

Supplementary Table 1. Compiled Data Output File for Mascot MS Searches, screening Swiss-Prot and TrEMBL, corresponding to the tyrosine phosphoproteome analysis of CRP-stimulated platelets.

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score
(P42655) 14-3-3 protein ϵ	143E_HUMAN	2 peptides matched DSTLIMQLLR (0) + 1 Oxidation (M) AAFDDAIAELDTLSEESYK (0) 11.37% sequence coverage	59.37
(P29312) 14-3-3 protein ζ/δ	143Z_HUMAN	4 peptides matched TAFDEAIAELDTLSEESYK (0) DICNDVLSLLEK (0) DSTLIMQLLR (0) + 1 Oxidation (M) SVTEQGAELSNEER (0) 22.44% sequence coverage	164.45
(P12814) Alpha-actinin 1	AAC1_HUMAN	6 peptides matched VGWEQLLTTIAR (0) MTLGMIWTHILR (0) + 2 Oxidation (M) FAIQDISVEETSAK (0) ELPPDQAEYCIAR (0) LLETIDQLYLEYAKR (1) IDQLEGDHQLIQEALIFDNK (0) 9.64% sequence coverage	254.8
(P07355) Annexin A2 (Annexin II)	ANX2_HUMAN	2 peptides matched GVDEVTIVNILTNR (0) SALSGHLETVILGLLK (0) 8.87% sequence coverage	79.13
(P08758) Annexin A5 (Annexin V)	ANX5_HUMAN	1 peptides matched GLGTDEESILTLLTSR (0) 5.01% sequence coverage	81.47
(Q14155) Rho guanine nucleotide exchange factor 7 (Beta-Pix)	ARH7_HUMAN	2 peptides matched ELELQILTEAIR (0) SLVDTVYALKDEVQELR (1) 4.48% sequence coverage	61.72
(Q06187) Tyrosine-protein kinase BTK (Bruton's tyrosine kinase)	BTK_HUMAN	6 peptides matched NCLVNDQGVVKVSDFGLSR (1) LSYYEYDFER (0) FPYPFQVVYDEGPLYVFSPTTEELR (0) VVALYDYMPMNANDLQLR (0) + 2 Oxidation (M) ILLSNILDVMDEES (0) QRPIFIITEYMANGCLLNLYR (0) 16.08% sequence coverage	134.45
(P22681) CBL E3	CBL_HUMAN	4 peptides matched	179.36

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ubiquitin protein ligase		ALVIAQNNIEMAK (0) + 1 Oxidation (M) VCVPSSASALGTASK (0) GIFPSGLFQGDTR (0) NSPPYILDLLPDTYQHLR (0) 6.62% sequence coverage	
(O60496) Dok-2 (Downstream of tyrosine kinase 2)	DOK2_HUMAN	1 peptides matched QGNEIFLALEEISAQK (0) Multi-Hit 4.12% sequence coverage	70.82
(P07332) Proto-oncogene tyrosine-protein kinase FES/FPS (C-FES)	FES_HUMAN	1 peptides matched QVLQEALQGLQVALCSQAK (0) 2.31% sequence coverage	32.5
(O15117) ADAP (SLAP-130)	FYB_HUMAN	3 peptides matched LTGPIQVIHLAK (0) TTAVEIDYDSLK (0) INQEELASGTPPARFPK (1) 5.23% sequence coverage	135.79
(P06241) Proto-oncogene tyrosine-protein kinase FYN (P59-FYN)	FYN_HUMAN	4 peptides matched SDVWSFGILLTELVTK (0) IADFGLAR (0) ALKLPNLVDMAAQVAAGMAYIER (1) + 2 Oxidation (M) QLLSFGNPR (0) 10.44% sequence coverage	176.68
(O75791) GRB2-related adaptor protein 2 (Gads protein)	GRP2_HUMAN	4 peptides matched NFIDIQFPKWFHEGLSR (1) ILSNQEEWFKAELGSEQGYVPK (1) ALYDFEALEDDELGFHSGEVVEVLDSSNPSWWTGR (0) HQAENLLMGKEVGFFIIR (1) + 1 Oxidation (M) 27.87% sequence coverage	167.48
(P08631) Tyrosine-protein kinase HCK (Hemopoietic cell kinase)	HCK_HUMAN	3 peptides matched IADFGLAR (0) TMKPGSMSVEAFLAEANVMK (0) + 3 Oxidation (M) VAVKTMKPGSMSVEAFLAEANVMK (1) + 1 Oxidation (M) 6.09% sequence coverage	52.06
(P43405) Tyrosine-protein kinase SYK (Spleen tyrosine kinase)	KSYK_HUMAN	7 peptides matched LRNYYYDVVN (1) NEANDPALKDELLAEANVMQQLDNPYIVR (1) + 1 Oxidation (M) IGTQGNVNFQGRPQLPGSHPATWSAGGIISR (0) YLEESNFVHRDLAAR (1) SDVWSFGVLMWEAFSYGQKPYR (0) + 1 Oxidation (M) EYVKQTWNLQGGQALEQAIISQKPQLEK (1)	174.18

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score
		MIGICEAESWMLVMEMAELGPLNKYLQQNR (1) + 4 Oxidation (M) 25.82% sequence coverage	
(Q13094) Lymphocyte cytosolic protein 2 (SH2 domain-containing leucocyte protein of 76 kDa) (SLP-76 tyrosine phosphoprotein) (SLP76)	LCP2_HUMAN	10 peptides matched FLNLTENDIQKFPK (1) Multi-Hit YQKESQVYLLGTGLR (1) GKEDFLSVSDIIDYFR (1) Multi-Hit EDFLSVSDIIDYFR (0) SEVLGWDPDSLADYFK (0) NVPFRSEVLGWDPDSLADYFK (1) LRVPILSK (1) YQCTLTHAAGYP (0) ENEDDDVHQRPLQPALLPMSNTFPSR (0) TPQQPPVPPQRPMAALPPPAGR (0) + 1 Oxidation (M) 25.70% sequence coverage	417.36
(P07948) Tyrosine-protein kinase LYN	LYN_HUMAN	2 peptides matched SLDNGGYIISPR (0) TLKPGTMSVQAFLEEANLMK (0) + 2 Oxidation (M) 6.26% sequence coverage	54.16
(Q16539) Mitogen-activated protein kinase 14 (MAP kinase p38alpha)	MK14_HUMAN	12 peptides matched SLEEFNDVYLVTHLMGADLNNIVK (0) Multi-Hit LTDDHVQFLIYQILR (0) Multi-Hit ITAAQALAHAYFAQYHDPDDEPVADPYDQSFESR (0) Multi-Hit DLKPSNLAVNEDCELKILDFGLAR (1) ILDFGLAR (0) TIWEVPERYQNLSPVGSVCAAFDTK (1) LTDDHVQFLIYQILRGLK (1) NYIQSLTQMPK (0) + 1 Oxidation (M) DLKPSNLAVNEDCELEK (0) DLLIDEWKSLTYDEVISFVPPPLDQEEMES (1) + 1 Oxidation (M) NYIQSLTQMPKMNANVFIGNPLAVDLLEK (1) + 2 Oxidation (M) KLSRPFQSIHAK (1) 56.66% sequence coverage	497.53
(P35579) Myosin heavy chain, nonmuscle type A (Myosin 9)	MYH9_HUMAN	18 peptides matched DLGEELEALKTELEDTLTDSTAAQQELR (1) QLLQANPILEAFGNAK (0) TRLQQELDDLLVDLDHQR (1) KFDQLLAEEK (1) LQQELDDLLVDLDHQR (0) VISGVLQLGNIVFKK (1) DFSALESQEQDTQELLQEENR (0) EQADFAIEALAK (0) ALELDSNLYR (0) IIGLDQVAGMSETALPGAFK (0) + 1 Oxidation (M) NLPIYSEEIVEMYK (0) + 1 Oxidation (M) VVFQEFR (0)	962.11

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		DFSALESQIQDTQELLQEENRQK (1) IAQLEEQLDNETK (0) ANLQIDQINTDLNLER (0) KANLQIDQINTDLNLER (1) IAQLEEQLDNETKER (1) DVLLQVDDERR (1) 10.96% sequence coverage	
(O00145) SH2 containing inositol-5-phosphatase (SHIP)	O00145	1 peptides matched LSQLTSLSSIEDKVK (1) ^c 1.34% sequence coverage	57.43
(O75563) SRC kinase-associated phosphoprotein 55-related protein (SKAP-HOM)	O75563	1 peptides matched NLLADVETFVADILK (0) 4.17% sequence coverage	65.25
(P16885) PLC-gamma-2 (Phospholipase C-gamma-2)	PIG2_HUMAN	9 peptides matched GILDLNTYNVVK (0) ILHQEAMNASTPTIIESWLR (0) + 1 Oxidation (M) VTFEYDPNLAFLR (0) IQQYFSPNYVEDISTADFEELKQIIEDNPLGSLCR (1) SIACPFVEVEICGAEYDNNKFK (1) AFKEVFGDLLLTKPTEASADQLPSPSQLR (1) YYLTDNLTFFSIYALIQHYR (0) ESETFPNDYTLFWR (0) TTVVNDNGLSPIWAPTQEKVTFEYDPNLAFLR (1) 14.78% sequence coverage	389.83
(Q9H939) PSTPIP2 (Proline-serine-threonine phosphatase-interacting protein 2)	PSP2_HUMAN	4 peptides matched DIEYFVNQRK (1) NALWLHVNQLSQCVTSDEMYEQVR (0) + 1 Oxidation (M) ALEVFKQQVDNVAQCHIQLAQLR (1) GNFWSADILSTIGYDNIQHLNNGR (0) 25.22% sequence coverage	124.44
(Q7Z5H2) G6f protein	Q96QC7_HUMAN	7 peptides matched AADGSPCNVLLCSVVPSR (0) VQSFWGSEAALLLVCPGEGLEPR (0) Multi-Hit GAPGRDASIPQFKPEIQVYENIHLAR (1) + 1 Phospho (Y) Multi-Hit VYDVLVLKGSQLSAR (1) GRVQSFWGSEAALLLVCPGEGLEPR (1) Multi-Hit DASIPQFKPEIQVYENIHLAR (0) + 1 Phospho (Y) VYDVLVLK (0) 29.31% sequence coverage	401.39
(Q15404) Ras suppressor protein	RSU1_HUMAN	2 peptides matched LTVLPPELGNLDTGQK (0)	80.79

Protein Name ^{a)}	Database Entry	Peptide Sequences ^{b)}	Protein Score
1 (RSP-1)		NLEVLNFFNNQIEELPTQISSLQK (0) Multi-Hit 14.85% sequence coverage	
(Q9NZQ3) SH3 adapter protein SPIN90* (Dip-interacting protein-1) (DIP-1)	SP90_HUMAN	2 peptides matched LQGLEQDVLQAIDR (0) SAEPNALAFAAGETFLVLER (0) 4.70% sequence coverage	167.27
(P12931) Proto-oncogene tyrosine-protein kinase Src (c-Src)	SRC_HUMAN	4 peptides matched LFGGFNSSDTVTSPQR (0) SDVWSFGILLTELTTK (0) AGPLAGGVTTFVALYDYESR (0) LIEDNEYTAR (0) 11.58% sequence coverage	118.09
(Q14247) Src substrate cortactin	SRC8_HUMAN	2 peptides matched YGLFPANYVELRQ (1) ASAGHAVSIAQDDAGADDWETDPDFVNDVSEKEQR (1) 8.72% sequence coverage	131.94
(P15498) Vav proto-oncogene	VAV_HUMAN	2 peptides matched LNPGDIVELTKAEAEQNWWEGR (1) MEVFQEYYGLPPPPGAIGPFLR (0) + 1 Oxidation (M) 5.20% sequence coverage	50.58
(Q9UDY2) Tight junction protein ZO-2	ZO2_HUMAN	3 peptides matched LAGGNDVGIFVAGIQEGTSAEQEGLQEGDQILK (0) LAGGNDVGIFVAGIQEGTSAEQEGLQEGDQILKVNTQDFR (1) INGTVTENMSLTDAR (0) + 1 Oxidation (M) 4.62% sequence coverage	105.20

^{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)}Although the only peptide sequenced had one missed cleavage, the identification was accepted because it was confirmed by western blot (not shown).