



Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
GLLGLAAADP	AIFYKEQFLDGDWATNR	N-ter +28.03 Da, K +28.03 Da	26.4	91.9	3	2129.25	-6.64	0.00	CALR_MOUSE		Calreticulin;	CRP55;Calregulin;Endoplasmic reticulum resident protein 60;HACBP;	0.00 - 0.15
DPHRCEKAMT TAVKVAGSVA	AKGGDVSVCEIYWR AKLPSLLVDR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da N-ter +34.06 Da, K +34.06 Da	32.6 28.8	78.8 46.9	3 3	1581.89 1352.93	-2.25 0.58	0.21 0.01	CX681_MOUSE STBD1_MOUSE	Q147V6_MOUSE	Cytochrome c oxidase subunit 6B1; Starch-binding domain-containing protein 1;	Cytochrome c oxidase subunit Vlb isoform 1; Genethonin-1; Beta-2-globin;Hemoglobin beta-2 chain;Hemoglobin beta-minor chain; SR type 1;Steroid 5-alpha-reductase 1; Heparin-binding protein 44;Low density lipoprotein receptor-related protein-associated protein 1;	0.00 - 0.15 0.25 - 0.75
AEKSAVSLCW ASWSLQGVVF	AKVNPDEVGGEALGR ALFTLCALFTR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, C +57.02 Da	43.3 26.6	76.1 4.6	3 3	1566.96 1345.77	0.89 -1.69	0.07 0.38	HBB2_MOUSE SSA1_MOUSE		Hemoglobin subunit beta-2; 3-oxo-5-alpha-steroid 4-dehydrogenase 1;		0.75 - 0.85 0.00 - 0.15
RKDAQMVHNS	ALNEDTQDELGDPR	N-ter +34.06 Da	33.1	69.4	3	1605.88	0.94	0.09	AMRP_MOUSE	F6Y09_MOUSE	Alpha-2-macroglobulin receptor-associated protein;		0.75 - 0.85
ERHRTLTEMV AVGPVPTANA SLVSQMIQLA	ALNPDPFKPADYKPPATR ALPADPPASVIVVGPVVVPR ALSEASQTDPDPSGPPPR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +34.06 Da	17.8 51.7 61.8	70.9 77.1 67.7	4 3 3	2081.28 1867.24 1642.95	1.41 0.32 -0.92	0.09 0.02 0.04	SFO1_MOUSE FETUA_MOUSE F134C_MOUSE	Q3U45_MOUSE	Splicing factor 1; Alpha-2-HS-glycoprotein; Protein FAM134C;		0.75 - 0.85 0.25 - 0.75 0.15 - 0.25
KTDQVIQIFI GMLPEKDCRY	ALVNDPQPEHPLR ALYDASFETKESR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	40.6 25.9 25.3	58.6 75.6 51.1	3 3 4	1512.89 1571.90 2994.50	1.50 -0.92 4.59	0.08 0.05 0.26	UB2L3_MOUSE DEST_MOUSE E9QG06_MOUSE		Ubiquitin-conjugating enzyme E2 L3; Destrin;		0.85 - 1.00 0.15 - 0.25
VQMGAVDLLG LALAFGLAHA	AMDDDIJALVVVDSGSMCKAGFAGDDAPR AMEGPPWKTVAIAADR	N-ter +34.06 Da, K +34.06 Da	27.1	58.8	3	1683.04	0.15	0.00	AZAEN9_MOUSE	Q9D3H2_MOUSE			0.85 - 1.00 0.25 - 0.75
PREIFKQKER SPVSSGVNLF EAVVSSVNTV CDIDIRKDLV HHSFYNELRV QSKGQWLTLT M	AMSTTSVTSQQPKLR ANDGSFLEFKR ANKTVEEENIVVTTGVVR ANNVMSGTMTMYPIADR APEEHPHTLLEAPLNPKANR APLDTINVHLR APNVLASEPEIKGIR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	34.8 23.2 27.2 36.7 38.9 37.6 43.7	99.5 87.0 82.7 49.0 70.1 56.8 66.2	3 3 3 3 3 3 3	1706.07 1451.90 2096.39 1888.00 2253.37 1275.80 1746.12	-2.12 -0.30 -1.09 -3.84 1.06 -0.12 0.73	0.37 0.02 0.07 0.55 0.09 0.01 0.07	DBNL_MOUSE CS043_MOUSE SYUG_MOUSE ACTA_MOUSE ACTC_MOUSE LYAG_MOUSE KAD2_MOUSE	ACTA_MOUSE	Drebrin-like protein; Uncharacterized protein C19orf43 homolog; Gamma-synuclein; Actin, alpha skeletal muscle; Actin, alpha cardiac muscle 1; Lysosomal alpha-glucosidase; Adenylate kinase 2, mitochondrial;	Actin-binding protein 1;SH3 domain-containing protein 7; Persyn; Alpha-actin-1; Alpha-cardiac actin; Acid maltase; ATP-AMP transphosphorylase 2;	0.00 - 0.15 0.25 - 0.75 0.15 - 0.25 0.00 - 0.15 0.75 - 0.85 0.25 - 0.75 0.25 - 0.75
TSQLTAFPLG	APPPWPIQDSSGPELGSR	N-ter +34.06 Da	50.1	58.5	3	2021.16	0.54	0.02	GORS1_MOUSE		Golgi reassembly-stacking protein 1;	Golgi peripheral membrane protein p65;Golgi reassembly-stacking protein of 65 kDa;	0.25 - 0.75
ATSASGALLS VAGPOPAQTG NAILVRYTQK TISKIKGLRV M	APPSGPPISGVSGETTYDITR APOGSLGELYFER APOVSTPTLVEAAR APQVYILPPAEQLSR APVEHVADAGAFLR	N-ter +34.06 Da N-ter +34.06 Da N-ter +28.03 Da N-ter +34.06 Da N-ter +28.03 Da	51.7 44.3 42.0 43.1 29.0	68.1 53.8 43.8 52.7 69.8	3 3 3 3 3	2153.27 1499.86 1466.87 1812.13 1578.96	-0.25 1.68 0.28 -0.79 -1.32	0.03 0.06 0.01 0.01 0.10	PRRC1_MOUSE FRIL1_MOUSE ALBU_MOUSE IGG2B_MOUSE NOB1_MOUSE	Q9CFX4_MOUSE F6YBB8_MOUSE	Protein PRRC1; Ferritin light chain 1; Serum albumin; Ig gamma-2B chain C region; RNA-binding protein NOB1;	Proline-rich and coiled-coil-containing protein 1; Ferritin L subunit 1;	0.25 - 0.75 0.85 - 1.00 0.25 - 0.75 0.15 - 0.25 0.15 - 0.25
LLATVWHGQG NLQSRFRIL GRVQEPKPGM	APVIEPSPGPELVPEGETVTLR AQMGTGEYMQDPDEEAR ARPAPASPAARFPHTQGQRLR	N-ter +28.03 Da N-ter +34.06 Da N-ter +34.06 Da	49.2 23.4 34.3	52.3 26.0 37.6	3 3 4	2316.38 2118.00 2344.41	0.03 -2.25 -2.40	0.01 0.21 0.13	CSF1R_MOUSE E9PYJ9_MOUSE KIFC3_MOUSE	Q3TBH6_MOUSE LDB3_MOUSE	Macrophage colony-stimulating factor 1 receptor; Kinesin-like protein KIFC3;	CSF-1 receptor;Proto-oncogene c-Fms;	0.25 - 0.75 0.00 - 0.15 0.00 - 0.15
SVQSGNLALA SPCLLRVHL	ASAAAVDAGMAMAGQSPVLR ASAFGSSTESLVAR	N-ter +28.03 Da N-ter +34.06 Da	34.7 49.3	37.9 25.5	3 2	1901.02 1415.78	1.25 0.01	0.03 0.00	PTBP1_MOUSE THEM5_MOUSE	Q922I7_MOUSE	Poly(pyrimidine) tract-binding protein 1; Thioesterase superfamily member 5;	Heterogeneous nuclear ribonucleoprotein I;	0.75 - 0.85 0.25 - 0.75
GNTGFSAGLD SSCLVLAARH KNVREATESF	ASAQTSHELTPINDLIGCIGR ASASNTLNKDLVSLNLPKEQAR ASDPILYRPAVALDTKGPEIR	N-ter +34.06 Da, C +57.02 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da	29.6 28.2 23.7	31.3 70.3 77.7	4 4 4	2500.40 2443.62 2436.56	-3.18 -0.20 -1.09	0.58 0.02 0.07	PCBP2_MOUSE CISY_MOUSE KPYM_MOUSE		Poly(rC)-binding protein 2; Citrate synthase, mitochondrial; Pyruvate kinase isozymes M1/M2;	Alpha-CP2;CTBP;Putative heterogeneous nuclear ribonucleoprotein X;	0.00 - 0.15 0.25 - 0.75 0.15 - 0.25
LALLVRSTAP ENNVGVCHIF	ASFFGENHLEVPVPSALTR ASFNDFVHVHTDLSGKETICR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	33.1 39.7	73.3 102.2	3 4	2098.24 2452.46	-1.89 -4.64	0.42 1.16	CSPG4_MOUSE RS14_MOUSE	D3YVF4_MOUSE	Chondroitin sulfate proteoglycan 4; 40S ribosomal protein S14;	Chondroitin sulfate proteoglycan NG2;Proteoglycan AN2;	0.00 - 0.15
ARGAAVTRSM	ASGGGVPTDEEQATGLER	N-ter +28.03 Da	51.7	69.4	3	1800.97	-0.60	0.03	COX5B_MOUSE	Q9D881_MOUSE	Cytochrome c oxidase subunit 5B, mitochondrial;	Cytochrome c oxidase polypeptide Vb; Aldehyde dehydrogenase family 5 member A1;NAD(+)-dependent succinic semialdehyde dehydrogenase;	0.25 - 0.75
EPAGTPRRSY	ASGPGGLHADLLR	N-ter +34.06 Da	29.7	31.2	3	1296.78	-0.15	0.00	SSDH_MOUSE		Succinate-semialdehyde dehydrogenase, mitochondrial;		0.25 - 0.75
DIQVKELEKR QEVRCLEERSY	ASGQAFELISPR ASKPTLNEVIVSAIR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	23.2 44.7	87.5 75.7	3 3	1415.90 1752.18	5.05 -0.15	0.22 0.01	STMN1_MOUSE THIL_MOUSE	D3Z1Z8_MOUSE	Stathmin; Acetyl-CoA acetyltransferase, mitochondrial;	Leukemia-associated gene protein;Leukemia-associated phosphoprotein p18;Metablastin;Oncoprotein p18;Phosphoprotein p19;Proslin;Protein Pr22;pp17;	0.85 - 1.00 0.25 - 0.75
SSSPVKGYW TGAEDTRMPP VYSSAKNSS	ASLDASTQTTHELTPNNGIICIGR ASLEQSLASPKISVR ASNTQDGVGSLCSR	N-ter +28.03 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, C +57.02 Da	43.4 29.3 25.8	76.2 58.8 77.7	4 3 3	2822.68 1770.09 1478.79	-1.40 -3.64 0.21	0.26 0.46 0.02	PCBP1_MOUSE Q3URZ6_MOUSE PAXI_MOUSE	F7DBB3_MOUSE F8VQ28_MOUSE	Poly(rC)-binding protein 1; Paxillin;	Alpha-CP1;Heterogeneous nuclear ribonucleoprotein E1;	0.15 - 0.25 0.00 - 0.15 0.25 - 0.75
M	ASQTQGIQQLQAEKR	N-ter +28.03 Da, K +28.03 Da	33.1	14.1	3	1854.06	4.26	0.31	VATG2_MOUSE		V-type proton ATPase subunit G 2;	V-ATPase 13 kDa subunit 2;Vacuolar proton pump subunit G 2;	0.85 - 1.00

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MKAARFVMS	ASSLSSASLVPR	N-ter +34.06 Da	41.1	23.9	2	1207.73	0.25	0.01	PKD4_MOUSE		[Pyruvate dehydrogenase [lipoamide]] kinase isozyme 4, mitochondrial;	Pyruvate dehydrogenase kinase isoform 4; Alpha-CP1;Heterogeneous nuclear ribonucleoprotein E1;	0.25 - 0.75
EVKGYWASLD	ASTQTTHELTPNNLIGCIGR	N-ter +34.06 Da, C +57.02 Da	38.3	21.6	3	2442.36	-0.17	0.03	PCBP1_MOUSE		Poly(rC)-binding protein 1; WD repeat domain phosphoinositide-interacting protein 2;		0.25 - 0.75
WTGYFVKVLM	ASTSYLPSQVTEMFNQGR	N-ter +34.06 Da	27.9	76.8	3	2049.16	-3.84	0.55	WIPI2_MOUSE	D3YWK1_MOUSE			0.00 - 0.15
IREGEVEVLK	ATEMVEVGPEDDEVGAER	N-ter +34.06 Da	49.1	69.6	3	1966.04	-0.84	0.12	PTRF_MOUSE		Polymerase I and transcript release factor;	Cav-p60;Cavin-1;	0.15 - 0.25
NWYKMGQLVL	ATIEKIPFESAFR	N-ter +34.06 Da, K +34.06 Da	25.5	67.9	3	1576.04	-0.43	0.04	FACR2_MOUSE		Fatty acyl-CoA reductase 2;	Male sterility domain-containing protein 1;	0.25 - 0.75
VIQHRPSQY	ATLDVYNPFENR	N-ter +34.06 Da	21.6	50.5	3	1471.83	-1.18	0.08	SCAM3_MOUSE	Q3UXS0_MOUSE	Secretory carrier-associated membrane protein 3;		0.15 - 0.25
KHKKEKAVTI	ATPATAAPAASVSAATTTSAQEEPAAPAEPR	N-ter +28.03 Da	45.8	78.0	4	2833.63	-1.94	0.30	SRRM1_MOUSE	A2A8V8_MOUSE	Serine/arginine repetitive matrix protein 1;	Plenty-of-prolines 101;	0.00 - 0.15
SSSAPRVSR	ATTVSAPDLKSVR	N-ter +34.06 Da, K +34.06 Da	44.1	82.2	3	1411.98	-1.03	0.08	F7CK47_MOUSE	MAP4_MOUSE	Microtubule-associated protein;		0.15 - 0.25
SDTTTPKLL	AVAATAPPDAPNREEVFDER	N-ter +28.03 Da	28.4	100.0	4	2182.28	-1.40	0.29	VINC_MOUSE		Vinculin;	Metavinclin;	0.15 - 0.25
QERQTAQVL	AVADKVKEDSQVPATQLQR	N-ter +28.03 Da, K +28.03 Da	33.2	80.3	4	2267.43	-0.58	0.03	AKA12_MOUSE		A-kinase anchor protein 12;		0.25 - 0.75
QLAAQPSTYL	AVAELENVSGKYFDGLR	N-ter +28.03 Da, K +28.03 Da	27.2	89.8	3	2052.24	-3.18	0.58	RDH13_MOUSE		Retinol dehydrogenase 13;		0.00 - 0.15
DDGLADLFLV	AVEEQSYCEYSGSR	N-ter +34.06 Da, C +57.02 Da	48.6	79.2	3	1667.86	-2.94	0.45	E9PX16_MOUSE				0.00 - 0.15
IIPASTGAAK	AVGKVIPELNKLGTMAFR	N-ter +28.03 Da, K +28.03 Da	37.7	79.3	4	2084.38	0.01	0.00	G3P_MOUSE	F8WJL5_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase;	Peptidyl-cysteine S-nitrosylase GAPDH;	0.25 - 0.75
MGASGRLLR	AVIMGAPSGKGTVSSR	N-ter +34.06 Da, K +34.06 Da	38.7	82.1	3	1642.09	-0.30	0.06	KAD3_MOUSE		GTP:AMP phosphotransferase, mitochondrial;	Adenylate kinase 3;Adenylate kinase 3 alpha-like 1;	0.25 - 0.75
QRLYAREATQ	AVLDKPETLSSDASTR	N-ter +28.03 Da, K +28.03 Da	19.3	90.9	3	1745.08	-4.32	0.86	ACADV_MOUSE		Very long-chain specific acyl-CoA dehydrogenase, mitochondrial;	MVLCAD;	0.00 - 0.15
GPEPTTDCFV	AVMHGETEGTVPGNALVVDPEKPFRR	N-ter +28.03 Da, K +28.03 Da	35.6	66.0	4	2705.56	0.41	0.02	EHD2_MOUSE		EH domain-containing protein 2;		0.25 - 0.75
RSLVIPNTL	AVNAAQDSTDLVAKLR	N-ter +28.03 Da, K +28.03 Da	41.5	59.9	3	1727.06	1.20	0.08	TCPA_MOUSE		T-complex protein 1 subunit alpha;	CCT-alpha;Tailless complex polypeptide 1A;Tailless complex polypeptide 1B;	0.75 - 0.85
VLTFGFMTL	AVPIAQKSEQSLNEALMR	N-ter +28.03 Da, K +28.03 Da	33.1	92.8	4	2224.40	0.12	0.01	Q542V8_MOUSE	D3Z3K5_MOUSE			0.25 - 0.75
QKEKSPDQCS	AVPNTPPSTPVKLEELDPQEPSTR	N-ter +28.03 Da, K +28.03 Da	30.9	72.9	4	2657.58	0.16	0.02	ADDA_MOUSE		Alpha-adducin;	Erythrocyte adducin subunit alpha;	0.25 - 0.75
LSLEVQELQA	AVRPLQLLGTCAELCR	N-ter +34.06 Da, C +57.02 Da	56.0	55.5	3	1890.14	-0.94	0.11	Q8BT6_MOUSE				0.15 - 0.25
ERNEWQKFL	AVSQNPQDVLTPVPTGQSQEEAAGDQDDLR	N-ter +28.03 Da	42.9	81.4	4	3139.76	-1.89	0.21	GOGA2_MOUSE	E9PUQ5_MOUSE	Golgin subfamily A member 2;	130 kDa cis-Golgi matrix protein;	0.00 - 0.15
TGQAAPVLGL	AVSSELIQQSFPVDECPR	N-ter +34.06 Da, C +57.02 Da	51.9	55.7	3	2223.23	-0.40	0.03	FKBP9_MOUSE		Peptidyl-prolyl cis-trans isomerase FKBP9;	63 kDa FK506-binding protein;FK506-binding protein 9;FKBP65R5;Rotamase;	0.25 - 0.75
VNVKTSASR	AVSSLATKGGPSEVR	N-ter +34.06 Da, K +34.06 Da	20.7	96.8	3	1597.10	0.37	0.07	DCLK1_MOUSE	Q8BRN4_MOUSE	Serine/threonine-protein kinase DCLK1;	1;Doublecortin-like kinase 1;	0.25 - 0.75
LSKDJANTW	AVTVDFPCSTNAKR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	25.1	101.1	3	1570.97	-2.74	0.37	PPR3A_MOUSE		Protein phosphatase 1 regulatory subunit 3A;	Protein phosphatase 1 glycogen-associated regulatory subunit;Protein phosphatase type-1 glycogen targeting subunit;	0.00 - 0.15
LWSAVGASNM	AVVTCGSVVKLLNTR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	31.2	46.6	3	1684.11	0.53	0.07	SDF2_MOUSE		Stromal cell-derived factor 2;		0.25 - 0.75
TISLQMGTK	CASQVGMTAPGTR	N-ter +34.06 Da, C +57.02 Da	28.9	63.8	3	1368.76	-0.17	0.01	CNN2_MOUSE	D3Z7R6_MOUSE	Calponin-2;	Calponin H2, smooth muscle;Neutral calponin;	0.25 - 0.75
ARNLGRVGTK	CCTLPEDQR	N-ter +34.06 Da, C +57.02 Da	33.6	57.5	2	1211.62	0.29	0.05	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
MEPYS	CDTFVALPPTVGNR	N-ter +34.06 Da, C +57.02 Da	37.3	45.0	3	1650.94	-0.45	0.01	SCRN3_MOUSE	A2AWQ9_MOUSE	Secernin-3;		0.25 - 0.75
M	CEEETLALVCDNGSLCKAGFAGDDAPR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	23.8	56.5	4	3055.50	4.17	0.39	ACTH_MOUSE	D3ZY0_MOUSE	Actin, gamma-enteric smooth muscle;	Alpha-actin-3;Gamma-2-actin;Smooth muscle gamma-actin;	0.85 - 1.00
HNLPLGRFCE	CEIGYELDR	N-ter +28.03 Da, C +57.02 Da	32.0	84.6	2	1181.64	0.12	0.02	FBN1_MOUSE	A2AQ53_MOUSE	Fibrillin-1;		0.25 - 0.75
WLLDHCQESY	CEPTVCQPTCYQR	N-ter +28.03 Da, C +57.02 Da	41.6	90.3	3	1725.88	3.83	1.04	E9QZ9_MOUSE				0.85 - 1.00
TCCKAADKDT	CFSTEGPNLVTR	N-ter +28.03 Da, C +57.02 Da	31.3	64.7	3	1407.77	-0.34	0.02	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
SGGAAGATSL	CFVYPLDFAR	N-ter +34.06 Da, C +57.02 Da	32.1	44.9	2	1320.73	-1.94	0.15	ADT1_MOUSE	ADT2_MOUSE	ADP/ATP translocase 1;	ADP.ATP carrier protein 1;ADP.ATP carrier protein, heart/skeletal muscle isoform T1;Adenine nucleotide translocator 1;Solute carrier family 25 member 4;mANC1;	0.00 - 0.15
QAGRFRHNL	CGEEQGAADALHFNPR	N-ter +28.03 Da, C +57.02 Da	66.2	72.0	3	1798.94	1.46	0.15	LEG7_MOUSE	Q9CRB1_MOUSE	Galectin-7;		0.85 - 1.00
SRTTSTSTM	CGYYGNYGGGR	N-ter +28.03 Da, C +57.02 Da	30.7	60.4	2	1356.64	1.26	0.10	KR168_MOUSE	O09048_MOUSE	Keratin-associated protein 16-8;	Keratin-associated protein 16.8;	0.75 - 0.85
CRVPITPENP	CKEIHGTSSEPEMLSHTR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	18.5	87.5	4	2298.40	-2.00	0.40	RN219_MOUSE		RING finger protein 219;		0.00 - 0.15
CQVGGISTV	CQPVGGISTVCQPTCGVSR	N-ter +28.03 Da, C +57.02 Da	37.6	55.3	3	2090.09	2.29	0.13	E9QZ9_MOUSE				0.85 - 1.00
KPTDGASSN	CVTDIHLVR	N-ter +28.03 Da, C +57.02 Da	33.0	68.0	3	1226.73	2.29	0.11	NASP_MOUSE	B1AU75_MOUSE	Nuclear autoantigenic sperm protein;		0.85 - 1.00
AEFKAADFDMF	DADGGGDISVKELGTVMR	N-ter +34.06 Da, K +34.06 Da	32.4	88.0	3	1887.17	0.01	0.00	TNNC2_MOUSE		Troponin C, skeletal muscle;	STNC;	0.25 - 0.75
MQN	DAGEFVDLVPR	N-ter +34.06 Da	33.8	73.3	3	1413.84	1.41	0.06	RS21_MOUSE		40S ribosomal protein S21;		0.75 - 0.85
LGVKSQKLL	DAVDYIPVPTR	N-ter +34.06 Da	44.4	30.2	2	1379.79	1.63	0.11	EFTU_MOUSE	D3YVN7_MOUSE	Elongation factor Tu, mitochondrial;		0.85 - 1.00
LPLLARLSAG	DCPCSEALCQPIR	N-ter +28.03 Da, C +57.02 Da	43.3	56.6	3	1703.84	1.43	0.13	DIAC_MOUSE		Di-N-acetylchitobiase;		0.75 - 0.85
RPKVKREVKV	DCSEYLALSKR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	19.8	82.1	3	1408.88	1.05	0.06	Q8BM18_MOUSE	Q148R4_MOUSE			0.75 - 0.85
IFKAVLVTG	DDEATLADNCKMCTR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	39.8	94.4	3	1980.13	-2.94	0.45	IGJ_MOUSE		Immunoglobulin J chain;		0.00 - 0.15

Table S8, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
VLLTFGFVRA MTEAEQQQLI	DDEVDVDTGVEEDLGKSR DDHFLFDKVPSPLLASGMAR	N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da, K +34.06 Da	73.1 30.3	68.4 117.7	3 4	2045.15 2396.60	0.62 -0.06	0.09 0.00	ENPL_MOUSE KCRM_MOUSE	KCRB_MOUSE	Endoplasmic reticulum resident protein 99;Heat shock protein 90 kDa beta member 1;Polymorphic tumor rejection antigen 1;Tumor rejection antigen gp96; Creatine kinase M-type;	94 kDa glucose-regulated protein;Endoplasmic reticulum resident protein 99;Heat shock protein 90 kDa beta member 1;Polymorphic tumor rejection antigen 1;Tumor rejection antigen gp96; Creatine kinase M chain;M-CK;	0.25 - 0.75 0.25 - 0.75
PPPCPGRELF DSELSTSELE EDEYTESYSD	DDPSVYNIQNLDKAR DDISIMGYKLDQTDVQIMAR DDSNMEDYPPQSANPMNSLLSLYR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da	38.7 23.1 21.0	76.0 43.7 69.3	3 3 4	1803.05 2466.38 2986.50	1.87 -1.94 6.66	0.12 0.30 0.85	SHC1_MOUSE SLAI1_MOUSE NLV_MOUSE	F7D4S5_MOUSE	SHC-transforming protein 1; SLAIN motif-containing protein 1; Nuclear valosin-containing protein-like;	SHC-transforming protein A;Src homology 2 domain-containing-transforming protein C1; Creatine kinase M chain;M-CK;	0.85 - 1.00 0.00 - 0.15 0.85 - 1.00
TNLRDDIMRL	DDTVHVVIATPGR	N-ter +28.03 Da	22.0	96.4	3	1406.89	2.21	0.34	DDX6_MOUSE		Probable ATP-dependent RNA helicase DDX6;	ATP-dependent RNA helicase p54;DEAD box protein 6;Oncogene RCK homolog;	0.85 - 1.00
TWKLVSENF	DDYMKEVGVGFATR	N-ter +34.06 Da, K +34.06 Da	36.2	77.0	3	1654.99	-0.03	0.00	FABP4_MOUSE		Fatty acid-binding protein, adipocyte;	3T3-L1 lipid-binding protein;Adipocyte lipid-binding protein;Adipocyte-type fatty acid-binding protein;Fatty acid-binding protein 4;Myelin P2 protein homolog;P15;P2 adipocyte protein;Protein 422;	0.25 - 0.75
DVIRNAFACF	DEEATGIQEDYLR	N-ter +28.03 Da	27.0	41.9	3	1666.84	0.85	0.05	ML12B_MOUSE		Myosin regulatory light chain 12B;	Myosin regulatory light chain 2-B, smooth muscle isoform;Myosin regulatory light chain 20 kDa;Myosin regulatory light chain MRLC2;	0.25 - 0.75
KAVLSAEKLR IENHEGVRFR NFASQMSYGY DKDKSGFIEE DDFRFASAGD SASNRHIAAK	DEEVHTGLGELLR DEILEASDGIMVAR DEKSAGVSPVPGMGPSPGR DELGSLKGFSSDAR DGIIVVWNAQTGEKLELR DHASIQMNVAEVDR	N-ter +28.03 Da N-ter +34.06 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	37.2 42.8 36.0 25.2 16.7 33.8	71.2 68.4 75.3 90.1 112.4 94.7	3 3 3 3 4 3	1494.87 1551.91 1892.15 1650.01 2209.50 1611.92	1.51 -1.03 -2.40 -0.17 2.04 0.14	0.15 0.04 0.25 0.03 0.10 0.02	SERPH_MOUSE KPYM_MOUSE CO1A1_MOUSE PRVA_MOUSE WDR41_MOUSE RS21_MOUSE	F8WGB7_MOUSE	Serpin H1; Pyruvate kinase isozymes M1/M2; Collagen alpha-1(I) chain; Parvalbumin alpha; WD repeat-containing protein 41; 40S ribosomal protein S21;	47 kDa heat shock protein;Collagen-binding protein;Serine protease inhibitor J6; Pyruvate kinase muscle isozyme; Alpha-1 type I collagen;	0.85 - 1.00 0.15 - 0.25 0.00 - 0.15 0.25 - 0.75 0.85 - 1.00 0.25 - 0.75
MDD LLFWIPASRG LLLWFPGARC PMSRRTEISI QQLDHDFLF	DIAALVVDNGSGMCKAGFAGDDAPR DILLTQSPALVSPGER DIQMOTSPSSLASLGER DISSKQVESTASAGPSR DKPVPSPLLASGMAR	+57.02 Da N-ter +28.03 Da N-ter +28.03 Da N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da	49.4 49.6 56.8 40.7 37.5	87.1 73.1 73.8 88.0 49.2	4 3 3 3 3	2562.44 1923.21 1934.08 1846.11 1622.07	-0.49 -0.62 -1.03 -0.79 0.83	0.09 0.11 0.19 0.12 0.07	ACTB_MOUSE KV5A9_MOUSE KV5A7_MOUSE SEPT9_MOUSE KCRM_MOUSE	E9Q1F2_MOUSE KV5A8_MOUSE A2A6U3_MOUSE KCRB_MOUSE	Actin, cytoplasmic 1; Ig kappa chain V-V region L7; Ig kappa chain V-V region MOPC 41; Septin-9; Creatine kinase M-type;	Beta-actin;	0.25 - 0.75 0.25 - 0.75 0.15 - 0.25 0.15 - 0.25 0.25 - 0.75
NRVYKEMYKT KQEVNENFAI	DLEKDIISDTSGDFR DLIAQQPVEVEHR	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da	24.2 24.2	75.8 86.9	3 3	1778.07 1675.01	-1.89 -0.69	0.14 0.10	ANXA2_MOUSE NDU56_MOUSE	B0V2N7_MOUSE D3YW32_MOUSE	Annexin A2; NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial; NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial;	Annexin II;Annexin-2;Calpactin I heavy chain;Calpactin-1 heavy chain;Chromobindin-8;Lipocortin II;Placental anticoagulant protein IV;Protein I;p36; Complex I-13kD-A;NADH-ubiquinone oxidoreductase 13 kDa-A subunit; Complex I-9kD;NADH-ubiquinone oxidoreductase 9 kDa subunit;	0.00 - 0.15 0.25 - 0.75
HHDYNTYTLF GGSLSVLMAR LTSSESRPTR	DLNLDLSKFR DLPAAAAPAGPASFAR DLSSDLSLASKIVK	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	24.3 52.5 43.6 42.8	50.2 64.2 76.2 67.6	3 3 3 3	1287.85 1509.89 1634.04 1925.20	-0.86 4.97 1.31 2.33	0.09 0.80 0.18 0.20	NDUV3_MOUSE 6PGL_MOUSE A2M_MOUSE Q9D1B1_MOUSE	Q3U422_MOUSE Q8CBG6_MOUSE D3YW52_MOUSE	mitochondrial; 6-phosphogluconolactonase; Alpha-2-macroglobulin;	Pregnancy zone protein;	0.15 - 0.25 0.85 - 1.00 0.75 - 0.85 0.85 - 1.00
CEEETALVC DDEETALVC NKNMKRQKSL QDSILMKDKS KSKENPRFIS	DNGSGLCKAGFAGDDAPR DNGSGLVKAGFAGDDAPR DNLLKVTPEVNR DNLYNIIINR DNQLQEGKNVIGLQMGNTNR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	38.0 49.5 30.8 21.6 36.2	96.3 83.9 74.9 88.1 68.6	3 3 3 3 3	1863.04 1802.05 1452.94 1275.77 2170.27	-3.18 -1.29 1.65 0.43 0.61	0.58 0.16 0.13 0.01 0.07	ACTA_MOUSE ACTC_MOUSE SCEL_MOUSE HSF3_MOUSE TAGL2_MOUSE	ACTH_MOUSE ACTS_MOUSE	Actin, aortic smooth muscle; Actin, alpha cardiac muscle 1; Sciellin; Heat shock factor protein 3; Transgelin-2;	Alpha-actin-2; Alpha-cardiac actin;	0.00 - 0.15 0.15 - 0.25 0.85 - 1.00 0.25 - 0.75 0.25 - 0.75
LLGLLGLAAA LLTACLASRA VPTANAALPA	DPAIYFKEQLDGDWATNR DPASTLPDIQVENFSES DPPASVVVGVVPR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da N-ter +28.03 Da	27.9 51.0 50.3	96.5 66.3 75.4	4 3 3	2341.36 2166.21 1515.00	-1.47 -0.30 0.74	0.12 0.05 0.05	CALR_MOUSE AMB_MOUSE FETUA_MOUSE		Calreticulin; Protein AMBP; Alpha-2-HS-glycoprotein;	Calreticulin; Protein AMBP; Alpha-2-HS-glycoprotein;	0.15 - 0.25 0.25 - 0.75 0.25 - 0.75
PTSYPEPSKL LLVILPATGS	DPTSVTLPKPEIR DPVLCFTQYEESGR	N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da, C +57.02 Da	24.1 45.7	84.5 67.5	3 3	1554.04 1820.97	0.68 0.57	0.04 0.02	MA2B_MOUSE PRZB1_MOUSE		Lysosomal alpha-mannosidase; Properdin;	Lysosomal alpha-mannosidase; Mannosidase alpha class 2B member 1;Mannosidase alpha-B; Complement factor P;	0.25 - 0.75 0.25 - 0.75
SWASRNEAAP GLPGLAGLHG	DQDEIDCLPLGAKQPSFR DQGAGPVGPAQPR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da N-ter +28.03 Da	38.3 46.6	53.2 47.1	3 2	2144.17 1302.73	0.19 -0.11	0.01 0.01	PPGB_MOUSE CO1A2_MOUSE	A2A5I9_MOUSE E9Q6U9_MOUSE	Lysosomal protective protein; Collagen alpha-2(I) chain;	Carboxypeptidase C;Carboxypeptidase L;Cathepsin A;Protective protein cathepsin A;Protective protein for beta-galactosidase; Alpha-2 type I collagen; Alpha-1 protease inhibitor 1;Alpha-1-antiproteinase;Serine protease inhibitor 1-1;Serine protease inhibitor A1a;	0.25 - 0.75 0.25 - 0.75
DVQETDTSQK	DQSPASHEIATNLGDFAIPLYR	N-ter +28.03 Da	64.9	71.3	3	2432.37	0.28	0.08	A1AT1_MOUSE	A1AT2_MOUSE	Alpha-1-antitrypsin 1-1;	Alpha-1-antitrypsin 1-1;	0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
DVQETDTSQK	DQSPASHEIATNLGDFALR	N-ter +34.06 Da	45.4	65.8	3	2075.19	-0.94	0.05	A1AT4_MOUSE		Alpha-1-antitrypsin 1-4;	Alpha-1 protease inhibitor 4;Serine protease inhibitor 1-4;Serine protease inhibitor A1d;	0.15 - 0.25
EGSSNVFSMF	DQTQIQEFKEAFTVIDQNR	N-ter +28.03 Da, K +28.03 Da	44.8	92.8	4	2365.41	-2.74	0.37	MLRS_MOUSE	F6ULR7_MOUSE	Myosin regulatory light chain 2, skeletal muscle isoform;	Fast skeletal myosin light chain 2;MLC2F;	0.00 - 0.15
FWSLLAICAS	DSFRDQAVAIMR	N-ter +34.06 Da	29.1	52.8	3	1441.83	-0.36	0.03	DPEP1_MOUSE		Dipeptidase 1;	Membrane-bound dipeptidase 1;Microsomal dipeptidase;Renal dipeptidase;	0.25 - 0.75
QTRGFVSDSS	DSMDTGAGSIR	N-ter +28.03 Da	40.0	77.5	2	1136.60	0.94	0.04	ATIF1_MOUSE	Q9D879_MOUSE	ATPase inhibitor, mitochondrial;	Inhibitor of F(1)F(o)-ATPase;	0.75 - 0.85
PRQPSQSS	DSQVHSGVQVEGR	N-ter +28.03 Da	38.7	101.1	3	1424.85	2.94	0.45	E9Q019_MOUSE	FILA_MOUSE			0.85 - 1.00
KVLQTRGFVS	DSSDSMDTGAGSIR	N-ter +34.06 Da	46.7	52.1	2	1431.71	2.11	0.20	ATIF1_MOUSE	Q9D879_MOUSE	ATPase inhibitor, mitochondrial;	Inhibitor of F(1)F(o)-ATPase;	0.85 - 1.00
DVEPTYCRY	DSVSFNGAVSDDSKR	N-ter +28.03 Da, K +28.03 Da	61.0	85.5	3	1738.00	-0.07	0.01	PCOC1_MOUSE	D3ZE3_MOUSE	Procollagen C-endopeptidase enhancer 1;	P14;Procollagen COOH-terminal proteinase enhancer 1;Type 1 procollagen C-proteinase enhancer protein;Type 1 procollagen COOH-terminal proteinase enhancer;	0.25 - 0.75
QGVVMVGMGQK	DSYVGDQAQSKR	N-ter +34.06 Da, K +34.06 Da	31.3	96.3	3	1421.88	0.30	0.06	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
RHNRIKEIGA	DTFSQLGSLQALDLSWNAIR	N-ter +34.06 Da	42.1	48.9	3	2268.31	-3.32	0.66	LGR6_MOUSE	D3Z6S4_MOUSE	Leucine-rich repeat-containing G-protein coupled receptor 6;		0.00 - 0.15
PKKQALYLMF	DTPQESPVKSPPPR	N-ter +28.03 Da, K +28.03 Da	29.9	96.7	3	1592.01	0.60	0.06	TACC2_MOUSE	E9Q8T1_MOUSE	Transforming acidic coiled-coil-containing protein 2;	D4;Rho-GDI beta;	0.25 - 0.75
LTKYKTLTG	DVPVVDPTVFNVTVTR	N-ter +34.06 Da	54.2	70.7	3	1812.15	-1.22	0.17	GDIR2_MOUSE		Rho GDP-dissociation inhibitor 2;	Alpha-1 protease inhibitor 1;Alpha-1-antiprotease;Serine protease inhibitor 1-1;Serine protease inhibitor A1a;	0.15 - 0.25
CCLVP5FLAE	DVQETDTSQKQSPASHEIATNLGDFAIISLYR	N-ter +34.06 Da, K +34.06 Da	46.7	84.6	4	3604.10	-1.40	0.18	A1AT1_MOUSE	A1AT2_MOUSE	Alpha-1-antitrypsin 1-1;		0.15 - 0.25
LVLILKGVQC	DVQLVESGGGLVQPGGSR	N-ter +28.03 Da	43.9	33.4	3	1781.99	0.03	0.00	HVM16_MOUSE		Ig heavy chain V region MOPC 21;		0.25 - 0.75
TDKPLRLPLQ	DVYKIGGIGTVPVGR	N-ter +28.03 Da, K +28.03 Da	50.0	73.1	3	1586.03	-0.11	0.01	EF1A1_MOUSE	EF1A2_MOUSE	Elongation factor 1-alpha 1;	Elongation factor Tu;Eukaryotic elongation factor 1 A-1;	0.25 - 0.75
LVFAPVGVQK	DWLSLSLPHR	N-ter +34.06 Da	34.3	84.1	3	1256.81	-0.84	0.03	Q9EQY5_MOUSE	D3YYJ5_MOUSE			0.15 - 0.25
HSGALQRQKR	DWWIPPINPENSIR	N-ter +28.03 Da	29.3	60.4	3	1676.99	1.04	0.14	CADH2_MOUSE	D3YYT0_MOUSE	Cadherin-2;	Neural cadherin;	0.75 - 0.85
VLHFGIAVLY	EACCVLLLWLLALFISQIPR	N-ter +28.03 Da, C +57.02 Da	32.4	56.7	4	2428.48	4.06	0.38	MFS6L_MOUSE		Major facilitator superfamily domain-containing protein 6-like;		0.85 - 1.00
DGSSAGTLL	EALDCILPPTRPDKPLR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	31.4	72.2	4	2159.40	1.58	0.06	EF1A1_MOUSE	D3YZ68_MOUSE	Elongation factor 1-alpha 1;	Elongation factor Tu;Eukaryotic elongation factor 1 A-1;	0.85 - 1.00
FEGRSRRRR	EAPKVVVEEQSR	N-ter +28.03 Da, K +28.03 Da	22.1	37.1	3	1455.81	0.14	0.00	CO4B_MOUSE		Complement C4-B;		0.25 - 0.75
GSYYEKPTQ	EAPQVTGPIEVPVVR	N-ter +28.03 Da	38.4	26.2	3	1617.95	-0.74	0.04	CRIP2_MOUSE		Cysteine-rich protein 2;	Heart LIM protein;	0.25 - 0.75
GTEAAATVF	EAVPMSMPPILR	N-ter +28.03 Da	29.5	87.0	3	1367.85	-0.04	0.00	A1AT2_MOUSE		Alpha-1-antitrypsin 1-2;	Alpha-1 protease inhibitor 2;Alpha-1-antiprotease;Serine protease inhibitor 1-2;Serine protease inhibitor A1b;	0.25 - 0.75
LGTPRLGVQK	EDGLDFPEYDGVDR	N-ter +34.06 Da	39.9	20.8	2	1659.78	-1.18	0.14	CASQ1_MOUSE	E9Q489_MOUSE	Calsequestrin-1;	Calsequestrin, skeletal muscle isoform;	0.15 - 0.25
PKLPGRVAFG	EDIDLPEFDAR	N-ter +34.06 Da	38.8	38.3	2	1453.77	-5.64	0.00	CATB_MOUSE		Cathepsin B;	Cathepsin B1;	0.00 - 0.15
GATALLTHGQ	EDIPEVSCIHNGLR	N-ter +34.06 Da, C +57.02 Da	46.4	72.7	3	1671.97	0.76	0.04	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.25 - 0.75
SHIDKTLMLN	EDKPADDDYSAVLQR	N-ter +34.06 Da, K +34.06 Da	33.5	82.8	3	1674.03	-1.47	0.16	SRCA_MOUSE		Sarcalumenin;		0.15 - 0.25
TLTAVHDAIL	EDLVFSEIVGKR	N-ter +34.06 Da, K +34.06 Da	44.9	75.4	3	1556.04	2.38	0.23	RS7_MOUSE	F6SVV1_MOUSE	40S ribosomal protein S7;		0.85 - 1.00
LGTLPARAAH	EDPVEKIVIEGFSR	N-ter +34.06 Da, K +34.06 Da	31.4	97.8	3	1572.04	0.43	0.02	SBSN_MOUSE	E9QP82_MOUSE	Suprabasin;		0.25 - 0.75
LCCLVPSFLA	EDVQETDTSQKQSPASHEIATNLGDFAIISLYR	N-ter +34.06 Da, K +34.06 Da	31.3	86.9	4	3733.16	-1.69	0.76	A1AT1_MOUSE	A1AT2_MOUSE	Alpha-1-antitrypsin 1-1;	Alpha-1 protease inhibitor 1;Alpha-1-antiprotease;Serine protease inhibitor 1-1;Serine protease inhibitor A1a;	0.00 - 0.15
LCCLVPSFLA	EDVQETDTSQKQSPASHEIATNLGDFALR	N-ter +34.06 Da, K +34.06 Da	47.7	44.3	3	3369.81	-0.81	0.06	A1AT4_MOUSE		Alpha-1-antitrypsin 1-4;	Alpha-1 protease inhibitor 4;Serine protease inhibitor 1-4;Serine protease inhibitor A1d;	0.15 - 0.25
ARQASRSTAY	EDYHHPPRR	N-ter +28.03 Da	24.9	71.3	3	1363.72	2.04	0.32	Q8VHMS_MOUSE				0.85 - 1.00
LVQDVANNTN	EEAGDGTTTATVLR	N-ter +34.06 Da	32.0	75.8	3	1524.90	-0.04	0.00	CH60_MOUSE	D3Z2F2_MOUSE	60 kDa heat shock protein, mitochondrial;	60 kDa chaperonin;Chaperonin 60;HSP-65;Heat shock protein 60;Mitochondrial matrix protein P1;	0.25 - 0.75
SGLLLTGTQ	EEAQEIDCNDEAVQAVDSLKLNAR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	46.7	111.6	4	3146.91	-5.18	0.58	Q6S9I3_MOUSE	Q6S9I2_MOUSE			0.00 - 0.15
M	EEEIAALVIDNGSMCKAGFAGDDAPR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	28.6	55.2	4	2979.54	0.71	0.05	ACTG_MOUSE	B1ATY1_MOUSE	Actin, cytoplasmic 2;	Gamma-actin;	0.25 - 0.75
EDEKAAAEIY	EEFLAAFEGSDGNKVKTFVR	N-ter +28.03 Da, K +28.03 Da	30.7	75.4	4	2327.39	0.70	0.06	SR140_MOUSE	E9QM87_MOUSE	U2 snRNP-associated SURP motif-containing protein;	associated protein SR140;	0.25 - 0.75
GHACTQKFSN	EEIAMATVTALR	N-ter +28.03 Da	44.5	29.2	2	1331.75	-0.45	0.04	ALDOA_MOUSE	ALDOC_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.25 - 0.75
MPCKI	EEIKDFLLTAR	N-ter +34.06 Da, K +34.06 Da	29.5	58.9	3	1401.93	0.14	0.01	RL38_MOUSE		60S ribosomal protein L38;		0.25 - 0.75
LLLSGELYA	EEKQCDPFTVENGR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	32.7	66.3	3	1776.00	0.21	0.02	F13B_MOUSE	B1AY02_MOUSE	Coagulation factor XIII B chain;	Protein-glutamine gamma-glutamyltransferase B chain;Transglutaminase B chain;	0.25 - 0.75
PHLSYKEAF	EEMEGTSPSPHVSAR	N-ter +28.03 Da	66.4	100.5	3	1825.02	-0.25	0.04	E9Q056_MOUSE	E9Q6Y2_MOUSE			0.25 - 0.75
ERGNPVIQW	EEVEDASEEAPLRDR	N-ter +34.06 Da	30.0	77.1	3	1777.99	-2.18	0.20	SRCA_MOUSE		Sarcalumenin;		0.00 - 0.15
ERGNPVIQW	EEVEDASEEAPLR	N-ter +34.06 Da	56.6	40.8	2	1506.79	-1.52	0.17	SRCA_MOUSE		Sarcalumenin;		0.00 - 0.15
AVLSAEKLRD	EEVHTGLGELLR	N-ter +34.06 Da	24.4	57.8	3	1385.85	0.71	0.06	SERPH_MOUSE		Serpin H1;	47 kDa heat shock protein;Collagen-binding protein;Serine protease inhibitor J6;	0.25 - 0.75

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FRHACVPVDF	EEHVSSNADEEDIR	N-ter +28.03 Da	45.4	79.5	3	1755.93	1.09	0.18	IDHG1_MOUSE	Q3TKM5_MOUSE	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial;	Isocitric dehydrogenase subunit gamma;NAD(+)-specific ICDB subunit gamma;	0.75 - 0.85
TEEHLRDYF	EYKIDTIEITDR	N-ter +34.06 Da, K +34.06 Da	34.4	79.8	3	1862.18	-0.04	0.01	ROA2_MOUSE	F6U106_MOUSE	Heterogeneous nuclear ribonucleoproteins A2/B1;		0.25 - 0.75
EVTDRAYTGR	EFDDLPLAEQR	N-ter +28.03 Da	28.5	49.2	3	1359.73	0.16	0.00	AT2A1_MOUSE		Sarcoplasmic/endoplasmic reticulum calcium ATPase 1;	Calcium pump 1;Calcium-transporting ATPase sarcoplasmic reticulum type, fast twitch skeletal muscle isoform;Endoplasmic reticulum class 1/2 Ca(2+) ATPase;	0.25 - 0.75
RLSLESEGAN	EGATAAPELSALEEAFR	N-ter +28.03 Da	45.2	30.9	2	1788.95	0.71	0.14	TPPP_MOUSE		Tubulin polymerization-promoting protein;		0.25 - 0.75
IIRNVKGPVQ	EGDVLTLLESER	N-ter +28.03 Da	45.5	37.8	2	1387.77	0.99	0.06	RS28_MOUSE	D3YVD9_MOUSE	40S ribosomal protein S28;		0.75 - 0.85
KKAGHPFMWN	EHLGYVLTCPNSLGTGLR	N-ter +28.03 Da, C +57.02 Da	42.6	81.7	3	2014.20	-2.84	0.61	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.00 - 0.15
DAYGPPSNFL	EIDVSNPQTVGVGR	N-ter +28.03 Da	27.9	45.8	3	1497.85	0.88	0.06	SNX3_MOUSE	Q78ZM0_MOUSE	Sorting nexin-3;		0.75 - 0.85
DPLNLGRTL	EIPGSSDPNIVPDGDFSSLVR	N-ter +28.03 Da	35.8	74.1	3	2228.26	0.38	0.04	CO4B_MOUSE		Complement C4-B;		0.25 - 0.75
NLVKTNCDLY	EKLGEYGFQNAILVR	N-ter +28.03 Da, K +28.03 Da	29.7	71.2	3	1792.12	-0.49	0.02	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
LLAVLPTTTA	EKNIGDIYSLTVDSR	N-ter +34.06 Da, K +34.06 Da	45.9	57.5	3	1777.09	1.08	0.06	Q9DBK8_MOUSE	Q8C7G9_MOUSE			0.75 - 0.85
KLPSLAFLYM	EKNQLEEVPSALPR	N-ter +34.06 Da, K +34.06 Da	33.2	67.8	3	1677.09	-0.52	0.04	PRELP_MOUSE		Prolargin;	Proline-arginine-rich end leucine-rich repeat protein;	0.25 - 0.75
NIGGAGSYIY	EKPQTEAPQVTGPIEVPVVR	N-ter +28.03 Da, K +28.03 Da	21.4	66.2	4	2229.38	3.43	0.11	CRIP2_MOUSE		Cysteine-rich protein 2;	Heart LIM protein;	0.85 - 1.00
AIPNLRNYG	ELADCTKQEPER	N-ter +28.03 Da, K +28.03 Da	29.2	73.7	3	1424.94	0.43	0.03	ALBU_MOUSE		Serum albumin;		0.00 - 0.15
HIFCNCSN	ELALPSPYKPVPR	N-ter +28.03 Da, K +28.03 Da	29.2	73.7	3	1424.94	0.43	0.03	RUN_MOUSE		RUN and FYVE domain-containing protein 1;	Rab4-interacting protein;	0.25 - 0.75
SAKSGDELQD	ELFELLGPEGLDLIEKLLQNR	N-ter +34.06 Da, K +34.06 Da	19.9	66.9	4	2506.64	-3.84	0.00	E9PZJ8_MOUSE				0.00 - 0.15
KPGAVQETTF	ELGGDVHSGTALPASR	N-ter +28.03 Da	41.0	101.7	3	1593.97	-0.62	0.07	AFAD_MOUSE	E9PYX7_MOUSE	Afadin;	Protein AF-6;	0.25 - 0.75
QKRRKNDLDM	ELQALDHSFEAR	N-ter +34.06 Da	34.5	68.4	3	1561.94	0.25	0.02	TNNT3_MOUSE	A2A6J0_MOUSE	Troponin T, fast skeletal muscle;	Fast skeletal muscle troponin T;	0.25 - 0.75
RQMRHRSLAR	ELSGTIKEILTAQSGVGNVDGR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	39.3	84.1	4	2459.48	1.42	0.15	RL12_MOUSE		60S ribosomal protein L12;		0.75 - 0.85
QTTALMAHLF	EMGFCDRQLNLRLLR	N-ter +28.03 Da, C +57.02 Da	28.2	56.7	3	1948.12	1.55	0.09	NBR1_MOUSE	A2A4N8_MOUSE	Next to BRCA1 gene 1 protein;	Membrane component chromosome 17 surface marker 2 homolog;Neighbor of BRCA1 gene 1 protein;	0.85 - 1.00
TDKHKTDLNF	ENLKGDDLDLPNVLSR	N-ter +34.06 Da, K +34.06 Da	39.3	68.5	3	2059.23	-1.56	0.14	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.00 - 0.15
DLLLTPEMF	ENPLYGVSVPFKLVR	N-ter +28.03 Da, K +28.03 Da	27.1	66.6	3	1945.20	-0.38	0.03	SHIP1_MOUSE		Phosphatidylinositol-3,4,5-trisphosphate 5-phosphatase 1;	Inositol polyphosphate-5-phosphatase of 145 kDa;SH2 domain-containing inositol-5'-phosphatase 1;p150Ship;	0.25 - 0.75
DKLCAIPNLR	ENYGELADCTKQEPER	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	37.1	96.4	3	2154.14	-2.64	0.50	ALBU_MOUSE		Serum albumin;		0.00 - 0.15
TGHFMGKSL	EPPSLSLVGTAPPNTR	N-ter +28.03 Da	29.2	61.8	3	1760.06	0.35	0.01	NMB_MOUSE	D3Z621_MOUSE	Neurodin-B;		0.25 - 0.75
LRSLFSAEN	EPVPVLVGNWRPPQVKGR	N-ter +34.06 Da, K +34.06 Da	23.7	67.6	4	2190.45	-0.43	0.01	CAH3_MOUSE		Carbonic anhydrase 3;	Carbonate dehydratase III;Carbonic anhydrase III;	0.25 - 0.75
LQLVSWTLAA	EPVDVLEAWGVHR	N-ter +28.03 Da	46.1	92.9	3	1533.94	0.96	0.07	Q9JL12_MOUSE				0.75 - 0.85
LLWAAACAQS	EQDFYDFKAVNIR	N-ter +28.03 Da, K +28.03 Da	20.5	59.9	3	1699.96	-1.03	0.13	GPX7_MOUSE	E9PVY3_MOUSE	Glutathione peroxidase 7;		0.15 - 0.25
LIWDMGVLG	EQEVDNELQELSTQGSR	N-ter +28.03 Da	58.6	45.5	3	2076.06	1.16	0.07	CLU5_MOUSE	E9Q988_MOUSE	Clusterin;	Apolipoprotein J;Clustrin;Sulfated glycoprotein 2;	0.75 - 0.85
GPPGSPGSPG	EQQPSGASGPAGPR	N-ter +34.06 Da	41.3	9.7	2	1300.67	-0.54	0.05	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.25 - 0.75
TLFQSPFIGM	ESAGIHETTYNSIMKCDIDIR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	26.1	66.9	4	2508.37	-1.12	0.15	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.15 - 0.25
RTLPRDAVEK	ESALSPEGDVQR	N-ter +34.06 Da	30.9	75.3	3	1320.77	-0.86	0.05	PCOC1_MOUSE	D3YUE2_MOUSE	Procollagen C-endopeptidase enhancer 1;	P14;Procollagen COOH-terminal proteinase enhancer 1;Type 1 procollagen C-proteinase enhancer protein;Type 1 procollagen COOH-terminal proteinase enhancer;	0.15 - 0.25
GPRGERGTPG	ESGAAGSPGIGSR	N-ter +34.06 Da	55.3	48.1	2	1275.72	1.44	0.23	CO1A2_MOUSE	E9Q6U9_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.85 - 1.00
FIVFYSKSC	ESLQTSLLHAAR	N-ter +28.03 Da	38.0	53.8	3	1352.81	1.48	0.07	F8VQ07_MOUSE				0.85 - 1.00
RSPRRSPVHP	ESSEGEHVSVPQR	N-ter +34.06 Da	30.7	90.5	3	1602.92	-5.64	2.82	FILA2_MOUSE	FILA2_MOUSE	Filaggrin-2;	Intermediate filament-associated protein;	0.00 - 0.15
GPAGKNGDRG	ETGPAGPAGPIGAGAR	N-ter +28.03 Da	42.7	51.5	3	1502.86	1.47	0.09	CO1A1_MOUSE		Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.85 - 1.00
RRSGRLLTRW	ETTSIPEAGEGQIR	N-ter +34.06 Da	38.4	62.6	3	1607.92	0.75	0.08	ISCA2_MOUSE		Iron-sulfur cluster assembly 2 homolog, mitochondrial;	HESB-like domain-containing protein 1;	0.25 - 0.75
LASLLSGQA	EVEDASEEAPLR	N-ter +34.06 Da	42.4	48.3	2	1377.75	-1.64	0.10	SRCA_MOUSE		Sarcalumenin;		0.00 - 0.15
FSRGLSNAER	EVGKALEGINNGITQAGR	N-ter +34.06 Da, K +34.06 Da	43.4	48.2	3	1894.18	-1.32	0.13	SBSN_MOUSE	E9QP82_MOUSE	Suprabasin;		0.15 - 0.25
VLSAEKLRDE	EVHTGLGELLR	N-ter +34.06 Da	38.0	48.5	3	1256.79	0.70	0.07	SERPH_MOUSE			47 kDa heat shock protein;Collagen-binding protein;Serine protease inhibitor J6;	0.25 - 0.75
RLVDSGSLA	EVPKEAPKVGILGSGDFAR	N-ter +34.06 Da, K +34.06 Da	42.1	61.3	4	2071.38	0.92	0.07	STEA3_MOUSE	E9QN92_MOUSE	Metalloendopeptidase STEAP3;	Dudulin-2;Protein nm1054;Six-transmembrane epithelial antigen of prostate 3;Tumor suppressor-activated pathway protein 6;	0.75 - 0.85
LMAVVIGINS	EVQLQQSGAELVR	N-ter +34.06 Da	40.8	39.9	3	1489.89	0.31	0.02	HVM02_MOUSE		Ig heavy chain V region 93G7;		0.25 - 0.75
DKRSALQISN	EWASQTTDGKLPVTKDVER	N-ter +34.06 Da, K +34.06 Da	33.3	82.0	4	2390.51	0.89	0.09	SERPH_MOUSE			47 kDa heat shock protein;Collagen-binding protein;Serine protease inhibitor J6;	0.75 - 0.85
VTASKAIEK	EYQPHVIVSTTGNPNTLDR	N-ter +34.06 Da	26.6	112.4	4	2519.57	-2.40	0.13	ADDA_MOUSE	E9Q1K3_MOUSE	Alpha-adducin;	Erythrocyte adducin subunit alpha;	0.00 - 0.15



Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
MSDN ACGSVYMSNP	GELEFDKPPAPPVR GESSFDLADR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da	31.6 44.5	96.7 53.5	3 2	1459.95 1129.61	2.66 -0.56	0.19 0.05	PAK2_MOUSE SODE_MOUSE		Serine/threonine-protein kinase PAK 2; Extracellular superoxide dismutase [Cu-Zn];	Gamma-PAK;p21-activated kinase 2;	0.85 - 1.00 0.25 - 0.75
AWSKDINAYN KGVVPLAGTN	GETPTEKLPFPIIDDKGR GETTTQGLDGLSER	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	23.5 42.5	81.4 67.6	4 3	2114.42 1490.82	0.40 -0.34	0.05 0.04	PRDX6_MOUSE ALDOA_MOUSE	Q6GT24_MOUSE Q9CPQ9_MOUSE	Peroxioredoxin-6; Fructose-bisphosphate aldolase A;	1-Cys peroxioredoxin;Acidic calcium-independent phospholipase A2;Antioxidant protein 2;Non-selenium glutathione peroxidase; Aldolase 1;Muscle-type aldolase;	0.25 - 0.75 0.25 - 0.75
KDLTELSRF DLHLKGNPKV	GEVVDCTIKTDPVTGR GEYDVTVPR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da N-ter +34.06 Da	28.0 33.4	87.9 44.0	3 2	1814.15 1068.61	-0.89 0.01	0.10 0.00	HNRDL_MOUSE E9Q616_MOUSE	F6VQH5_MOUSE F7BRM2_MOUSE	Heterogeneous nuclear ribonucleoprotein D-like; E9Q616_MOUSE	JKT41-binding protein;	0.15 - 0.25 0.25 - 0.75
SKQNLNPKV TLFGPKGVNI	GFCSGSGR GGAGSYIYKPPQTEAPQVTGPIEVPVVR	N-ter +34.06 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da	8.0 48.1	43.9 86.8	2 4	860.44 2997.84	-2.94 -1.32	0.23 0.10	ALG13_MOUSE CRIP2_MOUSE		UDP-N-acetylglucosamine transferase subunit ALG13 homolog; Cysteine-rich protein 2;	Asparagine-linked glycosylation 13 homolog;Glycosyltransferase 28 domain-containing protein 1; Heart LIM protein;	0.00 - 0.15 0.15 - 0.25
GGNFGFGDSR SNIAKAAWGKI	GGGNFGPGPGSNFR GGHGAEGAEALER	N-ter +28.03 Da N-ter +34.06 Da	48.6 53.6	115.6 85.3	3 3	1404.82 1449.83	1.01 -0.36	0.05 0.04	ROA2_MOUSE HBA_MOUSE	F6U106_MOUSE Q91V88_MOUSE	Heterogeneous nuclear ribonucleoproteins A2/B1; Hemoglobin subunit alpha;	Alpha-globin;Hemoglobin alpha chain; Adapter-related protein complex 1 subunit beta-1;Adaptor protein complex AP-1 subunit beta-1;Beta-1-adaptin;Beta-adaptin 1;Clathrin assembly protein complex 1 beta large chain;Golgi adaptor HA1/AP1 adaptin beta subunit;	0.75 - 0.85 0.25 - 0.75
VQMGAVDLLG YGGGGGGYGG GHPTSPRRPP	GGDLSDIGSNFGAPASVAAPAPAR GGSGYGGGGGGYGGEGYSISPNYSR GGSIITVYKPIR	N-ter +28.03 Da N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da	49.4 23.4 26.9	76.5 66.2 60.6	4 4 3	2496.45 2460.24 1487.96	0.19 -6.64 0.01	0.02 0.00 0.00	AP1B1_MOUSE E9QNN1_MOUSE MAP2B_MOUSE	Q5VGS5_MOUSE	AP-1 complex subunit beta-1; Epididymis-specific alpha-mannosidase;	Mannosidase alpha class 2B member 2; Cytokeratin-1B;Embryonic type II keratin-1;Keratin-77;Type-II keratin Kb39; Metastatic lymph node gene 50 protein; Scaffold attachment factor A;	0.25 - 0.75 0.00 - 0.15 0.25 - 0.75
GFSSRSLYL PQQQMTSSY DEEEGAGDEN	GGSKIFGNLVGR GGYKPAAPVSIQR GHGEQQSQPPAAAAQQPSQQR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	42.1 42.4 19.3	63.7 90.7 118.7	3 3 4	1346.85 1527.98 2356.41	-0.06 0.62 1.70	0.00 0.11 0.27	K2C1B_MOUSE LASP1_MOUSE HNRPU_MOUSE	A2A6H0_MOUSE	Keratin, type II cytoskeletal 1b; LIM and SH3 domain protein 1; Heterogeneous nuclear ribonucleoprotein U;		0.25 - 0.75 0.25 - 0.75 0.85 - 1.00
VCYGRRYGPK	GIGFGQAGCLSTDTGHEHLGLQFQKSPKPAR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	67.3	65.8	4	3281.90	-0.01	0.00	CSR3_MOUSE		Cysteine and glycine-rich protein 3;		0.25 - 0.75
NIKRNDFQL LTVPCILGQN GISTVCQPVG ARYASICQQN M	GIQDGVLSLLQDSGEVR GISDVVKVLTPEFEAR GISTVCQPTGVSFR GIVRIVEPELPGDDHDLKX GKDYIQTGLAR	N-ter +34.06 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da	49.4 45.1 28.0 45.2 35.8	69.6 57.7 80.7 81.6 46.6	3 3 3 4 3	1883.12 1910.21 1548.86 2267.44 1451.91	1.01 -0.69 1.07 -0.81 2.15	0.09 0.09 0.04 0.10 0.19	IF5A1_MOUSE LDHA_MOUSE E9Q2E9_MOUSE ALDOA_MOUSE DNIB1_MOUSE		Eukaryotic translation initiation factor 5A-1; L-lactate dehydrogenase A chain; E9Q2E9_MOUSE Fructose-bisphosphate aldolase A; DnaJ homolog subfamily B member 1;	Eukaryotic initiation factor 5A isoform 1;eIF-4D; LDH muscle subunit; Aldolase 1;Muscle-type aldolase; Heat shock 40 kDa protein 1;	0.75 - 0.85 0.00 - 0.15 0.75 - 0.85 0.15 - 0.25 0.85 - 1.00
PSNQVIMLTF KAENGLVIN	GKFDVEPDTYCR GKPIITFQER	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da	29.9 29.8	68.1 52.2	3 3	1553.89 1243.79	-6.64 -0.36	0.00 0.01	PCOC1_MOUSE G3P_MOUSE	D3Y2E3_MOUSE F8WJL5_MOUSE	Procollagen C-endopeptidase enhancer 1; Glyceraldehyde-3-phosphate dehydrogenase;		0.00 - 0.15 0.25 - 0.75
AEKAAVSCWLW	GKVNSEVGGALGR	N-ter +34.06 Da, K +34.06 Da	45.1	77.9	3	1554.98	-0.01	0.00	HBB1_MOUSE		Hemoglobin subunit beta-1; Potassium voltage-gated channel subfamily A member 7;	Beta-1-globin;Hemoglobin beta-1 chain;Hemoglobin beta-major chain;	0.25 - 0.75
PDFRDRDDP	GLAPVAATGPFLAR	N-ter +34.06 Da	19.0	84.6	3	1444.98	-1.94	0.15	KCNA7_MOUSE		Voltage-gated potassium channel subunit Kv1.7; Carboxypeptidase N 83 kDa chain;Carboxypeptidase N large subunit;Carboxypeptidase N polypeptide 2;Carboxypeptidase N regulatory subunit;		0.00 - 0.15 0.25 - 0.75 0.25 - 0.75
NPGHLSFRAL VTVVRNLEY SGLQGLPLA	GLDEGEPAGSWDLTVEGR GLDPCSVAAILQQR GLHGDDQAGPVGVPAGPR	N-ter +34.06 Da N-ter +28.03 Da, C +57.02 Da N-ter +28.03 Da	36.0 37.7 38.6	81.1 25.7 80.7	3 3 3	1921.08 1554.86 1666.99	-0.04 -0.14 1.16	0.00 0.00 0.07	CPN2_MOUSE EIF2D_MOUSE CO1A2_MOUSE	E9PUG7_MOUSE E9Q6U9_MOUSE	Carboxypeptidase N subunit 2; Eukaryotic translation initiation factor 2D; Collagen alpha-2(I) chain; Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic;		0.25 - 0.75 0.25 - 0.75 0.75 - 0.85
LIKVDGEGPN	GLKJSEVIGER	N-ter +34.06 Da, K +34.06 Da	35.8	43.2	3	1380.96	-0.43	0.01	GPDA_MOUSE	E0CXN5_MOUSE			0.25 - 0.75
TASHCLARGF	GLLSNPADGVAWTCFR	N-ter +34.06 Da, C +57.02 Da	48.3	74.8	3	1854.07	-2.00	0.16	CAF17_MOUSE	B2FDE8_MOUSE	Putative transferase CAF17 homolog, mitochondrial;	Iron-sulfur cluster assembly factor homolog; GCS heavy chain;Gamma-ECS;Gamma-glutamylcysteine synthetase;	0.00 - 0.15
M M NSQAFSTNA ERRRLAERY KGYMRPTKSR SSNTDSSSP	GLLSQGSPLSWEETQR GLPKGPEGQGLPEVETR GLPPSYETIKEEYGVTELGEPSNSAVVR GLTLDPEADSEYLSR GLTDPKPSASQER GNSHTSSSSSSSSSSSSSSSR	N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	47.8 31.1 23.8 41.8 30.9 9.3	45.7 49.8 92.0 28.6 97.8 9.4	3 3 4 2 3 4	1815.00 1831.14 3088.91 1698.90 1566.06 2177.91	0.52 0.16 4.86 0.62 -0.56 2.87	0.04 0.00 1.08 0.05 0.04 0.35	GSH1_MOUSE CCD93_MOUSE IFM2_MOUSE SVIL_MOUSE F7CK47_MOUSE E9PXS2_MOUSE	E9Q9A4_MOUSE Q8K4L2_MOUSE F7DF66_MOUSE	Glutamate--cysteine ligase catalytic subunit; Coiled-coil domain-containing protein 93; Interferon-induced transmembrane protein 2; Supervillin; Microtubule-associated protein;		0.25 - 0.75 0.25 - 0.75 0.85 - 1.00 0.25 - 0.75 0.25 - 0.75 0.85 - 1.00
LAGLVFVSEA SMPDVLHLK DEEEPLPACN QDHPSSMGVY	GPAGAGESKCLPMVKVLDVAVR GPNVKGEYDVTVPR GPTPAPASPAAEVGSQEEALSSSAQSPGR QQESGGFSGPGENR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +34.06 Da	34.0 27.1 36.5 48.8	69.5 79.2 78.0 88.8	3 3 4 3	2238.38 1585.97 2763.55 1411.78	0.77 -0.23 -2.06 0.53	0.04 0.00 0.17 0.05	TTHY_MOUSE E9Q616_MOUSE D3Z6Q9_MOUSE EWS_MOUSE	F7BRM2_MOUSE	Transthyretin;	Prealbumin;	0.25 - 0.75 0.25 - 0.75 0.00 - 0.15 0.25 - 0.75
MYIFVHWQF	GLDQHPIDGYLSHTELAPLR	N-ter +34.06 Da	39.9	65.4	4	2393.41	-0.01	0.00	SPRC_MOUSE	Q5NCU4_MOUSE	SPARC;	Basement-membrane protein 40;Osteonectin;Secreted protein acidic and rich in cysteine;	0.25 - 0.75



Table S8, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
KHAPPPAAVN	GQPPPEPSAPAKVVR	N-ter +28.03 Da, K +28.03 Da	19.0	98.5	3	1585.06	2.20	0.27	LARP1_MOUSE		La-related protein 1;	La ribonucleoprotein domain family member 1; Syndet; Vesicle-membrane fusion protein SNAP-23;	0.85 - 1.00
VSKQPSRITN	GQPQQTGAASGGYIKR	N-ter +34.06 Da, K +34.06 Da	34.4	80.4	3	1787.14	0.61	0.10	SNP23_MOUSE	Q9D3L3_MOUSE	Synaptosomal-associated protein 23;		0.25 - 0.75
											Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex;	Branched-chain alpha-keto acid dehydrogenase complex component E2; Dihydroipoamide acetyltransferase component of branched-chain alpha-keto acid dehydrogenase complex; Dihydroipoamide branched chain transacylase; Dihydrolipoylysine-residue (2-methylpropanoyl)transferase;	0.25 - 0.75
HSLRTAAVLQ	GQVVQFKLSDIGEGIR	N-ter +34.06 Da, K +34.06 Da	45.7	44.3	3	1813.15	0.07	0.01	ODB2_MOUSE		mitochondrial;		0.25 - 0.75
NDLTYLPEWE	GRVPDSIDYR	N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	27.3	66.8	3	1204.70	-0.36	0.04	CATK_MOUSE		Cathepsin K;		0.25 - 0.75
EETALVCDN	GSGLCKAGFAGDDAPR	N-ter +28.03 Da, K +28.03 Da	25.0	11.5	3	1645.87	-6.64	0.00	ACTA_MOUSE	ACTH_MOUSE	Actin, aortic smooth muscle;	Alpha-actin-2;	0.00 - 0.15
EETALVCDN	GSGLVKAGFAGDDAPR	N-ter +28.03 Da, K +28.03 Da	43.8	89.7	3	1572.97	-0.86	0.14	ACTC_MOUSE	ACTS_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.15 - 0.25
HPTSPRRPG	GSITIVPKIIR	N-ter +28.03 Da, K +28.03 Da	37.6	89.5	3	1430.98	0.39	0.02	MA2B2_MOUSE		Epididymis-specific alpha-mannosidase;	Mannosidase alpha class 2B member 2;	0.25 - 0.75
GGRPAMEPGN	GSLDLGGDAAGR	N-ter +28.03 Da	52.9	59.9	2	1115.62	1.98	0.03	HNRPU_MOUSE		Heterogeneous nuclear ribonucleoprotein U;	Scaffold attachment factor A;	0.85 - 1.00
M	GSSQVIEIPGGGTGEGYHLR	N-ter +28.03 Da	62.4	69.5	3	2057.16	0.47	0.07	GORS2_MOUSE	A2AT18_MOUSE	Golgi reassembly-stacking protein 2;	Golgi reassembly-stacking protein of 55 kDa;	0.25 - 0.75
GQSSSANRRA	GSSSGVQVQASAGGLAASDR	N-ter +28.03 Da	68.0	61.6	3	1877.00	2.27	0.31	FILA_MOUSE	F7BVV1_MOUSE	Filaggrin;		0.85 - 1.00
												CW17; Mammalian branch point-binding protein; Transcription factor ZFM1; Zinc finger gene in MEN1 locus; Zinc finger protein 162;	
HGPPMDQYL	GSTPVGSGVYR	N-ter +34.06 Da	39.2	49.1	2	1112.66	0.72	0.06	SF01_MOUSE	Q3UI45_MOUSE	Splicing factor 1;		0.25 - 0.75
ALERGARGGP	GSVELAHLHGILR	N-ter +28.03 Da	24.5	81.8	3	1428.94	6.73	0.37	FGF20_MOUSE		Fibroblast growth factor 20;		0.85 - 1.00
VRNIKSMWEK	GSVFSAPSASGTPNKETAGLKVGVSSR	N-ter +28.03 Da, K +28.03 Da	26.3	70.1	4	2674.62	0.33	0.03	Q8VCQ8_MOUSE	E9Q0M9_MOUSE			0.25 - 0.75
												Annexin II; Annexin-2; Calpactin I heavy chain; Calpactin-1 heavy chain; Chromobindin-8; Lipocortin II; Placental anticoagulant protein IV; Protein I p36;	0.25 - 0.75
GDHSTPSSAY	GSVKPYNTFAER	N-ter +28.03 Da, K +28.03 Da	37.5	67.1	3	1538.88	-0.34	0.06	ANXA2_MOUSE	B0V2N7_MOUSE	Annexin A2;		0.25 - 0.75
ISTSVCLRAH	GSVKSSEDYAFPTYADR	N-ter +28.03 Da, K +28.03 Da	48.0	81.2	3	1960.12	-1.64	0.21	COX41_MOUSE		Cytochrome c oxidase subunit 4 isoform 1, mitochondrial;	Cytochrome c oxidase polypeptide IV; Cytochrome c oxidase subunit IV isoform 1; Protein cypher; Protein oracle; Z-band alternatively spliced PDZ-motif protein;	0.00 - 0.15
RSFRILAQMT	GTEYMQDPDEEALRR	N-ter +28.03 Da	19.9	78.8	3	1836.98	2.29	0.24	LDB3_MOUSE	E9PYJ9_MOUSE	LIM domain-binding protein 3;		0.85 - 1.00
RSFRILAQMT	GTEYMQDPDEEALR	N-ter +28.03 Da	30.3	87.7	3	1680.88	0.00	0.00	E9PYJ9_MOUSE	LDB3_MOUSE			0.25 - 0.75
ILTRLRLQKR	GTGGVDTAAVAVFDISNADR	N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	75.0	71.4	3	2020.13	2.01	0.12	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain; M-CK;	0.85 - 1.00
VEAARNLRV	GTKCCTLPEDQR	N-ter +28.03 Da	26.5	43.8	3	1531.84	-3.06	0.26	ALBU_MOUSE		Serum albumin;		0.00 - 0.15
SVCVHLRNL	GTLDNPSLDETAYER	N-ter +28.03 Da	39.9	72.9	3	1794.96	0.60	0.08	FRDA_MOUSE	E9QZP9_MOUSE	Frataxin, mitochondrial;		0.25 - 0.75
FDQTTISLQM	GTNKGASQAGMLPAGTR	N-ter +28.03 Da, K +28.03 Da	33.1	59.9	3	1671.97	1.40	0.07	CNN3_MOUSE		Calponin-3;	Calponin; acidic isoform;	0.75 - 0.85
TIDCDVITLM	GTPSGTAEPYDGTAKAR	N-ter +34.06 Da, K +34.06 Da	42.8	49.6	3	1674.97	0.55	0.05	BSDC1_MOUSE		BSD domain-containing protein 1;		0.25 - 0.75
QRRSIIIRLF	GTSPPAAEVTSPPEPALEAPAR	N-ter +34.06 Da	41.9	71.7	3	2346.40	0.12	0.01	PARF_MOUSE		Putative GTP-binding protein Parf;		0.25 - 0.75
RLRLKRGRTG	GVDTAAVAVFDISNADR	N-ter +34.06 Da	58.1	51.9	3	1811.02	0.16	0.01	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain; M-CK;	0.25 - 0.75
LDHGRTLREQ	GVEEHETLLLR	N-ter +28.03 Da	35.6	48.2	3	1322.78	0.18	0.01	TLN1_MOUSE	A2AIM2_MOUSE	Talin-1;		0.25 - 0.75
EYVSPNSEDV	GVEGKGDGPGQGR	N-ter +28.03 Da, K +28.03 Da	34.5	95.4	3	1502.93	1.10	0.38	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.75 - 0.85
												12.6 kDa FK506-binding protein; FK506-binding protein 1B; Immunophilin FKBP12.6; Rotamase;	0.25 - 0.75
M	GVEIETISPGDGR	N-ter +28.03 Da	31.3	65.7	3	1356.78	0.35	0.02	FKB1B_MOUSE		Peptidyl-prolyl cis-trans isomerase FKBP1B;		0.25 - 0.75
												Calcium-activated neutral proteinase small subunit; Calcium-dependent protease small subunit; Calcium-dependent protease small subunit 1; Calpain regulatory subunit; Low molecular mass dual specificity phosphatase 3;	0.25 - 0.75
GGGTAMRILG	GVISAISEAAQYNEPPPPR	N-ter +34.06 Da	37.6	84.6	4	2197.34	0.10	0.00	CPNS1_MOUSE	D3YW48_MOUSE	Calpain small subunit 1;		0.25 - 0.75
M	GVQPNNFWSVLPGR	N-ter +28.03 Da	33.0	57.6	3	1580.94	0.65	0.08	DUS23_MOUSE		Dual specificity protein phosphatase 23;		0.25 - 0.75
												12 kDa FK506-binding protein; FK506-binding protein 1A; Immunophilin FKBP12; Rotamase;	0.85 - 1.00
M	GVQVETISPGDGR	N-ter +28.03 Da	44.9	51.8	2	1341.76	1.53	0.05	FKB1A_MOUSE	Q1JUQ8_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP1A;		0.85 - 1.00
WQEGDKVIRP	GVSQAGEEMEQFGGQVGR	N-ter +28.03 Da	50.6	42.9	3	1835.93	0.45	0.04	SBSN_MOUSE	E9QP82_MOUSE	Suprabasin;		0.25 - 0.75
GNFAAQYSDK	GVSSGPGMGLMGR	N-ter +28.03 Da	57.6	30.7	2	1426.75	0.11	0.00	CO1A2_MOUSE	E0CXI2_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.25 - 0.75
RAMSLSDALK	GVTDNVDTVVHYVPLPR	N-ter +34.06 Da	38.7	72.1	3	2013.26	-1.79	0.25	PLIN1_MOUSE		Perilipin-1;	Lipid droplet-associated protein; Perilipin A;	0.00 - 0.15
MSN	GYEDHMAEDCR	N-ter +28.03 Da, C +57.02 Da	35.3	99.8	3	1409.67	7.24	1.54	ELAV1_MOUSE		ELAV-like protein 1;	Elav-like generic protein; Hu-antigen R; MelG;	0.85 - 1.00
QQQQTSSYG	GKYEPAAPVSIQR	N-ter +28.03 Da, K +28.03 Da	44.5	58.3	3	1470.91	-0.92	0.05	LASP1_MOUSE	A2AGH0_MOUSE	LIM and SH3 domain protein 1;	Metastatic lymph node gene 50 protein;	0.15 - 0.25
KGHRGLPLGK	GYSGLQGLPLAGLHGDDQAPVPGVAGPR	N-ter +28.03 Da	41.3	102.6	4	2780.72	-1.89	0.28	CO1A2_MOUSE	E9Q6U9_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.00 - 0.15
TQCEKIVQKY	GYTHLSTGDLR	N-ter +34.06 Da	42.9	57.1	3	1365.82	-1.15	0.13	KAD1_MOUSE		Adenylate kinase isoenzyme 1;	ATP-AMP transphosphorylase 1; Myokinase;	0.15 - 0.25
SRVTRGRSIK	GTYLPPHCSR	N-ter +34.06 Da, C +57.02 Da	24.7	92.6	3	1220.73	-2.40	0.50	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain; M-CK;	0.00 - 0.15





Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
KCCTLPEDQR	LPCVEDYLSAILNR	N-ter +28.03 Da, C +57.02 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	31.3	73.2	3	1690.00	2.41	0.33	ALBU_MOUSE		Serum albumin;		0.85 - 1.00
M	LPNTGKLAGCTVITGASR		23.7	71.4	4	2161.36	-2.00	0.16	HSDL2_MOUSE	E9PYC8_MOUSE	Hydroxysteroid dehydrogenase-like protein 2; WD repeat domain phosphoinositide-interacting protein 2;		0.00 - 0.15
GKVLMASTSY ALLCAGRAQG	LPSQVTEFNFQGR LQCCEYGVPIETSCPAVTCR	N-ter +28.03 Da N-ter +34.06 Da, C +57.02 Da	33.6 57.7	48.3 29.2	3 3	1533.84 2596.24	0.77 -1.43	0.04 0.08	WIPI2_MOUSE LY6C1_MOUSE	D3YWK1_MOUSE LY6C2_MOUSE	Lymphocyte antigen G6C1;		0.25 - 0.75 0.15 - 0.25
PRKIISLSQL	LQEDSLNVADLSSLR	N-ter +34.06 Da	27.9	61.1	3	1693.01	0.49	0.01	PSME2_MOUSE	E0CZ90_MOUSE	Proteasome activator complex subunit 2;	11S regulator complex subunit beta;Activator of multicatalytic protease subunit 2;Proteasome activator 28 subunit beta; C-terminal LIM domain protein 1;Elfin;LIM domain protein CLP-36;	0.25 - 0.75
PPKQSTSLV ARRQHLKSLV DESTGSIARR DESTGSIARR	LQEIIESDGGKDPNKPSPGFR LQIAATELEKEESR LQSIGTENTEENRR LQSIGTENTEENR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +28.03 Da	21.0 35.6 19.3 26.6	98.6 79.3 81.2 70.4	4 3 3 3	2270.41 1672.04 1673.97 1571.84	-2.32 1.35 1.58 3.19	0.23 0.09 0.17 0.14	PDL1_MOUSE TNNI2_MOUSE ALDOA_MOUSE ALDOA_MOUSE	A2A6K0_MOUSE Q9CPQ9_MOUSE Q9CPQ9_MOUSE	PDZ and LIM domain protein 1; Troponin I, fast skeletal muscle; Fructose-bisphosphate aldolase A; Fructose-bisphosphate aldolase A;		0.00 - 0.15 0.75 - 0.85 0.85 - 1.00 0.85 - 1.00
ALSVPDSRA HSGITESQEF	LRPGDCEVCISYLGR LSGGAOSSSKSPSESR	N-ter +34.06 Da, C +57.02 Da N-ter +34.06 Da, K +34.06 Da	59.6 27.0	63.3 85.0	3 3	1828.03 1769.08	1.54 -2.84	0.19 0.41	MANF_MOUSE E9Q8I5_MOUSE	Q3TMX5_MOUSE	Mesencephalic astrocyte-derived neurotrophic factor;	Arginine-rich protein;Protein ARMET;	0.85 - 1.00 0.00 - 0.15
ASCRAHLTM	LSLDFLDDVRR	N-ter +34.06 Da	24.8	50.8	3	1512.90	-1.47	0.21	SC11A_MOUSE	D3Z569_MOUSE	Signal peptidase complex catalytic subunit SEC11A;	Endopeptidase SP18;Microsomal signal peptidase 18 kDa subunit;SEC11 homolog A;SEC11-like protein 1;SPC18;Sid 2895; GCS heavy chain;Gamma-ECS;Gamma-glutamylcysteine synthetase;	0.15 - 0.25 0.25 - 0.75
MGL	LSQGSPLSWEETQR	N-ter +28.03 Da	39.3	51.2	3	1644.90	0.18	0.01	GSH1_MOUSE		Glutamate-cysteine ligase catalytic subunit;	AKAP expressed in kidney and lung;Protein kinase A-anchoring protein 2; Creatine kinase M-type; Protein QLL1;	0.25 - 0.75 0.25 - 0.75 0.25 - 0.75
DQFSRVNVS GIWHNDNKSF KGSVAGGAVY	LTQEELSDGLDELVSR LWVVNEEDHLR LVYDQELLGSPDKSEAAALR	N-ter +28.03 Da N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da	47.4 42.3 21.8	56.6 57.2 70.6	3 3 3	1831.02 1436.82 2171.36	0.67 -0.76 -0.45	0.03 0.06 0.05	AKAP2_MOUSE KCRM_MOUSE QLL1_MOUSE	A2AP18_MOUSE	A-kinase anchor protein 2; Creatine kinase M-type; Protein QLL1;		0.25 - 0.75 0.15 - 0.25 0.25 - 0.75
AGNKVTVYDF SCTFLAVSG	LVYDVLQDHR LYSSDDVIELPSNFNR	N-ter +34.06 Da N-ter +34.06 Da	28.4 52.2	63.7 60.0	3 3	1290.80 2090.16	-0.94 0.10	0.05 0.01	GSTM2_MOUSE PDIAB_MOUSE	GSTM6_MOUSE	Glutathione S-transferase Mu 2; Protein disulfide-isomerase A6;	GST 5-5;GST class-mu 2;Glutathione S-transferase pmGT2; Thioredoxin domain-containing protein 7;	0.15 - 0.25 0.25 - 0.75
TARGAAVTRS EQEDNAIKAI	MASGGVPTDEEQATGLER MEIPKTLQTAADGTR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	44.7 28.0	64.6 87.8	3 3	1932.01 1816.10	-1.18 2.09	0.05 0.20	COX5B_MOUSE E9PVX6_MOUSE	Q9D881_MOUSE	Cytochrome c oxidase subunit 5B, mitochondrial;	Cytochrome c oxidase polypeptide Vb;	0.15 - 0.25 0.85 - 1.00
GKPLSLAFLY GEHTPSALAI SLLLSVQGY	MEKNQLEEVPSALPR MENANVLAR MEQASKTVQDALSSVQESDIJAVVAR	N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	32.0 26.7 31.0	67.0 57.9 99.1	3 2 4	1808.14 1050.63 2729.72	0.01 -0.01 -2.84	0.00 0.00 0.20	PRELP_MOUSE ALDOA_MOUSE APOC3_MOUSE	Q9CPQ9_MOUSE E9QP56_MOUSE	Prolargin; Fructose-bisphosphate aldolase A; Apolipoprotein C-III;		0.25 - 0.75 0.25 - 0.75 0.00 - 0.15
ETLQPSFIG	MESAGIHETTYNSIMKCDIDIR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	23.7	59.9	4	2651.46	-0.23	0.03	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
DTPKQALYL KLEWIKAFEN	MFDTPQESPVKSPVPR MHLETLVLSLPR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da	26.0 29.3	72.3 49.1	3 3	1870.10 1505.92	0.71 0.71	0.08 0.02	TACC2_MOUSE Q9D1Q5_MOUSE	E9Q8T1_MOUSE	Transforming acidic coiled-coil-containing protein 2;		0.25 - 0.75 0.25 - 0.75
SVILQHLRMS	MHTEAAEVLLER	N-ter +28.03 Da	41.7	107.5	3	1425.88	-0.76	0.03	HIBCH_MOUSE	E0CX19_MOUSE	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial;	3-hydroxyisobutyryl-coenzyme A hydrolase;	0.15 - 0.25
WAATPKQGR	MKVFVTGPLPAEGR MLGAPEEADANEEGVR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da	33.1 49.9	83.9 63.5	3 3	1557.01 1720.92	-0.67 0.49	0.07 0.03	GRHPR_MOUSE CYTC_MOUSE	D6REG4_MOUSE A2APX3_MOUSE	Glyoxylate reductase/hydroxypruvurate reductase; Cystatin-C;	Cystatin-3; Calgizzarin;Endothelial monocyte-activating polypeptide;Protein S100-C;S100 calcium-binding protein A11;	0.25 - 0.75 0.25 - 0.75
QLSKTEFLSF	MNTELAFTKNQKDPGVLDLR	N-ter +28.03 Da, K +28.03 Da	26.9	83.2	4	2331.42	0.60	0.06	S10AB_MOUSE	F6S135_MOUSE	Protein S100-A11;		0.25 - 0.75
LPYNPMMVVM	MPPPPPVSTAVQPPGAPPVR	N-ter +28.03 Da	34.5	26.3	3	2116.21	2.36	0.10	DVL2_MOUSE		Segment polarity protein dishevelled homolog DVL-2;	DSH homolog 2; Protein cypher;Protein oracle;Z-band alternatively spliced PDZ-motif protein;	0.85 - 1.00 0.75 - 0.85 0.85 - 1.00
ILAQMTGTEY	MQDPDEALRR MQQVEASLQPETLR	N-ter +34.06 Da N-ter +28.03 Da	25.2 26.8	83.2 52.6	3 3	1392.80 1656.94	1.13 1.87	0.13 0.11	LDB3_MOUSE SPA3G_MOUSE	E9PYJ9_MOUSE SPA3C_MOUSE	LIM domain-binding protein 3; Serine protease inhibitor A3G;	Serine protease inhibitor 2A; Protein phosphatase 2B regulatory subunit 1;Protein phosphatase 3 regulatory subunit B alpha isoform 1; Alpha-1 type I collagen; Tumor protein D52-like 2; Protein cypher;Protein oracle;Z-band alternatively spliced PDZ-motif protein;	0.75 - 0.85 0.75 - 0.85 0.25 - 0.75 0.25 - 0.75 0.00 - 0.15 0.75 - 0.85 0.25 - 0.75
NSGSLSEEF PGLGGNFASQ SPNKGVLSDF	MSLPELQQNPLVQR MSYGYDEKASGVSPGPMGSPGR MTDVPVDPGVVHR	N-ter +34.06 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da	38.6 53.8 54.6	59.9 60.3 87.4	3 3 3	1686.04 2493.38 1448.87	0.41 -0.34 -0.23	0.02 0.06 0.03	CANB1_MOUSE C01A1_MOUSE Q3TUJ9_MOUSE	F8WGB7_MOUSE	Calcineurin subunit B type 1; Collagen alpha-1(I) chain; Tumor protein D54;		0.25 - 0.75 0.25 - 0.75 0.25 - 0.75
QSRFRILAQ QSRFRILAQ PTSGMIGNLS	MTGTEYMQDPDEEALRR MTGTEYMQDPDEEALR MTPELSSAHNVIVTER	N-ter +28.03 Da N-ter +28.03 Da N-ter +28.03 Da	22.4 41.0 35.7	76.9 41.5 64.1	3 3 3	2069.08 1912.90 1811.04	-6.64 1.42 -0.42	0.00 0.22 0.01	LDB3_MOUSE E9PYJ9_MOUSE D5G1A_MOUSE	E9PYJ9_MOUSE LDB3_MOUSE	LIM domain-binding protein 3; LIM domain-binding protein 3; Desmoglein-1-alpha;	DG1;DG1;Desmosomal glycoprotein I; Alpha-tubulin 1;Alpha-tubulin isotype M-alpha-1;Tubulin alpha-1 chain;	0.00 - 0.15 0.75 - 0.85 0.25 - 0.75
TLEHSDCAF DHHIVPLTA EIFKAGHPF	MVDNEAIYDRC MVIENDAGDER MWNHGLGYLTCPSNLGTLGR	N-ter +34.06 Da, C +57.02 Da N-ter +34.06 Da N-ter +34.06 Da, C +57.02 Da	32.5 32.4 37.4	36.5 59.6 70.6	3 2 3	1531.78 1281.69 2451.40	-0.52 0.72 -4.32	0.02 0.05 0.86	TBA1A_MOUSE ITH2_MOUSE KCRM_MOUSE	TBA1B_MOUSE	Tubulin alpha-1A chain; Inter-alpha-trypsin inhibitor heavy chain H2; Creatine kinase M-type;		0.25 - 0.75 0.25 - 0.75 0.00 - 0.15
TIKRLETTY	NATEPVISFYDKR	N-ter +34.06 Da, K +34.06 Da	38.2	69.7	3	1607.01	0.68	0.08	KAD1_MOUSE		Adenylate kinase isoenzyme 1;	ATP-AMP transphosphorylase 1;Myokinase;	0.25 - 0.75
TGGRTTWTART	NATLSVEPEGR	N-ter +28.03 Da	36.9	50.3	2	1199.68	-0.32	0.02	ACOT2_MOUSE		Acyl-coenzyme A thioesterase 2, mitochondrial;	Acyl coenzyme A thioester hydrolase;MTE-1;Very-long-chain acyl-CoA thioesterase;	0.25 - 0.75





Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
KTMIVHDVE DSPERELIS	SEPAMTPKSEGLTVLR SEPSPAVTPVPTTLIAPR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da	27.6 44.2	80.9 84.5	3 3	1771.10 1967.28	-0.34 -1.03	0.02 0.11	M4K4_MOUSE SNX2_MOUSE	B7ZNR9_MOUSE	Mitogen-activated protein kinase kinase kinase kinase 4; Sorting nexin-2;	HPK/GCK-like kinase HGK;MAPK/ERK kinase kinase kinase 4;Nck-interacting kinase;	0.25 - 0.75 0.15 - 0.25
PRQPTVTSVC LLLLSGDAHS WTHEVFSSRS	SESAQELAEGQR SEVPGAAAEGPGGSVGLGDR SEVLSGGDEDDYQR	N-ter +28.03 Da N-ter +34.06 Da N-ter +34.06 Da	33.3 45.8 37.1	72.9 48.8 80.6	3 3 3	1331.73 1873.03 1644.90	0.65 -0.45 -1.52	0.03 0.02 0.17	PDU5_MOUSE CO024_MOUSE E9Q616_MOUSE	E9Q8P5_MOUSE	PDZ and LIM domain protein 5; UPFD480 protein C15orf24 homolog;	Enigma homolog;Enigma-like PDZ and LIM domains protein;	0.25 - 0.75 0.25 - 0.75 0.00 - 0.15
ANEVEAVKVH GLVRGQKVLV RNLHQSGFSL	SFPTLKFFPASADR SGAPIKIPVGPETLGR SGAQIDNNIPR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	23.2 37.8 35.1	66.9 59.3 52.8	3 3 2	1638.99 1659.13 1212.67	0.04 0.37 1.12	0.00 0.01 0.05	PDIA1_MOUSE ATPB_MOUSE DPYL2_MOUSE	E9Q8G8_MOUSE	Protein disulfide-isomerase; ATP synthase subunit beta, mitochondrial; Dihydropyrimidinase-related protein 2;	Cellular thyroid hormone-binding protein;Endoplasmic reticulum resident protein 59;Prolyl 4-hydroxylase subunit beta;p55;	0.25 - 0.75 0.25 - 0.75 0.75 - 0.85
KLEDGPKFL AAASWRPVSA SHORAAADSQN NIDIRSAFKR VLDGADCI ML KVFHILDKDK QAPPVRLNHQ	SGDAIIVDMVPGKPMCVESFSDYPLGR SGEEFVPGQSAADILSGAASR SGEGNTSAEESFSQEVAR SGEGQADAGELDFSGLLKR SGETAKGDYPLEAVR SGFIEEDELKILGFSDDAR SGFSLSGAQIDNNIPR	N-ter +28.03 Da N-ter +28.03 Da N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da	49.4 61.6 52.0 50.4 32.5 32.0 33.7	79.6 65.4 71.8 74.8 86.3 68.3 53.4	4 3 3 3 3 3 3	3062.76 2163.17 1941.01 2075.24 1660.05 2312.31 1709.97	-1.79 -1.12 2.32 -2.32 -0.89 -0.45 2.47	0.31 0.24 0.29 0.12 0.15 0.08 0.19	EF1A1_MOUSE OFUT2_MOUSE Q7M739_MOUSE D3YU50_MOUSE KPYM_MOUSE PRVA_MOUSE DPYL2_MOUSE	E9PZ23_MOUSE Q6P65_MOUSE	Elongation factor 1-alpha 1; GDP-fucose protein O-fucosyltransferase 2; Elongation factor 1-alpha 1; Pyruvate kinase isozymes M1/M2; Parvalbumin alpha; Dihydropyrimidinase-related protein 2;	Unc-33-like phosphoprotein 2; Elongation factor Tu;Eukaryotic elongation factor 1 A-1; Peptide-O-fucosyltransferase 2;	0.00 - 0.15 0.15 - 0.25 0.85 - 1.00 0.00 - 0.15 0.15 - 0.25 0.25 - 0.75 0.85 - 1.00
RGAAVTRMA RKDLANTVL VSVERALADE ETTALCDNG GKTVIRLPSG AAQYSDKGV SLSKERHQCT	SGGGVPTDEEQATGLER SGGTTMYPGIADR SGLDYSLSGGGGVPLVLR SGLVKAGFAGDDAPR SGPASPTTGSVDIR SGPGMGLMGPR SGPIVTLQNGDKSTPDDWSSQLER	N-ter +34.06 Da N-ter +34.06 Da N-ter +34.06 Da N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da N-ter +34.06 Da N-ter +34.06 Da, K +34.06 Da	43.3 40.2 60.8 30.0 68.4 42.9 38.7	67.1 51.7 59.2 63.6 43.3 54.0 82.6	3 2 3 3 2 2 4	1735.96 1358.74 1867.14 1527.97 1448.83 1189.68 2881.71	-0.79 -0.60 0.49 0.39 0.12 -1.18 -0.15	0.05 0.03 0.04 0.03 0.02 0.05 0.02	COX5B_MOUSE ACTS_MOUSE A2BFA6_MOUSE ACTC_MOUSE E9Q616_MOUSE CO1A2_MOUSE SYNP2_MOUSE	Q9D881_MOUSE ACTA_MOUSE ACTA_MOUSE ACTS_MOUSE D3YVV9_MOUSE	Cytochrome c oxidase subunit 5B, mitochondrial; Actin, alpha skeletal muscle; Actin, alpha cardiac muscle 1; Synaptopodin-2;	Cytochrome c oxidase polypeptide Vb; Alpha-actin-1;	0.15 - 0.25 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75 0.15 - 0.25 0.25 - 0.75
FFTGLVKMYH PSGVPKQDGR SSANRRAGSS	SGPVVAMVWEGLNVVKTGR SQQPGVPGAGVR SGSGVQASAGGLAADASR	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da N-ter +28.03 Da	21.0 33.8 67.3	75.4 50.1 62.4	3 2 3	2066.35 1205.71 1645.90	-0.25 0.14 1.63	0.01 0.01 0.14	NDKA_MOUSE CO1A2_MOUSE FILA_MOUSE	NDK8_MOUSE E9Q6U9_MOUSE F7BVV1_MOUSE	Nucleoside diphosphate kinase A; Collagen alpha-2(I) chain; Filaggrin;	Alpha-2 type I collagen; Myopodin; Metastasis inhibition factor NM23;NDPK-A;Tumor metastatic process-associated protein;nm23-M1;	0.25 - 0.75 0.25 - 0.75 0.85 - 1.00
MYTPIQ	SGSPFPASVQDPLHIWR	N-ter +34.06 Da	23.2	82.0	3	1984.20	-1.52	0.39	CAPG_MOUSE	Q99L84_MOUSE	Macrophage-capping protein;	Actin regulatory protein CAP-G;Actin-capping protein GCAP39;Myc basic motif homolog 1;	0.00 - 0.15
ASSREGSPAR MA	SGTPVHCPSPIR SGVAVSDGVKIVFNDMKVR	N-ter +34.06 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da	41.7 21.4	53.8 115.1	3 4	1340.78 2104.41	0.26 4.16	0.01 0.25	BAG3_MOUSE COF1_MOUSE	E9Q1T2_MOUSE	BAG family molecular chaperone regulator 3; Cofilin-1;	Bcl-2-associated athanogene 3;Bcl-2-binding protein Bts; Cofilin, non-muscle isoform; Alpha-1 protease inhibitor 1;Alpha-1-antiprotease;Serine protease inhibitor 1-	0.25 - 0.75 0.85 - 1.00
DTSQKQDSPA	SHEIATNLGDFAI SLYR	N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	45.5	76.5	3	1940.17	0.25	0.03	A1AT1_MOUSE	A1AT2_MOUSE	Alpha-1-antitrypsin 1-1;	1;Serine protease inhibitor A1a;	0.25 - 0.75
RSTCHNQNSM ASTSQSSRAA LQTRFPLDY	SICEEFSQADKGCFCFR SIFGGAKPVDTAAR SIPFPTPTTLTGR	N-ter +34.06 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da	45.9 24.9 26.7	79.9 83.4 60.3	3 3 3	2132.10 1456.99 1511.93	-4.32 2.47 2.49	0.86 0.47 0.12	A2M_MOUSE IF48_MOUSE UBP2L_MOUSE	D3YW52_MOUSE Q3TDD8_MOUSE E9PZA1_MOUSE	Alpha-2-macroglobulin; Eukaryotic translation initiation factor 4B; Ubiquitin-associated protein 2-like;	Pregnancy zone protein;	0.00 - 0.15 0.85 - 1.00 0.85 - 1.00
LSEKISSVQ RTSPVPRQKR LGSSCEEIFY	SIVPALEIANHR SIVVSPILIPENQR SKDSEGSWFR	N-ter +28.03 Da N-ter +34.06 Da N-ter +34.06 Da, K +34.06 Da	31.4 41.1 23.3	57.6 95.7 92.7	3 3 3	1417.89 1598.12 1265.79	1.18 -0.14 -6.64	0.08 0.01 0.00	CH60_MOUSE CAD13_MOUSE NIPS1_MOUSE	Q5SVG6_MOUSE	60 kDa heat shock protein, mitochondrial; Cadherin-13; Protein NipSnap homolog 1;	60 kDa chaperonin;Chaperonin 60;HSP-65;Heat shock protein 60;Mitochondrial matrix protein P1; Heart cadherin;Truncated cadherin;	0.75 - 0.85 0.25 - 0.75 0.00 - 0.15
NRPLAAGAN	SKGPPDFSSDEEREPTVLGSGASVGR	N-ter +28.03 Da, K +28.03 Da	51.5	79.8	4	2813.61	-0.56	0.07	LAP2A_MOUSE	LAP2B_MOUSE	Lamina-associated polypeptide 2, isoforms alpha/zeta;	Thymopoietin isoforms alpha/zeta;	0.25 - 0.75
KIGGAQNRNY	SKLLCGLLSDR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	30.7	47.5	3	1316.81	-0.20	0.01	MIF_MOUSE		Macrophage migration inhibitory factor;	Delayed early response protein 6;Glycosylation-inhibiting factor;L-dopachrome isomerase;L-dopachrome tautomerase;Phenylpyruvate tautomerase;	0.25 - 0.75
PPPATHYSTL	SKPAPLTGTLVLR	N-ter +28.03 Da, K +28.03 Da	30.1	52.9	3	1423.92	1.73	0.19	PKN1_MOUSE	D6RH37_MOUSE	Serine/threonine-protein kinase N1;	Protein kinase C-like 1;Protein kinase C-like PKN;Protein-kinase C-related kinase 1;Serine-threonine protein kinase N;	0.85 - 1.00
TITESMDML	SKVEAANFR	N-ter +34.06 Da, K +34.06 Da	12.6	66.7	2	1088.73	-6.64	0.00	GGT7_MOUSE		Gamma-glutamyltransferase 7;	Gamma-glutamyltransferase-like 3;Gamma-glutamyltranspeptidase 7;	0.00 - 0.15
LWSLVATLLG	SKWPEPVFGR	N-ter +34.06 Da, K +34.06 Da	27.9	53.6	3	1269.82	0.03	0.00	MASP2_MOUSE		Mannan-binding lectin serine protease 2;	MBL-associated serine protease 2;Mannose-binding protein-associated serine protease 2;	0.25 - 0.75
ISRRLVSDG	SLAEVPEAKVGVILGSGDFAR	N-ter +28.03 Da, K +28.03 Da	21.2	85.8	4	2324.51	1.47	0.16	STEA3_MOUSE	E9QN92_MOUSE	Metalloreductase STEAP3;	Dudulin-2;Protein nm1054;Six-transmembrane epithelial antigen of prostate 3;Tumor suppressor-activated pathway protein 6;	0.85 - 1.00

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
STVHEILCKL NEMATAASSS	SLEGDHSTPPSAYGSVKPYTFNDAER SLEKSYELPDGGQVITIGNER	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da	30.1 45.2	66.4 78.1	4 3	2880.55 2315.45	0.07 -1.79	0.01 0.25	ANXA2_MOUSE ACTC_MOUSE	BOV2N7_MOUSE ACTA_MOUSE	Annexin A2; Actin, alpha cardiac muscle 1;	Annexin II;Annexin-2;Calpactin I heavy chain;Calpactin-1 heavy chain;Chromobindin-8;Lipocortin II;Placental anticoagulant protein IV;Protein I;p36; Alpha-cardiac actin; Carbonate dehydratase III;Carbonic anhydrase III;	0.25 - 0.75 0.00 - 0.15
VSSDQMAKLR	SLFSSAENEPVPLVGNWRPPQPVKGR	N-ter +28.03 Da, K +28.03 Da	33.8	103.9	4	3013.93	-2.00	0.24	CAH3_MOUSE		Carbonic anhydrase 3;	Carbonate dehydratase III;Carbonic anhydrase III;	0.00 - 0.15
FEHRLGEAAR	SLGNAGNEIGR	N-ter +28.03 Da	44.2	62.9	2	1114.64	-1.06	0.11	DMKN_MOUSE	E9QLW7_MOUSE	Dermokine;	Epidermis-specific secreted protein SK30/SK89;	0.15 - 0.25
SLPQNQPFV	SLGTGQVIKWDQGLGMCEGEKR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	31.7	109.6	4	2720.78	-3.32	0.33	FKBP2_MOUSE		Peptidyl-prolyl cis-trans isomerase FKBP2;	13 kDa FK506-binding protein;FK506-binding protein 2;Immunophilin FKBP13;Rotamase; Lysosomal pepstatin-insensitive protease;Tripeptidyl aminopeptidase;Tripeptidyl-peptidase I;	0.00 - 0.15
RPEPQQVTV SIRSAPPKLA	SLHLGVTPSVLR SLKGVPEADAVETLAGSLGTR	N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da	30.7 48.5	33.7 80.9	3 3	1305.82 2166.43	-0.38 -0.79	0.04 0.12	TPP1_MOUSE ICAL_MOUSE	Q921U7_MOUSE	Tripeptidyl-peptidase 1; Calpastatin;	Tripeptidyl-peptidase 1; Calpain inhibitor; Alcohol sulfotransferase;Hydroxysteroid sulfotransferase 2;	0.25 - 0.75 0.15 - 0.25
AMKANTMSNY LSPQTKRAKR	SLLPASLLDHR SLLSGETGSLPGNYLVIPIYSGR	N-ter +34.06 Da N-ter +34.06 Da	45.4 29.9	63.0 44.7	3 3	1254.83 2442.40	-1.64 -3.18	0.05 0.58	STZB1_MOUSE MYOM1_MOUSE	E9QK1_MOUSE	Sulfotransferase family cytosolic 2B member 1; Myomesin-1;	Sulfotransferase; Myomesin family member 1;Skelemin;	0.00 - 0.15 0.00 - 0.15
FQTSSFSAM RLLSGETG	SLPGAPTASSGTAAYALPNR SLPGNYLVIPIYSGR	N-ter +28.03 Da N-ter +34.06 Da	32.5 44.9	59.8 32.7	3 2	2026.17 1568.93	-0.58 -0.12	0.06 0.01	ARNT_MOUSE MYOM1_MOUSE	Q3ULM2_MOUSE	Aryl hydrocarbon receptor nuclear translocator; Myomesin-1;	Dioxin receptor, nuclear translocator;Hypoxia-inducible factor 1-beta; Myomesin family member 1;Skelemin;	0.25 - 0.75 0.25 - 0.75
LLGSPRRSY	SLPPHQVPLPSLPTMQAGTIAR	N-ter +28.03 Da, K +28.03 Da	44.6	55.2	4	2581.58	-0.58	0.01	ODP2_MOUSE		Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex;Pyruvate dehydrogenase complex component E2;	0.25 - 0.75
QTPGMRRCSS TDPKFDQTTI	SLPPIQAPSHPPPQPTQPR SLQMGTKNGASQAGMLAPGTR	N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da	35.5 39.7	44.4 101.8	4 4	2169.27 2143.37	1.20 1.78	0.04 0.13	RHG17_MOUSE CNN3_MOUSE	F8WJ58_MOUSE	Rho GTPase-activating protein 17; Calponin-3;	Neuron-associated developmentally-regulated protein;Rho-type GTPase-activating protein 17; Calponin, acidic isoform;	0.75 - 0.85 0.85 - 1.00
ASVILQHRM ASGPFNFQVG	SMHTEAAEVLIER SMPPAQQTISQGMHR	N-ter +34.06 Da N-ter +34.06 Da	54.7 62.0	60.8 85.6	3 3	1518.89 1830.07	-1.40 -4.32	0.11 0.86	HIBCH_MOUSE TLN1_MOUSE	E0CX19_MOUSE F8WGT0_MOUSE	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial; Talin-1;	3-hydroxyisobutyryl-coenzyme A hydrolase; Phosphatidylinositol-binding clathrin assembly protein;	0.15 - 0.25 0.00 - 0.15
STAASRATL TPGHACTQK EQFLPMMQAI	SNAVSSLASTGLSLTKVDER SNEEIAMATVTLR SNNKDQGGYEDFVEGLR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	32.9 36.7 77.0	78.9 41.8 48.0	3 3 3	2090.29 1532.85 1983.03	1.15 -0.20 0.70	0.09 0.02 0.10	PICA_MOUSE ALDOA_MOUSE MYL1_MOUSE	Q9CPQ9_MOUSE E9PWG4_MOUSE	Fructose-bisphosphate aldolase A; Myosin light chain 1/3, skeletal muscle isoform;	Clathrin assembly lymphoid myeloid leukemia; Aldolase 1;Muscle-type aldolase; Myosin light chain alkali 1/2;	0.75 - 0.85 0.25 - 0.75 0.25 - 0.75
KSFVNLGKD LLAACGSVTM TSGDSLTVAS KIPRHVEVEI LHPTLILAQ RSIISRLFGT	SNNLCLHFNPR SNPGESSFDLADRLDPVEKIDR SNTDFAFSLYR SNTDVEVTPQPKTVIR SNVDELGCSHLGQSYESR SPAEEVTPSPPEPAPALEAPAR	N-ter +34.06 Da, C +57.02 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, C +57.02 Da N-ter +28.03 Da	26.8 25.5 42.0 41.2 45.7 27.1	56.4 70.0 68.8 94.7 69.3 54.8	3 4 2 3 3 3	1404.79 2527.50 1347.74 1712.14 2065.06 2182.25	-0.56 0.16 4.33 0.10 0.79 1.09	0.03 0.02 1.41 0.01 0.12 0.04	LEG1_MOUSE SODE_MOUSE SPA3G_MOUSE E9Q616_MOUSE CO3A1_MOUSE PARF_MOUSE		Galectin-1; Extracellular superoxide dismutase [Cu-Zn]; Serrine protease inhibitor A3G; E9Q616_MOUSE Collagen alpha-1(III) chain; Putative GTP-binding protein Parf;	14 kDa lectin;Beta-galactoside-binding lectin L-14-I;Galactin;Lactose-binding lectin 1;Lectin galactoside-binding soluble 1;S-Lac lectin 1;	0.25 - 0.75 0.25 - 0.75 0.85 - 1.00 0.25 - 0.75 0.25 - 0.75 0.75 - 0.85
QETDTSQKDQ NSTHPMHSRC	SPASHEIATNLGDFALR SPDPGLTALLSDHR	N-ter +34.06 Da N-ter +28.03 Da	46.9 64.7	59.7 67.7	3 3	1832.07 1505.89	0.03 0.79	0.00 0.08	A1AT4_MOUSE HEMO_MOUSE		Alpha-1-antitrypsin 1-4; Hemopexin;	Alpha-1 protease inhibitor 4;Serrine protease inhibitor 1-4;Serrine protease inhibitor A1d;	0.25 - 0.75 0.25 - 0.75
MPGVGLPELG	SPGLPLPSLPPR	N-ter +34.06 Da	32.0	60.9	3	1360.91	-0.06	0.00	GORS2_MOUSE	A2AT19_MOUSE	Golgi reassembly-stacking protein 2;	Golgi reassembly-stacking protein of 55 kDa;	0.25 - 0.75
RGKTKATKSC KEEQAPPMLG	SPPPPPPEPTSEGR SQEGHLVEEVLIR	N-ter +34.06 Da N-ter +34.06 Da	50.9 24.1	73.9 45.8	3 3	1477.87 1541.93	0.42 -1.89	0.03 0.14	BCAS1_MOUSE SYNP2_MOUSE	A2AVX1_MOUSE D3YV9_MOUSE	Breast carcinoma-amplified sequence 1 homolog; Synaptopodin-2;	Novel amplified in breast cancer 1 homolog; Myopodin;	0.25 - 0.75 0.00 - 0.15
PVRNRKVVYD	SQFQESDDADEYGR	N-ter +34.06 Da	47.3	80.9	3	1794.89	1.25	0.23	NUCK5_MOUSE		Nuclear ubiquitous casein and cyclin-dependent kinases substrate;	JC7;	0.75 - 0.85
TFLPRKIISL GSYSQAPSQY ISKVRVHIQ	SQLLQEDSLNVADLSSLR SQSSSYGQSSFR SRGESQEVALPSR	N-ter +28.03 Da N-ter +34.06 Da N-ter +34.06 Da	57.9 27.5 35.9	67.2 88.5 82.5	3 3 3	2015.19 1609.90 1448.90	-3.84 -1.32 -0.30	0.55 0.10 0.02	PSME2_MOUSE EWS_MOUSE Q3UR26_MOUSE	E0CZ90_MOUSE Q5SU58_MOUSE F7DBB3_MOUSE	Proteasome activator complex subunit 2; RNA-binding protein EWS;	11S regulator complex subunit beta;Activator of multicatalytic protease subunit 2;Proteasome activator 28 subunit beta;	0.00 - 0.15 0.15 - 0.25 0.25 - 0.75
DQMAKLRSLF	SSAENEPVPLVGNWRPPQPVKGR	N-ter +28.03 Da, K +28.03 Da	33.4	95.0	4	2666.68	1.26	0.14	CAH3_MOUSE		Carbonic anhydrase 3;	Carbonate dehydratase III;Carbonic anhydrase III;	0.75 - 0.85
RSPGASRAAM VLQTRGFVSD	SSDAQWLTAER SSDSMDTGAGSIR	N-ter +34.06 Da N-ter +34.06 Da	43.8 47.2	32.8 51.7	2 2	1425.74 1316.68	-0.60 0.84	0.06 0.07	PHS2_MOUSE ATIF1_MOUSE	Q9D879_MOUSE	Pterin-4-alpha-carbinolamine dehydratase 2; ATPase inhibitor, mitochondrial;	4-alpha-hydroxy-tetrahydropterin dehydratase 2;DcoH-like protein DcoHm;Dimerization cofactor of hepatocyte nuclear factor 1 from muscle;HNF-1-alpha dimerization cofactor; Inhibitor of F(1)(alpha)-ATPase;	0.25 - 0.75 0.25 - 0.75





Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
LQKRTGGVD GSWEFFASGK	TAAVGAVFDSINADR TAESGELHLGLTTDEKFEVGVYR	N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da	44.7 36.9	42.4 69.7	3 4	1533.84 2505.48	-0.12 -0.32	0.00 0.05	KCRM_MOUSE TTHY_MOUSE		Creatine kinase M-type; Transthyretin;	Creatine kinase M chain;M-CK; Prealbumin; V-ATPase 28 kDa accessory protein;Vacuolar proton pump subunit D;	0.25 - 0.75 0.25 - 0.75
AFLSLAEAKF NEDLSEKIF DTCKAAADKD	TAGDFSTTVIQNVNKAQVKIR TASNVSVPPLAENVITTAGQR TCFSTEGPNLVTR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +28.03 Da, C +57.02 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	30.8 46.5 42.3	78.1 57.5 36.7	4 3 2	2373.52 2239.31 1508.79	-0.17 0.60 1.15	0.01 0.06 0.11	VATD_MOUSE UBP2L_MOUSE ALBU_MOUSE	E9Q0D9_MOUSE E9Q3Q3_MOUSE	V-type proton ATPase subunit D; Ubiquitin-associated protein 2-like; Serum albumin;		0.25 - 0.75 0.25 - 0.75 0.75 - 0.85
MVHL	TDAEKAASVSLWGKVSDEVGGALGR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	43.8	74.9	4	2920.76	0.24	0.03	HBB1_MOUSE		Hemoglobin subunit beta-1;	Beta-1-globin;Hemoglobin beta-1 chain;Hemoglobin beta-major chain;	0.25 - 0.75
MVHL	TDAEKASVSLWAKVNPDEVGGALGR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	46.4	104.5	4	2960.89	-5.06	0.00	HBB2_MOUSE		Hemoglobin subunit beta-2; WD repeat domain phosphoinositide-interacting protein 2;	Beta-2-globin;Hemoglobin beta-2 chain;Hemoglobin beta-minor chain;	0.00 - 0.15
TYGTAALKAY	TDDLGAVGAGCLEDEASALR	N-ter +28.03 Da, C +57.02 Da	61.3	74.7	3	2047.11	-0.97	0.08	WIPI2_MOUSE	D3YWK1_MOUSE			0.15 - 0.25
RELPSFLGER	TDEAAFQKVMNSLDSNR	N-ter +28.03 Da, K +28.03 Da	26.3	80.0	3	1981.12	1.20	0.18	S10A4_MOUSE	D3YU9_MOUSE	Protein S100-A4;	Metastasin;Metastatic cell protein;PEL98;Placental calcium-binding protein;Protein 18A2;Protein Mts1;S100 calcium-binding protein A4;	0.75 - 0.85
VLKAMKGLG AESGELHGLT	TDDESIINLLTSR TDEKFEVGVYR	N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da	34.1 21.6	55.6 96.1	3 3	1509.89 1397.85	-0.18 1.12	0.03 0.05	ANXA5_MOUSE TTHY_MOUSE		Annexin A5; Transthyretin;	Anchorin CII;Annexin V;Annexin-5;Calphobindin I;Endonexin II;Lipocortin V;Placental anticoagulant protein 4;Placental anticoagulant protein I;Thromboplastin inhibitor;Vascular anticoagulant-alpha;	0.25 - 0.75 0.75 - 0.85
INRVKEMKY GGYKPTDKHK SRRSTQGVTL	TDEKDIISDTSQDFR TDLNHNELKGGDDLPNVLSLR TDLQEAETIGR	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	26.3 38.2 25.8	62.0 75.4 68.1	3 4 3	1879.10 2627.48 1427.92	-0.79 0.51 1.05	0.11 0.08 0.12	ANXA2_MOUSE KCRM_MOUSE MYPT1_MOUSE	BOV2N7_MOUSE	Annexin A2; Creatine kinase M-type; Protein phosphatase 1 regulatory subunit 12A;		0.15 - 0.25 0.25 - 0.75 0.75 - 0.85
AHVDHGKSTL ILSVASTVMT PRHEVTEISN LRQIKNEVQ	TDSLVCAGIASAR TDTEDEKGFLEGGVGR TDVETQPKTVIR TDVSDTKHQTLQGVAFPISR	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da	29.1 33.5 21.7 41.1	64.8 94.3 89.9 48.8	3 3 3 4	1629.06 1864.13 1498.97 2354.37	1.10 -2.40 0.42 -1.47	0.06 0.63 0.08 0.16	EF2_MOUSE Q99K47_MOUSE E9Q616_MOUSE TWF1_MOUSE	E9PV24_MOUSE	Elongation factor 2;  Twinfilin-1;		0.75 - 0.85 0.00 - 0.15 0.25 - 0.75 0.15 - 0.25
WLLCALGLQA	TEALPSAPALPGGAACLSR	N-ter +34.06 Da, C +57.02 Da	42.2	63.8	3	2130.22	1.59	0.20	SPIT1_MOUSE		Kunitz-type protease inhibitor 1; cAMP-dependent protein kinase type I-alpha regulatory subunit;	Hepatocyte growth factor activator inhibitor type 1;	0.85 - 1.00
RRGASIAEYV KDWSPYLAH AGNWNWAGHY	TEEDAASYVR TEFTPTETDYACR TEGAELVDSLVGVYR	N-ter +34.06 Da N-ter +28.03 Da, C +57.02 Da N-ter +28.03 Da	29.8 26.9 51.8	56.7 49.2 67.3	2 3 3	1173.64 1718.83 1628.97	0.00 2.61 0.20	0.00 0.21 0.04	KAP0_MOUSE B2MG_MOUSE TBB2A_MOUSE	A2A169_MOUSE Q91X8_MOUSE TBB2B_MOUSE	Beta-2-microglobulin; Tubulin beta-2A chain;		0.25 - 0.75 0.85 - 1.00 0.25 - 0.75
VTEEAASAAQ	TEGPSTPSSFPAQEHR	N-ter +34.06 Da	29.9	101.9	3	1890.09	-2.06	0.43	AKA12_MOUSE		A-kinase anchor protein 12;	Germ cell lineage protein gercelin;Src-suppressed C kinase substrate;	0.00 - 0.15
KLEERHTLI	TEMVVALNPDFKPPADYKPPATR	N-ter +34.06 Da, K +34.06 Da	39.0	73.1	4	2559.61	0.40	0.06	SFO1_MOUSE	Q3U45_MOUSE	Splicing factor 1;	CW17;Mammalian branch point-binding protein;Transcription factor ZFM1;Zinc finger gene in MEN1 locus;Zinc finger protein 162;	0.25 - 0.75
KKRLETYNA ETGAGISETV ESVRSPPSSR TLNAANVPAG	TEPVISFYDKR TETTIVTETTIVTETPENQSLIMKLR TEVLVTPAGVASKR TEVVCAPPTAYIDFAR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, C +57.02 Da	26.7 41.2 52.7 45.1	55.7 95.4 55.7 56.9	3 4 3 3	1409.83 3007.81 1495.02 1837.01	0.68 0.28 1.73 1.04	0.06 0.03 0.18 0.09	KAD1_MOUSE PP1RB_MOUSE LAD1_MOUSE TPIS_MOUSE		Adenylate kinase isoenzyme 1; Protein phosphatase 1 regulatory subunit 11; Ladinin-1; Triosephosphate isomerase;	ATP-AMP transphosphorylase 1;Myokinase; T-complex testis expressed protein 5; Linear IgA disease antigen homolog; Triose-phosphate isomerase;	0.25 - 0.75 0.25 - 0.75 0.85 - 1.00 0.75 - 0.85
SFRILAQMTG SFRILAQMTG	TEYMQDPEDEALRR TEYMQDPEDEALR	N-ter +28.03 Da N-ter +34.06 Da	27.2 37.5	75.6 85.6	3 3	1779.94 1629.88	-0.01 -0.52	0.00 0.07	LDB3_MOUSE E9PYJ9_MOUSE	E9PYJ9_MOUSE LDB3_MOUSE	LIM domain-binding protein 3;	Protein cypher;Protein oracle;Z-band alternatively spliced PDZ-motif protein;	0.25 - 0.75 0.25 - 0.75
IAPSNQVIML	TFGKDFVEPTYCR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	41.2	64.5	3	1789.95	-0.62	0.06	PCOC1_MOUSE	D3YE3_MOUSE	Procollagen C-endopeptidase enhancer 1;	P14;Procollagen COOH-terminal proteinase enhancer 1;Type 1 procollagen C-proteinase enhancer protein;Type I procollagen COOH-terminal proteinase enhancer; Metastasis inhibition factor NM23;NDPK-A;Tumor metastatic process-associated protein;nm23-M1;	0.25 - 0.75
MANSER VTTLDIVRAN	TFIAIKPDGVQR TFVAELKGLDPR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	28.0 26.2	74.7 87.7	3 3	1399.92 1484.03	0.52 -0.23	0.05 0.01	NDKA_MOUSE MDHM_MOUSE	NDKB_MOUSE	Nucleoside diphosphate kinase A; Malate dehydrogenase, mitochondrial;		0.25 - 0.75 0.25 - 0.75
FKEAFLFDR LTRLRLQKRG	TGECKITLSQVGDVLR TGGVDVTAAGVAFDINADR	N-ter +34.06 Da N-ter +34.06 Da	41.7 58.9	66.8 56.8	3 3	1831.11 1969.11	0.55 0.62	0.03 0.04	MYL1_MOUSE KCRM_MOUSE	E9PWG4_MOUSE	Myosin light chain 1/3, skeletal muscle isoform; Creatine kinase M-type;	Myosin light chain alkali 1/2; Creatine kinase M chain;M-CK;	0.25 - 0.75 0.25 - 0.75
KVCYAKNGFP	TGIGFGLTQVQVEKK	N-ter +28.03 Da, K +28.03 Da	25.6	65.9	3	1775.10	-0.22	0.02	CSR3_MOUSE		Cysteine and glycine-rich protein 3;	Cysteine-rich protein 3;LIM domain protein, cardiac;Muscle LIM protein;	0.25 - 0.75
FRAAVPSGAS PAGKNGDRGE HTVEKGGKHK	TGIYEALER TGPAGPAGPIGPAR TGPNLHGLFGR	N-ter +28.03 Da N-ter +28.03 Da N-ter +34.06 Da	42.4 40.0 30.8	32.1 48.8 57.2	2 2 3	1191.69 1373.81 1201.75	0.04 1.35 0.25	0.00 0.10 0.02	ENOA_MOUSE CO1A1_MOUSE CYC_MOUSE	ENOB_MOUSE F8WGB7_MOUSE	Alpha-enolase; Collagen alpha-1(I) chain; Cytochrome c, somatic;	1;Non-neural enolase; Alpha-1 type I collagen;	0.25 - 0.75 0.75 - 0.85 0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
LHASNRLQK	TGTAEMSSILEER	N-ter +28.03 Da	45.2	27.9	2	1450.74	1.53	0.09	ATPA_MOUSE	D6R16_MOUSE	ATP synthase subunit alpha, mitochondrial;		0.85 - 1.00
VHKAVLDVAE	TGTEAAAATGVIGIR	N-ter +34.06 Da	48.1	37.5	3	1477.89	0.89	0.05	SPA3K_MOUSE		Serine protease inhibitor A3K;	Contrapsin;SPI-2;	0.75 - 0.85
IKTKGKEAFP	THFDPSCLFPACR	N-ter +28.03 Da, C +57.02 Da	36.8	79.5	3	1634.86	-0.22	0.01	CAH3_MOUSE		Carbonic anhydrase 3;	Carbonate dehydratase III;Carbonic anhydrase III;	0.25 - 0.75
GGDVAFVKHT	TIFEVLPEKADR	N-ter +28.03 Da, K +28.03 Da	37.9	68.7	3	1472.93	0.66	0.05	TRFE_MOUSE	D3YR8_MOUSE	Serotransferrin;	Beta-1 metal-binding globulin;Siderophilin;	0.25 - 0.75
M	TIGSMENVEFTSEKGR	N-ter +34.06 Da, K +34.06 Da	51.1	61.4	3	2008.18	-1.52	0.13	SMYD1_MOUSE		SET and MYND domain-containing protein 1;	CD8b-opposite;Zinc finger protein BOP;	0.00 - 0.15
EQLVDEGLVK	TIGVSNFNLQIER	N-ter +34.06 Da	22.9	62.3	3	1621.01	-1.22	0.14	ALDR_MOUSE		Aldose reductase;	Aldehyde reductase;	0.15 - 0.25
LSQSPQGRVM	TIPYQMPASSVICAGGQDR	N-ter +28.03 Da, C +57.02 Da	51.7	61.8	3	2272.24	1.34	0.11	PCBP1_MOUSE		Poly(rC)-binding protein 1;	Alpha-CP1;Heterogeneous nuclear ribonucleoprotein E1;	0.75 - 0.85
LDAYSIQGH	TISPLDLAKLNQVAR	N-ter +28.03 Da, K +28.03 Da	24.5	57.6	3	1694.11	0.14	0.01	PCBP1_MOUSE		Poly(rC)-binding protein 1;	Alpha-CP1;Heterogeneous nuclear ribonucleoprotein E1;	0.25 - 0.75
DALNIETAVK	TKGVDEVTIVNLTNR	N-ter +34.06 Da, K +34.06 Da	48.7	82.6	3	1839.26	-0.20	0.01	ANXA2_MOUSE	B0V2N7_MOUSE	Annexin A2;	Annexin II;Annexin-2;Calpactin I heavy chain;Calpactin-1 heavy chain;Chromobindin-8;Lipocortin II;Placental anticoagulant protein IV;Protein I;p36;	0.25 - 0.75
KPRESEKVKI	TKVDFDFAGEEVR	N-ter +28.03 Da, K +28.03 Da	38.5	27.8	3	1452.80	0.77	0.02	CFDP1_MOUSE		Craniofacial development protein 1;	27 kDa craniofacial protein;Buccantaur;Protein Cp27;	0.25 - 0.75
NLDPLNLLGR	TLEIPGSSDPNIVPDGFSSLR	N-ter +28.03 Da	29.2	68.4	3	2442.40	-0.17	0.04	CO4B_MOUSE		Complement C4-B;		0.25 - 0.75
ELLSQFLLH	TLEQXNIAVENEVR	N-ter +34.06 Da, K +34.06 Da	29.1	101.4	3	1710.17	-0.69	0.09	ASHWN_MOUSE		Ashwin;		0.25 - 0.75
SAANCKSLH	TFLGDKLCAIPNLR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	22.8	38.8	3	1673.00	0.54	0.04	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
SLPSTAVTSE	TLPGLSPPVEKYR	N-ter +28.03 Da, K +28.03 Da	27.4	80.3	3	1599.03	2.33	0.13	DLG1_MOUSE	E9Q9H_MOUSE	Disks large homolog 1;	Embryo-dlg/synapse-associated protein 97;Synapse-associated protein 97;	0.85 - 1.00
NPWEKARPEF	TLPVHFYGR	N-ter +34.06 Da	29.0	45.3	3	1122.69	-1.69	0.16	PYGM_MOUSE	E9PUM3_MOUSE	Glycogen phosphorylase, muscle form;	Myophosphorylase;	0.00 - 0.15
WDGLDPGKLY	TLVLTPDAPSR	N-ter +28.03 Da	49.9	38.7	2	1311.75	0.99	0.05	PEBP1_MOUSE	D3ZLV4_MOUSE	Phosphatidylethanolamine-binding protein 1;	HCNPPP;	0.75 - 0.85
CNAHYPKGSF	TMVADTPENLR	N-ter +34.06 Da	37.1	47.4	2	1279.73	0.14	0.02	LASP1_MOUSE	A2A6G_MOUSE	LIM and SH3 domain protein 1;	Metastatic lymph node gene 50 protein;	0.25 - 0.75
VDKGVVPLAG	TNGETTTGLDGLSER	N-ter +28.03 Da	40.4	66.1	3	1705.92	0.03	0.01	ALDOA_MOUSE	Q9CPQ_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.25 - 0.75
DQSPASHEIA	TNLGDFALSYR	N-ter +28.03 Da	52.4	44.8	2	1396.80	0.68	0.11	A1AT2_MOUSE	A1AT1_MOUSE	Alpha-1-antitrypsin 1-2;	Alpha-1-protease inhibitor 2;Alpha-1-antiprotease;Serine protease inhibitor 1-2;Serine protease inhibitor A1b;	0.25 - 0.75
EDPNQVPLN	TNPTVELEKR	N-ter +34.06 Da, K +34.06 Da	32.7	26.8	3	1253.80	-0.40	0.02	ADDG_MOUSE		Gamma-adducin;	Adducin-like protein 70;	0.25 - 0.75
MALLISLPGE	TPAMAQILLLSACLHAGNSAR	N-ter +34.06 Da, C +57.02 Da	24.9	66.1	4	2428.48	-5.64	0.00	PILR2_MOUSE	F8WHI2_MOUSE	Paired immunoglobulin-like type 2 receptor beta-2;	Activating receptor PILR-beta-2;	0.00 - 0.15
SRLTYDIAH	TPGVAADLSHIETR	N-ter +28.03 Da	39.8	45.6	3	1493.85	0.49	0.02	MDHM_MOUSE		Malate dehydrogenase, mitochondrial;		0.25 - 0.75
WRCLKIGEH	TPSALAIEMANVLAR	N-ter +28.03 Da	39.1	57.2	3	1698.01	0.43	0.08	ALDOA_MOUSE	A6Z44_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.25 - 0.75
GLPGSMGPPG	TPSVDHGFLVTR	N-ter +28.03 Da	26.9	73.8	3	1355.82	2.04	0.04	CO4A1_MOUSE		Collagen alpha-1(IV) chain;		0.85 - 1.00
MVKIVTVK	TQAYPDQKPGTSGLR	N-ter +34.06 Da, K +34.06 Da	26.6	86.3	3	1686.08	-1.89	0.21	PGM1_MOUSE		Phosphoglucomutase-1;	Glucose phosphomutase 1;	0.00 - 0.15
GFQNALVRY	TQKAPQVSTPLVEAAR	N-ter +34.06 Da, K +34.06 Da	39.0	53.2	3	1864.21	0.29	0.02	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
PNMVTTPGHAC	TQKFSNEEIAMATVTR	N-ter +34.06 Da, K +34.06 Da	39.5	56.0	3	2077.27	0.33	0.05	ALDOA_MOUSE	Q9CPQ_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.25 - 0.75
LNVDPGARAR	TQLSQLSTR	N-ter +28.03 Da	34.6	58.1	2	1060.65	0.11	0.00	KLC3_MOUSE		Kinesin light chain 3;		0.25 - 0.75
DEESKPASSN	TQVEGDEEAALLER	N-ter +28.03 Da	64.0	26.8	2	1586.82	1.71	0.14	Q8VCQ8_MOUSE	E9Q0M9_MOUSE			0.85 - 1.00
TVCQCTCYQR	TSCISTPAQVTCNR	N-ter +28.03 Da, C +57.02 Da	36.8	67.5	3	1621.87	6.07	0.37	E9Q2E9_MOUSE				0.85 - 1.00
M	TSDDQAKVVAEPOAQR	N-ter +28.03 Da, K +28.03 Da	29.3	92.0	3	1798.09	-0.25	0.04	LAR4B_MOUSE		La-related protein 4B;	La ribonucleoprotein domain family member 4B;La ribonucleoprotein domain family member 5;La-related protein 5;	0.25 - 0.75
AATTTATTTT	TSGGHPLEFLR	N-ter +28.03 Da	17.8	68.3	3	1240.74	0.01	0.00	RD23B_MOUSE	Q3TJ52_MOUSE	UV excision repair protein RAD23 homolog B;	XP-C repair-complementing complex 58 kDa protein;	0.25 - 0.75
LIIGDRQTGK	TSIADTIINQKR	N-ter +34.06 Da, K +34.06 Da	26.4	51.5	3	1540.04	0.65	0.05	ATPA_MOUSE	D3Z6F5_MOUSE	ATP synthase subunit alpha, mitochondrial;		0.25 - 0.75
VGLTSLRAVS	TSSMGLPKQVKIVEVGR	N-ter +28.03 Da, K +28.03 Da	24.1	87.7	4	2110.40	-0.15	0.02	HMGCL_MOUSE		Hydroxymethylglutaryl-CoA lyase, mitochondrial;	3-hydroxy-3-methylgluturate-CoA lyase;	0.25 - 0.75
LEAWYRHGRT	TSSYSALSEPSR	N-ter +28.03 Da	43.6	54.9	2	1311.70	-0.25	0.03	MCCR_MOUSE	A2A845_MOUSE	Trans-2-enoyl-CoA reductase, mitochondrial;		0.25 - 0.75
RTVHTRVCL	TTFNVDQGFDFQDR	N-ter +28.03 Da	37.6	37.5	3	1666.82	0.99	0.03	THIOM_MOUSE	Q3TUS3_MOUSE	Thioredoxin, mitochondrial;	Thioredoxin-2;	0.75 - 0.85
FKLPKARKTG	TTIAGVVYKDGIVLGADTR	N-ter +34.06 Da, K +34.06 Da	32.4	70.5	3	2016.33	0.64	0.03	PSB7_MOUSE		Proteasome subunit beta type-7;	Macropain chain Z;Multicatalytic endopeptidase complex chain Z;Proteasome subunit Z;	0.25 - 0.75
GGDVAFVKH	TTIFEVLPEKADR	N-ter +28.03 Da, K +28.03 Da	45.2	67.3	3	1573.98	1.07	0.17	TRFE_MOUSE	D3YR8_MOUSE	Serotransferrin;	Beta-1 metal-binding globulin;Siderophilin;	0.75 - 0.85
AQAVTAYIK	TTLESTPESASR	N-ter +28.03 Da	38.9	46.9	2	1376.74	-0.12	0.01	PPR3A_MOUSE		Protein phosphatase 1 regulatory subunit 3A;	Protein phosphatase 1 glycogen-associated regulatory subunit;Protein phosphatase type-1 glycogen targeting subunit;	0.25 - 0.75
VPLAGNGET	TTQGLDGLSER	N-ter +34.06 Da	27.1	55.4	2	1209.71	0.16	0.01	ALDOA_MOUSE	Q9CPQ_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.25 - 0.75
AAATTTATTT	TTSGGHPLEFLR	N-ter +28.03 Da	29.5	74.1	3	1341.80	0.06	0.00	RD23B_MOUSE	Q3TJ52_MOUSE	UV excision repair protein RAD23 homolog B;		0.25 - 0.75
VVPLAGNNGE	TTTQGLDGLSER	N-ter +34.06 Da	41.0	46.2	2	1310.75	0.20	0.01	ALDOA_MOUSE	Q9CPQ_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.25 - 0.75
QRPLRLQKPR	TVATPLNQVANPNSAIFGGAR	N-ter +34.06 Da	52.0	49.9	3	2131.27	0.74	0.05	IF4H_MOUSE	Q80U88_MOUSE	Eukaryotic translation initiation factor 4H;	1 protein homolog;	0.25 - 0.75
EKAKREVCSW	TVEGDVNTDPWAGYR	N-ter +28.03 Da	39.1	49.9	3	1706.88	0.29	0.04	AMPM1_MOUSE		Methionine aminopeptidase 1;	Peptidase M 1;	0.25 - 0.75
LRGENLVSM	TVEGPPPKDGTGIAR	N-ter +28.03 Da, K +28.03 Da	26.9	113.6	3	1492.99	2.75	0.62	RSMB_MOUSE	RSMN_MOUSE	Small nuclear ribonucleoprotein-associated protein B;	Sm protein B;	0.85 - 1.00
GCVAGDEESY	TVFKDLDFPIQDR	N-ter +28.03 Da, K +28.03 Da	48.3	36.7	3	1762.03	-0.17	0.04	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
QNADCPKNSG	TVGAVALDCR	N-ter +34.06 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	36.8	54.3	2	1094.66	-2.06	0.17	ASGL1_MOUSE		L-asparaginase;	Asparaginase-like protein 1;L-asparagine amidohydroxylase;	0.00 - 0.15
VDNPGHPFIM M	TVGCVAGDEESYTVFKDLFDPIIQDR TVHNLVLFDR	N-ter +34.06 Da	57.3 33.3	91.5 57.3	4 3	3029.75 1310.80	-3.32 -0.84	0.33 0.08	KCRM_MOUSE TPPC1_MOUSE	B1ASW5_MOUSE	Creatine kinase M-type; Trafficking protein particle complex subunit 1;	Creatine kinase M chain;M-CK;	0.00 - 0.15 0.15 - 0.25
KDVVVYIFG	TVIQEVKTSNVAR	N-ter +34.06 Da, K +34.06 Da	30.3	93.9	3	1512.07	0.56	0.06	ECHB_MOUSE	D3YXU1_MOUSE	Trifunctional enzyme subunit beta, mitochondrial;	TP-beta;	0.25 - 0.75
GNNITVKTES TSLPFLLEIL VDIRKDLVAN VVQVPSAYQK ASLPPDPPL	TVKTVFVSCNLGKFDETTADGR TVLPPEVHSR TVLSGGTTMYPGIADR TVPIEAVTSKSNIR TVPQTHNAR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da N-ter +34.06 Da N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da	47.0 30.7 40.1 24.2 11.3	75.9 69.6 74.7 51.0 22.4	4 3 3 3 2	2659.52 1199.76 1671.94 1671.04 1056.61	1.65 -0.64 0.07 0.90 -1.12	0.23 0.03 0.01 0.03 0.02	FABP5_MOUSE TNPO3_MOUSE ACTB_MOUSE SRCB_MOUSE Q9QU1_MOUSE	E9Q964_MOUSE	Fatty acid-binding protein, epidermal; Transportin-3; Actin, cytoplasmic 1; Src substrate cortactin;	Fatty acid-binding protein;Fatty acid-binding protein 5;Keratinocyte lipid-binding protein;Psoriasis-associated fatty acid-binding protein homolog;	0.85 - 1.00 0.25 - 0.75 0.25 - 0.75 0.75 - 0.85 0.15 - 0.25
RQRPEPQVQG YSFPVKIKK SPGMKDLGA	TVSLHLGVTSPVLR TWKVFELGINDFSR TWWVLGHSER	N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da	33.7 32.2 30.0	70.4 90.6 58.0	3 3 3	1512.03 1864.16 1216.75	-0.45 0.82 -0.69	0.02 0.07 0.01	TPP1_MOUSE MDHC_MOUSE TPIS_MOUSE		Tripeptidyl-peptidase 1; Malate dehydrogenase, cytoplasmic; Triosephosphate isomerase;	Tripeptidyl aminopeptidase;Tripeptidyl-peptidase 1; Cytosolic malate dehydrogenase; Triose-phosphate isomerase;	0.25 - 0.75 0.25 - 0.75 0.25 - 0.75
NEETIKRLE TPKGVGRHST VSGRQQLVEL SEAVVSSVNT PLPVIHQKV TSQLVACTKV	TYYNATEPVISFYDKR VAAASPSHEAKGLVISPEGLSPA VAEQADLEQAFSPSPDPCVDR VANKTVEEAENIVTTGVVR VANS PANADYQER VAPTISPVCQEQLVEAGR	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da N-ter +28.03 Da, C +57.02 Da	34.4 21.0 42.6 34.1 35.9 42.1	76.4 55.9 74.7 99.5 64.4 57.1	3 4 4 4 3 3	2034.23 2555.55 2376.23 2183.43 1467.81 2068.18	-1.22 2.67 -0.25 -0.58 -0.20 -0.54	0.14 0.13 0.05 0.05 0.02 0.04	KAD1_MOUSE ACD10_MOUSE APUS_MOUSE SYU9_MOUSE E9PYJ9_MOUSE TLN1_MOUSE	D3Z7X0_MOUSE	Adenylate kinase isoenzyme 1; Acyl-CoA dehydrogenase family member 10; Apoptosis inhibitor 5; Gamma-synuclein;	ATP-AMP transphosphorylase 1;Myokinase; AAC-11; Persyn;	0.15 - 0.25 0.85 - 1.00 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75
MADEIAKAQ VGPEPTDCF	VAQPGGDTIFGKIIR VAVMHGTEGTVPGNALVVDPEKPF	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da	26.4 43.4	51.6 51.9	3 4	1639.09 2804.60	-0.38 1.40	0.02 0.07	HINT1_MOUSE EHD2_MOUSE	B0R1E3_MOUSE	Histidine triad nucleotide-binding protein 1; EH domain-containing protein 2;	Adenosine 5'-monophosphoramidase;Protein kinase C inhibitor 1;Protein kinase C-interacting protein 1;	0.25 - 0.75 0.75 - 0.85
SPDSLFTAKF GGRGAGDSGC	VAYDEEEDYGPAGPNSYSGAGTAVGAYDAPR VDAYALCDALGRPAVGGGGEWR	N-ter +28.03 Da N-ter +28.03 Da, C +57.02 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	49.4 17.3 18.0	85.7 112.5 49.8	4 4 3	3392.75 2416.47 1507.91	-2.84 1.74 0.33	0.41 0.21 0.02	AFAD_MOUSE RAIN_MOUSE Q8BM18_MOUSE	F7C3I9_MOUSE	Afadin; Ras-interacting protein 1;	Protein AF-6;	0.00 - 0.15 0.85 - 1.00 0.25 - 0.75
FRPKVKREKV LTIQLIHNH AGKHVPRAVF	VDCSEYLALSKR VDEYDPTIEDSYR VDLEPTVIDEVR	N-ter +28.03 Da N-ter +28.03 Da N-ter +34.06 Da	18.0 32.0 48.3	49.8 70.9 46.1	3 3 2	1507.91 1628.84 1417.85	0.33 0.60 1.55	0.02 0.09 0.15	Q8BM18_MOUSE RASH_MOUSE TBA1A_MOUSE	Q148R4_MOUSE	GTase HRas; Tubulin alpha-1A chain;	H-Ras-1;Transforming protein p21;c-H-ras;p21ras; Alpha-tubulin 1;Alpha-tubulin isotype M-alpha-1;Tubulin alpha-1 chain; Protein cypher;Protein oracle;Z-band alternatively spliced PDZ-motif protein;	0.25 - 0.75 0.25 - 0.75 0.85 - 1.00
LASLPVKDLA LRLQKRGTTG EKLGGQGVQK	VDSASPVYQAVIKTQSKPEDEADEWAR VDTAAVGAVFDISNADR VDVPAADLSDQVPDQSETR	N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da N-ter +28.03 Da	24.6 40.0 50.7	81.7 68.3 63.5	4 3 3	3120.90 1754.03 2157.14	-1.94 0.31 -0.30	0.22 0.02 0.06	LDB3_MOUSE KCRM_MOUSE CO3_MOUSE	E9PYJ9_MOUSE	LIM domain-binding protein 3; Creatine kinase M-type; Complement C3;	Creatine kinase M chain;M-CK; HSE-MSF;	0.00 - 0.15 0.25 - 0.75 0.25 - 0.75
LNKQKGYFF	VEGELYCETHAR	N-ter +28.03 Da, C +57.02 Da	42.0	87.9	3	1490.81	0.45	0.08	PDL3_MOUSE		PDZ and LIM domain protein 3;	Actinin-associated LIM protein;Alpha-actinin-2-associated LIM protein;	0.25 - 0.75
LIKEKILPY	VELDLHSYDLGIENR	N-ter +28.03 Da	39.6	84.9	3	1800.06	0.30	0.02	IDHC_MOUSE	F8W1Y0_MOUSE	Isocitrate dehydrogenase [NADP] cytoplasmic;	Cytosolic NADP-isocitrate dehydrogenase;DP;NADP(+)-specific ICDH;Oxalosuccinate decarboxylase;	0.25 - 0.75
AAAAAAVAV EEVANPLLT EVEVLKATEM CVAAGDEEY AVQGGAAAPM AVQGGAAAPV	VESMVTATEVAPPPVEVPIR VEVEYPENAILDLTR VEVGPEDEVGAEAR VFKDLFDPIIQDR VGAVQVPLVGMPPMPQAPR VGAVQVPLVGMPPMPQAPR	N-ter +28.03 Da N-ter +28.03 Da N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da N-ter +34.06 Da	42.1 38.9 57.9 32.0 31.8 49.3	80.8 69.6 45.4 79.1 60.2 59.3	4 3 2 3 3 3	2342.45 1788.06 1527.78 1673.12 1872.12 1862.12	1.95 0.70 0.86 -0.49 2.93 1.36	0.14 0.06 0.12 0.03 0.20 0.10	CHD4_MOUSE ITIH3_MOUSE PTRF_MOUSE KCRM_MOUSE F8VQ88_MOUSE SNRPA_MOUSE	E9QA55_MOUSE E9PVS1_MOUSE	Chromodomain-helicase-DNA-binding protein 4; Inter-alpha-trypsin inhibitor heavy chain H3; Polymerase I and transcript release factor; Creatine kinase M-type;	Chromodomain-helicase-DNA-binding protein 4; Inter-alpha-trypsin inhibitor heavy chain H3; Cav-p60;Cavin-1; Creatine kinase M chain;M-CK;	0.85 - 1.00 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75 0.85 - 1.00 0.75 - 0.85
YAKRAFVHWY ASGETLHSPK M	VGEGMEEGEFSER VGQPGAAGPVSPMCPGR VGVKPVGSDPDFQPELSGAGSR	N-ter +34.06 Da N-ter +34.06 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da	47.0 53.8 35.2	41.2 71.0 76.2	2 3 3	1559.76 1670.96 2254.33	0.42 -0.45 -1.60	0.06 0.03 0.29	TBA1A_MOUSE FETUA_MOUSE TXNL1_MOUSE	TBA1B_MOUSE	Tubulin alpha-1A chain; Alpha-2-HS-glycoprotein; Thioredoxin-like protein 1;	Alpha-tubulin 1;Alpha-tubulin isotype M-alpha-1;Tubulin alpha-1 chain; Countertrypsin;Fetuin-A; 32 kDa thioredoxin-related protein; Acetyl-CoA acyltransferase;Beta-ketothiolase;Mitochondrial 3-oxoacyl-CoA thiolase;	0.25 - 0.75 0.25 - 0.75 0.00 - 0.15
AYLARHVGLR TKFENAFLSH DVDLHLKGNP M E	VGVPTETGALTNR VISQHSLSGNIR VKGEYDVTVP VKLTAEIEQAAQYTNVAVR VKLVESGGGLVQPGGSLR	N-ter +28.03 Da N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da	34.3 31.0 38.7 43.9 36.3	29.4 47.8 58.8 95.8 62.2	3 3 3 4 3	1454.85 1491.92 1317.81 2173.42 1937.22	0.74 0.43 -0.45 0.49 0.50	0.05 0.02 0.04 0.08 0.06	THIM_MOUSE ATPA_MOUSE E9Q616_MOUSE RU2A_MOUSE HVM17_MOUSE	D3Z6F5_MOUSE F7BRM2_MOUSE	3-ketoacyl-CoA thiolase, mitochondrial; ATP synthase subunit alpha, mitochondrial;		0.25 - 0.75 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75
FFVKNMISNQ N FSPYHEGEV	VKNLGGGGSEKKEGGTSPDAAAKGMTR VLAASEPEIKGIR VLDDGGEVDLGLNYER	N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da	19.8 20.3 46.8	52.1 62.5 61.0	4 3 3	3177.95 1476.03 1906.01	-5.64 0.88 0.39	0.00 0.16 0.02	CPLX4_MOUSE KAD2_MOUSE PYR1_MOUSE	F7BP55_MOUSE	Complexin-4; Adenylate kinase 2, mitochondrial; CTP synthase 1;	Complexin IV; ATP-AMP transphosphorylase 2; CTP synthetase 1;UTP-ammonia ligase 1;	0.00 - 0.15 0.75 - 0.85 0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
LYASGRITGI	VLDSDGDVYTHNVPIYEGALPHAIMR	N-ter +28.03 Da	52.8	99.8	4	2851.72	-2.84	0.20	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin; 26S proteasome regulatory subunit RPN10;26S proteasome regulatory subunit	0.00 - 0.15
M	VLESTMVQVDNSEMYR	N-ter +34.06 Da, C +57.02 Da	48.3	52.1	3	1966.01	1.80	0.22	P5MD4_MOUSE		26S proteasome non-ATPase regulatory subunit 4;	SSA;Multiubiquitin chain-binding protein;	0.85 - 1.00
WAAEANLVL	VLPGSEGESEPLTPALGEAAR	N-ter +28.03 Da	44.4	67.8	3	2107.22	4.03	0.38	IRGQ_MOUSE		Immunity-related GTPase family Q protein;		0.85 - 1.00
EPPKQSTFL	VLQEILESDGKGDPNKPSGFR	N-ter +28.03 Da, K +28.03 Da	21.7	80.8	4	2369.45	0.20	0.02	PDL1_MOUSE		PDZ and LIM domain protein 1;	C-terminal LIM domain protein 1;Elfin;LIM domain protein CLP-36;	0.25 - 0.75
HRMTTLFCIN	VLSEVCGDITTKHMLPTVLR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	42.6	85.4	4	2452.53	0.72	0.07	ZAAA_MOUSE		Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform;	PP2A subunit A isoform PR65-alpha;PP2A subunit A isoform R1-alpha;	0.25 - 0.75
M	VLSNEPAASAAEEVEDDALVR	N-ter +34.06 Da	66.9	68.2	3	2347.32	-1.89	0.21	TBCD_MOUSE		Tubulin-specific chaperone D;	Beta-tubulin cofactor D;Tubulin-folding cofactor D;	0.00 - 0.15
PFMWNEHLGY	VLTCPSNLGTGLR	N-ter +34.06 Da, C +57.02 Da	29.8	37.3	3	1420.84	0.40	0.04	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.25 - 0.75
LSKHNNHMAK	VLTPDLYNKLR	N-ter +34.06 Da, K +34.06 Da	30.3	77.0	3	1398.99	0.33	0.03	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.25 - 0.75
VTECVKQICL	VMLETLSQSPQGR	N-ter +28.03 Da	28.1	52.8	3	1472.84	0.86	0.06	PCBP1_MOUSE		Poly(rC)-binding protein 1;	Alpha-CP1;Heterogeneous nuclear ribonucleoprotein E1;	0.25 - 0.75
KKLRPDGSEV	VNAIQVPGPPRQLVEELQSR	N-ter +28.03 Da	24.8	69.1	4	2576.60	0.60	0.04	MIB2_MOUSE		E3 ubiquitin-protein ligase MIB2;	Dystrophin-like protein;Mind bomb homolog 2;Skatrophin;	0.25 - 0.75
DQVIQFIAL	VNDPQPEHLR	N-ter +28.03 Da	20.9	91.9	3	1328.81	1.47	0.14	UB2L3_MOUSE		Ubiquitin-conjugating enzyme E2 L3;	UbcM4;Ubiquitin carrier protein L3;Ubiquitin-protein ligase L3;	0.85 - 1.00
M	VNPTVFFDITADDEPLGR	N-ter +28.03 Da	54.1	44.9	3	2033.10	0.99	0.17	PP1A_MOUSE	E9Q1E3_MOUSE	Peptidyl-prolyl cis-trans isomerase A;	Cyclophilin A;Cyclosporin A-binding protein;Rotamase A;SP18;	0.75 - 0.85
RASSSTINLM	VNTEPLFTKTDICKLSR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	25.7	85.7	4	2236.53	-1.03	0.13	E9PWQ3_MOUSE	F6R0L1_MOUSE			0.15 - 0.25
NGKLTGMAFR	VPTPNVSVVDLTCR	N-ter +28.03 Da, C +57.02 Da	43.4	32.0	3	1583.88	1.45	0.10	G3PT_MOUSE	G3P_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific;	Spermatogenic cell-specific glyceraldehyde 3-phosphate dehydrogenase 2;Spermatogenic glyceraldehyde-3-phosphate dehydrogenase;	0.85 - 1.00
M	VQAWYMDDESTADPR	N-ter +34.06 Da	31.7	58.5	3	1701.89	0.37	0.04	MTND_MOUSE		1,2-dihydroxy-3-keto-5-methylthiopentene oxoxygenase;	metalloproteinase cytoplasmic tail-binding protein 1;	0.25 - 0.75
LSGTAGVQSQ	VQLQQSGAELVK	N-ter +28.03 Da, K +28.03 Da	44.8	27.9	3	1483.87	1.37	0.06	HVM00_MOUSE		Ig heavy chain V region;	Anti-arsenate antibody;	0.75 - 0.85
ERTISKIKGL	VRAPQVYILPPAEQLSR	N-ter +34.06 Da	40.6	68.6	3	2067.35	-0.15	0.01	IGG2B_MOUSE		Ig gamma-2B chain C region;		0.25 - 0.75
FYADHPFIFL	VRDNQSGSLIFIGR	N-ter +34.06 Da	53.6	58.3	3	1594.99	0.14	0.01	SERPH_MOUSE		Serpin H1;	47 kDa heat shock protein;Collagen-binding protein;Serine protease inhibitor J6;	0.25 - 0.75
RSIIRNVKGP	VREGDVLTLLESESR	N-ter +28.03 Da	47.4	92.8	3	1643.04	-0.32	0.04	RS28_MOUSE		40S ribosomal protein S28;		0.25 - 0.75
TSVVRPFAKL	VRPPVQVYIEGR	N-ter +28.03 Da	45.6	43.0	3	1496.91	-0.62	0.04	ATPD_MOUSE	D3Z4J0_MOUSE	ATP synthase subunit O, mitochondrial;	Oligomycin sensitivity conferral protein;	0.25 - 0.75
VGENKASAK	VSDAISTQPVVDHEFDVAVVGGAGGLR	N-ter +34.06 Da	39.5	83.6	4	2962.77	-4.32	0.86	DHSA_MOUSE		Succinate dehydrogenase [ubiquinone] flavoprotein subunit, mitochondrial;	Flavoprotein subunit of complex II;	0.00 - 0.15
SEGNELLVQE	VSDLSVTADGFSASYR	N-ter +34.06 Da	40.1	65.6	3	1707.96	0.12	0.01	PCOC1_MOUSE	D3YUE2_MOUSE	Procollagen C-endopeptidase enhancer 1;	P14;Procollagen COOH-terminal proteinase enhancer 1;Type 1 procollagen C-proteinase enhancer protein;Type 1 procollagen COOH-terminal proteinase enhancer;	0.25 - 0.75
DNGMVLGEQE	VSDNELQELSTQSGR	N-ter +34.06 Da	43.8	61.6	3	1695.95	0.86	0.08	CLUS_MOUSE	E9Q9B8_MOUSE	Clusterin;	Apolipoprotein J;Clustrin;Sulfated glycoprotein 2;	0.25 - 0.75
GMKVLIQTRGF	VSDSDSDMTGAGSIR	N-ter +28.03 Da	65.3	50.7	2	1611.79	1.17	0.18	ATIF1_MOUSE	Q9D879_MOUSE	ATPase inhibitor, mitochondrial;	Inhibitor of F(1)F(o)-ATPase;	0.75 - 0.85
GRRGQFGARG	VSEGSAAAMAGESMAQR	N-ter +28.03 Da	53.2	63.0	3	1679.87	0.07	0.01	ORN_MOUSE		Oligoribonuclease, mitochondrial;	RNA exonuclease 2 homolog;Small fragment nuclease;	0.25 - 0.75
IESTECKRTR	VSGEHMDLTTCPAAGGQKQLR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	41.4	83.0	4	2553.48	0.93	0.11	Q9D1B1_MOUSE				0.75 - 0.85
VWAAVPGKTF	VSITPAEVGVLVGKDR	N-ter +34.06 Da, K +34.06 Da	30.1	51.2	3	1707.14	0.37	0.03	PROF1_MOUSE	Q5X49_MOUSE	Profilin-1;	Profilin I;	0.25 - 0.75
ALSVRNLSPY	VSNELLEAFSQFGPIER	N-ter +28.03 Da	48.0	73.7	3	2092.20	0.29	0.04	SFPQ_MOUSE		Splicing factor, proline- and glutamine-rich;	DNA-binding p52/p100 complex, 100 kDa subunit;Polypyrimidine tract-binding protein-associated-splicing factor;	0.25 - 0.75
GQAAAPVLGLA	VSSELQIQQSFVPDECPR	N-ter +34.06 Da, C +57.02 Da	42.0	32.2	3	2152.14	-0.58	0.02	FKBP9_MOUSE		Peptidyl-prolyl cis-trans isomerase FKBP9;	63 kDa FK506-binding protein;FK506-binding protein 9;FKBP6SR5;Rotamase;	0.25 - 0.75
RDDGLADLFL	VSSGPTNASAFTR	N-ter +28.03 Da	36.6	51.1	2	1450.78	-0.15	0.02	MAP4_MOUSE	E9QPW8_MOUSE	Microtubule-associated protein 4;		0.25 - 0.75
MKAATPVV	VTAAAPAMEPGPSVSPGSPR	N-ter +28.03 Da	25.0	66.8	3	1906.09	0.24	0.01	F6U6G6_MOUSE			Porphobilinogen synthase;	0.25 - 0.75
SASNLYPIF	VTDVPDDVQPIASLPGVAR	N-ter +28.03 Da	44.9	74.4	3	1976.20	-0.14	0.01	HEM2_MOUSE		Delta-aminolevulinic acid dehydratase;		0.25 - 0.75
M	VTEQEIEAGKTLVDPKQLQAR	N-ter +28.03 Da, K +28.03 Da	19.7	87.2	4	2646.73	-1.40	0.18	DOHH_MOUSE	D3Z7J7_MOUSE	Deoxyhypusine hydroxylase;	Deoxyhypusine dioxygenase;Deoxyhypusine monoxygenase;	0.15 - 0.25
ARQSRRTQGG	VTLDLQEAETIGR	N-ter +34.06 Da, K +34.06 Da	19.8	56.3	3	1741.12	-0.69	0.07	MYPT1_MOUSE		Protein phosphatase 1 regulatory subunit 12A;	Myosin phosphatase-targeting subunit 1;	0.25 - 0.75
SPLPVIHQK	VVANSPANADYQER	N-ter +34.06 Da	49.6	79.2	3	1566.91	-0.38	0.04	E9PVJ9_MOUSE				0.25 - 0.75
STSQLVACTK	VVAPTSSPVCQEQLEVEAGR	N-ter +34.06 Da, C +57.02 Da	47.6	53.5	3	2173.28	0.31	0.04	TLN1_MOUSE	F8WGT0_MOUSE	Talin-1;		0.25 - 0.75
IINVKQFAKF	VVDLSQVAPTDIEEGMR	N-ter +28.03 Da	54.9	85.4	3	2001.14	1.88	0.34	PRS7_MOUSE	Q8BVQ9_MOUSE	26S protease regulatory subunit 7;	RPT1;Proteasome 26S subunit ATPase 2;Protein M5S1;	0.85 - 1.00
AKRQSRMEKY	VVDSDTVQAHTVR	N-ter +34.06 Da	46.5	91.3	3	1459.92	0.15	0.02	SYNP2_MOUSE	D3YV9_MOUSE	Synaptodin-2;	Myopodin;	0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log <sub>2</sub> ) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
SRMAKPEEVL	VVENDQGEVVR	N-ter +28.03 Da	20.3	40.9	2	1270.70	0.99	0.08	XPO1_MOUSE		Exportin-1;	Chromosome region maintenance 1 protein homolog;	0.75 - 0.85
MFWIPASSSD	VVMTQTPLSLVPSLGDQASISCR	N-ter +34.06 Da, C +57.02 Da	58.9	49.7	3	2607.48	-1.56	0.32	KV2A7_MOUSE		Ig kappa chain V-II region 26-10;		0.00 - 0.15
IWHNDNKSFL	VWVNEEDHLR	N-ter +34.06 Da	20.7	71.2	3	1329.78	-1.18	0.03	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.15 - 0.25
KIKGLVRAPQ	VYLPPPAEQLSR	N-ter +34.06 Da	36.4	50.7	3	1515.96	-0.69	0.05	IGG2B_MOUSE		Ig gamma-2B chain C region;		0.25 - 0.75
SPDDDLGSSN	WEAADLGNEER	N-ter +28.03 Da	32.5	57.1	2	1316.68	4.94	0.75	SMAP_MOUSE	D6RI64_MOUSE	Small acidic protein;	Sid 2057;	0.85 - 1.00
DAEKAAVSCL	WGKVNSEVGEALGR	N-ter +34.06 Da, K +34.06 Da	22.5	58.3	3	1741.04	-3.84	0.00	HBB1_MOUSE		Hemoglobin subunit beta-1;	Beta-1-globin;Hemoglobin beta-1 chain;Hemoglobin beta-major chain;	0.00 - 0.15
LAHFDPRVTM	WVFEEDIGGR	N-ter +34.06 Da	32.3	27.8	2	1240.66	2.66	0.24	GPDA_MOUSE	E0CXN5_MOUSE	Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic;		0.85 - 1.00
LNDNFVKLIS	WYDNEYGYSNR	N-ter +28.03 Da	26.3	77.5	3	1493.74	0.32	0.04	G3P_MOUSE	G3PT_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase; Electron transfer flavoprotein subunit alpha, mitochondrial;	Peptidyl-cysteine S-nitrosylase GAPDH;	0.25 - 0.75
LKSGENFKLL	YDLADQLHAAVGASR	N-ter +28.03 Da	41.8	81.2	3	1613.95	0.47	0.06	ETFA_MOUSE				0.25 - 0.75
LREDPAYLHY	YDPAGGEDPLGAVHLR	N-ter +28.03 Da	61.6	68.2	3	1693.96	0.60	0.06	PLEK_MOUSE	Q8CAG6_MOUSE	Plectstrin;		0.25 - 0.75
VNIGGAGSYI	YEQPTEAPQVTGPIEVPVVR	N-ter +34.06 Da, K +34.06 Da	47.9	90.6	4	2404.58	4.92	1.00	CRIP2_MOUSE		Cysteine-rich protein 2;	Heart LIM protein;	0.85 - 1.00
AASSSLEKS	YELPDGQVITIGNER	N-ter +34.06 Da	36.6	60.2	3	1737.02	-0.40	0.03	ACT5_MOUSE	ACTA_MOUSE	Actin, alpha skeletal muscle;	Alpha-actin-1;	0.25 - 0.75
TWSPSEWQMA	YEPQGGSGYDYSYAGGR	N-ter +28.03 Da	39.3	69.0	3	1853.91	-0.06	0.01	HNRPK_MOUSE	E9Q8D6_MOUSE	Heterogeneous nuclear ribonucleoprotein K;	CRP55;Calregulin;Endoplasmic reticulum resident protein 60;HACBP;	0.25 - 0.75
LGAAADPAI	YFKEQFLDGDWNTNR	N-ter +34.06 Da, K +34.06 Da	34.5	66.4	3	1957.13	1.28	0.16	CALR_MOUSE		Calreticulin; Swi5-dependent recombination DNA repair protein 1 homolog;		0.75 - 0.85
KLTLELIDF	YGIDNLLHYNR	N-ter +28.03 Da	29.1	63.8	3	1519.84	-0.81	0.11	SFR1_MOUSE			Meiosis protein 5 homolog;	0.15 - 0.25
LGGNFASQMS	YGYDEKSAGVSPGPMGSPGR	N-ter +34.06 Da, K +34.06 Da	42.5	45.6	3	2275.26	-5.64	0.00	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.00 - 0.15
GTQCEKIVQK	YGYTHLSTGDLR	N-ter +34.06 Da	25.7	49.6	3	1528.89	-0.30	0.02	KAD1_MOUSE		Adenylate kinase isoenzyme 1;	ATP-AMP transphosphorylase 1;Myokinase;	0.25 - 0.75
ENQKFNFSVL	YKEDVSPGTAIKGTPEMLR	N-ter +28.03 Da, K +28.03 Da	20.2	87.2	4	2175.35	0.81	0.04	A2AQ82_MOUSE	A2AQA9_MOUSE			0.25 - 0.75
QQQMTSSYVG	YKEPAAPVSIQR	N-ter +28.03 Da, K +28.03 Da	30.3	84.3	3	1413.92	1.47	0.14	LASP1_MOUSE	A2AGH0_MOUSE	LIM and SH3 domain protein 1; WD repeat domain phosphoinositide-interacting protein 2;	Metastatic lymph node gene 50 protein;	0.85 - 1.00
FGKVLMASTS	YLP5QVTEMFNQGR	N-ter +28.03 Da	31.6	53.7	3	1696.92	1.51	0.19	WIPI2_MOUSE	D3YWK1_MOUSE			0.85 - 1.00
LGKPLSFL	YMEKNQLEEVPSALPR	N-ter +28.03 Da, K +28.03 Da	40.9	79.6	3	1959.17	-0.43	0.03	PRELP_MOUSE		Prolargin; WD repeat domain phosphoinositide-interacting protein 2;	Proline-arginine-rich end leucine-rich repeat protein;	0.25 - 0.75
VGASDGYLYM	YNLDPQEGGECALMR	N-ter +34.06 Da, C +57.02 Da	37.0	76.6	3	1785.96	1.48	0.20	WIPI2_MOUSE	D3YWK1_MOUSE			0.85 - 1.00
PLGSTIPMAY	YVPGIYPPGSAVLVEGGYDAGAR	N-ter +28.03 Da	38.9	67.4	3	2432.40	1.12	0.13	DAZ2_MOUSE		DAZ-associated protein 2;	Deleted in azoospermia-associated protein 2;Proline-rich protein expressed in brain; NFAT pre-existing subunit;T-cell transcription factor NFAT1;	0.75 - 0.85
SKSLSPGLLG	YQQPSLLAAPLGLADHR	N-ter +28.03 Da	32.6	76.5	3	1948.20	1.21	0.06	NFAC2_MOUSE	B5B2Q6_MOUSE	Nuclear factor of activated T-cells, cytoplasmic 2;		0.75 - 0.85
PGLTGNFAAQ	YSDKGVSSGGPMGLMGR	N-ter +28.03 Da, K +28.03 Da	60.4	77.4	3	1948.11	-2.00	0.08	CO1A2_MOUSE	E0CXI2_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.00 - 0.15
AAMKANTMSN	YSLLPASLLDHR	N-ter +28.03 Da	57.0	90.9	3	1411.91	2.03	0.13	ST2B1_MOUSE	E9QKC1_MOUSE	Sulfotransferase family cytosolic 2B member 1;	Sulfotransferase 2;	0.85 - 1.00
CTFFLAVSGL	YSSDDVIELTSPNFNR	N-ter +34.06 Da	38.8	59.3	3	1977.07	0.40	0.04	PDI6_MOUSE	Q3TML0_MOUSE	Protein disulfide-isomerase A6;	Thioredoxin domain-containing protein 7; Actinin-associated LIM protein;Alpha-actinin-2-associated LIM protein;	0.25 - 0.75
SASYNPIGL	YSTSNIQDALHGQLR	N-ter +34.06 Da	31.0	58.7	3	1736.01	0.16	0.01	PDLI3_MOUSE		PDZ and LIM domain protein 3;	Sterile alpha motif domain-containing protein 4B;	0.25 - 0.75
QQIIITPIKA	YSVLQATPTAKDEGR	N-ter +28.03 Da, K +28.03 Da	37.6	97.2	3	1691.05	-1.15	0.10	SMAG2_MOUSE		Protein Smaug homolog 2;		0.15 - 0.25
GAGNNWAKGH	YTEGAEVLDSVLDVVR	N-ter +28.03 Da	53.2	68.5	3	1792.05	0.00	0.00	TBB2A_MOUSE	TBB2B_MOUSE	Tubulin beta-2A chain;		0.25 - 0.75
RSESIYEML	YTPPEPNGMASEVTEKER	N-ter +28.03 Da, K +28.03 Da	26.9	91.4	3	2122.18	-1.94	0.37	E9Q3A1_MOUSE	E9Q6H8_MOUSE			0.00 - 0.15
QKIGQPTLL	YVDAGAETMTQR	N-ter +34.06 Da	38.4	85.8	3	1374.78	0.79	0.08	KAD1_MOUSE		Adenylate kinase isoenzyme 1;	ATP-AMP transphosphorylase 1;Myokinase;	0.25 - 0.75
MYAKRAFVHW	YVGEGMEEGFSEAR	N-ter +28.03 Da	17.8	29.7	2	1716.78	2.97	0.40	TBA1A_MOUSE	TBA1B_MOUSE	Tubulin alpha-1A chain;	Alpha-tubulin 1;Alpha-tubulin isotype M-alpha-1;Tubulin alpha-1 chain;	0.85 - 1.00
KAPEGETEF	YVSPEDLEAQLQSDER	N-ter +34.06 Da	52.8	59.2	3	1912.04	1.22	0.12	DNJC5_MOUSE		Onaj homolog subfamily C member 5;	Cysteine string protein;	0.75 - 0.85
SLWKFETSKY	YVTIIDAPGHR	N-ter +34.06 Da	36.7	59.6	3	1274.80	1.14	0.03	EF1A1_MOUSE	D3Z3I8_MOUSE	Elongation factor 1-alpha 1;	Elongation factor Tu;Eukaryotic elongation factor 1 A-1;	0.75 - 0.85
NRPFAAERL	YYSMKAGTDDSTLVR	N-ter +28.03 Da, K +28.03 Da	17.9	110.9	3	1819.08	-2.47	0.28	ANXA7_MOUSE	F8WGC2_MOUSE	Annexin A7;	Annexin VII;Annexin-7;Synexin;	0.00 - 0.15