

Supplementary Table 3. Compiled Data Output File for Mascot MS Searches, screening Swiss-Prot and TrEMBL, corresponding to the 2DE-differential analysis files.

a) pI 4-7

File#1

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(Q9Y490) Talin 1	TLN1_HUMAN	13 peptides matched QVAASTAQLLVACK (0) LNEAAAGLNQAATELVQASR (0) AVAEQIPLLQGVGR (0) LAQAAQSSVATITR (0) ALSTDPAAPNLKSQLAAAAR (1) AVAAGNSCRQEDVIATANLSR (1) LLAALLEDEGGSGRPLLQAAK (0) AAMEPIVISAQTMLESAGGLIQTAR (0) + 2 Oxidation (M) NGNLPEFGDAISTASK (0) ASAGPQPLLQVQSK (0) AATAPLLEAVDNLSAFASNPEFSSIPAQISPEGR (0) LNEAAAGLNQAATELVQASRGTPQDLAR (1) AVAEQIPLLQGVGRGSAQPDSQAQLALIAASQSFLQPGGK (1) 9.79% sequence coverage	460.25	223886	5.38	B
(Q9Y490) Talin 1	TLN1_HUMAN	30 peptides matched TLAESALQLLYTAK (0) AVSSAIAQLLGEVAQGNENYAGIAAR (0) Multi-Hit QAAASATQTIAAAQHAASPK (0) LAQAAQSSVATITR (0) GLAGAVSELLR (0) AATAPLLEAVDNLSAFASNPEFSSIPAQISPEGR (0) Multi-Hit LNEAAAGLNQAATELVQASR (0) ASAGPQPLLQVQSK (0) TLAESALQLLYTAKEAGGNPK (1) VGAIPANALDDGQWSQGLISAAR (0) AVAEQIPLLQGVGR (0) ASVPTIQDQASAMQLSQCAKNLGTALAELR (1) + 1 Oxidation (M)	1388.41	219847	5.40	-3.13

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
		Multi-Hit EGISQEALHTQMLTAVQEISHLIEPLANAAR (0) + 1 Oxidation (M) AIAVTVQEMVTKSNTSPEELGPLANQLTSDYGR (1) VVAPTISSPVCQEQLVEAGR (0) LLAALLEDEGGSGRPLLQAAK (0) ILAQATSDLVNAIKADAEGESDLENSR (1) GLAGAVSELLRSAQPASAEPR (1) NGNLPEFGDAISTASK (0) TMLESAGGLIQTAR (0) + 1 Oxidation (M) ANQAIQMACQSLGEPGCTQAQVLSAATIVAKHTSALCNSCR (1) + 1 Oxidation (M) MVAAATNNLCEAANAAVQGHASQEKLISAK (1) + 1 Oxidation (M) QFVQSAKEVANSTANLVK (1) LNEAAAGLNQAATELVQASRGTPQDLAR (1) ASAGPQPLLVQSCKAVAEQIPLLVQGVV (1) GSQAQPDSPSAQLALIAASQSFLQPGGKMVAAAK (1) VLGEAMTGISQNAK (0) ASVPTIQDQASAMQLSQCAK (0) ALSTDPAAPNLKSQLAAAAR (1) ECANGYLELLDHVLLTLQKPSPELK (0) 23.25% sequence coverage				
(P21333) Filamin A (Alpha-filamin) (Filamin 1) (Endothelial actin-binding protein) (ABP-280) (Nonmuscle filamin)	FLNA_HUMAN	6 peptides matched VAQPTITDNKDGTVTVR (1) AGNNMLLVGVHGPR (0) + 1 Oxidation (M) VNQPASFVSLNGAK (0) VGSAADIPINISSETDLSLLTATVVPPSGR (0) YAPSEAGLHEMDIR (0) + 1 Oxidation (M) VTYTPMAPGSYLISIK (0) + 1 Oxidation (M) 3.96% sequence coverage	206.76	116946	5.98	B
(P02679) Fibrinogen gamma chain precursor	FIBG_HUMAN	6 peptides matched ASTPNGYDNGIHWATWK (0) YLQEIYNSNNQK (0) AIQLTYNPDESSKPNMIDAATLK (0) + 1 Oxidation (M) Multi-Hit CHAGHLNGVYYYQGGTYSK (0) EGFGHLSPTGTTEFWLGNEK (0)	272.18	109393	5.32	-2.51

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P02679) Fibrinogen gamma chain precursor	FIBG_HUMAN	8 peptides matched ASTPNGYDNGHIWATWK (0) YLQEIYNSNNQK (0) AIQLTYNPDESSKPNMIDAATLK (0) + 1 Oxidation (M) Multi-Hit CHAGHLNGVYYQGGTYSK (0) EGFGHLSPTGTTEFWLGNEK (0) QSGLYFIKPLK (0) AIQLTYNPDESSKPNMIDAATLKSR (1) + 1 Oxidation (M) VAQLEAQCQEPCKDTVQIHDITGK (1) 25.16% sequence coverage	293.36	108073	5.36	B
(P18206) Vinculin (Metavinculin)	VINC_HUMAN	9 peptides matched MLGQMTDQVADLR (0) + 2 Oxidation (M) CDRVDQLTAQLADLAAR (1) AQQVSQGLDVLTAK (0) ELTPQVVSAAR (0) MTGLVDEAIDTK (0) + 1 Oxidation (M) AAAVGTANKSTVEGIQASVK (1) GILSGTSDLLLTFDEAEVRK (1) NFTVEKMSAEINEIIR (1) + 1 Oxidation (M) Multi-Hit SLLDASEEAIKK (1) 11.91% sequence coverage	305.08	105481	5.30	B
(P18206) Vinculin (Metavinculin)	VINC_HUMAN	25 peptides matched GILSGTSDLLLTFDEAEVR (0) MLGQMTDQVADLR (0) + 2 Oxidation (M) MTGLVDEAIDTK (0) + 1 Oxidation (M) AQQVSQGLDVLTAKVENAAR (1) MSAEINEIIR (0) + 1 Oxidation (M) LVQAAQMLQSDPYSPARDYLIDGSR (1) + 1 Oxidation (M) AQQVSQGLDVLTAK (0) VAMANIQPQMLVAGATSIAR (0) + 1 Oxidation (M) Multi-Hit VLQLTSWDEDAWASK (0) CDRVDQLTAQLADLAAR (1) AVAGNISDPGLQKSFLDSGYR (1)	1169.81	103578	5.34	-3.08

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
		ALASQLQDSLKDLK (1) ELLPVLISAMK (0) SLGEISALTSK (0) GILSGTSDLLLTFDEAEVRK (1) EILGTCKMLGQMTDQVADLR (1) + 2 Oxidation (M) WIDNPTVDDRGVGGQAAIR (1) LVQAAQMLQSDPYSPAR (0) + 1 Oxidation (M) NFTVEKMSAEINEIR (1) Multi-Hit AIPDLTAPVAAVQAAVSNLVR (0) Multi-Hit ELTPQVVSAAR (0) MLGQMTDQVADLRAR (1) + 2 Oxidation (M) VGKETVQTTEDQILK (1) AVAGNISDPGLQK (0) MQEAMTQEVSDVFSDTTTPIK (0) + 2 Oxidation (M) 27.44% sequence coverage				
(P21333) Filamin A (Alpha-filamin) (Filamin 1) (Endothelial actin-binding protein) (ABP-280) (Nonmuscle filamin)	FLNA_HUMAN	2 peptides matched VAQPTITDNKDGTVTVR (1) LVSNHSLHETSSVFVDSLTK (0) 1.39% sequence coverage	72.79	103578	5.44	B
(P21333) Filamin A (Alpha-filamin) (Filamin 1) (Endothelial actin-binding protein) (ABP-280) (Nonmuscle filamin)	FLNA_HUMAN	8 peptides matched LVSNHSLHETSSVFVDSLTK (0) THEAEIVEGENHTYCIR (0) AEAGVPAEFSIWTR (0) VGSAADIPINISSETDLSLLTATVVPPSGR (0) YGGPYHIGGSPFK (0) VNQPASFAVSLNGAK (0) LTVSSLQESGLKVNQPASFAVSLNGAK (1) YAPSEAGLHEMDIR (0) + 1 Oxidation (M) 5.06% sequence coverage	339.65	102951	5.49	B
(P21333) Filamin A (Alpha-filamin) (Filamin 1) (Endothelial actin-binding protein)	FLNA_HUMAN	12 peptides matched VAQPTITDNKDGTVTVR (1) VNQPASFAVSLNGAK (0) YNEQHVPGPSFTAR (0)	404.85	101709	5.60	B

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(ABP-280) (Nonmuscle filamin)		AEAGVPAEFSIWTR (0) YGGPYHIGGSPFK (0) VGSAADIPINISSETDLSLLTATVVPPSGR (0) Multi-Hit YAPSEAGLHEMDIR (0) + 1 Oxidation (M) THEAEIVEGENHTYCIR (0) FNEEHIPDSPFVVPVASPSGDAR (0) LTVSSLQESGLK (0) VTYTPMAPGSYLISIK (0) + 1 Oxidation (M) DGSCGVAYVVQEPGDYEVSVK (0) 7.74% sequence coverage				
(P00488) Coagulation factor XIII A chain precursor (Protein-glutamine gamma-glutamyltransferase A chain)	F13A_HUMAN	6 peptides matched DGTHVVENV DATHIGK (0) STVLTIP EIIIK (0) GVNLQEFLNVT SVHLFK (0) GVNLQEFLNVT SVHLFKER (1) LALETALMYGAK (0) + 1 Oxidation (M) MYVAVWTPYGVLR (0) + 1 Oxidation (M) 9.84% sequence coverage	187.61	101709	5.60	B
(P06396) Gelsolin precursor, plasma (Actin-depolymerizing factor) (ADF) (Brevin) (AGEL)	GELS_HUMAN	3 peptides matched AGALNSNDAFVLK (0) EVQGFESATFLGYFK (0) TPSAAYLWVGTGASEAEKTGAQELLR (1) 6.90% sequence coverage	140.93	101709	5.60	B
(P21333) Filamin A (Alpha-filamin) (Filamin 1) (Endothelial actin-binding protein) (ABP-280) (Nonmuscle filamin)	FLNA_HUMAN	11 peptides matched LTVSSLQESGLK (0) FNEEHIPDSPFVVPVASPSGDAR (0) AEAGVPAEFSIWTR (0) YGGPYHIGGSPFK (0) Multi-Hit RLTVSSLQESGLK (1) VAQPTITDNKDGT VTVR (1) VTYTPMAPGSYLISIK (0) + 1 Oxidation (M) YAPSEAGLHEMDIR (0) + 1 Oxidation (M) Multi-Hit NGQHVASSPIPVVISQSEIGDASR (0) LVSNHSLHETSSVFVDSLTK (0) VTYCPTEPGNYIINIK (0)	411.85	99269	5.63	B

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)} 6.42% sequence coverage	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P00488) Coagulation factor XIII A chain precursor (Protein-glutamine gamma-glutamyltransferase A chain)	F13A_HUMAN	3 peptides matched STVLTIP EIIK (0) GTYPVPIVSELQSGK (0) SETSRTAFGGR (1) 5.33% sequence coverage	42.71	99269	5.63	B
(Q96S64) MacGAP	Q96S64	2 peptides matched ELPQPLLSVEYLK (0) STNDADVPQGVIR (0) 4.20% sequence coverage	66.82	93423	5.95	B
(Q8WUM4) Programmed cell death 6-interacting protein (PDCD6-interacting protein) (ALG-2 interacting protein 1) (Hp95)	PD6I_HUMAN	3 peptides matched FYNELTEILVR (0) YYDQICSIEPK (0) HCIMQANA EYHQSILAK (0) + 1 Oxidation (M) 4.49% sequence coverage	78.94	89068	5.97	B
(Q99704) Docking protein 1 (p62(dok)) (Downstream of tyrosine kinase 1) (Dok-1)	DOK1_HUMAN	2 peptides matched IAPCPSQDSL YSDPLDSTSAQAGEGVQR (0) GSWTLAPTDNPPK (0) 8.52% sequence coverage	113.85	59479	5.94	B
(P12931) Proto-oncogene tyrosine-protein kinase Src (p60-Src) (c-Src)	SRC_HUMAN	8 peptides matched TQFNSLQQLVAYYSK (0) AANILVGENLVCK (0) GSLLDLFLKGETGK (1) GAYCLSVSDFD NAK (0) LTTVCPTSKPQTQGLAK (0) GPSAAFAPAAAEPK (0) LFGGFNSSDTVTSPQR (0) AANILVGENLVCKVADFG LAR (1)	358.21	58294	6.01	-2.16

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)} 20.56% sequence coverage	Protein Score	Mass (Da)	pI	Fold ^{c)}
(Q16555) Dihydropyrimidinase related protein-2 (DRP-2) (Collapsin response mediator protein 2) (CRMP-2) (N2A3)	DPY2_HUMAN	6 peptides matched DIGAIAQVHAENGDIIEEQQR (0) GLYDGPVCEVSVTPK (0) AITIANQTNCPYITKVMMSK (1) + 1 Oxidation (M) AVGKDNFTLIPEGTNGTEER (1) AITIANQTNCPYITK (0) ILDLGITGPEGHVLSRPEEVEAEAVNR (0) 18.18% sequence coverage	135.21	57324	5.43	B
(O60496) Docking protein 2 (p56(dok-2)) (Downstream of tyrosine kinase 2)	DOK2_HUMAN	4 peptides matched GQEGEYAVPFDAVAR (0) QGNEIFLALEEAIQAQK (0) Multi-Hit CVSGEGNFEFETR (0) QSRPCMEENELYSSAVTVGPHK (0) + 1 Oxidation (M) 16.26% sequence coverage	117	51384	5.46	B
(P12931) Proto-oncogene tyrosine-protein kinase Src (p60-Src) (c-Src)	SRC_HUMAN	4 peptides matched TQFNSLQQLVAYYSK (0) AANILVGENLVCK (0) LTTVCPTSKPQTQGLAK (0) GAYCLSVSDFDNAK (0) 11.02% sequence coverage	149.48	50832	5.99	B
(P55209) Nucleosome assembly protein 1-like 1 (NAP-1 related protein) (hNRP)	NPL1_HUMAN	6 peptides matched LDGLVETPTGYIESLPR (0) YAVLYQPLFDK (0) FYEEVHDLER (0) NVDLLSDMVQEHDEPILK (0) + 1 Oxidation (M) GIPEFWLTVFK (0) FYEEVHDLERK (1) 17.39% sequence coverage	272.71	49880	4.50	B
(Q02750) Dual specificity mitogen-activated protein kinase kinase 1 (MAP kinase kinase 1) (MAPKK 1) (ERK activator kinase	MPK1_HUMAN	2 peptides matched ISELGAGNGGVVFK (0) DVKPSNILVNSR (0) 6.63% sequence coverage	122.01	44532	5.99	B

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
1) (MAPK/ERK kinase 1) (MEK1)						
(P20073) Annexin A7 (Annexin VII) (Synexin)	ANX7_HUMAN	3 peptides matched GFGTDEQAIVDVVANR (0) LYYAMKGAGTDDSTLVR (1) + 1 Oxidation (M) LGTDESCFNMILATR (0) + 1 Oxidation (M) 10.30% sequence coverage	118.48	44532	5.99	B
(O00231) 26S proteasome non-ATPase regulatory subunit 11 (26S proteasome regulatory subunit S9) (26S proteasome regulatory subunit p44.5)	PSDB_HUMAN	2 peptides matched EQSILELGSLLAK (0) LYDNLLEQNLIR (0) 5.92% sequence coverage	54.28	44532	5.99	B
(Q9Y490) Talin 1	TLN1_HUMAN	8 peptides matched LLAALLEDEGGSGRPLLQAAK (0) Multi-Hit VVAPTISSPVCQEQLVEAGR (0) Multi-Hit AVEGCVSASQAATEDGQLLR (0) Multi-Hit GLAGAVSELLR (0) AVASAAAALVLK (0) GVKLLAALLEDEGGSGRPLLQAAK (1) VVAPTISSPVCQEQLVEAGRLVAK (1) GLAGAVSELLRSAQPASAEPR (1) 3.97% sequence coverage	403.95	40735	5.08	B
(Q16539) Mitogen-activated protein kinase 14 (Mitogen-activated protein kinase p38alpha) (MAP kinase p38alpha)	MK14_HUMAN	9 peptides matched NYIQSLTQMPK (0) + 1 Oxidation (M) Multi-Hit SLEEFNDVYLVTHLMGADLNNIVK (0) + 1 Oxidation (M) DLLIDEWK (0) LTDDHVQFLIYQILR (0) DLKPSNLAVNEDCELKILDFGLAR (1) LVGTPGAELLK (0) ISSESARNYIQSLTQMPK (1) + 1 Oxidation (M)	191.3	39865	5.41	B

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
		TLFPGTDHIDQLKLILR (1) DLKPSNLAVNEDCELK (0) 32.5% sequence coverage				
(P01137) Transforming growth factor beta 1 precursor (TGF-beta 1)	TGF1_HUMAN	2 peptides matched DNTLQVDINGFTTGR (0) VAGESAEPEPEPEADYYAKEVTR (1) 9.74% sequence coverage	125.13	39865	5.41	B
(Q9Y490) Talin 1	TLN1_HUMAN	8 peptides matched VVAPTISSPVCQEQLVEAGR (0) Multi-Hit AVEGCVSASQAATEDGQLLR (0) LLAALLEDEGGSGRPLLQAAK (0) GVKLLAALLEDEGGSGRPLLQAAK (1) Multi-Hit GLAGAVSELLR (0) GLAGAVSELLRSAQPASAEPR (1) TEDSGLQTQVIAAATQCALSTSQLVACTK (0) VVAPTISSPVCQEQLVEAGRLVAK (1) 4.64% sequence coverage	464.45	37566	5.01	-2.23
(P04792) Heat shock 27 kDa protein (HSP 27)	HS27_HUMAN	2 peptides matched LATQSNEITIPVTFESR (0) RVPFSLLR (1) 12.19% sequence coverage	148.47	26798	5.54	B
(Q92882) Osteoclast stimulating factor 1	OSF1_HUMAN	1 peptides matched GYADIVQLLLAK (0) 5.60% sequence coverage	64.57	26798	5.54	B
(P04792) Heat shock 27 kDa protein (HSP 27)	HS27_HUMAN	8 peptides matched LATQSNEITIPVTFESR (0) KYTLPPGVDPTQVSSSLSPGTLTVEAPMPK (1) VSLDVNHFAPDELTVK (0) Multi-Hit LFDQAFGLPR (0) VSLDVNHFAPDELTVKTK (1) RVPFSLLR (1) YTLPPGVDPTQVSSSLSPGTLTVEAPMPK (0) + 1 Oxidation (M) Multi-Hit GPSWDPFRDWYPHSR (1)	447.38	26458	5.82	-3.43

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
		48.29% sequence coverage				
(Q9UKN4) Bridging integrator-2	Q9UKN4	2 peptides matched TMEIYVAQFSEIKER (1) + 1 Oxidation (M) IGCYVTIFQNISNLR (0)	79.88	26373	5.94	B
or		5.31% sequence coverage				
(Q86VV0) Breast cancer associated protein BRAP1	Q86VV0	2 peptides matched TMEIYVAQFSEIKER (1) + 1 Oxidation (M) IGCYVTIFQNISNLR (0)	79.88			
		5.30% sequence coverage				
(Q13201) Multimerin 1 precursor (Endothelial cell multimerin 1)	EMI4_HUMAN	2 peptides matched LAFESENINSEIHCDR (0) LVEENALAPDFSKGSYR (1)	72.93	26373	5.94	B
		2.68% sequence coverage				
(Q9UKN4) Bridging integrator-2	Q9UKN4	5 peptides matched TMEIYVAQFSEIKER (1) + 1 Oxidation (M) VSETLQEIYSSEWDGHEELK (0) FEQSASNFYQQQAEGHK (0) TMEIYVAQFSEIK (0) + 1 Oxidation (M) FEQSASNFYQQQAEGHKLYK (1)	113.67	25955	5.80	B
or		9.75% sequence coverage				
(Q86VV0) Breast cancer associated protein BRAP1	Q86VV0	5 peptides matched TMEIYVAQFSEIKER (1) + 1 Oxidation (M) VSETLQEIYSSEWDGHEELK (0) FEQSASNFYQQQAEGHK (0) TMEIYVAQFSEIK (0) + 1 Oxidation (M) FEQSASNFYQQQAEGHKLYK (1)	113.67	25955	5.80	
		9.73% sequence coverage				
(Q01518) Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1_HUMAN	2 peptides matched NSLDCEIVSAK (0) VENQENVSNLVIEDTELK (0)	46.12	20756	5.95	B
		6.11% sequence coverage				

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P37802) Transgelin 2 (SM22-alpha homolog)	TAG2_HUMAN	13 peptides matched YGINTTDIFQTVDLWEGK (0) TLMNLGGLAVAR (0) Multi-Hit QMEQISQFLQAAER (0) + 1 Oxidation (M) Multi-Hit IQASTMAFKQMEQISQFLQAAER (1) + 2 Oxidation (M) Multi-Hit DGTVLCELINALYPEGQAPVKK (1) Multi-Hit IEKQYDADLEQILIQWITTQCR (1) DGTVLCELINALYPEGQAPVK (0) Multi-Hit YGINTTDIFQTVDLWEGKNMACVQR (1) + 1 Oxidation (M) Multi-Hit DDGLFSGDPNWFPPK (0) DDGLFSGDPNWFPPK (1) TLMNLGGLAVARDDGLFSGDPNWFPPK (1) Multi-Hit QYDADLEQILIQWITTQCR (0) QYDADLEQILIQWITTQCRK (1) 60.30% sequence coverage	736.85	18764	5.44	B
(O00151) PDZ and LIM domain protein 1 (LIM domain protein CLP-36)	PDL1_HUMAN	3 peptides matched GCTDNLTTLTVAR (0) AALANLCIGDVITAIDGENTSNMTHLEAQNR (0) + 1 Oxidation (M) TTQQIDLQGGPWFRLVGGK (1) 19.45% sequence coverage	58.37	13145	5.78	B
(O00151) PDZ and LIM domain protein 1 (LIM domain protein CLP-36)	PDL1_HUMAN	1 peptides matched GCTDNLTTLTVAR (0) 3.64% sequence coverage	57.69	12417	6.29	B
(O00151) PDZ and LIM domain protein 1 (LIM domain protein CLP-36)	PDL1_HUMAN	2 peptides matched VWSPLVTEEGK (0) AALANLCIGDVITAIDGENTSNMTHLEAQNR (0) + 1 Oxidation (M) 12.76% sequence coverage	38.98	12155	6.35	B

File#2

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	2 peptides matched NRQEGLMIASSLLNEGYLEQAGDMSK (1) + 1 Oxidation (M) FILREDPAYLHYYDPAGAEDPLGAIHLR (1) 15.42% sequence coverage	67.69	42940	6.34	3.23
(Q8IY23) Similar to CG4946 gene product (Mob4A protein)	Q8IY23	1 peptides matched ELAPLQELIEK (0) 5.09% sequence coverage	36.57	26174	5.63	CRP
or						
(Q9H3T5) Mob1 protein (Hypothetical protein) (Mob4B protein)	Q9H3T5	1 peptides matched ELAPLQELIEK (0) 5.09% sequence coverage	36.57			

File#3

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P49591) Seryl-tRNA synthetase	SYS_HUMAN	4 peptides matched EVMQEVAQLSQFDEELYKVVIGK (1) + 1 Oxidation (M) EIGNLLHPSVPISNDEDVDNKVER (1) DVTLENRLQNMEVTDA (1) + 1 Oxidation (M) EFMPPGLQELIPFVKPAPIEQEPSKK (1) + 1 Oxidation (M) 17.15% sequence coverage	57.01	58176	5.88	CRP
(O75351) SKD1 protein (Vacuolar sorting protein 4b)	SKD1_HUMAN	1 peptides matched GILLFGPPGTGK (0) 2.70% sequence coverage	50.84	56027	6.20	CRP
or						
(Q9UN37) Vacuolar protein sorting factor 4A)	Q9UN37	1 peptides matched GILLFGPPGTGK (0) 2.74% sequence coverage	50.84			

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	7 peptides matched QQDHFFQAAFLEER (0) NRQEGLMIASSLLNEGYLELQAGDMSK (1) + 1 Oxidation (M) Multi-Hit SEEENLFEIITADEVHYFLQAATPK (0) IFNHCFTGNCVIDWLVSNQSVR (0) GSTLTSPCQDFGKR (1) KSEEENLFEIITADEVHYFLQAATPK (1) Multi-Hit ITTTKQQDHFFQAAFLEER (1) 30.57% sequence coverage	364.66	43704	5.93	CRP
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	10 peptides matched IFNHCFTGNCVIDWLVSNQSVR (0) NRQEGLMIASSLLNEGYLELQAGDMSK (1) + 2 Oxidation (M) Multi-Hit MFVFKITTTK (1) + 1 Oxidation (M) GSTLTSPCQDFGKR (1) Multi-Hit QQDHFFQAAFLEER (0) EDPAYLHYYPAGAEDPLGAIHLR (0) Multi-Hit LPETIDLGALYLSMKDTEK (1) + 1 Oxidation (M) LPETIDLGALYLSMK (0) + 1 Oxidation (M) QEGLMIASSLLNEGYLELQAGDMSK (0) + 2 Oxidation (M) GMIPLKGSTLTSPCQDFGK (1) + 1 Oxidation (M) 38.57% sequence coverage	370.19	43465	5.81	CRP

File#4

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(O95671) N-acetylserotonin O-methyltransferase-like protein (ASMTL)	ASML_HUMAN	1 peptides matched LLDICAAMGLLEK (0) + 1 Oxidation (M) 2.09% sequence coverage	61.53	73329	5.64	CRP

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P04792) Heat shock 27 kDa protein (HSP 27)	HS27_HUMAN	5 peptides matched LATQSNEITIPVTFESR (0) LFDQAFGLPR (0) RVPFSLLR (1) YTLPPGVDPTQVSSSLSPGTLTVEAPMPK (0) + 1 Oxidation (M) VSLDVNHFAPDELTVK (0) 39.51% sequence coverage	207.3	28188	4.96	CRP
(P04792) Heat shock 27 kDa protein (HSP 27)	HS27_HUMAN	3 peptides matched LATQSNEITIPVTFESR (0) LFDQAFGLPR (0) RVPFSLLR (1) 17.07% sequence coverage	155.8	27468	5.21	2.81
(Q9H3T5) Mob1 protein (Hypothetical protein) (Mob4B protein)	Q9H3T5	1 peptides matched ELAPLQELIEK (0) 5.09% sequence coverage	32.21	24449	5.97	CRP
or	Or					
(Q8IY23) Similar to CG4946 gene product (Mob4A protein)	Q8IY23					
(O43665) Regulator of G-protein signaling 10 (RGS10)	RGSA_HUMAN	3 peptides matched TEEEEEEDLPDAQTAAK (0) RTEEEEEEDLPDAQTAAK (1) EFSEENVLFWLACEDFKK (1) 20.23% sequence coverage	88.60	21439	5.37	5.31
(O43665) Regulator of G-protein signaling 10 (RGS10)	RGSA_HUMAN	5 peptides matched TEEEEEEDLPDAQTAAK (0) EIYMTFLSSK (0) + 1 Oxidation (M) LQDQIFNLMKYDSYSR (1) + 1 Oxidation (M) RTEEEEEEDLPDAQTAAK (1) LQDQIFNLMK (0) + 1 Oxidation (M) 24.85% sequence coverage	134.89	21205	5.64	CRP

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P24844) Myosin regulatory light chain 2, smooth muscle isoform (Myosin RLC) (LC20)	MLRN_HUMAN	2 peptides matched LNGTDPEDVIR (0) GNFNYYVEFTR (0) 12.28% sequence coverage	116.23	20667	4.60	2.67
(O43665) Regulator of G-protein signaling 10 (RGS10)	RGSA_HUMAN	2 peptides matched EIYMTFLSSK (0) + 1 Oxidation (M) TEEEEEEDLPDAQTAAKR (1) 15.60% sequence coverage	74.73	20366	5.64	CRP
(P19105) Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC)	MLRM_HUMAN	2 peptides matched GNFNYYIEFTR (0) NAFACFDEEATGTIQEDYLR (0) 17.64% sequence coverage	74.83	19996	4.42	CRP
(P19105) Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC)	MLRM_HUMAN	5 peptides matched GNFNYYIEFTR (0) LNGTDPEDVIR (0) ELLTTMGDRFTDEEVDELYR (1) + 1 Oxidation (M) DGFIDKEDLHDMLASLGK (1) + 1 Oxidation (M) NAFACFDEEATGTIQEDYLR (0) 46.47% sequence coverage	159.39	18925	4.52	CRP
(P19105) Myosin regulatory light chain 2, nonsarcomeric (Myosin RLC)	MLRM_HUMAN	6 peptides matched NAFACFDEEATGTIQEDYLR (0) LNGTDPEDVIR (0) ATSNVFMFDQSQIQEFK (0) + 1 Oxidation (M) GNFNYYIEFTR (0) FTDEEVDELYR (0) DGFIDKEDLHDMLASLGK (1) + 1 Oxidation (M) 51.76% sequence coverage	286.5	18856	4.59	2.17

File#5

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P11413) Glucose-6-phosphate 1-dehydrogenase (G6PD)	G6PD_HUMAN	14 peptides matched NSYVAGQYDDAASYQR (0) DGLLPENTFIVGYAR (0) GGYFDEFGIIR (0) VGFQYEGTYK (0) IIVEKPFGR (0) GYLDDPTVPR (0) KPGMFFNPEESELDTYGNRYK (1) + 1 Oxidation (M) Multi-Hit NIHESCMSQIGWNR (0) + 1 Oxidation (M) Multi-Hit DNIACVILTFKEPFGTEGR (1) LILDVFCGSQMHFVR (0) + 1 Oxidation (M) LQFHDVAGDIFHQQCK (0) LFYLALPPTVYEAVTK (0) IDHYLGKEMVQNLMVLR (1) + 2 Oxidation (M) IFTPLLHQIELEKPKPIPIYIYGSR (0) 41.63% sequence coverage	471.55	56094	6.51	B
(P12931) Proto-oncogene tyrosine-protein kinase Src (EC 2.7.1.112) (p60-Src) (c-Src)	SRC_HUMAN	3 peptides matched LFGGFNSSDTVTSPQR (0) AANILVGENLVCK (0) TQFNLSLQQLVAYYSK (0) 8.22% sequence coverage	97.64	56094	6.51	B
(Q9UJU6) SRC homology 3 domain-containing protein HIP-55 (Drebrin F)	Q9UJU6	6 peptides matched FQDVGPQAPVGSVYQK (0) FVLINWTGEGVNDVR (0) NGPALQEAYVR (0) VVTEKSPTDWALFTYEGNSNDIR (1) TWEQQQEVVSR (0) ESGRFQDVGPQAPVGSVYQK (1) 18.60% sequence coverage	245.61	30391	5.79	B
(P07203) Glutathione peroxidase 1 (GSHPx-1) (Cellular glutathione peroxidase)	GPX1_HUMAN	1 peptides matched EALPAPSDDATALMTDPK (0) + 1 Oxidation (M) 8.95% sequence coverage	30.61	24726	5.75	-2.52

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(Q01518) Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1_HUMAN	3 peptides matched NSLDCEIVSAK (0) VENQENVSNLVIEDTELK (0) TLWNGQKLVTTVTEIAG (1) 9.70% sequence coverage	109.03	18706	5.91	B
(O15117) ADAP (FYN-T-binding protein) (FYB-120/130) (p120/p130) (SLP-76 associated phosphoprotein) (SLAP-130)	FYB_HUMAN	1 peptides matched DLQVKPGESLEVIQTTDDTK (0) 2.55% sequence coverage	49.24	16914	5.33	B

File#6

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P46109) Crk-like protein	CRKL_HUMAN	4 peptides matched DSSTCPGDYVLSVSENSR (0) VGMIPVPYVEK (0) + 1 Oxidation (M) VSHYIINSLPNRR (1) IFDPQNPENE (0) 17.49% sequence coverage	156.79	39222	5.84	CRP
(P29354) Growth factor receptor-bound protein 2 (GRB2 adapter protein) (SH2/SH3 adapter GRB2) (ASH protein)	GRB2_HUMAN	2 peptides matched ESESAPGDFSLSVK (0) QRHDGAFLIR (1) 11.05% sequence coverage	101	27564	5.46	CRP

File#7

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P21333) Filamin A (Alpha-filamin) (Filamin 1) (Endothelial actin-	FLNA_HUMAN	9 peptides matched DAGEGGLSLAIEGPSK (0) VAQPTITDNKDGTVTVR (1) Multi-Hit	600.10	101861	5.53	B

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
binding protein) (ABP-280) (Nonmuscle filamin)		LVSNHSLHETSSVFVDSLTK (0) YGGPYHIGGSPFK (0) LTVSSLQESGLK (0) AEAGVPAEFSIWTR (0) THEAEIVEGENHTYCIR (0) VTYTPMAPGSYLISIK (0) + 1 Oxidation (M) RLTVSSLQESGLK (1) 4.76% sequence coverage				
(P00488) Coagulation factor XIII A chain precursor	F13A_HUMAN	5 peptides matched LALETALMYGAK (0) + 1 Oxidation (M) Multi-Hit GTYIPVPIVSELQSGK (0) QIGGDGMMDITDTYK (0) + 2 Oxidation (M) MYVAVWTPYGVLR (0) Multi-Hit STVLTPEIIHK (0) 9.30% sequence coverage	225.27	101861	5.53	B
(P06396) Gelsolin precursor, plasma (Actin-depolymerizing factor) (ADF) (Brevin) (AGEL)	GELS_HUMAN	2 peptides matched EVQGFESATFLGYFK (0) HVVPNEVVVQR (0) 3.32% sequence coverage	43.76	101861	5.53	B
(P30740) Leukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (M/NEI) (EI)	ILEU_HUMAN	5 peptides matched LGVQDLFNSSK (0) TYGADLASVDFQHASEDAR (0) FQSLNADINKR (1) TYGADLASVDFQHASEDARK (1) TYNFLPEFLVSTQK (0) 14.77% sequence coverage	330.36	43874	5.77	B
(P01892) HLA class I histocompatibility antigen, A-2 alpha chain precursor (MHC class I antigen A*2)	1A02_HUMAN	3 peptides matched APWIEQEGPEYWDGETR (0) WAAVVVPSGQEQR (0) AHSQTHRVDLGTLR (1) 12.05% sequence coverage	180.14	43090	5.99	B

or

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P79603) MHC class I HLA-A protein	P79603	3 peptides matched APWIEQEGPEYWDGETR (0) WAAVVVPSGQEQR (0) AHSQTHRVDLGTLR (1) 12.05% sequence coverage	180.14			
(Q86UX7) Unc-112 related protein 2 (Kindlin-3) (MIG2-like)	URP2_HUMAN	4 peptides matched ASFSQPLFQAVAAICR (0) VFVGEEDPEAESVTLR (0) TASGDYIDSSWELR (0) VVLAGGVAPALFR (0) 8.84% sequence coverage	333.06	37756	5.62	B
(O75563) SKAP-HOM	O75563	1 peptides matched GEFAIDGYSVR (0) 3.06% sequence coverage	64.44	36971	4.67	B
(P07996) Thrombospondin 1 precursor	TSP1_HUMAN	2 peptides matched GGVNDNFQGVLQNVR (0) FVFGTTPEDILR (0) 2.30% sequence coverage	151.68	31435	5.38	B
(P24410) Ras-related protein Rab-11A (Rab-11) (24KG) (YL8)	R11A_HUMAN	1 peptides matched STIGVEFATR (0) 4.62% sequence coverage	60.8	20104	5.37	B
or						
(Q15907) Ras-related protein Rab-11B (GTP-binding protein YPT3)	R11B_HUMAN	1 peptides matched STIGVEFATR (0) 4.58% sequence coverage	60.8			
(Q9UJU6) SRC homology 3 domain-containing protein HIP-55 (Drebrin F)	Q9UJU6	4 peptides matched FVLINWTGEGVNDVR (0) FQDVGPQAPVGSVYQK (0) NGPALQEAYVR (0) AEEDVEPECIMEK (0) + 1 Oxidation (M) 12.79% sequence coverage	267.78	17844	5.29	B

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(Q9Y3F5) A6 related protein (Protein tyrosine kinase 9-like)	Q9Y3F5	3 peptides matched VVIEDEQLVLGASQEPVGR (0) HLSSCAAPPLTSAER (0) Multi-Hit AVLPLLLDAQPCYLLYR (0) 14.89% sequence coverage	274.11	16806	5.54	-2.72
(Q9P005) HSPC159	Q9P005	1 peptides matched IQTLSAIDTIK (0) 6.39% sequence coverage	90.00	15361	5.45	-2.95

File#8

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P27924) Ubiquitin-conjugating enzyme E2-25 kDa (Ubiquitin-protein ligase) (Huntingtin interacting protein 2)	UBC1_HUMAN	1 peptides matched TVLLSLQALLAAAEPPDDPQDAVVANQYK (0) 14% sequence coverage	33.51	24851	5.07	B
(Q9Y3C8) Ubiquitin-fold modifier conjugating enzyme 1	UFC1_HUMAN	1 peptide matched VVSEIPVLK 5% Sequence coverage	37	20245	6.57	B
(P52566) Rho GDP-dissociation inhibitor 2 (Rho GDI 2) (Rho-GDI beta) (Ly-GDI)	GDIS_HUMAN	5 peptides matched LTLVCESAPGPITMDLTGDLEALKK (1) DIVSGLKYVQHTYR (1) ATFMVGSYGPRPEEYEFLLTPVEEAPK (0) + 1 Oxidation (M) Multi-Hit LTLVCESAPGPITMDLTGDLEALK (0) + 1 Oxidation (M) Multi-Hit ATFMVGSYGPRPEEYEFLLTPVEEAPKGMLAR (1) + 2 Oxidation (M) 34.82% sequence coverage	169.65	16967	5.77	-2.2

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(Q86UX7) Unc-112 related protein 2 (Kindlin-3) (MIG2-like)	URP2_HUMAN	5 peptides matched ARGEELDEDLFLQLTGGHEAF (1) Multi-Hit IDLAVGDVVK (0) ILEAHQNVAQLSLAEALR (0) GEELDEDLFLQLTGGHEAF (0) ILEAHQNVAQLSLAEALRFIQAWQSLPDFGISYVMVR (1) + 1 Oxidation (M) 10.34% sequence coverage	247.33	15221	5.96	B

b) pI 6-11

File#1

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	2 peptides matched NRQEGLMIASSLLNEGYLQPAGDMSK (1) + 2 Oxidation (M) MFVFKITTTK (1) + 1 Oxidation (M) 10.28% sequence coverage	109.16	42892	7.04	-2.22
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	4 peptides matched NRQEGLMIASSLLNEGYLQPAGDMSK (1) + 2 Oxidation (M) MFVFKITTTK (1) + 1 Oxidation (M) GSTLTSPCQDFGKR (1) IFNHCFGTGNCVIDWLVSNSVR (0) 20.57% sequence coverage	158.55	42782	7.09	B
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	3 peptides matched GSTLTSPCQDFGKR (1) NRQEGLMIASSLLNEGYLQPAGDMSK (1) + 2 Oxidation (M) MFVFKITTTK (1) + 1 Oxidation (M) 14.28% sequence coverage	119.06	42782	7.21	B
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	2 peptides matched NRQEGLMIASSLLNEGYLQPAGDMSK (1) + 2 Oxidation (M) LPETIDLGALYLSMK (0) + 1 Oxidation (M) 11.71% sequence coverage	50.95	42672	7.29	B

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(O75791) GRB2-related adaptor protein 2 (Gads protein) (Growth factor receptor binding protein) (GRBLG) (Grf40 adaptor protein) (Grf-40) (GRB-2-like protein) (GRB2L) (GRBX) (P38)	GRP2_HUMAN	2 peptides matched LGLFPANYVAPMTR (0) + 1 Oxidation (M) AELGSQEGYVPK (0) 7.87% sequence coverage	64.97	39101	6.29	B

File#2

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P05092) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein)	PPIA_HUMAN	8 peptides matched HTGPGILSMANAGPNTNGSQFFICTAK (0) + 1 Oxidation (M) Multi-Hit VNPTVFFDIAVDGEPLGR (0) Multi-Hit IIPGFMCQGGDFTR (0) Multi-Hit SIYGEEKFEDENFILK (1) Multi-Hit KITIADCGQLE (1) VSFELFADKVPK (1) HTGPGILSMANAGPNTNGSQFFICTAKTEWLDGK (1) + 1 Oxidation (M) EGMNIVEAMER (0) + 1 Oxidation (M) 70.12% sequence coverage	435.29	16760	7.55	-3.83
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	2 peptides matched NRQEGLMIASSLLNEGYLQPAGDMSK (1) + 2 Oxidation (M) GSTLTSPCQDFGKR (1) Multi-Hit 11.42% sequence coverage	98.83	42614	6.12	-2.08
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	4 peptides matched GSTLTSPCQDFGKR (1) Multi-Hit MFVFKITTTK (1) + 1 Oxidation (M) NRQEGLMIASSLLNEGYLQPAGDMSK (1) + 2 Oxidation (M) LPETIDLGALYLSMKDTEK (1) + 1 Oxidation (M) 19.71% sequence coverage	132.65	42495	6.86	B

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	6 peptides matched QQDHFFQAAFLEER (0) MFVFKITTTK (1) + 1 Oxidation (M) GSTLTSPCQDFGKR (1) Multi-Hit NRQEGLMIASSLLNEGYLQPAGDMSK (1) + 2 Oxidation (M) LPETIDLGALYLSMKDTEK (1) + 1 Oxidation (M) SDNSPKGMIPLK (1) + 1 Oxidation (M) 27.14% sequence coverage	251.83	42495	6.65	-2.97
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	3 peptides matched NRQEGLMIASSLLNEGYLQPAGDMSK (1) + 2 Oxidation (M) MFVFKITTTK (1) + 1 Oxidation (M) GSTLTSPCQDFGKR (1) Multi-Hit 14.28% sequence coverage	154.61	42495	6.73	B
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	5 peptides matched IFNHCFTGNCVIDWLVSNSQSVR (0) NRQEGLMIASSLLNEGYLQPAGDMSK (1) + 2 Oxidation (M) GSTLTSPCQDFGKR (1) Multi-Hit KSEEEENLFEIITADEVHYFLQAATPK (1) SIRLPETIDLGALYLSMK (1) + 1 Oxidation (M) 30.28% sequence coverage	225.38	42377	6.88	B
(P08567) Pleckstrin (Platelet p47 protein)	PLEK_HUMAN	5 peptides matched NRQEGLMIASSLLNEGYLQPAGDMSK (1) + 2 Oxidation (M) LPETIDLGALYLSMK (0) + 1 Oxidation (M) GSTLTSPCQDFGKR (1) Multi-Hit LPETIDLGALYLSMKDTEK (1) + 1 Oxidation (M) SIRLPETIDLGALYLSMK (1) + 1 Oxidation (M) 17.71% sequence coverage	184.73	42495	7.15	B
(O00151) PDZ and LIM domain protein 1 (LIM domain protein CLP-36) (C-terminal LIM domain protein 1) (Elfin)	PDL1_HUMAN	13 peptides matched IKGCTDNLTLTVAR (1) CGTGIVGVFVK (0) MNLASEPQEV LHIGSAHNR (0) + 1 Oxidation (M) GCTDNLTLTVAR (0) ERVTPPEGYEVVTVFPK (1) VITNQYNNPAGLYSSENISNFNNALESK (0) GHFFVEDQIYCEK (0)	561.95	35246	6.87	B

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
		HRHPECYVCTDCGTNLK (1) SAMPFTASPASSTTAR (0) + 1 Oxidation (M) LPMCDKCGTGIVGVFVK (1) + 1 Oxidation (M) VTPPEGYEVVTVFPK (0) TAASGVEANSRPLDHAQPPSSLVIDKESEVYK (1) VAASIGNAQKLPMSDK (1) + 1 Oxidation (M) Multi-Hit 55.62% sequence coverage				
(Q9H479) Fructosamine-3-kinase (EC 2.7.1.-)	FN3K_HUMAN	3 peptides matched QMFEGEVASLEALR (0) + 1 Oxidation (M) AFGGPGAGCISEGR (0) AYDTDAGPVFVK (0) 12.94% sequence coverage	117.33	35246	6.87	B
(O75558) Syntaxin 11	STXB_HUMAN	4 peptides matched QADTLNVIELNVQK (0) LAELLDLSK (0) DIRDIQDENQLLVADVK (1) TLCCFCCPCLK (0) 17.77% sequence coverage	192.12	29896	6.28	B
(Q9NS28) Regulator of G-protein signaling 18 (RGS18)	RGSI_HUMAN	3 peptides matched VYQLMEQDSYTR (0) + 1 Oxidation (M) EVITNSITQPTLHSFDAAQSR (0) LSLLVQKPEFHEDTR (0) 20.42% sequence coverage	146.77	27681	6.93	B
(Q9UJ68) Peptide methionine sulfoxide reductase (Protein-methionine-S-oxide reductase)	MSRA_HUMAN	1 peptides matched GVYSTQVGFAGGYTSNPTYK (0) 8.51% sequence coverage	40.45	24170	6.87	B
(Q06830) Peroxiredoxin 1 (Thioredoxin peroxidase 2) (Thioredoxin-dependent peroxide reductase 2)	PDX1_HUMAN	4 peptides matched QITVNDLPVGR (0) GLFIHDDKGILR (1) TIAQDYGVLK (0) LVQAFQFTDK (0) 21.60% sequence coverage	198.22	22627	8.15	B

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P37802) Transgelin 2 (SM22-alpha homolog)	TAG2_HUMAN	4 peptides matched IQASTMAFKQMEQISQFLQAAER (1) + 2 Oxidation (M) TLMNLGGLAVAR (0) + 1 Oxidation (M) QMEQISQFLQAAER (0) + 1 Oxidation (M) DDGLFSGDPNWFPK (0) 24.62% sequence coverage	169.39	21965	7.36	B
(P15153) Ras-related C3 botulinum toxin substrate 2 (p21-Rac2) (Small G protein) (GX)	RAC2_HUMAN	1 peptides matched YLECSALTQR (0) 5.20% sequence coverage	64.12	21965	7.36	B
or	or					
(P6300) p21-Rac1	RAC1_HUMAN					
(P30086) Phosphatidylethanolamine-binding protein (PEBP) (Raf kinase inhibitor protein) (RKIP)	PEBP_HUMAN	1 peptides matched LYTLVLTDPDAPSR (0) 7.52% sequence coverage	50.75	21965	7.36	B
(P37802) Transgelin 2 (SM22-alpha homolog)	TAG2_HUMAN	4 peptides matched QMEQISQFLQAAER (0) + 1 Oxidation (M) TLMNLGGLAVAR (0) + 1 Oxidation (M) NFSDNQLQEGKNVIGLQMG TNR (1) + 1 Oxidation (M) IQASTMAFKQMEQISQFLQAAER (1) + 2 Oxidation (M) 28.64% sequence coverage	176.94	21965	7.43	B
(O43665) Regulator of G-protein signaling 10 (RGS10)	RGSA_HUMAN	8 peptides matched AKEIYMTFLSSK (1) + 1 Oxidation (M) FLKSDLFLK (1) EIYMTFLSSK (0) + 1 Oxidation (M) TEEEEEEDLPDAQTA AK (0) TEEEEEEDLPDAQTA AKR (1) LQDQIFNLMK (0) + 1 Oxidation (M) LQDQIFNLMKYDSYSR (1) + 1 Oxidation (M) ILEEPHPLMFQK (0) + 1 Oxidation (M) 38.15% sequence coverage	237.38	20160	6.88	B

File#3

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P05092) Peptidyl-prolyl cis-trans isomerase A (EC 5.2.1.8) (PPIase) (Rotamase) (Cyclophilin A) (Cyclosporin A-binding protein)	PPIA_HUMAN	8 peptides matched SIYGEKFEDEFILK (1) Multi-Hit VNPTVFFDIAVDGEPLGR (0) KITIADCGQLE (1) Multi-Hit IIPGFMCQGGDFTR (0) Multi-Hit VSFELFADKVPK (1) EGMNIVEAMER (0) + 1 Oxidation (M) VKEGMNIVEAMER (1) + 1 Oxidation (M) EGMNIVEAMERFGSR (1) + 2 Oxidation (M) 53.04% sequence coverage	348.54	17133	7.37	2.61
(P02671) Fibrinogen alpha/alpha-E chain precursor [Contains: Fibrinopeptide A]	FIBA_HUMAN	6 peptides matched HRHPDEAAFFDTASTGK (1) GLIDEVNQDFTNR (0) MKPVPDLVPGNFK (0) + 1 Oxidation (M) Multi-Hit NSLFEYQK (0) TFPGFFSPMLGEFVSETESR (0) + 1 Oxidation (M) DSHSLTTNIMEILR (0) + 1 Oxidation (M) 9.81% sequence coverage	207.63	62215	7.07	CRP
(Q9ULV4) Coronin 1C (Coronin 3) (hCRNN4)	CO1C_HUMAN	2 peptides matched AIFLADGNVFTTGFSR (0) YFEITDESPYVHYLNTFSSK (0) 7.59% sequence coverage	119.33	57779	6.61	CRP
(P36871) Phosphoglucomutase (EC 5.4.2.2) (Glucose phosphomutase) (PGM)	PGMU_HUMAN	5 peptides matched SIFDFSALKELLSGPNR (1) SIFDFSALK (0) INQDPQVMLAPLISIALK (0) + 1 Oxidation (M) Multi-Hit AIGGIILTASHNPGGPNDFGIK (0) FNISNGGPAPEAITDKIFQISK (1) 14.26% sequence coverage	104	57779	6.61	CRP
(Q01518) Adenylyl cyclase-associated protein 1 (CAP 1)	CAP1_HUMAN	9 peptides matched NSLDCEIVSAK (0) LSDLLAPISEQIK (0) ALLVTASQCQQAENK (0)	252.53	53924	7.07	2.38

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
		SALFAQINQGESITHALK (0) Multi-Hit LSDLLAPISEIQIKEVITFR (1) VENQENVSNLVIEDTELKQVAYIYK (1) VPTISINKTDGCHAYLSK (1) ALLVTASQCQQAENKLSDLLAPISEQIK (1) SSEMNVLIPTTEGGDFNEFPVPEQFK (0) + 1 Oxidation (M) 27.84% sequence coverage				
(P12931) Proto-oncogene tyrosine-protein kinase Src (p60-Src) (c-Src)	SRC_HUMAN	4 peptides matched LFGGFNSSDTVTSPQR (0) AANILVGENLVCK (0) GSLLDLFLKGETGK (1) KLDSGGFYITSR (1) 10.09% sequence coverage	186.79	55544	5.92	CRP
(P07954) Fumarate hydratase, mitochondrial precursor	FUMH_HUMAN	1 peptides matched IYELAAGGTAVGTGLNTR (0) 3.52% sequence coverage	70.48	45156	7.07	CRP
(Q13418) Integrin-linked protein kinase 1 (EC 2.7.1.-) (ILK-1) (59 kDa serine/threonine protein kinase) (p59ILK)	ILK1_HUMAN	7 peptides matched GMAFLHTLEPLIPR (0) + 1 Oxidation (M) FSFQCPGR (0) EVPFADLSNMEIGMK (0) + 2 Oxidation (M) SAVVEMLIMR (0) + 2 Oxidation (M) MYAPAWVAPEALQK (0) + 1 Oxidation (M) QLNFLTK (0) FDMIVPILEKMQDK (1) + 2 Oxidation (M) 18.14% sequence coverage	208.45	49710	7.22	2.54
(P04406) Glyceraldehyde 3-phosphate dehydrogenase, liver (EC 1.2.1.12) (GAPDH)	G3P2_HUMAN	8 peptides matched LISWYDNEFGYSNR (0) IISNASCTTNCLAPLAK (0) VPTANVSVVDLTCR (0) LVINGNPITIFQER (0) LVINGNPITIFQERDPSK (1) LTGMAFRVPTANVSVVDLTCR (1) + 1 Oxidation (M)	373.3	35745	7.29	CRP

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
		VIHDNFGIVEGLMTTVHAIATQK (0) + 1 Oxidation (M) Multi-Hit GALQNIIPASTGAAK (0) 32.63% sequence coverage				
(O75791) GRB2-related adaptor protein 2 (Gads protein)	GRP2_HUMAN	3 peptides matched ASQSSPGDFSISVR (0) LGLFPANYVAPMTR (0) + 1 Oxidation (M) AELGSQEGYVPK (0) 12.12% sequence coverage	92.14	39305	5.92	CRP
(P36959) GMP reductase 1 (Guanosine 5'-monophosphate oxidoreductase 1)	GMP1_HUMAN	2 peptides matched MTSILEAVPQVK (0) + 1 Oxidation (M) LFYGMSSDTAMNK (0) + 2 Oxidation (M) 7.24% sequence coverage	73.56	37696	6.79	CRP
(P25789) Proteasome subunit alpha type 4 (EC 3.4.25.1) (Proteasome component C9)	PSA4_HUMAN	3 peptides matched ATCIGNNSAAAVSMLK (0) + 1 Oxidation (M) LLDEVFFSEK (0) LSAEKVEIATLTR (1) 14.94% sequence coverage	196.64	27474	7.22	CRP
(Q15404) Ras suppressor protein 1 (Rsu-1) (RSP-1)	RSU1_HUMAN	1 peptides matched LTVLPPELGNDLTGQK (0) 6.15% sequence coverage	43.57	27474	7.22	CRP
(P00338) L-lactate dehydrogenase A chain	LDHA_HUMAN	3 peptides matched LVIITAGAR (0) QVVESAYEVIK (0) FIIPNVVK (0) 8.45% sequence coverage	92.22	32433	7.52	CRP
(P54819) Adenylate kinase isoenzyme 2, mitochondrial (EC 2.7.4.3) (ATP-AMP transphosphorylase)	KAD2_HUMAN	6 peptides matched NGFLLDGFPR (0) AVLLGPPGAGKGTQAPR (1) LQAYHTQTTPLEIYYR (0) LVSDEMVELIEK (0) + 1 Oxidation (M) APSVPAAEPEYPKGIR (1) APSVPAAEPEYPK (0) 30.25% sequence coverage	219.18	26819	7.51	CRP

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P00338) L-lactate dehydrogenase A chain	LDHA_HUMAN	3 peptides matched QVVESAYEVIK (0) LVIIITAGAR (0) FIIPNVVK (0) 8.45% sequence coverage	80.42	32433	7.62	CRP
(P04406) Glyceraldehyde 3-phosphate dehydrogenase, liver (GAPDH)	G3P2_HUMAN	2 peptides matched IISNASCCTTNCLAPLAK (0) GALQNIIPASTGAAK (0) 9.58% sequence coverage	147.8	25620	7.30	CRP
(P37802) Transgelin 2 (SM22-alpha homolog)	TAG2_HUMAN	7 peptides matched IQASTMAFKQMEQISQFLQAAER (1) + 2 Oxidation (M) QMEQISQFLQAAER (0) + 1 Oxidation (M) TLMNLGGLAVAR (0) + 1 Oxidation (M) NFSDNQLQEGKNVIGLQMGTR (1) + 1 Oxidation (M) ENFQNWVK (0) DDGLFSGDPNWFVK (0) DGTVLCELINALYPEGQAPVKK (1) 50.75% sequence coverage	300.89	21864	7.69	3.09
(P23528) Cofilin, non-muscle isoform (18 kDa phosphoprotein) (P18)	COF1_HUMAN	6 peptides matched EILVGDVGQTVDDPYATFVK (0) LGGSAVISLEGKPL (0) YALYDATYETK (0) KEDLVFIFWAPESAPLK (1) AVLFCLSEDKK (1) Multi-Hit CTLAEKLGSAVISLEGKPL (1) 47.59% sequence coverage	316.38	18099	7.60	CRP

File#4

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P12931) Proto-oncogene tyrosine-protein kinase Src (p60-Src) (c-Src)	SRC_HUMAN	2 peptides matched TQFNSLQQLVAYYSK (0) GSLLDLFLKGETGK (1) 5.23% sequence coverage	84.75	55467	6.48	B
(O14818) Proteasome subunit alpha type 7	PSA7_HUMAN	1 peptides matched LTVEDPVTVEYITR (0) 5.64% sequence coverage	53.34	26137	8.44	B

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score	Mass (Da)	pI	Fold ^{c)}
(P00338) L-lactate dehydrogenase A chain (LDH-A) (LDH muscle subunit) (LDH-M)	LDHA_HUMAN	6 peptides matched DQLIYNLLKKEEQTPQNK (1) LVIITAGAR (0) QVVESAYEVIK (0) FIIPNVVK (0) GEMMDLQHGSFLR (0) + 2 Oxidation (M) ITVVGVGAVGMACAISILMK (0) + 2 Oxidation (M) Multi-Hit 23.86% sequence coverage	225.44	31941	7.56	CRP
(Q9NS28) Regulator of G-protein signaling 18 (RGS18)	RGSI_HUMAN	2 peptides matched VYQLMEQDSYTR (0) + 1 Oxidation (M) EVITNSITQPTLHSFDAAQSR (0) 14.04% sequence coverage	76.86	27732	5.91	CRP

^{a)}Accession numbers are shown in brackets before the protein name.

^{b)}Number of missed tryptic cleavage sites are shown in brackets after peptide sequences. Modifications detected according to the searching parameters and sequence coverage are also highlighted.

^{c)}fold change (CRP versus basal), a negative value indicates that the feature is expressed to a higher extent in basal samples; B = Protein feature only present in basal gels, CRP = Feature only present in CRP gels.