Supplementary Table 12: Quantitative comparison of down-regulated N-termini from FFPE liver tissues of C57BL/6 wild type mice and C57BL/6 cathepsin L C*ctsl*$^{-/-}$) knock out mice. Identified prime-site sequences, protein names, average fold change values (log$_2$ ratio of ctsl-/- versus wild type; Fc < -0.58) and *p*-values (moderated t-test using linear models for microarray data [42, 43] with Benjamini-Hochberg procedure 5% FDR, n=3) are shown.

Non-prime Sequence	Prime Sequence	UniProt ID	Protein Name	Position	Length	Average Fc	*p*-value
KDLMPHDLAR	AALSGLLHR	Q99JY0	Trifunctional enzyme subunit beta, mitochondrial;	83	475	-10.00	6.52E-06
DLYTAKGLFR	AAVPSGASTGIYEALELR	P17182	Alpha-enolase;	33	434	-10.00	6.52E-06
QFMVQNGLSR	AEAEAQAEELSFPR	Q05920	Pyruvate carboxylase, mitochondrial;	929	1178	-10.00	6.52E-06
GTIGDLRVAR	AEFGFDLSHIPR	Q9DBB8	Trans-1,2-dihydrobenzene-1,2-diol dehydrogenase;	152	333	-10.00	6.52E-06
RKADIDLTKR	AGELTEDEVER	P62270	40S ribosomal protein S18;	56	152	-10.00	6.52E-06
CCGFEPYHIR	AIAEELAPER	O35490	Betaine--homocysteine S-methyltransferase 1;	309	407	-10.00	6.52E-06
VDRRSNQVAR	ALHDQLGLR	O35488	Very long-chain acyl-CoA synthetase;	94	620	-10.00	6.52E-06
CDVDIRKDLY	ANTVLSGGTTMYPGIADR	P60710	Actin, cytoplasmic 1;	295	375	-10.00	6.52E-06
LAQYREVAAF	AQFGSDLDAATQQLLSR	Q03265	ATP synthase subunit alpha, mitochondrial;	447	553	-10.00	6.52E-06
AEIEALKGQR	ASLEAAIADAEQR	P11679	Keratin, type II cytoskeletal 8;	335	490	-7.49	6.52E-06
FLSGGQSEEE	ASLNLNAINR	P05063	Fructose-bisphosphate aldolase C;	280	363	-10.00	6.52E-06
LGQAAWKEAR	ASLQNLLSASQAR	P35505	Fumarylacetoacetase;	83	419	-10.00	6.52E-06
VHPGGGSTSR	ASSFVLALEPELESR	Q91YQ5	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 1;	67	608	-10.00	6.52E-06
FASCFYGPFR	DAAQSSPAFGDR	P10518	Delta-aminolevulinic acid dehydratase;	210	330	-10.00	6.52E-06
SWGNHTPIFR	DAGMQLQGYR	P05202	Aspartate aminotransferase, mitochondrial;	171	430	-10.00	6.52E-06
HVEDAGVHSG	DATLMLPTQTISQGAIEKVKDATR	Q8C196	Carbamoyl-phosphate synthase (ammonia), mitochondrial;	1205	1500	-0.62	6.52E-06
LKVFLENVIR	DAVTYTEH	P62806	Histone H4;	69	103	-10.00	6.52E-06
EDDEEEDDED	DDEEEEEEEPVKAAPGKR	P09405	Nucleolin;	265	707	-10.00	6.52E-06
VLSLSFPIRR	DDGSWEVIEGYR	P26443	Glutamate dehydrogenase 1, mitochondrial;	125	558	-10.00	6.52E-06
YMLLKFAKLR	DEFDIVGDVR	Q3UEG6	Alanine--glyoxylate aminotransferase 2, mitochondrial;	422	513	-10.00	6.52E-06
IGANGLANPR	DFLIPVAWYEDR	O09173	Homogentisate 1,2-dioxygenase;	226	445	-10.00	6.52E-06
PPPLPRLKRR	DFTPAELR	O55022	Membrane-associated progesterone receptor component 1;	72	195	-10.00	6.52E-06
KIKAPVVLSR	DHHDVSGTDSPFR	Q8VC12	Urocanate hydratase;	544	676	-10.00	6.52E-06
REFQTSVISR	DIDTAAKF	P56384	ATP synthase F(0) complex subunit C1, mitochondrial;	67	136	-10.00	0.000295

Non-prime Sequence	Prime Sequence	UniProt ID	Protein Name	Position	Length	Average Fc	*p*-value
REFQTSVISR	DIDTAAKFIGAGAA	P56384	ATP synthase F(0) complex subunit C1, mitochondrial;	67	136	-10.00	6.52E-06
VVACGLRHID	DKVFLTTAEVISQQVSDKHLQEGR	P06801	NADP-dependent malic enzyme;	475	572	-10.00	6.52E-06
KSGENFKLLY	DLADQLHAAVGASR	Q99LC5	Electron transfer flavoprotein subunit alpha, mitochondrial;	236	333	-10.00	6.52E-06
TPDCGKQGFI	DLPEFPFGLEPR	O35490	Betaine--homocysteine S-methyltransferase 1;	263	407	-10.00	6.52E-06
LTAVHDAILE	DLVFPSEIVGKR	P62082	40S ribosomal protein S7;	132	194	-10.00	6.52E-06
DFGSNLKPAR	DMGMVTILVHNTASALR	P34914	Bifunctional epoxide hydrolase 2;	195	554	-10.00	6.52E-06
ISVEMVIVED	DSAFTVLKKAGR	Q8VC30	Bifunctional ATP-dependent dihydroxyacetone kinase/FAD-AMP lyase (cyclizing);	140	578	-10.00	6.52E-06
MSSKVSR	DTLYEAVR	P53026	60S ribosomal protein L10a;	8	217	-10.00	6.52E-06
VYCKWRYQRR	DVDFEAIWGAVR	P25688	Uricase;	203	303	-10.00	6.52E-06
CFSVNELITY	EALGLCPEGQGGTLVDR	P32020	Non-specific lipid-transfer protein;	317	547	-10.00	6.52E-06
DTDDTATALR	EAQEEVGLHPH	Q99P30	Peroxisomal coenzyme A diphosphatase NUDT7;	92	236	-10.00	6.52E-06
SLLLRRPPGR	EAYPGDVFYLH	Q03265	ATP synthase subunit alpha, mitochondrial;	335	553	-10.00	6.52E-06
SLLLRRPPGR	EAYPGDVFYLHSR	Q03265	ATP synthase subunit alpha, mitochondrial;	335	553	-10.00	6.52E-06
IIRNVKGPVR	EGDVLTLLESER	P62858	40S ribosomal protein S28;	52	69	-10.00	6.52E-06
LEGDKVKVER	EIDGGLETLR	Q9DCW4	Electron transfer flavoprotein subunit beta;	165	255	-10.00	6.52E-06
GSPENTRRRR	EIENLILNDPDFQHEDYNFLTR	Q9R0H0	Peroxisomal acyl-coenzyme A oxidase 1;	35	661	-10.00	6.52E-06
QLCEEHGILR	ENIIDLSNANR	B5X0G2	Major urinary protein 17;	164	180	-10.00	6.52E-06
EHPGGEEVLR	EQAGGDATENFEDVGH	P56395	Cytochrome b5;	53	134	-10.00	6.52E-06
EHPGGEEVLR	EQAGGDATENFEDVGHSTDAR	P56395	Cytochrome b5;	53	134	-10.00	6.52E-06
PQGSRPALGR	ESVQVPDDQDFR	Q9JMD3	PCTP-like protein;	20	291	-10.00	6.52E-06
FLANGIQRRS	FHQDQSSVGGLTAEDIEKAR	Q60936	Atypical kinase ADCK3, mitochondrial {ECO:0000305};	160	645	-10.00	6.52E-06
IHGRVYDITR	FLSEHPGGEEVLLEQAGADATESFEDVGHSPDAR	Q9CQX2	Cytochrome b5 type B;	51	146	-10.00	6.52E-06
TVSRARKIQR	FLSQPFQVAEVFTGH	P56480	ATP synthase subunit beta, mitochondrial;	463	529	-10.00	6.52E-06
PFETLLAQNR	GGQSFIVGDQISFADYR	F6RWR5	Protein BC021614 {ECO:0000313|Ensembl:ENSMUSP00000075779};	139	210	-10.00	6.52E-06
PDTGISSKAM	GIMNSFVNDIFER	P10853	Histone H2B type 1-F/J/L;	61	126	-10.00	6.52E-06
TKYPQLLSGIR	GISEETTTGVHNLY	P50247	Adenosylhomocysteinase;	152	432	-10.00	6.52E-06
RALQSIEKER	GLGTEVPGNFQGPDPYR	Q91XE8	Transmembrane protein 205;	125	189	-10.00	6.52E-06
DILNMDKTLK	GLNSDSVTEETLR	Q8C196	Carbamoyl-phosphate synthase (ammonia), mitochondrial;	893	1500	-0.93	6.52E-06

Non-prime Sequence	Prime Sequence	UniProt ID	Protein Name	Position	Length	Average Fc	*p*-value
AAVAAAREER	GLSPIWAINSPATAEVIR	G3X982	Aldehyde oxidase 3;	1291	1335	-10.00	6.52E-06
AMDGTEGLVR	GQKVLDSGAPIKIPVGPETLGR	P56480	ATP synthase subunit beta, mitochondrial;	122	529	-10.00	6.52E-06
NWDDMEKIWH	HTFYNELR	P60710	Actin, cytoplasmic 1;	88	375	-0.77	6.52E-06
FMAILCRGID	HTVVYWLGRR	Q3V0D6	Protein 4930544L04Rik {ECO:0000313|Ensembl:ENSMUSP00000095596};	26	104	-10.00	6.52E-06
ADIALVELLY	HVEELDPGVVDNFPLLKALR	P30115	Glutathione S-transferase A3;	166	221	-10.00	6.52E-06
KAQQALVQKR	HYLFDVQR	Q9CQQ7	ATP synthase F(0) complex subunit B1, mitochondrial;	164	256	-1.37	6.52E-06
DFGKWRAVLR	IADQCPSSLAIQENANALAR	Q91Y97	Fructose-bisphosphate aldolase B;	154	364	-10.00	6.52E-06
QPGAGAIMAR	IAQFLSGIPETVPLSTVNR	Q8VCH0	3-ketoacyl-CoA thiolase B, peroxisomal;	103	424	-10.00	6.52E-06
WVGCHPNGMR	IFFYDAENPPGSEVLR	P52430	Serum paraoxonase/arylesterase 1;	291	355	-10.00	6.52E-06
AEGFKGKILF	IFIDSDHTDNQR	P09103	Protein disulfide-isomerase;	291	509	-10.00	6.52E-06
KKLTDVGIRR	IFSSEHDIFR	P51174	Long-chain specific acyl-CoA dehydrogenase, mitochondrial;	52	430	-10.00	6.52E-06
RSVVEFLQGY	IGIPHGGFPEPFR	Q05920	Pyruvate carboxylase, mitochondrial;	952	1178	-10.00	6.52E-06
FTMELAKKGF	IGPGIDVPAPDMSTGER	P26443	Glutamate dehydrogenase 1, mitochondrial;	215	558	-10.00	6.52E-06
GSECCTRKTR	IIDVVYNASNNELVR	P62242	40S ribosomal protein S8;	78	208	-10.00	6.52E-06
MGCKAAGASR	IIGIDINKDKF	Q64437	Alcohol dehydrogenase class 4 mu/sigma chain;	220	374	-0.91	6.52E-06
REDSATLYER	IMSAGQEEGIGDFGTYALNALR	Q9DBT9	Dimethylglycine dehydrogenase, mitochondrial;	691	869	-10.00	6.52E-06
SILEADCDIL	IPAASEKQLTKSNAPR	P26443	Glutamate dehydrogenase 1, mitochondrial;	380	558	-10.00	6.52E-06
GSEVSALLGR	IPSAVGYQPTLATDMGTMQER	P56480	ATP synthase subunit beta, mitochondrial;	325	529	-10.00	6.52E-06
SRDEKVQLYR	IQFNESFAEMNR	P19783	Cytochrome c oxidase subunit 4 isoform 1, mitochondrial;	84	169	-10.00	6.52E-06
PAERYYRDAR	ITEIYEGTSEIQR	Q07417	Short-chain specific acyl-CoA dehydrogenase, mitochondrial;	387	412	-10.00	6.52E-06
EIIANDQGNR	ITPSYVAFTPEGER	P20029	78 kDa glucose-regulated protein;	62	655	-10.00	6.52E-06
RDVKMKKKGN	IYSLNEGYAKDFDPAINEYLQR	Q9QXD6	Fructose-1,6-bisphosphatase 1;	209	338	-0.82	6.52E-06
FRPVASQLPR	IYTSIGEDYDER	P67778	Prohibitin;	106	272	-10.00	6.52E-06
NIGVTAVAFN	KELDPVQKLFVDKIR	P97450	ATP synthase-coupling factor 6, mitochondrial;	34	108	-10.00	6.52E-06
GIKLDQGGAP	LAGTNKETTIQGLDGLSER	Q91Y97	Fructose-bisphosphate aldolase B;	116	364	-0.96	6.52E-06
HYDSIKLYER	LEEETGQVVGFHQPGSIR	Q9DBT9	Dimethylglycine dehydrogenase, mitochondrial;	112	869	-10.00	6.52E-06
YMNKVELESR	LEGLTDEINFLR	P11679	Keratin, type II cytoskeletal 8;	220	490	-10.00	6.52E-06
PSPDKMLQGR	LFAYPDTHR	P24270	Catalase;	355	527	-10.00	6.52E-06

Non-prime Sequence	Prime Sequence	UniProt ID	Protein Name	Position	Length	Average Fc	*p*-value
EVGALAKVLR	LFEENEINLTHIESR	P16331	Phenylalanine-4-hydroxylase;	54	453	-10.00	6.52E-06
MAGVGAAFRR	LGALSGAGALGLASYGAH	Q5F285	Transmembrane protein 256;	11	113	-10.00	6.52E-06
FDHLDSTMRR	LIPPFHAASAQLTSLVDADAR	Q91XD4	Formimidoyltransferase-cyclodeaminase;	394	541	-10.00	6.52E-06
LSKPLSVPTR	LLLGPGPSNLAPR	O35423	Serine--pyruvate aminotransferase, mitochondrial;	46	414	-10.00	6.52E-06
RTGVKLKKGR	LQFWTETLPR	Q63880	Carboxylesterase 3A;	544	571	-10.00	6.52E-06
AYNNRAQARR	LQGDVAGALEDLER	Q8VBW8	Tetratricopeptide repeat protein 36;	94	186	-10.00	6.52E-06
SYQCLVVSRS	LSSVEYEPKEKTFDKILIANR	Q91ZA3	Propionyl-CoA carboxylase alpha chain, mitochondrial;	47	724	-10.00	6.52E-06
LLKNSPLVSR	LTLYDIAHTPGVAADLSHIETR	P08249	Malate dehydrogenase, mitochondrial;	53	338	-10.00	6.52E-06
ALTITASVQA	LTPTHYLTKQDVER	Q9DBG6	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2;	23	631	-5.14	6.52E-06
ALEVQGRDSR	LVLEVAQHLGESTVR	P56480	ATP synthase subunit beta, mitochondrial;	95	529	-10.00	6.52E-06
ELIFPPELMR	MAEESQNTVLTFR	G3X982	Aldehyde oxidase 3;	225	1335	-10.00	6.52E-06
FEESFQKALR	MCHPSVDGFTPR	Q8C196	Carbamoyl-phosphate synthase (ammonia), mitochondrial;	815	1500	-10.00	6.52E-06
IPKEEVKEVY	MGNVIQGGEGQAPTR	Q8QZT1	Acetyl-CoA acetyltransferase, mitochondrial;	88	424	-10.00	6.52E-06
GGFLGQRIVR	MLVQEEELQEIR	Q61694	3 beta-hydroxysteroid dehydrogenase type 5;	22	373	-10.00	6.52E-06
	MRGQVGDLSPQQQEALAR	Q8R0F9	SEC14-like protein 4;	1	403	-0.63	6.52E-06
LQDCMSKMQR	MVQESSSGGLLDR	Q571F8	Glutaminase liver isoform, mitochondrial;	118	602	-10.00	6.52E-06
NEAIYDICRR	NLDIERPTYTNLNR	P05213	Tubulin alpha-1B chain;	216	451	-10.00	6.52E-06
SITSVQAIYV	PADDLTDPAPATTFAHLDATTVLSR	P56480	ATP synthase subunit beta, mitochondrial;	363	529	-10.00	6.52E-06
M	PAHMLQEISSSYTTTTTITAPPSGNER	P13516	Acyl-CoA desaturase 1;	2	355	-10.00	6.52E-06
ETELFYKGIR	PAINVGLSVSR	Q03265	ATP synthase subunit alpha, mitochondrial;	406	553	-10.00	6.52E-06
RCIPALDSLK	PANEDQKIGIEIIKR	P63038	60 kDa heat shock protein, mitochondrial;	456	573	-10.00	6.52E-06
TPRLPMNKEW	PANLDLKKELSEPSSTR	Q8C196	Carbamoyl-phosphate synthase (ammonia), mitochondrial;	834	1500	-10.00	6.52E-06
VGILALEVYF	PAQYVDQTDLEKFNNVEAGKYTVGLGQTR	P54869	Hydroxymethylglutaryl-CoA synthase, mitochondrial;	64	508	-10.00	6.52E-06
KVNVTVDYIR	PASPATETVPAFSER	Q78PY7	Staphylococcal nuclease domain-containing protein 1;	424	910	-10.00	6.52E-06
KRCPSQSSSR	PATGISQPPTTPTGQATR	Q6ZQ58	La-related protein 1;	1038	1072	-10.00	6.52E-06
GYDKVKLQSR	PAVPPAPGPGQLTLR	Q62465	Synaptic vesicle membrane protein VAT-1 homolog;	81	406	-10.00	6.52E-06
LGMMTSVLIC	PDGKTVEAEAAHGTVTR	O88844	Isocitrate dehydrogenase (NADP) cytoplasmic;	298	414	-10.00	6.52E-06
FQLMGLYGRE	PDLSSDIKER	B5X0G2	Major urinary protein 17;	142	180	-10.00	6.52E-06
GLKGMSLNLE	PDNVGVVVFGNDKLIKEGDVVKR	Q03265	ATP synthase subunit alpha, mitochondrial;	111	553	-10.00	6.52E-06

Non-prime Sequence	Prime Sequence	UniProt ID	Protein Name	Position	Length	Average Fc	*p*-value
SWWTHVEMGP	PDPILGVTEAFKR	P05202	Aspartate aminotransferase, mitochondrial;	41	430	-10.00	6.52E-06
SEQYRTGKPN	PDQLLKELPFPLNTR	Q78JT3	3-hydroxyanthranilate 3,4-dioxygenase {ECO:0000255|HAMAP-Rule:MF_03019};	161	286	-10.00	6.52E-06
KRLDSRRRMS	PEEFTEIMNQR	P54869	Hydroxymethylglutaryl-CoA synthase, mitochondrial;	457	508	-10.00	6.52E-06
WTFLHCLPRK	PEEVDDEVFYSPR	P11725	Ornithine carbamoyltransferase, mitochondrial;	308	354	-10.00	6.52E-06
M	PEFLEDPSVLTKDKLKSELVANNVTLPAGEQR	Q61029	Lamina-associated polypeptide 2, isoforms beta/delta/epsilon/gamma;	2	452	-10.00	6.52E-06
RHGNPWEKAR	PEFMLPVHFYGR	Q9ET01	Glycogen phosphorylase, liver form;	195	850	-10.00	6.52E-06
DSLTEISGLI	PEVLNMFPILLR	P24456	Cytochrome P450 2D10;	224	504	-10.00	6.52E-06
EQPVAVFLGV	PFAKPPLGSLR	P23953	Carboxylesterase 1C;	54	554	-10.00	6.52E-06
M	PFVELETNLPASRIPAGLENR	O35215	D-dopachrome decarboxylase;	2	118	-10.00	6.52E-06
VNHDEKQWKD	PFVFRPER	P00186	Cytochrome P450 1A2;	422	513	-0.95	6.52E-06
FPRMASGSWR	PFVTVAPLGSPLR	Q8CC88	von Willebrand factor A domain-containing protein 8;	1166	1905	-10.00	6.52E-06
EKINYTGRFL	PGFEAPTYKDTLLPKLPR	P49429	4-hydroxyphenylpyruvate dioxygenase;	158	393	-10.00	6.52E-06
LVCGGNQVPR	PGFFFQPTVFTDVEDH	Q8R0Y6	Cytosolic 10-formyltetrahydrofolate dehydrogenase;	772	902	-10.00	6.52E-06
QASWVTHGVP	PGFGKELFESDLDR	Q9DBT9	Dimethylglycine dehydrogenase, mitochondrial;	324	869	-10.00	6.52E-06
ATEGPCKLSR	PGFWDPIGR	Q5XG73	Acyl-CoA-binding domain-containing protein 5;	91	508	-10.00	6.52E-06
QMAFDPSNMP	PGIEPSPDKMLQGR	P24270	Catalase;	341	527	-10.00	6.52E-06
AVSSPPTSPR	PGSAATISSSASNIVPPR	E9Q740	Protein Srp72 {ECO:0000313|Ensembl:ENSMUSP00000113312};	567	610	-10.00	6.52E-06
FREPNAQVSR	PIPDIGGGYIPTEEEWR	Q9CRD0	OCIA domain-containing protein 1;	17	247	-10.00	0.00639
VSTPPPFQGR	PITPVYTVAPNVQR	Q91WT8	RNA-binding protein 47;	517	590	-10.00	0.009565
RVSKDASPGS	PLEKLVSSVSDLPKR	P54869	Hydroxymethylglutaryl-CoA synthase, mitochondrial;	434	508	-10.00	6.52E-06
GNGLIKVNGR	PLEMIEPR	P14131	40S ribosomal protein S16;	38	146	-10.00	6.52E-06
ICNGVPMVMM	PLFGDQMDNAKR	P70691	UDP-glucuronosyltransferase 1-2;	392	533	-10.00	6.52E-06
GGPGNPALAQ	PLIQNVKKILESDR	Q8C196	Carbamoyl-phosphate synthase (ammonia), mitochondrial;	273	1500	-10.00	6.52E-06
IEGRPGASLP	PLNLKELEKDLIDR	Q05920	Pyruvate carboxylase, mitochondrial;	984	1178	-10.00	6.52E-06
QSTVYAFSAR	PLTGGEPVSLGSLR	P11352	Glutathione peroxidase 1;	21	201	-10.00	6.52E-06
VESQLKILIR	PLYSNPPLNGAR	P05202	Aspartate aminotransferase, mitochondrial;	314	430	-10.00	6.52E-06
KDVLKLVEAR	PMIHELLTEGR	P70168	Importin subunit beta-1;	841	876	-10.00	6.52E-06
QYNGVPLDGR	PMNIQLVTSQIDTQR	O08583	THO complex subunit 4;	174	255	-10.00	6.52E-06

Non-prime Sequence	Prime Sequence	UniProt ID	Protein Name	Position	Length	Average Fc	*p*-value
VNISLRVLSR	PNAQELPSMYQR	O35129	Prohibitin-2;	112	299	-10.00	6.52E-06
LNQAKGWLRD	PNASPGDAGEQAIR	Q64727	Vinculin;	287	1066	-0.95	6.52E-06
RCGKKKVWLD	PNETNEIANANSR	P84099	60S ribosomal protein L19;	26	196	-0.74	6.52E-06
RRLQELRELI	PNIPFQMLLR	Q05920	Pyruvate carboxylase, mitochondrial;	635	1178	-10.00	6.52E-06
PLDSTSRIMD	PNIVGNEHYDVAR	P56480	ATP synthase subunit beta, mitochondrial;	410	529	-0.68	6.52E-06
DGSIDLVINL	PNNNTKFVHDNYVIR	Q8C196	Carbamoyl-phosphate synthase (ammonia), mitochondrial;	1439	1500	-10.00	6.52E-06
EQMAFDPSNM	PPGIEPSPDKMLQGR	P24270	Catalase;	340	527	-1.13	6.52E-06
AKHEQILVLD	PPSDLKFKGPFTDVVTTNLKLQNPSDR	Q9WV55	Vesicle-associated membrane protein-associated protein A;	19	249	-10.00	6.52E-06
FLCDLQEKFR	PSIAYFPQIVSVAAR	P85094	Isochorismatase domain-containing protein 2A, mitochondrial;	29	206	-10.00	6.52E-06
ISLRNLLLGR	PSLEQLAQEVTYANLR	Q9QYC7	Vitamin K-dependent gamma-carboxylase;	711	757	-10.00	6.52E-06
M	PSVALKSPR	P32020	Non-specific lipid-transfer protein;	2	547	-10.00	6.52E-06
KDINAYNGET	PTEKLPFPIIDDKGR	O08709	Peroxiredoxin-6;	94	224	-10.00	6.52E-06
VHSGDATLML	PTQTISQGAIEKVKDATR	Q8C196	Carbamoyl-phosphate synthase (ammonia), mitochondrial;	1211	1500	-10.00	6.52E-06
EVCFPGGKRD	PVDTDDTATALR	Q99P30	Peroxisomal coenzyme A diphosphatase NUDT7;	80	236	-0.62	6.52E-06
TVLPEALERW	PVELVEKLLPR	Q9ET01	Glycogen phosphorylase, liver form;	389	850	-10.00	6.52E-06
MAGK	PVLHYFDGR	P30115	Glutathione S-transferase A3;	5	221	-0.95	6.52E-06
VDGLMIHSGD	PVNYYVDTAVR	P62908	40S ribosomal protein S3;	163	243	-10.00	6.52E-06
EEATRVSQEH	PVVLTKFVEGAR	Q8C196	Carbamoyl-phosphate synthase (ammonia), mitochondrial;	1163	1500	-10.00	6.52E-06
M	PYEIKKVFASLPQVER	O88342	WD repeat-containing protein 1;	2	606	-10.00	6.52E-06
M	PYLLISTQIR	P99025	GTP cyclohydrolase 1 feedback regulatory protein;	2	84	-0.79	6.52E-06
WQNLRIASGR	PYNPSMSRPDAWG	O35490	Betaine--homocysteine S-methyltransferase 1;	362	407	-10.00	6.52E-06
DKIREYKSKR	QASGGPVDIGPEYQQDLDR	P97450	ATP synthase-coupling factor 6, mitochondrial;	55	108	-10.00	6.52E-06
FIIDDKGILR	QITINDLPVGR	P35700	Peroxiredoxin-1;	141	199	-10.00	6.52E-06
VPYVTYDEDY	QQLIEDIVR	Q6NZL8	Signal peptide, CUB and EGF-like domain-containing protein 1;	945	1018	-10.00	6.52E-06
KKGGEKKKGR	SAINEVVTR	P62900	60S ribosomal protein L31;	15	125	-1.15	6.52E-06
AVSCLWGKVN	SDEVGGEALGR	P02088	Hemoglobin subunit beta-1;	21	147	-1.16	6.52E-06
TITLVLKEEA	SDYLELDTIKNLVR	P08113	Endoplasmin;	256	802	-0.68	6.52E-06
FNIERAHDER	SEASGPQLLPVR	Q8C5H8	NAD kinase 2, mitochondrial;	250	452	-10.00	6.52E-06

Non-prime Sequence	Prime Sequence	UniProt ID	Protein Name	Position	Length	Average Fc	*p*-value
MGAHVVLTAR	SEEGLQKVVSR	P50172	Corticosteroid 11-beta-dehydrogenase isozyme 1;	67	292	-10.00	6.52E-06
M	SETAPAAPAAPAPAEKTPVKKK	P43274	Histone H1.4;	2	219	-10.00	6.52E-06
KDLKVLKTTQ	SGFEGFLKDQFTTLPEVKDR	P25688	Uricase;	168	303	-10.00	6.52E-06
RHRSPCMQDR	SHMPYTDAMIHEVQR	Q64458	Cytochrome P450 2C29;	343	490	-10.00	6.52E-06
RRFTTSVVRR	SHYEEGPGKNLPF	P17665	Cytochrome c oxidase subunit 7C, mitochondrial;	17	63	-10.00	6.52E-06
KSLNCTVKTY	SISHTLEDLDR	Q62452	UDP-glucuronosyltransferase 1-9;	76	528	-1.20	6.52E-06
MVDSVYRTR	SLGVAAEGLPDQYADGEAAR	Q9QXF8	Glycine N-methyltransferase;	10	293	-2.12	6.52E-06
SLLQQQKTSR	SNMDNMFESYINNLR	P11679	Keratin, type II cytoskeletal 8;	140	490	-10.00	6.52E-06
WLTFHAGPSL	SSAASSKELLMKLR	Q9CZR8	Elongation factor Ts, mitochondrial {ECO:0000255|HAMAP-Rule:MF_03135};	40	324	-10.00	6.52E-06
PFSQHVRRLR	SSITPGTVLIILTGR	P47911	60S ribosomal protein L6;	150	296	-10.00	6.52E-06
AKDPFAHLPK	STFVLDEFKR	Q9D8N0	Elongation factor 1-gamma;	286	437	-10.00	6.52E-06
PSPSPSPSLS	STQSAVSKAGAGAVVPKLSHLPR	Q9DC70	NADH dehydrogenase (ubiquinone) iron-sulfur protein 7, mitochondrial;	46	224	-10.00	6.52E-06
AMTNQILVER	SVTGWKEIEYEVVR	Q8C196	Carbamoyl-phosphate synthase (ammonia), mitochondrial;	625	1500	-1.37	6.52E-06
EPVWAIGTGK	TATPQQAQEVHEKLR	P17751	Triosephosphate isomerase;	226	299	-0.97	6.52E-06
CMQDRSRMPY	TDAMIHEVQR	P56654	Cytochrome P450 2C37;	348	490	-1.05	6.52E-06
LIKEGDVVKR	TGAIVDVPVGEELLGR	Q03265	ATP synthase subunit alpha, mitochondrial;	134	553	-2.14	6.52E-06
CRCKFNQQQR	TGEPDEEEGTFR	Q9Z239	Phospholemman;	70	92	-10.00	6.52E-06
CDFSNASKPQ	TIQESTGGIVEVLHKVDSEGISPNR	P51660	Peroxisomal multifunctional enzyme type 2;	287	735	-0.71	6.52E-06
IIKHPNFNRK	TLNNDIMLIK	Q9Z1R9	MCG124046;	103	246	-10.00	6.52E-06
KTQDPAKAPN	TPDVLEIEFKKGVPVKVTNIKDGTTR	J3QNG0	Uncharacterized protein {ECO:0000313|Ensembl:ENSMUSP00000136734};	219	412	-10.00	6.52E-06
WVQSTIANER	TPWIEFENNYR	E9QAK1	Sulfotransferase {ECO:0000256|RuleBase:RU361155};	75	189	-10.00	6.52E-06
FKIAMGAFDR	TRPTVAAGAVGLAQR	P45952	Medium-chain specific acyl-CoA dehydrogenase, mitochondrial;	280	421	-1.61	6.52E-06
MVDSVYR	TRSLGVAAEGLPDQYADGEAAR	Q9QXF8	Glycine N-methyltransferase;	8	293	-10.00	6.52E-06
RRLSELLRYH	TSQSGDEMTSLSEYVSR	P11499	Heat shock protein HSP 90-beta;	459	724	-10.00	6.52E-06
AVLSLYASGR	TTGIVMDSGDGVTHTVPIYEGY	E9Q1F2	Actin, cytoplasmic 1;	68	295	-10.00	6.52E-06
AVLSLYASGR	TTGIVMDSGDGVTHTVPIYEGYALPH	E9Q1F2	Actin, cytoplasmic 1;	68	295	-10.00	6.52E-06
HSTDARELSK	TYIIGELHPDDR	P56395	Cytochrome b5;	78	134	-10.00	6.52E-06
MGNHLTNLRR	VAGPQPAQTGAPQGSLGEYLFER	P29391	Ferritin light chain 1;	155	183	-10.00	6.52E-06

Non-prime Sequence	Prime Sequence	UniProt ID	Protein Name	Position	Length	Average Fc	*p*-value
WDTVSNQVQR	VAVDAPVSSVALR	Q64374	Regucalcin;	52	299	-1.52	6.52E-06
PLDTEVPLER	VFDYSEYWEGAR	Q05920	Pyruvate carboxylase, mitochondrial;	831	1178	-10.00	6.52E-06
TKKVQQELSR	VGLLEALLPGQPEAVAR	P51855	Glutathione synthetase;	314	474	-10.00	6.52E-06
AYLARHVGLR	VGVPTETGALTLNR	Q8BWT1	3-ketoacyl-CoA thiolase, mitochondrial;	77	397	-10.00	6.52E-06
M	VHLTDAEKAAVSCLWGKVNSDEVGGEALGR	P02088	Hemoglobin subunit beta-1;	2	147	-1.33	6.52E-06
GVANVSIEDR	VISLSGEHSIIGR	P08228	Superoxide dismutase (Cu-Zn);	104	154	-10.00	6.52E-06
M	VLSGEDKSNIKAAWGKIGGH	P01942	Hemoglobin subunit alpha;	2	142	-10.00	6.52E-06
GARGTQLLPR	VVGVPVALDLITSGR	Q9DBM2	Peroxisomal bifunctional enzyme;	140	718	-10.00	6.52E-06
ELRLLEVDNR	VVLPMELPIR	P00405	Cytochrome c oxidase subunit 2;	142	227	-10.00	6.52E-06
IGLFVKAGSR	YEDSNNLGTSHLLR	Q9DB77	Cytochrome b-c1 complex subunit 2, mitochondrial;	71	453	-10.00	6.52E-06
NRRRLSELLR	YHTSQSGDEMTSLSEYVSR	P11499	Heat shock protein HSP 90-beta;	457	724	-10.00	6.52E-06
GAGNNWAKGH	YTEGAELVDSVLDVVR	P68372	Tubulin beta-4B chain;	106	445	-10.00	6.52E-06