKNESSPIRFD
F27	DSFLQRYSSDPTG	I1	RKPGLRRSPIKKV	K5	SCKDDINSYECWC
F28	YVVAKRESRGLKS	I2	EGNNANYTEYVAT	K6	QIRRRRPTPATLV
F29	NMRDDEITQDENT	I3	VDLSKVTSKCGSL	K7	LSAFRRTSLAGGG
F30	Kemptide*	I4	VPSDNIDSQGRNC	K8	QVEFRRLSISAES
G1	APNVHINTIEPVN	I5	ESIRMKRYILHFH	K9	FGMSRNLYAGDYY
G2	REEEATRSEKKKA	I6	TGIMQLKSEIKQV	K10	GQKFARKSTRRSI
G3	AGGGRRISDSHED	I7	DFGFFSSSESGAP	K11	GGPGPERTPGSGS
G4	DTSPRHLSNVSST	I8	QAPGPALTPSLLP	K12	LDRDGSRSLDADE
G5	RKSVPTVSKGTVE	I9	VPTVSKGTVEGNY	K13	FKKSFKLSGFSFK
G6	LDSCNSLTPKSTP	I10	PKRGFLRSASLGR	K14	DIMRDSNYISKGS
G7	QARPGPQSPGSPL	I11	TEATATDYHTTSH	K15	PSFLRAPSWFDTG
G8	TEASGYISSLEYP	I12	LNVAAVNTHRDRP	K16	GGPTTPLSPTRLS
G9	RFIGRRQSLIEDA	I13	NEEESSYSYEEIN	K17	AFDLFKLTPEEKN
G10	GEAGGPLTPRRVS	I14	PWLKPGRSPLPSH	K18	QSTKVPQTPLHTS
G11	FDKDGNGYISAAE	I15	TSSSQLSTPKSKQ	K19	RSGSRRGSFDATG
G12	IVAENPEYLSEFS	I16	DSDLSRRSSSTMS	K20	KKDTETVYSEVRK
G13	VISDGGDSEQFID	I17	NRYGMGTSVERAA	K21	CQRHLDISRELND
G14	HLESGMKSSKSKD	I18	DSLSRYDSDGDKS	K22	FGEKRKNSILNPI
G15	RGGVKRISGLIYE	I19	RYAQDDFSLDENE	K23	KSNVKIQSTPVKQ
G16	AAEERRKSHEAEV	I20	LEDIKRLTPRFTL	K24	DEVPSQDSPGAAE
G17	QRSRGRASSHSSQ	I21	QSKVPFRSRSPSE	K25	IENEEQEYVQTVK
G18	HPGYINFSYEVLT	I22	TSVSAVASNMRDD	K26	FVQLRRKSDLETS
G19	GPFPGSQTSDTLP	I23	DLILNRCSESTKR	K27	DGPKGTGYIKTEL
G20	AVRDMRQTVAVGV	I24	YSYQMALTPVVVT	K28	LDDFDGTYETQGG
G21	RGAPPRRSSIRNA	I25	AQAFPVSYSSSGA	K29	QIEMKKRSPISTD
G22	FCKRRVESGEGSD	I26	FMRLRRLSTKYRT	K30	P2*
G23	EQRMKESSFYSLC	I27	DNTPHTPTPFKNA	L1	LVNSIAKTYVGTN
G24	AMNREVSSLKNKL	I28	TRQPVELTPTDKL	L2	GIPVRCYSAEVVT
G25	EVEEEDSSESEES	I29	QDAYRRNSVRFLQ	L3	TPRTPPPSQGKGR
G26	HQDQEGDTDAGLK	I30	P4*	L4	PLPSHARSQPGLC
G27	VGEEEHVYSFPNK	J1	AGERRKGTDVNVF	L5	YVQLPATYMNLGP
G28	QAFELILSPRSKE	J2	LEKIGEGTYGTVF	L6	SNVSPAISIHEIG
G29	PAPSRTASFYESM	J3	ATDYHTTSHPGTH	L7	VQGEEKESSNDST
G30	Tab2*	J4	PVVSGDTSPRHLS	L8	EYTKEDGSKRIGM
H1	ASAASFEYTILDP	J5	DDIDLFGSDDEEE	L9	TRHPPVLTPPDQE
H2	EAILPRISVISTG	J6	PRAFSSRSYTSGP	L10	RGAPKRGSGKVPW
H3	GAEIVYKSPVVSG	J7	NHCDMASTLIGTP	L11	IHRKTTASTRKVS
H4	AHSIHQRSRKRLS	J8	DDSSAYRSVDEVN	L12	SKYLATASTMDHA
H5	PSLSRHSSPHQSE	J9	KIPKRPGSVHRTP	L13	FMSSRRQSVLVKS
H6	LDIPTGTTPQRKS	J10	KNSDLLTSPDVGL	L14	GLAKSFGSPNRAY
H7	EDDPEATYTTSGG	J11	GVPVRTYTHEVVT	L15	VLDIEQFSTVKGV
H8	TPLHRDKTPLHQK	J12	PQATRQTSVSGPA	L16	KTPDGNKSPAPKP
H9	GRSLSVTSLGGLP	J13	SGLYRSPSMPENL	L17	YQAEENTYDEYEN
H10	PEEKTTNTVSKFD	J14	KAPRDPVTENCVQ	L18	LMPVSAQTPKGRR
H11	PGRSPLPSHARSQ	J15	RKGAGDGSDEEVD	L19	QCKDKEATKLTEE
H12	NTWGCGNSLRTAL	J16	EKESSNDSTSVSA	L20	GRKGSGDYMPMSP
H13	PGETPPLSPIDME	J17	RYMEDSTYYKASK	L21	VSGQLIDSMANSF
H14	EFPSRGKSSSYSK	J18	ADSEMTGYVVTRW	L22	SSMPGGSTPVSSA
H15	LSSLRASTSKSES	J19	EAIKMGRYTEIFM	L23	RGVQRKVSGSRGS
H16	SQITSQVTGQIGW	J20	EREGSKRYCIQTK	L24	PTAENPEYLGLDV
H17	KNAKKEDSDEEED	J21	VSNEDPSSPRASP	L25	YPTGNHTYQEIAV
H18	IGHGTKVYIDPFT	J22	GDRSGYSSPGSPG	L26	QCALCRRSTTDCG
H19	RGLKRSLSEMEIG	J23	AGALASSSKEENR	L27	LCYESHESMESYE

L28	KKKKKRFSFKKSF	O2	TKAQVPDSAGTAT	Q6	GAGFGSRSLYGLG
L29	FPTSTSLSPFYLR	O3	SYEEHIPYTHMNG	Q7	SPVMRSSSTLPVP
L30	P2*	O4	EEGFGSSSPVKSP	Q8	VSQREAEYEPETV
M1	NNFDQDFTREEPV	O5	SVPEFPLSPPKKK	Q9	EPHVTRRTPDYFL
M2	QSRPRSCTWPLQR	O6	DFVGHQGTVPSDN	Q10	ERLKLSPSPSSRV
M3	EETGTEEYMKMDL	O7	AGPTRQASQAGPV	Q11	DGKKRKRSRKESY
M4	REEAIKFSEEQRF	O8	RHLSNVSSTGSID	Q12	VCNGGIMTPPKST
M5	MLRGRSLSVTSLG	O9	YASSNPEYLSASD	Q13	KGTVEGNYVSLTR
M6	VRYIKENSPCVTP	O10	DMYDKEYYSVHNK	Q14	DPGSVLSTACGTP
M7	SSNYMAPYDNYVP	O11	KGRGLSLSRFSWG	Q15	VCDCKRNSDVMDC
M8	AAGERRKSQEAQV	O12	FLPRHRDTGILDS	Q16	QASSTPLSPTRIT
M9	FKLGGRDSRSGSP	O13	KKKTAKISQSAQT	Q17	DQPSEPPSPATTP
M10	KRFSFKKSFKLSG	O14	LVEPLTPSGEAPN	Q18	CNKAFRDTFRLLL
M11	PAYSRALSRQLSS	O15	EQQLFYISQPGSS	Q19	QLTWGRPSTRIQQ
M12	GKKTKFASDDEHD	O16	QRSELDKSSAHSY	Q20	KEREKEISDDEAE
M13	LCNMYKDSHHPAR	O17	LSPIDMESQERIK	Q21	KDKMAEAYSEIGM
M14	DPSSPRASPAHSP	O18	LLNKRRGSVPILR	Q22	GGGGGEFYGYMTM
M15	LCEDLPGTEDFVG	O19	CYEQLNDSSEEED	Q23	GGRERLASTNDKG
M16	FYYEILNSPEKAC	O20	LIDSMANSFVGTR	Q24	RAGETRFTDTRKD
M17	SKQSPISTPTSPG	O21	SLGFKRSYEEHIP	Q25	TSFMMTPYVVTRY
M18	EYLTRDSSILGPH	O22	SNFDKEFTRQPVE	Q26	RKSKRRNSEFEIF
M19	SSVTVTRSYRSVG	O23	EYVQTVKSSKGGP	Q27	REEADGVYAASGG
M20	QKFARKSTRRSIR	O24	RAGKRRPSRLVAL	Q28	GAVVPQGSRQVPV
M21	FGMSRDVYSTDYY	O25	SGFQVSETPRQAP	Q29	APTKRNSSPPPSP
M22	GLGRSITSPTTLY	O26	FPVSNTNSPTKIL	Q30	SLPDHKKTLEHLC
M23	DSPSDGGTPGRMP	O27	AATKIQASFRGHI	R1	RSPKENLSPGFSH
M24	RPNPCAYTPPSLK	O28	ITKALGISYGRKK	R2	MILLSELSRRRIR
M25	NIHLEKKYVRRDS	O29	KENSPCVTPVSTA	R3	KSISERLSVLKGA
M26	YNYEGRGSVAGSV	O30	RLMTGDTYTAHAG	R4	EPPSPATTPCGKV
M27	APAPKKGSKKAVT	P1	ASATVSKTETSQV	R5	DSSESEESAGPLL
M28	HHKLVLPSNTPNV	P2	PPDAADASPVVAA	R6	ESHESMESYELNP
M29	GVHHIDYYKKTSN	P3	SGRPRTTSFAESC	R7	SSLGFKRSYEEHI
M30	KNGCRRGSSLGQI	P4	KLPGLRTYVDPHT	R8	SNVSSTGSIDMVD
N1	TPSDSLIYDDGLS	P5	MSSSEEVSWISWF	R9	KKNGRILTLPRSN
N2	LLADLTRSLSDNI	P6	SAYGGLTSPGLSY	R10	YRIQEQESSGEED
N3	RYIEDEDYYKASV	P7	VSSDGHEYIYVDP	R11	EKIGEGTYGVVYK
N4	ESIKMQQYTEHFM	P8	WTETKKQSFKQTG	R12	AGMEFSRSKSDNS
N5	PKINRSASEPSLH	P9	NTIDLPMSPRALD	R13	TDNLLPMSPEEFD
N6	EEGTFRSSIRRLS	P10	NSLTPKSTPVKTL	R14	NRFTRRASVCAEA
N7	PSSSIDEYFSEQP	P11	VPEMPGETPPLSP	R15	SSVIGWPTVRERM
N8	WGRGTDEYFIRKP	P12	DGSRKIGSMDELE	R16	ASGSKKHSRPPRG
N9	TYIDPETYEDPNR	P13	SSPTAAGTPNKET	R17	RLFVENDSPSDGG
N10	EEQEYVQTVKSSK	P14	VDAQGTLSKIFKL	R18	KDIIRQPSEEEII
N11	KDGNGYISAAELR	P15	ARTAHYGSLPQKS	R19	SKDESVDYVPMLD
N12	GSPESPESTEITE	P16	VGLLKLASPELER	R20	VPWEDRMSLVNSR
N13	YKPLYIPSNRVND	P17	SQKVVVTTPLHRD	R21	LGQTLKASMRELG
N14	ERAKRNGSIVSMN	P18	KKKFRTPSFLKKS	R22	KSFLDSGYRILGA
N15	NLLKKFRSSTSSS	P19	SGASTGIYEALEL	R23	GTPTRKISASEFD
N16	RRAASMDSSSKLL	P20	DSMKDEEYEQMVK	R24	TASTRKVSLAPQA
N17	THIGPRTTRAQGI	P21	HHVPGHESRGPPP	R25	KMQLRRPSDQEVS
N18	HFFKNIVTPRTPP	P22	EYEDENLYEGLNL	R26	STATKDTYDALHM
N19	LDTSSVLYTAVQP	P23	AKALGKRTAKYRW	R27	PSGSQASSPQSSD
N20	DIKNDSNYVVKGN	P24	VSTQLVNSIAKTY	R28	LALHIRSSWSGLH
N21	QQKIRKYTMRRLL	P25	ATRGRGSSVGGGS	R29	AEPEKMESSISSS
N22	RPASVPPSPSLSR	P26	SGISSVPTPSPLG	R30	AKAKTRSSRAGLQ
N23	RVPTMRPSMSGLH	P27	GPPEPGPYAQPSV	S1	TFPPAPGSPEPPH
N24	VAYSPKRSPKENL	P28	QRRSARLSAKPAP	S2	SDGEFLRTSCGSP
N25	HQRRKYRSNKGES	P29	CYALCNRTFRKTF	S3	RVKGRTWTLCGTP
N26	KLSPSPSSRVTVS	P30	TGESDGGYMDMSK	S4	FDNNEEESSYSYE
N27	EEEDIRVSITEKC	Q1	PTAGALYSGSEGD	S5	YLSWGTASPYSAM
N28	NFHLMAPSEEDHS	Q2	AFIAARGSFDGSS	S6	EKGNVFSSPTAAG
N29	SAIKMVQYRDSFL	Q3	ITSTLASSFKRRR	S7	FACTYVGTPYYVP
N30	SLKDMEESIRNLE	Q4	WKVLRRFSVTTMR	S8	SQGRNCSTNDSLL
O1	PSDLLPMSPSVYA	Q5	PRASPAHSPRENG	S9	EDPDIPESQMEEP

S10	EEDTDEDSDNEIH
S11	FESERRGSHPYID
S12	QLKPLKTYVDPHT
S13	GSPGMKIYIDPFT
S14	DKKGNFNYVEFTR
S15	KVTSKCGSLGNIH
S16	STTTTRRSCSKTV
S17	KVDNEDIYESRHE
S18	LQARRRQSVLNLM
S19	AITSTLASSFKRR
S20	FLSEETPYSYPTG
S21	GHQGTVPSDNIDS
S22	PGLGRKLSDFGQE
S23	KTPSSPVYQDAVS
S24	CNRTFRKTFKMLL
S25	TLTTNEEYLDLSQ
S26	ILVKCQGSRLDDQ
S27	LEHVTRRTLSMDK
S28	RALSRQLSSGVSE
S29	KNIVTPRTPPPSQ
S30	NENTEDQYSLVED
T1	ALALARETIESLS
T2	DSQGRNCSTNDSL
T3	KQDSNPLYKSAIT
T4	DLLSRFQSNRMDD
T5	ALRADENYYKAQT
T6	ANRERRPSYLPTP
T7	YIYTIDGSRKIGS
T8	QNLNEDVSQEESP
T9	DDTSDPTYTSSLG
T10	SSEDLSAYASISF
T11	SSQGVDTYVEMRP
T12	HFDERDKTSRNMR
T13	DEICIAGSPLTPR
T14	PHLDRLVSARSVS
T15	RDMYDKEYYSVHN
T16	AEKHLEISREVGD
T17	VVRTPPKSPSSAK
T18	PRSKGQESFKKQE
T19	KIYSGDYYRQGCA
T20	RLSISAESQSPGT
T21	SSTYQSTSETVSI
T22	IYISPLKSPYKIS
T23	TCSPQPEYVNQPD
T24	TIESLSSSEESIT
T25	SDTEEQEYEEEQP
T26	EKKRRKMSKGLPD
T27	SEETPAISPSKRA
T28	LRTHNGASPYQCT
T29	HGDRPRASGCLAR
T30	RDTGILDSIGRFF
U1	KELEKRASGQAFE
U2	STPKSKQSPISTP
U3	SRKVGPGYLGSGG
U4	QALDNPEYHNASN
U5	TVSRASSSRSVRT
U6	LAKAQETSGEEIS
U7	EPSGPYESDEDKS
U8	NGDDPLLTYRFPP
U9	TVTSTDEYLDLSA
U10	AALRQLRSPRRTQ
U11	ELKGTTHSLLDDK
U12	KDLYLPLSLDDSD
U13	TFLPVPEYINQSV
U14	GSVQNPVYHNQPL
U15	DEEEDDDSEEDEE
U16	MEQKKRVTMILQS
U17	LKGKRGDSGSPAT
U18	HYTLDFLSPKTFQ
U19	LRAQRASSNVFSN
U20	VLCLRKGSGAKDA
U21	DAIKMGRYKESFV
U22	SPISTPTSPGSLR
U23	KAYGNGYSSNGNT
U24	YVHVNATYVNVKC
U25	MPLNVSFTNRNYD
U26	ERSKTVTSFYNQS
U27	NPLMRRNSVTPLA
U28	DSKNFDDYMKSLG
U29	TREEPVLTLVDEA
U30	KGMMPPLSEEEEL
V1	GSRSRTPSLPTPP
V2	ELILKPPSPISEA
V3	HSWPWQVSLRTRF
V4	PPSEGEESTVRFA
V5	SALLGDHYVQLPA
V6	RGRRKKKTPRKAE
V7	TPQTQSTSGRRRR
V8	DIYKDPDYVRKGS
V9	TLYDRYSSPPAST
V10	FTATEPQYQPGEN
V11	EGSFESRYQQPFE
V12	VRRLRRLTAREAA
V13	KKVAVVRTPPKSP
V14	RYFLDDQYTSSSG
V15	GRASDYKSAHKGF
V16	ENVPLDRSSHCQR
V17	TYRYHGHSMSDPG
V18	KEKMKELSMLSLI
V19	TASSGADYPDELQ
V20	EDENGDITPIKAK
V21	VNVIPPHTPVRTV
V22	RPPSAELYSNALP
V23	EYEPETVYEVAGA
V24	LHPPPQLSPFLQP
V25	ERLRLSPSPTSQR
V26	PGPMVDQSPSVST
V27	KDSSHYDSDGDKS
V28	RSAIRRASTIEMP
V29	EPLERRLSLVPDS
V30	TWIENKLYGMSDP
W1	PGPQSPGSPLEEE
W2	TMTFFKKSKISTY
W3	KKPRRKDTPALHI
W4	DAENRLQTMKEEL
W5	YSGSEGDSESGEE
W6	GSCRSDDYMPMSP
W7	SRLRRRASQLKIT
W8	VANQDPVSPSLVQ
W9	VVTLCYESHESME
W10	PKIEDVGSDEEDD
W11	IHFWSTLSPIAPR
W12	ENGRIHGSPLQKL
W13	ASLGRRASFHLEC
W14	FKYPRPSSVPPSP
W15	RGEPNVSYICSRY
W16	TQGGGSVTKKRKL
W17	AAAAAPASEDEDD
W18	PLASPEPTKKPRI
W19	RPRGQRDSSYYWE
W20	EKMESSISSSSEE
W21	ISSVPTPSPLGPL
W22	SGYSSPGSPGTPG
W23	ENFDKFFTRGQPV
W24	SGSSDSRSHQNSP
W25	PVIENPQYFGITN
W26	ELNKDRTSRDSSP
W27	EFPSLRVSAGFLL
W28	EKRHTRDSEAQRL
W29	SEHAQDTYLVLDK
W30	HSTPPSAYGSVKA
X1	DFRTRESTAKKIK
X2	PLPSGLLTPPQSG
X3	ESLSYAPSPLQKP
X4	SKALRISTPLTGV
X5	SQRQRSTSTPNVH
X6	INEWLTKTPDGNK
X7	DSLDSRLSPPAGL
X8	CIAGSPLTPRRVT
X9	PDLKKSRSASTIS
X10	AIETDKEYYTVKD
X11	GAKLRKVSKQEEA
X12	ALTSNQEYLDLSM
X13	SKEKIKQSSSSEC
X14	RPSQRHGSKYLAT
X15	PGKARKKSSCQLL
X16	RHTDDEMTGYVAT
X17	GSPSKSPSKKKKK
X18	LRGAQAASPAKGE
X19	NQNSRRPSRATWL
X20	FGYGGRASDYKSA
X21	QAIKMDRYKDNFT
X22	HIIENPQYFSDAC
X23	REDSARVYENVGL
X24	KKLERNLSFEIKK
X25	HGSKYLATASTMD
X26	LLLSNPAYRLLLA
X27	QEKRRQISIRGIV
X28	PLSYTRFSLARQV
X29	LLAVSEEYLDLRL
X30	AEHQYFMTEYVAT

*Control Peptides:

P2: GTAEPDYGALY
P4: GTDEGIpYDVPL
Tab2: VVSHFND
Kemptide: LRRASLG