

Table S10: Dimethylated (naturally unmodified) N-termini identified in the TAILS experiment comparing wild-type and *Cts1^Δ* skin (replicate 1). This is a comprehensive, non redundant listing. Up to two potential protein IDs per peptide are stated.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
CGTCGQPADK	AAGGAGAQQVSSISSGASSVTVTR	N-ter +28.03 Da	95.9	44.6	3	2249.23	0.18	0.05	LMNA_MOUSE		Prelamin-A/C;	Hematopoietic cell-specific LYN substrate	0.25 - 0.75
YGVEKDRDK	AALGYDYKGETEKHEQSR	N-ter +28.03 Da, K +28.03 Da	18.4	63.3	4	2165.21	-0.89	0.28	HCLS1_MOUSE		Hematopoietic lineage cell-specific protein;	1;LckBP1;	0.15 - 0.25
NAVGPVPTAN	AALPADPPASVVVGPVVPR	N-ter +28.03 Da	55.9	41.2	3	1938.21	-0.22	0.03	FETUA_MOUSE		Alpha-2-HS-glycoprotein;	Countertrypsin;Fetuin-A;	0.25 - 0.75
NTLHLDVYMA	AANLFAQTYLTGSQDR	N-ter +28.03 Da	46.2	49.9	3	1840.00	-0.07	0.01	UBA1_MOUSE		Ubiquitin-like modifier-activating enzyme 1;	Ubiquitin-activating enzyme E1;Ubiquitin-activating enzyme E1 X;Ubiquitin-like modifier-activating enzyme 1 X;	0.25 - 0.75
CLGELICTLN	AANVPAGTEVVCAPPTAYIDFAR	N-ter +28.03 Da, C +57.02 Da	48.4	39.0	3	2417.30	0.93	0.17	TPIS_MOUSE		Triosephosphate isomerase;	Triose-phosphate isomerase;	0.25 - 0.75
LRAMRGVING	AAPELPVPTGGPMAGAR	N-ter +28.03 Da	37.5	47.7	3	1618.93	-0.29	0.02	VATB2_MOUSE		V-type proton ATPase subunit B, brain isoform;	Endomembrane proton pump 58 kDa subunit;Vacuolar proton pump subunit B 2;	0.25 - 0.75
EKERALYAD	AAPGDKLLHYDPR	N-ter +34.06 Da, K +34.06 Da	25.9	57.8	4	1804.13	-1.32	0.20	SRCA_MOUSE		Sarcolumenin;		0.15 - 0.25
LERKPAAGLS	AAPVPPAAPALLDFSDVPPAPR	N-ter +28.03 Da	29.7	59.4	4	2370.40	-0.22	0.05	RTN4_MOUSE	Q8BHFS_MOUSE	Reticulon-4;	Neurite outgrowth inhibitor;	0.25 - 0.75
YALSSPLQLL	AAQASSSTPVVTR	N-ter +28.03 Da	29.3	46.7	3	1414.84	-0.11	0.01	FOXK1_MOUSE	E9Q4K6_MOUSE	Forkhead box protein K1;	Myocyte nuclear factor;	0.25 - 0.75
NSVQSGNLAL	AASAAVAVDAGMAMAGQSPVLR	N-ter +28.03 Da	61.8	43.9	3	1972.07	0.20	0.04	PTB1_MOUSE	Q92Z17_MOUSE	Polypyrimidine tract-binding protein 1;	Heterogeneous nuclear ribonucleoprotein I;	0.25 - 0.75
ASASTSQSSR	AASIFGGAKPVDTAAR	N-ter +34.06 Da, K +34.06 Da	39.3	39.9	3	1599.01	1.37	0.38	IF4B_MOUSE	Q3TDD8_MOUSE	Eukaryotic translation initiation factor 4B;		0.75 - 0.85
QKRGTGGVDT	AATGSVDFISNDR	N-ter +28.03 Da	35.9	48.1	3	1492.82	0.68	0.05	KCRU_MOUSE		Creatine kinase U-type, mitochondrial;	Acidic-type mitochondrial creatine kinase;Ubiquitous mitochondrial creatine kinase;	0.25 - 0.75
DLYTAKGLFR	AAVPSGASTGIYEALER	N-ter +34.06 Da	51.9	47.3	3	1838.09	-0.49	0.08	ENOA_MOUSE	ENOB_MOUSE	Alpha-enolase;		0.25 - 0.75
LTARDEARLR	AAVQQLQAEGLSPR	N-ter +28.03 Da	35.5	42.9	3	1494.88	0.31	0.02	Q8K354_MOUSE			2-phospho-D-glycerate hydro-lyase;Enolase 1;Non-neural enolase;	0.25 - 0.75
LWLLPSLALA	AAVTEPADLEYTEVPR	N-ter +28.03 Da	59.4	49.3	3	1787.98	2.69	0.82	Q8BVL6_MOUSE				0.85 - 1.00
LSGEDKSNK	AAWGKIGHGAEYGAELER	N-ter +34.06 Da, K +34.06 Da	44.8	56.7	4	2110.24	-2.74	0.18	HBA_MOUSE	Q91V88_MOUSE	Hemoglobin subunit alpha;	Alpha-globin;Hemoglobin alpha chain;	0.00 - 0.15
SVTREDSQY	AAYSNAVGAAYSSAR	N-ter +34.06 Da	37.7	46.0	3	1604.91	-4.64	1.16	OBSCN_MOUSE	E9QQ96_MOUSE	Obscurin;	Obscurin-RhoGEF;Obscurin-myosin light chain kinase;	0.00 - 0.15
GPQQLTRVR	ACGLNFADLMGR	N-ter +28.03 Da, C +57.02 Da	49.0	43.6	2	1351.70	2.06	0.61	VAT1_MOUSE		Synaptic vesicle membrane protein VAT-1 homolog;		0.85 - 1.00
IQNLHSFDFP	ADASKGDOLLPAGETEDYHIR	N-ter +28.03 Da, K +28.03 Da	73.9	64.1	4	2312.31	0.67	0.19	E1F1_MOUSE		Eukaryotic translation initiation factor 1;	Protein translation factor SUI1 homolog;	0.25 - 0.75
MSFSAQDI	ADFKEAFLFDR	N-ter +34.06 Da, K +34.06 Da	34.9	52.9	3	1538.96	-3.84	2.19	E9PWG4_MOUSE				0.00 - 0.15
LASSASAEFF	ADIALAPMEAAKVR	N-ter +28.03 Da, K +28.03 Da	36.7	47.2	3	1510.93	0.39	0.06	MPCP_MOUSE		Phosphate carrier protein, mitochondrial;	Phosphate transport protein;Solute carrier family 25 member 3;	0.25 - 0.75
DGETEERIR	ADIVENQVMDTR	N-ter +28.03 Da	32.2	53.8	3	1417.76	-1.18	0.16	GSTM1_MOUSE	A2AE89_MOUSE	Glutathione S-transferase Mu 1;	GST 1-1;GST class-mu 1;Glutathione S-transferase G78.7;pmGT10;	0.15 - 0.25
AGDEESEYVF	ADLDFPVIKLR	N-ter +28.03 Da, K +28.03 Da	30.0	51.6	3	1341.87	-2.56	0.60	KCRS_MOUSE		Creatine kinase S-type, mitochondrial;	Basic-type mitochondrial creatine kinase;Sarcomeric mitochondrial creatine kinase;	0.00 - 0.15
IWTTRHPVQG	ADLVQDLISICTR	N-ter +34.06 Da, C +57.02 Da	38.6	48.2	3	1510.86	-0.81	0.14	LYVE1_MOUSE		Lymphatic vessel endothelial hyaluronin acid receptor 1;	Cell surface retention sequence-binding protein 1;	0.15 - 0.25
EKEKEPVQDI	ADVNLPLPECFYAVSR	N-ter +28.03 Da, C +57.02 Da	35.0	56.1	3	1878.04	0.98	0.23	STAP1_MOUSE	E9PYX8_MOUSE	Signal-transducing adaptor protein 1;	Extracellular link domain-containing protein 1;	0.75 - 0.85
VREKEAQPLE	AEAPGVDLGLPEGR	N-ter +28.03 Da	39.6	47.2	3	1520.89	0.15	0.01	NIBAN_MOUSE		Protein Niban;	Stem cell adaptor protein 1;	0.25 - 0.75
RSTGVVNIPA	AECLDEYEDDEAGQKER	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	55.6	48.8	3	2112.00	0.30	0.10	PAWR_MOUSE		PRKC apoptosis WT1 regulator protein;	Prostate apoptosis response 4 protein;	0.25 - 0.75
SLQLVSWTLA	AEPPVDVLEAWGVHR	N-ter +28.03 Da	61.7	49.8	3	1604.91	0.77	0.12	Q9IUJ2_MOUSE				0.25 - 0.75
QLWYKARYTE	AERARGRPLGAVDKYRLR	N-ter +34.06 Da, K +34.06 Da	11.2	28.7	4	2151.38	-5.64	2.82	SIX4_MOUSE		Homeobox protein SIX4;	Sine oculis homeobox homolog 4;Skeletal muscle-specific ARE-binding protein AREC3;	0.00 - 0.15
QVQTVQISTI	AESEDSQESVDSVTSQKR	N-ter +34.06 Da, K +34.06 Da	56.2	46.3	3	2164.14	-1.60	0.53	CREB1_MOUSE	Q62347_MOUSE	Cyclic AMP-responsive element-binding protein 1;		0.00 - 0.15
HHAFQGRDM	AETFDQGAHAFQGGGR	N-ter +28.03 Da	41.0	67.3	4	1812.95	-0.45	0.12	S8SN_MOUSE	E9QP82_MOUSE	Suprabasin;		0.25 - 0.75
GAVISESTPI	AETIKASSNESLVANR	N-ter +28.03 Da, K +28.03 Da	37.3	47.4	3	1745.01	-0.84	0.16	LAP2B_MOUSE	Q3TNH0_MOUSE	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma;	Thymopoietin isoforms beta/delta/epsilon/gamma;	0.15 - 0.25
ARSKPSPQLS	AETPVAALPEFPR	N-ter +28.03 Da	37.0	43.4	3	1424.83	-0.36	0.06	E9Q056_MOUSE				0.25 - 0.75
GVKVLAFSL	AEVQVAVGPGQR	N-ter +28.03 Da	32.9	40.3	3	1292.74	2.08	0.26	CAND2_MOUSE		Cullin-associated NEDD8-dissociated protein 2;	Cullin-associated and neddylation-dissociated protein 2;TBP-interacting protein of 120 kDa B;p120 CAND2;	0.85 - 1.00
GLDNVHKQRV	AEVLNDPESMEKR	N-ter +28.03 Da, K +28.03 Da	37.5	51.1	3	1572.86	-0.92	0.09	KLC1_MOUSE	Q5UE59_MOUSE	Kinesin light chain 1;		0.15 - 0.25
ISLEVSRSGR	AEVSTHLSQSPR	N-ter +34.06 Da	29.1	45.6	3	1427.86	0.68	0.05	SYNEM_MOUSE	F6VN34_MOUSE	Synemin;	Desmuslin;	0.25 - 0.75
ATEEDIHDKR	AEYGEIKNIHLNDR	N-ter +34.06 Da, K +34.06 Da	24.3	59.0	4	1852.16	-1.89	0.14	RBM8A_MOUSE		RNA-binding protein 8A;	RNA-binding motif protein 8A;Ribonucleoprotein RBM8A;	0.00 - 0.15
PKHLRSKTLV	AFQKVMPPQAR	N-ter +28.03 Da, K +28.03 Da	34.1	38.6	3	1521.91	0.33	0.02	Q3U422_MOUSE				0.25 - 0.75
SSVLTPTPPQ	AFTVIDQNR	N-ter +34.06 Da	29.2	32.9	2	1096.64	-0.30	0.02	MLRS_MOUSE	F6ULR7_MOUSE	Myosin regulatory light chain 2, skeletal muscle isoform;	Fast skeletal myosin light chain 2;MLC2F;	0.25 - 0.75
DFRHMTMHVGR	AGDAFGDTSFLTSKAR	N-ter +28.03 Da, K +28.03 Da	44.5	52.8	3	1698.95	0.49	0.04	BORG4_MOUSE	A2A6Q2_MOUSE	Cdc42 effector protein 4;	Binder of rho GTPases 4;	0.25 - 0.75
RTFGTTGERR	AGEEAADSPELPR	N-ter +34.06 Da	35.2	55.3	3	1374.76	-0.43	0.04	ADKL_MOUSE		Adrenodoxin-like protein, mitochondrial;	Ferredoxin-1-like protein;	0.25 - 0.75
DKVIRPGVSK	AGEEMEQQFGQVGR	N-ter +28.03 Da	32.9	58.2	3	1464.75	-0.20	0.01	S8SN_MOUSE	E9QP82_MOUSE	Suprabasin;		0.25 - 0.75
VCDNGLSLCK	AGFAGDDAPR	N-ter +34.06 Da	35.7	38.7	2	1009.54	-0.12	0.01	ACTB_MOUSE	ACTB_MOUSE	Actin, aortic smooth muscle;	Alpha-actin-2;	0.25 - 0.75
M	AGGEGGVTLGQPHLSR	N-ter +28.03 Da	35.0	47.6	3	1562.89	-0.64	0.10	IF2G_MOUSE	A2AAW9_MOUSE	Eukaryotic translation initiation factor 2 subunit 3, X-linked;	Eukaryotic translation initiation factor 2 subunit gamma, X-linked;	0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
YSGLQGLPGL	AGLHGDQAGPVPVGPAGPR	N-ter +34.06 Da	47.5	47.2	3	1744.01	-2.40	0.50	CO1A2_MOUSE	E9Q6U9_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.00 - 0.15
MERGMFGGSF	AGSFGGAGGHPGVAR	N-ter +28.03 Da	45.7	47.6	3	1395.77	-0.86	0.08	HNRPM_MOUSE	B8JK32_MOUSE	Heterogeneous nuclear ribonucleoprotein M;		0.15 - 0.25
RGQSSANRR	AGSSGSGVQASAGLAADASR	N-ter +34.06 Da	79.2	37.2	3	1954.03	0.48	0.14	FILA_MOUSE	F7BVV1_MOUSE	Filaggrin;		0.25 - 0.75
IKVDKGVVPL	AGTNGETTQDGLDLSER	N-ter +34.06 Da	41.7	45.3	3	1839.99	-2.64	0.33	ALDOA_MOUSE	Q9CPQ9_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.00 - 0.15
QADCAVLIVA	AGVGEFEAGISKNGQTR	N-ter +28.03 Da, K +28.03 Da	37.7	46.1	3	1776.00	-1.89	0.21	EF1A1_MOUSE	EF1A2_MOUSE	Elongation factor 1-alpha 1; Histidine triad nucleotide-binding protein 2, mitochondrial;	Elongation factor Tu;Eukaryotic elongation factor 1 A-1;	0.00 - 0.15
GARGAQVRGN	AGVSDGSEVAKAQAAPGGASPTIFSR	N-ter +28.03 Da, K +28.03 Da	21.8	56.1	4	2642.55	0.52	0.13	HINT2_MOUSE		HINT3;		0.25 - 0.75
QMSYGYDEKS	AGVSVPGPMGPGSPR	N-ter +34.06 Da	38.8	56.4	3	1398.83	-2.18	0.30	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.00 - 0.15
VLLGLTPARA	AHEDPVEKVIIEGFSR	N-ter +28.03 Da, K +28.03 Da	35.0	68.0	4	1768.04	0.23	0.06	SBSN_MOUSE	E9QP82_MOUSE	Suprabasin;		0.25 - 0.75
IMELINNAK	AHGGYSVFAGVGER	N-ter +28.03 Da	26.4	57.8	3	1433.79	1.29	0.11	ATP_MOUSE		ATP synthase subunit beta, mitochondrial;		0.75 - 0.85
RAISTSVCLR	AHGSVVKSEDIYAFPTYARR	N-ter +34.06 Da, K +34.06 Da	25.1	65.6	4	2336.37	-0.81	0.14	COX41_MOUSE		Cytochrome c oxidase subunit 4 isoform 1, mitochondrial;	Cytochrome c oxidase polypeptide IV;Cytochrome c oxidase subunit IV isoform 1;	0.15 - 0.25
RAISTSVCLR	AHGSVVKSEDIYAFPTYARR	N-ter +34.06 Da, K +34.06 Da	29.2	61.7	4	2180.25	-1.09	0.19	COX41_MOUSE		Cytochrome c oxidase subunit 4 isoform 1, mitochondrial;	Cytochrome c oxidase polypeptide IV;Cytochrome c oxidase subunit IV isoform 1;	0.15 - 0.25
SELLHSITLL	AHLTGDIIQGSATSLR	N-ter +28.03 Da	39.0	55.8	3	1768.05	0.66	0.11	HIP1_MOUSE		Huntingtin-interacting protein 1;	Huntingtin-interacting protein I;	0.25 - 0.75
FSKOWSYFIL	AHTEFTPTETDTYACR	N-ter +28.03 Da, C +57.02 Da	53.6	54.8	3	1926.95	-0.89	0.23	B2MG_MOUSE	Q91XJ8_MOUSE	Beta-2-microglobulin;		0.15 - 0.25
DRQKEVNEF	AIDLIAQPVNEVEHR	N-ter +28.03 Da	49.4	46.3	3	1859.08	-1.00	0.16	NDU56_MOUSE	D3YV32_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial;	Complex I-13kD-A;NADH-ubiquinone oxidoreductase 13 kDa-A subunit;	0.15 - 0.25
RPRGPASYKR	AIGEDFVLLKER	N-ter +28.03 Da, K +28.03 Da	24.5	53.2	3	1444.91	0.52	0.08	MINK1_MOUSE	E9Q2Q5_MOUSE	Missshapen-like kinase 1;	Complex I-13kD-A;NADH-ubiquinone oxidoreductase 13 kDa-A subunit;	0.25 - 0.75
EAAGNKYVPR	AILVDLEPGTMDSVLR	N-ter +28.03 Da	32.7	49.6	3	1642.94	-1.22	0.17	TBB2A_MOUSE	TBB2B_MOUSE	Tubulin beta-2A chain;	GCK family kinase MINK;MAPK/ERK kinase kinase 6;Missshapen/NIK-related kinase;Mitogen-activated protein kinase kinase kinase 6;	0.15 - 0.25
EFEQLPMMQ	AISNKKDQGGYEDFVEGLR	N-ter +34.06 Da, K +34.06 Da	32.2	46.7	3	2179.22	0.37	0.11	MYL1_MOUSE	E9PWG4_MOUSE	Myosin light chain 1/3, skeletal muscle isoform;	Myosin light chain alkali 1/2; Cathepsin C;Cathepsin J;Dipeptidyl peptidase I;Dipeptidyl transferase;	0.25 - 0.75
FFKYVERGHT	AISYCHETMTGWVHDVLR	N-ter +28.03 Da, C +57.02 Da	34.9	68.6	4	2259.21	2.72	1.07	CATC_MOUSE	D3Z220_MOUSE	Dipeptidyl peptidase 1;	I;Dipeptidyl transferase;	0.85 - 1.00
IVEGLMTTVH	AITATQKTVDGSPSKLWR	N-ter +34.06 Da, K +34.06 Da	22.9	53.6	4	2030.35	-0.25	0.05	G3P_MOUSE	F8WJL5_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase;	Peptidyl-cysteine S-nitrosylase GAPDH;	0.25 - 0.75
RVLLPEGGIT	AIVFLEPLEAR	N-ter +28.03 Da	23.5	73.3	3	1413.89	1.14	0.17	RBM19_MOUSE		Probable RNA-binding protein 19;	RNA-binding motif protein 19;	0.75 - 0.85
LLPLLAGAQA	AIVFIKEPSQDALQGR	N-ter +34.06 Da, K +34.06 Da	23.1	47.7	3	1926.21	1.05	0.21	PTK7_MOUSE	Q3V2W2_MOUSE	Inactive tyrosine-protein kinase 7;	7;Pseudo tyrosine kinase receptor 7;Tyrosine-protein kinase-like 7;	0.75 - 0.85
GEDFSETLTR	AKFEELNMDLFR	N-ter +28.03 Da, K +28.03 Da	35.4	60.2	3	1567.90	1.46	0.28	GRP78_MOUSE		78 kDa glucose-regulated protein;	Heat shock 70 kDa protein 5;Immunoglobulin heavy chain-binding protein;	0.75 - 0.85
PDLSKHNNHM	AKVLTPLDYNKLR	N-ter +34.06 Da, K +34.06 Da	18.9	54.1	4	1632.17	0.53	0.08	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.25 - 0.75
FAPQLSVQK	ALDLDPSKTVNNGAIALHPLGGSGSR	N-ter +28.03 Da, K +28.03 Da	42.0	60.7	4	2702.60	0.68	0.20	THIM_MOUSE		3-ketoacyl-CoA thiolase, mitochondrial;	Acetyl-CoA acyltransferase;Beta-ketothiolase;Mitochondrial 3-oxoacyl-CoA thiolase;	0.25 - 0.75
RQNKDLMELQ	ALIDSHFEAR	N-ter +34.06 Da	28.8	51.8	3	1191.71	-0.81	0.03	TNNT3_MOUSE	A2A6J0_MOUSE	Troponin T, fast skeletal muscle;	Fast skeletal muscle troponin T; Heparin-binding protein 44;Low density lipoprotein receptor-related protein-associated protein 1;	0.15 - 0.25
RKDAQMVHNS	ALNEDTQDELGDPR	N-ter +28.03 Da	35.5	49.5	3	1599.82	-0.89	0.13	AMRP_MOUSE	F6SY09_MOUSE	Alpha-2-macroglobulin receptor-associated protein;	ATP-dependent helicase ATRX;HP1 alpha-interacting protein;HP1-BP38 protein;Heterochromatin protein 2;X-linked nuclear protein;	0.15 - 0.25
QTPYIPFNLG	ALSAMSNQLEDLINOGR	N-ter +34.06 Da	24.3	51.9	4	2021.15	-2.00	0.32	ATRX_MOUSE		Transcriptional regulator ATRX;	UbcM4;Ubiquitin carrier protein L3;Ubiquitin-protein ligase L3;	0.00 - 0.15
KTDQVIQFFI	ALVNDPQPEHLR	N-ter +28.03 Da	47.7	42.4	3	1512.87	4.25	0.95	UBZL3_MOUSE		Ubiquitin-conjugating enzyme E2 L3;		0.85 - 1.00
TLNAANVPAG	AMDDDIALVVDNGSGMCKAGFAGDDAPR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	23.6	30.5	4	2994.44	1.82	0.55	E9Q606_MOUSE				0.85 - 1.00
LALAFGLAHA	AMEGPWKTVAIAADR	N-ter +34.06 Da, K +34.06 Da	34.7	45.0	3	1683.02	2.48	0.29	A2AEN9_MOUSE	Q9D3H2_MOUSE	Sodium/potassium-transporting ATPase subunit beta-3;	Sodium/potassium-dependent ATPase subunit beta-3;	0.85 - 1.00
LAALFTTMMW	AMLQTLNDEVPKYR	N-ter +28.03 Da, K +28.03 Da	49.0	47.1	3	1733.00	0.25	0.04	AT1B3_MOUSE				0.25 - 0.75
IRYREPRRML	AMPLDLDALSPER	N-ter +28.03 Da	47.6	51.1	3	1583.87	0.98	0.09	RM55_MOUSE		395 ribosomal protein L55, mitochondrial;		0.75 - 0.85
EPKRRSARLS	AMPVPTPELKPGR	N-ter +28.03 Da, K +28.03 Da	24.2	56.7	4	1694.09	-0.25	0.03	HMGNS_MOUSE		High mobility group nucleosome-binding domain-containing protein 5;	Nucleosome-binding protein 1;Nucleosome-binding protein 45;Protein GARP45;	0.25 - 0.75
PREIFKQKER	AMSTTSVTSSQPKLR	N-ter +28.03 Da, K +28.03 Da	42.6	37.7	3	1705.97	1.70	0.58	DBNL_MOUSE		Drebrin-like protein;	Actin-binding protein 1;SH3 domain-containing protein 7;	0.85 - 1.00
SPVSSGVNLF	ANDGSFLEFKR	N-ter +28.03 Da, K +28.03 Da	42.1	57.9	3	1451.86	0.84	0.21	CS043_MOUSE		Uncharacterized protein C19orf43 homolog;		0.25 - 0.75
QPISNVRAIQ	ANINIPMGAFRPGAGQPPR	N-ter +28.03 Da	24.6	48.7	3	1991.15	0.21	0.02	SMPX_MOUSE		Small muscular protein;	Stretch-responsive skeletal muscle protein;	0.25 - 0.75
NPEESIEDIY	ANIPDLPSYIPSR	N-ter +28.03 Da	34.5	44.4	3	1556.89	-0.27	0.02	PALMD_MOUSE	Q3UV77_MOUSE	Palmdelphin;		0.25 - 0.75
CDIDIRKLDY	ANNVMMSGTTMYPGIADR	N-ter +28.03 Da	26.1	56.3	3	1881.98	-2.64	0.66	ACT5_MOUSE		Actin, alpha skeletal muscle;	Alpha-actin-1;	0.00 - 0.15
SPSEIGPMP	ANQDTIFEGIGGPR	N-ter +34.06 Da	40.8	47.3	3	1507.86	-3.47	0.39	COSA1_MOUSE		Collagen alpha-1(V) chain;		0.00 - 0.15
FGVTTLDVWR	ANTFVAELKGLDPR	N-ter +28.03 Da, K +28.03 Da	38.0	46.6	3	1657.00	1.00	0.09	MDHM_MOUSE		Malate dehydrogenase, mitochondrial;		0.75 - 0.85
CDVDIRKLDY	ANTVLSGGTTMYPGIADR	N-ter +28.03 Da	34.6	54.6	3	1851.02	-0.45	0.07	ACTB_MOUSE	ACTG_MOUSE	Actin, cytoplasmic 1;	Beta-actin;	0.25 - 0.75
DLSKVLFICT	ANVIDTIPELR	N-ter +28.03 Da	38.3	22.3	2	1364.80	0.86	0.06	LONM_MOUSE	E9Q120_MOUSE	Lon protease homolog, mitochondrial;	Lon protease-like protein;Mitochondrial ATP-dependent protease Lon;Serine protease 15;	0.25 - 0.75

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
QSQWQKVKDF	ANVVVDVAVKDSGR	N-ter +28.03 Da, K +28.03 Da	19.0	49.2	3	1448.83	1.32	0.08	APOA1_MOUSE	Q8BPD5_MOUSE	Apolipoprotein A-I;	Apolipoprotein A1;	0.75 - 0.85
LLSWASRNEA HTFYNELRV	APDQDEIDCLPGLAKQPSFR APEEHPVLLTEAPLNPKANR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da	38.4 50.1	59.5 58.0	4 4	2312.28 2251.36	0.96 1.35	0.12 0.15	PPGB_MOUSE ACTB_MOUSE	A2A5J9_MOUSE ACTG_MOUSE	Lysosomal protective protein; Actin, cytoplasmic 1;	Carboxypeptidase C;Carboxypeptidase L;Cathepsin A;Protective protein cathepsin A;Protective protein for beta-galactosidase; Beta-actin;	0.75 - 0.85 0.75 - 0.85
LRRFMQTFVL	APEGSVANKFYVHNDIFR	N-ter +28.03 Da, K +28.03 Da	27.2	59.7	4	2119.21	0.62	0.07	G3BP1_MOUSE	Q3UR88_MOUSE	Ras GTPase-activating protein-binding protein 1;	ATP-dependent DNA helicase VIII;GAP SH3 domain-binding protein 1;HDH-VIII;	0.25 - 0.75
SQPESLPAM	APLPDSDPDQPALLLAR APNVLASEPEIPKGIK	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	26.2 40.8	54.5 32.8	3 3	1816.07 1746.06	-0.42 1.42	0.04 0.19	C2D1B_MOUSE KAD2_MOUSE		Coiled-coil and C2 domain-containing protein 1B; Adenylate kinase 2, mitochondrial;	Five prime repressor element under dual repression-binding protein 2; ATP-AMP transphosphorylase 2;	0.25 - 0.75 0.75 - 0.85
ATSASGALLS VAGPQPAQTG NAILRVYTKG	APPSGPPISGFSVGTYYDITR APQGLSLEYLFR APQVSTPTLVEAAR	N-ter +28.03 Da N-ter +28.03 Da N-ter +28.03 Da	59.4 42.2 39.4	39.8 52.2 43.5	3 3 3	2147.18 1493.83 1466.87	-0.81 1.01 -2.12	0.13 0.08 0.37	PRRC1_MOUSE FRIL1_MOUSE ALBU_MOUSE	Q9CPX4_MOUSE	Protein PRRC1; Ferritin light chain 1; Serum albumin;	Proline-rich and coiled-coil-containing protein 1; Ferritin L subunit 1;	0.15 - 0.25 0.75 - 0.85 0.00 - 0.15
LLATVWHGQG	APVIEPSGPELVPEGETVTLR	N-ter +34.06 Da	62.7	43.6	3	2322.39	-0.14	0.04	CSF1R_MOUSE	Q3TBH6_MOUSE	Macrophage colony-stimulating factor 1 receptor;	CSF-1 receptor;Proto-oncogene c-Fms;	0.25 - 0.75
DMTSKFLTAL	AQDGVINEEALSVELDR	N-ter +28.03 Da	63.8	47.2	3	1986.08	2.22	0.38	PDC6I_MOUSE	B8JL8_MOUSE	Programmed cell death 6-interacting protein;	ALG-2-interacting protein 1;ALG-2-interacting protein X;E2F1-inducible protein;Eig2;	0.85 - 1.00
ITQQASMTSL	AQGPGTSAITFPPEEQDPR	N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	38.8 30.1	48.2 46.1	3 3	2164.15 1399.78	-0.64 -3.47	0.15 0.39	PRRC1_MOUSE 2AAA_MOUSE		Protein PRRC1; Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform;	Proline-rich and coiled-coil-containing protein 1; PP2A subunit A isoform PR65-alpha;PP2A subunit A isoform R1-alpha;	0.25 - 0.75 0.00 - 0.15
TIEHLLPFL	AQLKDECPVFR	N-ter +28.03 Da	48.2	47.1	3	2112.01	1.25	0.33	LDB3_MOUSE	E9PYJ9_MOUSE	LIM domain-binding protein 3;	Protein cypher;Protein oracle;Z-band alternatively spliced PDZ-motif protein;	0.75 - 0.85
NLQSRFRIL	AQMTGTGYMQDPEEALR	N-ter +28.03 Da	48.2	47.1	3	2112.01	1.25	0.33	LDB3_MOUSE	E9PYJ9_MOUSE	LIM domain-binding protein 3;	ATP-AMP transphosphorylase;Adenylate kinase 3-like;	0.25 - 0.75
LARAPLCERI	AQNFGQLHLSGGHLLR	N-ter +28.03 Da	60.6	60.7	4	1805.08	0.66	0.08	KAD4_MOUSE	A2ARF6_MOUSE	Adenylate kinase isoenzyme 4, mitochondrial; Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial;	Heat shock 70 kDa protein 8;	0.15 - 0.25 0.25 - 0.75
MRAAPRRAPA GIDFYTSIR SPCLLPRVHL QGRRGVSESEQ	AQPAAAAAPSVAAGSAAAPR ARFELNADLFR ASAFGSSTESLVAR ASDSEGHSDSDFEQAVGAHR	N-ter +34.06 Da N-ter +28.03 Da N-ter +34.06 Da N-ter +28.03 Da	60.6 39.2 48.5 51.7	60.4 66.5 35.5 60.2	3 3 2 4	1791.09 1507.88 1415.80 2071.02	-1.43 0.77 -0.12 1.68	0.39 0.08 0.02 0.43	CHCH2_MOUSE HSP7C_MOUSE THEM5_MOUSE E9Q019_MOUSE	B2RPU8_MOUSE HSP72_MOUSE FILA_MOUSE	Heat shock cognate 71 kDa protein; Thioesterase superfamily member 5;	Heat shock 70 kDa protein 8;	0.25 - 0.75 0.25 - 0.75 0.85 - 1.00
GKRHPYKMNL	ASEPQEVLIHIGSAHNR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	38.4 64.8	50.7 58.8	4 4	1771.99 2452.35	2.92 2.02	0.31 0.68	PDU11_MOUSE RS14_MOUSE		PDZ and LIM domain protein 1; 40S ribosomal protein S14;	C-terminal LIM domain protein 1;Elfin;LIM domain protein CLP-36;	0.85 - 1.00 0.85 - 1.00
ENNVGVCHIF	ASFNDTFVHVHDLGSKETICR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	64.8	58.8	4	2452.35	2.02	0.68	RS14_MOUSE	D3YVF4_MOUSE	40S ribosomal protein S14;		0.85 - 1.00
KSPQVILVNM ENAFRSRGG	ASFPECTAAAIKAIK ASGDKAEAGAPQVEAGKR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	37.3 31.1	49.6 61.4	3 4	1660.98 1883.09	-0.30 2.09	0.04 0.39	RRFM_MOUSE Q8VCQ8_MOUSE	E9Q0M9_MOUSE	Ribosome-recycling factor, mitochondrial;	Ribosome-releasing factor, mitochondrial;	0.25 - 0.75 0.85 - 1.00
ARGAAVTRSM	ASGGGVPTDEEQATGLER	N-ter +28.03 Da	40.7	50.4	3	1800.94	-0.22	0.02	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 KTGAAAGKRK QEVRCLEERSY ADPAKVEAFQ	ASGPGGLHADLLR ASGPPVSELITKAVAASKER ASKPTLNEVVIVSAIR ASLSKLDGVYVNDVAFGTAHR	N-ter +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, K +28.03 Da	42.4 30.6 38.6 56.4	53.3 70.1 47.0 62.2	3 4 3 4	1290.77 2094.35 1764.20 2176.26	0.01 0.26 -0.43 -0.45	0.00 0.01 0.06 0.06	SSDH_MOUSE H12_MOUSE THL1_MOUSE PGK1_MOUSE	H13_MOUSE	Succinate-semialdehyde dehydrogenase, mitochondrial; Histone H1.2; Acetyl-CoA acetyltransferase, mitochondrial; Phosphoglycerate kinase 1;	H1 VAR.1;H1C; Acetoacetyl-CoA thiolase;	0.25 - 0.75 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75
QHSSKFMVLV M	ASNQPEQDFWAINDR ASQTQGIQQLLQAEKR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	39.3 28.1	51.6 28.9	3 3	1817.93 1854.09	0.83 2.48	0.11 0.44	ATAD3_MOUSE VATG2_MOUSE		ATPase family AAA domain-containing protein 3; V-type proton ATPase subunit G 2;	AAA-ATPase TOB3; V-ATPase 13 kDa subunit 2;Vacuolar proton pump subunit G 2;	0.25 - 0.75 0.85 - 1.00
RSALQSIW GLLDWPOGTG	ASQTDGKLEPVTKDVER ASQVTEGDKVKVER	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da	20.4 28.7	57.4 60.9	4 4	2075.32 1742.10	-0.49 -0.03	0.04 0.00	SERPH_MOUSE ETFB_MOUSE		Serpin H1; Electron transfer flavoprotein subunit beta;	47 kDa heat shock protein;Collagen-binding protein;Serine protease inhibitor J6;	0.25 - 0.75 0.25 - 0.75
TTL5NAVSSL	ASTGLSLTKDVER	N-ter +28.03 Da, K +28.03 Da	25.9	44.4	3	1431.86	-0.45	0.09	PICA_MOUSE		Phosphatidylinositol-binding clathrin assembly protein;	Clathrin assembly lymphoid myeloid leukemia; HLA-B-associated transcript 2;Proline-rich and coiled-coil-containing protein 2A;	0.25 - 0.75
DGKPPSLTLA YVALDFENEM NGQNSRPKI IREGEVEVLK	ASTPGPEELTAATVPPPPR ATAASSSSLEKSYELPDGQVITIGNER ATALPDDIITR ATEMVEVGPEDDEVGAEAR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +28.03 Da	38.8 45.9 27.5 53.3	37.6 53.4 45.6 55.0	3 4 3 3	2016.13 2878.61 1340.79 1959.98	-0.36 3.02 0.21 1.02	0.03 0.89 0.01 0.22	PRC2A_MOUSE ACTC_MOUSE DNIC1_MOUSE PTRF_MOUSE	ACTA_MOUSE F6ZL86_MOUSE	Protein PRC2A; Actin, alpha cardiac muscle 1; Dnaj homolog subfamily C member 1; Polymerase I and transcript release factor;	Alpha-cardiac actin; Dnaj protein homolog MTJ1; Cav-p60;Cavin-1;	0.25 - 0.75 0.85 - 1.00 0.25 - 0.75 0.75 - 0.85
KRGTGGVDTA NWWKMGQLVL	ATGSVFDISNLDLR ATIEKIPFESAFR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	40.5 22.2	51.2 53.6	3 3	1421.79 1563.95	0.71 0.91	0.07 0.13	KCRU_MOUSE FACR2_MOUSE		Creatine kinase U-type, mitochondrial; Fatty acyl-CoA reductase 2;	Acidic-type mitochondrial creatine kinase;Ubiquitous mitochondrial creatine kinase; Male sterility domain-containing protein 1;	0.25 - 0.75 0.25 - 0.75
VIQHRSQYQY	ATLDVYNPFENR	N-ter +28.03 Da	24.5	55.8	3	1465.80	0.03	0.01	SCAM3_MOUSE	Q3UXS0_MOUSE	Secretory carrier-associated membrane protein 3;		0.25 - 0.75
LTGEFEKKVY	ATLGEVHPLVVFHTNR	N-ter +28.03 Da	33.7	55.7	4	1817.10	-0.49	0.06	RAN_MOUSE		GTP-binding nuclear protein Ran;	GTPase Ran;Ras-like protein TC4;Ras-related nuclear protein;	0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
DTLHRVKMIM	ATNRPDTLDPALLRPGR	N-ter +28.03 Da	21.4	59.2	4	1890.16	1.22	0.15	PRS10_MOUSE		26S protease regulatory subunit 10B;	26S proteasome AAA-ATPase subunit RPT4;Proteasome 26S subunit ATPase 6;Proteasome subunit p42;	0.75 - 0.85
KHKKEKAVTI	ATPATAAPAASAAITTSQAEEPAAPAEPR	N-ter +28.03 Da	57.5	43.7	4	2833.53	-1.69	0.11	SRRM1_MOUSE	A2A8V8_MOUSE	Serine/arginine repetitive matrix protein 1;	Plenty-of-prolines 101; Germ cell lineage protein gercelin;Src-suppressed C kinase substrate;	0.00 - 0.15
HLAQGSETVQ	ATPESLEVPEVTEVDVR	N-ter +34.06 Da	45.2	42.5	3	1919.04	-0.81	0.13	AKA12_MOUSE		A-kinase anchor protein 12;		0.15 - 0.25
GRRDSKSPTK	ATPLPAEGKKNLTLR	N-ter +28.03 Da, K +28.03 Da	24.9	56.1	4	1579.03	-0.20	0.02	E41L2_MOUSE		Band 4.1-like protein 2;	Generally expressed protein 4.1;	0.25 - 0.75
AVAAAAATTT	ATTTTTSGGHPLFLR	N-ter +34.06 Da	30.4	49.1	3	1722.00	0.20	0.02	RD23B_MOUSE	Q3TJ52_MOUSE	UV excision repair protein RAD23 homolog B;	XP-C repair-complementing complex 58 kDa protein;	0.25 - 0.75
QERQTOAVLQ	AVADKVKEDSQVPTQLQR	N-ter +34.06 Da, K +34.06 Da	34.8	48.1	4	2285.45	-1.56	0.32	AKA12_MOUSE		A-kinase anchor protein 12;	Germ cell lineage protein gercelin;Src-suppressed C kinase substrate;	0.00 - 0.15
QLAAQPSTYL	AVAEELNVSGKYFDGLR	N-ter +28.03 Da, K +28.03 Da	48.0	49.2	3	2052.15	1.67	0.29	RDH13_MOUSE		Retinol dehydrogenase 13;		0.85 - 1.00
LLENMEGLFL	AVDEIVDGGVILESDPQQVVRH	N-ter +28.03 Da	70.3	62.4	4	2402.39	2.66	0.64	COPZ1_MOUSE	Q8R3M1_MOUSE	Coatomer subunit zeta-1;	Zeta-1-coat protein;	0.85 - 1.00
QKIGQPSTLL	AVEEQYCEYSGSR	N-ter +34.06 Da, C +57.02 Da	45.2	40.6	3	1667.80	-1.52	0.43	E9PX16_MOUSE				0.00 - 0.15
LQFFNLDFTL	AVFHPETSTIQGLEGR	N-ter +28.03 Da	34.4	49.5	3	1769.00	1.23	0.15	FR10P_MOUSE		FGFR1 oncogene partner;		0.75 - 0.85
KRGTVGVDTA	AVGAVFDISNADR	N-ter +34.06 Da	36.7	48.7	3	1367.79	-2.18	0.30	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.00 - 0.15
IIPASTGAAK	AVGKVIPELNGKLTGMAFR	N-ter +28.03 Da, K +28.03 Da	38.8	60.5	4	2084.34	-1.52	0.26	G3P_MOUSE	F8WJL5_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase;	Peptidyl-cysteine S-nitrosylase GAPDH;	0.00 - 0.15
GERGLPGPPG	AVGPAGKDGEGAQAGPAGPAGER	N-ter +34.06 Da, K +34.06 Da	54.0	47.2	4	2312.32	-1.74	0.41	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.00 - 0.15
EATGGKYVPR	AVLVDLPEGTMDSVR	N-ter +28.03 Da	36.3	49.5	3	1628.93	-0.52	0.04	TBB2C_MOUSE	TBB4_MOUSE	Tubulin beta-4B chain;	Tubulin beta-2C chain;	0.25 - 0.75
GPEPTTDCVF	AVMHGETGETVPGNALVVDPEKPFRR	N-ter +28.03 Da, K +28.03 Da	56.3	54.7	4	2705.53	3.41	0.58	EHD2_MOUSE		EH domain-containing protein 2;		0.85 - 1.00
SSLLSPMSVN	AVMKVIDPATATVLDLR	N-ter +28.03 Da, K +28.03 Da	45.1	40.8	3	1842.10	-0.27	0.03	TCFD_MOUSE		T-complex protein 1 subunit delta;	A45;CCT-delta; CCT-alpha;Tailless complex polypeptide 1A;	0.25 - 0.75
RSLVIPNTL	AVNAAQDSTDLVAKLR	N-ter +28.03 Da, K +28.03 Da	41.8	41.2	3	1727.03	0.52	0.04	TCPA_MOUSE		T-complex protein 1 subunit alpha;	CT-alpha;Tailless complex polypeptide 1A;	0.25 - 0.75
VLTFGQMLTC	AVPIAQKSEPOSLSNEALMR	N-ter +28.03 Da, K +28.03 Da	34.8	58.6	4	2224.32	0.80	0.31	Q542V8_MOUSE	D3Z3K5_MOUSE			0.25 - 0.75
LSLEVLELQA	AVRPLQLLGTCAELCR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	69.6	45.0	3	1884.09	-0.30	0.06	Q8BTE6_MOUSE				0.25 - 0.75
AVPDKTVKWC	AVSEHENTKCISFR	N-ter +28.03 Da, C +57.02 Da	24.3	73.5	4	1732.98	-0.14	0.02	TRFE_MOUSE	D3YVR8_MOUSE	Serotransferrin;	Beta-1 metal-binding globulin;Siderophilin;	0.25 - 0.75
MDIQGDPKYR	AVSEQGVCTLEIR	N-ter +28.03 Da, C +57.02 Da	31.4	52.5	3	1488.84	-0.36	0.03	MY8PH_MOUSE		Myosin-binding protein H;	H-protein;	0.25 - 0.75
LQSEMLSLTL	AVSKEKEEETSPODTSIPR	N-ter +28.03 Da, K +28.03 Da	34.9	62.1	4	2215.26	1.34	0.33	E9Q705_MOUSE				0.75 - 0.85
TGQAAPVLGL	AVSSELIQSQSFVDPDEPR	N-ter +28.03 Da, C +57.02 Da	48.9	46.2	3	2217.18	1.26	0.18	FKBP9_MOUSE		Peptidyl-prolyl cis-trans isomerase FKBP9;	63 kDa FK506-binding protein;FK506-binding protein 9;FKBP65R;Rotamase;	0.75 - 0.85
TEEQGPEEDQ	AVSVFSGDPEGSALHEKSLR	N-ter +28.03 Da, K +28.03 Da	22.8	46.3	4	2141.21	-1.47	0.16	F22403_MOUSE				0.15 - 0.25
FISNPNSIIL	AVTAANTDMATSEALKISR	N-ter +28.03 Da, K +28.03 Da	44.8	42.3	3	2005.14	0.30	0.06	DNM1L_MOUSE	E9PUD2_MOUSE	Dynamin-1-like protein;	Dynamin family member proline-rich carboxyl-terminal domain less;Dynamin-related protein 1;	0.25 - 0.75
LLIATEEGFK	AVVGDDEVYLFHHR	N-ter +34.06 Da	34.6	64.0	4	1727.97	-0.09	0.03	LEG7_MOUSE	Q9CR81_MOUSE	Galectin-7;		0.25 - 0.75
ITKHNDDEQY	AWESSAGSFTVR	N-ter +28.03 Da	36.4	51.4	2	1381.73	-2.00	0.24	H590A_MOUSE	H590B_MOUSE	Heat shock protein HSP 90-alpha;	Heat shock 86 kDa;Tumor-specific transplantation 86 kDa antigen;	0.00 - 0.15
SGEDKSNKA	AWGKIGGHGAEYGAELER	N-ter +34.06 Da, K +34.06 Da	52.4	58.8	4	2039.21	-2.12	0.28	HBA_MOUSE	Q91V88_MOUSE	Hemoglobin subunit alpha;	Alpha-globin;Hemoglobin alpha chain;	0.00 - 0.15
GDMVPAISL	AYEQAESDIMKR	N-ter +28.03 Da, K +28.03 Da	23.7	52.7	3	1495.81	-1.60	0.15	AT1A1_MOUSE	E9QAV3_MOUSE		Sodium pump subunit alpha-1;	0.00 - 0.15
IFGDYIERLW	AYLTIEQLLEKR	N-ter +28.03 Da, K +28.03 Da	40.1	48.5	3	1531.97	2.79	0.57	ITIH3_MOUSE	F6ZJX7_MOUSE	Inter-alpha-trypsin inhibitor heavy chain H3;		0.85 - 1.00
LGEMLHEPTN	CAPYNTSDTETSNNYR	N-ter +34.06 Da, C +57.02 Da	22.0	68.2	3	2027.01	-6.64	0.00	Q6DFU8_MOUSE				0.00 - 0.15
ARNLGRVGTK	CCTLPEQDR	N-ter +28.03 Da, C +57.02 Da	33.6	37.6	2	1205.56	1.09	0.22	ALBU_MOUSE		Serum albumin;		0.75 - 0.85
CDDEETLTA	CDNGSLVKAGFAGDAPR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	62.6	46.4	3	1962.02	0.61	0.17	ACTC_MOUSE	ACTS_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
KVLLSICSLL	CDPNPDDPLVPEIAR	N-ter +28.03 Da, C +57.02 Da	29.9	54.7	3	1734.92	-0.43	0.05	UB2D2_MOUSE	UB2D3_MOUSE	Ubiquitin-conjugating enzyme E2 D2;	Ubiquitin carrier protein D2;Ubiquitin-conjugating enzyme E2(17)KB 2;Ubiquitin-conjugating enzyme E2-17 kDa 2;Ubiquitin-protein ligase D2;	0.25 - 0.75
MEPYS	CDTFVALPPATVGNR	N-ter +34.06 Da, C +57.02 Da	33.5	41.6	3	1650.93	-0.97	0.04	SCRN3_MOUSE	A2AWQ9_MOUSE	Secernin-3;		0.15 - 0.25
HNLPLGRFCE	CEIGYELDR	N-ter +28.03 Da, C +57.02 Da	40.1	57.1	2	1181.61	1.89	0.28	FBN1_MOUSE	A2AQ53_MOUSE	Fibrillin-1;		0.85 - 1.00
VTVAFNARD	CFLHLPR	N-ter +34.06 Da, C +57.02 Da	29.9	64.2	2	975.62	-4.64	1.16	PEX1_MOUSE		Peroxisome biogenesis factor 1;	Peroxin-1;	0.00 - 0.15
QAGRFRHVNL	CGEEQGADAAALHFNPR	N-ter +28.03 Da, C +57.02 Da	90.5	48.4	3	1798.89	1.99	0.54	Q9CRB1_MOUSE	LEG7_MOUSE			0.85 - 1.00
DDFAQFLDTC	CKAADKDCFTSTEGPNLVTR	N-ter +28.03 Da, C +57.02 Da	31.2	66.0	4	2353.30	0.59	0.06	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
GNSTHPMHSR	CSPDPGLTALLSDHR	N-ter +28.03 Da, C +57.02 Da	45.3	63.3	3	1665.92	2.64	0.51	HEMO_MOUSE		Hemopexin;		0.85 - 1.00
FNIFYELFTM	CTSITTEDEKGLHLHGR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	41.0	57.2	4	2021.15	-0.07	0.02	ASAH1_MOUSE	D3Z015_MOUSE	Acid ceramidase;	Acylsphingosine deacylase;N-acylsphingosine amidohydrolase;	0.25 - 0.75
NLLQHIGTNL	CVIGDGSGLTGANIFR	N-ter +28.03 Da, C +57.02 Da	38.1	44.2	3	1663.91	-0.17	0.02	K6PL_MOUSE		6-phosphofructokinase, liver type;	Phosphofructo-1-kinase isozyme B;Phosphofructokinase 1;Phosphohexokinase;	0.25 - 0.75
KPTDGASSSN	CYTDISHLVR	N-ter +28.03 Da, C +57.02 Da	43.3	64.6	3	1226.72	0.86	0.12	NASP_MOUSE	B1AU75_MOUSE	Nuclear autoantigenic sperm protein;		0.25 - 0.75
MQN	DAGEFVDLVPR	N-ter +28.03 Da	35.1	51.5	3	1407.78	0.00	0.00	RS21_MOUSE		40S ribosomal protein S21;		0.25 - 0.75
LGVSQVQLL	DAVDYIPVPR	N-ter +28.03 Da	17.4	48.7	3	1373.79	3.76	1.10	EFTU_MOUSE	D3YVN7_MOUSE	Elongation factor Tu, mitochondrial;		0.85 - 1.00
PPQCRFPFPG	DAVERPRPPPGPPWSPR	N-ter +34.06 Da	28.9	60.9	4	2195.31	-4.06	1.35	PDCD7_MOUSE	Q3U2X6_MOUSE	Programmed cell death protein 7;	ES18;	0.00 - 0.15
ASGTTLEAL	DCILPPTRPDTPKPLR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	24.1	69.5	4	1846.21	-2.25	0.11	EF1A1_MOUSE	D3Y268_MOUSE	Elongation factor 1-alpha 1;	Elongation factor Tu;Eukaryotic elongation factor 1A-1;	0.00 - 0.15
LPLLARLSAG	DCPCSEAAALCQPIR	N-ter +34.06 Da, C +57.02 Da	47.3	60.9	3	1709.88	-0.81	0.14	DIAC_MOUSE		Di-N-acetylchitobiase;		0.15 - 0.25
ESAAKDEAVF	DDEVAPDAAAENCLAER	N-ter +28.03 Da, C +57.02 Da	49.3	52.8	3	1872.91	0.81	0.23	E9PVP1_MOUSE				0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
VLLTFGFVRA AKLAEQAERY	DDEVDVDTVEEDLGKSR DDMAAAMKAVTEQGHLSNEER	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da	58.2 50.6	49.6 62.1	3 4	2033.04 2487.29	2.25 5.22	0.60 1.51	ENPL_MOUSE 1433B_MOUSE	A2A5N1_MOUSE	Endoplasmic reticulum resident protein 99;Heat shock protein 90 kDa beta member 1;Polymorphic tumor rejection antigen 1;Tumor rejection antigen gp96; 14-3-3 protein beta/alpha;	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; Protein kinase C inhibitor protein 1;	0.85 - 1.00 0.85 - 1.00
AKLAEQAERY AAGGGGGENY	DDMAACMKSVTEQGAELSNEER DDPHKTPASPVVHIR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da	49.8 37.0	51.5 59.2	4 4	2526.23 1724.04	3.17 -0.01	1.33 0.00	1433Z_MOUSE HNRPL_MOUSE	D3YXF4_MOUSE E9Q8W8_MOUSE	14-3-3 protein zeta/delta; Heterogeneous nuclear ribonucleoprotein L;	Protein kinase C inhibitor protein 1;SEZ-2;	0.85 - 1.00 0.25 - 0.75
VVWEKRSIGY	DDTDESHCVHEIESR	N-ter +28.03 Da, C +57.02 Da	36.2	57.5	4	1855.87	2.04	0.68	PLIN2_MOUSE		Perilipin-2;	Adipophilin;Adipose differentiation-related protein;	0.85 - 1.00
LAAGPRPSLG DVIRNAFACF	DEAIHCPCSEKRLAR DEEAIGTIQEDYLR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da N-ter +28.03 Da	27.3 34.5	55.8 44.7	4 3	1967.03 1678.88	-0.45 1.25	0.06 0.25	IBP4_MOUSE Q6ZWQ9_MOUSE		Insulin-like growth factor-binding protein 4;		0.25 - 0.75 0.75 - 0.85
DVIRNAFACF	DEEASGFHEDHLR	N-ter +28.03 Da	48.7	58.8	4	1681.87	1.47	0.31	MYL9_MOUSE		Myosin regulatory light polypeptide 9;	Myosin regulatory light chain 2, smooth muscle isoform;Myosin regulatory light chain 9;	0.75 - 0.85
DVIRNAFACF	DEEATGTIQEDYLR	N-ter +28.03 Da	35.4	45.5	3	1666.84	3.93	1.13	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;	0.85 - 1.00
KAVLSAEKLR VIGAVVDVQF	DEEVTGLGELLR DEGLPPILNALEVQGR	N-ter +28.03 Da N-ter +28.03 Da	40.4 45.9	47.0 46.7	3 3	1494.84 1748.03	1.73 -0.23	0.24 0.06	SERPH_MOUSE ATPB_MOUSE		Serpin H1; ATP synthase subunit beta, mitochondrial;	47 kDa heat shock protein;Collagen-binding protein;Serine protease inhibitor J6;	0.85 - 1.00 0.25 - 0.75
QTRDQLTIV NFASQMSYGY DKDKSGFIEE NYPKDNKRKM	DEKLDITLTVPEEHKTR DEKSAGVSVPGMGPSPGR DELGSLKGFSSDAR DETASSAVKVKR	N-ter +34.06 Da, K +34.06 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	49.4 39.4 33.6 26.7	65.6 37.0 54.2 67.4	4 4 3 4	2396.56 1892.08 1662.02 1488.92	-2.06 -3.06 -2.94 1.57	0.69 0.26 2.26 0.31	NDUS4_MOUSE CO1A1_MOUSE PRVA_MOUSE TADBP_MOUSE	E9QPX3_MOUSE F8WGB7_MOUSE Q8R0B4_MOUSE	NADH dehydrogenase [ubiquinone] iron-sulfur protein 4, mitochondrial; Collagen alpha-1(I) chain; Parvalbumin alpha; TAR DNA-binding protein 43;	Complex I-18 kDa;Complex I-AQDQ;NADH-ubiquinone oxidoreductase 18 kDa subunit; Alpha-1 type I collagen;	0.00 - 0.15 0.00 - 0.15 0.00 - 0.15 0.75 - 0.85
MTDAAVSFAK SQASDSEGHS	DFLAGGVAASIKTAVAPIER DFSEGGVAQGAHR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	23.7 47.7	54.7 54.6	4 3	2112.31 1300.69	2.66 -1.94	0.95 0.22	ADT2_MOUSE FILA_MOUSE	F7BVV1_MOUSE	ADP/ATP translocase 2; Filaggrin;	ADP,ATP carrier protein 2;Adenine nucleotide translocator 2;Solute carrier family 25 member 5;	0.85 - 1.00 0.00 - 0.15
GKSTTKRRR VFKVPMLNPN SASNRIIAK	DGDKLVVECVKMGVTSTR DGVIVGNRYR DHASIQMNVAEVDR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da N-ter +28.03 Da N-ter +34.06 Da	40.0 9.3 45.3	60.1 65.6 62.0	4 2 3	2077.22 1019.61 1617.90	3.05 -1.43 -0.38	0.53 0.12 0.07	FABP4_MOUSE CBPC2_MOUSE RS21_MOUSE	C8PC3_MOUSE	Fatty acid-binding protein, adipocyte; Cytosolic carboxypeptidase 2; 40S ribosomal protein S21;	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;	0.85 - 1.00 0.15 - 0.25 0.25 - 0.75
MDD KLPGRVAFGE LGGNSSPSAK LLWFPGKIC LLFWIPASRG LLWVFGARC	DIAALVVDNGSGMKAGFAGDDAPR DIDLPEFTDAR DIKKILDSVGEADDDR DIKMTQSPSSMYASLGER DILLTQSPAILSVSPGER DIQMTQSPSSLSASLGER	N-ter +28.03 Da, K +28.03 Da, C +57.02 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 N-ter +28.03 Da	30.1 48.5 48.5 54.0 50.5 49.6	54.4 41.5 55.1 54.0 46.2 45.1	4 2 3 3 3 3	2562.36 1318.70 1985.18 2056.11 1923.16 1934.03	1.92 3.16 3.55 -1.09 -3.18 -3.18	0.59 0.74 1.52 0.19 1.45 0.87	ACTB_MOUSE CATB_MOUSE RLA2_MOUSE KV5A5_MOUSE KV5A9_MOUSE KV5A7_MOUSE	E9Q1F2_MOUSE	Actin, cytoplasmic 1; Cathepsin B; 60S acidic ribosomal protein P2; Ig kappa chain V-V region T1; Ig kappa chain V-V region L7; Ig kappa chain V-V region MOPC 41;	Beta-actin; Cathepsin B1;	0.85 - 1.00 0.85 - 1.00 0.85 - 1.00 0.15 - 0.25 0.00 - 0.15 0.00 - 0.15
MVNPVTFF MLLWLSGVEG LDWTLYQLET	DITADDEPLGR DIVMTQSHKFMSTSVGDR DKFEFGKELKR	N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da	39.1 44.3 16.1	29.5 66.1 66.5	2 4 4	1234.66 2094.16 1532.11	-0.09 -1.52 -1.22	0.01 0.39 0.37	PPIA_MOUSE KV5A1_MOUSE TNNT3_MOUSE	E9Q1E3_MOUSE	Peptidyl-prolyl cis-trans isomerase A; Ig kappa chain V19-17; Troponin T, fast skeletal muscle;	Cyclophilin A;Cyclosporin A-binding protein;Rotamase A;SP18; Ig kappa chain V-V region MPC11; Fast skeletal muscle troponin T;	0.25 - 0.75 0.00 - 0.15 0.15 - 0.25
QQIDDHFLF	DKPVSPLLTAAAGMAR	N-ter +28.03 Da, K +28.03 Da	31.4	50.4	3	1581.97	0.21	0.03	KCRU_MOUSE	A2ARP5_MOUSE	Creatine kinase U-type, mitochondrial;	Acidic-type mitochondrial creatine kinase;Ubiquitous mitochondrial creatine kinase; Annexin I;Annexin-1;Calpactin II;Calpactin-2;Chromobindin-9;Lipocortin I;Phospholipase A2 inhibitory protein;p35;	0.25 - 0.75
NRVYREELKR	DLAKDITSSTSGDFR	N-ter +28.03 Da, K +28.03 Da	52.3	49.0	3	1695.92	0.11	0.02	ANXA1_MOUSE	E9QA30_MOUSE	Annexin A1;		0.25 - 0.75
KDASVGVFFR	DLFSDGHSEFLKAASNLR	N-ter +28.03 Da, K +28.03 Da	26.1	63.3	4	2062.18	3.26	0.80	PDIA3_MOUSE		Protein disulfide-isomerase A3; NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial;	58 kDa glucose-regulated protein;58 kDa microsomal protein;Disulfide isomerase ER-60;Endoplasmic reticulum resident protein 57;Endoplasmic reticulum resident protein 60;	0.85 - 1.00
QKEVNFAL TKVNKECCHG	DUIAQPVNEVEHR DLLECADDR	N-ter +28.03 Da N-ter +28.03 Da, C +57.02 Da	36.1 27.2	45.6 76.1	3 2	1674.95 1133.59	-0.94 0.51	0.11 0.04	NDUSE_MOUSE ALBU_MOUSE	D3YW32_MOUSE	Serum albumin; NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial;	Complex I-13kD-A;NADH-ubiquinone oxidoreductase 13 kDa-A subunit;	0.15 - 0.25 0.25 - 0.75
HHDYNTYFL GGSLVSMLAR	DLNLDSLKFR DLPAAAAPAGPASFAR	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da	24.9 45.7	56.4 41.2	3 3	1287.86 1509.86	0.59 3.09	0.13 0.44	NDUV3_MOUSE 6PGL_MOUSE	Q3U422_MOUSE Q8CBG6_MOUSE	6-phosphogluconolactonase;	Complex I-9kD;NADH-ubiquinone oxidoreductase 9 kDa subunit;	0.25 - 0.75 0.85 - 1.00

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
PRTLASPKKK	DLSEIEIQQKLEAAEER	N-ter +28.03 Da, K +28.03 Da	30.0	69.0	4	2084.28	2.23	0.75	STMN1_MOUSE	STMN2_MOUSE	Stathmin;	Leukemia-associated gene protein;Leukemia-associated phosphoprotein p18;Metablastin;Oncoprotein 18;Phosphoprotein p19;Prosolin;Protein Pr22;pp17;	0.85 - 1.00
LTSESSRPTR	DLSSSDLSTASKIVK	N-ter +28.03 Da, K +28.03 Da	51.2	51.9	3	1634.00	1.31	0.44	A2M_MOUSE	D3YW52_MOUSE	Alpha-2-macroglobulin;	Pregnancy zone protein;	0.75 - 0.85
LTSESSRPTR	DLSSSDLSTASK	N-ter +28.03 Da, K +28.03 Da	38.7	31.6	2	1265.67	-0.54	0.07	A2M_MOUSE	D3YW52_MOUSE	Alpha-2-macroglobulin;	Pregnancy zone protein;	0.25 - 0.75
IMKCDIDIRK	DLYANNVMSGTTMYPGIADR	N-ter +28.03 Da	50.0	55.5	3	2273.17	3.92	1.08	ACTS_MOUSE		Actin, alpha skeletal muscle;	Alpha-actin-1;	0.85 - 1.00
GAHAFGQGR	DMAETFDQGAHAFGQGR	N-ter +28.03 Da	45.4	59.6	4	2059.02	0.06	0.02	SBSN_MOUSE	E9QP82_MOUSE	Suprabasin;		0.25 - 0.75
DDEETALVLC	DNGSLVKAGFAGDGDAPR	N-ter +28.03 Da, K +28.03 Da	54.3	48.3	3	1801.98	-1.25	0.21	ACTC_MOUSE	ACTS_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.15 - 0.25
WPDARGIWHN	DNKSLVWVNEEDHLR	N-ter +34.06 Da, K +34.06 Da	48.4	70.4	4	2068.25	-1.32	0.33	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.15 - 0.25
LPTSLTLYL	DNNKISNIPDEYFKR	N-ter +28.03 Da, K +28.03 Da	29.1	65.9	4	1936.13	-1.09	0.12	LUM_MOUSE		Lumican;	Keratan sulfate proteoglycan lumican;	0.15 - 0.25
LLTACLASRA	DPASTLPDIQVENFSESR	N-ter +34.06 Da	48.1	47.7	3	2166.17	-0.23	0.04	AMBP_MOUSE		Protein AMBP;		0.25 - 0.75
VPTANAALPA	DPPASVVVGPVVVPR	N-ter +34.06 Da	51.6	43.1	3	1520.98	-0.32	0.04	FETUA_MOUSE		Alpha-2-HS-glycoprotein;	Countertryptin;Fetuin-A;	0.25 - 0.75
LLVLPATGS	DPVLCFTQYEESSGR	N-ter +34.06 Da, C +57.02 Da	43.2	49.2	3	1820.94	0.26	0.01	PROP_MOUSE		Properdin;	Complement factor P;	0.25 - 0.75
SWASRNEAAP	DQDEIDCLPLAKQPSFR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	57.0	51.0	3	2144.17	1.32	0.29	PPGB_MOUSE	A2A5I9_MOUSE	Lysosomal protective protein;	Carboxypeptidase C;Carboxypeptidase L;Cathepsin A;Protective protein cathepsin A;Protective protein for beta-galactosidase;	0.75 - 0.85
IFLLYKIVRG	DQPASGSDNDDEPPPLPR	N-ter +34.06 Da	28.7	48.8	3	2025.01	-0.64	0.05	PGRCL_MOUSE	Q3TFP8_MOUSE	Membrane associated progesterone receptor component 1;		0.25 - 0.75
DVQETDTSQK	DQSPASHEIATNLGDFALR	N-ter +28.03 Da	53.1	50.9	3	2069.12	-2.40	0.76	A1AT4_MOUSE		Alpha-1-antitrypsin 1-4;	Alpha-1 protease inhibitor 4;Serine protease inhibitor 1-4;Serine protease inhibitor A1d;	0.00 - 0.15
EGSSNVFSMF	DQIQQEFKEAFTVIDQNR	N-ter +34.06 Da, K +34.06 Da	41.6	50.6	4	2377.38	-0.71	0.49	MLRS_MOUSE	F6ULR7_MOUSE	Myosin regulatory light chain 2, skeletal muscle isoform;	Fast skeletal myosin light chain 2;MLC2f;	0.25 - 0.75
FEVLPEKADR	DQYELCLDNTR	N-ter +28.03 Da, C +57.02 Da	34.7	66.2	3	1566.84	1.53	0.20	TRFE_MOUSE	E9Q035_MOUSE	Serotransferrin;	Beta-1 metal-binding globulin;Siderophilin;	0.75 - 0.85
GPVGPAGKNG	DRGETGPAGPAGPIGAGAR	N-ter +34.06 Da	54.5	43.9	3	1837.05	-2.64	0.50	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.00 - 0.15
ASGRTTGIVL	DSGGDVTNHPYIYGALPHAIMR	N-ter +28.03 Da	62.0	59.7	4	2639.44	1.72	0.56	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.85 - 1.00
PRQPSQSS	DSQVHSGVQVEGR	N-ter +28.03 Da	28.8	44.0	3	1424.76	0.12	0.01	FILA_MOUSE	F7BVV1_MOUSE	Filaggrin;		0.25 - 0.75
DVEPDTYCRY	DSVSFVNGAVSDDSKR	N-ter +34.06 Da, K +34.06 Da	64.9	44.7	3	1750.00	-0.30	0.06	PCOC1_MOUSE	D3ZE3_MOUSE	Procollagen C-endopeptidase enhancer 1;	P14;Procollagen COOH-terminal proteinase enhancer 1;Type I procollagen C-proteinase enhancer protein;Type I procollagen COOH-terminal proteinase enhancer;	0.25 - 0.75
QGVVMGMGQK	DSYVGDEAQSRR	N-ter +28.03 Da, K +28.03 Da	31.9	63.8	3	1409.77	2.20	0.45	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.85 - 1.00
IEKKRILKR	DTDLEDELEPDR	N-ter +28.03 Da	32.7	53.9	3	1570.78	2.12	0.42	PROD_MOUSE		Vitamin K-dependent protein C;	Anticoagulant protein C;Autoprothrombin IIA;Blood coagulation factor XIV;	0.85 - 1.00
PHKNMFTVNR	DTGVISVLTSLDR	N-ter +28.03 Da	34.4	51.4	3	1459.86	1.66	0.68	CADH1_MOUSE		Cadherin-1;	ARC-1;Epithelial cadherin;Uvomorulin;	0.85 - 1.00
ASGVSLLEAL	DTILPPTPTDKPLR	N-ter +34.06 Da, K +34.06 Da	23.4	56.8	4	1787.20	-1.89	0.21	EF1A2_MOUSE	B72BW3_MOUSE	Elongation factor 1-alpha 2;	Eukaryotic elongation factor 1 A-2;Statin-S1;	0.00 - 0.15
WGMKMGDFP	DTIQCADVHLVPR	N-ter +28.03 Da, C +57.02 Da	23.6	72.5	3	1550.90	2.34	0.20	O88301_MOUSE	Q91Y82_MOUSE			0.85 - 1.00
TAGKHGDSLR	DTKNEIAELTR	N-ter +28.03 Da, K +28.03 Da	41.9	48.2	3	1344.79	-0.54	0.10	K2C79_MOUSE		Keratin, type II cytoskeletal 79;	Cytokeratin-79;Keratin-79;Type-II keratin Kb38;	0.25 - 0.75
CPPEKSKRR	DTQSNELIEINPQTEGKVYTR	N-ter +28.03 Da, K +28.03 Da	44.4	60.1	4	2490.41	0.66	0.15	COGAI_MOUSE	A3KRV3_MOUSE	Collagen alpha-1(XVI) chain;	Alpha-1 type I collagen;	0.25 - 0.75
PEEYVSPNSE	DVGVEGPKDPPGQGR	N-ter +28.03 Da, K +28.03 Da	28.8	43.5	3	1716.95	-0.49	0.10	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;		0.25 - 0.75
AS	DVLELTDENFESR	N-ter +28.03 Da	41.9	57.6	3	1593.84	0.55	0.09	PDIA3_MOUSE	F6Q404_MOUSE	Protein disulfide-isomerase A3;	58 kDa glucose-regulated protein;58 kDa microsomal protein;Disulfide isomerase ER-60;Endoplasmic reticulum resident protein 57;Endoplasmic reticulum resident protein 60;	0.25 - 0.75
LTKYKTLTG	DVPVVDPTVPVTVTR	N-ter +28.03 Da	52.1	52.2	3	1806.08	0.40	0.14	GDIR2_MOUSE		Rho GDP-dissociation inhibitor 2;	D4;Rho-GDI beta;	0.25 - 0.75
LVLLKGVQC	DVLQVESGGGLVQPQGSRR	N-ter +28.03 Da	49.7	48.0	3	1782.01	-3.18	0.87	HVM16_MOUSE		Ig heavy chain V region MOPC 21;		0.00 - 0.15
SVGDGETVEF	DVVEGEKAEAAANTVPGDVPVEGSR	N-ter +34.06 Da, K +34.06 Da	61.4	54.1	4	2606.49	-3.06	0.77	DBPA_MOUSE	F6TIF5_MOUSE	DNA-binding protein A;	Cold shock domain-containing protein A;Y-box protein 3;	0.00 - 0.15
RYAWVKRQLV	DYEEKYGR	N-ter +28.03 Da, K +28.03 Da	30.3	25.3	2	1114.56	2.86	0.48	VP53_MOUSE	E9PGX9_MOUSE	Vacuolar protein sorting-associated protein 53 homolog;		0.85 - 1.00
LQREKEFKAK	EAAALSHSGSCSEVEKETR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	42.1	58.1	4	2160.14	-0.64	0.16	VATG1_MOUSE		V-type proton ATPase subunit G 1;	V-ATPase 13 kDa subunit 1;Vacuolar proton pump subunit G 1;	0.25 - 0.75
VLHFGIIVLY	EACCVVLLWLLALFSLQIPR	N-ter +28.03 Da, C +57.02 Da	30.1	38.7	4	2428.43	3.19	0.50	MFS6L_MOUSE		Major facilitator superfamily domain-containing protein 6-like;		0.85 - 1.00
GTASTRRVTF	EADENENITVVKGIR	N-ter +28.03 Da, K +28.03 Da	28.8	50.4	3	1742.01	0.53	0.10	CHCH3_MOUSE	Q9D9P1_MOUSE	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial;		0.25 - 0.75
FDQTQIQEFK	EAFITVIDQNR	N-ter +34.06 Da	40.8	33.6	2	1225.69	-2.32	0.23	MLRS_MOUSE	F6ULR7_MOUSE	Myosin regulatory light chain 2, skeletal muscle isoform;	Fast skeletal myosin light chain 2;MLC2f;	0.00 - 0.15
DGSASGTTLL	EALDCILPPTPTDKPLR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	36.9	60.0	4	2159.37	-1.79	0.12	EF1A1_MOUSE	D3Y268_MOUSE	Elongation factor 1-alpha 1;	Elongation factor Tu;Eukaryotic elongation factor 1 A-1;	0.00 - 0.15
EGNASGVSLL	EALDTLPTPTPTDKPLR	N-ter +34.06 Da, K +34.06 Da	37.5	56.7	4	2100.38	-4.32	0.00	EF1A2_MOUSE	B72BW3_MOUSE	Elongation factor 1-alpha 2;	Eukaryotic elongation factor 1 A-2;Statin-S1;	0.00 - 0.15
KKQQEVVGL	EANKIDFKELDIAGDEDNR	N-ter +28.03 Da, K +28.03 Da	31.4	77.3	4	2275.31	-0.86	0.20	SH3BG_MOUSE	F7ABS0_MOUSE	SH3 domain-binding glutamic acid-rich protein;		0.15 - 0.25
FEGRRSRRRR	EAPKVVVEEQESR	N-ter +34.06 Da, K +34.06 Da	44.2	45.0	3	1467.89	-0.52	0.07	COAB_MOUSE		Complement C4-B;		0.25 - 0.75

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
GTEAAAATVF	EAVPMSMPPILR	N-ter +28.03 Da	25.1	47.2	3	1367.80	0.53	0.10	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
VRSLTMVEDN	EDDDEGDELLHHHR	N-ter +28.03 Da	41.6	62.9	4	1872.91	2.84	0.70	LMNA_MOUSE		Prelamin-A/C;		0.85 - 1.00
LGTPRLGVQG	EDGLDFPEYDGVDR	N-ter +34.06 Da	37.9	49.2	3	1659.83	-0.32	0.06	CASQ1_MOUSE	E9Q489_MOUSE	Calsequestrin-1;	Calsequestrin, skeletal muscle isoform;	0.25 - 0.75
GTDFITGKKY	EDICPSTHMDVPIKIR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	46.2	61.4	4	2081.13	-1.47	0.33	IF5A1_MOUSE	IF5A2_MOUSE	Eukaryotic translation initiation factor 5A-1;	Eukaryotic initiation factor 5A isoform 1;eIF-4D;	0.15 - 0.25
PKLPGRVAFG	EDIDLPEFDAR	N-ter +28.03 Da	36.5	48.6	3	1447.75	2.11	0.31	CATB_MOUSE		Cathepsin B;	Cathepsin B1;	0.85 - 1.00
GATALLTHGQ	EDIPEVSCIHNGLR	N-ter +34.06 Da, C +57.02 Da	52.6	44.5	3	1671.92	-0.94	0.16	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.15 - 0.25
TLTAVHDAIL	EDLVFPEIVGKIR	N-ter +28.03 Da, K +28.03 Da	48.3	53.0	3	1543.94	1.25	0.24	RS7_MOUSE	F6SVV1_MOUSE	40S ribosomal protein S7;		0.75 - 0.85
RKLVRSMTM	EDNEDDEDGELLHHHR	N-ter +34.06 Da	51.7	63.7	4	2237.07	-2.18	0.60	LMNA_MOUSE		Prelamin-A/C;		0.00 - 0.15
LGTLPARAAH	EDPVEKVIIEGFSR	N-ter +28.03 Da, K +28.03 Da	27.3	53.0	3	1559.90	0.33	0.01	SBSN_MOUSE	E9QP82_MOUSE	Suprabasin;		0.25 - 0.75
LCCLVPSFLA	EDVQETDTSQKQSPASHEIATNLGDFAIISLYR	N-ter +34.06 Da, K +34.06 Da	50.6	50.0	4	3733.03	-2.12	1.57	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	39.8	53.6	4	3369.84	-1.40	0.44	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
LAKYNQLMRI	EEALGDKAVFAGR	N-ter +34.06 Da, K +34.06 Da	21.8	44.4	3	1429.88	-5.06	1.69	ENOB_MOUSE		Beta-enolase;		0.00 - 0.15
IDSHFEARKK	EEEEELIALKER	N-ter +28.03 Da, K +28.03 Da	31.5	50.3	3	1413.84	-1.84	0.26	TNNT3_MOUSE	A2A6J0_MOUSE	Troponin T, fast skeletal muscle;	Fast skeletal muscle troponin T;	0.00 - 0.15
SFYNELRVAP	EEHPTLLEAPLNPKANR	N-ter +28.03 Da, K +28.03 Da	43.0	55.6	4	2085.24	-1.32	0.17	ACT5_MOUSE	ACTA_MOUSE	Actin, alpha skeletal muscle;	Alpha-actin-1;	0.15 - 0.25
TFYNELRVAP	EEHPVLLLEAPLNPKANR	N-ter +28.03 Da, K +28.03 Da	31.8	57.8	4	2083.26	1.58	0.15	ACTB_MOUSE	ACTG_MOUSE	Actin, cytoplasmic 1;	Beta-actin;	0.75 - 0.85
MPCKI	EEIKDFLLTAR	N-ter +28.03 Da, K +28.03 Da	25.6	57.4	3	1389.87	-5.64	0.00	RL38_MOUSE		60S ribosomal protein L38;		0.00 - 0.15
QQQFVEGVRM	EEIVEGCTGALHILAR	N-ter +28.03 Da, C +57.02 Da	30.3	41.3	3	1795.00	0.65	0.08	CTN1_MOUSE	PLAK_MOUSE	Catenin beta-1;	Beta-catenin;	0.25 - 0.75
WWNPQEKTI	EEQLDEEHLESHR	N-ter +28.03 Da	28.6	67.8	4	1677.87	0.12	0.03	AKAP2_MOUSE	A2AP18_MOUSE	A-kinase anchor protein 2;	AKAP expressed in kidney and lung;Protein kinase A-anchoring protein 2;	0.25 - 0.75
PPSVGVADKK	EETQPPVALKKEGIR	N-ter +28.03 Da, K +28.03 Da	17.6	49.0	4	1778.12	-0.34	0.04	PAIRB_MOUSE		Plasminogen activator inhibitor 1 RNA-binding protein;	PAI1 RNA-binding protein 1;SERPINE1 mRNA-binding protein 1;	0.25 - 0.75
ERGNPVIAQW	EEVEDASEEAPLR	N-ter +34.06 Da	47.0	44.6	3	1506.79	3.66	0.55	SRC_MOUSE		Sarcalumenin;		0.85 - 1.00
FRHACVPVDF	EEVHVSSNADEEDIR	N-ter +28.03 Da	67.4	50.7	3	1755.88	-0.12	0.03	IDHG1_MOUSE	Q3TKM5_MOUSE	Isocitrate dehydrogenase [NAD] subunit gamma 1, mitochondrial;	Isocitrate dehydrogenase subunit gamma;NAD(+)-specific ICODH subunit gamma;	0.25 - 0.75
TEEHLRDYF	EEYGKIDTIEITDR	N-ter +28.03 Da, K +28.03 Da	34.4	47.8	3	1850.06	-1.06	0.15	ROA2_MOUSE	F6U106_MOUSE	Heterogeneous nuclear ribonucleoproteins A2/B1;		0.15 - 0.25
EVTDRAYTGR	EFDDLPLAEQR	N-ter +28.03 Da	23.8	62.1	3	1359.75	-0.23	0.01	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
FSMFDQTIQ	EFKEAFTVIDQNR	N-ter +34.06 Da, K +34.06 Da	44.0	48.5	3	1664.00	-0.49	0.13	MLRS_MOUSE	F6ULR7_MOUSE	Myosin regulatory light chain 2, skeletal muscle isoform;	Fast skeletal myosin light chain 2;MLC2f;	0.25 - 0.75
RLSESEGAN	EGATAAPELSALEEAFRR	N-ter +28.03 Da	26.5	52.0	3	1945.09	0.57	0.17	TPPP_MOUSE		Tubulin polymerization-promoting protein;		0.25 - 0.75
RLSESEGAN	EGATAAPELSALEEAFR	N-ter +28.03 Da	35.9	47.8	3	1788.98	1.75	0.58	TPPP_MOUSE		Tubulin polymerization-promoting protein;		0.85 - 1.00
IIRNVKGPVQ	EGDVLTLLESER	N-ter +28.03 Da	42.3	58.3	2	1387.80	1.38	0.13	RS28_MOUSE	D3YVD9_MOUSE	40S ribosomal protein S28;		0.75 - 0.85
SYFPRGLKYR	EGGVESAFHKTTSGATPAAIR	N-ter +28.03 Da, K +28.03 Da	32.3	57.6	4	2142.23	0.75	0.11	Q99L84_MOUSE	D3YZN3_MOUSE			0.25 - 0.75
GVSESQASDS	EGHSDFSEGOAVGAHR	N-ter +28.03 Da	49.6	67.4	4	1710.89	1.36	0.31	F78VV1_MOUSE	FILA_MOUSE			0.75 - 0.85
AGSAIHWREP	EGKEVVDVYVTR	N-ter +28.03 Da, K +28.03 Da	39.3	55.0	3	1535.88	-0.49	0.01	RISC_MOUSE	Q3USP4_MOUSE	Retinoid-inducible serine carboxypeptidase;	Serine carboxypeptidase 1;	0.25 - 0.75
RFMQTFVLAP	EGSVANKFYVHNDIFR	N-ter +28.03 Da, K +28.03 Da	27.6	59.2	4	1951.11	1.01	0.13	G38P1_MOUSE	Q3UR88_MOUSE	Ras GTPase-activating protein-binding protein 1;	Golgi peripheral membrane protein p65;Golgi reassembly-stacking protein of 65 kDa;	0.75 - 0.85
KKAGHPFMWN	EHLGYVLTCPNSLGTGLR	N-ter +28.03 Da, C +57.02 Da	54.0	44.3	3	2014.12	-0.97	0.21	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.15 - 0.25
MNHLLLUKQF	EHLNHQNPNTFESR	N-ter +28.03 Da	25.1	63.6	4	1749.93	1.46	0.45	NUC2_MOUSE		Nucleobindin-2;	DNA-binding protein NEFA;	0.75 - 0.85
FYNELRVAPE	EHPVLLLEAPLNPKANR	N-ter +28.03 Da, K +28.03 Da	25.1	51.8	4	1956.18	-0.18	0.02	ACT5_MOUSE	ACTA_MOUSE	Actin, alpha skeletal muscle;	Alpha-actin-1;	0.25 - 0.75
CLLHEKTPVS	EHVTKCCSGSLVER	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	35.5	53.0	3	1716.92	2.94	0.54	ALBU_MOUSE		Serum albumin;		0.85 - 1.00
RKLPQRQLRV	EIAQDFKTLDR	N-ter +28.03 Da, K +28.03 Da	26.2	54.5	3	1390.82	-0.18	0.02	H31_MOUSE	H32_MOUSE	Histone H3.1;		0.25 - 0.75
FILKARSTVR	EIDPQNDLFTLR	N-ter +28.03 Da	29.0	55.1	3	1487.84	0.60	0.06	DLR1_MOUSE	A2AVR9_MOUSE	Dynein light chain roadblock-type 1;	Dynein light chain 2A, cytoplasmic;	0.25 - 0.75
MGYMAAKKHL	EINPDHPIVETLR	N-ter +28.03 Da	48.3	54.6	3	1559.92	-0.52	0.04	H590B_MOUSE	Q71LX8_MOUSE	Heat shock protein HSP 90-beta;	Heat shock 84 kDa;Tumor-specific transplantation 84 kDa antigen;	0.25 - 0.75
IILFDAHKL	EISDEFSEIAGLR	N-ter +28.03 Da	27.1	55.1	3	1563.86	-1.09	0.14	EHD2_MOUSE	Q8R2X0_MOUSE	EH domain-containing protein 2;		0.15 - 0.25
GEATWSGSEF	EISFPDSPGAQAQADHLPR	N-ter +28.03 Da	54.5	44.4	3	2063.10	0.59	0.13	GORS1_MOUSE		Golgi reassembly-stacking protein 1;		0.25 - 0.75
YPGIADRMQK	EITALAPSTMKIKIAPPPEP	N-ter +28.03 Da, K +28.03 Da	40.5	61.5	4	2262.48	4.85	1.18	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.85 - 1.00
KMGLQLVATI	EKIPFESAFR	N-ter +28.03 Da, K +28.03 Da	34.5	53.3	3	1278.77	0.98	0.08	FACR2_MOUSE		Fatty acyl-CoA reductase 2;	Male sterility domain-containing protein 1;	0.75 - 0.85
NLVKTNCDLY	EKLGEYGFQNALVR	N-ter +28.03 Da, K +28.03 Da	49.2	38.3	3	1792.06	-0.32	0.03	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
LLAVLPTTTA	EKNGIDYSLTVDSR	N-ter +28.03 Da, K +28.03 Da	39.2	61.3	3	1765.03	0.57	0.03	Q9DBK8_MOUSE	Q8C7G9_MOUSE			0.25 - 0.75
KLPSLFLYIM	EKNQLFEVPSALPR	N-ter +28.03 Da, K +28.03 Da	38.4	38.1	3	1664.97	-1.32	0.20	PRELP_MOUSE		Prolargin;	Proline-arginine-rich end leucine-rich repeat protein;	0.15 - 0.25
MEVKVQKSSK	ELEDMMNQLFDLDR	N-ter +28.03 Da, K +28.03 Da	35.4	49.9	3	1705.96	-0.89	0.13	TNNI2_MOUSE	A2A6K0_MOUSE	Troponin I, fast skeletal muscle;	Troponin I, fast-twitch isoform;	0.15 - 0.25
KDKSGFIEED	ELGSILKGFSSDAR	N-ter +28.03 Da, K +28.03 Da	25.4	46.4	3	1534.91	-1.47	0.29	PRVA_MOUSE		Parvalbumin alpha;		0.15 - 0.25

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
FYSNKEIFLR	ELISNASDALDKIR	N-ter +28.03 Da, K +28.03 Da	51.1	46.6	3	1599.96	0.79	0.14	HS90B_MOUSE	ENPL_MOUSE	Heat shock protein HSP 90-beta;	Heat shock 84 kDa;Tumor-specific transplantation 84 kDa antigen;	0.25 - 0.75
LTPKKYEGGR	ELNDFISYLQR	N-ter +28.03 Da	31.4	51.5	3	1424.80	-0.22	0.05	PDIA3_MOUSE		Protein disulfide-isomerase A3;	58 kDa glucose-regulated protein;58 kDa microsomal protein;Disulfide isomerase ER-60;Endoplasmic reticulum resident protein 57;Endoplasmic reticulum resident protein 60;	0.25 - 0.75
ASSSLEKSY	ELPDGQVITIGNER	N-ter +28.03 Da	32.9	46.3	3	1567.89	0.91	0.08	ACTB_MOUSE	ACTA_MOUSE	Actin, cytoplasmic 1;	Beta-actin;	0.25 - 0.75
EGAEPMGYSA	ELSGEILDRNEEKR	N-ter +28.03 Da, K +28.03 Da	27.6	62.0	4	1945.10	-0.97	0.08	EZR1_MOUSE		Ezrin;	Cytovillin;Villin-2;p81;	0.15 - 0.25
NVFGKESKKK	ELVNNLGEIVQKIER	N-ter +28.03 Da, K +28.03 Da	39.0	39.3	3	1873.10	-0.58	0.05	EHD1_MOUSE	F6Y7R7_MOUSE	EH domain-containing protein 1;	PAST homolog 1;	0.25 - 0.75
LGQQLNLL	ENWDTLGTVSQIQER	N-ter +28.03 Da	45.5	48.1	3	1890.00	2.09	0.42	APOA1_MOUSE	Q8BPD5_MOUSE	Apolipoprotein A-I;	Apolipoprotein A1;	0.85 - 1.00
DKLCAIPNLR	ENYGELADCCTKQEPER	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	45.2	40.8	3	2154.02	3.44	0.75	ALBU_MOUSE		Serum albumin;		0.85 - 1.00
FSAGSAIHWR	EPEGKEVWDYVTVR	N-ter +28.03 Da, K +28.03 Da	12.5	51.4	3	1761.98	0.06	0.01	RISC_MOUSE	Q3U5P4_MOUSE	Retinoid-inducible serine carboxypeptidase;	Serine carboxypeptidase 1;	0.25 - 0.75
KDCKEPRKR	EQCCYNCCKPGHLLAR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	25.6	65.0	4	1904.97	-0.36	0.18	CNBP_MOUSE	D3YF6_MOUSE	Cellular nucleic acid-binding protein;	Zinc finger protein 9;	0.25 - 0.75
LLWAAACAQS	EQDFYDFKAVNIR	N-ter +28.03 Da, K +28.03 Da	28.8	52.3	3	1699.95	-0.62	0.11	GPX7_MOUSE	E9PVY3_MOUSE	Glutathione peroxidase 7;		0.25 - 0.75
LIWDNGMVLG	EQEVSDFNEQLSELSTQSSR	N-ter +34.06 Da	61.1	43.6	3	2082.08	2.10	0.48	CLU3_MOUSE	E9Q9B8_MOUSE	Clusterin;	Apolipoprotein J;Clustrin;Sulfated glycoprotein 2;	0.85 - 1.00
KGKSCRTITF	EQFQEALEELAKKR	N-ter +28.03 Da, K +28.03 Da	32.6	66.4	4	1802.11	-0.30	0.07	TPPP_MOUSE		Tubulin polymerization-promoting protein;		0.25 - 0.75
TLFQPSFIGM	ESAGIHETTYNSIMKCDIDIR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	39.2	54.9	4	2508.34	0.77	0.17	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
LQVFRQFVRH	ESEVASSVLVLR	N-ter +28.03 Da	41.4	30.9	2	1345.75	3.98	0.76	SSBP_MOUSE	Q8R2K3_MOUSE	Single-stranded DNA-binding protein, mitochondrial;		0.85 - 1.00
VSEAGPAGAG	ESKCPMLVKKVLDVAVR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	24.5	62.5	4	1846.24	0.65	0.03	TTHY_MOUSE		Transthyretin;	Prealbumin;	0.25 - 0.75
LSIFVSGCFS	ESPTKVQLVGGAAHR	N-ter +28.03 Da, K +28.03 Da	22.2	60.9	4	1533.96	0.16	0.04	CDS1_MOUSE		CDS5 antigen-like;	Apoptosis inhibitor expressed by macrophages;Apoptosis inhibitory 6;CT-2;SP-alpha;	0.25 - 0.75
ADROGRRGVS	ESQASDSEGHSDSEGAQVAAHR	N-ter +28.03 Da	57.0	65.9	4	2415.19	-0.56	0.25	E9Q019_MOUSE	F7BVV1_MOUSE			0.25 - 0.75
GRYDATSQY	ESVMKTEPSVAEYTVR	N-ter +28.03 Da, K +28.03 Da	34.2	48.8	3	1881.05	-0.43	0.07	DNIC3_MOUSE		Dnaj homolog subfamily C member 3;	Interferon-induced, double-stranded RNA-activated protein kinase inhibitor;Protein kinase inhibitor of 58 kDa;	0.25 - 0.75
HAFQGRDMA	ETFDQGAHHAFQGGRR	N-ter +28.03 Da	34.2	61.0	4	1741.90	0.33	0.08	SBSN_MOUSE	E9QP82_MOUSE	Suprabasin;		0.25 - 0.75
GPAGKNGDRG	ETGPAAGPAGPIGAGAR	N-ter +34.06 Da	40.5	41.3	3	1508.88	0.26	0.04	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.25 - 0.75
LPTFSNLNR	ETNLESPLVDTHSKR	N-ter +28.03 Da, K +28.03 Da	19.6	59.8	4	1894.13	0.63	0.05	VIME_MOUSE	E9PZV5_MOUSE	Vimentin;		0.25 - 0.75
RRSGRLLTRW	ETTSIPEAGEGQIR	N-ter +34.06 Da	40.3	44.6	3	1607.89	0.43	0.08	ISCA2_MOUSE		Iron-sulfur cluster assembly 2 homolog, mitochondrial;	HESB-like domain-containing protein 1;	0.25 - 0.75
VQGRSRLVL	EVAQHLGESTVR	N-ter +28.03 Da	34.4	47.8	3	1352.77	0.54	0.03	ATPB_MOUSE		ATP synthase subunit beta, mitochondrial;		0.25 - 0.75
LASLLSGQA	EVEDASEEAPLR	N-ter +28.03 Da	31.7	51.2	3	1371.72	0.71	0.07	SRCB_MOUSE		Sarcalumenin;		0.25 - 0.75
FSRGLSNAER	EVGKALEGINGITQAGR	N-ter +28.03 Da, K +28.03 Da	54.9	36.1	3	1882.10	-1.18	0.16	SBSN_MOUSE	E9QP82_MOUSE	Suprabasin;		0.15 - 0.25
LAPSLWLHRF	EVIDDLNHWHDATKLR	N-ter +28.03 Da, K +28.03 Da	32.0	70.1	4	2017.18	-0.20	0.02	APRV1_MOUSE		Retroviral-like aspartic protease 1;	Skin-specific retroviral-like aspartic protease;TPA-inducible aspartic proteinase-like protein;	0.25 - 0.75
LTKLPGYPVK	EVKCDMEVSCPEGYTCR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	45.1	47.6	3	2347.12	0.99	0.36	GRN_MOUSE	Q3U9N4_MOUSE	Granulins;	PC cell-derived growth factor;Proepithelin;	0.75 - 0.85
GAGFRPKVKR	EKVDCSEYLALSKR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	36.2	60.6	4	1880.12	-0.71	0.07	Q148R4_MOUSE	Q8BM18_MOUSE			0.25 - 0.75
GAGFRPKVKR	EKVDCSEYLALSK	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	33.9	80.1	3	1724.05	-0.32	0.04	Q8BM18_MOUSE	Q148R4_MOUSE			0.25 - 0.75
VLMDFQVKA	EVLDMAENAFDDEYLKCKSR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	61.3	58.4	4	2516.34	-0.43	0.15	NAR3_MOUSE	E9Q1U7_MOUSE	Ecto-ADP-ribosyltransferase 3;	Mono(ADP-ribosyl)transferase 3;NAD(P)(+)-arginine ADP-ribosyltransferase 3;	0.25 - 0.75
HCSPSVGLS	EVQALVAGKPNMTR	N-ter +28.03 Da, K +28.03 Da	26.6	62.6	3	1568.97	-2.47	0.55	BTBD7_MOUSE		BTB/POZ domain-containing protein 7;		0.00 - 0.15
LMAAVIGINS	EVQLQQSGAELVR	N-ter +34.06 Da	31.2	39.4	3	1489.89	-0.74	0.12	HVM02_MOUSE		Ig heavy chain V region 93G7;		0.25 - 0.75
VNNMVFVKY	EYVAAAELVGLIQYITER	N-ter +34.06 Da	22.6	18.5	4	2255.30	-0.36	0.05	PRKC_MOUSE		DNA-dependent protein kinase catalytic subunit;	p460;	0.25 - 0.75
TFQQMWSKQ	EYDEAGPSIVHR	N-ter +28.03 Da	51.6	56.5	3	1399.75	-0.43	0.05	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
ASRVLASRN	FANDATFEIKCDLHR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	32.0	59.0	4	2066.27	1.65	0.27	ODPA_MOUSE		Pyruvate dehydrogenase E1 component subunit alpha, somatic form, mitochondrial;	PDHE1-A type I;	0.85 - 1.00
LLTQPGDWTL	FAPTNDAFKGMTSEER	N-ter +28.03 Da, K +28.03 Da	29.6	52.2	3	1855.97	-0.18	0.04	POSTN_MOUSE		Periostin;	Osteoblast-specific factor 2;	0.25 - 0.75
SLGRDGHFTL	FAPTNEAFKLPK	N-ter +28.03 Da, K +28.03 Da	23.3	50.0	3	1574.92	0.20	0.02	POSTN_MOUSE		Periostin;	Osteoblast-specific factor 2;	0.25 - 0.75
LDYVMAAANL	FAQTYGLTGSQDR	N-ter +28.03 Da	37.0	48.6	3	1470.78	0.26	0.05	UBA1_MOUSE		Ubiquitin-like modifier-activating enzyme 1;	Ubiquitin-activating enzyme E1;Ubiquitin-activating enzyme 1 X;	0.25 - 0.75
GTWKLVSSEN	FDDYMKVGVGFATR	N-ter +28.03 Da, K +28.03 Da	25.8	50.9	3	1789.96	-0.49	0.09	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
EIFDKARVLF	FDELDSIAKAR	N-ter +28.03 Da, K +28.03 Da	19.7	50.0	3	1319.77	1.77	0.29	TERA_MOUSE		Transitional endoplasmic reticulum ATPase;	15S Mg(2+)-ATPase p97 subunit;Valosin-containing protein;	0.85 - 1.00

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
ESEKVKITKV	FDFAEEVVR	N-ter +34.06 Da	25.4	49.3	2	1102.61	0.06	0.01	CFDP1_MOUSE		Craniofacial development protein 1;	27 kDa craniofacial protein;Buccentaur;Protein Cq27;	0.25 - 0.75
MVNPPTVF	FDITADDEPLGR	N-ter +34.06 Da	32.6	44.3	3	1381.76	2.04	0.40	PPIA_MOUSE	E9Q1E3_MOUSE	Peptidyl-prolyl cis-trans isomerase A;	Cyclophilin A;Cyclosporin A-binding protein;Rotamase A;SP18;	0.85 - 1.00
KDGRHCCLKC	FDKFCANTCVDCR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	41.0	48.3	3	1759.90	-3.47	1.16	FHL1_MOUSE	A2AE8_MOUSE	Four and a half LIM domains protein 1;	Kyot;RBP-associated molecule 14-1;Skeletal muscle LIM-protein 1;	0.00 - 0.15
QQQLIDHFL	FDKPVSPLLTAAGMAR	N-ter +28.03 Da, K +28.03 Da	36.2	44.3	3	1729.04	0.71	0.10	KCRU_MOUSE	A2ARP5_MOUSE	Creatine kinase U-type, mitochondrial;	Acidic-type mitochondrial creatine kinase;Ubiquitous mitochondrial creatine kinase;	0.25 - 0.75
SYTSLGFF	FDRDDVALEGVGHFFR	N-ter +28.03 Da	58.0	78.7	4	1907.08	3.09	0.46	FRIL1_MOUSE	FRIL2_MOUSE	Ferritin light chain 1;	Ferritin L subunit 1;	0.85 - 1.00
TEGVKGAKNF	FEAKVQAINVSSR	N-ter +28.03 Da, K +28.03 Da	30.3	45.4	3	1503.91	0.21	0.04	EFHD2_MOUSE	Q8C845_MOUSE	EF-hand domain-containing protein D2;	Swiprosin-1;	0.25 - 0.75
TGAEQVSLT	FEDVAFLTR	N-ter +28.03 Da	29.3	70.4	2	1223.74	4.48	0.73	Z354A_MOUSE	Z354B_MOUSE	Zinc finger protein 354A;	Kidney, ischemia, and developmentally-regulated protein 1;Renal transcription factor Kid-1;Transcription factor 17;	0.85 - 1.00
DTEYNLRDY	FEKYGKIEVEMEDR	N-ter +34.06 Da, K +34.06 Da	28.7	58.7	4	2088.29	-0.86	0.08	ROA3_MOUSE	A2AL12_MOUSE	Heterogeneous nuclear ribonucleoprotein A3;		0.15 - 0.25
GTVSSRIKX	FELKHLSSGDLR	N-ter +28.03 Da, K +28.03 Da	30.6	65.2	4	1569.99	-1.25	0.27	KAD3_MOUSE		GTP:AMP phosphotransferase, mitochondrial;	Adenylate kinase 3;Adenylate kinase 3 alpha-like 1;	0.15 - 0.25
RRSRGFVY	FENVDDAKEAKER	N-ter +34.06 Da, K +34.06 Da	20.6	46.3	4	1652.00	-1.52	0.26	TRA2B_MOUSE	F8WJG3_MOUSE	Transformer-2 protein homolog beta;	Silica-induced gene 41 protein;Splicing factor, arginine/serine-rich 10;Transformer-2 protein homolog B;	0.00 - 0.15
LSCIAMMCNE	FFEGCPDKEPR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	24.3	63.3	3	1436.77	0.51	0.07	S10A4_MOUSE	D3YUT9_MOUSE	Protein S100-A4;	Metastasin;Metastatic cell protein;PEL98;Placental calcium-binding protein;Protein 18A2;Protein Mts1;S100 calcium-binding protein A4;	0.25 - 0.75
EDRQAGP	FGDEKEDAGPQQEAAAR	N-ter +34.06 Da, K +34.06 Da	24.7	67.6	3	1872.06	-3.18	0.29	USBP1_MOUSE		Usher syndrome type-1C protein-binding protein 1;		0.00 - 0.15
GGPKLPGRVA	FGEDIDLPEFDAR	N-ter +28.03 Da	31.0	53.5	3	1651.86	1.29	0.25	CATB_MOUSE		Cathepsin B;	Cathepsin B1;	0.75 - 0.85
DEKLRKR	FGIVTSSAGTGTTEDEAKKR	N-ter +34.06 Da, K +34.06 Da	51.3	52.1	4	2257.38	-0.84	0.16	SARNP_MOUSE		SAP domain-containing ribonucleoprotein;	Nuclear protein Hcc-1;	0.15 - 0.25
SGFLAGFSL	FGLGSEPAAGEAEVSDGGTVDLR	N-ter +28.03 Da	79.6	44.5	3	2332.22	-0.20	0.02	IMPA3_MOUSE		Inositol monophosphatase 3;	Golgi 3-prime phosphoadenosine 5-prime phosphate 3-prime phosphatase;Inositol monophosphatase domain-containing protein 1;Inositol-1(or 4)-monophosphatase 3;Myo-inositol monophosphatase A3;	0.25 - 0.75
EQALEDHSS	FGPISEVVVKDR	N-ter +28.03 Da, K +28.03 Da	36.3	48.8	3	1499.94	0.07	0.01	RBM3_MOUSE	Q8BG13_MOUSE	Putative RNA-binding protein 3;	RNA-binding motif protein 3;	0.25 - 0.75
QYREVAFAAQ	FGSDLAATQQLSR	N-ter +28.03 Da	30.6	59.0	3	1648.94	0.72	0.11	ATPA_MOUSE	D3Z6F5_MOUSE	ATP synthase subunit alpha, mitochondrial;		0.25 - 0.75
TQICPNLVA	FHDSSDLENVPHLR	N-ter +28.03 Da	39.0	66.9	4	1840.01	3.13	0.86	PRELP_MOUSE		Prolargin;	Proline-arginine-rich end leucine-rich repeat protein;	0.85 - 1.00
PVNGSSMQSL	FIEIHSVSAKNR	N-ter +28.03 Da, K +28.03 Da	23.6	65.3	4	1584.97	0.48	0.07	SKT_MOUSE	E9QAU4_MOUSE	Sickle tail protein;	Enhancer trap locus 4;	0.25 - 0.75
AAEGFKGKIL	FIFDSDHTDNQR	N-ter +28.03 Da	45.4	57.4	3	1634.86	2.05	0.35	PDIA1_MOUSE		Protein disulfide-isomerase;	Cellular thyroid hormone-binding protein;Endoplasmic reticulum resident protein 59;Prolyl 4-hydroxylase subunit beta;p55;	0.85 - 1.00
EQLNVIKIL	FIPLSQDLLENLKAEEVAR	N-ter +28.03 Da, K +28.03 Da	25.1	55.7	4	2154.36	3.04	0.81	K0664_MOUSE		Protein KIAA0664;		0.85 - 1.00
SMFDQIQE	FKEAFTVIDQNR	N-ter +28.03 Da, K +28.03 Da	47.3	51.1	3	1522.89	-0.29	0.06	MLRS_MOUSE	F6ULR7_MOUSE	Myosin regulatory light chain 2, skeletal muscle isoform;	Fast skeletal myosin light chain 2;MLC2F;	0.25 - 0.75
VARGKLHLL	FKEETEIPAR	N-ter +28.03 Da, K +28.03 Da	38.1	50.1	3	1274.75	2.56	0.59	PRDBP_MOUSE		Protein kinase C delta-binding protein;	Cavin-3;Serum deprivation response factor-related gene product that binds to C-kinase;	0.85 - 1.00
AQKQLPAL	FKLDNQDFGDHATLKR	N-ter +28.03 Da, K +28.03 Da	20.8	35.0	4	1988.12	-2.64	0.33	A2AP_MOUSE	Q5ND35_MOUSE	Alpha-2-antiplasmin;	Alpha-2-plasmin inhibitor;Serpin F2;	0.00 - 0.15
PEGKTIKQ	FLEELLTQCDR	N-ter +28.03 Da, C +57.02 Da	24.7	87.1	3	1551.90	-0.97	0.08	MLRS_MOUSE		Myosin regulatory light chain 2, skeletal muscle isoform;	Fast skeletal myosin light chain 2;MLC2F;	0.15 - 0.25
HAQLAYCVVQ	FLEKDTLTPVIR	N-ter +28.03 Da, K +28.03 Da	27.3	28.4	3	1717.01	-0.17	0.02	ZASA_MOUSE	F6VYL0_MOUSE	Serine/threonine-protein phosphatase 2A 56 kDa regulatory subunit alpha isoform;	PP2A B subunit isoform B'-alpha;PP2A B subunit isoform B56-alpha;PP2A B subunit isoform PR61-alpha;PP2A B subunit isoform R5-alpha;NEDD8 carrier protein;NEDD8 protein ligase;Ubiquitin-conjugating enzyme E2 M;	0.25 - 0.75
NSIYGLQYL	FLEPNPEDPLNKEAEVLQNNR	N-ter +28.03 Da, K +28.03 Da	31.2	51.7	4	2592.45	2.50	0.33	UBC12_MOUSE	F7CDT0_MOUSE	NEDD8-conjugating enzyme Ubc12;		0.85 - 1.00
LGFGNNLNYM	FLETLALENHGLAR	N-ter +28.03 Da	50.1	47.1	3	1610.95	-0.07	0.01	ITH3_MOUSE	E9PVS1_MOUSE	Inter-alpha-trypsin inhibitor heavy chain H3;		0.25 - 0.75
LAQNERCLHM	FLQDEIHKSYTPSKIR	N-ter +28.03 Da, K +28.03 Da	30.4	58.0	4	2136.31	-0.01	0.00	SNX3_MOUSE	Q78ZM0_MOUSE	Sorting nexin-3;	SDP3 protein;	0.25 - 0.75
FALYKPTVDL	FLQLVDSGKVDPEAR	N-ter +28.03 Da, K +28.03 Da	33.6	46.7	3	1631.96	-0.92	0.09	LPPRC_MOUSE		Leucine-rich PPR motif-containing protein, mitochondrial;	130 kDa leucine-rich protein;	0.15 - 0.25
VFGVCHIFAS	FNDTFVHTDLSGKETICR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	41.0	67.3	4	2294.29	0.15	0.03	RS14_MOUSE	D3YVF4_MOUSE	40S ribosomal protein S14;		0.25 - 0.75
EEFDARWVY	FNKPDIDAWELR	N-ter +34.06 Da, K +34.06 Da	34.3	54.2	3	1570.96	-0.97	0.23	COX5A_MOUSE		Cytochrome c oxidase subunit 5A, mitochondrial;	Cytochrome c oxidase polypeptide Va;Gamma-glutamyl leukotrienase;Gamma-glutamyltransferase-like activity 1;Gamma-glutamyltranspeptidase 5;	0.15 - 0.25
SKGHVEYEPK	FNQEVQKGLQDR	N-ter +28.03 Da, K +28.03 Da	18.5	114.6	4	1516.97	-0.97	0.08	GGT5_MOUSE	Q8C7B4_MOUSE	Gamma-glutamyltransferase 5;		0.15 - 0.25
GDKGDQGLAG	FPGSPGKEGKGSAGTGMGPGSPGR	N-ter +28.03 Da, K +28.03 Da	24.4	23.7	4	2522.32	0.86	0.13	COA1_MOUSE		Collagen alpha-1(V) chain;		0.25 - 0.75
EAASGALSMF	FQGEETENEENLSEKAGLDR	N-ter +28.03 Da, K +28.03 Da	45.0	61.5	4	2593.41	2.27	0.60	A2AIX1_MOUSE	E9QAT4_MOUSE			0.85 - 1.00

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
IILEYQHGA	FQSGQVLSALPR	N-ter +34.06 Da	23.7	43.9	3	1335.83	-0.74	0.09	CBBP2_MOUSE		Carboxypeptidase B2;	Carboxypeptidase R;Carboxypeptidase	0.25 - 0.75
ELNGKLTGMA	FRVPTPNVSVDLTCR	N-ter +28.03 Da, C +57.02 Da	47.4	56.2	3	1887.11	1.57	0.21	G3P_MOUSE	G3PT_MOUSE	Glyceraldheyde-3-phosphate dehydrogenase;	Peptidyl-cysteine S-nitrosylase GAPDH;	0.75 - 0.85
QASDSEGHSD	FSEQAQVAHHR	N-ter +28.03 Da	32.0	52.9	3	1185.65	3.51	0.85	FILA_MOUSE	F7BVV1_MOUSE	Flaggrin;		0.85 - 1.00
VLRPPGGGSN	FSLGFDEPAEQVVR	N-ter +28.03 Da	35.7	48.6	3	1618.88	0.03	0.00	HN1_MOUSE		Hematological and neurological expressed 1 protein;		0.25 - 0.75
QLQDMGLIDL	FSPEKSQLPGVAGGR	N-ter +28.03 Da, K +28.03 Da	24.6	45.1	3	1698.02	0.63	0.14	ANT3_MOUSE		Antithrombin-III;	Serpin C1;	0.25 - 0.75
MIASHMIACL	FTELNQNVQVQVQYLYHMR	N-ter +28.03 Da, K +28.03 Da	50.6	75.6	4	2609.50	1.38	0.22	HKK2_MOUSE		Hexokinase-2;	Hexokinase type II;	0.75 - 0.85
VLLFDINFR	FTQAGSEVALLGR	N-ter +28.03 Da	48.1	42.6	3	1462.84	0.25	0.02	ATPB_MOUSE		ATP synthase subunit beta, mitochondrial;		0.25 - 0.75
PGAHUVKKI	FVGGIKEDTEEHLR	N-ter +34.06 Da, K +34.06 Da	23.8	66.0	4	1834.12	-2.64	0.83	ROA1_MOUSE	ROA2_MOUSE	Heterogeneous nuclear ribonucleoprotein A1;		0.00 - 0.15
RYLSPKYIKM	FVLDEADEMLR	N-ter +28.03 Da	50.7	51.6	3	1451.77	0.61	0.12	IF4A2_MOUSE	IF4A2_MOUSE	Eukaryotic initiation factor 4A-I;	ATP-dependent RNA helicase eIF4A-1;	0.25 - 0.75
RTSTASVPLN	FVPLTNPKEVQEMR	N-ter +28.03 Da, K +28.03 Da	30.1	46.0	3	1857.07	0.04	0.01	ADDA_MOUSE	ESQ1K3_MOUSE	Alpha-adducin;	Erythrocyte adducin subunit alpha;	0.25 - 0.75
LNTSFKHFIF	FVQEFNLIDRR	N-ter +28.03 Da	22.8	52.9	3	1463.87	0.74	0.12	MOL1A_MOUSE	MOL1B_MOUSE	MOB kinase activator 1B;	HDP-1;Helix-destabilizing protein;Single-strand-binding protein;Topoisomerase-inhibitor	0.25 - 0.75
HRDDGLADLL	FVSSGPTNASAFTR	N-ter +28.03 Da	40.2	48.7	3	1597.85	-0.92	0.10	MAP4_MOUSE	E9QPW8_MOUSE	Microtubule-associated protein 4;	suppressed;hnRNP core protein A1;	0.15 - 0.25
GMRSRGRGFQ	FVSSSLPDICVR	N-ter +28.03 Da, C +57.02 Da	24.2	59.4	3	1470.81	-0.38	0.02	CNBP_MOUSE	D3YF6_MOUSE	Cellular nucleic acid-binding protein;	Zinc finger protein 9;	0.25 - 0.75
NFDYHDHAFI	GAEAKSFDQLTPESKER	N-ter +28.03 Da, K +28.03 Da	27.7	61.1	4	2234.24	0.65	0.09	CALL_MOUSE	Q6XU8_MOUSE	Calumenin;	Crocalbin;	0.25 - 0.75
NNWAKGHYTE	GAEVDSVLDVVR	N-ter +28.03 Da	34.1	46.4	3	1398.84	-0.74	0.16	TBB2C_MOUSE	TBB2A_MOUSE	Tubulin beta-4B chain;	Tubulin beta-2C chain;	0.25 - 0.75
NPLKNSGIEH	GAFQGLKLSYIR	N-ter +28.03 Da, K +28.03 Da	28.0	47.2	3	1494.93	0.12	0.00	PGS2_MOUSE		Decorin;	Bone proteoglycan II;PG-S2;PG40;	0.25 - 0.75
LLRGPVVARA	GAGAVGAGPVVR	N-ter +28.03 Da	51.8	33.4	2	1037.63	-1.36	0.14	Q6PE62_MOUSE				0.15 - 0.25
MSVFGKLF	GAGGGKAGKGGPTPQEIQR	N-ter +28.03 Da, K +28.03 Da	33.5	49.9	4	1920.15	2.33	0.66	CHM4B_MOUSE		Charged multivesicular body protein 4b;	Chromatin-modifying protein 4b;	0.85 - 1.00
PPGADKAAEA	GAGSATEFQFR	N-ter +28.03 Da	48.0	50.1	2	1197.64	-0.97	0.08	RS10_MOUSE		40S ribosomal protein S10;		0.15 - 0.25
ATPKQGRML	GAPAEADANEEGVRR	N-ter +34.06 Da	31.5	52.3	3	1632.88	-2.74	0.73	CYT1_MOUSE	A2APX3_MOUSE	Cystatin-C;	Cystatin-3;	0.00 - 0.15
RVAGPQPAQT	GAPQGLSEGLFGR	N-ter +28.03 Da	41.6	49.0	3	1550.85	2.25	0.31	FRL1_MOUSE	Q9CPX4_MOUSE	Ferritin light chain 1;	Ferritin L subunit 1;	0.25 - 0.75
TISLQMGTKN	GASQAQMLAPGTR	N-ter +28.03 Da	49.3	32.4	2	1243.68	0.95	0.10	CNN3_MOUSE		Calponin-3;	Calponin, acidic isoform;	0.75 - 0.85
GTGGVDAAV	GAVFDISNADR	N-ter +34.06 Da	42.8	41.9	2	1197.67	-2.00	0.08	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.00 - 0.15
AYGRSPMVAF	GAVGFDPHPHMR	N-ter +28.03 Da	30.2	54.8	3	1307.72	-0.30	0.02	TLF3_MOUSE	Q3TY99_MOUSE	Transducin-like enhancer protein 3;		0.25 - 0.75
GKSGSAGVSK	GAVSAEQVIAGFNR	N-ter +28.03 Da	39.6	49.3	3	1445.83	0.33	0.02	PFDF_MOUSE	F8WJ30_MOUSE	Prefoldin subunit 2;		0.25 - 0.75
DYKSAHKGFK	GAYDAQTGLSKIFKLGGR	N-ter +34.06 Da, K +34.06 Da	23.1	75.1	4	1983.35	-2.12	0.55	F7A0B0_MOUSE	F6RT34_MOUSE			0.00 - 0.15
SRKRELKEVF	GDDSEISKSSGVKKR	N-ter +28.03 Da, K +28.03 Da	23.3	69.4	4	1833.11	1.78	0.54	PRP3_MOUSE			Pre-mRNA-splicing factor 3;	0.85 - 1.00
RGARINVMNR	GDDTPLHLAASHGHR	N-ter +28.03 Da	21.9	71.6	4	1610.91	-0.07	0.01	ILK_MOUSE	D3YZAS_MOUSE	Integrin-linked protein kinase;		0.25 - 0.75
LASYAVQSKY	GDFNKEVHKSGLAGDKLLPQR	N-ter +34.06 Da, K +34.06 Da	41.1	64.5	4	2607.71	-4.06	0.68	MOES_MOUSE		Moesin;	Membrane-organizing extension spike protein;	0.00 - 0.15
CFSGMSDHRH	GDGSSFSQSTTGHCVHMR	N-ter +28.03 Da, C +57.02 Da	34.0	51.2	4	1947.93	0.66	0.24	HNRH2_MOUSE		Heterogeneous nuclear ribonucleoprotein H2;	Heterogeneous nuclear ribonucleoprotein H';	0.25 - 0.75
CFSGMSDHRH	GDGGSFTQSTTGHCVHMR	N-ter +28.03 Da, C +57.02 Da	48.8	60.8	4	1961.97	0.26	0.07	HNRH1_MOUSE	Q8C2Q7_MOUSE	Heterogeneous nuclear ribonucleoprotein H;		0.25 - 0.75
KSTTIKRRD	GDKLVECVMKGVSTSR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	32.8	52.3	4	1962.17	-0.86	0.08	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;	0.15 - 0.25
EDERKMLTGS	GDPKEEEELVDPLTTR	N-ter +34.06 Da, K +34.06 Da	43.9	47.0	3	2252.28	-0.20	0.04	QCR6_MOUSE		Cytochrome b-c1 complex subunit 6, mitochondrial;		0.25 - 0.75
PGVPVAGKGN	GDRGETGPAGPAGPIGAPGAR	N-ter +28.03 Da	68.3	39.9	3	1888.03	-2.00	0.40	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.00 - 0.15
LSSANPVRRM	GDSASKVISAEALPR	N-ter +28.03 Da, K +28.03 Da	66.1	45.4	3	1742.00	-0.30	0.03	MSRA_MOUSE		Mitochondrial peptide methionine sulfoxide reductase;	Peptide-methionine (S)-S-oxide reductase;Protein-methionine-S-oxide reductase;	0.25 - 0.75
CLSGMYDRHY	GDSEFTVQSTTGHCVHMR	N-ter +28.03 Da, C +57.02 Da	40.0	61.8	4	2076.04	1.04	0.37	HNRPF_MOUSE		Heterogeneous nuclear ribonucleoprotein F;		0.75 - 0.85
DNLNKGSKVK	GDVDSIGPKLEGDIKVR	N-ter +28.03 Da, K +28.03 Da	26.1	56.7	4	1978.22	-0.67	0.13	E9Q616_MOUSE				0.25 - 0.75
SLTKYKTLI	GDVPPVADPTVFNVTTR	N-ter +28.03 Da	57.1	46.6	3	1863.10	-0.49	0.13	GDIR2_MOUSE		Rho GDP-dissociation inhibitor 2;	D4;Rho-GDI beta;	0.25 - 0.75
PGPAGASGDR	GEAGAAGPSGAPGR	N-ter +28.03 Da	45.4	48.6	3	1278.69	4.45	1.66	CO1A2_MOUSE	E9Q6U9_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.85 - 1.00
KEAFLFDTR	GECKITLSQVGDVLR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	48.4	31.3	3	1742.06	0.77	0.10	MYL1_MOUSE	E9PWG4_MOUSE	Myosin light chain 1/3, skeletal muscle isoform;	Myosin light chain alkali 1/2;	0.25 - 0.75
PPDAAVECHR	GECDQSEGLVFFQGNR	N-ter +28.03 Da, C +57.02 Da	44.1	44.2	3	1754.88	1.49	0.20	HEMOM_MOUSE		Hemopexin;		0.75 - 0.85
PKPLPGRVAF	GEDIDLPEPFDAR	N-ter +28.03 Da	30.8	51.0	3	1504.78	0.32	0.03	CATB_MOUSE		Cathepsin B;	Cathepsin B1;	0.25 - 0.75
PDGRRRRRR	GEEGHDPKEPEQLR	N-ter +28.03 Da, K +28.03 Da	17.4	69.1	4	1675.93	-1.43	0.39	CATB_MOUSE	A2AL12_MOUSE	Heterogeneous nuclear ribonucleoprotein A3;		0.15 - 0.25
AGRFBVNLIC	GEEQDAAALHFNPR	N-ter +34.06 Da	72.5	55.7	3	1644.90	0.26	0.06	LEG7_MOUSE	Q9CR81_MOUSE	Galectin-7;		0.25 - 0.75
GGSGNSTGF	GEHGSSHPLPSSGQNESSGQSSR	N-ter +34.06 Da	17.6	55.3	4	2516.27	-2.64	0.99	FILA2_MOUSE	EQPZ3_MOUSE	Filaggrin-2;	Intermediate filament-associated protein;	0.00 - 0.15
STECKRTRYS	GEHMDLTTCPLAAGQOQEKLR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	36.4	56.8	4	2367.30	3.36	0.33	Q9D1B1_MOUSE				0.85 - 1.00
DLNFKGPKLK	GEIDASVPMEADLR	N-ter +34.06 Da	36.5	57.3	3	1664.91	-0.42	0.06	E9Q616_MOUSE				0.25 - 0.75
EKIREYFGQF	GEIEAIELPDPLKLNKR	N-ter +34.06 Da, K +34.06 Da	23.2	41.6	4	2036.36	-3.64	0.91	ROAA_MOUSE	Q8DXR6_MOUSE	Heterogeneous nuclear ribonucleoprotein A/B;	CarG-binding factor-A;	0.00 - 0.15
MSDN	GELEDPPAPVPR	N-ter +28.03 Da, K +28.03 Da	32.2	49.2	3	1459.88	0.74	0.10	PAK2_MOUSE		Serine/threonine-protein kinase PAK 2;	Gamma-PAK;p21-activated kinase 2;	0.25 - 0.75
ACGSVMTSNP	GESSFDLADRLDPVEKIDR	N-ter +34.06 Da, K +34.06 Da	34.4	65.5	4	2229.34	0.19	0.05	SODE_MOUSE		Extracellular superoxide dismutase [Cu-Zn];		0.25 - 0.75
ACGSVMTSNP	GESSFDLADR	N-ter +28.03 Da	47.5	44.1	2	1123.56	-0.71	0.05	SODE_MOUSE		Extracellular superoxide dismutase [Cu-Zn];		0.25 - 0.75

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
DCTKVKYRC	GETGHVAINCKTSEVNCYR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	54.4	64.2	4	2337.23	0.35	0.15	CNBP_MOUSE		Cellular nucleic acid-binding protein;	Zinc finger protein 9;	0.25 - 0.75
VGPAGKNGDR	GETGPAGPAGPIGAPGAR	N-ter +28.03 Da	63.7	42.2	3	1559.87	1.76	0.26	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.85 - 1.00
NVVKTGRVML	GETNPADSKPGTIR	N-ter +28.03 Da, K +28.03 Da	38.1	52.8	3	1497.86	0.37	0.11	NDKA_MOUSE	NDK8_MOUSE	Nucleoside diphosphate kinase A;	Tumor metastatic process-associated protein;nm23-M1;	0.25 - 0.75
KGVVPLAGTN	GETTQGLDGLSER	N-ter +28.03 Da	37.8	42.1	3	1490.78	-0.97	0.17	ALDOA_MOUSE	Q9CPQ9_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.15 - 0.25
KDLKDYFTKF	GEVVDCTIKMDPNTGR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	29.3	52.3	3	1859.05	-1.94	0.37	ROAA_MOUSE	Q80XR6_MOUSE	Heterogeneous nuclear ribonucleoprotein A/B;	CarG-binding factor-A;	0.00 - 0.15
KDLTEVLSRF	GEVVDCTIKDPVTGR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	37.1	39.3	3	1814.06	-2.32	0.46	HNRDL_MOUSE	F6VQH5_MOUSE	Heterogeneous nuclear ribonucleoprotein D-like;	JKT41-binding protein;	0.00 - 0.15
KDLKDYFSKF	GEVVDCTIKLDPITGR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	41.5	43.9	3	1840.12	-1.64	0.15	HNRPD_MOUSE	E9Q5B6_MOUSE	Heterogeneous nuclear ribonucleoprotein D0;	AU-rich element RNA-binding protein 1;	0.00 - 0.15
LIKVDNKKL	GEWVGLCKIDR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	31.1	64.9	3	1387.82	1.90	0.31	RS12_MOUSE	D3Z6B6_MOUSE	40S ribosomal protein S12;		0.85 - 1.00
KHCSQVDSVR	GFGKGFVQMDR	N-ter +28.03 Da, K +28.03 Da	26.6	50.4	3	1353.76	0.04	0.01	SRC8_MOUSE	Q921L6_MOUSE	Src substrate cactin;		0.25 - 0.75
CDLYEKLGEY	GFQNALIVR	N-ter +28.03 Da	39.9	31.0	2	1044.64	-2.00	0.24	ALBU_MOUSE		Serum albumin;		0.00 - 0.15
DPGYPRNISE	GFSGIPDNVDAAFALPAHR	N-ter +34.06 Da	24.2	91.8	4	1988.22	-6.64	0.00	VTNC_MOUSE		Vitronectin;	S-protein;Serum-spreading factor;	0.00 - 0.15
KEEFEKNKKG	GFSVVAADTPELQR	N-ter +28.03 Da	25.7	50.5	3	1445.82	0.88	0.10	LASP1_MOUSE	A2A6G6_MOUSE	LIM and SH3 domain protein 1;	Metastatic lymph node gene 50 protein;	0.25 - 0.75
KVLEVPALSL	GGAISGAHLKEASGELR	N-ter +28.03 Da, K +28.03 Da	24.5	61.4	4	1837.08	-1.25	0.12	SYNEM_MOUSE	F6VN34_MOUSE	Synemin;	Desmuslin;	0.15 - 0.25
KTDLNDPNLQ	GGDDLDPNVYLSR	N-ter +34.06 Da	40.8	49.2	3	1540.83	-1.64	0.10	KCRM_MOUSE	KCRB_MOUSE	Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.00 - 0.15
GGNFGFGDSR	GGGGNFGPGGPNFR	N-ter +28.03 Da	47.7	69.3	3	1404.75	-0.79	0.08	ROA2_MOUSE	F6U106_MOUSE	Heterogeneous nuclear ribonucleoproteins A2/B1;		0.25 - 0.75
MN	GGGKAKEKTPSEANLQEEVVR	N-ter +28.03 Da, K +28.03 Da	42.2	67.5	4	2455.38	2.26	0.60	RBPMS_MOUSE	Q9CPUS_MOUSE	RNA-binding protein with multiple splicing;	Heart and RRM expressed sequence;	0.85 - 1.00
SNKAAWGGKI	GGHGAEYGAELER	N-ter +34.06 Da	56.9	52.5	3	1449.78	-1.74	0.17	HBA_MOUSE	Q91V88_MOUSE	Hemoglobin subunit alpha;	Alpha-globin;Hemoglobin alpha chain;	0.00 - 0.15
AHLIVKIFV	GGIKEDTEEHLR	N-ter +34.06 Da, K +34.06 Da	19.4	68.7	4	1587.97	-0.58	0.15	ROA1_MOUSE	ROA2_MOUSE	Heterogeneous nuclear ribonucleoprotein A1;	HDP-1;Helix-destabilizing protein;Single-strand-binding protein;Topoisomerase-inhibitor suppressed;hnRNP core protein A1;	0.25 - 0.75
VQMGAVDLLG	GGDLSLIGDSNFGAPASVAAPAPAR	N-ter +28.03 Da	60.8	36.0	3	2496.35	0.14	0.05	AP1B1_MOUSE	Q5SVG5_MOUSE	AP-1 complex subunit beta-1;	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;	0.25 - 0.75
GGGTAMRIL	GGVISAIEAAQYNPEPPPPR	N-ter +28.03 Da	52.7	51.4	4	2248.26	1.51	0.13	CPNS1_MOUSE	D3YW48_MOUSE	Calpain small subunit 1;	Calcium-activated neutral proteinase small subunit;Calcium-dependent protease small subunit;Calcium-dependent protease small subunit 1;Calpain regulatory subunit;	0.75 - 0.85
PQQQMTSSY	GGYKEPAAPVSIQR	N-ter +28.03 Da, K +28.03 Da	55.3	42.3	3	1527.91	0.81	0.22	LASP1_MOUSE	A2A6H0_MOUSE	LIM and SH3 domain protein 1;	Metastatic lymph node gene 50 protein;	0.25 - 0.75
TFGLGSKSK	GHYEVTGSDEAGLQGGVSLASKKSR	N-ter +28.03 Da, K +28.03 Da	48.4	57.9	4	2974.71	0.83	0.37	E9Q1H8_MOUSE	E9Q616_MOUSE			0.25 - 0.75
PLAKLAAEK	GIDLTVKGTGPEGR	N-ter +28.03 Da, K +28.03 Da	23.4	47.0	3	1582.94	0.72	0.08	ODP2_MOUSE		Dihydrodipolyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;	Dihydrodipolamide acetyltransferase component of pyruvate dehydrogenase complex;Pyruvate dehydrogenase complex component E2;	0.25 - 0.75
IAHRIVAPGK	GILAADSTGSIAKR	N-ter +34.06 Da, K +34.06 Da	41.3	41.8	3	1555.99	-0.17	0.02	ALDOA_MOUSE	A6ZI44_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.25 - 0.75
NIKRNDFQLI	GIQDGYLSLLQDSGEVR	N-ter +28.03 Da	54.2	48.9	3	1877.04	-0.18	0.07	IF5A1_MOUSE		Eukaryotic translation initiation factor 5A-1;	Eukaryotic initiation factor 5A isoform 1;eIF-4D;	0.25 - 0.75
LSVPCILGQN	GISDVKVLTPEEAR	N-ter +34.06 Da, K +34.06 Da	60.8	44.0	3	1910.18	-0.84	0.11	LDHA_MOUSE		L-lactate dehydrogenase A chain;	LDH muscle subunit;	0.15 - 0.25
MD	GIVPDIAGVTKR	N-ter +28.03 Da, K +28.03 Da	42.9	51.0	3	1280.85	1.35	0.16	PTBP1_MOUSE	Q922I7_MOUSE	Poly(pyrimidine tract-binding protein 1);	Heterogeneous nuclear ribonucleoprotein I;	0.75 - 0.85
ARYASICQQN	GIVRIVEPELPGDHDHLKR	N-ter +34.06 Da, K +34.06 Da	47.9	54.3	4	2279.44	-0.79	0.16	ALDOA_MOUSE	ALDOC_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.25 - 0.75
EKLKRRKEEF	GIVTSSAGTGTEDTEAKKR	N-ter +28.03 Da, K +28.03 Da	40.8	59.6	4	2092.23	-1.00	0.28	SARNP_MOUSE		SAP domain-containing ribonucleoprotein;	Nuclear protein Hcc-1;	0.15 - 0.25
TVLSRAIAEL	GIVPAVDPLDTSR	N-ter +28.03 Da	41.0	45.6	3	1517.84	0.97	0.11	ATPB_MOUSE		ATP synthase subunit beta, mitochondrial;		0.75 - 0.85
SFYQDHEAFL	GKEDSKTFDQLSPDESKER	N-ter +28.03 Da, K +28.03 Da	30.8	63.2	4	2307.31	-0.18	0.04	RCN1_MOUSE		Reticulocalbin-1;		0.25 - 0.75
RWKTMSAKEK	GKFEDMAKADKAR	N-ter +28.03 Da, K +28.03 Da	25.4	70.0	4	1577.97	1.04	0.21	HMG81_MOUSE	D3YVC6_MOUSE	High mobility group protein B1;	High mobility group protein 1;	0.75 - 0.85
HHLRDYFEY	GKIDTIEIHDR	N-ter +28.03 Da, K +28.03 Da	34.4	50.4	3	1428.89	-1.60	0.19	ROA2_MOUSE	F6U106_MOUSE	Heterogeneous nuclear ribonucleoproteins A2/B1;		0.00 - 0.15
YNLRDYFEKY	GKIEFIEVMEDR	N-ter +28.03 Da, K +28.03 Da	37.6	50.5	3	1474.84	-1.36	0.14	ROA3_MOUSE	A2AL12_MOUSE	Heterogeneous nuclear ribonucleoprotein A3;		0.15 - 0.25
EDKSNIAKAW	GKIGGHGAYGAELER	N-ter +34.06 Da, K +34.06 Da	27.4	55.9	4	1782.07	-3.18	0.58	HBA_MOUSE	Q91V88_MOUSE	Hemoglobin subunit alpha;	Alpha-globin;Hemoglobin alpha chain;	0.00 - 0.15
KAENGLVIN	GKPIPIFQER	N-ter +34.06 Da, K +34.06 Da	29.6	46.1	3	1255.85	-1.79	0.19	G3P_MOUSE	F8WJL5_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase;	Peptidyl-cysteine S-nitrosylase GAPDH;	0.00 - 0.15
SWLDGKHVVF	GKVLGMDVVR	N-ter +34.06 Da, K +34.06 Da	34.8	50.4	3	1269.84	-0.94	0.05	PPIB_MOUSE		Peptidyl-prolyl cis-trans isomerase B;	CYP-51;Cyclophilin B;Rotamase B;5-cyclophilin;	0.15 - 0.25
QDKRKQISVR	GLAGVENVSELKKNFNR	N-ter +28.03 Da, K +28.03 Da	37.3	61.3	4	1958.21	-2.47	0.28	PYGM_MOUSE	E9PUM3_MOUSE	Glycogen phosphorylase, muscle form;	Myophosphorylase;	0.00 - 0.15
FSKYLALNGR	GLDVKQAFNPEGEFQR	N-ter +28.03 Da, K +28.03 Da	34.7	51.9	3	1890.06	-1.22	0.17	MYOTI_MOUSE		Myotilin;	Myofibrillar titin-like Ig domains protein;Titin immunoglobulin domain protein;	0.15 - 0.25
KTFSEHLSDF	GLESTTGEVPPVAIR	N-ter +28.03 Da	42.7	42.3	3	1554.93	-0.81	0.07	PDIA3_MOUSE		Protein disulfide-isomerase A3;	58 kDa glucose-regulated protein;58 kDa microsomal protein;Disulfide isomerase ER-60;Endoplasmic reticulum resident protein 57;Endoplasmic reticulum resident protein 60;	0.15 - 0.25

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
PWINTPKKQG	GLGPMNIPUSDPKR	N-ter +28.03 Da, K +28.03 Da	39.7	58.0	3	1663.05	-0.30	0.06	PRDX1_MOUSE	B1AXW6_MOUSE	Peroxiredoxin-1;	Macrophage 23 kDa stress protein;Osteoblast-specific factor 3;Thioredoxin peroxidase 2;	0.25 - 0.75
MFGGLSSWL	GLKPPGAAAEIEEPPSR	N-ter +28.03 Da, K +28.03 Da	49.7	46.4	3	1847.03	1.46	0.24	SYAP1_MOUSE		Synapse-associated protein 1;	Thioredoxin-dependent peroxide reductase 2;	0.75 - 0.85
YLECSALTQR	GLKTVFDEAIR	N-ter +28.03 Da, K +28.03 Da	34.5	55.1	3	1303.82	-0.04	0.01	RAC1_MOUSE	RAC2_MOUSE	Ras-related G3 botulinum toxin substrate 1;	p21-Rac1;	0.25 - 0.75
M	GLLSQGSPLSWEETQR	N-ter +28.03 Da	44.6	47.2	3	1815.00	-0.03	0.00	GS11_MOUSE		Glutamate-cysteine ligase catalytic subunit;	GCS heavy chain;Gamma-ECS;Gamma-glutamylcysteine synthetase;	0.25 - 0.75
QPRGSLRSVR	GLSAPSCPLDDKTEASAR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	41.3	41.1	3	1987.05	3.29	0.70	PLIN1_MOUSE		Perilipin-1;	Lipid droplet-associated protein;Perilipin A;	0.85 - 1.00
LSLPCILNAR	GLTSVINQKDKDEVAQLR	N-ter +28.03 Da, K +28.03 Da	26.6	51.8	4	2210.38	0.66	0.09	LDHB_MOUSE		L-lactate dehydrogenase B chain;	LDH heart subunit;	0.25 - 0.75
KAGYTDQVVI	GMDVAASEFYR	N-ter +34.06 Da	49.1	43.3	2	1278.67	-4.64	1.16	ENO1_MOUSE	ENO2_MOUSE	Alpha-enolase;	2-phospho-D-glycerate hydro-lyase;Enolase 1;Non-neural enolase;	0.00 - 0.15
RAVHVWYVGE	GMEEGEFSEAR	N-ter +28.03 Da	38.1	33.8	2	1268.58	0.42	0.09	TBA1A_MOUSE	TBA1B_MOUSE	Tubulin alpha-1A chain;	Alpha-tubulin 1;Alpha-tubulin isotype M-alpha-1;Tubulin alpha-1 chain;	0.25 - 0.75
PETLFQPSFI	GMESAGIHETTYNSIMKCDIDIR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	39.9	69.9	4	2696.45	4.60	1.55	ACT5_MOUSE	ACTA_MOUSE	Actin, alpha skeletal muscle;	Alpha-actin-1;	0.85 - 1.00
GRPRHQVMVM	GMGQKDSYVGEAQSQR	N-ter +34.06 Da, K +34.06 Da	37.7	55.4	4	1957.15	1.01	0.32	ACT5_MOUSE	ACTA_MOUSE	Actin, alpha skeletal muscle;	Alpha-actin-1;	0.75 - 0.85
ANRIVLDFRR	GNDVAFHFNPR	N-ter +28.03 Da	37.7	81.2	3	1300.74	0.51	0.10	LEG3_MOUSE	Q8C253_MOUSE	Galectin-3;	35 kDa lectin;Carbohydrate-binding protein 35;Galactose-specific lectin 3;IgE-binding protein;L-34 galactoside-binding lectin;Laminin-binding protein;Lectin L-29;Mac-2 antigen;	0.25 - 0.75
IFAREILDSR	GNPTVEVDLHTAKGR	N-ter +28.03 Da, K +28.03 Da	27.2	60.4	4	1648.99	0.06	0.01	ENO2_MOUSE	Q5SX59_MOUSE	Beta-enolase;	2-phospho-D-glycerate hydro-lyase;Enolase 3;Muscle-specific enolase;Skeletal muscle enolase;	0.25 - 0.75
LAGLVFVSEA	GPAGAGESKCLPMVKLVDAVR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	25.1	53.0	4	2256.44	0.38	0.02	TTHY_MOUSE		Transthyretin;	Prealbumin;	0.25 - 0.75
IGIPGRPGPQ	GPPGAGEKGLPGEKGPQGPAGR	N-ter +28.03 Da, K +28.03 Da	30.2	35.1	3	2194.26	1.31	0.19	COSA1_MOUSE		Collagen alpha-1(V) chain;		0.75 - 0.85
NPGIGTQGR	GPPGAPGSPGSRPGSPGPPGSPGR	N-ter +34.06 Da	25.3	60.7	4	2339.32	-3.06	0.51	COE1_MOUSE	B7ZNH7_MOUSE	Collagen alpha-1(XIV) chain;		0.00 - 0.15
QDHPSSMGVY	GQESGGFSGPGENR	N-ter +34.06 Da	33.4	48.5	3	1411.72	-2.47	0.28	EWS_MOUSE	Q5SU8_MOUSE	RNA-binding protein EWS;		0.00 - 0.15
ATEEKIREVF	GQFGEIEAELPIDKLNKR	N-ter +34.06 Da, K +34.06 Da	42.7	56.9	4	2368.56	-1.94	0.45	ROAA_MOUSE	Q8XR6_MOUSE	Heterogeneous nuclear ribonucleoprotein A/B;	CarG-binding factor-A;	0.00 - 0.15
PRHQVMVMGM	GQKDSYVGEAQSQR	N-ter +28.03 Da, K +28.03 Da	23.4	62.7	4	1750.99	-0.79	0.20	ACT5_MOUSE	ACTA_MOUSE	Actin, alpha skeletal muscle;	Alpha-actin-1;	0.25 - 0.75
AMDGTGLVLR	GQKVLDSGAPIKVPGETLGR	N-ter +28.03 Da, K +28.03 Da	54.7	63.0	4	2315.50	-1.12	0.20	ATP8_MOUSE		ATP synthase subunit beta, mitochondrial;		0.15 - 0.25
MYIFVHWQF	GLLDQHPIDGYSHTLAPLR	N-ter +28.03 Da	48.7	66.7	4	2387.38	0.75	0.20	SPRC_MOUSE	Q5NCU4_MOUSE	SPARC;	Basement-membrane protein 40;Osteonectin;Secreted protein acidic and rich in cysteine;	0.25 - 0.75
ARGDLGPF5R	GQMQRPFEDASALR	N-ter +28.03 Da, K +28.03 Da	42.7	49.1	3	1779.99	-0.22	0.12	PIN1_MOUSE		Peptidyl-prolyl cis-trans isomerase NIMA-interacting 1;	Peptidyl-prolyl cis-trans isomerase Pin1;	0.25 - 0.75
GGTDIISCFM	GQNSIPVVKGEIQAR	N-ter +28.03 Da, K +28.03 Da	32.2	43.4	3	1802.05	0.41	0.08	AACS_MOUSE		Acetoacetyl-CoA synthetase;		0.25 - 0.75
FQLRSICYLL	GQPEPLAPGTTLPADR	N-ter +28.03 Da	42.2	37.8	3	1743.98	0.52	0.05	RN123_MOUSE	Q05CH9_MOUSE	E3 ubiquitin-protein ligase RN123;	Kip1 ubiquitination-promoting complex protein 1;RING finger protein 123;	0.25 - 0.75
VSKQSRITN	GQPQQTGAASGGYIKR	N-ter +28.03 Da, K +28.03 Da	36.6	49.7	3	1775.02	0.16	0.02	SNP23_MOUSE	Q9D3L3_MOUSE	Synaptosomal-associated protein 23;	Syndet;Vesicle-membrane fusion protein SNAP-23;	0.25 - 0.75
HSLRTAAVLQ	GQVVQFKLSDIGEGIR	N-ter +28.03 Da, K +28.03 Da	39.2	37.4	3	1801.08	0.91	0.13	ODB2_MOUSE		Lipoamide acyltransferase component of branched-chain alpha-keto acid dehydrogenase complex, mitochondrial;	Regulator of ubiquitous kinase;SH3-containing, expressed in tumorigenic astrocytes;	0.25 - 0.75
EGPVGLGID	GRPGIGPAGPR	N-ter +34.06 Da	33.4	47.3	3	1164.75	-2.47	0.41	CO1A2_MOUSE	E9Q6U9_MOUSE	Collagen alpha-2(I) chain;	Alpha-cardiac actin;	0.00 - 0.15
RGDSPKIDLA	GSALSGLDKLDSLR	N-ter +34.06 Da, K +34.06 Da	29.5	57.8	3	1614.02	0.21	0.04	SH3K1_MOUSE	B0R0Y8_MOUSE	SH3 domain-containing kinase-binding protein 1;		0.25 - 0.75
YREVAFAQF	GSDLDAATQQLSLR	N-ter +28.03 Da	43.6	48.5	3	1501.85	-0.58	0.07	ATPA_MOUSE	D3Z6F5_MOUSE	ATP synthase subunit alpha, mitochondrial;		0.25 - 0.75
AQAAVASHNM	GSDSLYYFR	N-ter +28.03 Da	33.1	50.1	2	1134.59	-1.43	0.16	Q9D1B1_MOUSE				0.15 - 0.25
DYSQQGHVSS	GSEVTCQCCDLCNER	N-ter +28.03 Da, C +57.02 Da	46.8	55.3	3	1983.92	2.36	0.81	LY6D_MOUSE		Lymphocyte antigen 6D;	Thymocyte B-cell antigen;	0.85 - 1.00
EETALVCDN	GSGLVKAGFAGDDAPR	N-ter +28.03 Da, K +28.03 Da	50.7	47.0	3	1572.90	-0.12	0.03	ACTC_MOUSE	ACTS_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
HPTSPRRPPG	GSIIITVPKEIR	N-ter +28.03 Da, K +28.03 Da	52.1	37.4	3	1430.90	0.86	0.10	MAZ2_MOUSE		Epididymis-specific alpha-mannosidase;	Mannosidase alpha class 2B member 2;	0.25 - 0.75
GGRPAMEPGN	GSLDLGDAAGR	N-ter +28.03 Da	59.7	47.6	2	1115.61	2.65	0.18	HNRPU_MOUSE		Heterogeneous nuclear ribonucleoprotein U;	Scaffold attachment factor A;	0.85 - 1.00
DYLGRAGSPR	GSPLAEGPQAFFPER	N-ter +28.03 Da	34.0	52.9	3	1629.90	-2.00	0.24	IASRP_MOUSE		RelA-associated inhibitor;	Inhibitor of ASPP protein;Nf-kB-interacting protein 1;PPP1R13B-like protein;	0.00 - 0.15
M	GSSQSVEIPGGTEGYHVL	N-ter +28.03 Da	59.7	44.8	3	2057.11	0.12	0.02	GORS2_MOUSE	A2AT8_MOUSE	Golgi reassembly-stacking protein 2;	Golgi reassembly-stacking protein of 55 kDa;	0.25 - 0.75
GQSSSANRRA	GSSSGSGVQASAGGLAADASR	N-ter +28.03 Da	79.3	40.0	3	1876.96	1.11	0.16	FILA_MOUSE	F7BVV1_MOUSE	Filaggrin;		0.75 - 0.85
EFLRELSFGR	GSTAPVGGSGFPITTPR	N-ter +28.03 Da	39.9	48.0	3	1628.93	0.14	0.01	PDI6_MOUSE	Q3TML0_MOUSE	Protein disulfide-isomerase A6;	Thioredoxin domain-containing protein 7;	0.25 - 0.75
HGPPMDQYL	GSTPVGSGVYR	N-ter +28.03 Da	39.3	40.2	2	1106.62	0.25	0.02	SF01_MOUSE	Q3UI45_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
VRNIKSMWEK	GVSFASAPASGTPNKETAGLKVGVSSR	N-ter +28.03 Da, K +28.03 Da	54.9	57.8	4	2674.58	2.08	0.61	Q8VCQ8_MOUSE	E9Q0M9_MOUSE			0.85 - 1.00

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
GDHSTPPSAY ILTRLRLQKR	GSVKPYTNFDAER GTGGVDTAAVAVFDISNADR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	47.5 71.0	52.8 45.8	3 3	1538.85 2020.08	-0.09 1.75	0.02 0.40	ANXA2_MOUSE KCRM_MOUSE	BOV2N7_MOUSE	Annexin A2; Creatine kinase M-type;	Annexin II;Annexin-2;Calpactin I heavy chain;Calpactin-1 heavy chain;Chromobindin-8;Lipocortin II;Placental anticoagulant protein IV;Protein I;p36; Creatine kinase M chain;M-CK;	0.25 - 0.75 0.85 - 1.00
VEAARNLGRV SVCVHLRNL	GTKCCTLPEDQR GTLDPSSLDETAYER	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da N-ter +34.06 Da	23.3 40.1	87.9 51.2	3 3	1519.85 1800.95	1.86 -0.14	0.34 0.02	ALBU_MOUSE FRDA_MOUSE	E9Q2P9_MOUSE	Serum albumin; Frataxin, mitochondrial;		0.85 - 1.00 0.25 - 0.75
RKNKMASNIF TIDCDITLM QRRSISRFL	GTPEENPPSWAKSAGSKSSGGR GTPSGTAEPYDGTAKAR GTPSPAIVTPSPPEPAPALEAPAR	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	33.5 47.7 46.9	56.8 49.5 47.1	4 3 3	2288.35 1662.90 2340.31	0.07 0.23 -0.71	0.01 0.08 0.06	HN1_MOUSE BSDC1_MOUSE PARF_MOUSE		Hematological and neurological expressed 1 protein; BSD domain-containing protein 1; Putative GTP-binding protein Parf;		0.25 - 0.75 0.25 - 0.75 0.25 - 0.75
AALHKAIMVK LDHGRTLREQ	GVDEATHIDILTKR GVEEHETLLLR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da	54.3 25.3	49.6 60.3	3 3	1599.00 1328.83	0.90 -0.74	0.38 0.04	ANXA1_MOUSE TLN1_MOUSE	E9QA30_MOUSE A2AIM2_MOUSE	Annexin A1; Talin-1;	Annexin I;Annexin-1;Calpactin II;Calpactin-2;Chromobindin-9;Lipocortin I;Phospholipase A2 inhibitory protein;p35;	0.25 - 0.75 0.25 - 0.75
SGNRLDGKKK	GVPEPSPKPGDIKR	N-ter +28.03 Da, K +28.03 Da	23.5	51.8	4	1760.11	0.03	0.00	UFD1_MOUSE		Ubiquitin fusion degradation protein 1 homolog;		0.25 - 0.75
ADCAVLIVAA AVPVFDLIL	GVGEFFAGISKNGQTR GVGPDGHTCSLFPDHPHLLQER	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, C +57.02 Da	26.4 46.3	52.7 65.6	3 4	1717.03 2359.29	-1.25 3.11	0.12 0.31	EF1A1_MOUSE 6PGL_MOUSE	EF1A2_MOUSE Q8CBG6_MOUSE	Elongation factor 1-alpha 1; Elongation factor 1-alpha 1;	Elongation factor Tu;Eukaryotic elongation factor 1 A-1;	0.15 - 0.25 0.85 - 1.00
GGGTAMRILG KESCLTPKLD PSIVGRPRHQ	GVISAISEAAAQYNEPPPPR GVKEKALVSSVR GVMVGMGQKDSYVGEAQSKR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da	45.7 20.4 44.8	52.7 59.3 61.0	4 3 4	2191.24 1355.93 2325.29	0.39 1.14 0.52	0.03 0.29 0.09	CPN1_MOUSE ALBU_MOUSE ACT5_MOUSE	D3YW48_MOUSE	Calpain small subunit 1; Serum albumin; Actin, alpha skeletal muscle;	Calcium-activated neutral proteinase small subunit;Calcium-dependent protease small subunit;Calcium-dependent protease small subunit 1;Calpain regulatory subunit;	0.25 - 0.75 0.75 - 0.85 0.25 - 0.75
YTLGKVLQIV	GVNKMDSTPEPYSQKR	N-ter +28.03 Da, K +28.03 Da	35.5	68.0	4	1920.11	-3.06	0.51	EF1A1_MOUSE	D3Z3I8_MOUSE	Elongation factor 1-alpha 1; Cleavage and polyadenylation specificity factor subunit 5;	Elongation factor Tu;Eukaryotic elongation factor 1 A-1; Nucleoside diphosphate-linked moiety X motif 21;	0.00 - 0.15 0.25 - 0.75
PNRSQTGWPR RGERGPFGER	GVNQFGNKYIQTKPLTLER GVQPPGPAQPR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	32.0 63.6	50.8 30.3	4 2	2417.47 1116.64	0.06 0.71	0.01 0.09	CP5F5_MOUSE CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.25 - 0.75 0.25 - 0.75
M	GVQVETISPGDGR	N-ter +28.03 Da	31.4	44.4	3	1341.75	-0.25	0.04	FKB1A_MOUSE	Q1JUQ8_MOUSE	Peptidyl-prolyl cis-trans isomerase FKBP1A; NADH dehydrogenase [ubiquinone] iron-sulfur protein 6, mitochondrial;	12 kDa FK506-binding protein;FK506-binding protein 1A;Immunophilin FKBP12;Rotamase; Complex I-13kD-A;NADH-ubiquinone oxidoreductase 13 kDa-A subunit;	0.25 - 0.75 0.00 - 0.15
LTLPRAARGF	GVQVSPSGEKITHGQVYDEKDYR	N-ter +34.06 Da, K +34.06 Da	39.9	56.0	4	2794.66	-1.79	0.68	NDU56_MOUSE	D3YW32_MOUSE	Histidine triad nucleotide-binding protein 2, mitochondrial;	HINT-3;	0.25 - 0.75 0.85 - 1.00
ARGAQVRGNA GSSADRQGR GNFAAQYSDK	GVSDGSEVAKAQAAPGASPTIFSR GVSEQASDSEGHDFSEGGQAVGAHR GVSSGPGPMGLMGR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +34.06 Da	27.9 63.2 59.2	56.1 63.9 55.9	4 4 3	2571.51 2658.32 1432.82	0.43 2.79 -1.74	0.15 1.27 0.12	HINT2_MOUSE E9Q019_MOUSE EOCXI2_MOUSE	F7BVV1_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.00 - 0.15 0.85 - 1.00 0.00 - 1.00
HQALKGFSSK	GVTSVSIQFHSPDLAIR	N-ter +28.03 Da	50.5	51.0	3	1854.09	1.56	0.18	IC1_MOUSE	A2ATR8_MOUSE	Plasma protease C1 inhibitor;	C1 esterase inhibitor;C1-inhibiting factor;Serpin G1;	0.75 - 0.85
LIPEYLFIR GNFASQMSY QQQQMTSSYG DYLKMLTER DYLKMLTER	GVVDSIDLPLNISR GYDEKSAGVSVPGMGPSGPR GYKEPAAPVSIQR GYSFTTTER GYSFVTTTER	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 N-ter +28.03 Da	30.5 27.6 34.9 34.4 34.7	48.6 43.8 31.2 31.9 39.0	3 3 3 2 2	1540.88 2112.19 1482.93 1159.59 1157.62	0.14 -1.89 2.06 -2.74 1.90	0.01 0.35 0.37 0.18 0.20	H590A_MOUSE CO1A1_MOUSE LASP1_MOUSE ACTB_MOUSE ACTC_MOUSE	H590B_MOUSE F8WGB7_MOUSE A2AGH0_MOUSE ACTG_MOUSE ACTA_MOUSE	Heat shock protein HSP 90-alpha; Collagen alpha-1(I) chain; LIM and SH3 domain protein 1; Actin, cytoplasmic 1; Actin, alpha cardiac muscle 1;	Heat shock 86 kDa;Tumor-specific transplantation 86 kDa antigen; Alpha-1 type I collagen; Metastatic lymph node gene 50 protein; Beta-actin; Alpha-cardiac actin;	0.25 - 0.75 0.00 - 0.15 0.85 - 1.00 0.00 - 0.15 0.85 - 1.00
TQCARIVEKY	GYTHLSAGELLR	N-ter +28.03 Da	27.0	71.8	3	1343.82	-0.20	0.03	KCY_MOUSE		UMP-CMP kinase;		0.25 - 0.75
TQCEKIVQKY SRVRTGRSJK SDHRTYDLR	GYTHLSTGDLRL GYTLPPHCSR HAFSPVASVESASGETLHSPK	N-ter +28.03 Da N-ter +34.06 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da	42.1 33.2 55.1	51.1 51.6 68.3	3 3 4	1359.78 1220.68 2193.26	-0.79 -4.06 -0.45	0.19 0.68 0.06	KAD1_MOUSE KCRM_MOUSE FETUA_MOUSE		Adenylate kinase isoenzyme 1; Creatine kinase M-type; Alpha-2-HS-glycoprotein;	ATP-AMP transphosphorylase 1;Myokinase; Creatine kinase M chain;M-CK; Countertrypsin;Fetuin-A; ICD-M;IDP;NADP(+)-specific ICDH;Oxalosuccinate decarboxylase;	0.25 - 0.75 0.00 - 0.15 0.25 - 0.75
GWTKPITIGR GIVEGLMTTV GKKSQDDVAR	HAHGDQYKATDFVDR HAITATQKTVDPGSGKLWR HAQVSSSSIVSLGIGDR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	26.5 27.8 55.5	69.2 59.2 45.4	4 4 3	1914.07 2149.33 1823.07	-0.56 -0.42 3.59	0.12 0.06 0.37	IDHP_MOUSE G3P_MOUSE E9PWQ3_MOUSE	D6RIL6_MOUSE F8WJL5_MOUSE D3YWD1_MOUSE	Isocitrate dehydrogenase [NADP], mitochondrial; Glyceraldehyde-3-phosphate dehydrogenase;	decarboxylase; Peptidyl-cysteine S-nitrosylase GAPDH;	0.25 - 0.75 0.25 - 0.75 0.85 - 1.00
KGTFASEL	HCDKLHVDPENFR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	23.3	63.8	4	1721.94	2.71	0.81	HBB1_MOUSE	HBB2_MOUSE	Hemoglobin subunit beta-1;	Beta-1-globin;Hemoglobin beta-1 chain;Hemoglobin beta-major chain;	0.85 - 1.00
QICPNLIVAF RQIRTKVMDV YGHYEPGEF LLGLPARAA YWKTLGISPF PTDKHKTDLN	HDFSSDLENVPHLR HDGKVVSTHEQVLR HDVEDAETYKMLAR HEDPVKEVGFGR HEFADVVFANDSGHR HENLKGDDLDPNVYSSLR	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 +34.06 Da, K +34.06 Da N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da	30.3 25.2 19.6 44.8 34.9 43.3	78.1 68.4 54.6 68.3 84.8 60.4	3 4 4 4 4 4	1692.95 1660.02 1889.08 1709.06 1829.01 2196.28	0.20 1.48 0.57 0.53 3.59 -1.25	0.04 0.37 0.07 0.03 0.56 0.12	PRELP_MOUSE K1C14_MOUSE RCN3_MOUSE SBSN_MOUSE TTHY_MOUSE KCRM_MOUSE		Prolargin; Keratin, type I cytoskeletal 14; Reticulocalbin-3; Suprabasin; Transthyretin; Creatine kinase M-type;		0.25 - 0.75 0.75 - 0.85 0.25 - 0.75 0.25 - 0.75 0.85 - 1.00 0.15 - 0.25

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
HRWRPYSLSL	HGIEGAFSGSGAKTVIPR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	21.6	48.8	4	1839.09	5.06	0.61	CNDP2_MOUSE	F6XEL6_MOUSE	Cytosolic non-specific dipeptidase;	CNDP dipeptidase 2;Glutamate carboxypeptidase-like protein 1;	0.85 - 1.00
LIGALGCAIC	HGNPVDVDCIAKPR	N-ter +28.03 Da	15.4	56.3	4	1646.95	-0.52	0.08	ANT3_MOUSE		Antithrombin-III;	Serpin C1;	0.25 - 0.75
ENLATAFTIL	HHPEFTPDQPTER	N-ter +28.03 Da	36.0	56.9	3	1617.85	0.89	0.20	TXLNB_MOUSE		Beta-taxilin;	Muscle-derived protein 77;	0.25 - 0.75
TNWDDMEKIW	HHTFYNELR	N-ter +28.03 Da	21.8	61.3	3	1243.69	0.37	0.03	ACTC_MOUSE	ACTB_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
LLSRPKHKS	HHVLVIENKYMR	N-ter +28.03 Da, K +28.03 Da	28.2	65.4	4	1593.99	0.57	0.07	MA2B1_MOUSE		Lysosomal alpha-mannosidase;	Mannosidase alpha class 2B member 1;Mannosidase alpha-B;	0.25 - 0.75
MEDVTL	HIVERPYSFPDASSEPEPTQGEAR	N-ter +28.03 Da	55.0	61.2	4	2840.51	7.76	2.75	PTRF_MOUSE	Q3U4N4_MOUSE	Polymerase I and transcript release factor;	Cav-p60;Cavin-1;	0.85 - 1.00
LRLALQALQEQ	HKAEIITVSDGR	N-ter +28.03 Da, K +28.03 Da	25.0	46.4	3	1380.84	-1.36	0.17	VP525_MOUSE	A2A4J8_MOUSE	Vacuolar protein-sorting-associated protein 25;	ESCRT-II complex subunit VPS25;	0.15 - 0.25
STMGYMMAK	HLEINPDHPIVETLR	N-ter +28.03 Da	32.3	76.0	4	1810.11	2.48	0.22	H590B_MOUSE	Q71X8_MOUSE	Heat shock protein HSP 90-beta;	Heat shock 84 kDa;Tumor-specific transplantation 84 kDa antigen;	0.85 - 1.00
PMGRGKTIVL	HLKEDQTEYLEER	N-ter +28.03 Da, K +28.03 Da	20.6	61.9	4	1744.97	1.55	0.16	H590B_MOUSE	H590A_MOUSE	Heat shock protein HSP 90-beta;	Heat shock 84 kDa;Tumor-specific transplantation 84 kDa antigen;	0.75 - 0.85
GTFLEYYSRR	HPDYVSLLLR	N-ter +28.03 Da	35.2	65.0	3	1326.82	2.97	0.19	ALBU_MOUSE		Serum albumin;		0.85 - 1.00
NRSLRHNHIR	HPEYDYSNDMLLLR	N-ter +34.06 Da	40.5	51.1	3	1798.97	-3.64	0.46	K1K89_MOUSE		Kallikrein 1-related peptidase b9;	Epidermal growth factor-binding protein type C;Glandular kallikrein K9;Tissue kallikrein-9;	0.00 - 0.15
GLCLQLLSLA	HPHQDIDLNVTCR	N-ter +28.03 Da, C +57.02 Da	54.9	52.4	3	1644.90	0.82	0.14	A2APM2_MOUSE	A2APM5_MOUSE			0.25 - 0.75
SPOTIKTTAR	HQDLDFKFKVNPVLTNNQR	N-ter +28.03 Da, K +28.03 Da	24.9	61.0	4	2477.49	1.12	0.13	SCEL_MOUSE	Q14DQ7_MOUSE	Sciellin;		0.75 - 0.85
VFPISVGRPG	HQGVMMVMGMQKDSYVGEAQSKR	N-ter +28.03 Da, K +28.03 Da	67.5	62.3	4	2590.42	3.54	0.69	ACTA_MOUSE	ACTB_MOUSE	Actin, aortic smooth muscle;	Alpha-actin-2;	0.85 - 1.00
SESQASDSEF	HSDFSEGAAGAHNR	N-ter +28.03 Da	53.9	55.2	3	1524.79	2.92	0.98	F78VV1_MOUSE	FILA_MOUSE			0.85 - 1.00
PSPLAVPRRA	HSILPVDDIDINGLNEEQQLR	N-ter +28.03 Da, K +28.03 Da	63.1	61.0	4	2488.44	0.63	0.12	IVD_MOUSE		Isovaleryl-CoA dehydrogenase, mitochondrial;		0.25 - 0.75
QAQQAMDVQL	HSPAFQFPDVFLLR	N-ter +28.03 Da	37.7	50.3	3	1702.93	0.04	0.03	CLUS_MOUSE		Clusterin;	Apolipoprotein J;Clustrin;Sulfated glycoprotein 2;	0.25 - 0.75
LILPYVELDL	HSYDLGIENR	N-ter +28.03 Da	39.3	62.7	3	1230.68	0.88	0.08	IDHC_MOUSE	F8WIY0_MOUSE	Isocitrate dehydrogenase [NADP] cytoplasmic;		0.25 - 0.75
VILQHLRMSM	HTEAAEVLLEER	N-ter +28.03 Da	35.9	48.3	3	1294.75	-0.79	0.05	HIBCH_MOUSE	E0CX19_MOUSE	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial;	3-hydroxyisobutyryl-coenzyme A hydrolase; Acylcholine acylhydrolase;Butyrylcholine esterase;Choline esterase;	0.25 - 0.75
LLLCMPFGKS	HTEEDFIITTKTR	N-ter +28.03 Da, K +28.03 Da	24.8	72.8	4	1703.01	1.03	0.08	CHLE_MOUSE		Cholinesterase;	I;Pseudocholinesterase;	0.75 - 0.85
SCLDHVISYY	HVASDTEKHIR	N-ter +28.03 Da, K +28.03 Da	31.1	50.8	3	1323.82	0.77	0.13	EXOC7_MOUSE	A2AAN4_MOUSE	Exocyst complex component 7;	Exocyst complex component Exo70;	0.25 - 0.75
KHGGPADEER	HVGDLEGNVTAGKDGVANVSIEDR	N-ter +28.03 Da, K +28.03 Da	60.0	61.2	4	2378.36	1.42	0.26	SODC_MOUSE		Superoxide dismutase [Cu-Zn];		0.75 - 0.85
GMYPDQAGRF	HVNLLCGEEGADAAHLFNPR	N-ter +28.03 Da, C +57.02 Da	48.5	60.4	4	2375.29	1.96	0.33	Q9CRB1_MOUSE	LEG7_MOUSE			0.85 - 1.00
QPRNWLFLAC	HVTNEVAQLQGGGR	N-ter +28.03 Da	57.2	46.8	3	1548.91	-0.27	0.04	BR44L_MOUSE	D3Z5S0_MOUSE	Brain protein 44-like protein;		0.25 - 0.75
HRSGETEDTF	IADLVVGLCTGQKKTGAPCR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	44.4	55.4	4	2196.36	-1.40	0.22	ENOB_MOUSE	ENOA_MOUSE	Beta-enolase;	2-phospho-D-glycerate hydro-lyase;Enolase 3;Muscle-specific enolase;Skeletal muscle enolase;	0.15 - 0.25
LDATTVLSRA	IAELGIYPVAVDPLDSTSR	N-ter +28.03 Da	48.3	42.3	3	1944.10	0.99	0.30	ATPB_MOUSE		ATP synthase subunit beta, mitochondrial;		0.75 - 0.85
FPKKSRTAR	IASDEEIIQGTDAVIOQLER	N-ter +28.03 Da, K +28.03 Da	38.1	64.7	4	2285.32	-2.74	0.55	PALLD_MOUSE		Palladin;		0.00 - 0.15
DIFTGKKYED	ICPSTHNMVDPNIKR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	27.0	62.8	4	1837.05	-1.79	0.25	IF5A1_MOUSE	IF5A2_MOUSE	Eukaryotic translation initiation factor 5A-1;	Eukaryotic initiation factor 5A isoform 1;eIF-4D; 15S Mg(2+)-ATPase p97 subunit;Valosin-containing protein;	0.00 - 0.15
AEKNAPAIIF	IDELDAIAPKR	N-ter +28.03 Da, K +28.03 Da	32.1	42.3	3	1295.80	0.85	0.08	TERRA_MOUSE		Transitional endoplasmic reticulum ATPase;		0.25 - 0.75
ESDAADIVFL	IDSDDAVKPDGIAHIR	N-ter +28.03 Da, K +28.03 Da	38.2	60.8	4	1749.05	-0.01	0.00	E9PWQ3_MOUSE	D3YWD1_MOUSE			0.25 - 0.75
EAPVGVETDL	IDVGFDDVKKGGPGR	N-ter +34.06 Da, K +34.06 Da	28.9	61.2	4	1762.16	1.04	0.33	IST1_MOUSE	Q8BHC2_MOUSE	IST1 homolog;		0.75 - 0.85
RLAKYNQLMR	IEEALGDKAVFAGR	N-ter +28.03 Da, K +28.03 Da	30.4	35.0	3	1530.89	-0.25	0.06	ENOB_MOUSE		Beta-enolase;	2-phospho-D-glycerate hydro-lyase;Enolase 3;Muscle-specific enolase;Skeletal muscle enolase;	0.25 - 0.75
FVPNDGCLNF	IEENDEVLVAGFGR	N-ter +34.06 Da	41.8	45.9	3	1580.90	0.87	0.11	RS23_MOUSE	Q9CZ15_MOUSE	40S ribosomal protein S23;		0.25 - 0.75
EGNKEQIQKI	IETLSQQLQAKGKELNEFR	N-ter +34.06 Da, K +34.06 Da	26.0	53.3	4	2333.51	-1.43	0.19	PF02_MOUSE		Prefoldin subunit 2;		0.15 - 0.25
AEFGKGIKLF	IFIDSHTDNQR	N-ter +28.03 Da	27.6	76.2	3	1487.81	-0.06	0.01	PDIA1_MOUSE		Protein disulfide-isomerase;	Cellular thyroid hormone-binding protein;Endoplasmic reticulum resident protein 59;Prolyl 4-hydroxylase subunit beta;p55;	0.25 - 0.75
R	IFQTTERFPIQKLF	N-ter +34.06 Da, K +34.06 Da	27.8	28.1	4	2248.41	-2.12	1.20	F7D9Q0_MOUSE				0.00 - 0.15
KSNIKAAWGW	IGGHGAEYGAELER	N-ter +34.06 Da	54.4	51.5	3	1562.87	-2.06	0.43	HBA_MOUSE	Q91V88_MOUSE	Hemoglobin subunit alpha;	Alpha-globin;Hemoglobin alpha chain;	0.00 - 0.15
VPRKCSASNR	IIAAKDHASIQMNVVAEVDNR	N-ter +28.03 Da, K +28.03 Da	21.6	56.3	4	2136.26	0.11	0.01	RS21_MOUSE		40S ribosomal protein S21;		0.25 - 0.75
PKHPVDQVQR	IIGGSMDAKGSFFWQAK	N-ter +28.03 Da, K +28.03 Da	15.0	43.4	3	1876.07	0.37	0.08	HPT_MOUSE		Haptoglobin;		0.25 - 0.75
GTIAGLNVLFR	IIINEPTAAAIAGLDKK	N-ter +28.03 Da, K +28.03 Da	32.1	33.0	3	1871.14	0.33	0.03	HSP7C_MOUSE	HSP72_MOUSE	Heat shock cognate 71 kDa protein;	Heat shock 70 kDa protein 8;	0.25 - 0.75
MSFSKDWSLY	IIAHTFTPTTDTYACR	N-ter +34.06 Da, C +57.02 Da	40.5	48.0	3	2159.15	-0.32	0.11	B2MG_MOUSE	Q91XJ8_MOUSE	Beta-2-microglobulin;		0.25 - 0.75
IYSQVGSKKK	IIATPPQEDAPSVDIANIR	N-ter +28.03 Da	32.5	11.9	3	2047.12	1.08	0.21	TKT_MOUSE		Transketolase;	P68;	0.75 - 0.85
VEKSAFAFK	ILDPAAYQVKGGKVR	N-ter +34.06 Da, K +34.06 Da	23.5	50.8	4	1760.19	-2.12	0.09	D3YU50_MOUSE	Q6P6L5_MOUSE			0.00 - 0.15
AAVCAQPRGR	ILGGQEAAAHAR	N-ter +34.06 Da	35.3	49.6	3	1226.76	-1.00	0.34	CFAD_MOUSE		Complement factor D;	28 kDa adipocyte protein;Adipsin;C3 convertase activator;Properdin factor D;	0.15 - 0.25
APMTDEIQQQ	ILNLPESWDWR	N-ter +28.03 Da	36.0	38.2	2	1455.81	1.61	0.54	CATC_MOUSE	D3Z220_MOUSE	Dipeptidyl peptidase 1;	l;Dipeptidyl transferase;	0.75 - 0.85
FTVNRPLFF	IMEDTIGVPLFVGSVR	N-ter +28.03 Da	38.7	48.1	3	1760.04	1.32	0.22	A2AP_MOUSE		Alpha-2-antiplasmin;	Alpha-2-plasmin inhibitor;Serpin F2;	0.75 - 0.85
YTTISVPQML	INLWGSTKTIYSYLR	N-ter +28.03 Da, K +28.03 Da	27.9	38.5	3	1707.04	-1.43	0.12	Q8VEY4_MOUSE				0.15 - 0.25

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
GAIEECVSR D KPHEAGTAF QGVRVGTVMR	IPVPRPSSIEEFFIVK IQMTQTTSLSASLGD IQTQQLHAAMADTFLEHMCR IRGMVDPQAGR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da N-ter +28.03 Da, C +57.02 Da N-ter +28.03 Da	21.1 45.0 55.9 35.1	75.6 44.3 62.7 59.7	4 3 4 3	1877.24 1944.06 2428.30 1226.73	0.65 -1.79 0.06 -0.01	0.10 0.74 0.01 0.00	GWL_MOUSE KV5AA_MOUSE KPYM_MOUSE Q9CRB1_MOUSE	KV5AB_MOUSE	Serine/threonine-protein kinase greatwall; Ig kappa chain V-V region MOPC 173; Pyruvate kinase isozymes M1/M2;	Microtubule-associated serine/threonine-protein kinase-like; Pyruvate kinase muscle isozyme;	0.25 - 0.75 0.00 - 0.15 0.25 - 0.75 0.25 - 0.75
LLGPPSVLG ASLSTFQQMW	ISFHLPVNSR ISKQEYDESGPSIVHR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	30.2 35.5	55.4 59.0	3 4	1196.73 1900.08	-0.94 0.99	0.20 0.17	TMEDA_MOUSE ACTB_MOUSE	ACTG_MOUSE	Transmembrane emp24 domain-containing protein 10; Actin, cytoplasmic 1;	21 kDa transmembrane-trafficking protein;Transmembrane protein Tmp21;p24 family protein delta-1; Beta-actin;	0.15 - 0.25 0.75 - 0.85
SNKEIFLREL IALNDFVKL	ISNASDALDKIR ISWYDNEYGSNR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	22.2 37.0 29.9	44.6 54.9 56.4	3 3 4	1357.82 1693.83 2425.29	3.48 2.31 -0.06	0.58 1.11 0.03	H590B_MOUSE G3P_MOUSE Q148R4_MOUSE	ENPL_MOUSE F8WJ5_MOUSE	Heat shock protein HSP 90-beta; Glyceroldehyde-3-phosphate dehydrogenase;	Heat shock 84 kDa;Tumor-specific transplantation 84 kDa antigen; Peptidyl-cysteine S-nitrosylase GAPDH;	0.85 - 1.00 0.85 - 1.00
RRKKEGENQR KKELSDIAHR DAVTRQVRT SICQQNGIVP LLWVPGSTGD	ITSGESSGGNPKAKDECAQYR IVAPGKGLADESTGSIKR IVEEVQDGKVISSR IVEFEIPDGDHDLKR IVLTQSPASLAVSLGQR	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, K +28.03 Da N-ter +34.06 Da	43.7 26.3 23.7 62.3	48.3 46.5 70.4 42.6	3 3 4 3	2137.35 1613.97 1901.17 1888.16	0.72 4.48 -0.64 -1.64	0.15 1.33 0.04 0.67	ALDOA_MOUSE K1C17_MOUSE ALDOA_MOUSE KV3A1_MOUSE	A6Z144_MOUSE D3YXP7_MOUSE ALDOC_MOUSE KV3A2_MOUSE	Fructose-bisphosphate aldolase A; Keratin, type I cytoskeletal 17; Fructose-bisphosphate aldolase A; Ig kappa chain V-III region PC 2880/PC 1229;	Aldolase 1;Muscle-type aldolase; Cytokeratin-17;Keratin-17; Aldolase 1;Muscle-type aldolase;	0.25 - 0.75 0.25 - 0.75 0.85 - 1.00 0.25 - 0.75 0.00 - 0.15
GSKGQTQCEK LTAASEACL GVNIGGAGSY VTHGQVGVGK	IVQKYGYTHLSTGDLRL IVSDETIKNR IYEKPTQTEAPQVTGPIEVPVVR KAEAVATVVAADVQAR	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 N-ter +28.03 Da, K +28.03 Da	24.3 20.4 47.0 56.0	54.5 39.9 52.9 41.5	4 3 4 3	2019.23 2137.94 2517.58 1654.01	-0.42 -1.22 -1.94 -0.81	0.06 0.26 0.75 0.09	KAD1_MOUSE TCFH_MOUSE CRIP2_MOUSE TTIN_MOUSE	E9Q8M7_MOUSE	Adenylate kinase isoenzyme 1; T-complex protein 1 subunit eta; Cysteine-rich protein 2; Titin;	ATP-AMP transphosphorylase 1;Myokinase; CCT-eta; Heart LIM protein; Connectin;	0.25 - 0.75 0.15 - 0.25 0.00 - 0.15 0.15 - 0.25
DGRADAIEVLR QNAILVRYTQ KIREGEVEVL APPWKDSKFF DEPOSQWDVKV	KAMKGLGTEDESINLLTSR KAPQVSTPLVEAAR KATEMVEVGPEDDEVGAEAR KDAPDGPVTLVDGR KDFANVYDAVKDSSGR	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, K +28.03 Da N-ter +28.03 Da, K +28.03 Da	33.3 45.6 65.0 37.9 26.1	76.9 37.7 42.4 46.6 63.2	4 3 3 3 4	2245.41 1623.00 2116.09 1695.00 1867.10	0.87 0.11 -0.29 0.00 -0.45	0.15 0.01 0.04 0.00 0.05	ANXAS_MOUSE ALBU_MOUSE PTRF_MOUSE F612_MOUSE APOA1_MOUSE	Annexin A5; Serum albumin; Polymerase I and transcript release factor; Coagulation factor XII; Apolipoprotein A-I;	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 0.25 - 0.75 0.25 - 0.75 0.00 - 0.15 0.25 - 0.75	
YKNSKFHRVI LNCESFKQRR CSANSRIIAA	KDFMIQGDGFR KDGDFICPDSSTSSVCGTDGKTYR KDHASIQMNVAEVDR	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	32.3 50.2 60.4	50.3 60.8 55.4	3 4 3	1481.87 2649.37 1780.06	-3.47 0.01 -1.52	0.77 0.00 0.35	PPIB_MOUSE Q148R4_MOUSE RS21_MOUSE	Q8BM18_MOUSE	Peptidyl-prolyl cis-trans isomerase B; 40S ribosomal protein S21;	CYP-S1;Cyclophilin B;Rotamase B;S-cyclophilin;	0.00 - 0.15 0.25 - 0.75 0.00 - 0.15
AGELHLEICL AGDEESYTVF LSKRPEEPPR LPMMQAISNN	KDLEEDHACIPIKSDPVVSYR KDLFDPIQDR KDPSSNDPLTETIR KQGGYEDFVEGLR	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 +34.06 Da, K +34.06 Da, C +57.02 Da	35.3 29.7 24.1 36.0	59.8 61.9 65.1 49.0	4 3 3 3	2734.73 1414.87 1627.95 1679.96	-0.01 0.31 1.37 0.03	0.00 0.03 0.09 0.01	EF2_MOUSE KCRM_MOUSE MUG1_MOUSE E9PWG4_MOUSE	MYL1_MOUSE	Elongation factor 2; Creatine kinase M-type; Muringlobulin-1; E9PWG4_MOUSE	Creatine kinase M chain;M-CK;	0.25 - 0.75 0.25 - 0.75 0.75 - 0.85 0.25 - 0.75
FLDTCCAAD MAF	KDTCFSTEGPNLVR KDTGKTPVEVAIHR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da	51.0 32.1	53.3 56.0	3 4	1779.98 1860.15	0.32 1.81	0.07 0.34	ALBU_MOUSE RS20_MOUSE	Serum albumin; 40S ribosomal protein S20;	0.25 - 0.75 0.85 - 1.00		
CLLYRGDVIP MFDQTQIQEF TQDHISVYKQ	KDVNAAIATIKTR KEAFTVIDQNR KEAIGQGTPIPLDPEVKR	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, C +57.02 Da	29.7 27.1 37.9 27.7	63.9 46.6 62.2 70.9	4 3 4 4	1640.14 1375.81 2031.30 1945.01	0.45 -1.43 1.66 0.07	0.09 0.23 0.09 0.02	TBA1A_MOUSE MLR5_MOUSE A2AQ82_MOUSE ALBU_MOUSE	TBA1B_MOUSE F6ULR7_MOUSE A2AQ9_MOUSE	Tubulin alpha-1A chain; Myosin regulatory light chain 2, skeletal muscle isoform;	Alpha-tubulin 1;Alpha-tubulin isotype M-alpha-1;Tubulin alpha-1 chain;	0.25 - 0.75 0.15 - 0.25 0.85 - 1.00
KLATDLTKVN NESEKRELVF NQKNFSSVLY	KECCGDLLECADDR KEDGQEYAQVKMLGNR KEDVSPGTGAIKTPPEMLR	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	27.0 36.3	70.2 54.8	4 4	2137.36 2012.21	-1.74 0.33	0.17 0.02	IF1AX_MOUSE A2AQ82_MOUSE	IF1A_MOUSE A2AQ9_MOUSE	Serum albumin; Eukaryotic translation initiation factor 1A, X-chromosomal;	Eukaryotic translation initiation factor 4C;	0.25 - 0.75 0.00 - 0.15 0.25 - 0.75
EKSCLDWESF QSELSQVRY ALEPASAQA	KEEEGIEELAIHR KEEFKNGKGSFVADTPELOR KEELAAAMVR	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	19.4 32.8 18.1	55.6 65.8 91.8	4 4 3	1779.02 2805.86 1184.83	-0.18 -0.06 0.31	0.02 0.02 0.05	CFDP1_MOUSE LASP1_MOUSE RASL3_MOUSE	A2AG66_MOUSE D3Z6Z7_MOUSE	Craniofacial development protein 1; LIM and SH3 domain protein 1; RAS protein activator like-3;	27 kDa craniofacial protein;Bucentaur;Protein Cp27; Metastatic lymph node gene 50 protein;	0.25 - 0.75 0.25 - 0.75 0.25 - 0.75
DEATDGGGDN SLARELSGTI NIGVAVAFN DMEVKVQKSS AEQEELERQM QOMTSSYGGY DLSAKIEFS	KEGEDSSVHYDDKAIER KEILGTAQSGCNDVGR KELDPVQKLFVDKIR KELEDNMNQLFDLR KELQAANENKQQLVESR KEPAAPVSIQR KEQQEDFKEAFLFDR	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, K +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 +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	31.2 57.9 18.4 40.9 42.1 23.6 28.4	60.2 41.8 71.7 56.0 53.9 47.3 60.8	4 3 4 4 4 3 4	2174.22 1871.10 1963.46 1880.20 1297.29 1250.79 2144.33	0.38 -0.67 0.47 -1.22 0.15 -0.06 -5.64	0.09 0.16 0.08 0.20 0.03 0.01 0.00	CHD4_MOUSE RL12_MOUSE ATP5J_MOUSE TNNI2_MOUSE SWP70_MOUSE LASP1_MOUSE MYL1_MOUSE	E9QAS5_MOUSE E9QAD6_MOUSE E9QAD6_MOUSE D3Z6Z7_MOUSE A2AG6H_MOUSE E0CZ30_MOUSE	Chromodomain-helicase-DNA-binding protein 4; 60S ribosomal protein L12; ATP synthase-coupling factor 6, mitochondrial; Troponin I, fast skeletal muscle; Switch-associated protein 70; LIM and SH3 domain protein 1; Myosin light chain 1/3, skeletal muscle isoform;	0.25 - 0.75 0.25 - 0.75 0.25 - 0.75 0.15 - 0.25 0.25 - 0.75 0.25 - 0.75 0.00 - 0.15	
LLTKLPGYV LEEVTKMKQIC QEHEKGVRSW	KEVKCDMEVSCPGEVTCR KEVYENYPAYDLTER KGDSPVANGAEPAGQR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da	46.7 41.4 27.8	55.2 42.1 33.1	4 3 3	2491.21 1957.09 1723.91	2.30 -1.52 0.58	0.73 0.26 0.05	GRN_MOUSE DEK_MOUSE EPN3_MOUSE	Q3U9N4_MOUSE E9Q1Q2_MOUSE	Granulins; Protein DEK; Epsin-3;	PC cell-derived growth factor;Proepithelin; EPS-15-interacting protein 3;	0.85 - 1.00 0.00 - 0.15 0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
EIVPVLVSSR	KGLTEVKIDFFPR	N-ter +28.03 Da, K +28.03 Da	38.1	68.6	4	1615.05	0.35	0.04	THIC_MOUSE	Q80X81_MOUSE	Acetyl-CoA acetyltransferase, cytosolic;	Cytosolic acetoacetyl-CoA thiolase;	0.25 - 0.75
ISMPDVLNDF	KGPKLKGDEIASVPEMEADLR	N-ter +28.03 Da, K +28.03 Da	26.6	81.5	4	2394.52	0.10	0.01	E9Q616_MOUSE				0.25 - 0.75
MSMN	KGPTLDGDLPEQENVLQR	N-ter +28.03 Da, K +28.03 Da	46.8	59.5	4	2177.30	0.21	0.04	PLIN1_MOUSE		Perilipin-1;	Lipid droplet-associated protein;Perilipin A;	0.25 - 0.75
RIGRGRFR	KGVAINMVTEEDKR	N-ter +28.03 Da, K +28.03 Da	31.5	53.4	4	1673.01	-0.71	0.08	IF4A1_MOUSE		Eukaryotic initiation factor 4A-I;	ATP-dependent RNA helicase eIF4A-1;	0.25 - 0.75
AAAAAVYQTQ	KHSPQEAHPVQYER	N-ter +28.03 Da, K +28.03 Da	22.7	67.8	4	1761.02	0.63	0.11	CNTRF_MOUSE	Q9D586_MOUSE	Ciliary neurotrophic factor receptor subunit alpha;		0.25 - 0.75
DKSNKAAWG	KIGGHGAEGAEALER	N-ter +34.06 Da, K +34.06 Da	33.7	53.9	4	1725.04	-0.97	0.08	HBA_MOUSE	Q91V88_MOUSE	Hemoglobin subunit alpha;	Alpha-globin;Hemoglobin alpha chain;	0.15 - 0.25
NSSPSAKDIK	KILDSVGEADDDR	N-ter +28.03 Da, K +28.03 Da	40.3	48.1	3	1600.91	-0.89	0.15	RLA2_MOUSE		60S acidic ribosomal protein P2;		0.15 - 0.25
QSNVNLAKFR	KIQHELEEAER	N-ter +34.06 Da, K +34.06 Da	27.7	50.3	4	1577.95	-2.56	0.45	MYH4_MOUSE	MYH1_MOUSE	Myosin-4;	Myosin heavy chain 2b;Myosin heavy chain 4;	0.00 - 0.15
QDAYVLLSEK	KISSVQSIIVPALEIANHR	N-ter +28.03 Da, K +28.03 Da	46.6	59.8	4	2088.33	1.36	0.08	CH60_MOUSE		60 kDa heat shock protein, mitochondrial;		0.75 - 0.85
EDTMTEVKAY	KKELEEQLGPVAEETR	N-ter +28.03 Da, K +28.03 Da	28.1	58.3	4	1939.18	0.06	0.00	APOE_MOUSE	E9Q327_MOUSE	Apolipoprotein E;		0.25 - 0.75
STFKNTEISF	KLGVFEDEITADDR	N-ter +28.03 Da, K +28.03 Da	30.3	55.0	3	1662.94	0.45	0.10	FABP4_MOUSE		Fatty acid-binding protein, adipocyte;		0.25 - 0.75
DYISDLDLQR	KLLSVVDDEAFIR	N-ter +28.03 Da, K +28.03 Da	37.8	56.5	3	1623.98	-1.22	0.11	PYGM_MOUSE	E9PUM3_MOUSE	Glycogen phosphorylase, muscle form;	Myophosphorylase;	0.15 - 0.25
QRGAIVIKAR	KLSSAMSAAKAIADHIR	N-ter +28.03 Da, K +28.03 Da	29.5	63.5	4	1853.17	0.51	0.05	MDHC_MOUSE		Malate dehydrogenase, cytoplasmic;	Cytosolic malate dehydrogenase;	0.25 - 0.75
SDRKYEVAR	KLIVILEGELER	N-ter +28.03 Da, K +28.03 Da	35.6	50.0	3	1353.89	2.20	0.24	TPM2_MOUSE	A2AIM4_MOUSE	Tropomyosin beta chain;	Beta-tropomyosin;Tropomyosin-2;	0.85 - 1.00
GPSAGDVEAI	KNAIANASTLAEVER	N-ter +34.06 Da, K +34.06 Da	34.6	48.6	3	1654.05	0.15	0.02	RU2A_MOUSE		U2 small nuclear ribonucleoprotein A';		0.25 - 0.75
M	KNPFAHLAEPLDAAQPKR	N-ter +34.06 Da, K +34.06 Da	68.8	74.4	4	2292.50	0.23	0.02	ACOC_MOUSE	Q8VDC3_MOUSE	Cytoplasmic aconitate hydratase;	Citrate hydro-lyase;Iron regulatory protein	0.25 - 0.75
MKKKILAEER	KPLNIDHLSDDKLR	N-ter +34.06 Da, K +34.06 Da	19.1	49.1	4	1765.18	-1.74	0.35	TNNT3_MOUSE	A2A6J0_MOUSE	Troponin T, fast skeletal muscle;	Fast skeletal muscle troponin T;	0.00 - 0.15
M	KPPAACAGDVVDAASPSTVNHRL	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	71.6	58.0	4	2459.40	0.99	0.20	THOP1_MOUSE		Thimet oligopeptidase;		0.75 - 0.85
LSTFQMQWIS	KQEYDEAGPSIVHR	N-ter +28.03 Da, K +28.03 Da	49.0	63.6	4	1863.97	-0.52	0.09	ACTA_MOUSE	ACTA_MOUSE	Actin, alpha skeletal muscle;	Alpha-actin-1;	0.25 - 0.75
LSTFQMQWIS	KQEYDESGPSIVHR	N-ter +28.03 Da, K +28.03 Da	44.4	62.0	4	1699.96	0.55	0.07	ACTB_MOUSE	ACTG_MOUSE	Actin, cytoplasmic 1;	Beta-actin;	0.25 - 0.75
DTGMNHLLL	KQFELNHQNPMTFESR	N-ter +28.03 Da, K +28.03 Da	32.4	65.9	4	2181.22	3.24	1.37	NUCB2_MOUSE		Nucleobindin-2;	DNA-binding protein NEFA;	0.85 - 1.00
LDPEGKTIK	KQFLEELLTQCDDR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	55.0	56.6	3	1836.05	0.66	0.13	MLRS_MOUSE		Myosin regulatory light chain 2, skeletal muscle isoform;	Fast skeletal myosin light chain 2;MLC2F;	0.25 - 0.75
FKRSTPFFNW	KQIEGSDLSLQKR	N-ter +28.03 Da, K +28.03 Da	38.0	47.6	4	1672.03	-0.45	0.05	DMKN_MOUSE	E9QLW7_MOUSE	Dermokine;	Epidermis-specific secreted protein SK30/SK89;	0.25 - 0.75
FVREPPIMVT	KQLEDMNAYCGER	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	38.7	57.0	3	1680.92	-4.06	0.68	D3YU50_MOUSE	Q6P6L5_MOUSE			0.00 - 0.15
AGLILPGILA	KSIGTLDSPCKDPTR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	20.1	55.8	4	1776.13	0.53	0.14	CDSN_MOUSE		Corneodesmosin;		0.25 - 0.75
ATAASSSLE	KSVELPDGQVITIGNER	N-ter +28.03 Da, K +28.03 Da	46.6	48.4	3	1974.14	1.84	0.31	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.85 - 1.00
EINRVVKEMY	KTDLEKDIISDTSGDFR	N-ter +28.03 Da, K +28.03 Da	38.6	61.3	4	2023.17	0.41	0.06	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
DFHLLNEVN	KTDPGILKLTENR	N-ter +28.03 Da, K +28.03 Da	23.8	54.2	4	1568.01	-1.29	0.19	Q3UWK8_MOUSE				0.15 - 0.25
NLHASNRLQ	KTGTAEMSSILEER	N-ter +34.06 Da, K +34.06 Da	45.9	48.5	3	1618.97	-0.40	0.08	ATPA_MOUSE	D6R16_MOUSE	ATP synthase subunit alpha, mitochondrial;		0.25 - 0.75
HLEEVVLAML	KTPAQFDADLR	N-ter +28.03 Da, K +28.03 Da	43.4	54.9	3	1445.83	0.77	0.05	ANXA1_MOUSE	E9QA30_MOUSE	Annexin A1;	Annexin I;Annexin-2;Calpactin II;Calpactin-2;Chromobindin-9;Lipocortin I;Phospholipase A2 inhibitory protein;p35;	0.25 - 0.75
EEGPRKDG	KVDVVGATGQAGGSCSR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	55.0	41.3	3	1774.97	1.52	0.39	IF4B_MOUSE	Q3TDD8_MOUSE	Eukaryotic translation initiation factor 4B;		0.75 - 0.85
GILHENFQTL	KVEDNFEDIKPPVR	N-ter +28.03 Da, K +28.03 Da	32.0	56.0	4	1983.21	1.36	0.14	DC1L1_MOUSE		Cytoplasmic dynein 1 light intermediate chain 1;	Dynein light chain A,Dynein light intermediate chain 1, cytosolic;	0.75 - 0.85
AKLSDGVAVL	KVGGTSDVVEKDKDR	N-ter +28.03 Da, K +28.03 Da	27.0	73.6	4	1872.17	2.31	0.70	CH60_MOUSE		60 kDa heat shock protein, mitochondrial;		0.85 - 1.00
LSPMSVNAV	KVIDPATATSVDLR	N-ter +28.03 Da, K +28.03 Da	42.7	43.6	3	1540.95	-0.03	0.00	TCPD_MOUSE		T-complex protein 1 subunit delta;	A45;CCT-delta;	0.25 - 0.75
SINQGLDLRL	KVSHQGYGSTTEFEPR	N-ter +28.03 Da, K +28.03 Da	22.4	63.1	4	2007.10	-0.34	0.10	AMRP_MOUSE	F6WMD1_MOUSE	Alpha-2-macroglobulin receptor-associated protein;		0.25 - 0.75
NPNRVAQTK	KVTQLDLDPKELSR	N-ter +28.03 Da, K +28.03 Da	26.9	57.0	4	1782.13	-0.74	0.14	HAP28_MOUSE		28 kDa heat- and acid-stable phosphoprotein;		0.25 - 0.75
RQELKARAY	LAEKYEWDAEAR	N-ter +34.06 Da, K +34.06 Da	30.4	48.5	3	1646.97	-1.74	0.29	EF2_MOUSE		Elongation factor 2;		0.00 - 0.15
EQMRESLAQR	LAELKSNPTLNEYHTR	N-ter +28.03 Da, K +28.03 Da	33.0	55.3	4	1941.14	0.39	0.04	APOA1_MOUSE	Q8BPDS_MOUSE	Apolipoprotein A-1;	Apolipoprotein A1;	0.25 - 0.75
KMSPAKSIND	LAPPEWDWR	N-ter +28.03 Da	27.6	63.3	2	1196.67	1.21	0.19	CATF_MOUSE		Cathepsin F;		0.75 - 0.85
FDMTSKFLTA	LAQGVINEEALSVELDR	N-ter +28.03 Da	59.4	38.5	3	2099.16	0.64	0.14	PDC61_MOUSE	B8JL8_MOUSE	Programmed cell death 6-interacting protein;	ALG-2-interacting protein 1;ALG-2-interacting protein X;E2F1-inducible protein;Eig2;	0.25 - 0.75
DALKRGLREH	LCEQQAEALDYLCGR	N-ter +34.06 Da, C +57.02 Da	34.0	79.0	3	1787.98	-3.32	1.00	FA65C_MOUSE		Protein FAM65C;		0.00 - 0.15

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
DOAGRFHVNL	LCGEEQGADAAALHFNPR	N-ter +28.03 Da, C +57.02 Da	66.1	52.8	3	1911.99	-0.54	0.16	Q9CRB1_MOUSE	LEG7_MOUSE			0.25 - 0.75
NRVMMVAKKF	LDAGHKLNFVAASR	N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	25.3	60.8	4	1566.03	-2.56	0.30	PDIA3_MOUSE		Protein disulfide-isomerase A3;	58 kDa glucose-regulated protein;58 kDa microsomal protein;Disulfide isomerase ER-60;Endoplasmic reticulum resident protein 57;Endoplasmic reticulum resident protein 60;	0.00 - 0.15
SASGTLLLEA	LDLILPPTPTDKPLR	N-ter +28.03 Da, C +57.02 Da	21.0	49.5	4	1959.26	-2.40	0.13	EF1A1_MOUSE	D3Y268_MOUSE	Elongation factor 1-alpha 1;	Factor 1 A-1;	0.00 - 0.15
LSYSKIKHLR	LDGNPLTQSSLPDMEYCLR	N-ter +28.03 Da, C +57.02 Da	42.8	54.1	3	2333.23	3.62	0.20	LUM_MOUSE		Lumican;	Keratan sulfate proteoglycan lumican;	0.85 - 1.00
ADTFLEHMCR	LDIDSAPITAR	N-ter +28.03 Da	40.8	35.9	2	1198.70	0.88	0.08	KPYM_MOUSE		Pyruvate kinase isozymes M1/M2;	Pyruvate kinase muscle isozyme;	0.25 - 0.75
PLQKERGVKL	LDISELNTVGAGR	N-ter +28.03 Da	29.5	41.0	3	1371.79	0.03	0.00	NELFA_MOUSE		Negative elongation factor A;	Wolf-Hirschhorn syndrome candidate 2 homolog;	0.25 - 0.75
LAKMFKPQAL	LDKAKTNQGWLDSSR	N-ter +34.06 Da, K +34.06 Da	27.2	54.7	4	1820.16	-2.84	0.20	FERM2_MOUSE	A6X941_MOUSE	Fermitin family homolog 2;	Kindlin-2;Pleckstrin homology domain-containing family C member 1;	0.00 - 0.15
QHHDYNTYTF	LDLNLDSLKFR	N-ter +28.03 Da, K +28.03 Da	24.5	59.3	3	1388.89	-5.64	2.82	NDUV3_MOUSE	Q3U422_MOUSE	NADH dehydrogenase [ubiquinone] flavoprotein 3, mitochondrial;	Complex I-9kD;NADH-ubiquinone oxidoreductase 9 kDa subunit;	0.00 - 0.15
PSPEGALHL	LDLPCTPPPPAPIPSVR	N-ter +28.03 Da, C +57.02 Da	46.7	48.9	3	1854.10	1.66	0.19	AP1G2_MOUSE		AP-1 complex subunit gamma-like 2;	Gamma2-adaptin;	0.85 - 1.00
SGTRSSELC	LDLPEAPDDPAALETR	N-ter +28.03 Da	29.6	41.7	3	1749.95	-0.52	0.07	KANK2_MOUSE		KN motif and ankyrin repeat domain-containing protein 2;	Ankyrin repeat domain-containing protein 25;	0.25 - 0.75
GLPTSLTLY	LDNNKISNPDEYFKR	N-ter +28.03 Da, K +28.03 Da	25.9	57.8	4	2049.21	0.71	0.12	LUM_MOUSE		Lumican;	Keratan sulfate proteoglycan lumican;	0.25 - 0.75
EKSAAFAKI	LDPAYQVQKGGKVR	N-ter +34.06 Da, K +34.06 Da	19.9	59.6	4	1647.12	-3.18	0.58	D3YU50_MOUSE	Q6P6L5_MOUSE			0.00 - 0.15
SPSAKDIKI	LDVSGIEADDDR	N-ter +28.03 Da	51.9	45.7	2	1331.68	-1.03	0.08	RLA2_MOUSE		60S acidic ribosomal protein P2;		0.15 - 0.25
KTMVDDFAQF	LDTCKAADKDTCFSTEGPNLVR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	42.0	61.2	4	2842.50	2.87	0.86	ALBU_MOUSE		Serum albumin;		0.85 - 1.00
NASGVSLLEA	LDLILPPTPTDKPLR	N-ter +34.06 Da, K +34.06 Da	25.3	39.9	4	1900.25	-2.74	0.18	EF1A2_MOUSE	B7ZBW3_MOUSE	Elongation factor 1-alpha 2;	Eukaryotic elongation factor 1 A-2;Statin-S1;	0.00 - 0.15
KGQWLTLLEA	LDLTLNHLR	N-ter +28.03 Da	32.0	55.6	3	1107.70	-0.01	0.01	LYAG_MOUSE		Lysosomal alpha-glucosidase;	Acid maltase;	0.25 - 0.75
VEPEMLPTQV	LDTYQEATVEKTLR	N-ter +34.06 Da, K +34.06 Da	22.6	52.8	4	1896.24	-1.64	0.21	TITIN_MOUSE	F6ZV7_MOUSE	Titin;	Connectin;	0.00 - 0.15
TGTGTLVLL	LDVNDNAPIPEPR	N-ter +28.03 Da	29.6	63.9	3	1476.85	2.84	0.31	CADH1_MOUSE		Cadherin-1;	ARC-1;Epithelial cadherin;Uvomorulin;	0.85 - 1.00
HGHHPHGDF	LDYGPCDPPSNSQELKQYHR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	31.2	60.5	4	2516.33	-0.20	0.04	HRG_MOUSE		Histidine-rich glycoprotein;	Histidine-proline-rich glycoprotein;	0.25 - 0.75
KDGASGTTL	LEALDCLPPTPTDKPLR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	38.3	61.3	4	2260.40	-2.74	0.18	EF1A1_MOUSE	D3Y268_MOUSE	Elongation factor 1-alpha 1;	Elongation factor Tu;Eukaryotic elongation factor 1 A-1;	0.00 - 0.15
KEGNASGVL	LEALDILPPTPTDKPLR	N-ter +34.06 Da, K +34.06 Da	39.5	63.3	4	2213.48	-3.84	0.55	EF1A2_MOUSE	B7ZBW3_MOUSE	Elongation factor 1-alpha 2;	Eukaryotic elongation factor 1 A-2;Statin-S1;	0.00 - 0.15
VLPDMYSTY	LEALGIKEGTIPPEYR	N-ter +28.03 Da, K +28.03 Da	27.0	50.4	3	1841.12	-0.45	0.02	ICAL_MOUSE	Q921U7_MOUSE	Calpastatin;	Calpain inhibitor;	0.25 - 0.75
PLLLCEGAQA	LECYSCVQKADGCSPPHR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	58.1	66.8	4	2237.12	2.97	0.93	LYPD3_MOUSE		Ly6/PLAUR domain-containing protein 3;	GPI-anchored metastasis-associated protein C4.4A homolog;	0.85 - 1.00
EKGKTIKKQF	LEELLTQCDR	N-ter +34.06 Da, C +57.02 Da	24.8	31.1	3	1410.77	-1.56	0.18	MLRS_MOUSE		Myosin regulatory light chain 2, skeletal muscle isoform;	Fast skeletal myosin light chain 2;MLC2F;	0.00 - 0.15
DFDENDILRE	LEELSLEAQGIR	N-ter +28.03 Da	31.0	47.8	3	1384.82	0.20	0.02	IF2P_MOUSE		Eukaryotic translation initiation factor 5B;	Translation initiation factor IF-2;	0.25 - 0.75
NDAYGPPSNF	LEIDVSNPQTIVGVGR	N-ter +34.06 Da	34.9	42.3	3	1616.96	-1.12	0.12	SNX3_MOUSE	Q78ZM0_MOUSE	Sorting nexin-3;	SOP3 protein;	0.15 - 0.25
YRIWRDTANW	LEINPETGAIFTR	N-ter +28.03 Da	42.0	41.4	3	1487.86	-2.00	0.24	CADH1_MOUSE		Cadherin-1;	ARC-1;Epithelial cadherin;Uvomorulin;	0.00 - 0.15
TFLRMHHVLL	LEVQVLEGLQCPESGR	N-ter +28.03 Da, C +57.02 Da	43.0	44.6	3	1929.04	0.37	0.08	TR112_MOUSE		tRNA methyltransferase 112 homolog;	TRM112-like protein;	0.25 - 0.75
AANDCKSLHT	LFGDKLCAIPNLR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	15.0	51.2	3	1584.03	-0.32	0.04	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
LPEGTPEKY	LGAEYMQSVGNMR	N-ter +28.03 Da	24.6	68.4	3	1482.80	-0.12	0.01	TRFE_MOUSE	E9Q035_MOUSE	Serotransferrin;	Beta-1 metal-binding globulin;Siderophilin;	0.25 - 0.75
SPASHEIATN	LGDFAISLYR	N-ter +34.06 Da	15.0	43.3	2	1187.73	0.66	0.17	A1AT1_MOUSE	A1AT2_MOUSE	Alpha-1-antitrypsin 1-1;	Alpha-1 protease inhibitor 1;Alpha-1-antipeptidase;Serine protease inhibitor 1-1;Serine protease inhibitor A1a;	0.25 - 0.75
TVKTVFVFCN	LGEKFEDETTADGR	N-ter +28.03 Da, K +28.03 Da	24.1	58.0	3	1493.82	-6.64	0.00	FABP5_MOUSE	E9Q964_MOUSE	Fatty acid-binding protein, epidermal;	Epidermal-type fatty acid-binding protein;Fatty acid-binding protein 5;Keratinocyte lipid-binding protein;Psoriasis-associated fatty acid-binding protein homolog;	0.00 - 0.15
DAQSVLDAKE	LGMEEPRVSSR	N-ter +34.06 Da	22.4	111.3	3	1357.84	-3.64	0.91	ARHL2_MOUSE		Poly(ADP-ribose) glycohydrolase ARH3;	ADP-ribosylhydrolase 3;[Protein ADP-ribosylarginine] hydrolase-like protein 2;	0.00 - 0.15
PEPQQVGTVS	LHLGVTPSVLR	N-ter +34.06 Da	27.6	51.6	3	1224.84	-0.18	0.05	TPP1_MOUSE		Tripeptidyl-peptidase 1;	protease;Tripeptidyl aminopeptidase;Tripeptidyl-peptidase I;	0.25 - 0.75
RALGVDRWRR	LHTVYQSVELPETHQMLR	N-ter +34.06 Da	38.5	50.5	4	2214.28	0.71	0.10	ACADS_MOUSE		Short-chain specific acyl-CoA dehydrogenase, mitochondrial;	Butyryl-CoA dehydrogenase;	0.25 - 0.75
KHKTDLNHEN	LKGGDLDPNYVLSR	N-ter +34.06 Da, K +34.06 Da	46.8	37.1	3	1816.07	-1.12	0.12	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.15 - 0.25
GQLLCSALYA	LKGGMLFPKESPSR	N-ter +28.03 Da, K +28.03 Da	26.8	57.1	4	1630.02	-0.18	0.03	BGLR_MOUSE	Q99JK6_MOUSE	Beta-glucuronidase;		0.25 - 0.75
GCLVLPVGEA	LKGPKEISGFEGDVTSLR	N-ter +28.03 Da, K +28.03 Da	27.5	86.1	4	2016.30	-0.45	0.07	CLM9_MOUSE		CMRF35-like molecule 9;	CD300 antigen-like family member G;Nepmucin;	0.25 - 0.75
ELDGGLETLR	LKLPVAVTADLR	N-ter +28.03 Da, K +28.03 Da	35.3	46.2	3	1350.92	2.40	0.36	ETFB_MOUSE		Electron transfer flavoprotein subunit beta;		0.85 - 1.00
PDOAGRFHVNL	LLCGEEQGADAAALHFNPR	N-ter +28.03 Da, C +57.02 Da	68.4	54.2	3	2025.08	0.85	0.33	LEG7_MOUSE	Q9CRB1_MOUSE	Galectin-7;		0.25 - 0.75
KKILARRKP	LNIDHLSDDKLR	N-ter +34.06 Da, K +34.06 Da	25.4	59.2	4	1505.97	-1.64	0.41	TNNT3_MOUSE	A2A6J0_MOUSE	Troponin T, fast skeletal muscle;	Fast skeletal muscle troponin T;	0.00 - 0.15
QVLVQSSSN	LPDTSIPGGSTPTVQTPQLETR	N-ter +28.03 Da	46.5	54.4	3	2421.41	-2.12	0.46	PGBM_MOUSE	B1B0C7_MOUSE	Basement membrane-specific heparan sulfate proteoglycan core protein;		0.00 - 0.15

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
PRKIISLSQL	LQEDSLNVADLSSLR	N-ter +28.03 Da	54.5	43.4	3	1686.95	0.40	0.06	PSME2_MOUSE	E0C290_MOUSE	Proteasome activator complex subunit 2;	11S regulator complex subunit beta;Activator of multicatalytic protease subunit 2;Proteasome activator 28 subunit beta;	0.25 - 0.75
SRDGKALEQF	LQEYFDGNLKR	N-ter +34.06 Da, K +34.06 Da	28.9	40.1	3	1449.88	-1.60	0.34	PDIA3_MOUSE		Protein disulfide-isomerase A3;	58 kDa glucose-regulated protein;58 kDa microsomal protein;Disulfide isomerase ER-60;Endoplasmic reticulum resident protein 57;Endoplasmic reticulum resident protein 60;	0.00 - 0.15
ARRQHLKSVM	LQIAATELEKEESR	N-ter +28.03 Da, K +28.03 Da	23.3	57.4	3	1672.00	0.62	0.07	TNNI2_MOUSE	A2AGK0_MOUSE	Troponin I, fast skeletal muscle;	Troponin I, fast-twitch isoform;	0.25 - 0.75
PAAGMRRRRR	LQQEDGISFEYHR	N-ter +28.03 Da	31.2	49.6	3	1648.87	0.38	0.06	CBPE_MOUSE		Carboxypeptidase E;	Carboxypeptidase H;Enkephalin convertase;Prohormone-processing carboxypeptidase;	0.25 - 0.75
DESTGSIAGR	LQSIGTENTEENRR	N-ter +28.03 Da	26.1	49.8	3	1673.92	2.72	0.38	ALDOA_MOUSE	Q9CPQ9_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.85 - 1.00
DESTGSIAGR	LQSIGTENTEENR	N-ter +28.03 Da	33.7	48.0	3	1517.80	0.52	0.04	ALDOA_MOUSE	Q9CPQ9_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.25 - 0.75
NTFYSNKEIF	LREUSNASDALDKIR	N-ter +28.03 Da, K +28.03 Da	38.2	59.1	4	1869.18	0.32	0.05	H590B_MOUSE	ENPL_MOUSE	Heat shock protein HSP 90-beta;	Heat shock 84 kDa;Tumor-specific transplantation 84 kDa antigen;	0.25 - 0.75
FGDKLCAIPN	LRENYGELADCTCKEPPER	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	45.9	63.2	4	2423.27	0.43	0.10	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
LPLPTFSSLN	LRETNLESPLVDTHSKR	N-ter +28.03 Da, K +28.03 Da	24.4	60.9	4	2163.33	1.48	0.20	VIME_MOUSE	E9PZV5_MOUSE	Vimentin;		0.75 - 0.85
ALSVLPDSRA	LRPGDCEVCISYLGR	N-ter +34.06 Da, C +57.02 Da	55.3	52.9	3	1828.02	0.74	0.20	MANF_MOUSE	Q3TMX5_MOUSE	Mesencephalic astrocyte-derived neurotrophic factor;	Arginine-rich protein;Protein ARMET;	0.25 - 0.75
DIEPVEGRYM	LSGGSDGVVVLVDLENASR	N-ter +28.03 Da	27.3	51.2	3	1978.10	-0.42	0.08	ERCC8_MOUSE	D3YU16_MOUSE	DNA excision repair protein ERCC-8;	Cockayne syndrome WD repeat protein CSA homolog;	0.25 - 0.75
KAEEKGHDL	LSKVTLKNR	N-ter +28.03 Da, K +28.03 Da	17.8	65.9	3	1254.92	6.71	1.67	FILL1_MOUSE	E0CYM1_MOUSE	Filamin A-interacting protein 1-like;	Protein down-regulated in ovarian cancer 1 homolog;	0.85 - 1.00
FQLIGIQDGY	LSLLQDSGEVR	N-ter +34.06 Da	25.7	38.8	2	1249.76	-2.84	0.20	IF5A1_MOUSE		Eukaryotic translation initiation factor 5A-1;	Eukaryotic initiation factor 5A isoform 1;eIF-4D;	0.00 - 0.15
LLVTLCQCSHA	LSPTNCDASEPLAEKVLVDLINKGR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	39.7	58.9	4	2741.71	0.93	0.47	HRG_MOUSE		Histidine-rich glycoprotein;	Histidine-proline-rich glycoprotein;	0.25 - 0.75
RVAPEEHPTL	LTEAPLNPKANR	N-ter +28.03 Da, K +28.03 Da	23.0	57.1	3	1378.87	1.91	0.35	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.85 - 1.00
LLIATGPTTA	LTEDEKQTMVDLHNQYR	N-ter +28.03 Da, K +28.03 Da	23.0	62.5	4	2175.20	0.42	0.11	PI16_MOUSE	D3Z6T6_MOUSE	Peptidase inhibitor 16;	Cysteine-rich protease inhibitor;	0.25 - 0.75
GDYIERLWAY	LTIEQLLEKR	N-ter +28.03 Da, K +28.03 Da	22.3	50.8	3	1297.86	3.50	1.38	ITH3_MOUSE	F6ZJ7_MOUSE	Inter-alpha-trypsin inhibitor heavy chain H3;		0.85 - 1.00
LLKNSPLVSR	LTLYDIAHTPGVAADLSHIETR	N-ter +28.03 Da	72.9	58.9	4	2420.41	-6.64	0.00	MDHM_MOUSE		Malate dehydrogenase, mitochondrial;		0.00 - 0.15
ALTITASVQA	LTPHYLTQKQDVER	N-ter +28.03 Da, K +28.03 Da	20.6	65.4	4	1756.07	-0.71	0.13	RPN2_MOUSE	A2ACG7_MOUSE	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase subunit 2;	Dolichyl-diphosphooligosaccharide-protein glycosyltransferase 63 kDa subunit;Ribophorin II;Ribophorin-2;	0.25 - 0.75
MEVNRKDIVF	LVDGSSLSGPSNFAIR	N-ter +28.03 Da	29.1	46.8	3	1760.99	-0.52	0.03	E9PWQ3_MOUSE	D3YWD1_MOUSE			0.25 - 0.75
GMDGSLERV	LVGELLTSPEVDERPCR	N-ter +34.06 Da, C +57.02 Da	22.5	58.8	4	2116.27	-3.06	0.51	DEN5A_MOUSE		DENN domain-containing protein 5A;	Rab6-interacting protein 1;	0.00 - 0.15
ALEVQGRDSR	LVLEVAQHLGESTVR	N-ter +28.03 Da	46.9	48.5	3	1678.02	0.36	0.05	ATPB_MOUSE		ATP synthase subunit beta, mitochondrial;		0.25 - 0.75
TDQVIQFFIA	LVNDPQPPEHLR	N-ter +28.03 Da	38.9	49.5	3	1441.84	0.43	0.04	UB2L3_MOUSE		Ubiquitin-conjugating enzyme E2 L3;	UbcM4;Ubiquitin carrier protein L3;Ubiquitin-protein ligase L3;	0.25 - 0.75
EVGGEALGRL	LVVYPWTQR	N-ter +28.03 Da	17.4	31.2	2	1188.70	0.64	0.10	HBB1_MOUSE	HBB2_MOUSE	Hemoglobin subunit beta-1;	Beta-1-globin;Hemoglobin beta-1 chain;Hemoglobin beta-major chain;	0.25 - 0.75
GIWHNDNKSF	LVVVNEEDHLR	N-ter +28.03 Da	46.5	56.4	3	1436.82	-1.56	0.23	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.00 - 0.15
KGSVAGGAVY	LVYDQELGPSDKSEAAALR	N-ter +34.06 Da, K +34.06 Da	39.2	47.3	3	2171.31	-1.84	0.26	QIL1_MOUSE		Protein QIL1;		0.00 - 0.15
LRVPPRMDYR	LYLGHNVYTAIR	N-ter +28.03 Da	40.2	50.6	3	1446.87	1.62	0.22	TRFE_MOUSE	E9Q035_MOUSE	Serotransferrin;	Beta-1 metal-binding globulin;Siderophilin;	0.75 - 0.85
VLGKPLSLAF	LYMEKNLEEVPSALPR	N-ter +34.06 Da, K +34.06 Da	20.1	45.1	3	2084.26	0.19	0.04	PRELP_MOUSE		Prolargin;	Proline-arginine-rich end leucine-rich repeat protein;	0.25 - 0.75
SCTFFLAVSG	LYSSDDVIELTPSNFNR	N-ter +28.03 Da	49.6	50.8	3	2084.11	0.37	0.08	PDIA6_MOUSE	Q3TML0_MOUSE	Protein disulfide-isomerase A6;	Thioredoxin domain-containing protein 7;	0.25 - 0.75
EQKIGQPTLL	LYVDAGAETMTOR	N-ter +28.03 Da	45.1	54.3	3	1481.80	-0.36	0.06	KAD1_MOUSE		Adenylate kinase isoenzyme 1;	ATP-AMP transphosphorylase 1;Myokinase;	0.25 - 0.75
AHHAFGQGRD	MAETFDQGAHHAFFGQGR	N-ter +28.03 Da	50.1	69.1	4	1944.00	0.29	0.07	SBSN_MOUSE	E9QP82_MOUSE	Suprabasin;		0.25 - 0.75
AREHAPSIIF	MDEIDSIGSSR	N-ter +28.03 Da	32.8	38.2	2	1236.61	-0.29	0.02	PR58_MOUSE	E9Q0L5_MOUSE	26S protease regulatory subunit 8;	26S proteasome AAA-ATPase subunit RPT6;Proteasome 26S subunit ATPase 5;Proteasome subunit p45;p45/SUG;	0.25 - 0.75
LKKAIKLVV	MDSALEALSGLIGKVPBMWAKR	N-ter +28.03 Da, K +28.03 Da	20.9	38.2	4	2685.56	1.06	0.32	DYH12_MOUSE	F6V109_MOUSE	Dynein heavy chain 12, axonemal;	Axonemal beta dynein heavy chain 12;Axonemal dynein heavy chain 12-like protein;Axonemal dynein heavy chain 7-like protein;Ciliary dynein heavy chain 12;	0.75 - 0.85
SKMFEELKNR	MDVLAQEVALLEK	N-ter +28.03 Da, K +28.03 Da	42.4	49.4	3	1670.05	-1.64	0.31	TETN_MOUSE	Q8CFZ6_MOUSE	Tetranectin;	C-type lectin domain family 3 member B;Plasminogen kringle 4-binding protein;	0.00 - 0.15
GKPLSLAF	MEKNLEEVPSALPR	N-ter +34.06 Da, K +34.06 Da	42.4	43.0	3	1808.09	-0.01	0.00	PRELP_MOUSE		Prolargin;	Proline-arginine-rich end leucine-rich repeat protein;	0.25 - 0.75
KKPFELGKL	MELHGGEGSSGKAAGDETGAIKVER	N-ter +34.06 Da, K +34.06 Da	41.8	62.8	4	2474.45	-2.84	1.42	R53A_MOUSE	D3Z7W7_MOUSE	40S ribosomal protein S3a;	Protein TU-11;	0.00 - 0.15
ETLFPQFSFIG	MESAGIHETTYNSIMKCDIDIR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	33.9	62.6	4	2639.41	2.83	0.70	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.85 - 1.00
DTPKKQALYL	MFDTPQESPVKSPVVR	N-ter +28.03 Da, K +28.03 Da	33.3	41.7	3	1870.04	0.21	0.02	TACC2_MOUSE	E9Q8T1_MOUSE	Transforming acidic coiled-coil-containing protein 2;		0.25 - 0.75
TYGICRAIRR	MGESDDSLR	N-ter +28.03 Da	26.3	32.3	2	1149.57	0.35	0.04	RS21_MOUSE		40S ribosomal protein S21;		0.25 - 0.75
RPRHQGVVMG	MGQKDCYVGEAQSKR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	26.0	63.4	4	1973.15	0.99	0.45	ACTBL_MOUSE		Beta-actin-like protein 2;	Kappa-actin;	0.75 - 0.85

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
RPRHQGVVMVG	MGQKDSYVGDEAQSQR	N-ter +34.06 Da, K +34.06 Da	25.7	60.6	4	1900.14	1.08	0.30	ACTS_MOUSE	ACTA_MOUSE	Actin, alpha skeletal muscle;	Alpha-actin-1;	0.75 - 0.85
SVILQHLRMS	MHTEAAEVLLER	N-ter +34.06 Da	44.1	52.8	3	1431.84	0.03	0.01	HIBCH_MOUSE	E0CX19_MOUSE	3-hydroxyisobutyryl-CoA hydrolase, mitochondrial; CKL-like MARVEL transmembrane domain-containing protein 2B;	3-hydroxyisobutyryl-coenzyme A hydrolase;	0.25 - 0.75
RELVPVYLTG	MILMGVTFAFISIDLCLR	N-ter +28.03 Da, C +57.02 Da	26.4	76.9	4	2221.37	1.48	0.19	CLF2B_MOUSE			Chemokine-like factor superfamily member 2B;	0.75 - 0.85
AGNKLAMQEF	MILPVGASSFKAEAMR	N-ter +34.06 Da, K +34.06 Da	34.6	49.3	3	1704.06	-0.06	0.01	ENOB_MOUSE	Q5SX59_MOUSE	Beta-enolase;		0.25 - 0.75
	MKQLPILEPGDKPR	N-ter +28.03 Da, K +28.03 Da	26.2	56.8	4	1705.09	-0.20	0.02	RABEK_MOUSE	BOR054_MOUSE	Rab9 effector protein with kelch motifs;		0.25 - 0.75
	MKVFTVGPLPAEGR	N-ter +34.06 Da, K +34.06 Da	33.0	48.7	3	1569.02	-0.74	0.16	GRHPR_MOUSE	D6REG4_MOUSE	Glyoxylate reductase/hydroxyypyruvate reductase;		0.25 - 0.75
TARRQHLSKV	MLQJAATELEKESRR	N-ter +34.06 Da, K +34.06 Da	21.2	58.3	4	1971.22	-2.12	0.09	TNNI2_MOUSE	A2A6K0_MOUSE	Troponin I, fast skeletal muscle;	Troponin I, fast-twitch isoform;	0.00 - 0.15
QLSKTEFLSF	MNTELAFTKNQKDPGLVDR	N-ter +28.03 Da, K +28.03 Da	26.5	56.1	4	2331.36	2.11	0.44	S10AB_MOUSE	F6S3J5_MOUSE	Protein S100-A11;		0.85 - 1.00
ILAQMTGTEY	MQDPDEALRR	N-ter +34.06 Da	27.3	57.3	3	1392.77	0.33	0.07	LDB3_MOUSE	E9PYJ9_MOUSE	LIM domain-binding protein 3;		0.25 - 0.75
TTMYPGIADR	MQKEITALAPSTMKIIAPPER	N-ter +28.03 Da, K +28.03 Da	41.1	62.4	4	2677.73	2.31	0.36	ACTS_MOUSE	ACTA_MOUSE	Actin, alpha skeletal muscle;	Alpha-actin-1;	0.85 - 1.00
TTMYPGIADR	MQKEITALAPSTMKIK	N-ter +28.03 Da, K +28.03 Da	30.7	56.9	4	1901.22	3.79	0.81	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.85 - 1.00
TTMYPGIADR	MQKEITALAPSTMK	N-ter +28.03 Da, K +28.03 Da	44.6	41.7	3	1631.97	0.75	0.09	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
RIALQEDTNR	MSANALAIIVFAPCILR	N-ter +28.03 Da, C +57.02 Da	19.0	63.2	3	1774.08	-0.14	0.02	MYO9A_MOUSE	D3Z3A8_MOUSE	Myosin-Ix;	Unconventional myosin-9a;	0.25 - 0.75
												Protein phosphatase 2B regulatory subunit 1;Protein phosphatase 3 regulatory subunit B alpha isoform 1;	
NSGSLVEEF	MSLPELQQNPLVQR	N-ter +28.03 Da	35.9	43.7	3	1679.98	0.60	0.04	CANB1_MOUSE		Calcineurin subunit B type 1;		0.25 - 0.75
PGLGGNFASQ	MSYGYDEKASAGVSPGPMGPSGR	N-ter +28.03 Da, K +28.03 Da	57.6	48.5	3	2481.29	-3.18	0.87	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type 1 collagen;	0.00 - 0.15
IVGRPRHOGV	MVGMGQKDSYVGDEAQSQR	N-ter +28.03 Da, K +28.03 Da	23.5	71.4	4	2169.21	0.07	0.02	ACTS_MOUSE	ACTA_MOUSE	Actin, alpha skeletal muscle;	Alpha-actin-1;	0.25 - 0.75
DHHIVTPLTA	MVIEADGDER	N-ter +28.03 Da	33.0	33.7	2	1275.62	1.38	0.08	ITIH2_MOUSE		Inter-alpha-trypsin inhibitor heavy chain H2;		0.75 - 0.85
ISKEWGFTKF	NADEFEDMVAEKR	N-ter +28.03 Da, K +28.03 Da	25.5	51.8	3	1608.83	-0.22	0.05	RL10_MOUSE		60S ribosomal protein L10;	Protein QM homolog;	0.25 - 0.75
TIKKRLETTY	NATEPVISFYDKR	N-ter +28.03 Da, K +28.03 Da	34.8	44.3	3	1594.91	-0.38	0.05	KAD1_MOUSE		Adenylate kinase isoenzyme 1;	ATP-AMP transphosphorylase 1;Myokinase;	0.25 - 0.75
TGGRRTWART	NATLSVEPEGR	N-ter +28.03 Da	42.5	38.0	2	1199.66	-0.47	0.05	ACOT2_MOUSE		Acyl-coenzyme A thioesterase 2, mitochondrial;	Acyl coenzyme A thioesterase;MTE-1;Very-long-chain acyl-CoA thioesterase;	0.25 - 0.75
FGVCHIFASF	NDTFVHVDTLSGKETICR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	25.3	64.1	4	2147.21	-0.07	0.01	RS14_MOUSE	D3YVF4_MOUSE	40S ribosomal protein S14;		0.25 - 0.75
FSKYLALNGR	NDVGVTSASLAPGPSR	N-ter +28.03 Da	25.5	56.9	3	1651.95	-0.79	0.03	E9Q2R7_MOUSE				0.25 - 0.75
RDKRSALQSI	NEWASQTTDGKLEPKVDKVER	N-ter +34.06 Da, K +34.06 Da	39.8	59.4	4	2504.51	-2.18	0.50	SERPH_MOUSE		Serpin H1;	47 kDa heat shock protein;Collagen-binding protein;Serine protease inhibitor I6;	0.00 - 0.15
												Bone morphogenetic protein-binding endothelial cell precursor-derived regulator;Protein crossveinless-2;	
KRDDLIGDGD	NFKFDVDDFAESWR	N-ter +28.03 Da, K +28.03 Da	25.9	58.3	3	1830.96	2.46	0.50	BMPER_MOUSE		BMP-binding endothelial regulator protein;		0.85 - 1.00
DHPMLPNYK	NFKGTIQELGQNYAVSGEIFVDR	N-ter +28.03 Da, K +28.03 Da	22.7	41.1	4	2867.60	4.37	1.03	TOP2B_MOUSE	F6U5K2_MOUSE	DNA topoisomerase 2-beta;	DNA topoisomerase II, beta isozyme;	0.85 - 1.00
												Phosphatase 2A inhibitor I2PP2A;Template-activating factor I;	
IPNFVWTFV	NHPQVALLGDEEEDHEALYLR	N-ter +28.03 Da	41.5	57.3	4	2548.40	3.96	0.83	SET_MOUSE	A2BE93_MOUSE	Protein SET;		0.85 - 1.00
TVRLPFGCHK	NICSLTIQIKIPR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	29.9	98.5	3	1599.08	0.49	0.05	WIPI2_MOUSE	D3YWK1_MOUSE	WD repeat domain phosphoinositide-interacting protein 2;		0.25 - 0.75
ILLWLYGADG	NIVMTQSPKSMMSVGER	N-ter +34.06 Da, K +34.06 Da	35.8	43.7	3	2049.16	-1.32	0.20	KV5A2_MOUSE		Ig kappa chain V-V region MOPC 21;		0.15 - 0.25
FLPMMQAISN	NKDQGGYEDFVEGLR	N-ter +34.06 Da, K +34.06 Da	45.4	47.5	3	1794.01	-1.12	0.34	E9PWG4_MOUSE	MYL1_MOUSE			0.15 - 0.25
KAAQAQAVASY	NMGSDSLYFR	N-ter +28.03 Da	29.0	39.9	2	1379.67	2.23	0.50	Q9D1B1_MOUSE				0.85 - 1.00
GALGCAICHG	NPVDDICIAKPR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	22.2	39.6	3	1464.90	-0.36	0.03	ANT3_MOUSE		Antithrombin-III;	Serpin C1;	0.25 - 0.75
												Proline-arginine-rich end leucine-rich repeat protein;	
PSLAFLYMEK	NQLLEVPALPR	N-ter +28.03 Da	33.2	35.2	2	1379.79	0.30	0.02	PRELP_MOUSE		Prolargin;		0.25 - 0.75
SGDSLTVASS	NTDFAFSLYR	N-ter +28.03 Da	33.8	51.2	2	1260.68	-1.09	0.19	SPA3G_MOUSE	D3Z450_MOUSE	Serine protease inhibitor A3G;	Serine protease inhibitor 2A;	0.15 - 0.25
DIDSAPITAR	NTGIICITGPASR	N-ter +28.03 Da, C +57.02 Da	31.1	56.6	3	1386.81	0.08	0.01	KPYM_MOUSE		Pyruvate kinase isozymes M1/M2;	Pyruvate kinase muscle isozyme;	0.25 - 0.75
												Cell surface antigen CD96;T cell-activated increased late expression protein;	
SNSSMTTKDG	NYLEASSGTDAKNSSR	N-ter +34.06 Da, K +34.06 Da	28.4	66.7	3	1767.02	-2.18	0.20	TACT_MOUSE		T-cell surface protein tactile;		0.00 - 0.15
IGKIGGAQNR	NYSKLLCGLLSDR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	38.7	60.2	3	1593.95	1.92	0.30	MIF_MOUSE		Macrophage migration inhibitory factor;	Delayed early response protein 6;Glycosylation-inhibiting factor;L-dopachrome isomerase;L-dopachrome tautomerase;Phenylpyruvate tautomerase;	0.85 - 1.00
DKIREYKSKR	QASGGPVDIGPEYQQDLDR	N-ter +28.03 Da	46.2	46.6	3	2072.08	-1.74	0.17	ATP5J_MOUSE	E9QAD6_MOUSE	ATP synthase-coupling factor 6, mitochondrial;		0.00 - 0.15
GRKTETVCTF	QDQALVHQHQWDGKESTITR	N-ter +28.03 Da, K +28.03 Da	34.1	55.0	4	2352.31	1.54	0.32	FABP5_MOUSE		Fatty acid-binding protein, epidermal;	Epidermal-type fatty acid-binding protein;Fatty acid-binding protein 5;Keratinocyte lipid-binding protein;Psoriasis-associated fatty acid-binding protein homolog;	0.75 - 0.85
ESQVLDEQTY	QEDEPTIASPVGWPR	N-ter +28.03 Da	38.3	30.1	3	1708.89	0.45	0.03	ETV6_MOUSE	Q80WR3_MOUSE			0.25 - 0.75
VFSMFQDTQJ	QEFKEAFTVIDQNR	N-ter +34.06 Da, K +34.06 Da	47.9	42.0	3	1792.05	-2.94	0.68	MLRS_MOUSE	F6ULR7_MOUSE	Myosin regulatory light chain 2, skeletal muscle isoform;		0.00 - 0.15
HGYAAAGQTW	QEGDKVIRPVGVSQAGEEMEQFGQGV	N-ter +28.03 Da, K +28.03 Da	39.7	63.0	4	2886.61	0.90	0.29	E9QP82_MOUSE			Fast skeletal myosin light chain 2;MLC2F;	0.25 - 0.75

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
LLTSRSNAQR	QEIAQEFKTLFGR	N-ter +28.03 Da, K +28.03 Da	44.5	51.0	3	1621.97	2.05	0.17	ANXAS_MOUSE		Annexin A5;	Ancholin CII;Annexin V;Annexin-5;Calphobindin I;Endonexin II;Lipocortin V;Placental anticoagulant protein 4;Placental anticoagulant protein I;Thromboplastin inhibitor;Vascular anticoagulant-alpha;	0.85 - 1.00
STFQQMWISK	QEYDEAGPSIVHR	N-ter +28.03 Da	45.4	47.9	3	1527.81	-0.89	0.10	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.15 - 0.25
RQFYRYITD	QEYIYSIHR	N-ter +28.03 Da	31.5	56.1	3	1336.75	-1.15	0.05	MAZB2_MOUSE	F6TMZ3_MOUSE	Epididymis-specific alpha-mannosidase;	Mannosidase alpha class 2B member 2;	0.15 - 0.25
FHVNLLCGEE	QGADAALHFNPR	N-ter +28.03 Da	28.6	73.4	3	1323.77	0.21	0.02	O9CRB1_MOUSE	LEG7_MOUSE			0.25 - 0.75
KDLVASVPDM	QGDGEDNHVDGDKGPR	N-ter +34.06 Da, K +34.06 Da	9.2	90.0	3	1763.01	-2.94	0.91	NC2A_MOUSE	D3YYC2_MOUSE	Dr1-associated corepressor;	Dr1-associated protein 1;Negative co-factor 2-alpha;	0.00 - 0.15
RRQHLKSVML	QJAATELEKEESR	N-ter +28.03 Da, K +28.03 Da	27.9	51.0	3	1558.90	-0.67	0.05	TNNI2_MOUSE	A2AGK0_MOUSE	Troponin I, fast skeletal muscle;	Troponin I, fast-twitch isoform;	0.25 - 0.75
RNLHASNTRL	QKTGTAEMSSILEER	N-ter +28.03 Da, K +28.03 Da	52.1	52.2	3	1734.97	-0.81	0.14	ATPA_MOUSE	D6RJ16_MOUSE	ATP synthase subunit alpha, mitochondrial;		0.15 - 0.25
KWKEDVELYR	QKVAPLGAELQESAR	N-ter +28.03 Da, K +28.03 Da	48.7	44.0	3	1652.00	-0.20	0.02	APOA1_MOUSE	Q8BPD5_MOUSE	Apolipoprotein A-I;	Apolipoprotein A1;	0.25 - 0.75
DEEKMEIQEM	QLKEAKHIAEDSDR	N-ter +28.03 Da, K +28.03 Da	22.6	62.8	4	1723.04	0.40	0.09	TPM2_MOUSE	A2AIM4_MOUSE	Tropomyosin beta chain;	Beta-tropomyosin;Tropomyosin-2;	0.25 - 0.75
NTEENRRFYR	QLLLTADDR	N-ter +28.03 Da	37.2	34.5	2	1071.63	1.84	0.14	ALDOA_MOUSE	Q9CPQ9_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.85 - 1.00
LYKPVTDLFL	QLVDSGVKDEAR	N-ter +28.03 Da, K +28.03 Da	26.7	47.1	3	1371.80	-0.60	0.08	LPFRC_MOUSE			130 kDa leucine-rich protein;	0.25 - 0.75
MTTASPSQVR	QNYHQDAEAANR	N-ter +28.03 Da	38.0	48.7	3	1556.81	-2.84	0.41	FRIH_MOUSE		Ferritin heavy chain;		0.00 - 0.15
FRRRDKDTE	QPGEVSALGGQPAR	N-ter +34.06 Da	24.0	66.4	3	1399.86	-2.40	0.50	KCNH2_MOUSE	Q53Z09_MOUSE	Potassium voltage-gated channel subfamily H member 2;	Ether-a-go-go-related gene potassium channel 1;Voltage-gated potassium channel subunit Kv11.1;	0.00 - 0.15
QSLPSSHGPPS	QPGLPAVLSSPPLSPR	N-ter +28.03 Da	26.4	48.8	4	1827.12	4.13	0.93	CB071_MOUSE		Uncharacterized protein C2orf71 homolog;		0.85 - 1.00
LQPNQLGPPS	QPHLSVSSAANGHLGR	N-ter +34.06 Da	23.4	61.8	3	1664.00	-3.84	1.64	NOTC1_MOUSE	Q7TQ50_MOUSE	Neurogenic locus notch homolog protein 1;	Notch A;mt14;p300;	0.00 - 0.15
LLALQPALGS	QPPSASSSHSMGSSR	N-ter +28.03 Da	25.0	67.1	3	1529.79	1.62	0.17	V510L_MOUSE		V-set and immunoglobulin domain-containing protein 10-like;		0.75 - 0.85
LLHPTLLAQ	QSNVDELGCSHLGQSYESR	N-ter +34.06 Da, C +57.02 Da	59.8	42.6	3	2199.10	-1.74	0.52	CO3A1_MOUSE	Q5DTG2_MOUSE	Collagen alpha-1(III) chain;		0.00 - 0.15
LGRFAVRDMR	QTVAVGVIAVDKK	N-ter +28.03 Da, K +28.03 Da	31.2	56.1	4	1567.10	1.11	0.17	EF1A1_MOUSE		Elongation factor 1-alpha 1;	Elongation factor Tu;Eukaryotic elongation factor 1 A-1;	0.75 - 0.85
EKVIVPNMEF	RAADEEAFEDNSEEYR	N-ter +28.03 Da	52.2	53.4	3	2071.02	4.27	1.04	XPO2_MOUSE	E9QAX7_MOUSE	Exportin-2;	Chromosome segregation 1-like protein;Importin-alpha re-exporter;	0.85 - 1.00
RRGQSSANR	RAGSSSGVQVASAGGLAADASRR	N-ter +34.06 Da	39.3	56.2	4	2266.29	-2.12	0.65	F78VV1_MOUSE	FILA_MOUSE	Filaggrin;		0.00 - 0.15
RRGQSSANR	RAGSSSGVQVASAGGLAADASR	N-ter +28.03 Da	79.1	48.8	3	2104.13	-1.03	0.40	FILA_MOUSE	F78VV1_MOUSE	Filaggrin;		0.15 - 0.25
QYHVAVSLCQ	RAKAMSHFPESEYR	N-ter +28.03 Da, K +28.03 Da	30.0	63.2	4	1976.15	-0.43	0.05	ACON_MOUSE		Aconitate hydratase, mitochondrial;	Citrate hydro-lyase;	0.25 - 0.75
MRAAPR	RAPAAQPPAAAPSVAAGSAPAAAPR	N-ter +34.06 Da	61.9	41.3	4	2186.30	1.96	0.44	CHCH2_MOUSE	B2RPU8_MOUSE	Coiled-coil-helix-coiled-coil-helix domain-containing protein 2, mitochondrial;		0.85 - 1.00
PFYLRPFSFL	RAPSWIOTGLSEMR	N-ter +28.03 Da	40.4	47.5	3	1645.90	-1.40	0.18	CRYAB_MOUSE		Alpha-crystallin B chain;	Alpha(B)-crystallin;P23;	0.15 - 0.25
PVPVQPSWLR	RASAPLPGFSAPGR	N-ter +28.03 Da	40.0	54.3	3	1410.85	-0.89	0.15	HSPB6_MOUSE		Heat shock protein beta-6;		0.15 - 0.25
VSSSLPDICY	RCGESHLAKDCDLQEDACYNCR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	44.8	60.2	4	2926.40	-0.01	0.01	D3YFF6_MOUSE				0.25 - 0.75
RRASALAQL	RCILDSELEGR	N-ter +28.03 Da, C +57.02 Da	33.4	42.2	3	1487.84	0.60	0.06	KBL_MOUSE	E9PWY6_MOUSE	2-amino-3-ketobutyrate coenzyme A ligase, mitochondrial;	Aminoacetone synthase;Glycine acetyltransferase;	0.25 - 0.75
AAGFNKLGML	RDDTLHETEDVKEAIR	N-ter +34.06 Da, K +34.06 Da	21.0	54.6	4	1994.18	0.11	0.02	QCR7_MOUSE	Q9CQB4_MOUSE	Cytochrome b-c1 complex subunit 7;	Complex III subunit 7;Complex III subunit VII;Ubiquinol-cytochrome c reductase complex 14 kDa protein;	0.25 - 0.75
KEMKESIKKF	RDEAKKLEESDALQEAR	N-ter +28.03 Da, K +28.03 Da	31.6	74.2	4	2071.24	0.08	0.03	TIM44_MOUSE	F7C189_MOUSE	Mitochondrial import inner membrane translocase subunit TIM44;		0.25 - 0.75
AKAVLSAEKL	RDEEVHTGLGELLR	N-ter +34.06 Da	29.9	55.6	3	1656.99	1.34	0.17	SERPH_MOUSE		Serpin H1;	47 kDa heat shock protein;Collagen-binding protein;Serine protease inhibitor J6;	0.75 - 0.85
LSLMPESEF	RDIDNPSAEAR	N-ter +28.03 Da	28.2	73.0	3	1399.77	0.63	0.11	PLIN1_MOUSE		Perilipin-1;	Lipid droplet-associated protein;Perilipin A;	0.25 - 0.75
APSDNRVTSF	RDLIHDQDEEEEEEQGR	N-ter +28.03 Da	53.6	66.5	4	2283.14	-0.36	0.13	NSF1C_MOUSE	A2AT02_MOUSE	NSF1 cofactor p47;	p97 cofactor p47;	0.25 - 0.75
DIKSKTYQVM	RDYEQAGSAAAPSVFSR	N-ter +28.03 Da	72.4	58.2	3	1767.96	-1.64	0.31	MSTN1_MOUSE		Musculoskeletal embryonic nuclear protein 1;		0.00 - 0.15
LVKDRNVATP	RDYFALAHTRVDRHLVGR	N-ter +28.03 Da	36.7	27.4	4	2216.22	5.97	1.65	PYGL_MOUSE	PYGM_MOUSE	Glycogen phosphorylase, liver form;		0.85 - 1.00
SIIRNVKGPV	REGDVLTLLESER	N-ter +28.03 Da	35.6	56.8	3	1543.91	-0.67	0.09	RS28_MOUSE		40S ribosomal protein S28;		0.25 - 0.75
MSYFPRGLKY	REGVESAFHKTTSGATPAAIR	N-ter +28.03 Da, K +28.03 Da	33.1	65.9	4	2298.36	0.03	0.01	Q99LB4_MOUSE	D3YZN3_MOUSE			0.25 - 0.75
QAQPNANEDY	REGPCAVNLVLR	N-ter +28.03 Da, C +57.02 Da	35.2	52.6	3	1410.85	-0.06	0.01	STK39_MOUSE		STE20/SPS1-related proline-alanine-rich protein kinase;	Serine/threonine-protein kinase 39;	0.25 - 0.75
IRKLPFQRLV	REIAQDFKTDLR	N-ter +34.06 Da, K +34.06 Da	33.5	63.3	4	1559.01	-0.81	0.11	H31_MOUSE	H32_MOUSE	Histone H3.1;		0.15 - 0.25
KQIQKLEXRV	RELEGEVENEQKR	N-ter +34.06 Da, K +34.06 Da	33.3	64.6	4	1683.03	-3.06	1.02	MYH1_MOUSE	MYH8_MOUSE	Myosin-1;	Myosin heavy chain 1;Myosin heavy chain 2x;Myosin heavy chain, skeletal muscle, adult 1;	0.00 - 0.15
TFYSNKIFL	RELISNASDALDKIR	N-ter +28.03 Da, K +28.03 Da	42.3	67.3	4	1756.10	-0.09	0.01	H590B_MOUSE	ENPL_MOUSE	Heat shock protein HSP 90-beta;	Heat shock 84 kDa;Tumor-specific transplantation 84 kDa antigen;	0.25 - 0.75
TFYSNKIFL	RELISNDSALDKIR	N-ter +28.03 Da, K +28.03 Da	26.2	56.9	4	1772.08	0.79	0.07	H590A_MOUSE	B7ZC49_MOUSE	Heat shock protein HSP 90-alpha;	Heat shock 86 kDa;Tumor-specific transplantation 86 kDa antigen;	0.25 - 0.75
ITNHDEYSLR	RELMEKKDEGTGLR	N-ter +28.03 Da, K +28.03 Da	22.7	65.4	4	1975.17	-0.62	0.26	TLN1_MOUSE	A2AIM2_MOUSE	Talin-1;		0.25 - 0.75
GFSAGSAIHW	REPEKGEVWDYVTVR	N-ter +28.03 Da, K +28.03 Da	31.0	62.4	4	1918.11	0.74	0.11	RISC_MOUSE	Q3USP4_MOUSE	Retinoid-inducible serine carboxypeptidase;	Serine carboxypeptidase 1;	0.25 - 0.75
SPFRKDKSPV	REPIDLNTPER	N-ter +28.03 Da	24.1	52.7	3	1495.84	-0.18	0.02	RBM39_MOUSE	Q3U313_MOUSE	RNA-binding protein 39;	Coactivator of activating protein 1 and estrogen receptors;RNA-binding motif protein 39;RNA-binding region-containing protein 2;Transcription coactivator CAPER;	0.25 - 0.75

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
DEKCSSTELFV	REPPIMVTKQLEDMNAYCGER	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	49.8	62.5	4	2604.48	-6.64	0.00	D3YU50_MOUSE	Q6P6L5_MOUSE		Autophagy-related protein LC3 B;Autophagy-related ubiquitin-like modifier LC3 B;MAP1 light chain 3-like protein 2;MAP1A/MAP1B light chain 3 B;Microtubule-associated protein 1 light chain 3 beta;	0.00 - 0.15
EQRVEDVRLI	REQHPTKIPVIER	N-ter +34.06 Da, K +34.06 Da	26.4	62.6	4	1783.22	-1.36	0.28	MLP3B_MOUSE		Microtubule-associated proteins 1A/1B light chain 3B;		0.15 - 0.25
PLPTFSSLNL	RETNLESLPLVDTHSKR	N-ter +28.03 Da, K +28.03 Da	32.0	61.7	4	2050.24	2.62	0.29	VIME_MOUSE	E9PZV5_MOUSE	Vimentin;		0.85 - 1.00
AKVQAINVSS	RFEEIEKAQEER	N-ter +28.03 Da, K +28.03 Da	34.8	62.2	4	1747.98	0.33	0.06	Q8C845_MOUSE	EFHD2_MOUSE			0.25 - 0.75
GKAFLRQLPF	RGDDGIFDDNFIEER	N-ter +28.03 Da	49.5	58.7	3	1824.93	-0.01	0.00	SNX3_MOUSE	Q78ZM0_MOUSE	Sorting nexin-3;	SDP3 protein;	0.25 - 0.75
GKALKRQLPF	RGDEGIFEEFIEER	N-ter +34.06 Da	55.0	62.2	3	1846.01	-0.06	0.01	SNX12_MOUSE	Q6ZWQ5_MOUSE	Sorting nexin-12;	SDP8 protein;	0.25 - 0.75
APGPAGASGD	RGEAGAAAGSPGAPGR	N-ter +28.03 Da	34.2	19.9	3	1434.76	1.43	0.32	CO1A2_MOUSE	E9Q6U9_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.75 - 0.85
PVGPAGKNGD	RGETGPAGPAGPIGAGAR	N-ter +34.06 Da	75.6	48.5	3	1722.02	-2.64	0.50	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.00 - 0.15
KETRANRAKR	RGGGGHDAKGNVCGSR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	37.2	68.8	4	1850.06	2.60	0.74	FBN1_MOUSE	A2AQ53_MOUSE	Fibrillin-1;		0.85 - 1.00
M	RGQVGLSPQQEAALAR	N-ter +28.03 Da	53.5	53.8	3	2011.14	1.69	0.39	S14L4_MOUSE		SEC14-like protein 4;		0.85 - 1.00
EILTRLRLQK	RGTGGVDTAAVAVFDISNADR	N-ter +34.06 Da	82.8	52.6	3	2182.23	-5.64	2.82	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.00 - 0.15
IGSSADRQGR	RGVSESQASDESGHDFSEGOAVGAHR	N-ter +28.03 Da	79.2	58.3	4	2814.42	3.43	1.31	F7BVV1_MOUSE	E9Q019_MOUSE			0.85 - 1.00
CGCDFSLTVR	RHHCHACGKIVCR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	17.8	42.7	4	1757.99	-3.47	0.77	FGD5_MOUSE	E9QLU9_MOUSE	FYVE, RhoGEF and PH domain-containing protein 5;		0.00 - 0.15
LGTFLYEYSR	RHPDYYSVLLLR	N-ter +28.03 Da	26.6	36.6	3	1482.89	-0.40	0.04	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
AGTIAGLNLV	RIINEPTAAAIAYGLDKKVAER	N-ter +28.03 Da, K +28.03 Da	62.1	62.4	4	2539.61	1.64	0.13	HSP7C_MOUSE	Q504P4_MOUSE	Heat shock cognate 71 kDa protein;	Heat shock 70 kDa protein 8;	0.75 - 0.85
TFKNYKRNW	RIVEDEPNKICEADR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	28.6	70.1	4	1899.09	1.58	0.26	XPO2_MOUSE	E9QA7_MOUSE	Exportin-2;	protein;importin-alpha re-exporter;	0.75 - 0.85
GGISETRIEK	RIVITGDAALDHDQALQAIAR	N-ter +28.03 Da	47.8	64.4	4	2274.39	-0.36	0.03	E41L2_MOUSE	Q811B2_MOUSE	Band 4.1-like protein 2;	Generally expressed protein 4.1;	0.25 - 0.75
DARGHRPVDR	RKEEPPSLRAPPPIGGGYR	N-ter +28.03 Da, K +28.03 Da	20.2	49.5	4	2316.39	-0.22	0.04	FIBB_MOUSE		Fibrinogen beta chain;		0.25 - 0.75
MPLGLGR	RKKAPPLVENEAEPSR	N-ter +28.03 Da, K +28.03 Da	34.0	57.8	4	2033.24	2.47	0.69	GIPC1_MOUSE		PDZ domain-containing protein GIPC1;	GAIP C-terminus-interacting protein;RGS-GAIP-interacting protein;RGS19-interacting protein 1;SemaF cytoplasmic domain-associated protein 1;Synectin;	0.85 - 1.00
LLALAGLLQA	RLLLPQQAQGECDR	N-ter +28.03 Da, C +57.02 Da	48.7	46.9	3	1787.00	-2.64	0.66	ENDD1_MOUSE	Q692Y2_MOUSE	Endonuclease domain-containing 1 protein;		0.00 - 0.15
RAAPRQSSSF	RLLQALEAEER	N-ter +28.03 Da	39.2	51.5	3	1483.88	0.45	0.04	PDL1_MOUSE	F7C957_MOUSE	PDZ and LIM domain protein 2;	PDZ-LIM protein mystique;	0.25 - 0.75
VETQPQKTVI	RLPSGSGPASPTTGSVDIR	N-ter +34.06 Da	52.0	54.2	3	1959.17	-1.79	0.55	E9Q616_MOUSE				0.00 - 0.15
APAAGMRRRR	RLQQEDGISFEYHR	N-ter +28.03 Da	48.4	52.2	3	1804.98	2.12	0.33	CBPE_MOUSE		Carboxypeptidase H;Enkephalin convertase;Prohormone-processing		0.85 - 1.00
ADESTGSIK	RLQSIGTENTEENR	N-ter +34.06 Da	19.0	59.7	4	1836.08	-1.47	0.45	ALDOA_MOUSE	Q9CPQ9_MOUSE	Fructose-bisphosphate aldolase A;	Carboxypeptidase;	0.85 - 1.00
ADESTGSIK	RLQSIGTENTEENR	N-ter +28.03 Da	37.3	47.1	3	1673.91	0.39	0.06	ALDOA_MOUSE	Q9CPQ9_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.15 - 0.25
KTYGICRAIR	RMGESDSSILR	N-ter +34.06 Da	31.4	68.1	3	1311.76	-0.92	0.09	RS21_MOUSE		40S ribosomal protein S21;	Aldolase 1;Muscle-type aldolase;	0.25 - 0.75
IIPRHLQLAI	RNDEELNKLGR	N-ter +28.03 Da, K +28.03 Da	27.7	66.4	4	1511.94	0.06	0.01	H2A1F_MOUSE	H2A1H_MOUSE	Histone H2A type 1-F;		0.15 - 0.25
GMDVAASEFY	RNGKYDLKFPDPPAR	N-ter +34.06 Da, K +34.06 Da	25.1	65.7	4	2095.29	-2.18	0.40	ENOB_MOUSE		Beta-enolase;	2-phospho-D-glycerate hydro-lyase;Enolase 3;Muscle-specific enolase;Skeletal muscle enolase;	0.00 - 0.15
MFLPILQHS	RNKEQGTDFVFEGLR	N-ter +28.03 Da, K +28.03 Da	23.9	54.6	3	1996.11	1.25	0.16	MYL4_MOUSE	Q9CZ19_MOUSE	Myosin light chain 4;	MLC1EMB;Myosin light chain 1, atrial/fetal isoform;	0.75 - 0.85
SVVRPFAKLV	RPPVQVYGIETR	N-ter +34.06 Da	30.6	34.5	3	1403.86	-2.40	0.13	ATPO_MOUSE	D3Z4J0_MOUSE	ATP synthase subunit O, mitochondrial;	Oligomycin sensitivity conferral protein;	0.00 - 0.15
VDKIREYKSK	RQASGGPVDIGPEYQDLDLR	N-ter +28.03 Da	73.8	50.6	3	2228.19	3.98	0.97	ATP5I_MOUSE	E9QAD6_MOUSE	ATP synthase-coupling factor 6, mitochondrial;		0.85 - 1.00
QDIAKMLPLL	RQELESVEAGVQGGAFEGTR	N-ter +28.03 Da	66.8	53.1	3	2276.22	4.63	1.63	EHD2_MOUSE	Q8R2X0_MOUSE	EH domain-containing protein 2;		0.85 - 1.00
LQAQRAFTTR	RQISEDVDGPDNR	N-ter +34.06 Da	48.7	38.4	3	1533.82	-0.84	0.09	NEDD4_MOUSE		E3 ubiquitin-protein ligase NEDD4;	Neural precursor cell expressed developmentally down-regulated protein 4;	0.15 - 0.25
GRSSNRDRP	RQPSPSSQSSQVHSGVQVEGR	N-ter +28.03 Da	44.5	63.1	4	2379.30	0.87	0.25	E9Q019_MOUSE	F7BVV1_MOUSE			0.25 - 0.75
PNIDIRSAFK	RSFEGGEDAGELDFGLLKR	N-ter +34.06 Da, K +34.06 Da	53.6	65.2	4	2231.33	-2.32	0.23	D3YU50_MOUSE	Q6P6L5_MOUSE			0.00 - 0.15
AAGGGGGENY	RSPVHPESSEDEHVSIPQR	N-ter +28.03 Da	50.2	68.0	4	2342.28	-0.62	0.12	E9QPZ3_MOUSE				0.25 - 0.75
SQSGSGRSPR	RSPVHPESSEGEHVSVPQR	N-ter +34.06 Da	46.3	62.3	4	2276.28	-1.56	0.41	FILA2_MOUSE	E9QPZ3_MOUSE	Filaggrin-2;	Intermediate filament-associated protein;	0.00 - 0.15
SQDCSPATSR	RSSVSGISLEDNR	N-ter +28.03 Da	34.4	53.4	3	1446.82	0.32	0.03	PDL1_MOUSE	A8Y5C3_MOUSE	PDZ and LIM domain protein 4;	LIM protein RIL;Reversion-induced LIM protein; Metastasin;Metastatic cell protein;PEL98;Placental calcium-binding protein;Protein 18A2;Protein Mts1;S100 calcium-binding protein A4;	0.25 - 0.75
TRELPSFLGE	RTDEAAQKVMNSLDSNR	N-ter +28.03 Da, K +28.03 Da	44.8	61.9	4	2137.19	0.57	0.07	S100A4_MOUSE	D3YU9_MOUSE	Protein S100-A4;	General transcription factor TFIIIB;RNA polymerase II alpha initiation factor;	0.25 - 0.75
YMASQASAEK	RTQKEIGDIAGVADVTIR	N-ter +28.03 Da, K +28.03 Da	25.7	61.0	4	1997.25	-0.36	0.02	TF2B_MOUSE		Transcription initiation factor IIB;		0.25 - 0.75
IWHHSFYNEL	RVAPPEEHTLLTEAPLNPKANR	N-ter +28.03 Da, K +28.03 Da	64.5	52.2	4	2508.51	3.30	0.19	ACTA_MOUSE	ACTC_MOUSE	Actin, aortic smooth muscle;	Alpha-actin-2;	0.85 - 1.00
IWHHTFYNEL	RVAPPEEHPVLLTEAPLNPKANR	N-ter +28.03 Da, K +28.03 Da	58.1	61.3	4	2506.56	4.28	0.40	ACTB_MOUSE	ACTG_MOUSE	Actin, cytoplasmic 1;	Beta-actin;	0.85 - 1.00
MATL	RVHPEAQAKVDVFR	N-ter +28.03 Da, K +28.03 Da	21.4	69.0	4	1707.08	-0.84	0.14	PSME1_MOUSE		Proteasome activator complex subunit 1;	11S regulator complex subunit alpha;Activator of multicatalytic protease subunit 1;Proteasome activator 28 subunit alpha;	0.15 - 0.25
NVVGARRSSW	RVISSIEQKTER	N-ter +28.03 Da, K +28.03 Da	30.2	60.1	4	1500.95	1.87	0.35	1433B_MOUSE	A2A5N1_MOUSE	14-3-3 protein beta/alpha;	Protein kinase C inhibitor protein 1;	0.85 - 1.00
LNGKLTGMAF	RVPTPNVSVVDLTCR	N-ter +28.03 Da, C +57.02 Da	48.4	43.8	3	1740.01	0.48	0.04	G3P_MOUSE	G3PT_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase;	Peptidyl-cysteine 5-nitrosylase GAPDH;	0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
ESLGLSPSEV	RVTHVHGCGEDGVATR	N-ter +34.06 Da, C +57.02 Da	18.5	72.6	4	1885.08	-1.43	0.12	ZKSC3_MOUSE	QSRJ53_MOUSE	Zinc finger protein with KRAB and SCAN domains 3;	SCAN-KRAB-zinc finger protein;Zinc finger protein 306;Zinc finger protein 307;Zinc finger protein 47 homolog;	0.15 - 0.25
VVFHYRAARD	RYALTFAEQEACTR	N-ter +34.06 Da, C +57.02 Da	12.8	65.6	4	1718.98	-1.89	0.42	NCAN_MOUSE		Neurocan core protein;	Chondroitin sulfate proteoglycan 3;	0.00 - 0.15
GPYDRPRTAR	RYIGIVKQAGLDR	N-ter +28.03 Da, K +28.03 Da	29.3	54.8	4	1544.00	0.47	0.05	HNRPF_MOUSE		Heterogeneous nuclear ribonucleoprotein F;		0.25 - 0.75
FLYKMGDDYY	RYLAEVATGDDKKR	N-ter +28.03 Da, K +28.03 Da	37.0	64.8	4	1705.06	0.89	0.14	14335_MOUSE		14-3-3 protein sigma;	Stratifin;	0.25 - 0.75
GGGVGGPGAK	SAAQAAAQNTNSNAAGKQLR	N-ter +34.06 Da, K +34.06 Da	43.5	46.4	3	1925.16	-4.06	1.35	PAIRB_MOUSE		Plasminogen activator inhibitor 1 RNA-binding protein;	PAI1 RNA-binding protein 1;SERPINE1 mRNA-binding protein 1;	0.00 - 0.15
QDEGAEPMGY	SAELSSSEGILDRNEEKR	N-ter +34.06 Da, K +34.06 Da	51.9	61.5	4	2115.24	0.64	0.12	EZRI_MOUSE		Ezrin;	Cytovillin;Villin-2;p81;	0.25 - 0.75
QDEGAEPMGY	SAELSSSEGILDDR	N-ter +28.03 Da	42.5	46.3	3	1418.75	0.03	0.00	EZRI_MOUSE		Ezrin;	Cytovillin;Villin-2;p81;	0.25 - 0.75
QHQGIPVFF	SAGIGDVLVEEVR	N-ter +28.03 Da	28.2	52.4	3	1384.83	0.42	0.10	SNT3_MOUSE		Cytosolic 5'-nucleotidase 3;	Cytosolic 5'-nucleotidase III;Lupin;Pyrimidine 5'-nucleotidase 1;	0.25 - 0.75
LFQPSFIGME	SAGIHETYSIMKCDIDIR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	38.0	62.4	4	2379.31	1.04	0.17	ACT5_MOUSE	ACTA_MOUSE	Actin, alpha skeletal muscle;	Alpha-actin-1;	0.75 - 0.85
MATRSVCVSRG	SAGSAAAGPVEAAR	N-ter +28.03 Da	42.2	42.3	3	1354.78	-0.12	0.01	BOLA1_MOUSE		BOLA-like protein 1;		0.25 - 0.75
SQMSYGYDEK	SAGVSVPGMPGSPGR	N-ter +28.03 Da	49.5	39.4	3	1479.81	-2.74	0.37	CO1A1_MOUSE	F8WGB7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.00 - 0.15
VLELYKTGNA	SALLLPDQGR	N-ter +34.06 Da	42.2	34.1	2	1215.78	-1.64	0.57	SPA3K_MOUSE		Serine protease inhibitor A3K;	Contrapsin;SPI-2;	0.00 - 0.15
VLHIGSAHNR	SAMPFTASPAPSTR	N-ter +28.03 Da	28.5	44.2	3	1447.78	0.84	0.08	PDU1_MOUSE		PD2 and LIM domain protein 1;	C-terminal LIM domain protein 1;Elfin;LIM domain protein CLP-36;	0.25 - 0.75
QEPKRSARL	SAMPVPFTEPKPKR	N-ter +28.03 Da, K +28.03 Da	30.7	60.1	4	1781.13	0.82	0.07	HMG5_MOUSE		High mobility group nucleosome-binding domain-containing protein 5;	Nucleosome-binding protein 1;Nucleosome-binding protein 45;Protein GARP45;	0.25 - 0.75
VTLINFWPVD	SAPASSQLSHDDTHSR	N-ter +28.03 Da	51.2	63.4	4	1819.96	0.00	0.00	DMD_MOUSE	A2A922_MOUSE	Dystrophin;		0.25 - 0.75
AVNSSYKRR	SAPCEDPFPKAKLR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	30.8	45.9	3	1757.00	-0.89	0.17	E9Q3G8_MOUSE				0.15 - 0.25
VPRASMSCSR	SAPPKLASLKGVPEDAVETLAGSLGR	N-ter +28.03 Da, K +28.03 Da	44.3	54.5	4	2846.77	0.86	0.48	ICAL_MOUSE	Q921U7_MOUSE	Calpastatin;	Calpain inhibitor;	0.25 - 0.75
KSMWEKVSF	SAPSASGTPNKETAGLKVGVSSR	N-ter +28.03 Da, K +28.03 Da	36.9	54.5	4	2284.36	0.08	0.02	Q8VCQ8_MOUSE	E9Q0M9_MOUSE			0.25 - 0.75
FEQQVQAAAY	SASKGGIVGMLPIAR	N-ter +34.06 Da, K +34.06 Da	35.4	40.7	3	1625.06	-0.30	0.02	Q99N15_MOUSE	A2AFQ2_MOUSE			0.25 - 0.75
SCLVLAARHA	SASSTNLKDVLSNLIPIKEQAR	N-ter +34.06 Da, K +34.06 Da	22.1	58.4	4	2372.55	0.14	0.05	CISY_MOUSE		Citrate synthase, mitochondrial;		0.25 - 0.75
RYEDMAAFMK	SAVEKGEELSCER	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	28.3	54.1	3	1677.88	0.26	0.05	14335_MOUSE		14-3-3 protein sigma;	Stratifin;	0.25 - 0.75
GEARDRTYRR	SAVPPGADKAEAGASGATFQFR	N-ter +28.03 Da, K +28.03 Da	50.9	56.5	4	2475.42	1.16	0.11	RS10_MOUSE		40S ribosomal protein S10;		0.75 - 0.85
GTRKPKVDAF	SCHLAQAPNHVVVSR	N-ter +34.06 Da, C +57.02 Da	45.4	58.5	4	1708.00	-0.52	0.10	TRFE_MOUSE	E9Q035_MOUSE	Serotransferrin;	Beta-1 metal-binding globulin;Siderophilin;	0.25 - 0.75
TQCCAEADKE	SCLTPKLDGVKEKALVSSVR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	25.8	61.3	4	2298.48	-0.29	0.03	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
TESTVKTTF	SCNLGEKFDETTADGR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	40.1	47.4	3	1854.93	1.56	0.24	FABP5_MOUSE	E9Q964_MOUSE	Fatty acid-binding protein, epidermal;	Epidermal-type fatty acid-binding protein;Fatty acid-binding protein 5;Keratinocyte lipid-binding protein;Psoriasis-associated fatty acid-binding protein homolog;	0.75 - 0.85
LWALLTPAEA	SCQGIQCAPGQR	N-ter +28.03 Da, C +57.02 Da	27.1	48.5	3	1388.70	0.77	0.22	E9PVG8_MOUSE				0.25 - 0.75
AIGIDLTTY	SCVGVFGHGKVEIANDQGNR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	52.6	54.6	4	2383.34	1.64	0.15	H571A_MOUSE	HS71B_MOUSE	Heat shock 70 kDa protein 1A;	Heat shock 70 kDa protein 3;Hsp68;	0.75 - 0.85
AARDKEIFG	SDADSEDDADSDDEDR	N-ter +34.06 Da	16.6	81.7	3	1789.79	-2.74	0.73	PAF1_MOUSE		RNA polymerase II-associated factor 1 homolog;		0.00 - 0.15
GTVTHLCRQY	SDAPPLLDGKIDR	N-ter +28.03 Da, K +28.03 Da	45.6	40.2	3	1552.91	0.88	0.05	ACPM_MOUSE	F8WJ64_MOUSE	Acyl carrier protein, mitochondrial;	Ci-SDAP;NADH-ubiquinone oxidoreductase 9.6 kDa subunit;	0.25 - 0.75
KIIRLCREPR	SDECGAGVFMGSHFDR	N-ter +28.03 Da, C +57.02 Da	54.4	63.9	3	1798.86	0.29	0.07	RS27A_MOUSE		Ubiquitin-40S ribosomal protein S27a;	Ubiquitin carboxyl extension protein 80;	0.25 - 0.75
QIGAKFWEVI	SDEHGIDPTGTYHGDSLDQLDR	N-ter +28.03 Da	54.3	61.2	4	2455.24	2.09	0.74	TBB5_MOUSE		Tubulin beta-5 chain;		0.85 - 1.00
QIGAKFWEVI	SDEHGIDPTGTYHGDSLDQLER	N-ter +28.03 Da	54.2	59.7	4	2469.25	1.22	0.23	TBB2C_MOUSE	TBB4_MOUSE	Tubulin beta-4B chain;	Tubulin beta-2C chain;	0.75 - 0.85
ASRKTFSEL	SDFGLESTTEGPVVVAIR	N-ter +28.03 Da	47.7	42.0	3	1904.07	0.60	0.14	PDI3_MOUSE		Protein disulfide-isomerase A3;	58 kDa glucose-regulated protein;58 kDa microsomal protein;Disulfide isomerase ER-60;Endoplasmic reticulum resident protein 57;Endoplasmic reticulum resident protein 60;	0.25 - 0.75
SPTRSVTSPI	SDFPAPPYSAVSPPEAFSR	N-ter +34.06 Da	26.9	81.0	3	2249.30	0.33	0.07	SYNP2_MOUSE	D3YVV9_MOUSE	Synaptodin-2;	Myopodin;	0.25 - 0.75
ESQASDSEGH	SDFSEGAQVGAHR	N-ter +28.03 Da	46.8	58.5	3	1387.73	-0.30	0.03	FILA_MOUSE	F7BVV1_MOUSE	Filaggrin;		0.25 - 0.75
TKDLGGNAK	SDFTEEICR	N-ter +28.03 Da, C +57.02 Da	36.2	41.3	2	1183.57	0.60	0.07	IDH3A_MOUSE		Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial;	Isocitric dehydrogenase subunit alpha;NAD(+)-specific ICDH subunit alpha;	0.25 - 0.75
ALYTAMKFGF	SDKESILELITSR	N-ter +28.03 Da, K +28.03 Da	30.5	48.0	3	1545.94	1.47	0.43	ANXA6_MOUSE	F8WIT2_MOUSE	Annexin A6;	67 kDa calelectrin;Annexin VI;Annexin-6;Calphobindin-II;Chromobindin-20;Lipocortin VI;Protein III;p68;p70;	0.75 - 0.85
SRDEFNTCP	SDKEVEIAYSVAKR	N-ter +28.03 Da, K +28.03 Da	32.1	56.7	4	1793.06	0.16	0.01	CLIC4_MOUSE		Chloride intracellular channel protein 4;		0.25 - 0.75
GLTGNFAAQY	SDKGVSSGPGMLGMGR	N-ter +28.03 Da, K +28.03 Da	65.3	50.4	3	1784.98	-1.52	0.13	CO1A2_MOUSE	E0CXI2_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.00 - 0.15
AVALHSVA	SDLELHPPSPWWSHR	N-ter +34.06 Da	38.4	64.4	4	1854.05	-0.67	0.04	CY1_MOUSE		Cytochrome c1, heme protein, mitochondrial;		0.25 - 0.75
HLSRSRPSA	SDLPQELVDQKCLLQKYTHR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	36.4	59.2	4	2701.66	-1.47	0.37	CFAI_MOUSE		Complement factor I;	C3B/C4B inactivator;	0.15 - 0.25
RERKNSITEI	SDNEDELLEYHR	N-ter +28.03 Da	23.8	63.5	3	1546.79	2.26	0.59	PHL1_MOUSE	D32OX5_MOUSE	Pleckstrin homology-like domain family B member 1;	Protein LLS-alpha;	0.85 - 1.00
KSKENPRNF	SDNQLQEGKNIQVGLQMGNTNR	N-ter +28.03 Da, K +28.03 Da	46.7	51.2	4	2257.26	0.21	0.04	TAGL2_MOUSE		Transgelin-2;	SM22-beta;	0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
TKQQTFTTY NVREATESFA	SDNQPGVLIQVYEGER SDPILYRPVAVALDTKGPEIR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	59.0 22.6	48.1 60.4	3 4	1831.00 2365.48	0.23 -0.07	0.02 0.01	H571A_MOUSE KPYM_MOUSE	H571B_MOUSE	Heat shock 70 kDa protein 1A; Pyruvate kinase isozymes M1/M2;	Heat shock 70 kDa protein 3;Hsp68; Pyruvate kinase muscle isozyme;	0.25 - 0.75 0.25 - 0.75
SGGGLLVDF	SDSASAVAPLAGSEDNFAR	N-ter +34.06 Da	46.4	53.0	3	1995.08	-0.25	0.05	AP2A2_MOUSE		AP-2 complex subunit alpha-2;	100 kDa coated vesicle protein C;Adapter-related protein complex 2 alpha-2 subunit;Adaptor protein complex AP-2 subunit alpha-2;Alpha-adaptin C;Alpha2-adaptin;Clathrin assembly protein complex 2 alpha-C large chain;Plasma membrane adaptor HAZ/AP2 adaptin alpha C subunit;	0.25 - 0.75
HRQSKLSSD LQTRGFVSDS RPRQSPSPQS MKVLQTRGFV	SDSGSGQVQGR SDSMDTGAGSIR SDSQVHSGVQVEGR SDSSDSMDTGAGSIR	N-ter +28.03 Da N-ter +28.03 Da N-ter +34.06 Da N-ter +28.03 Da	21.3 40.7 49.4 33.9	100.6 39.7 48.3 49.0	2 3 3 3	1104.63 1223.59 1517.84 1512.71	0.07 -0.32 -0.03 -1.74	0.03 0.02 0.01 0.17	SNPC1_MOUSE ATIF1_MOUSE FILA_MOUSE ATIF1_MOUSE	Q9D879_MOUSE F7BVV1_MOUSE Q9D879_MOUSE	snRNA-activating protein complex subunit 1; ATPase inhibitor, mitochondrial; Filaggrin; ATPase inhibitor, mitochondrial;	43 kDa subunit; Inhibitor of F(1)F(o)-ATPase; Carnitine deficiency-associated protein 3;Tyrosine-phosphorylated protein 36;	0.25 - 0.75 0.25 - 0.75 0.25 - 0.75 0.00 - 0.15
KTPQGPEIY	SDTFPFLSQSTAKHVESR	N-ter +28.03 Da, K +28.03 Da	36.9	63.7	4	2073.18	-0.38	0.02	CDV3_MOUSE	F8WGL9_MOUSE	Protein CDV3;		0.25 - 0.75
A	SDVLELTDENFESR	N-ter +28.03 Da	46.5	52.8	3	1680.87	2.31	0.75	PDIA3_MOUSE	F6Q404_MOUSE	Protein disulfide-isomerase A3;	58 kDa glucose-regulated protein;58 kDa microsomal protein;Disulfide isomerase ER-60;Endoplasmic reticulum resident protein 57;Endoplasmic reticulum resident protein 60;	0.85 - 1.00
RILGVISAI	SEAAAQYNPEPPPPR	N-ter +28.03 Da	38.9	40.0	3	1650.87	0.01	0.00	CPNS1_MOUSE	D3YW48_MOUSE	Calpain small subunit 1;		0.25 - 0.75
KKGFVLHKS	SEEAHAEDSVMDDHFR	N-ter +28.03 Da	58.1	64.4	4	1923.94	1.01	0.38	PAIRB_MOUSE		Plasminogen activator inhibitor 1 RNA-binding protein;	PAI1 RNA-binding protein 1;SERPINE1 mRNA-binding protein 1;	0.75 - 0.85
VDYRTRVLI RPNPNWGWG	SEEEELDTKLTR SEFGDSSSPATR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	27.4 42.7	49.5 37.2	3 2	1504.84 1267.61	-2.06 0.01	0.17 0.00	PEA15_MOUSE Q99K47_MOUSE	E9PV24_MOUSE	Astrocytic phosphoprotein PEA-15; Serine/threonine-protein phosphatase 6 regulatory subunit 3;	15 kDa phosphoprotein enriched in astrocytes;	0.00 - 0.15 0.25 - 0.75
PTKETGWASF PRRSPVHES RGVSEQASD	SEFTSSSLTKESLR SEGEHVSVPQR SEGHSDFSEGOAVGAHR	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da N-ter +28.03 Da	42.9 28.9 45.3	44.8 67.6 63.0	3 3 4	1638.98 1380.76 1797.92	0.25 -0.01 2.75	0.09 0.00 0.74	PP6R3_MOUSE FILA2_MOUSE E9Q019_MOUSE	FILA2_MOUSE FILA_MOUSE	Filaggrin-2;	SAPS domain family member 3; Intermediate filament-associated protein;	0.25 - 0.75 0.25 - 0.75 0.85 - 1.00
CEFQDAYVLL RRDHVLGLAR KQYAPRCVC	SEKKISSVQSPVALEIANHR SELEEDIIPEEDIIR SEPIPEPGRDETIVR	N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da N-ter +28.03 Da	57.6 44.5 30.1	70.7 45.0 47.4	4 3 3	2460.58 1920.07 1739.93	1.45 -0.89 0.93	0.17 0.17 0.11	CH60_MOUSE CO3_MOUSE ZYX_MOUSE	Q7TQE2_MOUSE	60 kDa heat shock protein, mitochondrial; Complement C3; Zyxin;		0.75 - 0.85 0.15 - 0.25 0.25 - 0.75
KRHPYKMNLA DSPERELLS	SEPQEVLIHGSANHR SEPSPAVTPVPTTLIAPR	N-ter +28.03 Da N-ter +28.03 Da	23.4 44.3	64.6 40.6	4 3	1700.97 1961.16	-0.09 0.71	0.01 0.10	PDL1_MOUSE SNX2_MOUSE		PDZ and LIM domain protein 1; Sorting nexin-2;	LIM domain protein CLP-36;	0.25 - 0.75 0.25 - 0.75
SSQPNLSTYS	SEQEYGGKAGGSPASYHGSTSPR	N-ter +28.03 Da, K +28.03 Da	30.7	58.3	4	2308.21	-0.29	0.07	EPN2_MOUSE	Q5NCM6_MOUSE	Epsin-2;	EPS-15-interacting protein 2;Intersectin-EH-binding protein 2;	0.25 - 0.75
PRQPTVTSVC SPLRSPPLLG SADROGRRGV	SESAQELAEQQR SESPYEDFLSADSKVLR SESQASDSEGHSDFSEGOAVGAHR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	38.2 40.9 55.7	55.0 63.3 63.9	3 3 4	1331.71 2055.15 2502.22	-0.07 0.06 0.90	0.01 0.01 0.29	PDL5_MOUSE MAP18_MOUSE E9Q019_MOUSE	E9Q8P5_MOUSE F7BVV1_MOUSE	PDZ and LIM domain protein 5; Microtubule-associated protein 1B;	Enigma homolog;Enigma-like PDZ and LIM domains protein;	0.25 - 0.75 0.25 - 0.75 0.25 - 0.75
MEKLSGMRF	SEVATQYSEDKAR	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	34.4	39.5	3	1550.88	-1.52	0.22	PIN4_MOUSE		Peptidyl-prolyl cis-trans isomerase NIMA-interacting 4; Serine/threonine-protein phosphatase 2A 65 kDa regulatory subunit A alpha isoform;	Parvulin-14;Peptidyl-prolyl cis-trans isomerase Pin4;Rotamase Pin4;	0.00 - 0.15
MITTLFCINVL	SEVCGQDITTKHMLPTVLR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	37.9	61.7	4	2240.30	0.11	0.01	ZAAA_MOUSE			PP2A subunit A isoform PR65-alpha;PP2A subunit A isoform R1-alpha;	0.25 - 0.75
KVLIRIMVSR WTHVFSSRS ERDRITALK GISLPQVELA DEQALEDHFS	SEVDMKLR SEVVLSDGDEDDYQR SFEVEIEPPNTPPR SFGAGPEIVAPSAEATAGSR SFGPISVVVVKDR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +28.03 Da N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da	17.8 44.5 33.2 39.5 32.6	51.9 47.3 60.3 45.6 53.3	3 3 3 3 3	1145.71 1638.82 1855.01 2023.10 1586.99	2.08 -0.03 0.40 -0.38 -0.30	0.19 0.01 0.01 0.05 0.03	ANXA2_MOUSE E9Q616_MOUSE SEPT9_MOUSE PRAX_MOUSE RBM3_MOUSE	BOV2N5_MOUSE A2A6U3_MOUSE Q6NVF7_MOUSE Q8BG13_MOUSE	Annexin A2; Septin-9; Periaxin; Putative RNA-binding protein 3;	Annexin I;Annexin-2;Calpactin I heavy chain;Calpactin-1 heavy chain;Chromobindin-8;Lipocortin II;Placental anticoagulant protein IV;Protein I;p36;	0.85 - 1.00 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75
ANEVEAVKVH ETPSQRATR	SFPTLKFPPASADR SGAQASSTPLSPTR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	30.5 28.3	53.8 37.9	3 3	1638.96 1386.76	-1.29 2.00	0.09 0.37	PDIA1_MOUSE LMNA_MOUSE	E9Q8G8_MOUSE D3YUF7_MOUSE	Protein disulfide-isomerase; Prelamin-A/C;	Cellular thyroid hormone-binding protein;Endoplasmic reticulum resident protein 59;Prolyl 4-hydroxylase subunit beta;p55;	0.15 - 0.25 0.85 - 1.00
GPEANVGPYG SHQRAADSQN	SGDSAPLQEAMAVLQHHDVAVSGTAR SGEGNTSAAESSFSQEVAR	N-ter +28.03 Da N-ter +28.03 Da	52.2 46.3	51.6 39.1	4 3	2575.38 1940.95	-1.47 0.20	0.49 0.04	MA2B1_MOUSE Q7M739_MOUSE	E9PZZ3_MOUSE	Lysosomal alpha-mannosidase;	Lysosomal acid alpha-mannosidase;Mannosidase alpha class 2B member 1;Mannosidase alpha-B;	0.15 - 0.25 0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
NIDIRSAFKR	SGEQDADAGELDFSGLLKR	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	42.3	50.1	3	2075.18	-0.79	0.15	D3YU50_MOUSE	Q6P6L5_MOUSE			0.25 - 0.75
ESTECRTRV	SGEHMDLTTCPAAGGQQEKLK	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	40.7	58.3	4	2454.34	3.28	0.31	Q9D1B1_MOUSE				0.85 - 1.00
EPFASGKTA	SGELHGLTTDEKFEVGVYR	N-ter +28.03 Da, K +28.03 Da	52.7	60.7	4	2192.25	-2.32	0.35	THY_MOUSE		Transthyretin;	Prealbumin;	0.00 - 0.15
VLDGADCIML	SGETAKGDYPLEAVR	N-ter +34.06 Da, K +34.06 Da	33.0	40.2	3	1659.98	-1.09	0.14	KPYM_MOUSE		Pyruvate kinase isozymes M1/M2;	Pyruvate kinase muscle isozyme;	0.15 - 0.25
EQFRQLQGN	SGEVESHFLFEKSLR	N-ter +28.03 Da, K +28.03 Da	28.1	60.4	4	1873.11	0.53	0.06	APOA4_MOUSE		Apolipoprotein A-IV;	Apolipoprotein A4;	0.25 - 0.75
PLPPTAQGN	SGSGAPGLAAAIAAGAKLR	N-ter +28.03 Da, K +28.03 Da	43.8	47.0	3	1680.05	-0.76	0.12	VASP_MOUSE		Vasodilator-stimulated phosphoprotein;		0.25 - 0.75
RKDLANTVL	SGGTTMPYGIADR	N-ter +28.03 Da	44.5	39.6	2	1352.69	-0.42	0.08	ACTB_MOUSE	ACTA_MOUSE	Actin, cytoplasmic 1;	Beta-actin;	0.25 - 0.75
AIMARIAQFL	SGIPETVPLSTVNR	N-ter +28.03 Da	34.1	41.7	3	1496.88	0.45	0.04	THIKA_MOUSE	THIKB_MOUSE	3-ketoacyl-CoA thiolase A, peroxisomal;	Acetyl-CoA acyltransferase A;Beta-ketothiolase A;	0.25 - 0.75
HRGLPLGKGY	SGLQGLPLAGLHGDQAGPVPVGPAGPR	N-ter +34.06 Da	51.1	55.1	4	2566.52	-1.74	0.52	CO1A2_MOUSE	E9Q6U9_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.00 - 0.15
ETTALVCDNG	SGLVKAGFAGDDAPR	N-ter +28.03 Da, K +28.03 Da	45.3	41.8	3	1515.87	0.49	0.11	ACTC_MOUSE	ACTS_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
DNG	SGMCKAGFAGDDAPR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	43.4	56.6	3	1594.81	-1.03	0.23	ACTB_MOUSE	ACTG_MOUSE	Actin, cytoplasmic 1;	Beta-actin;	0.15 - 0.25
AAQYSDKGV	SGPPMGLMGPR	N-ter +34.06 Da	32.5	43.5	2	1189.67	-2.74	0.18	CO1A2_MOUSE	E0CXI2_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.00 - 0.15
SPSLPPSAKR	SGQKPLVDVHAEALDR	N-ter +28.03 Da, K +28.03 Da	25.3	60.1	4	1806.07	0.87	0.10	DC1L1_MOUSE		Cytoplasmic dynein 1 light intermediate chain 1;	Dynein light chain A;Dynein light intermediate chain 1, cytosolic;	0.25 - 0.75
PSGPVKDGR	SGQPVPVGPAGVR	N-ter +34.06 Da	39.1	26.2	2	1211.72	-0.17	0.02	CO1A2_MOUSE	E9Q6U9_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.25 - 0.75
CWLAVGHSNG	SGSSKEGNECLSKTR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	19.6	73.3	4	1836.08	4.46	1.00	E9PYU6_MOUSE				0.85 - 1.00
HVVPDQLMTF	SGTNDPCALCSLHIGKIGKAQNR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	43.9	69.1	4	2568.43	1.20	0.21	MIF_MOUSE		Macrophage migration inhibitory factor;	Delayed early response protein 6;Glycosylation-inhibiting factor;L-dopachrome isomerase;L-dopachrome tautomerase;Phenylpyruvate tautomerase;	0.75 - 0.85
ASSREGSPAR	SGTPVHCPSPIR	N-ter +34.06 Da, C +57.02 Da	32.4	44.4	3	1340.77	0.69	0.04	BAG3_MOUSE		BAG family molecular chaperone regulator 3;	Bcl-2-associated athanogene 3;Bcl-2-binding protein Bis;	0.25 - 0.75
SVQVPEFTPK	SGVKIHVSQELQSANASVDDSR	N-ter +28.03 Da, K +28.03 Da	57.1	59.4	4	2497.39	2.60	0.58	UBA1_MOUSE		Ubiquitin-like modifier-activating enzyme 1;	Ubiquitin-activating enzyme E1;Ubiquitin-activating enzyme E1 X;Ubiquitin-like modifier-activating enzyme 1 X;	0.85 - 1.00
VVLFETATLR	SGYLLPDTKAYGDR	N-ter +28.03 Da, K +28.03 Da	27.2	44.0	3	1610.90	-0.54	0.05	ENPL_MOUSE		Endoplasmic reticulum resident protein 99;Heat shock protein 90 kDa beta member 1;Polymorphic tumor rejection antigen 1;Tumor rejection antigen gp96;	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;	0.25 - 0.75
DTSQKQDSPA	SHEIATNLGDFALSR	N-ter +34.06 Da	34.7	40.8	3	1940.10	0.08	0.04	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;	0.25 - 0.75
DTSQKQDSPA	SHEIATNLGDFALSR	N-ter +28.03 Da	23.4	47.5	3	1570.89	-2.32	0.58	A1AT4_MOUSE		Alpha-1-antitrypsin 1-4;	Alpha-1 protease inhibitor 4;Serine protease inhibitor 1-4;Serine protease inhibitor A1d;	0.00 - 0.15
QGPAPPNPF	SHLLEGELEYTKTIER	N-ter +34.06 Da, K +34.06 Da	34.5	65.7	4	2114.29	4.26	0.57	ADDG_MOUSE		Gamma-adducin;	Adducin-like protein 70;	0.85 - 1.00
GLNPVAVSRF	SHTDVKVPDFSDYRR	N-ter +28.03 Da, K +28.03 Da	23.7	70.9	4	1877.08	-1.60	0.15	UCRI_MOUSE		Cytochrome b-c1 complex subunit Rieske, mitochondrial;	Complex III subunit 5;Cytochrome b-c1 complex subunit 5;Rieske iron-sulfur protein;Ubiquinol-cytochrome c reductase iron-sulfur subunit;	0.00 - 0.15
GLNPVAVSRF	SHTDVKVPDFSDYR	N-ter +28.03 Da, K +28.03 Da	30.0	69.7	4	1720.96	-1.36	0.17	UCRI_MOUSE		Cytochrome b-c1 complex subunit Rieske, mitochondrial;	Complex III subunit 5;Cytochrome b-c1 complex subunit 5;Rieske iron-sulfur protein;Ubiquinol-cytochrome c reductase iron-sulfur subunit;	0.15 - 0.25
RSTCHNQNSM	SICEEFSQADDKGCFR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	52.5	41.4	3	2132.02	0.55	0.15	A2M_MOUSE	D3YW52_MOUSE	Alpha-2-macroglobulin;	Pregnancy zone protein;	0.25 - 0.75
NQQEGVCPGE	SIDNSPVKWCALSHLER	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	25.3	69.0	4	2067.20	-0.15	0.03	TRFE_MOUSE	E9Q035_MOUSE	Serotransferrin;	Beta-1 metal-binding globulin;Siderophilin;	0.25 - 0.75
ASTSQSRAA	SIFGGAKPVDTAAR	N-ter +28.03 Da, K +28.03 Da	27.8	50.3	3	1444.88	-1.18	0.14	IF4B_MOUSE	E9P2A1_MOUSE	Eukaryotic translation initiation factor 4B;		0.15 - 0.25
GLILPILAK	SIGTLDPCCKDPTDR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	21.8	51.3	3	1601.89	1.76	0.44	CDSN_MOUSE		Corneodesmosin;		0.85 - 1.00
QLPNQVLES	SIIDTGPLISGAKQR	N-ter +28.03 Da, K +28.03 Da	39.4	40.6	3	1611.00	-0.17	0.04	EHD2_MOUSE	Q8R2X0_MOUSE	EH domain-containing protein 2;		0.25 - 0.75
SAGIHETTYN	SIMKCDIDIR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	28.3	52.3	3	1305.75	0.25	0.04	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
LQTRFLDY	SIPFPPTTTLTR	N-ter +28.03 Da	25.8	36.1	3	1511.89	1.22	0.14	UBP2L_MOUSE	E9P2A1_MOUSE	Ubiquitin-associated protein 2-like;		0.75 - 0.85
SVATQQTL	SIPSHPSTAGKIFR	N-ter +28.03 Da, K +28.03 Da	18.3	60.6	4	1552.97	0.61	0.06	A2AQ82_MOUSE	A2AQ9_MOUSE			0.25 - 0.75
WAAPVKGTFV	SITPAEAVGLVGDNR	N-ter +28.03 Da, K +28.03 Da	31.7	40.5	3	1595.99	0.47	0.03	PROF1_MOUSE	Q5SX49_MOUSE	Profilin-1;	Profilin 1;	0.25 - 0.75
QLPKVNKNKN	SIVDPKVIHVGVDVAVSR	N-ter +28.03 Da, K +28.03 Da	31.1	57.1	4	2273.40	0.65	0.05	PLCD1_MOUSE		1-phosphatidylinositol-4,5-bisphosphate phosphodiesterase delta-1;	Phosphoinositide phospholipase C-delta-1;Phospholipase C-delta-1;	0.25 - 0.75
RTSPVPRQKR	SIVVSPILIPENQR	N-ter +28.03 Da	35.2	45.8	3	1592.00	0.38	0.11	CAD13_MOUSE		Cadherin-13;	Heart cadherin;Truncated cadherin;	0.25 - 0.75
IHQVQVQEMD	SKADDLCLKSSGVIQR	N-ter +28.03 Da, K +28.03 Da	44.7	61.7	4	1928.21	-0.76	0.08	C163A_MOUSE		Scavenger receptor cysteine-rich type 1 protein M130;		0.25 - 0.75
LLLYAAYAGA	SKAELHYPPQGEHR	N-ter +28.03 Da, K +28.03 Da	19.8	67.1	4	1735.98	2.91	0.60	RCN2_MOUSE	D6RHL9_MOUSE	Reticulocalbin-2;	Taipoxin-associated calcium-binding protein 49;	0.85 - 1.00
QALEGLILEK	SKDQEDAMGGVAQAEQAEQHSVIMR	N-ter +34.06 Da, K +34.06 Da	24.2	39.5	4	2911.52	-3.06	0.77	E9Q4L7_MOUSE				0.00 - 0.15
IDLSAKIEF	SKEQEQDFKFAFLFDR	N-ter +34.06 Da, K +34.06 Da	26.6	61.7	4	2231.37	-0.56	0.12	MYL1_MOUSE	E0CZ30_MOUSE	Myosin light chain 1/3, skeletal muscle isoform;	Myosin light chain alkali 1/2;	0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
AAVSTAQPIL	SKLEPQIATASEYahr	N-ter +28.03 Da, K +28.03 Da	35.4	54.4	4	1856.08	-0.34	0.03	PLIN3_MOUSE			Cargo selection protein TIP47;Mannose-6-phosphate receptor-binding protein 1;	0.25 - 0.75
AKVEAFQASL	SKLGDVYVNDafgTAHR	N-ter +28.03 Da, K +28.03 Da	22.6	80.0	4	1905.13	-0.84	0.06	PGK1_MOUSE	PGK2_MOUSE	Phosphoglycerate kinase 1;		0.15 - 0.25
QNTVRSFMKR	SKLGPYNEELR	N-ter +28.03 Da, K +28.03 Da	34.4	44.1	3	1360.79	0.74	0.10	TBCB_MOUSE		Tubulin-folding cofactor B;	Cytoskeleton-associated protein 1;Cytoskeleton-associated protein CkAP1;Tubulin-specific chaperone B;	0.25 - 0.75
ERSPLQSLAR	SKPSPQLSAETPVAALPEFPR	N-ter +28.03 Da, K +28.03 Da	49.3	58.2	4	2277.37	0.08	0.02	E9Q056_MOUSE				0.25 - 0.75
SLSTFQQMWI	SKQEYDESGPSIVHR	N-ter +28.03 Da, K +28.03 Da	39.4	65.7	4	1787.00	0.20	0.02	ACTB_MOUSE	ACTG_MOUSE	Actin, cytoplasmic 1;	Beta-actin;	0.25 - 0.75
LWSLVATLLG	SKWPEPVFGR	N-ter +34.06 Da, K +34.06 Da	25.6	47.8	3	1269.81	-0.07	0.01	MASP2_MOUSE		Mannan-binding lectin serine protease 2;	MBL-associated serine protease 2;Mannose-binding protein-associated serine protease 2;	0.25 - 0.75
ISRRVLVSDG	SLAEVPKEAPKVGILSGDFAR	N-ter +34.06 Da, K +34.06 Da	24.1	54.3	4	2342.53	-0.60	0.15	STEA3_MOUSE	E9QN92_MOUSE	Metalloreductase STEAP3;	Dudulin-2;Protein nm1054;Six-transmembrane epithelial antigen of prostate 3;Tumor suppressor-activated pathway protein 6;	0.25 - 0.75
NIGAARPIKR	SLEDLDLVIAGKKAR	N-ter +28.03 Da, K +28.03 Da	24.1	62.9	4	1711.13	0.71	0.14	ARISB_MOUSE		AT-rich interactive domain-containing protein 5B;	Developmentally and sexually retarded with transient immune abnormalities protein;MRF1-like;Modulator recognition factor protein 2;	0.25 - 0.75
STVHEILCKL	SLEGDHTSPPSAYGSVKPYTNFDAER	N-ter +34.06 Da, K +34.06 Da	40.7	58.8	4	2892.59	1.02	0.20	ANXA2_MOUSE	BOVZN7_MOUSE	Annexin A2;	Annexin I;Annexin-2;Calpactin I heavy chain;Calpactin-1 heavy chain;Chromobindin-8;Lipoprotein II;Placental anticoagulant protein IV;Protein I;p36;	0.75 - 0.85
LPKFSISMDN	SLEHILPELGR	N-ter +28.03 Da	30.4	50.2	3	1403.88	0.77	0.10	SPA3F_MOUSE	SPA3G_MOUSE	Serine protease inhibitor A3F;		0.25 - 0.75
NEMATAASSS	SLEKSYELPDGQVITIGNER	N-ter +28.03 Da, K +28.03 Da	58.4	46.7	3	2303.31	1.29	0.17	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.75 - 0.85
LRPPGGGSNF	SLGFDEPAEQPVR	N-ter +34.06 Da	36.1	43.6	3	1477.83	0.35	0.11	HN1_MOUSE		Hematological and neurological expressed 1 protein;		0.25 - 0.75
FEHRLGEAAR	SLGNAGNEIGR	N-ter +28.03 Da	37.2	34.0	2	1114.61	-0.94	0.13	DMKN_MOUSE	E9QLW7_MOUSE	Dermokine;	Epidermis-specific secreted protein SK30/SK89; Lysosomal pepstatin-insensitive protease;Tripeptidyl aminopeptidase;Tripeptidyl-peptidase I;	0.15 - 0.25
RPEPQQVGTV	SLHLGVTPSVLR	N-ter +34.06 Da	22.5	48.0	3	1311.87	0.77	0.17	TPP1_MOUSE		Tripeptidyl-peptidase 1;		0.25 - 0.75
ADESAANCDK	SLHTLFGDKLCAIPNLR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	29.5	60.6	4	2010.23	1.07	0.20	ALBU_MOUSE		Serum albumin;		0.75 - 0.85
SLTVIHDFLF	SLKESPEKFOIEAMFPR	N-ter +28.03 Da, K +28.03 Da	43.0	64.9	4	2103.27	-1.89	0.21	FAF2_MOUSE		FAS-associated factor 2;	UBX domain-containing protein 8;	0.00 - 0.15
SIRSAPPKLA	SLKGVVPEDAVETLAGSLGTR	N-ter +34.06 Da, K +34.06 Da	52.9	48.1	3	2166.36	0.93	0.50	ICAL_MOUSE	Q921U7_MOUSE	Calpastatin;	Calpain inhibitor; Alcohol sulfotransferase;Hydroxysteroid sulfotransferase 2;	0.25 - 0.75
AMKANTMSNY	SLLPASLLDHR	N-ter +28.03 Da	44.8	66.1	3	1248.80	3.02	0.54	STZB1_MOUSE	E9QKC1_MOUSE	Sulfotransferase family cytosolic 2B member 1;		0.85 - 1.00
QLIGIQDGYL	SLLQDSGEVR	N-ter +34.06 Da	48.4	24.9	2	1136.65	-0.38	0.05	IF5A1_MOUSE		Eukaryotic translation initiation factor 5A-1;	Eukaryotic initiation factor 5A isoform 1;eIF-4D;	0.25 - 0.75
RSPLQLLGR	SLPEGVVDGIEVYTKISCKVTSR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	59.9	52.3	4	2707.59	0.81	0.46	ITIH3_MOUSE	E9PVS1_MOUSE	Inter-alpha-trypsin inhibitor heavy chain H3;		0.25 - 0.75
SGLSVEEFM	SLPELQQNPLVQR	N-ter +28.03 Da	36.4	41.1	3	1548.93	-0.79	0.03	CANB1_MOUSE		Calcineurin subunit B type 1;	Protein phosphatase 2B regulatory subunit 1;Protein phosphatase 3 regulatory subunit B alpha isoform 1;	0.25 - 0.75
FQTSSFSFAM	SLPGAPTASSGTAAYPALPNR	N-ter +28.03 Da	35.1	40.5	3	2026.13	-3.06	0.77	ARNT_MOUSE	Q3ULM2_MOUSE	Aryl hydrocarbon receptor nuclear translocator;	Dioxin receptor, nuclear translocator;Hypoxia-inducible factor 1-beta;	0.00 - 0.15
LLGSPRRSY	SLPHQKVPPLPSLPTMQAGTIAR	N-ter +28.03 Da, K +28.03 Da	45.1	61.5	4	2581.60	1.12	0.04	ODP2_MOUSE		Dihydrolipoyllysine-residue acetyltransferase component of pyruvate dehydrogenase complex, mitochondrial;	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex;Pyruvate dehydrogenase complex component E2;	0.75 - 0.85
ACFATKDGK	SLTKDLGNNAKSDFTTEICR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	39.1	68.4	4	2484.37	4.19	0.98	IDH3A_MOUSE		Isocitrate dehydrogenase [NAD] subunit alpha, mitochondrial;	Isocitric dehydrogenase subunit alpha;NAD(+)-specific ICDH subunit alpha; Heparin-binding protein 44;Low density lipoprotein receptor-related protein-associated protein 1;	0.85 - 1.00
DGRKDAQMVH	SNALNEDTQDELGDPR	N-ter +28.03 Da	38.5	63.0	3	1800.93	-0.64	0.09	AMRP_MOUSE	F6SY09_MOUSE	Alpha-2-macroglobulin receptor-associated protein;	Heat shock 84 kDa;Tumor-specific transplantation 84 kDa antigen;	0.25 - 0.75
NKEIFLRELI	SNASDALDKIR	N-ter +28.03 Da, K +28.03 Da	23.8	47.2	3	1244.73	2.62	0.15	H590B_MOUSE	ENPL_MOUSE	Heat shock protein HSP 90-beta; Phosphatidylinositol-binding clathrin assembly protein;		0.85 - 1.00
STAASRATTL	SNAVSSTGLSLTKVDER	N-ter +28.03 Da, K +28.03 Da	52.0	46.1	3	2090.22	0.07	0.01	PICA_MOUSE			Clathrin assembly lymphoid myeloid leukemia;	0.25 - 0.75
TPGHACTQKF	SNEEIAMATVTALR	N-ter +28.03 Da	43.0	46.7	3	1532.86	-1.32	0.20	ALDOA_MOUSE	Q9CPQ9_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.15 - 0.25
DKDDLVTTEL	SNEELLQLVLR	N-ter +34.06 Da	28.5	39.3	3	1348.79	-0.89	0.07	LAP2A_MOUSE	LAP2B_MOUSE	Lamina-associated polypeptide 2, isoforms alpha/zeta;	Thymopoietin isoforms alpha/zeta; 56 kDa cytokeratin;Cytokeratin-10;Keratin, type I cytoskeletal 59 kDa;Keratin-10;	0.15 - 0.25
KSKELTVID	SNIEQMSSHSEITELR	N-ter +28.03 Da, K +28.03 Da	33.6	60.5	4	2044.15	-0.27	0.02	K1C10_MOUSE	A2A513_MOUSE	Keratin, type I cytoskeletal 10;		0.25 - 0.75
EQFLPMMQAI	SNNKDQGGYEDFVEGLR	N-ter +28.03 Da, K +28.03 Da	63.7	50.3	3	1983.03	-2.32	0.70	MYL1_MOUSE	E9PWG4_MOUSE	Myosin light chain 1/3, skeletal muscle isoform;	Myosin light chain alkali 1/2;	0.00 - 0.15
KSFVNLNGKD	SNNLCLHFNPR	N-ter +28.03 Da, C +57.02 Da	36.3	51.7	3	1398.76	-0.52	0.06	LEG1_MOUSE		Galectin-1;	14 kDa lectin;Beta-galactoside-binding lectin L-14-I;Galaplin;Lactose-binding lectin 1;Lectin galactoside-binding soluble 1;S-Lac lectin 1;	0.25 - 0.75
LLAACGSVTM	SNPGESSFLADRLDPVEKIDR	N-ter +28.03 Da, K +28.03 Da	44.8	59.7	4	2515.41	0.94	0.24	SODE_MOUSE		Extracellular superoxide dismutase [Cu-Zn];		0.25 - 0.75

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
ILEGNDIELV	SNSAAUIQQATTYKNDKDR	N-ter +28.03 Da, K +28.03 Da	31.4	56.7	4	2141.34	0.06	0.01	RL9_MOUSE		60S ribosomal protein L9;		0.25 - 0.75
TSGDSLTVAS	SNTDFAFSLYR	N-ter +28.03 Da	49.4	38.0	2	1347.70	2.52	0.58	SPA3G_MOUSE	D3Z450_MOUSE	Serine protease inhibitor A3G;	Serine protease inhibitor 2A;	0.85 - 1.00
KIPRHVETEI	SNTDVEOTGPKTVIR	N-ter +34.06 Da, K +34.06 Da	45.1	43.1	3	1712.05	-1.40	0.33	E9Q616_MOUSE				0.15 - 0.25
RSRCFGFVTY	SNVEEADAAAMAASHAVDGNTEVELKR	N-ter +28.03 Da, K +28.03 Da	104.1	59.3	4	2737.50	0.40	0.12	Q9CX86_MOUSE				0.25 - 0.75
QETDTSQKDK	SPASHEIATNLGDFALR	N-ter +28.03 Da	39.1	57.6	3	1826.04	-3.06	0.77	A1AT4_MOUSE		Alpha-1-antitrypsin 1-4;	Alpha-1 protease inhibitor 4;Serine protease inhibitor 1-4;Serine protease inhibitor A1d;	0.00 - 0.15
NSTHPMHSRC	SPDPLTALLSDHR	N-ter +28.03 Da	75.1	47.1	3	1505.85	0.00	0.00	HEMO_MOUSE		Hemopexin;		0.25 - 0.75
YPKRLEKELG	SPPGISLETIDAAFSCPGSSR	N-ter +28.03 Da, C +57.02 Da	56.9	43.9	3	2176.14	-0.42	0.16	HEMO_MOUSE		Hemopexin;		0.25 - 0.75
LVTLCSHAL	SPTNCDASEPLAEKVLINKGR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	26.8	56.4	4	2610.52	3.77	1.76	HRG_MOUSE		Histidine-rich glycoprotein;	Histidine-proline-rich glycoprotein;	0.85 - 1.00
QSGSRRPRR	SPVHPESSEGEESVVPQR	N-ter +28.03 Da	37.3	58.4	4	2114.13	-1.74	0.41	FILA2_MOUSE	FILA2_MOUSE	Filaggrin-2;	Intermediate filament-associated protein;	0.00 - 0.15
DGDLGNLSL	SPVQADVVFPR	N-ter +28.03 Da	26.7	41.4	3	1305.73	0.00	0.00	LEGLA_MOUSE	E9QAC6_MOUSE	Galectin-related protein A;	Lectin galactoside-binding-like protein A;	0.25 - 0.75
M	SQAQFDKAAAEVKK	N-ter +28.03 Da, K +28.03 Da	25.6	56.4	4	1690.98	-0.06	0.01	ACBP_MOUSE		Acyl-CoA-binding protein;	Diazepam-binding inhibitor;Endozepine;	0.25 - 0.75
DRQGRRGVSE	SQASDSEGHSDFSEGGAVGAHR	N-ter +28.03 Da	44.8	65.7	4	2286.14	1.67	0.82	E9Q019_MOUSE	F7BVV1_MOUSE			0.85 - 1.00
YGSGLSGYL	SQDTSVSPCKSDQSKAR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	26.1	64.9	4	1976.13	-0.12	0.03	CATD_MOUSE	Q8C243_MOUSE	Cathepsin D;		0.25 - 0.75
PVRNRKVDVY	SQFQESDDADEDYGR	N-ter +34.06 Da	49.4	60.7	3	1794.85	0.99	0.35	NUCK5_MOUSE		Nuclear ubiquitously casein and cyclin-dependent kinases substrate;	JC7;	0.75 - 0.85
FENAFLSHVI	SQHQLSLGNIR	N-ter +28.03 Da	33.7	46.9	3	1279.76	-0.56	0.04	ATPA_MOUSE	D3Z6F5_MOUSE	ATP synthase subunit alpha, mitochondrial;		0.25 - 0.75
TFLPKRIKL	SLLQEDSLNVDLSSLR	N-ter +28.03 Da	49.3	42.8	3	2015.14	0.06	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;	0.25 - 0.75
AVVRVGRRL	SQQSASGAPVLLR	N-ter +34.06 Da	49.3	47.1	3	1346.84	0.37	0.04	ETHE1_MOUSE		Protein ETHE1, mitochondrial;	Ethylmalonic encephalopathy protein 1 homolog;Hepatoma subtracted clone one protein;	0.25 - 0.75
RDRPRQPSP	SQSSDSQVHSGVQVEGR	N-ter +34.06 Da	58.9	43.2	3	1819.97	2.19	0.61	FILA_MOUSE	F7BVV1_MOUSE	Filaggrin;		0.85 - 1.00
QKIFAREILD	SRGNPTVEVDLHTAKGR	N-ter +28.03 Da, K +28.03 Da	28.4	67.5	4	1892.15	-0.30	0.07	ENOB_MOUSE	Q5X59_MOUSE	Beta-enolase;	2-phospho-D-glycerate hydro-lyase;Enolase 3;Muscle-specific enolase;Skeletal muscle enolase;	0.25 - 0.75
RASGPWGRSH	SSAAEASAALKVRPER	N-ter +34.06 Da, K +34.06 Da	26.5	46.3	4	1781.13	-1.52	0.17	ALAT2_MOUSE	D6RFQ8_MOUSE	Alanine aminotransferase 2;		0.00 - 0.15
QFLVLVLAGR	SSDAVAGPASSLQR	N-ter +28.03 Da, K +28.03 Da	44.5	49.7	3	1528.90	0.99	0.10	E9PWQ3_MOUSE	D3YWD1_MOUSE			0.75 - 0.85
VLQTRGFVSD	SSDSMDTGAISLR	N-ter +28.03 Da	55.8	49.4	2	1310.63	0.06	0.00	ATIF1_MOUSE	Q8D879_MOUSE	ATPase inhibitor, mitochondrial;	Inhibitor of F(1)F(o)-ATPase;	0.25 - 0.75
DRPRQPSPSQ	SSDQVHSGVQVEGR	N-ter +28.03 Da	60.6	42.3	3	1598.83	0.60	0.11	FILA_MOUSE	F7BVV1_MOUSE	Filaggrin;		0.25 - 0.75
GALAPTGPSA	SSEAPPLVNEVKR	N-ter +28.03 Da, K +28.03 Da	46.4	51.9	3	1595.93	-1.36	0.21	RPN1_MOUSE		Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1;	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase 67 kDa subunit;Ribophorin I;Ribophorin-1;	0.15 - 0.25
SPRRSPVHPE	SSEGEHSVVPQR	N-ter +34.06 Da	45.3	48.3	3	1473.80	0.06	0.01	FILA2_MOUSE	E9QPZ3_MOUSE	Filaggrin-2;	Intermediate filament-associated protein;	0.25 - 0.75
TWTHEVLESFR	SSEVLVSGDDEYQKR	N-ter +28.03 Da	37.7	57.3	3	1725.87	0.89	0.12	E9Q616_MOUSE				0.25 - 0.75
TDEQALDEHF	SSFGPISEVVVKDR	N-ter +28.03 Da, K +28.03 Da	48.9	50.1	3	1674.02	-1.36	0.21	RBM3_MOUSE	Q8B813_MOUSE	Putative RNA-binding protein 3;	RNA-binding motif protein 3;	0.15 - 0.25
SDVQTAVKTN	SSFIQGFVDHVKEDCDR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	33.2	65.4	4	2094.12	0.08	0.01	SAP_MOUSE	Q8BFQ1_MOUSE	Sulfated glycoprotein 1;	Prosaposin;	0.25 - 0.75
VVLLFETALL	SSGFSLDPQTHSNR	N-ter +28.03 Da	65.4	51.4	3	1688.86	3.89	0.49	H590B_MOUSE	Q71LX8_MOUSE	Heat shock protein HSP 90-beta;	Heat shock 84 kDa;Tumor-specific transplantation 84 kDa antigen;	0.85 - 1.00
CGLSDPNLTL	SSGKDGCPLVVEQVR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	47.6	32.5	3	1826.06	0.80	0.12	LRC47_MOUSE	F6Y733_MOUSE	Leucine-rich repeat-containing protein 47;		0.25 - 0.75
YTENGGGGQY	SSGAPASPETQGKANVTR	N-ter +34.06 Da, K +34.06 Da	39.1	59.4	3	1811.09	-0.58	0.22	CD34_MOUSE		Hematopoietic progenitor cell antigen CD34;		0.25 - 0.75
DGGLADLLEFV	SSGPTNASAFTR	N-ter +28.03 Da	58.4	42.3	2	1351.69	2.07	0.37	MAP4_MOUSE	E9QPW8_MOUSE	Microtubule-associated protein 4;		0.85 - 1.00
PLGYPVYNSV	SSHASSPYISSVQSPGSASLAQSR	N-ter +34.06 Da	27.3	27.2	3	2587.34	-1.47	0.25	DLX1_MOUSE		Homeobox protein DLX-1;		0.15 - 0.25
GGORAIAWRVL	SSIEQKSNEEGSEKGPVKEYR	N-ter +28.03 Da, K +28.03 Da	20.2	56.4	4	2750.52	2.96	1.24	14335_MOUSE		14-3-3 protein sigma;	Stratifin;	0.85 - 1.00
DLKTGESVLL	SSIPSPDDFKSTGIKYVEDR	N-ter +28.03 Da, K +28.03 Da	30.2	55.7	4	2437.41	3.18	0.87	PALMD_MOUSE	Q3UV77_MOUSE	Palmdelphin;		0.85 - 1.00
SSVATQQTLL	SSIPSPHSTAGKIFR	N-ter +34.06 Da, K +34.06 Da	27.2	56.0	4	1652.06	0.60	0.11	A2AQ82_MOUSE	A2AQ9_MOUSE			0.25 - 0.75
KYDMEVKVQK	SSKELEDMNQKLFDLR	N-ter +28.03 Da, K +28.03 Da	33.9	60.0	4	2036.18	0.29	0.05	TNNI2_MOUSE	A2A6K0_MOUSE	Troponin I, fast skeletal muscle;	Troponin I, fast-twitch isoform;	0.25 - 0.75
HVVSVYKPRY	SLSLNHYKPR	N-ter +28.03 Da, K +28.03 Da	22.7	60.4	3	1342.82	0.38	0.11	CLYBL_MOUSE		Citrate lyase subunit beta-like protein, mitochondrial;		0.25 - 0.75
PNHQKASSGK	SSPFKVSPSFR	N-ter +28.03 Da, K +28.03 Da	30.2	55.8	3	1463.90	1.69	0.08	SDPR_MOUSE		Serum deprivation-response protein;	Cavin-2;Phosphatidylserine-binding protein;	0.85 - 1.00
GGLLRLLGVR	SSAPVSPNVNR	N-ter +28.03 Da	41.8	17.7	2	1198.65	0.53	0.09	PYC_MOUSE	E9QPD7_MOUSE	Pyruvate carboxylase, mitochondrial;	Pyruvic carboxylase;	0.25 - 0.75
DDVARHGQRR	SSGIVSLGIGDR	N-ter +28.03 Da	56.9	36.7	2	1274.73	-0.43	0.02	E9PWQ3_MOUSE	D3YWD1_MOUSE			0.25 - 0.75
RSRGRGQFV	SSSLPDIQYR	N-ter +28.03 Da, C +57.02 Da	42.1	40.1	2	1224.63	2.00	0.43	CNBP_MOUSE	D3YF6_MOUSE	Cellular nucleic acid-binding protein;	Zinc finger protein 9;	0.85 - 1.00
LVLAARHASA	SSTNLKVDLSNLPKEQAR	N-ter +28.03 Da, K +28.03 Da	23.6	66.9	4	2196.39	0.60	0.14	C15V_MOUSE		Citrate synthase, mitochondrial;		0.25 - 0.75
KCLPLCAPRC	SSTSAPVQITHTYVHPR	N-ter +28.03 Da	36.7	57.1	4	2009.15	0.19	0.02	ETFD_MOUSE		Electron transfer flavoprotein-ubiquinone oxidoreductase, mitochondrial;	Electron-transferring-flavoprotein dehydrogenase;	0.25 - 0.75
GPTSNWARRQ	SSVAQPSLHTAQKPR	N-ter +28.03 Da, K +28.03 Da	27.7	54.7	4	1662.01	-0.12	0.02	GATB_MOUSE	Q3TLZ6_MOUSE	Glutamyl-tRNA(Gln) amidotransferase subunit B, mitochondrial;	Cytochrome oxidase assembly factor PET112 homolog;	0.25 - 0.75
LWSWLPSIFG	SSVEEMAESR	N-ter +28.03 Da	36.3	49.4	2	1222.61	-0.81	0.07	Q3URZ6_MOUSE	F7DBB3_MOUSE			0.15 - 0.25
EVREKPAK	SSVETQPAEVR	N-ter +28.03 Da	57.0	35.1	2	1358.72	0.93	0.12	E41L2_MOUSE	Q811B2_MOUSE	Band 4.1-like protein 2;	Generally expressed protein 4.1;	0.25 - 0.75
YQCLVVSRL	SSVEYEPKETFDKILIANR	N-ter +28.03 Da, K +28.03 Da	29.0	62.6	4	2478.53	0.21	0.04	PCCA_MOUSE	D3YZC0_MOUSE	Propionyl-CoA carboxylase alpha chain, mitochondrial;	Propanoyl-CoA:carbon dioxide ligase subunit alpha;	0.25 - 0.75

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile	
SPSGKSKQRY	SSVYGASVSDKDKR	N-ter +28.03 Da, K +28.03 Da	66.0	48.9	3	1667.92	-0.17	0.03	CHCH3_MOUSE	Q9D9P1_MOUSE	Coiled-coil-helix-coiled-coil-helix domain-containing protein 3, mitochondrial;		0.25 - 0.75	
LDKVKSATLS	STESTASGMQDEVR	N-ter +34.06 Da	46.4	60.1	3	1530.80	-0.76	0.09	AKA12_MOUSE	F8W121_MOUSE	A-kinase anchor protein 12;	Germ cell lineage protein gercelin;Src-suppressed C kinase substrate; E3 SUMO-protein ligase TRIM28;KRAB-A-interacting protein;KRIP-1;Tripartite motif-containing protein 28;	0.25 - 0.75	
KIVAERPBTN	STGPGPMAPPR	N-ter +28.03 Da	40.4	31.9	2	1094.59	-0.30	0.02	TIF1B_MOUSE		Transcription intermediary factor 1-beta;		0.25 - 0.75	
IHRAAAVAAM NKSVQKSGVR	STGTFFVVSQPLNYR STHQAAVSVSKIDSR	N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da	44.7 38.3	45.2 61.0	3 4	1601.94 1553.95	-0.58 1.13	0.07 0.23	AL9A1_MOUSE Q8VCQ8_MOUSE	Q3U367_MOUSE E9Q0M9_MOUSE	4-trimethylaminobutyraldehyde dehydrogenase;	Aldehyde dehydrogenase family 9 member A1;	0.25 - 0.75 0.75 - 0.85	
LPGPPPATHY	STLSKPAPLGTLEVR	N-ter +28.03 Da, K +28.03 Da	35.5	29.6	3	1725.05	-2.56	0.30	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;	0.00 - 0.15	
LCKLSLEGDH	STPPSAYGSVKPYTNFDAER	N-ter +28.03 Da, K +28.03 Da	28.7	40.7	3	2242.18	0.61	0.10	ANXA2_MOUSE	B0V2N7_MOUSE	Annexin A2;	Annexin II;Annexin-2;Calpactin I heavy chain;Calpactin-1 heavy chain;Chromobindin-8;Lipoprotein II;Placental anticoagulant protein IV;Protein I;p36;	0.25 - 0.75	
LVGLTSRAV GVHTSVASAT	STSSMGLTPKQVKIVEGPR SVATKKTEQPPSEYIFER	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da	24.7 38.7	57.7 60.0	4 4	2197.38 2337.36	1.09 -2.00	0.17 0.24	HMGCL_MOUSE OAT_MOUSE		Hydroxymethylglutaryl-CoA lyase, mitochondrial; Ornithine aminotransferase, mitochondrial;	3-hydroxy-3-methylglutarate-CoA lyase; Ornithine-oxo-acid aminotransferase;	0.75 - 0.85 0.00 - 0.15	
SSAFTEDKLV GNRGEFPGAG	SVFVTVITPMLNPIVYTLR SVGPGVAVGPR	N-ter +34.06 Da N-ter +28.03 Da	26.9 42.0	77.5 24.7	4 2	2260.45 1022.61	-2.40 -4.32	0.76 0.86	OL142_MOUSE E9Q6U9_MOUSE	Q8VG62_MOUSE E9Q6U9_MOUSE	Olfactory receptor 142; Olfactory receptor 219;	Olfactory receptor 227-2;Olfactory receptor 4C; Alpha-2 type I collagen;	0.00 - 0.15 0.00 - 0.15	
LESKSNKIVQ AITARRQHLK AITARRQHLK TDQVEAHVQN TKIFASNVS	SVIQTAVDQFAR SVMQLQAAETEKEESRR SVMQLQAAETEKEESRR SVPDEESKPASNTQVEGDEEAALLER SVLPAENVTITAGQR	N-ter +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, K +28.03 Da N-ter +28.03 Da	37.8 23.4 49.3 64.5 45.4	57.7 57.9 48.1 57.9 48.5	3 3 3 3 3	1361.81 2145.27 2001.21 2942.57 1680.00	-1.18 0.90 0.99 0.59 -4.32	0.08 0.06 0.13 0.13 0.86	AKA12_MOUSE TNN12_MOUSE TNN12_MOUSE Q8VCQ8_MOUSE UBP2L_MOUSE	A2A6K0_MOUSE A2A6K0_MOUSE E9Q0M9_MOUSE E9Q0M9_MOUSE	A-kinase anchor protein 12; Troponin I, fast skeletal muscle; Troponin I, fast skeletal muscle; Troponin I, fast-twitch isoform; Ubiquitin-associated protein 2-like;	Troponin I, fast-twitch isoform; Troponin I, fast-twitch isoform; Troponin I, fast-twitch isoform;	0.15 - 0.25 0.25 - 0.75 0.75 - 0.85 0.25 - 0.75 0.00 - 0.15	
VEPDTYCRYD RYDDMAACMK ALINDFVKLI	SVSVFNGAVSDDSKR SVTEQGAELSNERR SWYDNEYGSNR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da, C	47.9 46.7 34.6	44.2 50.7 46.0	3 3 3	1622.90 1575.82 1580.73	-1.74 0.12 4.76	0.17 0.01 0.83	PCOC1_MOUSE 1433Z_MOUSE G3P_MOUSE	D3Y2E3_MOUSE D3YXF4_MOUSE F8W1L5_MOUSE	Procollagen C-endopeptidase enhancer 1; 14-3-3 protein zeta/delta; Glyceraldehyde-3-phosphate dehydrogenase;	P14;Procollagen COOH-terminal proteinase enhancer 1;Type I procollagen C-proteinase enhancer protein;Type I procollagen COOH-terminal proteinase enhancer;	0.00 - 0.15 0.25 - 0.75 0.85 - 1.00	
HDPQLQPWSA TAASSSLEK QQPQQQMQMS GLGGNFASQM	SYDPGSAKTIINNGKTCR SYELPDGVQVITIGNER SYGGYKPAAPVSIQR SYGVDEKSGAVSVGPMPGSPGR	+57.02 Da N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da, K +34.06 Da	14.6 41.9 28.7 68.3	60.7 51.9 40.1 45.4	4 3 3 3	2065.19 1818.01 1778.01 2362.30	-0.71 0.19 -1.00 -0.74	0.11 0.02 0.16 0.21	CAH3_MOUSE ACTB_MOUSE LASP1_MOUSE CO1A1_MOUSE	ACTA_MOUSE A2A6H0_MOUSE F8WGB7_MOUSE	Carbonic anhydrase 3; Actin, cytoplasmic 1; LIM and SH3 domain protein 1; Collagen alpha-2(I) chain;	Carbonic anhydrase III; Beta-actin; Metastatic lymph node gene 50 protein; Alpha-1 type I collagen;	0.25 - 0.75 0.25 - 0.75 0.15 - 0.25 0.25 - 0.75	
VYLQNSHVHL VALDFENEMA LQKRGTGVD VYMAAVLYL GSWEPFASGK	SYVSKAESTPEIAEQR TAASSSLEKSYELPDGVQVITIGNER TAAVGAVDFISNADR TAEILELAGNAAR TAESGELHLTTDEKFEVGYR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da	35.6 42.7 45.8 34.1 41.6	41.2 59.9 45.6 48.8 66.4	3 4 3 3 4	1850.02 2807.59 1539.88 1361.84 2493.40	-0.36 1.87 -0.09 -0.47 0.65	0.04 0.50 0.01 0.03 0.15	CSN1_MOUSE ACTC_MOUSE KCRM_MOUSE H2A1F_MOUSE TTHY_MOUSE	B1ATU4_MOUSE ACTA_MOUSE H2A1F_MOUSE	COP9 signalosome complex subunit 1; Actin, alpha cardiac muscle 1; Creatine kinase M-type; Histone H2A type 1-F; Transthyretin;	COP9 signalosome subunit 1; Alpha-cardiac actin; Creatine kinase M chain;M-CK;	0.25 - 0.75 0.85 - 1.00 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75	
AAFSLAEAFK IEDGIFEVKS EQLAAELAEY GAORMFPMNR GPLVEQGRQR	TAGDFSTVIQNVNKAQVKIR TAGDTHLGGEDFDNR TAKIALLEEAR TAKPFLGSMNQPAAPSPTR TANLIGAGAAQPLR	N-ter +28.03 Da, K +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	50.8 46.0 36.0 39.5 44.8	58.8 53.6 43.7 60.3 38.7	4 3 3 4 3	2373.48 1631.81 1269.82 2173.27 1266.75	1.60 0.86 -0.94 1.06 -1.09	0.29 0.24 0.07 0.16 0.12	VATD_MOUSE HSP7C_MOUSE EZRI_MOUSE SYNP2_MOUSE APOE_MOUSE	E9Q0D9_MOUSE HS71A_MOUSE E9Q0M9_MOUSE D3YVV9_MOUSE	V-type proton ATPase subunit D; Heat shock cognate 71 kDa protein; Ezrin; Synaptopodin-2; Apolipoprotein E;		2-phospho-D-glycerate hydro-lyase;Enolase 1;Non-neural enolase; Restin;	0.75 - 0.85 0.25 - 0.75 0.15 - 0.25 0.75 - 0.85 0.15 - 0.25
QDDWGAWQKF ATPQSNLTK NEDLSLTKIF EPVWAIQTGK	TASAGIQVGGDDLTVTNPKR TASESINLSEAGSVKGER TASNSVSVLPANVTITAGQR TATPQQAQEVHEKLR	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 N-ter +34.06 Da, K +34.06 Da, C	84.5 34.9 41.6 29.8	42.3 39.8 40.7 51.0	3 3 3 4	2097.23 2133.21 2239.27 1803.12	0.63 0.25 0.52 0.32	0.09 0.04 0.10 0.08	ENOA_MOUSE CLIP1_MOUSE UBP2L_MOUSE TPIS_MOUSE	Q6PHC1_MOUSE Q8COS5_MOUSE E9Q0M9_MOUSE E0CXH5_MOUSE	Alpha-enolase; CAP-Gly domain-containing linker protein 1; Ubiquitin-associated protein 2-like; Triosephosphate isomerase;		0.25 - 0.75 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75	
VMDDFAAKLD DTCKAAADKD	TCCKAADKTCFSTGPNLVTR TCFSTGPNLVTR	+57.02 Da N-ter +34.06 Da, C +57.02 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	53.9 39.7	51.4 44.6	4 3	2632.45 1514.83	0.93 0.86	0.17 0.18	ALBU_MOUSE ALBU_MOUSE		Serum albumin; Serum albumin;		0.25 - 0.75 0.25 - 0.75	
RVSGEHMDLT	TCPLAAGGQKELR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	37.2	50.7	3	1583.93	2.68	0.59	Q9D1B1_MOUSE			Beta-1-globin;Hemoglobin beta-1 chain;Hemoglobin beta-major chain; Metastasin;Metastatic cell protein;PEL98;Placental calcium-binding protein;Protein 18A2;Protein Mts1;S100 calcium-binding protein A4;	0.85 - 1.00	
MVHL	TDAEKAAVSLGWKVNDSVGGGALGR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	63.5	56.3	4	2902.61	-1.25	0.36	HBB1_MOUSE		Hemoglobin subunit beta-1;		0.15 - 0.25	
RELPSFLGER	TDEAAFQKVMNLDSNR	N-ter +28.03 Da, K +28.03 Da	19.8	53.9	3	1981.06	2.02	0.39	S10A4_MOUSE	D3YUT9_MOUSE	Protein S100-A4;		0.85 - 1.00	
ERRGFCFITY	TDEEPVKLLESR	N-ter +34.06 Da, K +34.06 Da	20.8	49.6	4	1645.10	-2.18	0.30	HNRDL_MOUSE	F6VQH5_MOUSE	Heterogeneous nuclear ribonucleoprotein D-like;	JKT41-binding protein;	0.00 - 0.15	

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
QLKKAMEGAG	TDEKTUEILATR	N-ter +28.03 Da, K +28.03 Da	28.1	41.8	3	1557.96	-1.74	0.41	ANXA6_MOUSE	F8WITZ_MOUSE	Annexin A6;	67 kDa calelectrin;Annexin VI;Annexin-6;Calphobindin-II;Chromobindin-20;Lipocortin VI;Protein III;p68;p70;	0.00 - 0.15
ELKHALKGAG	TDEKVLTEIIASR	N-ter +28.03 Da, K +28.03 Da	31.1	49.2	3	1529.94	-0.30	0.05	ANXA5_MOUSE		Annexin A5;	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
SVSMIASRKP	TDGASSNCVTDISHLVR	N-ter +28.03 Da, C +57.02 Da	63.7	52.8	3	1946.02	0.93	0.20	NASP_MOUSE	B1AU75_MOUSE	Nuclear autoantigenic sperm protein;		0.25 - 0.75
INRVYKEMYK	TDLEKDIISDTSGDFR	N-ter +28.03 Da, K +28.03 Da	46.0	53.6	3	1867.02	0.49	0.08	ANXA2_MOUSE	B0VZNT_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
GGYKPTDKHK	TDLNHENLKGDDLPNVLSSR	N-ter +28.03 Da, K +28.03 Da	41.5	54.4	4	2627.43	-0.52	0.13	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.25 - 0.75
SRRTSQGVKL	TDLQEAETIGTR	N-ter +34.06 Da, K +34.06 Da	25.3	46.1	3	1427.89	0.53	0.11	MYPT1_MOUSE		Protein phosphatase 1 regulatory subunit 12A;	Myosin phosphatase-targeting subunit 1;	0.25 - 0.75
ADFAEITKLA	TDLTKNVKECCHGDLLCADDR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	33.0	65.6	4	2732.44	1.55	0.52	ALBU_MOUSE		Serum albumin;		0.75 - 0.85
AHVDHKGSTL	TDLSLVCKAGIASAR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	29.0	43.9	3	1629.03	-1.00	0.14	EF2_MOUSE		Elongation factor 2;		0.15 - 0.25
ILSVASTVWT	TDTEDKGFLSEGGGVR	N-ter +34.06 Da, K +34.06 Da	36.0	39.3	3	1864.02	0.77	0.19	Q99K47_MOUSE	E9PV24_MOUSE			0.25 - 0.75
PRHEVTEISN	TDVETQPGKTVIR	N-ter +28.03 Da, K +28.03 Da	33.7	46.1	3	1498.90	0.94	0.17	E9Q616_MOUSE				0.25 - 0.75
NASAEAIIG	TDVLQDHNALDFEHR	N-ter +28.03 Da	55.3	59.3	4	1936.06	0.86	0.12	APRV1_MOUSE		Retroviral-like aspartic protease 1;	Skin-specific retroviral-like aspartic protease;TPA-inducible aspartic proteinase-like protein;	0.25 - 0.75
KAVLDVAETG	TEAAAATVIGGIR	N-ter +34.06 Da	36.4	43.4	3	1319.82	-1.15	0.18	SPAK3_MOUSE		Serine protease inhibitor A3K;	Contrapsin;SPI-2;	0.15 - 0.25
WLLCALGLQA	TEAELPSAPALPGGAACLSR	N-ter +28.03 Da, C +57.02 Da	47.4	44.2	3	2124.15	1.12	0.12	SPIT1_MOUSE		Kunitz-type protease inhibitor 1;	Hepatocyte growth factor activator inhibitor type 1;	0.75 - 0.85
AGSYIEKPKQ	TEAPQVTGPVIVVVR	N-ter +28.03 Da	48.4	50.6	3	1719.04	0.04	0.01	CRIP2_MOUSE		Cysteine-rich protein 2;	Heart LIM protein;	0.25 - 0.75
QEPGQIVETY	TEEDPEGAMSVSVETDDGTTR	N-ter +28.03 Da	63.8	48.1	3	2453.19	0.75	0.20	CTND1_MOUSE	E9Q829_MOUSE	Catenin delta-1;	Cadherin-associated Src substrate;p120 catenin;p120(cas);	0.25 - 0.75
LFVRNLANTV	TEEILEKFSQFGKLER	N-ter +34.06 Da, K +34.06 Da	20.4	64.5	4	2142.38	-2.18	0.20	HNRPO_MOUSE		Heterogeneous nuclear ribonucleoprotein Q;	Skin-specific retroviral-like aspartic protease;TPA-inducible aspartic proteinase-like protein;	0.00 - 0.15
QPPVLLPQLL	TEGALPDITR	N-ter +28.03 Da	40.4	34.9	2	1228.67	-1.22	0.06	TB182_MOUSE		182 kDa tankyrase-1-binding protein;	Contrapsin;SPI-2;	0.15 - 0.25
VIRFQPGETL	TEILETPATNQEAEHQK	N-ter +28.03 Da	46.0	30.1	3	2123.08	-0.43	0.08	IQGA1_MOUSE	F6ZJ80_MOUSE	Ras GTPase-activating-like protein IQGAP1;	Hepatocyte growth factor activator inhibitor type 1;	0.25 - 0.75
SKTEFLFMN	TELAFTKNQKDPGVLDLR	N-ter +28.03 Da, K +28.03 Da	27.6	57.5	4	2086.26	2.39	0.50	S10AB_MOUSE	F6SJ35_MOUSE	Protein S100-A11;	Calgizarin;Endothelial monocyte-activating polypeptide;Protein S100-C;S100 calcium-binding protein A11;	0.85 - 1.00
NVNLAQRITF	TEMDSHEEKVFR	N-ter +28.03 Da, K +28.03 Da	19.8	59.3	4	1562.83	-1.18	0.27	COPD_MOUSE		Coatmer subunit delta;	Archain;Delta-coat protein;	0.15 - 0.25
KLEERHTLI	TEMVANLPDFKPPADYKPPATR	N-ter +28.03 Da, K +28.03 Da	35.5	63.4	4	2541.49	-0.71	0.13	SFO1_MOUSE	Q3U145_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
REGEVEVLKA	TEMVVEVGPEDDEVGAER	N-ter +28.03 Da	46.3	46.6	3	1888.92	1.14	0.33	PTRF_MOUSE		Polymerase I and transcript release factor;	Cav-p60;Cavin-1;	0.75 - 0.85
QLEEKELLA	TEQEDAIVAASKLR	N-ter +28.03 Da, K +28.03 Da	13.0	55.3	4	1629.00	-1.36	0.31	RRBP1_MOUSE	A2AVJ7_MOUSE	Ribosome-binding protein 1;	Ribosome receptor protein;	0.15 - 0.25
AAPCIYWLPL	TESQIVQKEAEQAEAR	N-ter +28.03 Da, K +28.03 Da	27.2	49.8	3	1801.01	0.72	0.17	ACINU_MOUSE	B8J9J3_MOUSE	Adaptin-1;	Linear IgA disease antigen homolog;	0.25 - 0.75
ESVRSPPSSR	TEVLVTPAGVASKR	N-ter +28.03 Da, K +28.03 Da	34.2	17.2	3	1482.90	1.08	0.11	LAD1_MOUSE		Ladimirin-1;	Triose-phosphate isomerase;	0.75 - 0.85
TLNAANVPAG	TEVVCAPPTAYIDFAR	N-ter +28.03 Da, C +57.02 Da	50.0	55.1	3	1837.01	-1.25	0.18	TPIS_MOUSE		Triosephosphate isomerase;	Protein cypher;Protein oracle;Z-band alternatively spliced PDZ-motif protein;	0.15 - 0.25
SFRILAQMTG	TEYMQDPDEEALRR	N-ter +28.03 Da	29.5	45.0	3	1779.89	0.59	0.14	LDB3_MOUSE	E9PYJ9_MOUSE	LIM domain-binding protein 3;	Protein cypher;Protein oracle;Z-band alternatively spliced PDZ-motif protein;	0.25 - 0.75
DDLTDPAATG	TEFAHLDATTVLSR	N-ter +28.03 Da	38.0	60.7	3	1458.87	-1.12	0.15	ATPB_MOUSE		ATP synthase subunit beta, mitochondrial;		0.15 - 0.25
AFGQGRDMAE	TFDQGAHAFGQGGGR	N-ter +28.03 Da	28.6	65.9	4	1612.86	1.13	0.21	SBSN_MOUSE	E9QP82_MOUSE	Suprabasin;		0.75 - 0.85
KWKISFPDQD	TFESEFYLDEKR	N-ter +28.03 Da, K +28.03 Da	54.7	48.1	3	1618.87	-1.89	0.42	SPAK3_MOUSE	SPA3M_MOUSE	Serine protease inhibitor A3K;	Contrapsin;SPI-2;	0.00 - 0.15
MANSER	TFIAIKPDGVQR	N-ter +34.06 Da, K +34.06 Da	27.0	45.7	3	1411.95	1.23	0.18	NDKA_MOUSE	NDKB_MOUSE	Nucleoside diphosphate kinase A;	Metastasis inhibition factor NM23;NDPK-A;Tumor metastatic process-associated protein;nm23-M1;	0.75 - 0.85
ADGRKTETVC	TFQDQALVQHQWQDQKSTITR	N-ter +28.03 Da, K +28.03 Da	58.1	65.4	4	2600.47	1.93	0.43	FABP5_MOUSE		Fatty acid-binding protein, epidermal;	Epidermal-type fatty acid-binding protein;Fatty acid-binding protein 5;Keratinocyte lipid-binding protein;Psoriasis-associated fatty acid-binding protein homolog;	0.85 - 1.00
VTTLDIVRAN	TFVAELKGLDPAR	N-ter +28.03 Da, K +28.03 Da	29.8	55.7	3	1471.92	0.07	0.02	MDHM_MOUSE		Malate dehydrogenase, mitochondrial;		0.25 - 0.75
QPDMAIMAVN	TFVKDCEDPNPLIR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	22.3	44.8	3	1758.98	-3.47	0.39	AP1B1_MOUSE	Q8CC13_MOUSE	AP-1 complex subunit beta-1;	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;	0.00 - 0.15
PSVWAAVPGK	TFVSTPAEVGLVGVKDR	N-ter +28.03 Da, K +28.03 Da	57.7	44.1	3	1943.19	0.53	0.10	PROF1_MOUSE	Q5SX49_MOUSE	Profilin-1;	Profilin I;	0.25 - 0.75

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
LKEGDVVKR	TGAIQVDPVGEELLGR	N-ter +34.06 Da	40.4	52.1	3	1658.03	2.60	0.67	ATPA_MOUSE	D3Z6F5_MOUSE	ATP synthase subunit alpha, mitochondrial;		0.85 - 1.00
FKEAFLFDR	TGCEKITLSQVGDVLR	N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	51.8	12.8	3	1843.07	-4.64	1.16	MYL1_MOUSE	E9PWG4_MOUSE	Myosin light chain 1/3, skeletal muscle isoform;	Myosin light chain alkali 1/2; ER-Golgi intermediate compartment 53 kDa protein;Lectin mannose-binding 1;p58;	0.00 - 0.15
SFSQFTGSDG	TGGDAAAPGAAGTQALPHR	N-ter +28.03 Da	52.1	49.9	3	1875.02	-0.60	0.09	LMAN1_MOUSE		Protein ERGIC-53;	Creatine kinase M chain;M-CK;	0.25 - 0.75
LTRLRLQKRG	TGGVDTAAVGAVFDSINADR	N-ter +34.06 Da	70.9	49.4	3	1969.09	0.20	0.04	KCRM_MOUSE		Creatine kinase M-type;		0.25 - 0.75
SSKDAIKKLL	TGIKHELQANCYEEVKDR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	26.5	63.6	4	2273.29	0.35	0.08	COF1_MOUSE	F8WGL3_MOUSE	Cofilin-1;	Cofilin, non-muscle isoform;	0.25 - 0.75
PAGKNGDRGE	TGPAGPAGPIGAGAR	N-ter +28.03 Da	47.2	41.2	3	1373.80	-3.47	0.77	CO1A1_MOUSE	F8WBG7_MOUSE	Collagen alpha-1(I) chain;	Alpha-1 type I collagen;	0.00 - 0.15
HTVEKGGKHK	TGPNLHGLFGR	N-ter +34.06 Da	30.2	54.6	3	1201.74	-0.42	0.04	CYC_MOUSE		Cytochrome c, somatic;		0.25 - 0.75
VHKAVLDVAE	TGTEAAAATGVIGGIR	N-ter +28.03 Da	48.9	47.1	3	1471.87	-3.64	0.46	SPA3K_MOUSE		Serine protease inhibitor A3K;	Contrapsin;SPI-2;	0.00 - 0.15
KCLPLCAPRC	TGTQLPTKIDPEQK	N-ter +28.03 Da, K +28.03 Da	13.9	52.6	4	1639.01	-1.74	0.35	F6XZJ7_MOUSE				0.00 - 0.15
NVARLNFSHG	THEYHAETIKNVR	N-ter +28.03 Da, K +28.03 Da	26.8	67.0	4	1652.97	0.35	0.07	KPYM_MOUSE		Pyruvate kinase isozymes M1/M2;	Pyruvate kinase muscle isozyme; Carbonate dehydratase III;Carbonic anhydrase III;	0.25 - 0.75
IKTKGKEAPF	THFDPSCLFPACR	N-ter +28.03 Da, C +57.02 Da	31.7	49.7	3	1634.82	-0.32	0.02	CAH3_MOUSE		Carbonic anhydrase 3;		0.25 - 0.75
IFEVKTAGD	THLGGEDFDNR	N-ter +28.03 Da	38.9	58.7	3	1287.66	1.07	0.19	HS71A_MOUSE	HS71B_MOUSE	Heat shock 70 kDa protein 1A;	Heat shock 70 kDa protein 3;Hsp68;	0.75 - 0.85
CEKIVQKYG	THLSTGDLR	N-ter +28.03 Da	30.3	51.1	3	1139.69	0.77	0.05	KAD1_MOUSE		Adenylate kinase isoenzyme 1;	ATP-AMP transphosphorylase 1;Myokinase;	0.25 - 0.75
AQHLGESTVR	TIAMDGETGLVR	N-ter +28.03 Da	40.3	38.5	2	1289.71	0.66	0.10	ATPB_MOUSE		ATP synthase subunit beta, mitochondrial;		0.25 - 0.75
NIPILSPDKR	TIAQDYGVKKADEGISFR	N-ter +28.03 Da, K +28.03 Da	33.2	45.1	3	2038.17	0.56	0.13	PRDX1_MOUSE	B1AXW6_MOUSE	Peroxioredoxin-1;	Macrophage 23 kDa stress protein;Osteoblast-specific factor 3;Thioredoxin peroxidase 2;Thioredoxin-dependent peroxide reductase 2;	0.25 - 0.75
GGDVAVFVKT	TIFEVLPEKADR	N-ter +28.03 Da, K +28.03 Da	40.5	51.2	3	1472.90	0.32	0.06	TRFE_MOUSE	D3YXR8_MOUSE	Serotransferrin;	Beta-1 metal-binding globulin;Siderophilin;	0.25 - 0.75
FKVLDPGEGK	TIKKQFLELLTTQCDR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	31.3	62.2	4	2206.34	0.55	0.05	MLRS_MOUSE		Myosin regulatory light chain 2, skeletal muscle isoform;	Fast skeletal myosin light chain 2;MLC2F;	0.25 - 0.75
AEVVRKDKKE	TIQDTQEELKGGAAKR	N-ter +28.03 Da, K +28.03 Da	31.7	58.3	4	1957.16	-0.89	0.12	E41L2_MOUSE	Q811B2_MOUSE	Band 4.1-like protein 2;	Generally expressed protein 4.1;	0.15 - 0.25
TIERKDLQYI	TISKEELSSGDSLDPDWKR	N-ter +28.03 Da, K +28.03 Da	39.0	63.7	4	2315.35	-0.30	0.04	AFAD_MOUSE	F7C3I9_MOUSE	Afadin;	Protein AF-6;	0.25 - 0.75
PRFNAHGDN	TIVCNTKEDGTWGTEHR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	37.5	63.7	4	2059.11	-0.20	0.03	LEG1_MOUSE		Galectin-1;	14-kDa lectin;Beta-galactoside-binding lectin L-14-I;Galaptin;Lactose-binding lectin 1;Lectin galactoside-binding soluble 1;S-Lac lectin 1;	0.25 - 0.75
RDAVTRQVR	TIVEVQDGKVISSR	N-ter +28.03 Da, K +28.03 Da	45.0	46.0	3	1715.03	4.82	1.26	K1C17_MOUSE	D3YXP7_MOUSE	Keratin, type I cytoskeletal 17;	Cytokeratin-17;Keratin-17;	0.85 - 1.00
ILLDALDKIK	TKGKEAPFTHFDPSCLFPACR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	27.5	67.7	4	2549.43	-0.25	0.02	CAH3_MOUSE		Carbonic anhydrase 3;	Carbonate dehydratase III;Carbonic anhydrase III;	0.25 - 0.75
SLSTFQQMWI	TKQEYDEAGPSIVHR	N-ter +28.03 Da, K +28.03 Da	50.4	55.3	4	1785.00	-0.47	0.09	ACTS_MOUSE		Actin, alpha skeletal muscle;	Alpha-actin-1;	0.25 - 0.75
AALTOAKSQR	TKQSTVLAPVIDLKR	N-ter +28.03 Da, K +28.03 Da	27.1	64.8	4	1752.20	0.40	0.02	SPPF45_MOUSE	A2AP40_MOUSE	Splicing factor 45;	45 kDa-splicing factor;RNA-binding motif protein 17;	0.25 - 0.75
VFEVFAFARG	TKSLMDVEVKATSR	N-ter +28.03 Da, K +28.03 Da	26.5	64.4	4	1648.03	-1.36	0.14	PGK1_MOUSE		Phosphoglycerate kinase 1;		0.15 - 0.25
YFIQVMKEYL	TRVDKLDAESLR	N-ter +28.03 Da, K +28.03 Da	32.0	54.1	4	1544.96	1.90	0.31	CLH_MOUSE	Q55XR6_MOUSE	Clathrin heavy chain 1;		0.85 - 1.00
AEITKLATDL	TKVNKECCHGDLLCADDR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	40.9	62.5	4	2421.35	0.82	0.27	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
QLVAGIKYK	TLDIESTECR	N-ter +28.03 Da, C +57.02 Da	33.8	33.3	2	1250.62	0.50	0.05	Q9D1B1_MOUSE				0.25 - 0.75
NLDPLNNLGR	TLEIPGSSDPNIVPDGDFSSSLVR	N-ter +28.03 Da	39.3	47.1	3	2442.34	0.52	0.23	CO4B_MOUSE		Complement C4-B;		0.25 - 0.75
ELLSQFLLL	TLEQKNIAVENEVR	N-ter +28.03 Da, K +28.03 Da	35.8	49.6	3	1698.02	1.95	0.40	ASHWN_MOUSE		Ashwin;		0.85 - 1.00
SAANCKSLH	TLFGDKLCAIPNLR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	28.2	42.7	3	1673.01	-3.18	0.29	ALBU_MOUSE		Serum albumin;		0.00 - 0.15
TGFEKKYVA	TLGVEVHPLVFHTNR	N-ter +28.03 Da	24.2	65.9	4	1746.07	-0.36	0.04	RAN_MOUSE		GTP-binding nuclear protein Ran;	GTPase Ran;Ras-like protein TC4;Ras-related nuclear protein;	0.25 - 0.75
ELRVAPPEHP	TLLEAPLNPKANR	N-ter +28.03 Da, K +28.03 Da	34.2	36.8	3	1592.98	0.15	0.03	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
GTGSLSLPT	TLPENALLSVEASGSAQENMPLARR	N-ter +34.06 Da	24.6	50.2	4	2774.58	-2.74	1.10	CH076_MOUSE		Uncharacterized protein C8orf76 homolog;		0.00 - 0.15
SLPSTAVTSE	TLPGSLSPVVEKYR	N-ter +28.03 Da, K +28.03 Da	27.4	53.0	3	1598.99	-0.62	0.05	DLG1_MOUSE	E9Q9H0_MOUSE	Disks large homolog 1;	Embryo-dlg/synapse-associated protein 97;Synapse-associated protein 97;	0.25 - 0.75
GKAPFALQVNI	TLPLNFDKAGDHR	N-ter +28.03 Da, K +28.03 Da	21.2	59.0	4	1538.91	1.04	0.12	A2M_MOUSE	D3YV52_MOUSE	Alpha-2-macroglobulin;	Pregnancy zone protein;	0.75 - 0.85
PFKLRSRKQR	TLSMIEEIR	N-ter +28.03 Da	38.1	43.1	2	1247.70	0.83	0.11	AKAP2_MOUSE	A2AP18_MOUSE	A-kinase anchor protein 2;	AKAP expressed in kidney and lung;Protein kinase A-anchoring protein 2;	0.25 - 0.75
WDLGDPGKLY	TLVLTDPDAPSR	N-ter +28.03 Da	46.4	34.3	2	1311.75	2.47	0.36	PEBP1_MOUSE	D3Z1V4_MOUSE	Phosphatidylethanolamine-binding protein 1;	HCNPPpp;	0.85 - 1.00
YANTVLSGGT	TMYPGIADR	N-ter +28.03 Da	33.9	45.3	2	1050.56	0.26	0.01	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
VDKGVVPLAG	TNGETTTQGLDGLSER	N-ter +28.03 Da	40.1	56.0	3	1705.91	-1.25	0.45	ALDOA_MOUSE	Q9CPQ9_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.15 - 0.25
PTFSSLNLR	TNLESPLVDTHSKR	N-ter +28.03 Da, K +28.03 Da	24.4	65.3	4	1765.09	1.56	0.13	VIME_MOUSE	E9PZV5_MOUSE	Vimentin;		0.75 - 0.85
DQSPASHEIA	TNLGDFAISLYR	N-ter +28.03 Da	53.6	37.5	2	1396.79	-1.03	0.29	A1AT2_MOUSE	A1AT1_MOUSE	Alpha-1-antitrypsin 1-2;	Alpha-1 protease inhibitor 2;Alpha-1-antiproteinase;Serine protease inhibitor 1-2;Serine protease inhibitor A1b;	0.15 - 0.25
DSLEIICSR	TNQLQEINR	N-ter +28.03 Da	30.7	46.5	3	1271.71	0.53	0.04	ANXA2_MOUSE	BOV2N7_MOUSE	Annexin A2;	Annexin II;Annexin-2;Calpactin I heavy chain;Calpactin-1 heavy chain;Chromobindin-8;Lipocortin II;Placental anticoagulant protein IV;Protein t;p36;	0.25 - 0.75
SRLTYDIAH	TPGVAADLSHIETR	N-ter +34.06 Da	32.2	33.0	3	1499.87	0.24	0.03	MDHM_MOUSE		Malate dehydrogenase, mitochondrial;		0.25 - 0.75
KTIIPLSQC	TPKVDFPDQDLTLTGR	N-ter +28.03 Da, K +28.03 Da	52.8	39.4	3	1942.13	-0.25	0.01	MDHM_MOUSE		Malate dehydrogenase, mitochondrial;		0.25 - 0.75
PGPYAQPSVN	TPLPQLNGPIYAR	N-ter +28.03 Da	26.7	40.0	3	1580.93	-0.60	0.04	CRK_MOUSE	F7D232_MOUSE	Adapter molecule crk;	Proto-oncogene c-Crk;p38;	0.25 - 0.75
WRCVLKIGEH	TPSALAIMENANVLAR	N-ter +34.06 Da	45.9	43.6	3	1704.02	0.12	0.05	ALDOA_MOUSE	A6Z144_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.25 - 0.75

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
GLPGSMGPPG	TPSVDHGFLVTR	N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	36.1	46.8	3	1355.78	0.24	0.03	CO4A1_MOUSE		Collagen alpha-1(V) chain;		0.25 - 0.75
LNRVCLLHK	TPVSEHVTKCCGSLVER	N-ter +28.03 Da, K +28.03 Da	37.6	59.3	4	2113.22	1.27	0.28	ALBU_MOUSE		Serum albumin;		0.75 - 0.85
GFOALILVRY	TQKAPQVSTPLVEAAR	N-ter +28.03 Da, K +28.03 Da	57.2	18.3	3	1852.08	-0.71	0.12	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
PNNMVTGPAC	TQKFSNEEIAMATVYTLAR	N-ter +28.03 Da, K +28.03 Da	34.7	45.2	3	2065.18	0.80	0.15	ALDOA_MOUSE	Q9CPQ9_MOUSE	Fructose-bisphosphate aldolase A;	Aldolase 1;Muscle-type aldolase;	0.25 - 0.75
LMITVHAIITA	TQKTVDGPFGKLR	N-ter +34.06 Da, K +34.06 Da	18.8	55.5	4	1674.12	-0.62	0.10	G3P_MOUSE	F8WJL5_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase;	Peptidyl-cysteine S-nitrosylase GAPDH;	0.25 - 0.75
RMRTHVDLSR	TQLAPHSEQMR	N-ter +28.03 Da	26.6	57.5	3	1324.73	-3.06	0.51	APOA1_MOUSE	Q8BPDS_MOUSE	Apolipoprotein A-I;	Apolipoprotein A1;	0.00 - 0.15
DEESKPASSN	TQVGEDEEAALLER	N-ter +28.03 Da	45.0	46.1	3	1586.85	1.92	0.33	Q8VC08_MOUSE	E9QOM9_MOUSE			0.85 - 1.00
PPRSTEDRLT	TQWREDEEEAAR	N-ter +28.03 Da	40.0	52.2	3	1675.83	1.98	0.55	LSP1_MOUSE	A2A6J7_MOUSE	Lymphocyte-specific protein 1;	52 kDa phosphoprotein;Lymphocyte-specific antigen WP34;S37 protein;	0.85 - 1.00
VVYLETETLV	TREAVTEILGIEPDR	N-ter +28.03 Da	51.6	57.3	3	1726.02	-0.52	0.06	TSN_MOUSE		Translin;		0.25 - 0.75
MA	TRGTVTDFPGDGR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	32.0	52.7	3	1552.85	-0.74	0.09	ANXA5_MOUSE		Annexin A5;	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
DQVELLCLDN	TRKPVDDQEDCYLAR	N-ter +28.03 Da, K +28.03 Da	34.5	68.8	4	1969.11	-0.58	0.11	TRFE_MOUSE	E9Q035_MOUSE	Serotransferrin;	Beta-1 metal-binding globulin;Siderophilin;	0.25 - 0.75
AAAMNLASAR	TSAIAPSVNLADSR	N-ter +28.03 Da	39.2	43.0	3	1428.82	-0.79	0.11	SRRM2_MOUSE	E9QMJ6_MOUSE	Serine/arginine repetitive matrix protein 2;		0.25 - 0.75
AALHFNPLRD	TSEVVFNTKEQGKWGR	N-ter +28.03 Da, K +28.03 Da	21.4	61.3	4	1949.16	0.20	0.02	Q9CRB1_MOUSE	D3Z141_MOUSE			0.25 - 0.75
FERPEAEAMC	TSFKENPTTFMGHYLHEVAR	N-ter +28.03 Da, K +28.03 Da	30.4	66.3	4	2420.36	2.24	0.31	ALBU_MOUSE		Serum albumin;		0.85 - 1.00
LIIGDRQTKG	TSIAIDTIINQKR	N-ter +28.03 Da, K +28.03 Da	39.1	42.3	3	1527.96	-0.34	0.07	ATPA_MOUSE	D3Z6F5_MOUSE	ATP synthase subunit alpha, mitochondrial;		0.25 - 0.75
LTTSESLCCE	TSSFSDKYGLGHVTEPR	N-ter +28.03 Da, K +28.03 Da	25.3	65.2	4	1936.10	-1.22	0.06	PLIN4_MOUSE		Perilipin-4;	Adipocyte protein S3-12;	0.15 - 0.25
VGLTSLRAVS	TSSMGLTPKQKIVEVGR	N-ter +28.03 Da, K +28.03 Da	20.4	64.0	4	2110.35	0.40	0.09	HMGCL_MOUSE		Hydroxymethylglutaryl-CoA lyase, mitochondrial;	3-hydroxy-3-methylglutarate-CoA lyase;	0.25 - 0.75
SLPKAALIRN	TSSMTEGLQPASVVLP	N-ter +34.06 Da	36.9	53.8	3	1905.15	-1.43	0.23	CN159_MOUSE	E9QMK9_MOUSE	UPF0317 protein C14orf159 homolog, mitochondrial;		0.15 - 0.25
VYQQPQQQM	TSSYGGYKEPAAPVSIQR	N-ter +28.03 Da, K +28.03 Da	24.9	53.4	3	1966.12	-0.92	0.21	LASP1_MOUSE	A2A6H0_MOUSE	LIM and SH3 domain protein 1;	Metastatic lymph node gene 50 protein;	0.15 - 0.25
LEAWYRHGRT	TSSYSALSPEPR	N-ter +34.06 Da	44.6	33.6	2	1317.71	-0.01	0.00	MECR_MOUSE	A2A845_MOUSE	Trans-2-enoyl-CoA reductase, mitochondrial;		0.25 - 0.75
RGVHTSVASA	TSVATKTEQGPSPSEYIFER	N-ter +28.03 Da, K +28.03 Da	51.3	52.7	4	2438.40	-0.84	0.15	OAT_MOUSE		Ornithine aminotransferase, mitochondrial;	Ornithine-oxo-acid aminotransferase;	0.15 - 0.25
APQRPIATQR	TTAAPKAGPVMVR	N-ter +28.03 Da, K +28.03 Da	20.2	50.0	3	1311.80	0.66	0.17	MARE1_MOUSE		Microtubule-associated protein RP/EB family member 1;	APC-binding protein EB1;End-binding protein 1;	0.25 - 0.75
MCDDEE	TTALVCDNCGSLVKAGFAGDAPR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	56.2	57.8	4	2447.35	0.71	0.19	ACTC_MOUSE	ACTS_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.25 - 0.75
TRVSGEHMDL	TTCPPLAAGGQEQELR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	51.8	46.8	3	1684.97	1.77	0.47	Q9D1B1_MOUSE				0.85 - 1.00
ADDLTDAPAA	TTFAHLDAITVLSR	N-ter +28.03 Da	50.9	52.8	3	1559.91	-0.71	0.08	ATPB_MOUSE		ATP synthase subunit beta, mitochondrial;		0.25 - 0.75
AMCTSFKENP	TTFMGHYHLEVAR	N-ter +28.03 Da	31.2	70.4	4	1588.89	0.86	0.07	ALBU_MOUSE		Serum albumin;		0.25 - 0.75
RTVHTTRVCL	TTFNVQDGPFQDR	N-ter +34.06 Da	45.9	53.9	3	1672.88	0.85	0.21	THIOM_MOUSE	Q3TUS3_MOUSE	Thioredoxin, mitochondrial;	Thioredoxin-2;	0.25 - 0.75
LRVPHARKTG	TTIAGLVFR	N-ter +28.03 Da	25.8	40.4	2	1004.64	2.10	0.59	PSB10_MOUSE			Low molecular mass protein 10;Macropain subunit MECl-1;Multicatalytic endopeptidase complex subunit MECl-1;Proteasome MECl-1;Proteasome subunit beta-2i;	0.85 - 1.00
FKLPKARKTG	TTIAGVVYKDGIVLGADTR	N-ter +34.06 Da, K +34.06 Da	33.7	47.3	3	2016.28	1.66	0.32	PSB7_MOUSE			Macropain chain Z;Multicatalytic endopeptidase complex chain Z;Proteasome subunit Z;	0.85 - 1.00
GGGDVAVFKH	TTIFEVLPEKADR	N-ter +28.03 Da, K +28.03 Da	45.3	47.4	3	1573.95	0.37	0.08	TRFE_MOUSE	D3YR8_MOUSE	Serotransferrin;	Beta-1 metal-binding globulin;Siderophilin;	0.25 - 0.75
LYANTVLSGG	TTMYPGIADR	N-ter +34.06 Da	26.4	31.8	2	1157.63	-4.64	1.16	ACTA_MOUSE	ACTB_MOUSE	Actin, aortic smooth muscle;	Alpha-actin-2;	0.00 - 0.15
EIIANDQGNR	TTPSYVAFTDTER	N-ter +28.03 Da	40.9	59.4	2	1514.82	1.24	0.21	HS71A_MOUSE	HS71B_MOUSE	Heat shock 70 kDa protein 1A;	Heat shock 70 kDa protein 3;Hsp68;	0.75 - 0.85
ISAVEQTAQR	TTTTAVHIQPAQEQAR	N-ter +28.03 Da	36.4	53.8	3	1779.02	0.29	0.05	TITIN_MOUSE	Q8BUJ6_MOUSE	Titin;	Connectin;	0.25 - 0.75
ITVKTESTVK	TTVFSCNLGKEDTADGR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	25.4	45.1	3	2303.18	2.59	0.71	FABP5_MOUSE	E9Q964_MOUSE	Fatty acid-binding protein, epidermal;	Epidermal-type fatty acid-binding protein;Fatty acid-binding protein 5;Keratinocyte lipid-binding protein;Psoriasis-associated fatty acid-binding protein homolog;	0.85 - 1.00
DFEHFLPMLQ	TVAKNKDQGTEDYVEGLR	N-ter +28.03 Da, K +28.03 Da	30.3	62.7	4	2269.30	0.31	0.03	MYL6_MOUSE	E9QLM0_MOUSE	Myosin light polypeptide 6;	17 kDa myosin light chain;Myosin light chain 3;Myosin light chain alkali 3;Smooth muscle and nonmuscle myosin light chain alkali 6;	0.25 - 0.75
QRPRQLKPR	TVATPLNQVANPNSAIFGGARPR	N-ter +28.03 Da	39.9	49.1	3	2378.40	1.77	0.43	IF4H_MOUSE	Q80U88_MOUSE	Eukaryotic translation initiation factor 4H;	Williams-Beuren syndrome chromosomal region 1 protein homolog;	0.85 - 1.00
QRPRQLKPR	TVATPLNQVANPNSAIFGGAR	N-ter +28.03 Da	63.4	43.9	3	2125.22	1.18	0.32	IF4H_MOUSE	Q80U88_MOUSE	Eukaryotic translation initiation factor 4H;	Williams-Beuren syndrome chromosomal region 1 protein homolog;	0.75 - 0.85
EKAKREVCWSV	TVEGDVNTDPWAGYR	N-ter +28.03 Da	32.4	53.6	3	1706.88	-0.40	0.04	AMPM1_MOUSE		Methionine aminopeptidase 1;	Peptidase M 1;	0.25 - 0.75
QTVSTKSSSN	TVESTSLYNKVAQGEVVR	N-ter +28.03 Da, K +28.03 Da	26.8	31.4	3	2106.20	2.09	0.18	SYEP_MOUSE		Bifunctional glutamate/proline-tRNA ligase;	Bifunctional aminoacyl-tRNA synthetase;	0.85 - 1.00
REILDSRGNP	TVEVDLHTAKGR	N-ter +34.06 Da, K +34.06 Da	23.4	52.7	3	1392.91	-1.89	0.42	ENOB_MOUSE	Q5X59_MOUSE	Beta-enolase;	2-phospho-D-glycerate hydro-lyase;Enolase 3;Muscle-specific enolase;Skeletal muscle enolase;	0.00 - 0.15
GCVAGDEESY	TVFKDLFDPIQDR	N-ter +28.03 Da, K +28.03 Da	44.6	50.4	3	1762.06	0.04	0.02	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 ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
QNAQCPKNSG NCGIVEGLMT	TVGAVALDCR TVHAITATKQTVDPGSPGLKWR	N-ter +28.03 Da, C +57.02 Da N-ter +34.06 Da, K +34.06 Da	32.8 41.4	75.7 56.7	2 4	1088.65 2367.55	-1.12 -0.71	0.10 0.11	ASGL1_MOUSE G3P_MOUSE		L-asparaginase; Glyceraldehyde-3-phosphate dehydrogenase;	Asparaginase-like protein 1;L-asparagine amidohydrolase; Peptidyl-cysteine 5-nitrosylase GAPDH; 60 kDa chaperonin;Chaperonin 60;HSP-65;Heat shock protein 60;Mitochondrial matrix protein P1;	0.15 - 0.25 0.25 - 0.75
VAVTMGPKGR	TVIEQSWGSPKVTGKGVTVAK	N-ter +28.03 Da, K +28.03 Da	41.5	60.8	4	2454.56	2.03	0.38	CH60_MOUSE	D3Z2F2_MOUSE	60 kDa heat shock protein, mitochondrial;		0.85 - 1.00
KDVVDYIFG VETELRGVCD VDIRKDLNAN	TVIQEVKTSNVAR TVLGLDLSHLIKAGDAESR TVLSGGTTMPGDIADR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	30.0 30.2 37.1	47.7 94.1 47.5	3 4 3	1499.94 2107.36 1665.92	0.90 1.29 0.06	0.17 0.25 0.01	ECHB_MOUSE 14335_MOUSE ACTB_MOUSE	D3YXU1_MOUSE ACTG_MOUSE	Trifunctional enzyme subunit beta, mitochondrial; 14-3-3 protein sigma; Actin, cytoplasmic 1;	TP-Beta; Stratifin; Beta-actin;	0.25 - 0.75 0.75 - 0.85 0.25 - 0.75
RQRPEPQVQG	TVSLHLGVTPSVLR	N-ter +28.03 Da	44.1	48.8	3	1505.97	0.40	0.07	TPP1_MOUSE		Tripeptidyl-peptidase 1;		0.25 - 0.75
IVWLLKPEM VCPSNFYFCK	TVSSDQMAKLR TVTSVEPLNGLNLR	N-ter +34.06 Da, K +34.06 Da N-ter +28.03 Da	24.0 40.7	42.0 41.8	3 3	1302.81 1525.91	0.41 2.12	0.06 0.31	CAH3_MOUSE LY6D_MOUSE		Carbonic anhydrase 3; Lymphocyte antigen 6D;	Carbonate dehydratase III;Carbonic anhydrase III; Thymocyte B-cell antigen; AKAP expressed in kidney and lung;Protein kinase A-anchoring protein 2;	0.25 - 0.75 0.85 - 1.00
GEFTSARAVL SPGMKDLGA	TVVKDEDHIGLDQFSR TWVVLGHSEER	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	26.2 41.5	58.8 48.3	4 3	1914.10 1210.70	1.22 -0.32	0.19 0.03	AKAP2_MOUSE TPIS_MOUSE	A2API8_MOUSE E0CXH5_MOUSE	A-kinase anchor protein 2; Triosephosphate isomerase;	kinase A-anchoring protein 2; Triose-phosphate isomerase;	0.75 - 0.85 0.25 - 0.75
QGQGDPIFFY VSGRQQQLVEL MGNHNTLRLR KNCGHRFLVL WHHSFYNELR WHHTFYNELR EERSVNCGTM	TYEEGLSHLTAEGQATLER VAEQADLEQAFSPSPDPCVDR VAGPQPAQTGAPQGLSLEYLFEER VANQDFVENLVR VAPEHPHTLLTEAPLNPKANR VAPEHPVLLTEAPLNPKANR VAQPKNLEGVYGFANLPNQVYR	N-ter +34.06 Da N-ter +28.03 Da, C +57.02 Da 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	29.0 53.3 53.1 48.4 41.1 52.4 52.1	55.8 43.5 42.3 51.2 55.7 57.5 56.0	3 3 3 3 4 4 4	2138.19 2376.16 2400.31 1529.90 2352.41 2350.44 2532.49	-1.89 2.44 3.27 0.59 4.38 3.47 1.21	0.28 0.76 0.77 0.03 0.81 0.75 0.22	ICLN_MOUSE API5_MOUSE FRIL1_MOUSE TOM1_MOUSE ACTC_MOUSE ACTB_MOUSE E9Q9F5_MOUSE	Q923F1_MOUSE Q9CPX4_MOUSE Q3UDC3_MOUSE ACTG_MOUSE	Methylosome subunit pICln; Apoptosis inhibitor 5; Ferritin light chain 1; Target of Myb protein 1; Actin, alpha cardiac muscle 1; Actin, cytoplasmic 1;	Chloride channel, nucleotide sensitive 1A;Chloride conductance regulatory protein ICl;Chloride ion current inducer protein; AAC-11; Ferritin L subunit 1;	0.00 - 0.15 0.85 - 1.00 0.85 - 1.00 0.25 - 0.75 0.85 - 1.00 0.85 - 1.00 0.75 - 0.85
AHQLFGRF5F	VATGLMEDDGKPR	N-ter +28.03 Da, K +28.03 Da	37.3	62.8	3	1443.83	-0.52	0.09	K56A1_MOUSE	Q505N6_MOUSE	Ribosomal protein S6 kinase alpha-1; kinase-activated protein kinase 1a;Ribosomal S6 kinase 1;		0.25 - 0.75
HLTGEFEKYY VGPPEPTDCF DVDEYDENKF EYKRDIVFL LMDVGNMGQS	VATLGEVHPVLFHTNR VAVMHGTEGTVPGNALVWDPKPFPR VDEEDGGDQAGPDEGEVDSCLR VDGSSSLGSPNFNAIR VDISGLQLALAEAR	N-ter +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 N-ter +34.06 Da	41.8 51.8 61.7 39.0 19.4	61.7 42.4 54.7 54.9 100.8	4 4 3 3 3	1922.21 2804.61 2433.09 1647.91 1417.98	-1.03 0.71 0.51 0.53 -3.18	0.15 0.15 0.21 0.03 0.29	RAN_MOUSE EH02_MOUSE ARPC5_MOUSE E9PWQ3_MOUSE CB029_MOUSE	Q3UA72_MOUSE D3YWD1_MOUSE	GTP-binding nuclear protein Ran; EH domain-containing protein 2; Actin-related protein 2/3 complex subunit 5; UPF0760 protein C2orf29 homolog;		0.15 - 0.25 0.25 - 0.75 0.25 - 0.75 0.25 - 0.75 0.00 - 0.15
AGKHVPRAVF	VDLEPTVIDEVR	N-ter +28.03 Da	27.6	45.4	3	1411.82	2.35	0.36	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
SPTESKDILL	VDLNSEIDTNQNSLR	N-ter +28.03 Da	47.0	48.6	3	1744.94	-0.64	0.09	DAB2_MOUSE	E9QL31_MOUSE	Disabled homolog 2;	DOC-2;Mitogen-responsive phosphoprotein; 265 proteasome AAA-ATPase subunit RPT1;Proteasome 265 subunit ATPase 2;Protein MSS1;	0.25 - 0.75
INVKQFAKFV	VDSLQVAPTIDIEGMR	N-ter +28.03 Da	44.7	53.0	3	1902.00	0.38	0.05	PRS7_MOUSE	Q8BVQ9_MOUSE	26S protease regulatory subunit 7;	Alpha-tubulin 1;Alpha-tubulin isotype M-alpha-1;Tubulin alpha-1 chain;	0.25 - 0.75
ASLRFQDALN MNGTRNWCTL EKLGGQGVQK MRKLVRSLTM AVTTROVRTI	VDLTFEQTNLVPPYR VDVHPSQATGSDVILR VDVPAADLSDQVPDSETR VEDNEDDDEGELHHR VEEVQDGKVISSR	N-ter +28.03 Da N-ter +28.03 Da N-ter +28.03 Da N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da	46.9 51.0 55.6 59.1 26.2	53.1 45.7 51.6 72.3 49.9	3 3 3 3 3	1819.05 1850.04 2157.12 2336.17 1500.89	-0.25 -1.03 0.81 -1.00 1.64	0.04 0.19 0.24 0.38 0.31	TBA1A_MOUSE TUFT1_MOUSE CO3_MOUSE LMNA_MOUSE K1C17_MOUSE	TBA1B_MOUSE D6RGP4_MOUSE	Tubulin alpha-1A chain; Tuftelin; Complement C3; Prelamin-A/C; Keratin, type I cytoskeletal 17;		0.25 - 0.75 0.15 - 0.25 0.25 - 0.75 0.15 - 0.25 0.75 - 0.85
LNLKQKGYFF M ICAKLSRQVV NEWRRPIHQ EVEANPLLTN EVEVLKATEM SEEEIEAFR GYEDFVEGLR AVQGGAAAPV MRGQ ELRGFDGVVC	VEGELYCETHAR VEKEEAGGGGGGSEEEAAQYDR VEKGAEGSQAEQSPHPR VESVDDKSSYFSMDSAEGR VEVEYPENAILDLTR VEVGPEDDEVGAER VFDKNGNYISAELR VFDKEGNGTVMGAELR VGAVQVPVGMPPMPQAPR VGDLSPPQQEALAR VGGDGSASEAAR	N-ter +28.03 Da, C +57.02 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 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 +34.06 Da N-ter +28.03 Da N-ter +28.03 Da	46.0 81.5 51.7 19.9 53.3 39.0 43.8 28.3 48.2 40.7 28.9	46.7 37.5 55.9 48.4 51.7 38.3 49.9 36.8 39.6 42.4 57.9	3 4 4 4 3 3 3 3 3 3 2	1490.75 2450.21 1975.12 2221.09 1788.02 1527.76 1810.02 1777.97 1862.09 1538.87 1103.58	-1.74 3.31 0.18 0.79 1.09 0.57 1.65 0.58 0.04 0.91 1.50	0.35 1.33 0.05 0.25 0.26 0.08 0.23 0.02 0.01 0.14 0.14	PDLJ3_MOUSE SAE1_MOUSE CASZ1_MOUSE TRI29_MOUSE ITHH3_MOUSE PTRF_MOUSE CALM_MOUSE MYL1_MOUSE SNRPA_MOUSE S14L4_MOUSE A2AQH1_MOUSE	B1A547_MOUSE E9PVS1_MOUSE Q3UKW2_MOUSE D3Z0S6_MOUSE	PDZ and LIM domain protein 3; SUMO-activating enzyme subunit 1; Zinc finger protein castor homolog 1; Tripartite motif-containing protein 29; Inter-alpha-trypsin inhibitor heavy chain H3; Polymerase I and transcript release factor; Calmodulin; Myosin light chain 1/3, skeletal muscle isoform; U1 small nuclear ribonucleoprotein A; SEC14-like protein 4;	Actinin-associated LIM protein;Alpha-actinin-2-associated LIM protein; Ubiquitin-like 1-activating enzyme E1A; Castor-related protein; Cav-p60;Cavin-1;	0.00 - 0.15 0.85 - 1.00 0.25 - 0.75 0.25 - 0.75 0.75 - 0.85 0.25 - 0.75 0.75 - 0.85 0.25 - 0.75 0.25 - 0.75 0.75 - 0.85
M	VGGEASAAVEKLVSGV	N-ter +28.03 Da, K +28.03 Da	22.1	43.8	3	1684.03	-0.03	0.00	C2AIL_MOUSE		CDKN2AIP N-terminal-like protein;	CDKN2A-interacting protein N-terminal-like protein;	0.25 - 0.75
GAHLVKKIF LVEAARNLGR QRHSGPSSYK	VGGIKEDTEEHLR VGTKCCTLPEDQR VGMTSEKFDCHYCR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	18.5 33.3 20.3	70.9 44.2 62.0	4 3 4	1674.99 1618.85 1856.98	-1.94 0.81 -5.06	0.52 0.27 1.69	ROA1_MOUSE ALBU_MOUSE AZAEX8_MOUSE	ROA2_MOUSE	Heterogeneous nuclear ribonucleoprotein A1; Serum albumin;	HDP-1;Helix-destabilizing protein;Single-strand-binding protein;Topoisomerase-inhibitor suppressed;hnRNP core protein A1;	0.00 - 0.15 0.25 - 0.75 0.00 - 0.15

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
M	VGVPKVGSDPDFQPELSGAGSR	N-ter +28.03 Da, K +28.03 Da	21.5	52.3	4	2254.28	3.07	0.53	TXNL1_MOUSE		Thioredoxin-like protein 1;	32 kDa thioredoxin-related protein; Acetyl-CoA acyltransferase; Beta-ketothiolase; Mitochondrial 3-oxoacyl-CoA thiolase;	0.85 - 1.00
AYLARHVGLR	VGVPTEGTGALTNR	N-ter +28.03 Da	37.5	47.5	3	1454.88	0.12	0.01	THIM_MOUSE		3-ketoacyl-CoA thiolase, mitochondrial;		0.25 - 0.75
TEAAAQAAYL	VGVSDFPNSQAGQQQLVEPTQFAR	N-ter +28.03 Da	51.6	52.5	4	2412.33	3.04	0.61	TLN1_MOUSE	F8WGT0_MOUSE	Talin-1;		0.85 - 1.00
GIFTGARVFF	VHEGYQGLVDGGHEIR	N-ter +34.06 Da	46.1	62.1	4	1799.03	-3.47	0.39	K6PF_MOUSE		6-phosphofructokinase, muscle type;	Phosphofructo-1-kinase isozyme A; Phosphofructokinase 1; Phosphohexokinase;	0.00 - 0.15
GSGRSPRRSP	VHPESSEGEHSHVVPQR	N-ter +28.03 Da	38.2	61.8	4	1930.04	-0.64	0.11	FILA2_MOUSE	E9QPZ3_MOUSE	Filaggrin-2;	Intermediate filament-associated protein;	0.25 - 0.75
HIFASFNDF	VHVTDLSGKETICR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	24.4	61.3	4	1669.98	0.06	0.01	RS14_MOUSE	D3YVF4_MOUSE	40S ribosomal protein S14;		0.25 - 0.75
ARRQSRMEKY	VISSGHAELAR	N-ter +34.06 Da	26.2	55.4	3	1301.79	-3.06	0.51	SYNP0_MOUSE	E9Q3E2_MOUSE	Synaptopodin;		0.00 - 0.15
KRNTHTRRKR	VIGGKPNVGDYDPWQVAIKDGQR	N-ter +28.03 Da, K +28.03 Da	19.9	65.0	4	2551.56	-1.06	0.13	CFAI_MOUSE		Complement factor I;	C3B/C4B inactivator;	0.15 - 0.25
FGYKNSFHR	VIKDFMIQGGDFTR	N-ter +34.06 Da, K +34.06 Da	42.5	47.0	3	1694.03	-2.94	0.45	PPIB_MOUSE		Peptidyl-prolyl cis-trans isomerase B;	CYP-51; Cyclophilin B; Rotamase B; Cyclophilin;	0.00 - 0.15
STGAAKAVGK	VIPELNGKLTGMAFR	N-ter +28.03 Da, K +28.03 Da	27.1	40.8	3	1701.03	0.01	0.00	G3P_MOUSE	F8WJL5_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase;	Peptidyl-cysteine S-nitrosylase GAPDH;	0.25 - 0.75
GVANVSIDDR	VISLSGHSIIGR	N-ter +28.03 Da	40.8	50.1	3	1394.86	-0.52	0.11	SODC_MOUSE		Superoxide dismutase [Cu-Zn];		0.25 - 0.75
TKFENAFSLH	VISQHSLSLGNIR	N-ter +28.03 Da	36.1	42.6	3	1491.92	0.81	0.10	ATPA_MOUSE	D3Z6F5_MOUSE	ATP synthase subunit alpha, mitochondrial;		0.25 - 0.75
DVAALHKAIM	VKGVEADIHTLTKR	N-ter +28.03 Da, K +28.03 Da	24.5	75.7	4	1854.26	-0.58	0.21	ANXA1_MOUSE	E9QA30_MOUSE	Annexin A1;	Annexin I; Annexin-1; Calpactin I; Calpactin-2; Chromobindin-9; Lipocortin I; Phospholipase A2 inhibitory protein; p35;	0.25 - 0.75
E	VKLVESGGGLVPGGSLR	N-ter +28.03 Da, K +28.03 Da	43.9	40.9	3	1937.17	-0.54	0.07	HVM17_MOUSE	HVM18_MOUSE	Ig heavy chain V region MOPC 47A;		0.25 - 0.75
LYASGRITGI	VLDSDGVTHTNPIYEGYALPHAIMR	N-ter +28.03 Da	51.1	69.0	4	2851.63	3.70	0.66	ACTC_MOUSE	ACTA_MOUSE	Actin, alpha cardiac muscle 1;	Alpha-cardiac actin;	0.85 - 1.00
M	VLESTMVCDNSEMYR	N-ter +28.03 Da, C +57.02 Da	47.4	66.7	3	1960.00	1.58	0.34	PSMD4_MOUSE		26S proteasome non-ATPase regulatory subunit 4;		0.75 - 0.85
LEVQGRDSRL	VLEVAQLGESTVR	N-ter +28.03 Da	46.5	30.0	3	1564.90	0.39	0.07	ATPB_MOUSE		ATP synthase subunit beta, mitochondrial;		0.25 - 0.75
EPPKQSTFSL	VLQEILESDGKDPNKPFGFR	N-ter +28.03 Da, K +28.03 Da	35.9	60.0	4	2369.40	1.25	0.22	PDL1_MOUSE		PDZ and LIM domain protein 1;	C-terminal LIM domain protein CLP-36; LIM domain protein CLP-36;	0.75 - 0.85
M	VLSNEPAASAAEEVEDDALVR	N-ter +28.03 Da	58.7	51.0	3	2341.25	-0.97	0.13	TBCD_MOUSE		Tubulin-specific chaperone D;	Beta-tubulin cofactor D; Tubulin-folding cofactor D;	0.15 - 0.25
IAEGVPQLLI	VLTAEPGDDVVR	N-ter +28.03 Da	32.7	30.4	2	1285.69	2.50	0.36	E9PWQ3_MOUSE	D3YWD1_MOUSE			0.85 - 1.00
PFMWNHGLGY	VLTCPSNLGTGLR	N-ter +34.06 Da, C +57.02 Da	28.7	48.0	3	1420.86	-0.58	0.09	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain; M-CK;	0.25 - 0.75
LSKHNNHMAK	VLTPDLYNKLRL	N-ter +28.03 Da, K +28.03 Da	18.8	45.3	3	1386.89	-1.94	0.52	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain; M-CK;	0.00 - 0.15
DRNLAENISR	VLYPDNFPEGKELR	N-ter +28.03 Da, K +28.03 Da	33.8	57.2	3	1896.09	-1.03	0.11	PYGB_MOUSE	PYGB_MOUSE	Glycogen phosphorylase, liver form;		0.15 - 0.25
IPESLKNMILL	VMDTAEIFHSADAR	N-ter +28.03 Da	53.9	48.7	3	1589.83	1.37	0.30	Q6DF21_MOUSE			Metastasis inhibition factor NM23; NDPK-A; Tumor metastatic process-associated protein; nm23-M1;	0.75 - 0.85
EGLNVKTKGR	VMLGETNPADSKPGTIR	N-ter +28.03 Da, K +28.03 Da	29.0	45.7	3	1841.06	-1.52	0.22	NDKA_MOUSE	NDKB_MOUSE	Nucleoside diphosphate kinase A;		0.00 - 0.15
SIVGRPRHQG	VMMVGMGQKDSYVGEAQSKR	N-ter +28.03 Da, K +28.03 Da	30.3	63.6	4	2268.27	-0.89	0.17	ACT5_MOUSE	ACTA_MOUSE	Actin, alpha skeletal muscle;	Alpha-actin-1;	0.15 - 0.25
DQVIQFFIAL	VNDPQPEHPLR	N-ter +28.03 Da	31.8	49.1	3	1328.75	1.50	0.26	UB2L3_MOUSE		Ubiquitin-conjugating enzyme E2 L3;	Ubiquitin-protein ligase L3;	0.75 - 0.85
KIPNFVWVTF	VNHFPQVSALLGEDEEALHYLTR	N-ter +28.03 Da	57.3	53.7	4	2647.47	1.57	0.53	SET_MOUSE	A2B93_MOUSE	Protein SET;	Phosphatase 2A inhibitor I2PP2A; Template-activating factor I;	0.75 - 0.85
KSAVSLWLAK	VNPDEVGGEALGR	N-ter +34.06 Da	36.0	36.9	2	1345.75	0.19	0.03	HBB2_MOUSE		Hemoglobin subunit beta-2;	Beta-2-globin; Hemoglobin beta-2 chain; Hemoglobin beta-minor chain;	0.25 - 0.75
M	VNPTVFFDITADDEPLGR	N-ter +28.03 Da	55.1	47.4	3	2033.11	0.43	0.16	PPIA_MOUSE	E9Q1E3_MOUSE	Peptidyl-prolyl cis-trans isomerase A;	Cyclophilin A; Cyclosporin A-binding protein; Rotamase A; SP18;	0.25 - 0.75
KAASVSLWGK	VNSDEVGGEALGR	N-ter +28.03 Da	41.0	76.7	3	1329.75	1.12	0.12	HBB1_MOUSE		Hemoglobin subunit beta-1;	Beta-1-globin; Hemoglobin beta-1 chain; Hemoglobin beta-major chain;	0.75 - 0.85
EAGERRKGTD	VNVFTILTISR	N-ter +28.03 Da	33.0	80.7	3	1277.84	-0.22	0.03	ANXA1_MOUSE	E9QA30_MOUSE	Annexin A1;	Annexin I; Annexin-1; Calpactin I; Calpactin-2; Chromobindin-9; Lipocortin I; Phospholipase A2 inhibitory protein; p35;	0.25 - 0.75
NGKLTGMAFR	VPTLNVSVDLTCR	N-ter +28.03 Da, C +57.02 Da	28.4	24.3	3	1599.90	0.12	0.01	D3Z1B7_MOUSE		Glyceraldehyde-3-phosphate dehydrogenase;		0.25 - 0.75
NGKLTGMAFR	VPTPNVSVDLTCR	N-ter +28.03 Da, C +57.02 Da	46.7	45.4	3	1583.91	2.71	0.30	G3PT_MOUSE	G3P_MOUSE	Glyceraldehyde-3-phosphate dehydrogenase, testis-specific;	Spermatogenic cell-specific glyceraldehyde 3-phosphate dehydrogenase 2; Spermatogenic glyceraldehyde-3-phosphate dehydrogenase; Acireductone dioxygenase (Fe(2+)-requiring); Membrane-type 1 matrix metalloproteinase cytoplasmic tail-binding protein 1;	0.85 - 1.00
M	VQAWYMDSTADPR	N-ter +28.03 Da	22.3	59.4	3	1695.86	0.25	0.04	MTND_MOUSE				0.25 - 0.75
SGKGTQCEKI	VQKYGYTHLSTGDLLR	N-ter +34.06 Da, K +34.06 Da	24.5	50.9	4	1918.19	-0.30	0.02	KAD1_MOUSE		Adenylate kinase isoenzyme 1;	ATP-AMP transphosphorylase 1; Myokinase;	0.25 - 0.75
LSGTAGVQSQ	VQLQQSGAELVK	N-ter +28.03 Da, K +28.03 Da	40.4	28.6	3	1483.87	0.04	0.01	HVM0_MOUSE		Ig heavy chain V region;	Anti-arsonate antibody;	0.25 - 0.75
FYADHPFIL	VRDNQSGSLIFIGR	N-ter +34.06 Da	51.5	46.2	3	1594.97	-0.92	0.16	SERPH_MOUSE		Serpin H1;	47 kDa heat shock protein; Collagen-binding protein; Serine protease inhibitor J6;	0.15 - 0.25
RSIIRNVKGP	VREGDVLTLLESER	N-ter +28.03 Da	41.3	58.3	3	1642.98	3.10	1.20	RS28_MOUSE		40S ribosomal protein S28;		0.85 - 1.00
KKQIQKLEXR	VRELEGEVENEQKR	N-ter +34.06 Da, K +34.06 Da	28.0	51.9	4	1782.08	-3.32	1.00	MYH1_MOUSE	MYH8_MOUSE	Myosin-1;	Myosin heavy chain 1; Myosin heavy chain 2x; Myosin heavy chain, skeletal muscle, adult 1;	0.00 - 0.15

Table S10, Tholen et al.

Non Prime Site	Prime Site	Modifications	Hyperscore	Mass error in ppm	Charge	Precursor neutral mass in Da	Fold change (log ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
KKIQKLEAR	VRELENEVEQKR	N-ter +34.06 Da, K +34.06 Da N-ter +34.06 Da, K +34.06 Da, C +57.02 Da	35.6	50.8	4	1839.11	-1.36	0.17	MYH4_MOUSE		Myosin-4;	Myosin heavy chain 2b;Myosin heavy chain 4;	0.15 - 0.25
GDEKCTELF	VREPPIMVTKLEEDMNAICGER		62.9	62.9	4	2703.55	-5.64	2.82	D3YU50_MOUSE	Q6P6L5_MOUSE		Apolipoprotein J;Clustrin;Sulfated glycoprotein 2;	0.00 - 0.15
DNGMVLGEQE GMKVLQTRGF	VSDNELQELSTQGSR VSDSSDSMDTGAGSIR	N-ter +28.03 Da N-ter +34.06 Da	45.6 29.9	49.2 46.6	3 3	1689.90 1617.81	-0.62 -0.67	0.09 0.10	CLUS_MOUSE ATIF1_MOUSE	E9Q988_MOUSE Q9D879_MOUSE	Clusterin; ATPase inhibitor, mitochondrial;	Inhibitor of F(1)F(o)-ATPase; RNA exonuclease 2 homolog;Small fragment nuclease;	0.25 - 0.75 0.25 - 0.75
GRRGQFGARG SSADROGRRG	VSEGAAMAAGESMAQR VSESQASDSEGHDFSEGOAVGAHR	N-ter +28.03 Da N-ter +28.03 Da	61.1 67.9	48.4 59.9	3 4	1679.84 2601.29	-0.71 3.27	0.12 1.40	ORN_MOUSE E9Q019_MOUSE	F7BVV1_MOUSE	Oligoribonuclease, mitochondrial;		0.25 - 0.75 0.85 - 1.00
LYASGRITGI	VSFELFADKVPKTAENFR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	23.3	62.6	4	2181.32	1.26	0.15	PPIA_MOUSE		Peptidyl-prolyl cis-trans isomerase A;	Cyclophilin A;Cyclosporin A-binding protein;Rotamase A;SP18;	0.75 - 0.85
IESTECKRTR VWAAVPGKTF GPLFLPKYTL SYGYDEKSAG EERHVGDGLN SASNLIPIF	VSGEHMDLTTCPAAGGQQEKLK VSITPAEVLVGVKDR VSTVSGMVFSEGAQR VSVPGPMGSPGR VTAGKDGVANVSDIR VTDVDDVQPIASLPGVAR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da N-ter +34.06 Da N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	59.4 31.9 36.8 39.6 19.1 30.8	57.5 49.2 50.1 27.6 43.0 41.1	4 3 3 2 3 3	2553.41 1695.08 1716.94 1270.73 1685.97 1976.14	2.68 -0.25 -0.43 -4.64 -1.56 -0.67	0.74 0.04 0.03 1.16 0.32 0.09	Q9D1B1_MOUSE PROF1_MOUSE RBP1_MOUSE CO1A1_MOUSE SODC_MOUSE HEM2_MOUSE	Q5X49_MOUSE A2AVJ7_MOUSE F8WGB7_MOUSE	Profilin-1; Ribosome-binding protein 1; Collagen alpha-1(I) chain; Superoxide dismutase [Cu-Zn]; Delta-aminolevulinic acid dehydratase;	Profilin I; Ribosome receptor protein; Alpha-1 type I collagen; 0.00 - 0.15 0.25 - 0.75	0.85 - 1.00 0.25 - 0.75 0.25 - 0.75 0.00 - 0.15 0.25 - 0.75
LVAAMQPRML	VTFDEELRPLVSVR	N-ter +28.03 Da	13.8	50.8	3	1784.07	0.83	0.13	PSMD2_MOUSE	Q80V77_MOUSE	26S proteasome non-ATPase regulatory subunit 2;	26S proteasome regulatory subunit RPN1;26S proteasome regulatory subunit p97;	0.25 - 0.75
LWKFETSKYY	VTIIDAPGHR	N-ter +34.06 Da	36.2	46.4	3	1111.71	-5.06	0.00	EF1A1_MOUSE	D3Z3I8_MOUSE	Elongation factor 1-alpha 1;	Elongation factor Tu;Eukaryotic elongation factor 1 A-1;	0.00 - 0.15
PNRVAQTKK	VTQLDLDPKELSR	N-ter +28.03 Da, K +28.03 Da	20.4	49.1	3	1625.98	1.06	0.08	HAP28_MOUSE		28 kDa heat- and acid-stable phosphoprotein;	PDGF-associated protein;PDGFA-associated protein 1;	0.75 - 0.85
YSPLAHRAYS SPLPVPKQ STSQVACTK M	VVAGGPEVLTPER VVANSPANADYQER VVAPITSSPVCQEQLEAGR VVEHPEFLKAGKEPLQIWR	N-ter +34.06 Da N-ter +34.06 Da N-ter +28.03 Da, C +57.02 Da N-ter +34.06 Da, K +34.06 Da	33.3 38.5 55.2 17.6	33.4 49.1 44.1 59.3	3 3 3 4	1457.88 1566.86 2167.23 2434.60	-1.94 -1.89 2.38 0.26	0.15 0.35 0.72 0.02	D2HDH_MOUSE E9PYJ9_MOUSE TLN1_MOUSE GELS_MOUSE	E9QN44_MOUSE F8WGT0_MOUSE A6PW55_MOUSE	D-2-hydroxyglutarate dehydrogenase, mitochondrial; Talin-1; Gelsolin;		0.00 - 0.15 0.00 - 0.15 0.85 - 1.00 0.25 - 0.75
LNKNRHPNLF RGENLVVME LIATEEGFKA	VVEKDTTINEIEDTR VVETLQEVTLR VVGDDYLFHHR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +28.03 Da	33.7 39.6 39.0	46.3 40.0 66.8	3 3 4	1964.10 1442.86 1650.90	1.51 -0.25 0.42	0.19 0.02 0.15	VATF_MOUSE GSDMA_MOUSE LEG7_MOUSE	Q9CR81_MOUSE	V-type proton ATPase subunit F; Gasdermin-A; Galectin-7;		0.75 - 0.85 0.25 - 0.75 0.25 - 0.75
TRAERREVER GESLQALFJA	VVDALSLKGDLAGR VVVPDESPLSWAQR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da	24.6 39.8	40.0 54.7	3 3	1625.02 1865.14	-0.17 2.24	0.02 0.21	KCRU_MOUSE ACSL1_MOUSE	A2ARP5_MOUSE D3Z041_MOUSE	Creatine kinase U-type, mitochondrial; Long-chain-fatty-acid--CoA ligase 1;	Acidic-type mitochondrial creatine kinase;Ubiquitous mitochondrial creatine kinase;	0.25 - 0.75 0.85 - 1.00
FSLGLSLLL GSVAGGAYVL	VVSVIGSQNSQLR VVDQELLGPKDSEALR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	32.1 30.1	35.7 43.7	3 3	1512.92 2046.15	1.78 1.16	0.18 0.32	MMGL_MOUSE QIL1_MOUSE	F8WHB7_MOUSE	Macrophage asialoglycoprotein-binding protein 1; Protein QIL1;	MMGL;Macrophage galactose/N-acetylgalactosamine-specific lectin;	0.85 - 1.00 0.75 - 0.85
DAEKSAVSL LLPQWPAASA GEDKSNKAA	WAKVNPDEVGGEALGR WELTLHTNDVHSR WKGIGGHGAEGAEALER	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da N-ter +34.06 Da, K +34.06 Da	46.6 30.2 36.6	55.5 65.9 53.3	3 3 4	1753.01 1748.02 1968.15	-2.32 -0.42 -0.43	0.46 0.08 0.04	HBB2_MOUSE SNTB_MOUSE HBA_MOUSE	Q91V88_MOUSE	Hemoglobin subunit beta-2; 5'-nucleotidase; Hemoglobin subunit alpha;	Beta-2-globin;Hemoglobin beta-2 chain;Hemoglobin beta-minor chain; Ecto-5'-nucleotidase; Alpha-globin;Hemoglobin alpha chain;	0.00 - 0.15 0.25 - 0.75 0.25 - 0.75
DAEKAASVCL LASLSTFQQM LASLSTFQQM LASLSTFQQM TYRIWRDTAN	WGKVNSEVVGGEALGR WISKQYDEAGPSIVHR WISKQYDESGPSIVHR WITKQYDEAGPSIVHR WLEINPETGAIFTR	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, K +34.06 Da N-ter +28.03 Da	35.9 24.9 31.9 35.5 41.2	49.4 65.9 52.7 56.3 49.4	3 4 4 4 3	1728.97 2070.19 2098.22 2096.25 1673.96	1.38 -1.43 0.20 -1.25 -0.40	0.35 0.23 0.05 0.18 0.07	HBB1_MOUSE ACTA_MOUSE ACTB_MOUSE ACTS_MOUSE CAOH1_MOUSE	ACTC_MOUSE ACTG_MOUSE	Hemoglobin subunit beta-1; Actin, aortic smooth muscle; Actin, cytoplasmic 1; Actin, alpha skeletal muscle; Cadherin-1;	Beta-1-globin;Hemoglobin beta-1 chain;Hemoglobin beta-major chain; Alpha-actin-2; Beta-actin; Alpha-actin-1; ARC-1;Epithelial cadherin;Uvomorulin;	0.75 - 0.85 0.15 - 0.25 0.25 - 0.75 0.15 - 0.25 0.25 - 0.75
VRCAAQRDGT	WLHSDKFTLKVR	N-ter +28.03 Da, K +28.03 Da	23.9	40.6	4	1613.01	-0.76	0.05	KIT_MOUSE	Q8C8K9_MOUSE	Mast/stem cell growth factor receptor Kit; Glycerol-3-phosphate dehydrogenase [NAD+], cytoplasmic;	Proto-oncogene c-Kit;Tyrosine-protein kinase Kit;	0.25 - 0.75
LAHFDPRVTM FQQMWISKQE NSPLVSRILT LREDPAYLHY VNIIGGAGSYI AASSSLEKS	VWFEEIDGGR YDESGPSIVHR YDIAHTPGVAADLSHIETR YDPAGGEDPLGAVHLR YEKPTQEAQVPTGPIEVPVVR YELPDGQVITIGNER	N-ter +28.03 Da N-ter +28.03 Da N-ter +28.03 Da N-ter +34.06 Da N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	32.1 34.8 40.0 73.0 52.6 49.0	59.9 50.7 60.9 56.2 54.0 47.7	2 3 3 4 3 3	1234.67 1286.69 2093.18 1699.97 2392.43 1730.97	-0.71 0.28 -1.60 0.52 1.44 0.51	0.08 0.05 0.34 0.11 0.50 0.10	GPDA_MOUSE ACTB_MOUSE MDHM_MOUSE PLEK_MOUSE CRIP2_MOUSE ACTB_MOUSE	E0CXN5_MOUSE ACTG_MOUSE ACTG_MOUSE Q8CAG6_MOUSE ACTA_MOUSE	cytoplasmic; Actin, cytoplasmic 1; Malate dehydrogenase, mitochondrial; Plectstrin; Cysteine-rich protein 2; Actin, cytoplasmic 1;	Beta-actin; 0.25 - 0.75 0.00 - 0.15 0.25 - 0.75 0.75 - 0.85 0.25 - 0.75	
DWLKNVLVTL PPLNPLSAN	YERDEGNLLTEKQKLR YERPVHLVALNTPVAGDIR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da	33.9 40.4	58.7 63.5	4 4	2189.31 2260.41	-0.52 1.93	0.12 0.20	SPRC_MOUSE COFA1_MOUSE	Q5NCU4_MOUSE A2AJY7_MOUSE	SPARC; Collagen alpha-1(XV) chain;		0.25 - 0.75 0.85 - 1.00
LGLAAADPAI	YFKEQFLDGDWNTNR	N-ter +28.03 Da, K +28.03 Da	47.4	58.8	3	1945.05	4.00	1.82	CALR_MOUSE		Calreticulin;	CRP55;Calregulin;Endoplasmic reticulum resident protein 60;HACBP;	0.85 - 1.00
GKFLVSSGKF PQQQQMTSS	YGDLEKDKLQTSQDAR YGYKPEAAPVSIQR	N-ter +28.03 Da, K +28.03 Da N-ter +28.03 Da, K +28.03 Da	31.2 22.5	57.6 44.5	4 3	2007.14 1690.98	3.28 0.58	0.95 0.12	CALR_MOUSE LASP1_MOUSE	A2A6H0_MOUSE	Calreticulin; LIM and SH3 domain protein 1;	CRP55;Calregulin;Endoplasmic reticulum resident protein 60;HACBP; Metastatic lymph node gene 50 protein;	0.85 - 1.00 0.25 - 0.75
KLTLTELDF LADQNKORY	YGIDNLLHYNR YGINDPVADKLLKR	N-ter +28.03 Da N-ter +28.03 Da, K +28.03 Da	38.3 26.9	53.3 61.2	3 4	1519.82 1685.09	-0.71 -0.14	0.14 0.02	SFR1_MOUSE RBM22_MOUSE		Swi5-dependent recombination DNA repair protein 1 homolog; Pre-mRNA-splicing factor RBM22;	Meiosis lymph 5 homolog; RNA-binding motif protein 22;	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 ₂) of ASAPRatio	FC-error of ASAPRatio	Uniprot ID 1	Uniprot ID 2	Protein Name 1	Protein Name 2	Quantile
LGGNFASQMS	YGYDEKSAAGVSVPGPMGPGSGPR	N-ter +34.06 Da, K +34.06 Da	50.2	42.8	3	2275.26	-3.32	1.00	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	38.1	49.4	3	1528.89	1.64	0.36	KAD1_MOUSE		Adenylyate kinase isoenzyme 1;	ATP-AMP transphosphorylase 1;Myokinase;	0.75 - 0.85
KAIMTVSSVF	YHAFSGAQAETAANR	N-ter +28.03 Da, K +28.03 Da	51.1	56.5	4	1776.99	1.66	0.42	ACTN1_MOUSE	ACTN4_MOUSE	Alpha-actinin-1;	Alpha-actinin cytoskeletal isoform;F-actin cross-linking protein;Non-muscle alpha-actinin-1;	0.85 - 1.00
DIDRVPFNS	YIDGVTMEEATVSGILGKR	N-ter +28.03 Da, K +28.03 Da	44.1	47.7	3	2094.20	0.33	0.09	ZCCHV_MOUSE	D3ZS1_MOUSE	Zinc finger CCCH-type antiviral protein 1;		0.25 - 0.75
TPDKPSPNMF	YIDPEKGDIVTVSPALLDR	N-ter +28.03 Da, K +28.03 Da	37.7	54.2	3	2255.36	1.53	0.63	CAD13_MOUSE		Cadherin-13;	Heart cadherin;Truncated cadherin;	0.75 - 0.85
HGSNGRSKTD	YKGLEEEGEGNKQLNR	N-ter +28.03 Da, K +28.03 Da	27.0	59.3	4	2076.17	1.23	0.22	E9Q019_MOUSE				0.75 - 0.85
QEINRVKEM	YKTDLKDIISDTSDFDR	N-ter +28.03 Da, K +28.03 Da	45.7	60.5	4	2186.24	0.43	0.05	ANXA2_MOUSE	BOV2N7_MOUSE	Annexin A2;	Annexin II;Annexin-2;Calpactin I heavy chain;Calpactin-1 heavy chain;Chromobindin-8;Lipoprotein II;Placental anticoagulant protein IV;Protein I;p36;	0.25 - 0.75
AGLPTSLTL	YLDNKNKISINPDEYFKR	N-ter +34.06 Da, K +34.06 Da	35.5	62.7	4	2230.39	-2.40	0.88	LUM_MOUSE		Lumican;	Keratan sulfate proteoglycan lumican;	0.00 - 0.15
KYQLVAGIKY	YLTLDIESTECR	N-ter +28.03 Da, C +57.02 Da	29.1	51.6	3	1526.81	-0.56	0.05	Q901B1_MOUSE				0.25 - 0.75
LGKLPALFL	YMEKNQLEEVPSALPR	N-ter +34.06 Da, K +34.06 Da	45.4	45.7	3	1971.17	2.07	0.27	PRELP_MOUSE		Prolargin;	Proline-arginine-rich end leucine-rich repeat protein;	0.85 - 1.00
ETIKKRELY	YNATEPVISFYDKR	N-ter +34.06 Da, K +34.06 Da	41.0	38.8	3	1770.03	-0.86	0.19	KAD1_MOUSE		Adenylyate kinase isoenzyme 1;	ATP-AMP transphosphorylase 1;Myokinase;	0.15 - 0.25
VGASDGYLYM	YNLDPQEGEGCALMR	N-ter +28.03 Da, C +57.02 Da	36.5	73.3	3	1779.92	-0.03	0.01	WIPI2_MOUSE	D3YWK1_MOUSE	WD repeat domain phosphoinositide-interacting protein 2;		0.25 - 0.75
STSSPVFHPK	YQACSGPLPHR	N-ter +28.03 Da, C +57.02 Da	35.2	50.2	3	1425.79	0.48	0.04	Q99M20_MOUSE				0.25 - 0.75
GRKSGKGYI	YQEGSKNKSLENSEMDNILANLR	N-ter +28.03 Da, K +28.03 Da	26.8	77.6	4	2607.54	1.94	0.32	ECHA_MOUSE		Trifunctional enzyme subunit alpha, mitochondrial;	TP-alpha;	0.85 - 1.00
DKAKELWDTL	YQLETDKFEFGEKLR	N-ter +34.06 Da, K +34.06 Da	23.0	63.1	4	2166.44	-2.94	0.45	TNNT3_MOUSE	A2A6J0_MOUSE	Troponin T, fast skeletal muscle;	Troponin T;	0.00 - 0.15
RLMEIYQEL	YRPPVLDALGR	N-ter +28.03 Da	36.0	51.8	3	1380.86	1.03	0.13	E9Q005_MOUSE	E9PVA8_MOUSE			0.75 - 0.85
PGLTGNFAAQ	YSDKGVSSGPGMGLMGR	N-ter +28.03 Da, K +28.03 Da	69.9	43.5	3	1948.04	-2.40	0.50	CO1A2_MOUSE	E0CXI2_MOUSE	Collagen alpha-2(I) chain;	Alpha-2 type I collagen;	0.00 - 0.15
VQVEEYIDL	YSEEPGEEPAWVQTER	N-ter +28.03 Da	51.0	49.1	3	2063.01	0.32	0.05	RCN3_MOUSE	D3ZT1_MOUSE	Reticulocalbin-3;		0.25 - 0.75
SPRRSQVHPE	YSEGEAHSEVSQR	N-ter +28.03 Da	18.8	46.9	3	1505.75	-0.14	0.05	FILA2_MOUSE	E9QPZ3_MOUSE	Filaggrin-2;	Intermediate filament-associated protein;	0.25 - 0.75
AAMKANTMSN	YSLLPASLLDHR	N-ter +28.03 Da	55.8	50.5	3	1411.85	2.80	0.79	STZB1_MOUSE	E9QK1_MOUSE	Sulfotransferase family cytosolic 2B member 1;	Alcohol sulfotransferase;Hydroxysteroid sulfotransferase 2;	0.85 - 1.00
FIHHLLAYL	YSSADQSSLMEEAEQAQR	N-ter +28.03 Da	61.6	54.2	3	2144.05	1.38	0.34	DYN2_MOUSE	Q91Z39_MOUSE	Dynamin-2;	Dynamin UDNM;	0.75 - 0.85
CTFFLAVSGL	YSSDDVIELTPSNFNR	N-ter +28.03 Da	50.2	48.6	3	1971.02	1.43	0.21	PDIAG_MOUSE	Q3TML0_MOUSE	Protein disulfide-isomerase A6;	Thioredoxin domain-containing protein 7;	0.75 - 0.85
SYMKIDELSL	YSVPEGQSKYVEEPR	N-ter +28.03 Da, K +28.03 Da	24.7	41.7	3	1822.99	-0.01	0.00	APOO_MOUSE	B1ASQ2_MOUSE	Apolipoprotein O;	Protein FAM121B;	0.25 - 0.75
YGFQNALVR	YTQKAPQVSTPTLVEAAR	N-ter +28.03 Da, K +28.03 Da	66.2	43.0	3	2015.19	3.52	0.54	ALBU_MOUSE		Serum albumin;		0.85 - 1.00
QKIGQPTLL	YVDAGAETMTQR	N-ter +34.06 Da	42.4	52.3	3	1374.74	1.56	0.40	KAD1_MOUSE		Adenylyate kinase isoenzyme 1;	ATP-AMP transphosphorylase 1;Myokinase;	0.75 - 0.85
MYAKRAFVHW	YVGEEMEEGFSEAR	N-ter +28.03 Da	44.6	50.2	3	1716.82	5.27	1.31	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
LGGADSGAA	YVLEQASSHIGNSTQAAVR	N-ter +28.03 Da	48.8	39.8	3	2058.13	1.36	0.27	ATLA3_MOUSE	E9PYT3_MOUSE	Atlastin-3;		0.75 - 0.85
HPFMWNEHLG	YVLTCPNSLGTGLR	N-ter +34.06 Da, C +57.02 Da	31.0	43.6	3	1583.92	-2.56	0.15	KCRM_MOUSE		Creatine kinase M-type;	Creatine kinase M chain;M-CK;	0.00 - 0.15
AFRPMEVANF	YYEPDCLAYGAKAAR	N-ter +28.03 Da, K +28.03 Da, C +57.02 Da	39.9	59.1	3	1802.97	-0.64	0.09	CEBPB_MOUSE		CCAAT/enhancer-binding protein beta;	AGP/EBP;Interleukin-6-dependent-binding protein;Liver-enriched transcriptional activator;	0.25 - 0.75
LQKRPKPDEK	YYSSIIWGPTCDGLDR	N-ter +34.06 Da, C +57.02 Da	25.7	101.6	4	1910.07	-6.64	0.00	DCOR_MOUSE	Q8CIC5_MOUSE	Ornithine decarboxylase;		0.00 - 0.15