

Table S4. Using cutoff criteria to define significance of $q < .05$ and fold change > 0 , 3,264 peptides representing 590 proteins were identified in a co-IP-MS assay performed on whole brain homogenate from wildtype C57/Bl6J mice. Data shown include accession number (column A), protein description (column B), modified peptide sequence (Column C), fold change (column D), the associated p-value (column E), corrected p-value (q value, Column F), and the number of significant peptides from that protein that were identified (Column G). Data are sorted in descending order of number of peptides identified for a protein. Note MAP2 is the protein with the most coverage, consistent with expected results from a MAP2 co-IP.

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P20357	MTAP2_MOUSE	VSDFGQM[+16]ASGM[+16]NVDAGK	5.57	4.27E-04	0.0143	128
P20357	MTAP2_MOUSE	M[+16]PC[+57]FPIESKEEEDKAEQAK	8.89	4.40E-04	0.0143	128
P20357	MTAP2_MOUSE	APHWTSASLTEAAAHPHSPSEM[+16]K	7.63	7.50E-04	0.0143	128
P20357	MTAP2_MOUSE	ARVDHGAEIITQSPSR	6.54	7.71E-04	0.0143	128
P20357	MTAP2_MOUSE	QDSFPISLEQAVTDAAM[+16]TSK	7.62	7.92E-04	0.0143	128
P20357	MTAP2_MOUSE	M[+16]PSKPGEDFEHAALVPDTSK	5.64	8.74E-04	0.0143	128
P20357	MTAP2_MOUSE	GEVQM[+16]EFIQLPK	2.02	9.46E-04	0.0143	128
P20357	MTAP2_MOUSE	VDHGAEIITQSPSR	6.34	9.49E-04	0.0143	128
P20357	MTAP2_MOUSE	M[+16]PC[+57]FPIESK	5.34	1.04E-03	0.0143	128
P20357	MTAP2_MOUSE	FPSSFAEPLDK	4.85	1.04E-03	0.0143	128
P20357	MTAP2_MOUSE	NGTVM[+16]APDLPEMLDLAGTR	8.14	1.16E-03	0.0143	128
P20357	MTAP2_MOUSE	VSDFGQMASGM[+16]NVDAGK	7.68	1.18E-03	0.0143	128
P20357	MTAP2_MOUSE	KETSAPSVQEPTLTETEPQTK	6.88	1.28E-03	0.0143	128
P20357	MTAP2_MOUSE	DLATDLSLIEVK	5.96	1.31E-03	0.0143	128
P20357	MTAP2_MOUSE	DWFIEM[+16]PTESK	6.00	1.34E-03	0.0143	128
P20357	MTAP2_MOUSE	VSDFGQM[+16]ASGMNVDAGK	6.29	1.36E-03	0.0143	128
P20357	MTAP2_MOUSE	ETSAPSVQEPTLTETEPQTK	6.38	1.50E-03	0.0143	128
P20357	MTAP2_MOUSE	TPGTPGTPSYPR	6.10	1.50E-03	0.0143	128
P20357	MTAP2_MOUSE	QFDSPM[+16]PSPFHGGSFLLPLDTM[+16]K	5.11	1.51E-03	0.0143	128
P20357	MTAP2_MOUSE	SM[+16]SINLPM[+16]SC[+57]LDSIALGFNFGR	8.94	1.57E-03	0.0143	128
P20357	MTAP2_MOUSE	QSTEPSIVM[+16]PSIGLSAEPAPK	5.97	1.68E-03	0.0143	128
P20357	MTAP2_MOUSE	LEGAGSATIAEVEM[+16]PFYEDK	5.31	1.73E-03	0.0143	128
P20357	MTAP2_MOUSE	NKLEGAGSATIAEVEM[+16]PFYEDK	6.83	1.75E-03	0.0143	128
P20357	MTAP2_MOUSE	SM[+16]SINLPMSC[+57]LDSIALGFNFGR	7.44	1.77E-03	0.0143	128
P20357	MTAP2_MOUSE	FAAPAQPEEER	6.08	1.79E-03	0.0143	128
P20357	MTAP2_MOUSE	STELGSDYYELSDSR	6.54	1.84E-03	0.0143	128
P20357	MTAP2_MOUSE	DDKTGVIQTSTEQSFSK	7.16	1.90E-03	0.0143	128
P20357	MTAP2_MOUSE	SGTSTPTTPGSTAITPGTPPSYSSF	6.52	1.95E-03	0.0143	128
P20357	MTAP2_MOUSE	KIDLSHVTSK	6.46	1.97E-03	0.0143	128
P20357	MTAP2_MOUSE	ANDKLDTVLEK	5.43	2.02E-03	0.0143	128
P20357	MTAP2_MOUSE	FPSSFAEPLDKGEM[+16]EFK	6.13	2.04E-03	0.0143	128
P20357	MTAP2_MOUSE	LILKPAIK	6.50	2.06E-03	0.0143	128
P20357	MTAP2_MOUSE	YFETSALKEDM[+16]TR	8.00	2.09E-03	0.0143	128
P20357	MTAP2_MOUSE	DGSPDAPATPEKEEVAFSEYK	5.43	2.19E-03	0.0143	128
P20357	MTAP2_MOUSE	EQGLFEK	6.04	2.26E-03	0.0143	128
P20357	MTAP2_MOUSE	KSEVQAHSR	5.58	2.32E-03	0.0143	128
P20357	MTAP2_MOUSE	EKDVLEDIPR	6.47	2.47E-03	0.0143	128
P20357	MTAP2_MOUSE	IGSTDNIK	6.34	2.48E-03	0.0143	128
P20357	MTAP2_MOUSE	EEFVETC[+57]PGELK	6.21	2.50E-03	0.0143	128
P20357	MTAP2_MOUSE	DEWGLAAPISPGPLTPMR	4.44	2.50E-03	0.0143	128
P20357	MTAP2_MOUSE	DVLEDIPR	5.59	2.53E-03	0.0143	128
P20357	MTAP2_MOUSE	QFDSPMPSPFHGGSFLLPLDTM[+16]K	5.26	2.57E-03	0.0143	128
P20357	MTAP2_MOUSE	GQEHTIDELKQDSFPISLEQAVTDAAMTSK	7.74	2.58E-03	0.0143	128
P20357	MTAP2_MOUSE	SQGTYSDTK	6.09	2.66E-03	0.0143	128
P20357	MTAP2_MOUSE	TTAASGDLAQAPGAFK	6.38	2.72E-03	0.0143	128
P20357	MTAP2_MOUSE	TGVIQTSTEQSFSK	6.25	2.81E-03	0.0143	128
P20357	MTAP2_MOUSE	GLSSVPEVAEVEPTTK	6.43	2.82E-03	0.0143	128
P20357	MTAP2_MOUSE	KDEWGLAAPISPGPLTPM[+16]R	6.64	2.83E-03	0.0143	128
P20357	MTAP2_MOUSE	ESEEM[+16]GGKVELFGLGITYDQASTK	6.83	2.85E-03	0.0143	128
P20357	MTAP2_MOUSE	NANGFPYREEEEGAFGEHR	8.38	2.88E-03	0.0143	128
P20357	MTAP2_MOUSE	LINQPLPDLK	6.14	2.90E-03	0.0143	128
P20357	MTAP2_MOUSE	VSLQDPSALATSK	6.40	2.94E-03	0.0143	128
P20357	MTAP2_MOUSE	GGQVQIVTK	6.29	2.95E-03	0.0143	128
P20357	MTAP2_MOUSE	ENGINEELTSADRETAEEVSAR	7.09	3.18E-03	0.0143	128
P20357	MTAP2_MOUSE	DQGGAGEGLSR	6.64	3.22E-03	0.0143	128
P20357	MTAP2_MOUSE	VNETEVK	5.90	3.22E-03	0.0143	128
P20357	MTAP2_MOUSE	SGILVPSEK	5.88	3.25E-03	0.0143	128
P20357	MTAP2_MOUSE	QFDSPM[+16]PSPFHGGSFLLPLDTMK	4.86	3.32E-03	0.0143	128
P20357	MTAP2_MOUSE	KANDKLDTVLEK	6.37	3.32E-03	0.0143	128
P20357	MTAP2_MOUSE	STVSIEEAVAK	5.98	3.34E-03	0.0143	128
P20357	MTAP2_MOUSE	VTSEPEAVSER	6.12	3.35E-03	0.0143	128
P20357	MTAP2_MOUSE	MPC[+57]FPIESK	6.39	3.63E-03	0.0146	128

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P20357	MTAP2_MOUSE	MPSKPGEDFEHAALVPDTSK	7.22	3.77E-03	0.0147	128
P20357	MTAP2_MOUSE	ETSPETSLIQDEVALK	7.23	3.78E-03	0.0147	128
P20357	MTAP2_MOUSE	QFDSPMPSPFHGGSFTLPLDTMK	8.06	3.80E-03	0.0147	128
P20357	MTAP2_MOUSE	EENSFSLNSSISSAR	6.42	3.83E-03	0.0147	128
P20357	MTAP2_MOUSE	ENGINEELTSADR	4.88	3.84E-03	0.0147	128
P20357	MTAP2_MOUSE	MPC[+57]FPIESKEEEDKAEQAK	7.79	3.89E-03	0.0147	128
P20357	MTAP2_MOUSE	FEVAQELTSSSEAPQEADSFM[+16]GVESGHIK	6.20	4.01E-03	0.0148	128
P20357	MTAP2_MOUSE	KQSTEPSIVM[+16]PSIGLSAEPAPK	6.10	4.09E-03	0.0148	128
P20357	MTAP2_MOUSE	FPSSFAEPLDKGEMEFK	5.91	4.24E-03	0.0149	128
P20357	MTAP2_MOUSE	NGTVMAPDLPEMLDLAGTR	8.95	4.30E-03	0.0150	128
P20357	MTAP2_MOUSE	VSDFGQMASGMNVDAGK	7.57	4.32E-03	0.0150	128
P20357	MTAP2_MOUSE	DLQGMERGEKLPVPFAQTFGTNLEDR	4.49	4.54E-03	0.0152	128
P20357	MTAP2_MOUSE	VSEGPRPFAPVFFQSDDK	4.63	4.55E-03	0.0152	128
P20357	MTAP2_MOUSE	YFETSALKEDMTR	6.73	4.82E-03	0.0154	128
P20357	MTAP2_MOUSE	SILTEQLETIPK	6.48	4.83E-03	0.0154	128
P20357	MTAP2_MOUSE	YTVPLPSPVQDSENLSGESGSFYEGTDDK	6.96	4.98E-03	0.0155	128
P20357	MTAP2_MOUSE	ETAEEVSAR	5.83	5.04E-03	0.0155	128
P20357	MTAP2_MOUSE	VTGGQTIQVETSSSESPFAK	6.19	5.09E-03	0.0155	128
P20357	MTAP2_MOUSE	KLILKPAIK	7.52	5.14E-03	0.0155	128
P20357	MTAP2_MOUSE	RPRPHDEELEIEM[+16]AAEAQAEPK	2.89	5.69E-03	0.0161	128
P20357	MTAP2_MOUSE	KTTAASGDLAQAPGAFK	3.96	5.70E-03	0.0161	128
P20357	MTAP2_MOUSE	SMSINLPM[+16]SC[+57]LDSIALGFNFGR	9.09	5.93E-03	0.0163	128
P20357	MTAP2_MOUSE	SILTEQLETIPKEER	6.44	6.01E-03	0.0164	128
P20357	MTAP2_MOUSE	GEVQMEFIQLPK	5.95	6.52E-03	0.0171	128
P20357	MTAP2_MOUSE	SDTLQISDLLVSESREEFVETC[+57]PGELK	3.26	6.61E-03	0.0171	128
P20357	MTAP2_MOUSE	LPPVPFAQTFGTNLEDR	7.34	6.66E-03	0.0172	128
P20357	MTAP2_MOUSE	RDLATDLSLIEVK	8.49	6.67E-03	0.0172	128
P20357	MTAP2_MOUSE	DLQGM[+16]EGEKLPVPFAQTFGTNLEDRK	4.64	6.94E-03	0.0174	128
P20357	MTAP2_MOUSE	DWFIEMPTESK	6.69	6.97E-03	0.0175	128
P20357	MTAP2_MOUSE	VTTDQEKK	5.52	7.03E-03	0.0175	128
P20357	MTAP2_MOUSE	SDTLQISDLLVSES	6.10	7.26E-03	0.0177	128
P20357	MTAP2_MOUSE	LEGAGSATIAEVEMPFYEDK	7.70	8.06E-03	0.0184	128
P20357	MTAP2_MOUSE	IVQVVTAEAVAVLK	6.09	8.48E-03	0.0189	128
P20357	MTAP2_MOUSE	LRDDKTGVIQTSTEQSFSK	2.43	8.48E-03	0.0189	128
P20357	MTAP2_MOUSE	AEPSQLDIK	7.29	8.64E-03	0.0191	128
P20357	MTAP2_MOUSE	KDEWGLAAPISPGPLTPMR	7.45	9.01E-03	0.0196	128
P20357	MTAP2_MOUSE	VELFGLGITYDQASTK	6.36	9.08E-03	0.0197	128
P20357	MTAP2_MOUSE	VNETEVKEK	5.41	9.12E-03	0.0197	128
P20357	MTAP2_MOUSE	NKLEGAGSATIAEVEMPFYEDK	3.70	9.54E-03	0.0202	128
P20357	MTAP2_MOUSE	RGVSGDREENSFSLNSSISSAR	8.79	1.04E-02	0.0211	128
P20357	MTAP2_MOUSE	YTRPTHLSLC[+57]VK	9.65	1.06E-02	0.0213	128
P20357	MTAP2_MOUSE	VGSLDNAHHVPGGGNVK	5.82	1.17E-02	0.0225	128
P20357	MTAP2_MOUSE	ESEEMGGKVELFGLGITYDQASTK	5.64	1.23E-02	0.0231	128
P20357	MTAP2_MOUSE	REIQGLFEK	1.64	1.28E-02	0.0235	128
P20357	MTAP2_MOUSE	NQHDEKELQAK	8.00	1.30E-02	0.0238	128
P20357	MTAP2_MOUSE	SSLPRPSSILPPR	7.89	1.40E-02	0.0249	128
P20357	MTAP2_MOUSE	GQEHTIDELK	2.74	1.40E-02	0.0249	128
P20357	MTAP2_MOUSE	RPRPHDEELEIEMAAEAQAEPK	5.12	1.44E-02	0.0254	128
P20357	MTAP2_MOUSE	VADVSISEVTLLGNVHSPVVEGYVGENISGEVK	3.37	1.47E-02	0.0257	128
P20357	MTAP2_MOUSE	GVSGDREENSFSLNSSISSAR	6.00	1.49E-02	0.0259	128
P20357	MTAP2_MOUSE	DEWGLAAPISPGPLTPM[+16]R	5.93	1.52E-02	0.0263	128
P20357	MTAP2_MOUSE	LPPVPFAQTFGTNLEDRK	3.37	1.53E-02	0.0264	128
P20357	MTAP2_MOUSE	LSVEIPC[+57]PPPVSEADLSTDEK	2.86	1.56E-02	0.0267	128
P20357	MTAP2_MOUSE	KQSTEPSIVMPSIGLSAEPAPK	6.08	1.60E-02	0.0271	128
P20357	MTAP2_MOUSE	FEVAQELTSSSEAPQEADSFMGVESGHIK	6.27	1.61E-02	0.0272	128
P20357	MTAP2_MOUSE	DDLTLR	2.43	1.65E-02	0.0276	128
P20357	MTAP2_MOUSE	QDSFPISLEQAVTDAAMTSK	8.85	1.69E-02	0.0281	128
P47911	RL6_MOUSE	6C SSITPGTVLIILTGR	4.34	1.78E-02	0.0290	128
P52480	KPYM_MOUSE	FGVEQDVMVFASFIR	9.35	2.06E-02	0.0323	128
O08638	MYH11_MOUSE	SLEADLM[+16]QLQEDLAAAER	5.62	2.09E-02	0.0326	128
P16546	SPTN1_MOUSE	KVEDLFLTFK	3.36	2.12E-02	0.0330	128
Q8VDM4	PSMD2_MOUSE	MNLASSFVNGFVNAAFGQDK	7.90	2.32E-02	0.0352	128

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
E9Q912	E9Q912_MOUSE	SVAQQASLTEQR	4.19	2.38E-02	0.0359	128
Q9D0F9	PGM1_MOUSE	TIEEYAIC[+57]PDLK	5.62	2.51E-02	0.0372	128
P80314	TCPB_MOUSE	LAVEAVLR	5.61	3.58E-02	0.0494	128
Q8VDD5	MYH9_MOUSE	LQLQEQLQAETELC[+57]AEAEELR	5.64	2.09E-02	0.0326	128
Q61879	MYH10_MOUSE	EEELQGALAR	3.03	9.82E-05	0.0143	125
Q61879	MYH10_MOUSE	NKQEVV[+16]SDLEER	4.68	1.61E-04	0.0143	125
Q61879	MYH10_MOUSE	NTDQASM[+16]PENTVAQK	2.66	3.10E-04	0.0143	125
Q61879	MYH10_MOUSE	ADM[+16]EDLM[+16]SSKDDVVGK	3.78	5.13E-04	0.0143	125
Q61879	MYH10_MOUSE	NILAEQLQAETELFAEAEEM[+16]R	3.44	5.34E-04	0.0143	125
Q61879	MYH10_MOUSE	VEGELEEM[+16]ER	3.94	5.35E-04	0.0143	125
Q61879	MYH10_MOUSE	ALEDETKNHEAQIQDM[+16]R	5.25	5.54E-04	0.0143	125
Q61879	MYH10_MOUSE	VEEEEEERNQILQNEK	4.12	8.28E-04	0.0143	125
Q61879	MYH10_MOUSE	QGLETDNKELAC[+57]EVK	4.15	8.45E-04	0.0143	125
Q61879	MYH10_MOUSE	ADM[+16]EDLM[+16]SSK	5.24	8.53E-04	0.0143	125
Q61879	MYH10_MOUSE	C[+57]M[+16]LQDREDQSILC[+57]TGESGAGK	5.09	9.29E-04	0.0143	125
Q61879	MYH10_MOUSE	ELDDATEANEGLSR	4.33	9.35E-04	0.0143	125
Q61879	MYH10_MOUSE	LDAQVQELHAK	4.24	9.59E-04	0.0143	125
Q61879	MYH10_MOUSE	KEEELQGALAR	4.07	9.78E-04	0.0143	125
Q61879	MYH10_MOUSE	M[+16]EEEEVLLLEDQNSK	4.53	1.03E-03	0.0143	125
Q61879	MYH10_MOUSE	MEIDLKDLEAQIEAANK	5.40	1.04E-03	0.0143	125
Q61879	MYH10_MOUSE	ELQAQIAELQEDFESEK	4.63	1.07E-03	0.0143	125
Q61879	MYH10_MOUSE	TSDVNDTQPPQSE	4.65	1.08E-03	0.0143	125
Q61879	MYH10_MOUSE	QLEEEKNSLQEQQEEEEEAR	5.93	1.09E-03	0.0143	125
Q61879	MYH10_MOUSE	DAAGLESQIQDTQELLQEETR	4.62	1.10E-03	0.0143	125
Q61879	MYH10_MOUSE	IAEC[+57]SSQLAEIEEEK	4.96	1.13E-03	0.0143	125
Q61879	MYH10_MOUSE	QLEEAEEEEATR	4.21	1.14E-03	0.0143	125
Q61879	MYH10_MOUSE	IAQLEEELEEEQSNM[+16]JELLNDR	3.79	1.14E-03	0.0143	125
Q61879	MYH10_MOUSE	KLDAQVQELHAK	4.12	1.14E-03	0.0143	125
Q61879	MYH10_MOUSE	LQNELDNVSTLLEAEK	4.48	1.16E-03	0.0143	125
Q61879	MYH10_MOUSE	SLEAEILQLQEELASSER	6.55	1.19E-03	0.0143	125
Q61879	MYH10_MOUSE	NLPIYSENIEM[+16]YR	4.89	1.22E-03	0.0143	125
Q61879	MYH10_MOUSE	ASRDEIFAQSK	3.91	1.24E-03	0.0143	125
Q61879	MYH10_MOUSE	HGFEAASIKEER	4.69	1.35E-03	0.0143	125
Q61879	MYH10_MOUSE	FLSNGYIPIPGQQDK	4.74	1.40E-03	0.0143	125
Q61879	MYH10_MOUSE	QLEEEKNSLQEQQEEEEEAR	5.12	1.47E-03	0.0143	125
Q61879	MYH10_MOUSE	GGPISFSSSR	4.16	1.51E-03	0.0143	125
Q61879	MYH10_MOUSE	M[+16]EIDLKDLEAQIEAANK	4.51	1.51E-03	0.0143	125
Q61879	MYH10_MOUSE	DLSEELEALK	4.63	1.54E-03	0.0143	125
Q61879	MYH10_MOUSE	QIVSNLEK	4.58	1.57E-03	0.0143	125
Q61879	MYH10_MOUSE	VEEEEEERNQILQNEKK	5.68	1.58E-03	0.0143	125
Q61879	MYH10_MOUSE	ATISALEAK	4.02	1.58E-03	0.0143	125
Q61879	MYH10_MOUSE	KM[+16]EEEEVLLLEDQNSK	3.54	1.76E-03	0.0143	125
Q61879	MYH10_MOUSE	NC[+57]AAYLK	4.77	1.84E-03	0.0143	125
Q61879	MYH10_MOUSE	HEM[+16]PPHIYAISESAYR	5.05	1.84E-03	0.0143	125
Q61879	MYH10_MOUSE	IGQLEEQLQEAK	4.77	1.86E-03	0.0143	125
Q61879	MYH10_MOUSE	TGLEDPER	4.26	1.88E-03	0.0143	125
Q61879	MYH10_MOUSE	LQELEGAVK	3.78	1.93E-03	0.0143	125
Q61879	MYH10_MOUSE	ELEAELEDER	4.29	1.94E-03	0.0143	125
Q61879	MYH10_MOUSE	KLDGETTDLQDQIAELQAQVDELK	6.09	1.94E-03	0.0143	125
Q61879	MYH10_MOUSE	NSLQEQQEEEEEAR	5.00	1.95E-03	0.0143	125
Q61879	MYH10_MOUSE	HAEQERDELADEIANSASGK	4.70	1.95E-03	0.0143	125
Q61879	MYH10_MOUSE	ALEQQVEEMR	4.43	2.01E-03	0.0143	125
Q61879	MYH10_MOUSE	DVEALSQR	3.62	2.02E-03	0.0143	125
Q61879	MYH10_MOUSE	DEIFAQSK	4.16	2.05E-03	0.0143	125
Q61879	MYH10_MOUSE	VLAYDKLEK	4.31	2.18E-03	0.0143	125
Q61879	MYH10_MOUSE	ALEEALAEKEEFER	4.70	2.19E-03	0.0143	125
Q61879	MYH10_MOUSE	ALELDPNLYR	4.76	2.22E-03	0.0143	125
Q61879	MYH10_MOUSE	NM[+16]DPLNDNVATLLHQSSDR	4.44	2.28E-03	0.0143	125
Q61879	MYH10_MOUSE	YEILTPNAIPK	4.57	2.32E-03	0.0143	125
Q61879	MYH10_MOUSE	LC[+57]HLLGMNVM[+16]EFTR	4.61	2.46E-03	0.0143	125
Q61879	MYH10_MOUSE	NTDQASMPENTVAQK	5.31	2.46E-03	0.0143	125
Q61879	MYH10_MOUSE	VDDDLGTIESLEEAK	3.57	2.50E-03	0.0143	125

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q61879	MYH10_MOUSE	M[+16]QAHIQDLEEQLDEEEGAR	4.23	2.51E-03	0.0143	125
Q61879	MYH10_MOUSE	QELEEILHDLESR	6.86	2.57E-03	0.0143	125
Q61879	MYH10_MOUSE	KMQAHIQDLEEQLDEEEGAR	5.05	2.58E-03	0.0143	125
Q61879	MYH10_MOUSE	QVLALQSQLADTK	4.44	2.72E-03	0.0143	125
Q61879	MYH10_MOUSE	TELEDLDTTAAQQLF	5.79	2.72E-03	0.0143	125
Q61879	MYH10_MOUSE	ALEEALAK	3.97	2.76E-03	0.0143	125
Q61879	MYH10_MOUSE	NLPIYSENIIEMYR	5.75	2.79E-03	0.0143	125
Q61879	MYH10_MOUSE	KLWVWIPSER	4.17	2.80E-03	0.0143	125
Q61879	MYH10_MOUSE	KKVDDDLGTIESLEEAK	4.65	2.90E-03	0.0143	125
Q61879	MYH10_MOUSE	QQQLSALK	4.56	2.99E-03	0.0143	125
Q61879	MYH10_MOUSE	ELEAELEDERK	4.60	3.02E-03	0.0143	125
Q61879	MYH10_MOUSE	SALLDEKR	4.31	3.02E-03	0.0143	125
Q61879	MYH10_MOUSE	KVDDDLGTIESLEEAKK	5.04	3.11E-03	0.0143	125
Q61879	MYH10_MOUSE	IVFQEFR	4.58	3.16E-03	0.0143	125
Q61879	MYH10_MOUSE	IAQLEEELEEEQSNMELLNDR	5.06	3.28E-03	0.0143	125
Q61879	MYH10_MOUSE	IVGLDQVTGMTETAFGSAYK	5.47	3.32E-03	0.0143	125
Q61879	MYH10_MOUSE	TTLQVDTLNTELAER	4.73	3.38E-03	0.0143	125
Q61879	MYH10_MOUSE	HATALEELSEQLEQAK	4.97	3.54E-03	0.0144	125
Q61879	MYH10_MOUSE	EQADFAVEALAK	4.53	3.56E-03	0.0145	125
Q61879	MYH10_MOUSE	QEEELQAKDEELLK	5.29	3.61E-03	0.0145	125
Q61879	MYH10_MOUSE	KVDDDLGTIESLEEAK	4.70	3.65E-03	0.0146	125
Q61879	MYH10_MOUSE	NILAEQLQAETELFAEAEEMF	5.16	3.69E-03	0.0147	125
Q61879	MYH10_MOUSE	SDLLLEGFNRYR	3.60	3.72E-03	0.0147	125
Q61879	MYH10_MOUSE	AVIYNPATQADWTAK	4.35	3.72E-03	0.0147	125
Q61879	MYH10_MOUSE	LC[+57]HLLGM[+16]NVM[+16]EFTR	3.70	3.76E-03	0.0147	125
Q61879	MYH10_MOUSE	KQQQLSALK	4.86	4.02E-03	0.0148	125
Q61879	MYH10_MOUSE	DELADEIANSASGK	4.29	4.14E-03	0.0148	125
Q61879	MYH10_MOUSE	AMVKNKDDIQK	4.26	4.23E-03	0.0149	125
Q61879	MYH10_MOUSE	QLHIEGASLELSDDDTESK	4.37	4.27E-03	0.0150	125
Q61879	MYH10_MOUSE	HEMPPHIYAISESAYR	4.22	4.37E-03	0.0150	125
Q61879	MYH10_MOUSE	VEDMAELTC[+57]LNEASVLHNLKDR	4.91	5.12E-03	0.0155	125
Q61879	MYH10_MOUSE	IVGLDQVTGM[+16]TETAFGSAYK	3.80	5.17E-03	0.0155	125
Q61879	MYH10_MOUSE	GDEVMVELAENGKK	6.76	5.29E-03	0.0158	125
Q61879	MYH10_MOUSE	KMEEEVLLLEDQNSK	4.59	5.30E-03	0.0158	125
Q61879	MYH10_MOUSE	DLEAQIEAANK	4.32	5.48E-03	0.0159	125
Q61879	MYH10_MOUSE	AM[+16]VKNKDDIQK	3.69	5.49E-03	0.0159	125
Q61879	MYH10_MOUSE	DHNIPGELER	4.46	5.84E-03	0.0163	125
Q61879	MYH10_MOUSE	RQLEEAEEEEATR	5.16	5.89E-03	0.0163	125
Q61879	MYH10_MOUSE	VVSSVLQFGNISFK	5.07	6.15E-03	0.0166	125
Q61879	MYH10_MOUSE	VEGELEEMER	3.90	6.19E-03	0.0167	125
Q61879	MYH10_MOUSE	HATALEELSEQLEQAKR	5.49	6.58E-03	0.0171	125
Q61879	MYH10_MOUSE	LDGETTDLQDQIAELQAQVDELK	5.69	6.70E-03	0.0172	125
Q61879	MYH10_MOUSE	QLLQANPILESFGNAK	5.09	7.02E-03	0.0175	125
Q61879	MYH10_MOUSE	LEVNMQAM[+16]K	3.09	7.25E-03	0.0177	125
Q61879	MYH10_MOUSE	KMEIDLKDLEAQIEAANK	6.78	7.29E-03	0.0177	125
Q61879	MYH10_MOUSE	LEVNMQAMK	4.03	7.55E-03	0.0180	125
Q61879	MYH10_MOUSE	NKQEVMSIDLEER	4.43	7.71E-03	0.0181	125
Q61879	MYH10_MOUSE	MEEEVLLLEDQNSK	4.22	7.80E-03	0.0182	125
Q61879	MYH10_MOUSE	LC[+57]HLLGM[+16]NVMFTR	5.48	7.89E-03	0.0183	125
Q61879	MYH10_MOUSE	LQNELDNVSTLLEEAEEK	7.24	7.91E-03	0.0183	125
Q61879	MYH10_MOUSE	HGFEAASIK	4.47	8.11E-03	0.0184	125
Q61879	MYH10_MOUSE	ADMEDLMSSKDDVGK	5.66	8.22E-03	0.0186	125
Q61879	MYH10_MOUSE	ADMEDLMSSK	4.18	8.27E-03	0.0187	125
Q61879	MYH10_MOUSE	GDEVMVELAENGK	3.83	1.03E-02	0.0209	125
Q61879	MYH10_MOUSE	LEVNM[+16]QAM[+16]K	3.08	1.03E-02	0.0209	125
Q61879	MYH10_MOUSE	NSLQEQEEEEEEARK	7.88	1.23E-02	0.0231	125
Q61879	MYH10_MOUSE	LC[+57]HLLGMNVMFTR	6.01	1.27E-02	0.0234	125
Q61879	MYH10_MOUSE	TFHIFYQLLSGAGEHLK	6.48	1.32E-02	0.0240	125
Q61879	MYH10_MOUSE	QEVN[+16]ISDLEER	2.39	1.37E-02	0.0246	125
Q61879	MYH10_MOUSE	ITDIIFFQAVC[+57]F	5.71	1.39E-02	0.0248	125
Q61879	MYH10_MOUSE	KTTLQVDTLNTELAER	5.03	1.40E-02	0.0249	125
P14873	MAP1B_MOUSE	SPPLLGSESPYEDFLSADSK	4.69	2.12E-02	0.0330	125

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q62261	SPTB2_MOUSE	HLLGVEDLLQK	5.30	2.24E-02	0.0344	125
Q99104	MYO5A_MOUSE	NTMTDSTILLEDVQK	4.92	2.43E-02	0.0364	125
P16546	SPTN1_MOUSE	GVIDM[+16]GNSLIER	2.92	2.50E-02	0.0371	125
A2AJI0	MA7D1_MOUSE	SLQLSAWESSIVDR	5.05	2.67E-02	0.0390	125
Q8K1M6	DNM1L_MOUSE	ALQGASQIAEIR	4.82	3.10E-02	0.0437	125
Q8VDD5	MYH9_MOUSE	QIATLHAQVTDM[+16]KK	4.31	4.81E-04	0.0143	117
Q8VDD5	MYH9_MOUSE	DLGEELEALK	4.29	5.23E-04	0.0143	117
Q8VDD5	MYH9_MOUSE	ALEQQVEEM[+16]KTQLEEELEDELQATEDAK	7.52	7.06E-04	0.0143	117
Q8VDD5	MYH9_MOUSE	KLEEDQIIM[+16]EDQNC[+57]K	4.23	7.18E-04	0.0143	117
Q8VDD5	MYH9_MOUSE	TEM[+16]EDLM[+16]SSKDDVVGK	3.39	9.94E-04	0.0143	117
Q8VDD5	MYH9_MOUSE	QAQQRDELADEIANSSGK	4.11	1.09E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	KM[+16]EDGVGC[+57]LETAAEAK	4.04	1.12E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	IIGLDQVAGM[+16]SETALPGAFK	3.79	1.14E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	LQEM[+16]ESAVK	3.76	1.22E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	ELEDATETADAM[+16]NR	3.88	1.23E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	KM[+16]QQNIQELEEQLLEEEESAR	4.54	1.25E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	SM[+16]M[+16]QDREDQSILC[+57]TGESGAGK	4.31	1.28E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	QLLQANPILEAFGNAK	4.48	1.31E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	LQQELDLLVLDLHQR	5.26	1.31E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	IM[+16]GIPEDQM[+16]GLLR	4.28	1.32E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	DFSALSQLQDTQELLQEENR	4.71	1.45E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	SM[+16]EAEMIQLQEELAAER	4.31	1.48E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	VAEFTTNLM[+16]EEEEK	3.61	1.50E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	KVEAQLQELQVK	3.29	1.57E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	EDQSILC[+57]TGESGAGK	4.49	1.57E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	ALELDSNLYR	4.11	1.64E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	VISGVLQLGNIAFK	4.56	1.64E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	LEVNLQAM[+16]K	3.98	1.70E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	NC[+57]AAYLR	4.65	1.70E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	FDQLLAEEK	3.65	1.72E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	VEDM[+16]AELTC[+57]LNEASVLHNLK	2.87	1.74E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	NTNPNFVR	4.41	1.76E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	MQQNIQELEEQLLEEEESAR	4.93	1.77E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	ALEQQVEEM[+16]K	3.39	1.78E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	HSQAVEELADQLEQTKR	4.67	1.79E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	QTLENERGELANEVK	5.95	1.79E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	DVLLQVEDERR	4.84	1.83E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	C[+57]NGVLEGIR	4.00	1.86E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	VIQYLAHVASSHK	4.57	1.86E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	KANLQIDQINTDLNLER	4.52	1.87E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	IAQLEEELEEEQGNTELINDR	4.47	1.89E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	GDLPFVTR	3.46	1.90E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	QLEEAEEEAQR	3.97	1.93E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	YEILTPNSIPK	4.47	1.96E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	ITDVIIGFQAC[+57]C[+57]R	4.79	1.99E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	KQELEEIC[+57]HDLEAR	4.59	2.04E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	ELETQISELQEDLESER	4.45	2.06E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	NLPIYSEEIVEM[+16]YK	4.36	2.06E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	TELEDTLDDSTAAQQLR	5.84	2.12E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	NFINNPLAQADWAAK	4.76	2.13E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	HEAMITDLEER	4.78	2.15E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	TDLLLEPYNK	4.05	2.19E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	IAQLEEQLDNETK	4.09	2.22E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	EQADFAIEALAK	4.15	2.23E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	IRELETQISELQEDLESER	5.59	2.24E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	TQLEEELEDELQATEDAK	4.57	2.32E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	IIGLDQVAGMSETALPGAFK	5.00	2.32E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	C[+57]QYLQAEK	3.97	2.34E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	RKLEGDSTLSDQIAELQAQIAELK	5.17	2.41E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	KEEELQAALAR	3.81	2.45E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	ANLQIDQINTDLNLER	4.40	2.45E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	VAAYDKLEK	4.25	2.47E-03	0.0143	117

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q8VDD5	MYH9_MOUSE	LQVELDSVTGLLSQSDSK	4.40	2.49E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	NKHEAMITDLEER	4.26	2.59E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	GALALEEKR	4.65	2.64E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	HEDELLAK	4.09	2.67E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	HSQAVEELADQLEQTK	4.64	2.72E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	AGVLAHLEEEER	5.22	2.76E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	LDPHLVLDQLR	5.04	2.93E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	VEAQLQELQVK	3.79	3.01E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	MEDGVGC[+57]LETAAEK	4.89	3.09E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	LEGDSTDLSDQIAELQAQIAELK	6.21	3.09E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	ADEWLM[+16]K	5.02	3.11E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	SMEAEMIQLQEELAAAER	5.53	3.16E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	LTEMETM[+16]QSQLMAEK	4.78	3.17E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	KFDQLLAEEK	3.98	3.17E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	VAEFTTNLMEEEEK	4.98	3.24E-03	0.0143	117
Q8VDD5	MYH9_MOUSE	NAEQFKDQADK	4.74	3.44E-03	0.0144	117
Q8VDD5	MYH9_MOUSE	NLPIYSEEIVEMYK	5.25	3.51E-03	0.0144	117
Q8VDD5	MYH9_MOUSE	NTDQASM[+16]PDNTAAQK	4.38	3.56E-03	0.0145	117
Q8VDD5	MYH9_MOUSE	VSHLLGINVTDFTR	5.00	3.60E-03	0.0145	117
Q8VDD5	MYH9_MOUSE	VVFQEFR	3.80	3.66E-03	0.0146	117
Q8VDD5	MYH9_MOUSE	ADFC[+57]IIHYAGK	4.99	3.82E-03	0.0147	117
Q8VDD5	MYH9_MOUSE	KLWVVPSSK	3.52	3.85E-03	0.0147	117
Q8VDD5	MYH9_MOUSE	LQEMESAVK	4.43	3.93E-03	0.0147	117
Q8VDD5	MYH9_MOUSE	KLEEDQIIMEDQNC[+57]K	4.35	3.97E-03	0.0148	117
Q8VDD5	MYH9_MOUSE	DLQGRDEQSEEK	6.37	4.04E-03	0.0148	117
Q8VDD5	MYH9_MOUSE	DVLLQVEDER	2.71	4.05E-03	0.0148	117
Q8VDD5	MYH9_MOUSE	EMEALEDER	4.78	4.06E-03	0.0148	117
Q8VDD5	MYH9_MOUSE	ALEQQVEEMKTQLEELEDELQATEDAK	8.79	4.08E-03	0.0148	117
Q8VDD5	MYH9_MOUSE	LQQLFNHTM[+16]FILEQEEYQR	5.08	4.14E-03	0.0148	117
Q8VDD5	MYH9_MOUSE	KM[+16]EDGVGC[+57]LETAAEAKR	4.81	4.16E-03	0.0149	117
Q8VDD5	MYH9_MOUSE	ELEDATETADAMNR	3.85	4.20E-03	0.0149	117
Q8VDD5	MYH9_MOUSE	KMQQNIQELEEQLLEEEESAR	4.40	4.34E-03	0.0150	117
Q8VDD5	MYH9_MOUSE	RGDLPFVTR	4.10	4.90E-03	0.0155	117
Q8VDD5	MYH9_MOUSE	THEAQIQEMR	5.12	4.93E-03	0.0155	117
Q8VDD5	MYH9_MOUSE	ALEEAMEQK	3.63	5.32E-03	0.0158	117
Q8VDD5	MYH9_MOUSE	EQLEEEEEAQR	4.35	5.44E-03	0.0158	117
Q8VDD5	MYH9_MOUSE	NGFEPASLKEEVGEEAIVLVENGK	5.35	5.97E-03	0.0164	117
Q8VDD5	MYH9_MOUSE	VEEEEEER	4.66	6.73E-03	0.0172	117
Q8VDD5	MYH9_MOUSE	QAC[+57]VLMIK	4.39	6.76E-03	0.0172	117
Q8VDD5	MYH9_MOUSE	LEEDQIIMEDQNC[+57]K	4.46	6.80E-03	0.0172	117
Q8VDD5	MYH9_MOUSE	GTGDC[+57]SDEEVDGKADGADAK	4.86	6.89E-03	0.0174	117
Q8VDD5	MYH9_MOUSE	NTDQASMPDNTAAQK	2.66	7.05E-03	0.0175	117
Q8VDD5	MYH9_MOUSE	LTEMETMQSQLM[+16]AEK	4.51	7.08E-03	0.0175	117
Q8VDD5	MYH9_MOUSE	SMEAEM[+16]QLQEELAAAER	4.34	7.11E-03	0.0176	117
Q8VDD5	MYH9_MOUSE	YLVDKNFINNPLAQADWAAK	5.46	7.14E-03	0.0176	117
Q8VDD5	MYH9_MOUSE	TFHIFYLLSGAGEHLK	6.14	7.42E-03	0.0179	117
Q8VDD5	MYH9_MOUSE	SMM[+16]QDREDQSILC[+57]TGESGAGK	6.30	7.63E-03	0.0181	117
Q8VDD5	MYH9_MOUSE	RQLEEAEEEEAQR	7.02	7.97E-03	0.0183	117
Q8VDD5	MYH9_MOUSE	SMMQDREDQSILC[+57]TGESGAGK	4.96	9.25E-03	0.0198	117
Q8VDD5	MYH9_MOUSE	LQQLFNHTMFILEQEEYQR	7.25	9.95E-03	0.0206	117
Q8VDD5	MYH9_MOUSE	SM[+16]EAEM[+16]IQLQEELAAAER	1.46	1.00E-02	0.0206	117
Q8VDD5	MYH9_MOUSE	KLEGDSTDLSDQIAELQAQIAELK	6.04	1.24E-02	0.0231	117
Q8VDD5	MYH9_MOUSE	ADEWLMK	4.67	1.62E-02	0.0273	117
Q8VDD5	MYH9_MOUSE	ALEQQVEEMK	1.82	1.68E-02	0.0279	117
Q7TQI3	OTUB1_MOUSE	AFGFHLEALLDDSKELQR	2.46	1.92E-02	0.0306	117
P67984	RL22_MOUSE	εAGNLGGGVVTIER	3.01	2.02E-02	0.0318	117
P62754	RS6_MOUSE	4(GC[+57]IVDANLSVLNLVIVK	2.30	2.02E-02	0.0318	117
Q9Z1B3	PLCB1_MOUSE	LNEILYPPLKQEQQVQLIEK	5.47	2.27E-02	0.0347	117
Q91ZU6	DYST_MOUSE	IVGGGWMALDEFLVK	4.14	2.37E-02	0.0358	117
O08709	PRDX6_MOUSE	DINAYNGETPTEK	5.54	2.95E-02	0.0420	117
Q99104	MYO5A_MOUSE	M[+16]LPELFQDDEK	4.11	1.34E-03	0.0143	98
Q99104	MYO5A_MOUSE	GEIQLSKEENNR	4.22	1.54E-03	0.0143	98

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q99104	MYO5A_MOUSE	TDDDAEAIC[+57]SM[+16]C[+57]NALTTAQIVk	5.62	1.76E-03	0.0143	98
Q99104	MYO5A_MOUSE	QYSGEEGFM[+16]K	4.96	1.83E-03	0.0143	98
Q99104	MYO5A_MOUSE	LGILDLLDEEC[+57]KM[+16]PK	4.79	1.98E-03	0.0143	98
Q99104	MYO5A_MOUSE	TSSIADEGTYTLDSILF	4.73	2.22E-03	0.0143	98
Q99104	MYO5A_MOUSE	AAITVQR	4.69	2.30E-03	0.0143	98
Q99104	MYO5A_MOUSE	VPLDMSLFLK	5.52	2.30E-03	0.0143	98
Q99104	MYO5A_MOUSE	ETLEPLIQAAQLLQVK	4.77	2.46E-03	0.0143	98
Q99104	MYO5A_MOUSE	QGGSPM[+16]IEGVDDAK	3.94	2.61E-03	0.0143	98
Q99104	MYO5A_MOUSE	NTM[+16]TDSTILLEDVQK	2.56	2.64E-03	0.0143	98
Q99104	MYO5A_MOUSE	LLESQLQSQK	4.27	2.76E-03	0.0143	98
Q99104	MYO5A_MOUSE	QAC[+57]TLLGISESYQM[+16]GIFR	5.87	2.78E-03	0.0143	98
Q99104	MYO5A_MOUSE	EQIPWTLIDFYDNQPC[+57]INLIESK	8.73	2.82E-03	0.0143	98
Q99104	MYO5A_MOUSE	AISPTSATSSGR	4.63	2.86E-03	0.0143	98
Q99104	MYO5A_MOUSE	QGGSPMIEGVDDAK	2.99	2.88E-03	0.0143	98
Q99104	MYO5A_MOUSE	DDKNTM[+16]TDSTILLEDVQK	4.01	2.97E-03	0.0143	98
Q99104	MYO5A_MOUSE	KLATATETYIKPISK	4.47	3.06E-03	0.0143	98
Q99104	MYO5A_MOUSE	SHENEAEALR	3.90	3.08E-03	0.0143	98
Q99104	MYO5A_MOUSE	FPPTFDEK	5.01	3.51E-03	0.0144	98
Q99104	MYO5A_MOUSE	YNVSQLLEEWLR	5.55	3.52E-03	0.0144	98
Q99104	MYO5A_MOUSE	NQSIIVSGESGAGK	4.46	3.78E-03	0.0147	98
Q99104	MYO5A_MOUSE	NKDTVFEQIK	4.46	3.79E-03	0.0147	98
Q99104	MYO5A_MOUSE	SAPEVTAPGAPAYR	4.89	3.84E-03	0.0147	98
Q99104	MYO5A_MOUSE	IGELEVQGM[+16]ENISPGQIIDEPIRPVNIPR	6.21	3.90E-03	0.0147	98
Q99104	MYO5A_MOUSE	DFQGMLEYK	1.05	3.94E-03	0.0147	98
Q99104	MYO5A_MOUSE	TDSTHSSNESEYTFSSFEAETEDIAPF	5.71	4.07E-03	0.0148	98
Q99104	MYO5A_MOUSE	VWIPDPEEVWK	4.48	4.08E-03	0.0148	98
Q99104	MYO5A_MOUSE	ISAAGFPSR	4.33	4.13E-03	0.0148	98
Q99104	MYO5A_MOUSE	IEASLQHEITR	4.80	4.26E-03	0.0150	98
Q99104	MYO5A_MOUSE	GTDDTWAQK	3.88	4.55E-03	0.0152	98
Q99104	MYO5A_MOUSE	AGQVAYLEK	4.57	4.72E-03	0.0153	98
Q99104	MYO5A_MOUSE	DSPQLLMDAK	3.54	4.79E-03	0.0154	98
Q99104	MYO5A_MOUSE	IGELEVQGMENISPGQIIDEPIRPVNIPR	6.72	4.96E-03	0.0155	98
Q99104	MYO5A_MOUSE	KEEVILIR	4.48	5.05E-03	0.0155	98
Q99104	MYO5A_MOUSE	HADYLNDDQK	5.04	5.12E-03	0.0155	98
Q99104	MYO5A_MOUSE	SLLTSTINSIKK	5.86	5.33E-03	0.0158	98
Q99104	MYO5A_MOUSE	YQNLLNEFSR	4.81	5.35E-03	0.0158	98
Q99104	MYO5A_MOUSE	LGILDLLDEEC[+57]KMPK	5.93	5.40E-03	0.0158	98
Q99104	MYO5A_MOUSE	LILDKDKYQFGK	3.06	5.43E-03	0.0158	98
Q99104	MYO5A_MOUSE	GVAVNLIPGLPAYILFM[+16]C[+57]VR	8.96	5.46E-03	0.0158	98
Q99104	MYO5A_MOUSE	QAC[+57]TLLGISESYQMGIFR	4.07	5.48E-03	0.0159	98
Q99104	MYO5A_MOUSE	LATATETYIKPISK	6.88	5.62E-03	0.0160	98
Q99104	MYO5A_MOUSE	GAELEYESLK	2.76	5.69E-03	0.0161	98
Q99104	MYO5A_MOUSE	TDDDAEAIC[+57]SMC[+57]NALTTAQIVk	5.71	5.86E-03	0.0163	98
Q99104	MYO5A_MOUSE	VVFQAEER	3.50	5.88E-03	0.0163	98
Q99104	MYO5A_MOUSE	EM[+16]TETM[+16]ER	4.27	5.94E-03	0.0163	98
Q99104	MYO5A_MOUSE	YFATVSGSASEANVEEK	5.23	5.98E-03	0.0164	98
Q99104	MYO5A_MOUSE	GEIAQAYIGLK	4.56	6.40E-03	0.0169	98
Q99104	MYO5A_MOUSE	AC[+57]GVLETIR	3.43	6.41E-03	0.0169	98
Q99104	MYO5A_MOUSE	SLLTSTINSIK	4.94	6.46E-03	0.0170	98
Q99104	MYO5A_MOUSE	VLSLQEEIAK	4.23	6.73E-03	0.0172	98
Q99104	MYO5A_MOUSE	QETDQLVSNLKEENTLLK	4.84	7.06E-03	0.0175	98
Q99104	MYO5A_MOUSE	VEYQC[+57]EGFLEK	5.00	7.11E-03	0.0176	98
Q99104	MYO5A_MOUSE	QLELDLNDER	2.72	7.26E-03	0.0177	98
Q99104	MYO5A_MOUSE	LTNLEGVYNSETEK	4.33	7.61E-03	0.0181	98
Q99104	MYO5A_MOUSE	KVPLDM[+16]SLFLK	2.90	8.04E-03	0.0184	98
Q99104	MYO5A_MOUSE	RGDDFETVSFWLSNTC[+57]R	7.16	8.21E-03	0.0186	98
Q99104	MYO5A_MOUSE	AIVYLQC[+57]C[+57]FR	4.59	8.32E-03	0.0187	98
Q99104	MYO5A_MOUSE	MLPELFQDDEK	4.68	8.34E-03	0.0188	98
Q99104	MYO5A_MOUSE	VLNLYTPVNEFEER	5.45	8.38E-03	0.0188	98
Q99104	MYO5A_MOUSE	DKGEIAQAYIGLK	3.87	8.39E-03	0.0188	98
Q99104	MYO5A_MOUSE	YIEIGFDK	5.55	8.48E-03	0.0189	98
Q99104	MYO5A_MOUSE	LLESQLQSQKR	3.05	8.56E-03	0.0190	98

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q99104	MYO5A_MOUSE	VLM[+16]EQLTSVSEELDVR	4.14	8.86E-03	0.0193	98
Q99104	MYO5A_MOUSE	VLMEQLTSVSEELDVRK	4.87	9.20E-03	0.0198	98
Q99104	MYO5A_MOUSE	QLMQDELDR	4.02	9.21E-03	0.0198	98
Q99104	MYO5A_MOUSE	VSVSFIR	4.59	9.27E-03	0.0199	98
Q99104	MYO5A_MOUSE	ILAGILHLGNVGFASR	6.04	9.71E-03	0.0204	98
Q99104	MYO5A_MOUSE	VLASNPIMESIGNAK	4.24	9.81E-03	0.0204	98
Q99104	MYO5A_MOUSE	VLASNPIM[+16]ESIGNAK	2.45	1.00E-02	0.0206	98
Q99104	MYO5A_MOUSE	QVLSDLAIQIYQQLVR	8.86	1.04E-02	0.0211	98
Q99104	MYO5A_MOUSE	EMTETMER	5.92	1.05E-02	0.0212	98
Q99104	MYO5A_MOUSE	HFADKVEYQC[+57]EGFLEK	5.73	1.06E-02	0.0213	98
Q99104	MYO5A_MOUSE	DDKNTMTDSTILLEDVQK	4.77	1.08E-02	0.0215	98
Q99104	MYO5A_MOUSE	LGNADSFHYTK	5.16	1.11E-02	0.0219	98
Q99104	MYO5A_MOUSE	LQQQFNMHVFK	5.35	1.12E-02	0.0219	98
Q99104	MYO5A_MOUSE	LEQEEYMK	1.87	1.15E-02	0.0223	98
Q99104	MYO5A_MOUSE	GAELEYESLKR	4.21	1.18E-02	0.0226	98
Q99104	MYO5A_MOUSE	LGILDLLDEEC[+57]K	4.90	1.23E-02	0.0231	98
Q99104	MYO5A_MOUSE	VLLHLHEEGKDLEYR	4.58	1.24E-02	0.0231	98
Q99104	MYO5A_MOUSE	YKQETDQLVSNLKEENTLLK	6.05	1.25E-02	0.0232	98
Q99104	MYO5A_MOUSE	AATIVIQSYLR	5.42	1.30E-02	0.0238	98
Q99104	MYO5A_MOUSE	KVPLDMSLFLK	5.37	1.43E-02	0.0253	98
Q99104	MYO5A_MOUSE	QNEHC[+57]LTNFDLAEYR	4.87	1.47E-02	0.0257	98
Q99104	MYO5A_MOUSE	NYHIFYQLC[+57]ASAK	5.83	1.57E-02	0.0268	98
P43277	H13_MOUSE	Hi SGVSLAALK	6.09	1.72E-02	0.0284	98
Q04447	KCRB_MOUSE	LGFEVELVQM[+16]VVDGVK	4.01	1.72E-02	0.0284	98
P61294	RAB6B_MOUSE	QITIEEGEQR	3.66	1.78E-02	0.0290	98
P14873	MAP1B_MOUSE	SIEEAC[+57]FTLQYLNK	8.18	1.82E-02	0.0295	98
P01869	IGH1M_MOUSE	VNSAAFPAPIEK	7.75	1.82E-02	0.0295	98
Q61937	NPM_MOUSE	NMTDQEAIQDLWQWR	4.19	1.89E-02	0.0302	98
O08539	BIN1_MOUSE	NVGFYVNTFQSIAGLEENFHK	3.80	2.19E-02	0.0338	98
Q7TPR4	ACTN1_MOUSE	GISQEQMNEFR	4.32	2.43E-02	0.0364	98
A0A0N5DKY8	A0A0N5DKY8_TRI	AFMTADLPNELIEILEK	4.01	2.50E-02	0.0371	98
Q9Z0E0	NCDN_MOUSE	NDSEQFAALLLVTK	3.35	2.78E-02	0.0402	98
P52480	KPYM_MOUSE	AGKPVIC[+57]ATQMLESNIK	6.47	2.92E-02	0.0417	98
Q99M74	KRT82_MOUSE	LAGLEEALQK	3.52	3.02E-02	0.0428	98
Q9JMH9	MY18A_MOUSE	LQQELEDKM[+16]EVEQQSR	3.85	5.45E-04	0.0143	63
Q9JMH9	MY18A_MOUSE	WQALSTLLEAFGNSPTIM[+16]NGSATR	6.59	1.18E-03	0.0143	63
Q9JMH9	MY18A_MOUSE	DLALGLVPGDR	2.87	1.87E-03	0.0143	63
Q9JMH9	MY18A_MOUSE	RFDSELSQAHEETQR	5.54	2.05E-03	0.0143	63
Q9JMH9	MY18A_MOUSE	LQALQSQVEFLEQSMVDK	5.30	2.48E-03	0.0143	63
Q9JMH9	MY18A_MOUSE	LQALQSQVEFLEQSM[+16]VDK	4.26	2.51E-03	0.0143	63
Q9JMH9	MY18A_MOUSE	AVEELLESLEK	4.51	2.79E-03	0.0143	63
Q9JMH9	MY18A_MOUSE	NQLEESEFTC[+57]AAAVK	4.76	3.29E-03	0.0143	63
Q9JMH9	MY18A_MOUSE	VVSLEAELQDISSQESKDEASLAK	5.36	3.45E-03	0.0144	63
Q9JMH9	MY18A_MOUSE	LQQELEDKMEVEQQSR	5.54	3.60E-03	0.0145	63
Q9JMH9	MY18A_MOUSE	NTGESASQLLDAETAER	5.59	3.83E-03	0.0147	63
Q9JMH9	MY18A_MOUSE	SEELSLPEGK	3.97	3.89E-03	0.0147	63
Q9JMH9	MY18A_MOUSE	DEEVEEAR	5.45	3.93E-03	0.0147	63
Q9JMH9	MY18A_MOUSE	LVEINGQNVENK	3.93	4.27E-03	0.0150	63
Q9JMH9	MY18A_MOUSE	LHLEGQQVR	6.08	4.29E-03	0.0150	63
Q9JMH9	MY18A_MOUSE	MSAAELR	4.37	4.39E-03	0.0150	63
Q9JMH9	MY18A_MOUSE	TFLQELER	4.46	4.77E-03	0.0154	63
Q9JMH9	MY18A_MOUSE	GFFNLNR	4.90	4.86E-03	0.0155	63
Q9JMH9	MY18A_MOUSE	ALLADAQIMLDHLK	5.80	4.89E-03	0.0155	63
Q9JMH9	MY18A_MOUSE	LTAELQDTK	4.11	5.37E-03	0.0158	63
Q9JMH9	MY18A_MOUSE	ALLADAQIM[+16]LDHLK	2.74	5.41E-03	0.0158	63
Q9JMH9	MY18A_MOUSE	LEISNPIPIK	4.96	5.42E-03	0.0158	63
Q9JMH9	MY18A_MOUSE	LGDLQADSDESQR	5.43	5.63E-03	0.0160	63
Q9JMH9	MY18A_MOUSE	QDQSIVLLGSSGSGK	5.18	5.76E-03	0.0161	63
Q9JMH9	MY18A_MOUSE	QNPATQNAPR	5.44	5.77E-03	0.0162	63
Q9JMH9	MY18A_MOUSE	AAEINGEVDDDDAGGEWR	4.90	5.84E-03	0.0163	63
Q9JMH9	MY18A_MOUSE	RFDVLAPHLTK	4.50	5.96E-03	0.0163	63
Q9JMH9	MY18A_MOUSE	NKDEEIQQLR	5.61	5.98E-03	0.0164	63

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9JMH9	MY18A_MOUSE	RPTGDFGFSLR	5.79	5.99E-03	0.0164	63
Q9JMH9	MY18A_MOUSE	DGFSLASQLK	4.74	5.99E-03	0.0164	63
Q9JMH9	MY18A_MOUSE	VVSLEAELQDISSQESK	3.23	6.12E-03	0.0166	63
Q9JMH9	MY18A_MOUSE	IISNLFGLR	5.81	6.32E-03	0.0169	63
Q9JMH9	MY18A_MOUSE	LEDLASLVYLNESVLTSLR	6.83	6.60E-03	0.0171	63
Q9JMH9	MY18A_MOUSE	QGPEESGLGEGTK	4.76	6.66E-03	0.0172	63
Q9JMH9	MY18A_MOUSE	SSC[+57]C[+57]LGLSR	3.68	6.79E-03	0.0172	63
Q9JMH9	MY18A_MOUSE	LPALVPPPPPALR	5.79	6.89E-03	0.0174	63
Q9JMH9	MY18A_MOUSE	DTKEEMSELAR	4.90	7.17E-03	0.0177	63
Q9JMH9	MY18A_MOUSE	EKDM[+16]LLAEAFSLK	5.03	7.79E-03	0.0182	63
Q9JMH9	MY18A_MOUSE	YGASLLHTYAGPSLLVLSTR	5.99	9.11E-03	0.0197	63
Q9JMH9	MY18A_MOUSE	VLAISPEEQK	4.42	9.24E-03	0.0198	63
Q9JMH9	MY18A_MOUSE	LQVDALIDTIK	6.27	1.15E-02	0.0223	63
Q9JMH9	MY18A_MOUSE	VSSSELDLPPGDPC[+57]EAGLLQLDVSLLR	7.54	1.24E-02	0.0231	63
Q9JMH9	MY18A_MOUSE	GSILDSGHLSTASSDDLKGEESFR	7.15	1.27E-02	0.0234	63
Q9JMH9	MY18A_MOUSE	VWLVHR	2.48	1.28E-02	0.0235	63
Q9JMH9	MY18A_MOUSE	VKDQEEELDEQAGSIQMLEQAK	4.25	1.30E-02	0.0238	63
Q9JMH9	MY18A_MOUSE	QMEVQLEEEYEDKQK	4.68	1.31E-02	0.0239	63
Q9JMH9	MY18A_MOUSE	EKDMLLAEAFSLK	6.19	1.31E-02	0.0239	63
Q9JMH9	MY18A_MOUSE	LQVDALIDTIKR	6.06	1.32E-02	0.0240	63
Q9JMH9	MY18A_MOUSE	FSHSYLSDSSTEAK	4.85	1.35E-02	0.0243	63
Q9JMH9	MY18A_MOUSE	VKLDHGDGAILDVDEDDIEK	5.72	1.38E-02	0.0247	63
Q9JMH9	MY18A_MOUSE	DLDIAGFTQK	2.35	1.49E-02	0.0259	63
Q9JMH9	MY18A_MOUSE	LFTTVRPLIQVQLSEEQIR	7.13	1.52E-02	0.0263	63
Q9JMH9	MY18A_MOUSE	AAYLLGC[+57]SLEELSSAIFK	8.02	1.54E-02	0.0265	63
Q9JMH9	MY18A_MOUSE	AGSATVLSGSIAGLEGGSQLALR	7.09	1.63E-02	0.0274	63
Q9JMH9	MY18A_MOUSE	RAVEELLESLDLEK	2.19	1.68E-02	0.0279	63
P17426	AP2A1_MOUSE	VAAQVDGGAQVQQLNIEC[+57]LR	8.26	1.76E-02	0.0288	63
P16546	SPTN1_MOUSE	DLTSWVTEMK	5.88	2.05E-02	0.0322	63
Q7TMM9	TBB2A_MOUSE	RISEQFTAMFR	4.29	2.22E-02	0.0342	63
P50518	VATE1_MOUSE	VSNTLESR	5.83	2.71E-02	0.0394	63
P05202	AATM_MOUSE	NLDKEYLPIGGLAEFC[+57]K	6.77	2.72E-02	0.0395	63
Q6IME9	K2C72_MOUSE	TAAENEFVVLK	3.25	2.85E-02	0.0409	63
P51863	VA0D1_MOUSE	NIVWIAEC[+57]IAQR	4.23	3.22E-02	0.0451	63
P63038	CH60_MOUSE	ISSVQSIVPALEIANAHR	2.46	3.22E-02	0.0451	63
Q6URW6	MYH14_MOUSE	RQEEEEAAVLEAGEEAR	4.03	3.24E-05	0.0143	61
Q6URW6	MYH14_MOUSE	AAEQAAASDLR	3.80	3.45E-04	0.0143	61
Q6URW6	MYH14_MOUSE	VLGLLPEEITAM[+16]LR	4.57	3.46E-04	0.0143	61
Q6URW6	MYH14_MOUSE	RLESQLQEVQGR	4.68	6.10E-04	0.0143	61
Q6URW6	MYH14_MOUSE	AEELLAQLGR	3.40	9.44E-04	0.0143	61
Q6URW6	MYH14_MOUSE	AEAELC[+57]SEAEETR	4.83	1.12E-03	0.0143	61
Q6URW6	MYH14_MOUSE	LAQAEELQEQESR	2.63	1.13E-03	0.0143	61
Q6URW6	MYH14_MOUSE	ELQSTQAQLSEWR	2.00	1.32E-03	0.0143	61
Q6URW6	MYH14_MOUSE	AELSSLQTSR	3.47	1.37E-03	0.0143	61
Q6URW6	MYH14_MOUSE	FLTNGPSSSPGQER	5.15	1.40E-03	0.0143	61
Q6URW6	MYH14_MOUSE	AELEALLSSK	4.61	1.49E-03	0.0143	61
Q6URW6	MYH14_MOUSE	QLEEAEEEEASR	5.99	1.62E-03	0.0143	61
Q6URW6	MYH14_MOUSE	VLGLLPEEITAMLR	7.32	1.68E-03	0.0143	61
Q6URW6	MYH14_MOUSE	LSQLEEEELQEQNSSELLK	5.99	1.70E-03	0.0143	61
Q6URW6	MYH14_MOUSE	LQQELDDATVDLGGQK	6.85	1.72E-03	0.0143	61
Q6URW6	MYH14_MOUSE	TPNVGGPGGPQVEWTAR	5.68	1.75E-03	0.0143	61
Q6URW6	MYH14_MOUSE	VGEEEEEC[+57]SR	6.14	1.79E-03	0.0143	61
Q6URW6	MYH14_MOUSE	LSLEAEVSELKAELSSLQTSR	5.73	1.86E-03	0.0143	61
Q6URW6	MYH14_MOUSE	GLEAEVLR	4.35	1.89E-03	0.0143	61
Q6URW6	MYH14_MOUSE	ELEDVTESAESMNR	5.55	1.98E-03	0.0143	61
Q6URW6	MYH14_MOUSE	TVSAVLQFGNIVLK	5.45	2.05E-03	0.0143	61
Q6URW6	MYH14_MOUSE	ELSSAESQLHDTQELLQEETR	4.83	2.11E-03	0.0143	61
Q6URW6	MYH14_MOUSE	TQVTELEDELTAEDAK	4.75	2.21E-03	0.0143	61
Q6URW6	MYH14_MOUSE	EQADFALEALAK	4.15	2.23E-03	0.0143	61
Q6URW6	MYH14_MOUSE	ILFQEFR	5.50	2.29E-03	0.0143	61
Q6URW6	MYH14_MOUSE	GELEDTLDDSTNAQQELR	2.19	2.49E-03	0.0143	61
Q6URW6	MYH14_MOUSE	MIQALELDPNLYR	4.61	2.54E-03	0.0143	61

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q6URW6	MYH14_MOUSE	LGEEDAGAR	4.05	2.54E-03	0.0143	61
Q6URW6	MYH14_MOUSE	LLGLGVTDFSR	4.64	2.80E-03	0.0143	61
Q6URW6	MYH14_MOUSE	LVLQVESLTTELSAER	4.87	2.81E-03	0.0143	61
Q6URW6	MYH14_MOUSE	RLQQELDDATVDLGQQK	4.22	2.83E-03	0.0143	61
Q6URW6	MYH14_MOUSE	LM[+16]ATLSNTNPSFVR	2.26	2.92E-03	0.0143	61
Q6URW6	MYH14_MOUSE	DEC[+57]SFHIFYQLLGAGEQLK	5.83	2.98E-03	0.0143	61
Q6URW6	MYH14_MOUSE	LSLEAEVSELK	4.49	3.09E-03	0.0143	61
Q6URW6	MYH14_MOUSE	LQQHIQELESHLEAEEGAR	5.23	3.15E-03	0.0143	61
Q6URW6	MYH14_MOUSE	KFEEDLLLLLEDQNSK	5.12	3.16E-03	0.0143	61
Q6URW6	MYH14_MOUSE	ALEAEAAGLR	4.55	3.18E-03	0.0143	61
Q6URW6	MYH14_MOUSE	KEDELQAALLR	5.05	3.32E-03	0.0143	61
Q6URW6	MYH14_MOUSE	VIQYLAHVASSPK	5.90	3.49E-03	0.0144	61
Q6URW6	MYH14_MOUSE	VASRPGVPPEAAQSFLYAPR	6.46	3.76E-03	0.0147	61
Q6URW6	MYH14_MOUSE	KQELELVVTELEAR	4.97	4.18E-03	0.0149	61
Q6URW6	MYH14_MOUSE	QAQQDRDEMAEEVASGNLSK	5.01	4.19E-03	0.0149	61
Q6URW6	MYH14_MOUSE	AQAELESVSTALSEAESK	2.67	4.51E-03	0.0152	61
Q6URW6	MYH14_MOUSE	ALEAEAAGLREQMEEVVAR	3.63	4.83E-03	0.0154	61
Q6URW6	MYH14_MOUSE	VAQLEEEER	3.54	5.56E-03	0.0159	61
Q6URW6	MYH14_MOUSE	DVEGIVGLEQVSSLGDGPPGGRPR	5.76	5.70E-03	0.0161	61
Q6URW6	MYH14_MOUSE	QRAEELLAQLGR	3.80	5.80E-03	0.0162	61
Q6URW6	MYH14_MOUSE	LMATLSNTNPSFVR	5.63	5.84E-03	0.0163	61
Q6URW6	MYH14_MOUSE	EQMEEVVAR	2.71	5.95E-03	0.0163	61
Q6URW6	MYH14_MOUSE	VTDIIVSFQAAAR	5.08	6.25E-03	0.0168	61
Q6URW6	MYH14_MOUSE	LQQLFNHTMFVLEQEEYQR	5.06	7.05E-03	0.0175	61
Q6URW6	MYH14_MOUSE	EAQAGLAEAQEDLEAER	3.49	7.13E-03	0.0176	61
Q6URW6	MYH14_MOUSE	LRLEVTVQALK	7.28	7.95E-03	0.0183	61
Q6URW6	MYH14_MOUSE	LKYEATISDMEDR	4.86	8.46E-03	0.0189	61
Q6URW6	MYH14_MOUSE	RRQEEEEAAVLEAGEEAR	3.30	1.27E-02	0.0234	61
Q6URW6	MYH14_MOUSE	VAQEQQSHPK	3.34	1.46E-02	0.0256	61
P12382	PFKAL_MOUSE	LNIIIIAEGAIDR	1.45	1.87E-02	0.0300	61
P62259	1433E_MOUSE	HLIPAANTGESK	2.74	2.46E-02	0.0367	61
Q9CQE8	RTRAF_MOUSE	INEAIVAVQAIADPK	8.15	2.49E-02	0.0370	61
Q99104	MYO5A_MOUSE	IMQLQR	6.92	2.92E-02	0.0417	61
Q8R1B4	EIF3C_MOUSE	VWDLFPEADKVR	4.68	3.47E-02	0.0481	61
P16546	SPTN1_MOUSE	VNDVC[+57]TNGQDLIK	2.81	4.53E-04	0.0143	61
P16546	SPTN1_MOUSE	DVTGAEALLER	2.96	1.24E-03	0.0143	61
P16546	SPTN1_MOUSE	MTLVASEDYGDTLAAIQGLLK	4.28	1.34E-03	0.0143	61
P16546	SPTN1_MOUSE	DLASVNNLLK	2.70	1.35E-03	0.0143	61
P16546	SPTN1_MOUSE	NQALNTDNYGHDLASVQALQR	3.08	1.62E-03	0.0143	61
P16546	SPTN1_MOUSE	KIEDLGAAMEEALILDNK	3.65	1.71E-03	0.0143	61
P16546	SPTN1_MOUSE	IAALQAFADQLIAVDHYAK	4.68	1.75E-03	0.0143	61
P16546	SPTN1_MOUSE	DVEDEETWIR	3.43	1.81E-03	0.0143	61
P16546	SPTN1_MOUSE	EAVTSEELGQDLEHVEVLQK	2.58	2.22E-03	0.0143	61
P16546	SPTN1_MOUSE	TKQDEVNAAWQR	2.80	2.92E-03	0.0143	61
P16546	SPTN1_MOUSE	QVEELYQSLELGEK	4.43	3.14E-03	0.0143	61
P16546	SPTN1_MOUSE	LLVSSDYGR	2.06	3.45E-03	0.0144	61
P16546	SPTN1_MOUSE	DLAALGDKVNSLGETAQR	2.02	3.56E-03	0.0145	61
P16546	SPTN1_MOUSE	LSDDNTIGQEEIQQR	2.89	3.83E-03	0.0147	61
P16546	SPTN1_MOUSE	DLTNVQNLQK	2.00	4.06E-03	0.0148	61
P16546	SPTN1_MOUSE	DLIGVQNLLK	2.66	4.53E-03	0.0152	61
P16546	SPTN1_MOUSE	LIQSHPESAEDLKEK	2.35	4.91E-03	0.0155	61
P16546	SPTN1_MOUSE	RQEENDKLR	3.01	4.93E-03	0.0155	61
P16546	SPTN1_MOUSE	HQAFEAEALSANQSR	3.09	5.03E-03	0.0155	61
P16546	SPTN1_MOUSE	VNEVSQFAAK	2.37	5.40E-03	0.0158	61
P16546	SPTN1_MOUSE	DLASVQALLR	2.51	5.50E-03	0.0159	61
P16546	SPTN1_MOUSE	EAFLNTEKDGSLDSVEALIK	3.47	5.51E-03	0.0159	61
P16546	SPTN1_MOUSE	LGESQTLQQFSR	2.73	5.54E-03	0.0159	61
P16546	SPTN1_MOUSE	SQLLGSAHEVQR	2.36	5.55E-03	0.0159	61
P16546	SPTN1_MOUSE	HQAFEAEELHANADR	3.82	5.61E-03	0.0160	61
P16546	SPTN1_MOUSE	VLETAEDIQER	2.44	5.74E-03	0.0161	61
P16546	SPTN1_MOUSE	ASAFNSWFENAEEDLTDPVR	6.47	5.94E-03	0.0163	61
P16546	SPTN1_MOUSE	SLGYDLPM[+16]VEEGEPDPEFEAILDTPVNR	6.92	6.48E-03	0.0170	61

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P16546	SPTN1_MOUSE	DLSSVQTLTLLTK	3.15	6.85E-03	0.0173	61
P16546	SPTN1_MOUSE	LAALADQWQFLVQK	3.87	6.90E-03	0.0174	61
P16546	SPTN1_MOUSE	QETFDAGLQAFQQEGIANITALKDQLLAAK	8.04	7.12E-03	0.0176	61
P16546	SPTN1_MOUSE	GLVSSDELAK	2.33	7.21E-03	0.0177	61
P16546	SPTN1_MOUSE	EANQQQQFNR	3.36	7.53E-03	0.0180	61
P16546	SPTN1_MOUSE	LDENSAFLQFNWK	4.05	7.55E-03	0.0180	61
P16546	SPTN1_MOUSE	VNSLGETAQR	2.66	7.67E-03	0.0181	61
P16546	SPTN1_MOUSE	HQLLEADISAHEDR	3.39	7.78E-03	0.0182	61
P16546	SPTN1_MOUSE	HQAFEAEVQANSQAIVK	2.60	7.96E-03	0.0183	61
P16546	SPTN1_MOUSE	YTEHSTVGLAQQWQDQLDQLGMR	4.32	8.66E-03	0.0191	61
P16546	SPTN1_MOUSE	TALLELWELR	4.72	8.92E-03	0.0194	61
P16546	SPTN1_MOUSE	LFGAAEVQR	2.45	9.01E-03	0.0196	61
P16546	SPTN1_MOUSE	ADVVESWIGEK	2.13	9.48E-03	0.0202	61
P16546	SPTN1_MOUSE	QEAFLLNEDLGDSLDSVEALLK	8.52	1.01E-02	0.0207	61
P16546	SPTN1_MOUSE	SADESGQALLAASHYASDEVK	3.12	1.03E-02	0.0209	61
P16546	SPTN1_MOUSE	DLMSWINGIR	5.99	1.22E-02	0.0230	61
P16546	SPTN1_MOUSE	QETFDAGLQAFQQEGIANITALK	5.06	1.25E-02	0.0232	61
P16546	SPTN1_MOUSE	LEESLEYQQFVANVEEEEEAWINEK	5.50	1.26E-02	0.0233	61
P16546	SPTN1_MOUSE	IDGITIQAR	2.18	1.31E-02	0.0239	61
P16546	SPTN1_MOUSE	WTQLLANSATR	2.73	1.35E-02	0.0243	61
P16546	SPTN1_MOUSE	TYLLDGSC[+57]MVEESGTLESQLEATK	3.15	1.48E-02	0.0258	61
P16546	SPTN1_MOUSE	LM[+16]VHTVATFNSIK	3.09	1.60E-02	0.0271	61
P16546	SPTN1_MOUSE	EKEPIVGSTDYGKDEDSAEALLK	3.92	1.61E-02	0.0272	61
P16546	SPTN1_MOUSE	GKDLIGVQNLLK	3.43	1.62E-02	0.0273	61
P62751	RL23A_MOUSE	LAPDYDALDVANK	3.19	1.79E-02	0.0292	61
P51410	RL9_MOUSE	6C DELILEGNDIELVSNAAALIQATTVK	3.70	1.80E-02	0.0293	61
Q8BH44	COR2B_MOUSE	SVVNVNGIDLLENVPPR	3.20	1.85E-02	0.0298	61
Q99KI0	ACON_MOUSE	QGLLPLTFADPSDYNK	3.07	1.88E-02	0.0301	61
P61205	ARF3_MOUSE	/MLAEDELK	7.44	1.94E-02	0.0308	61
P63318	KPCG_MOUSE	NDFMGAMSFVGSSELLK	3.15	2.04E-02	0.0321	61
Q60875	ARHG2_MOUSE	M[+16]QDIPEETESR	3.24	2.12E-02	0.0330	61
Q99104	MYO5A_MOUSE	VLMEQLTSVSEELDVR	1.79	2.50E-02	0.0371	61
Q9WUM4	COR1C_MOUSE	VGIVAWHPTAR	4.06	2.64E-02	0.0387	61
Q68FD5	CLH1_MOUSE	(ADDPSSYM[+16]EVVQAANASGNWEELVK	2.05	5.21E-04	0.0143	49
Q68FD5	CLH1_MOUSE	(AFM[+16]TADLPNELIELLEK	4.22	5.52E-04	0.0143	49
Q68FD5	CLH1_MOUSE	(VDKLDASESLR	1.50	5.96E-04	0.0143	49
Q68FD5	CLH1_MOUSE	(NLQNLLILTAIK	2.18	6.01E-04	0.0143	49
Q68FD5	CLH1_MOUSE	(LLLPLWLEAR	2.99	1.69E-03	0.0143	49
Q68FD5	CLH1_MOUSE	(TLQIFNIEM[+16]K	1.66	1.74E-03	0.0143	49
Q68FD5	CLH1_MOUSE	(LPVVIGGLLDVDC[+57]SEDDVIK	2.58	1.77E-03	0.0143	49
Q68FD5	CLH1_MOUSE	(SVNESLNNLFITEEDYQALR	2.69	1.85E-03	0.0143	49
Q68FD5	CLH1_MOUSE	(ESYVETELIFALAK	3.79	1.87E-03	0.0143	49
Q68FD5	CLH1_MOUSE	(SVDPTLALSVYLR	2.90	1.88E-03	0.0143	49
Q68FD5	CLH1_MOUSE	(AVDVFFPPEAQNDFPVAMQISEK	3.82	2.26E-03	0.0143	49
Q68FD5	CLH1_MOUSE	(HNIMDFAMPYFIQVMK	7.73	2.46E-03	0.0143	49
Q68FD5	CLH1_MOUSE	(NNRPSEGPLQTR	1.19	2.65E-03	0.0143	49
Q68FD5	CLH1_MOUSE	(VMEYINR	2.56	3.07E-03	0.0143	49
Q68FD5	CLH1_MOUSE	(ADDPSSYMEVVQAANASGNWEELVK	2.65	3.39E-03	0.0143	49
Q68FD5	CLH1_MOUSE	(VGYTPDWIFLLR	3.79	3.43E-03	0.0144	49
Q68FD5	CLH1_MOUSE	(AHIAQLC[+57]EK	1.44	3.65E-03	0.0146	49
Q68FD5	CLH1_MOUSE	(GQC[+57]DLELINVC[+57]NENSLFK	2.21	3.72E-03	0.0147	49
Q68FD5	CLH1_MOUSE	(IHEGC[+57]EPPATHNALAK	1.27	3.78E-03	0.0147	49
Q68FD5	CLH1_MOUSE	(NNLAGAEELFAR	1.62	3.92E-03	0.0147	49
Q68FD5	CLH1_MOUSE	(GQFSTDELVAEVEK	3.85	4.15E-03	0.0149	49
Q68FD5	CLH1_MOUSE	(FQSVPAQPGQTSPLLQYFGILLDQGLLNK	9.07	4.26E-03	0.0150	49
Q68FD5	CLH1_MOUSE	(AHMGMFTELAILYSK	5.44	4.79E-03	0.0154	49
Q68FD5	CLH1_MOUSE	(EVC[+57]FAC[+57]VDGK	1.46	4.88E-03	0.0155	49
Q68FD5	CLH1_MOUSE	(YHEQLSTQSLIELFESFK	8.25	4.97E-03	0.0155	49
Q68FD5	CLH1_MOUSE	(VIQC[+57]FAETGQVQK	2.35	6.31E-03	0.0169	49
Q68FD5	CLH1_MOUSE	(ISGETIFVTAPHEATAGIIGVNF	2.47	6.73E-03	0.0172	49
Q68FD5	CLH1_MOUSE	(LASTLVHLGEYQAAVDGAR	2.20	7.50E-03	0.0180	49
Q68FD5	CLH1_MOUSE	(KFDVNTSAVQVLIHIGNLDR	5.48	7.60E-03	0.0181	49

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q68FD5	CLH1_MOUSE	(KDPELWGSVLLLESNPYR	2.47	7.76E-03	0.0182	49
Q68FD5	CLH1_MOUSE	(KFNALFAQGNYSEAAK	1.69	7.93E-03	0.0183	49
Q68FD5	CLH1_MOUSE	(ALEHFTDLYDIK	2.24	7.96E-03	0.0183	49
Q68FD5	CLH1_MOUSE	(LHIIEVGTPTGNQPFPK	2.35	8.23E-03	0.0186	49
Q68FD5	CLH1_MOUSE	(VVGAMQLYSVDR	1.97	8.41E-03	0.0188	49
Q68FD5	CLH1_MOUSE	(LLYNNVSNFGR	1.66	8.96E-03	0.0195	49
Q68FD5	CLH1_MOUSE	(ALEHFTDLYDIKR	2.79	1.04E-02	0.0211	49
Q68FD5	CLH1_MOUSE	(VVGAM[+16]QLYSVDR	1.44	1.19E-02	0.0227	49
Q68FD5	CLH1_MOUSE	(LAELEEFINGPNNNAHIQQVGDR	1.70	1.24E-02	0.0231	49
Q68FD5	CLH1_MOUSE	(IAAYLFK	1.72	1.25E-02	0.0232	49
Q68FD5	CLH1_MOUSE	(VANVELYYK	1.74	1.26E-02	0.0233	49
Q68FD5	CLH1_MOUSE	(YIEIYVQK	2.20	1.34E-02	0.0242	49
Q68FD5	CLH1_MOUSE	(HDVVFLITK	2.06	1.41E-02	0.0250	49
Q68FD5	CLH1_MOUSE	(WLLLTGISAQQNR	3.06	1.48E-02	0.0258	49
Q68FD5	CLH1_MOUSE	(TLQIFNIEMK	2.64	1.51E-02	0.0262	49
Q68FD5	CLH1_MOUSE	(LTDQLPLIIVC[+57]DR	2.79	1.66E-02	0.0277	49
Q6URW6	MYH14_MOUSE	DLGEELEALRGELEDTL DSTNAQQELR	7.49	2.49E-02	0.0370	49
P05213	TBA1B_MOUSE	DVNAAIATIK	3.37	2.56E-02	0.0377	49
P28660	NCKP1_MOUSE	LKEFLALASSLLK	1.71	2.56E-02	0.0377	49
Q62261	SPTB2_MOUSE	MWEVLESTTQTK	1.70	2.74E-02	0.0397	49
P14873	MAP1B_MOUSE	SSYYVVSNDPAAEEPSR	5.33	3.44E-04	0.0143	44
P14873	MAP1B_MOUSE	NLISPDLGVVFLNVPENLK	6.01	7.32E-04	0.0143	44
P14873	MAP1B_MOUSE	QQDLNIMVLASSSTVVMQDESFPAC[+57]K	5.31	1.17E-03	0.0143	44
P14873	MAP1B_MOUSE	NVDVEFFK	2.95	1.33E-03	0.0143	44
P14873	MAP1B_MOUSE	AAEAGVTEEYGYLGTSK	3.40	1.69E-03	0.0143	44
P14873	MAP1B_MOUSE	TTEAAATAVGTAAATTA AVVAAAGIAASGPVI	3.38	2.22E-03	0.0143	44
P14873	MAP1B_MOUSE	SDISPLTPR	4.54	3.09E-03	0.0143	44
P14873	MAP1B_MOUSE	TSDVETMSSQSALALDER	4.11	3.42E-03	0.0144	44
P14873	MAP1B_MOUSE	ESSPLYSPGFSDSTSAK	4.88	3.88E-03	0.0147	44
P14873	MAP1B_MOUSE	SPSLSPSPPIEK	3.86	3.99E-03	0.0148	44
P14873	MAP1B_MOUSE	DLTTSSVEK	3.34	4.65E-03	0.0153	44
P14873	MAP1B_MOUSE	VLFPGNSTQYNILEGLEK	4.14	4.70E-03	0.0153	44
P14873	MAP1B_MOUSE	VDSILLTHIGDDNLPGINSM[+16]LQR	3.69	5.00E-03	0.0155	44
P14873	MAP1B_MOUSE	TPEEGGYSEISEK	3.01	5.01E-03	0.0155	44
P14873	MAP1B_MOUSE	SWDTNLI EC[+57]NLDQELK	4.86	5.11E-03	0.0155	44
P14873	MAP1B_MOUSE	TPEVSGYTYEK	3.63	6.12E-03	0.0166	44
P14873	MAP1B_MOUSE	TPQASTYSYETSDR	4.06	6.59E-03	0.0171	44
P14873	MAP1B_MOUSE	NLISPDLGVVFLNVPENLKDPEPNIK	5.20	6.64E-03	0.0172	44
P14873	MAP1B_MOUSE	TPEDGGYTC[+57]EITEK	4.56	6.92E-03	0.0174	44
P14873	MAP1B_MOUSE	ESPVSDLTSTGLYQDKQEEK	4.15	7.28E-03	0.0177	44
P14873	MAP1B_MOUSE	SPC[+57]DSGYSETIEK	4.75	7.30E-03	0.0178	44
P14873	MAP1B_MOUSE	SDVLETVVLINPSDEAVSTEV R	4.61	7.56E-03	0.0180	44
P14873	MAP1B_MOUSE	DFEELKAEIDVAK	3.86	7.57E-03	0.0180	44
P14873	MAP1B_MOUSE	VDSILLTHIGDDNLPGINSM LQR	4.40	7.63E-03	0.0181	44
P14873	MAP1B_MOUSE	EEGYEPDKTEAEDYVM[+16]JAVADK	3.93	8.14E-03	0.0185	44
P14873	MAP1B_MOUSE	DLTGQVPTPPVK	3.43	8.81E-03	0.0193	44
P14873	MAP1B_MOUSE	YESSLYSQEYSKPAVASFNGLSEGSK	5.10	9.25E-03	0.0198	44
P14873	MAP1B_MOUSE	DIKPQLELIEDEEK	3.45	9.37E-03	0.0200	44
P14873	MAP1B_MOUSE	GDSALFAVNGFNMLINGGSER	6.38	1.09E-02	0.0216	44
P14873	MAP1B_MOUSE	ASLTLFC[+57]PEEGDWK	4.06	1.15E-02	0.0223	44
P14873	MAP1B_MOUSE	SVNFSLTPNEIK	3.81	1.17E-02	0.0225	44
P14873	MAP1B_MOUSE	EMSLYASLASEK	5.44	1.19E-02	0.0227	44
P14873	MAP1B_MOUSE	SVGNTIEPVILFQK	4.64	1.21E-02	0.0229	44
P14873	MAP1B_MOUSE	AIGNIELGIR	4.04	1.21E-02	0.0229	44
P14873	MAP1B_MOUSE	HNLQDFINIK	3.51	1.28E-02	0.0235	44
P14873	MAP1B_MOUSE	LEMYVLNPVK	4.44	1.34E-02	0.0242	44
P14873	MAP1B_MOUSE	THDVGYYEYK	3.82	1.39E-02	0.0248	44
P14873	MAP1B_MOUSE	M[+16]SISEGTVSDK	3.62	1.51E-02	0.0262	44
P14873	MAP1B_MOUSE	QDVDLC[+57]LVSSC[+57]EJFK	4.49	1.55E-02	0.0266	44
Q8BP67	RL24_MOUSE	εVELC[+57]SFGSYK	4.34	1.81E-02	0.0294	44
Q61171	PRDX2_MOUSE	GLFIIDAK	4.21	2.12E-02	0.0330	44
Q61316	HSP74_MOUSE	FLEMC[+57]DDLLAR	3.73	2.58E-02	0.0380	44

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q68FD5	CLH1_MOUSE	(NLILVVR	4.64	2.75E-02	0.0398	44
P62889	RL30_MOUSE	εKSEIEYYAMLAK	1.83	3.59E-02	0.0495	44
Q62261	SPTB2_MOUSE	TQTAIASEDM[+16]PNTLTEAEK	2.58	1.77E-04	0.0143	44
Q62261	SPTB2_MOUSE	DASVAEAWLLGQEPYLSSR	5.00	2.36E-03	0.0143	44
Q62261	SPTB2_MOUSE	FANSLVGVQQQLQAFNTYR	3.40	2.82E-03	0.0143	44
Q62261	SPTB2_MOUSE	LVSQDNFGFDLPAVEAATK	3.71	3.20E-03	0.0143	44
Q62261	SPTB2_MOUSE	EAEKLESEHPDQAQAILSR	3.67	3.21E-03	0.0143	44
Q62261	SPTB2_MOUSE	EAASELLM[+16]R	2.80	3.36E-03	0.0143	44
Q62261	SPTB2_MOUSE	VIESTQDLGNLAGVMALQR	3.25	3.79E-03	0.0147	44
Q62261	SPTB2_MOUSE	LLEVELSGER	3.07	3.98E-03	0.0148	44
Q62261	SPTB2_MOUSE	EVDDLEQWIAER	4.19	4.75E-03	0.0154	44
Q62261	SPTB2_MOUSE	VLDNAIETEK	2.33	4.88E-03	0.0155	44
Q62261	SPTB2_MOUSE	DLDDFQSWLSR	3.61	4.93E-03	0.0155	44
Q62261	SPTB2_MOUSE	EGMQLISEKPETEAVVK	3.97	5.02E-03	0.0155	44
Q62261	SPTB2_MOUSE	IVSSNDVGHDEYSTQSLVK	3.25	5.15E-03	0.0155	44
Q62261	SPTB2_MOUSE	VAVVNQIAR	2.78	5.17E-03	0.0155	44
Q62261	SPTB2_MOUSE	KHEAIETDIAAYEER	4.21	5.39E-03	0.0158	44
Q62261	SPTB2_MOUSE	SALPAQSAATLPAR	3.27	5.49E-03	0.0159	44
Q62261	SPTB2_MOUSE	LSDGNEYLFQAK	2.96	5.67E-03	0.0160	44
Q62261	SPTB2_MOUSE	QALQDTLALYK	3.72	6.36E-03	0.0169	44
Q62261	SPTB2_MOUSE	LVSDGNINSDR	2.69	6.82E-03	0.0172	44
Q62261	SPTB2_MOUSE	GNLEVLLFTIQSK	4.36	6.92E-03	0.0174	44
Q62261	SPTB2_MOUSE	DALLSALSISQNYHLEC[+57]NETK	3.44	6.94E-03	0.0174	44
Q62261	SPTB2_MOUSE	HQILEQAVEDYAETVHQLSK	4.19	7.85E-03	0.0182	44
Q62261	SPTB2_MOUSE	LQALDTGWNELHK	3.63	7.91E-03	0.0183	44
Q62261	SPTB2_MOUSE	VQAVVAVAR	3.54	8.25E-03	0.0186	44
Q62261	SPTB2_MOUSE	DVEDEILWVGER	5.08	9.12E-03	0.0197	44
Q62261	SPTB2_MOUSE	DLTSVNILLK	3.37	9.24E-03	0.0198	44
Q62261	SPTB2_MOUSE	SQNIITDSSSLNAEAIR	4.22	9.50E-03	0.0202	44
Q62261	SPTB2_MOUSE	ALVADSHPESEK	4.93	1.13E-02	0.0221	44
Q62261	SPTB2_MOUSE	VAHMEFC[+57]YQELC[+57]QLAAER	3.35	1.15E-02	0.0223	44
Q62261	SPTB2_MOUSE	DQNTVETLQR	2.32	1.28E-02	0.0235	44
Q62261	SPTB2_MOUSE	AELFTQSC[+57]ADLDK	4.06	1.34E-02	0.0242	44
Q62261	SPTB2_MOUSE	LTTLELLEVR	3.46	1.36E-02	0.0244	44
Q62261	SPTB2_MOUSE	LFQLNR	2.96	1.49E-02	0.0259	44
Q62261	SPTB2_MOUSE	LQQFLR	1.98	1.54E-02	0.0265	44
Q9D8E6	RL4_MOUSE	6C APIRPDIVNFVHTNLR	5.13	1.72E-02	0.0284	44
Q08788	DCTN1_MOUSE	VDELTTDLEILK	3.49	2.07E-02	0.0324	44
Q9CWS5	Q9CWS5_MOUSE	VADALANAAGHLDDLPGALSALSDDLHAHK	4.32	2.15E-02	0.0334	44
P62717	RL18A_MOUSE	FWYFVSQLK	4.43	2.23E-02	0.0343	44
P63005	LIS1_MOUSE	P LLASC[+57]SADMTIK	2.33	2.50E-02	0.0371	44
P20357	MTAP2_MOUSE	LASVSADAEVAR	6.12	2.53E-02	0.0374	44
Q68FD5	CLH1_MOUSE	(IYIDSNNNPER	4.02	2.58E-02	0.0380	44
Q9DBG3	AP2B1_MOUSE	LLSTDPVTAK	2.32	2.74E-02	0.0397	44
Q6PIE5	AT1A2_MOUSE	DTAGDASESALLK	2.64	2.79E-02	0.0403	44
P80317	TCPZ_MOUSE	ALQFLEQVK	0.93	2.93E-02	0.0418	44
P14873	MAP1B_MOUSE	LGGDVSPQTQIDVVSQFGSFK	#REF!	#REF!	0.0495	43
Q9QYR6	MAP1A_MOUSE	SEPQDFQEDSWGDTK	3.17	3.11E-05	0.0143	41
Q9QYR6	MAP1A_MOUSE	DAEQTEPEQREPTYPDER	2.61	2.05E-04	0.0143	41
Q9QYR6	MAP1A_MOUSE	VPSAPGQESPVPDTK	2.13	2.89E-04	0.0143	41
Q9QYR6	MAP1A_MOUSE	TRHDEYLEVTK	1.94	5.71E-04	0.0143	41
Q9QYR6	MAP1A_MOUSE	VPEVTESHTRR	1.56	7.07E-04	0.0143	41
Q9QYR6	MAP1A_MOUSE	TADQDFFR	2.12	7.64E-04	0.0143	41
Q9QYR6	MAP1A_MOUSE	AQWGENLQVTLIPTHDEVTR	4.02	9.70E-04	0.0143	41
Q9QYR6	MAP1A_MOUSE	AVLDALLEGK	3.42	9.90E-04	0.0143	41
Q9QYR6	MAP1A_MOUSE	REEVLEEGAK	3.57	1.14E-03	0.0143	41
Q9QYR6	MAP1A_MOUSE	SAPC[+57]GSLAFSGDR	2.59	1.19E-03	0.0143	41
Q9QYR6	MAP1A_MOUSE	EQKDEASEEKEQVLEQK	2.70	1.21E-03	0.0143	41
Q9QYR6	MAP1A_MOUSE	NLISPELGVVFFNVDPK	3.38	1.48E-03	0.0143	41
Q9QYR6	MAP1A_MOUSE	GDSALFAVNGFNILVDGGSDRK	2.67	1.52E-03	0.0143	41
Q9QYR6	MAP1A_MOUSE	IDSVLLTHIGADNLPINGLLQR	4.49	1.93E-03	0.0143	41
Q9QYR6	MAP1A_MOUSE	EAELTPENIAAAR	2.09	2.05E-03	0.0143	41

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9QYR6	MAP1A_MOUSE	SPWASDFKDFQEPLPQK	2.87	2.12E-03	0.0143	41
Q9QYR6	MAP1A_MOUSE	VVSNTIEPLTLFHK	2.98	2.66E-03	0.0143	41
Q9QYR6	MAP1A_MOUSE	GAALQQTQAPEPR	2.03	3.19E-03	0.0143	41
Q9QYR6	MAP1A_MOUSE	SPQAQDTLGLSAGGQTGC[+57]TIQLLPEQDK	2.90	3.70E-03	0.0147	41
Q9QYR6	MAP1A_MOUSE	AVVFETGEAGAASGAGSLPGEVR	2.31	3.88E-03	0.0147	41
Q9QYR6	MAP1A_MOUSE	EGEGGAGAPDSSSFSSK	1.97	4.16E-03	0.0149	41
Q9QYR6	MAP1A_MOUSE	ELALSSPEDLTQDFEELKR	4.25	4.87E-03	0.0155	41
Q9QYR6	MAP1A_MOUSE	DLAAGAVPANLKPSK	2.25	4.92E-03	0.0155	41
Q9QYR6	MAP1A_MOUSE	NEPTTSPWLAIEPPWVPK	4.79	5.38E-03	0.0158	41
Q9QYR6	MAP1A_MOUSE	LSSFATSVAEDQSVASLTAPQTEETGK	2.35	5.63E-03	0.0160	41
Q9QYR6	MAP1A_MOUSE	ALGLEESPEEEGK	3.93	5.78E-03	0.0162	41
Q9QYR6	MAP1A_MOUSE	LGIAEPLYR	1.83	6.77E-03	0.0172	41
Q9QYR6	MAP1A_MOUSE	LSKPC[+57]C[+57]YIFPGGR	4.49	7.61E-03	0.0181	41
Q9QYR6	MAP1A_MOUSE	VLFPGNAPQNK	2.10	8.00E-03	0.0183	41
Q9QYR6	MAP1A_MOUSE	APDSGAEVER	1.92	8.63E-03	0.0191	41
Q9QYR6	MAP1A_MOUSE	EQDVVQGWR	2.15	9.53E-03	0.0202	41
Q9QYR6	MAP1A_MOUSE	ESTFLDEGPNQEITPLQHTPR	2.92	9.61E-03	0.0203	41
Q9QYR6	MAP1A_MOUSE	ALALVPGTPTR	1.57	9.65E-03	0.0203	41
Q9QYR6	MAP1A_MOUSE	SSLLLDVTTSIPSSR	2.40	1.13E-02	0.0221	41
Q9QYR6	MAP1A_MOUSE	FPTSTYDLSGPEGPGPFASQSAESAVPASSK	4.00	1.16E-02	0.0224	41
Q9QYR6	MAP1A_MOUSE	SPPC[+57]EDFSVTGESEK	2.82	1.18E-02	0.0226	41
Q9QYR6	MAP1A_MOUSE	GDSALFAVNGFNILVDGGSDR	5.82	1.26E-02	0.0233	41
Q9QYR6	MAP1A_MOUSE	QEPEPGPNVEPSFTPPAVPPR	2.55	1.27E-02	0.0234	41
Q9QYR6	MAP1A_MOUSE	LDMYVLNPVK	3.52	1.39E-02	0.0248	41
Q9QYR6	MAP1A_MOUSE	SFYADIYEQMMLTGLGPAC[+57]PTF	3.54	1.52E-02	0.0263	41
Q8R191	SNG3_MOUSE	AGAAFDPVSFAR	2.28	3.30E-02	0.0461	41
Q7TMM9	TBB2A_MOUSE	FWEVISDEHGIDPTGSYHGSDSLQLER	5.95	6.15E-04	0.0143	38
Q7TMM9	TBB2A_MOUSE	M[+16]SATFIGNSTAIQELFK	2.08	8.51E-04	0.0143	38
Q7TMM9	TBB2A_MOUSE	GHYTEGAELVDSVLDVVRK	3.70	8.82E-04	0.0143	38
Q7TMM9	TBB2A_MOUSE	M[+16]REIVHIQAGQC[+57]GNQIGAK	2.53	1.29E-03	0.0143	38
Q7TMM9	TBB2A_MOUSE	KLAVNM[+16]VPFPR	2.26	1.46E-03	0.0143	38
Q7TMM9	TBB2A_MOUSE	LAVNM[+16]VPFPR	1.92	1.57E-03	0.0143	38
Q7TMM9	TBB2A_MOUSE	NM[+16]MAAC[+57]DPR	2.01	1.91E-03	0.0143	38
Q7TMM9	TBB2A_MOUSE	NMM[+16]AAC[+57]DPR	1.95	2.11E-03	0.0143	38
Q7TMM9	TBB2A_MOUSE	MSATFIGNSTAIQELFKR	3.32	2.79E-03	0.0143	38
Q7TMM9	TBB2A_MOUSE	MSATFIGNSTAIQELFK	3.20	2.92E-03	0.0143	38
Q7TMM9	TBB2A_MOUSE	LTPTYGDLNHLVSATM[+16]SGVTTC[+57]LF	2.76	3.17E-03	0.0143	38
Q7TMM9	TBB2A_MOUSE	FPGQLNADLRK	3.04	3.85E-03	0.0147	38
Q7TMM9	TBB2A_MOUSE	EIVHIQAGQC[+57]GNQIGAK	2.28	4.11E-03	0.0148	38
Q7TMM9	TBB2A_MOUSE	ESESC[+57]DC[+57]LQGFQLTHSLGGGTGSGM[+16]GTLISK	3.11	4.17E-03	0.0149	38
Q7TMM9	TBB2A_MOUSE	LTPTYGDLNHLVSATMSGVTTC[+57]LF	4.28	4.55E-03	0.0152	38
Q7TMM9	TBB2A_MOUSE	SGPFGQIFRPDNFVFGQSGAGNNWAK	5.44	4.85E-03	0.0154	38
Q7TMM9	TBB2A_MOUSE	ALTVPELTQQMFDSK	2.66	4.93E-03	0.0155	38
Q7TMM9	TBB2A_MOUSE	ALTVPELTQQM[+16]FDSK	2.41	5.09E-03	0.0155	38
Q7TMM9	TBB2A_MOUSE	ISEQFTAM[+16]FR	2.19	5.64E-03	0.0160	38
Q7TMM9	TBB2A_MOUSE	INVYYNEAAGNK	2.31	7.49E-03	0.0180	38
Q7TMM9	TBB2A_MOUSE	LHFFM[+16]PGFAPLTSR	3.20	7.50E-03	0.0180	38
Q7TMM9	TBB2A_MOUSE	KLAVNMVPPFR	3.13	7.78E-03	0.0182	38
Q7TMM9	TBB2A_MOUSE	MSM[+16]KEVDEQM[+16]LNVQNK	1.88	7.90E-03	0.0183	38
Q7TMM9	TBB2A_MOUSE	LHFFMPGFAPLTSR	4.22	8.06E-03	0.0184	38
Q7TMM9	TBB2A_MOUSE	IM[+16]NTFSVMPSPK	1.73	8.20E-03	0.0186	38
Q7TMM9	TBB2A_MOUSE	FPGQLNADLR	2.21	8.23E-03	0.0186	38
Q7TMM9	TBB2A_MOUSE	AILVDLEPGTM[+16]DSVR	1.99	8.65E-03	0.0191	38
Q7TMM9	TBB2A_MOUSE	LAVNMVPPFR	2.81	8.72E-03	0.0191	38
Q7TMM9	TBB2A_MOUSE	MREIVHIQAGQC[+57]GNQIGAK	3.06	9.60E-03	0.0203	38
Q7TMM9	TBB2A_MOUSE	GHYTEGAELVDSVLDVVR	4.40	9.70E-03	0.0204	38
Q7TMM9	TBB2A_MOUSE	AILVDLEPGTMDSVR	2.65	1.00E-02	0.0206	38
Q7TMM9	TBB2A_MOUSE	ESESC[+57]DC[+57]LQGFQLTHSLGGGTGSGMGTLISK	3.72	1.29E-02	0.0237	38
Q7TMM9	TBB2A_MOUSE	ISEQFTAMFR	3.55	1.38E-02	0.0247	38
Q7TMM9	TBB2A_MOUSE	IMNTFSVM[+16]PSPK	1.80	1.40E-02	0.0249	38
Q62167	DDX3X_MOUSE	TAAFLLPILSQIYADGPGEALF	2.56	1.73E-02	0.0284	38
P16546	SPTN1_MOUSE	ENLLEEQGSIALR	3.03	1.88E-02	0.0301	38

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P26039	TLN1_MOUSE	TIGITNHDEYSLVR	4.36	2.21E-02	0.0341	38
P39053	DYN1_MOUSE	I GM[+16]EDLIPLVNR	2.67	2.73E-02	0.0396	38
P46460	NSF_MOUSE	V L FADAE E E E Q R	3.05	2.19E-04	0.0143	30
P46460	NSF_MOUSE	V GSM[+16]AGSTGVHDTVVNQLLSK	2.59	1.68E-03	0.0143	30
P46460	NSF_MOUSE	V I E V G L V V G N S Q V A F E K	3.85	2.20E-03	0.0143	30
P46460	NSF_MOUSE	V M[+16]EIGLPDEK	2.58	2.42E-03	0.0143	30
P46460	NSF_MOUSE	V Q K I E V G L V V G N S Q V A F E K	3.65	3.04E-03	0.0143	30
P46460	NSF_MOUSE	V M[+16]GIGGLDKEFSDIFR	3.04	3.34E-03	0.0143	30
P46460	NSF_MOUSE	V Q C[+57]IGTMTIEIDFLQK	3.90	3.38E-03	0.0143	30
P46460	NSF_MOUSE	V N F S G A E L E G L V R	2.89	4.04E-03	0.0148	30
P46460	NSF_MOUSE	V T P L V S V L L E G P P H S G K	3.18	4.10E-03	0.0148	30
P46460	NSF_MOUSE	V A E S L Q V T R	2.66	4.47E-03	0.0151	30
P46460	NSF_MOUSE	V I A E E S N F P F I K	3.07	4.62E-03	0.0153	30
P46460	NSF_MOUSE	V L L D Y V P I G P R	3.03	5.16E-03	0.0155	30
P46460	NSF_MOUSE	V M G I G G L D K E F S D I F R	5.19	5.24E-03	0.0157	30
P46460	NSF_MOUSE	V G I L L Y G P P G C[+57]GK	2.75	5.58E-03	0.0160	30
P46460	NSF_MOUSE	V A E N S S L N L I G K	2.46	6.39E-03	0.0169	30
P46460	NSF_MOUSE	V L G A N S G L H I I I F D E I D A I C[+57]K	4.25	6.47E-03	0.0170	30
P46460	NSF_MOUSE	V S Q L S C[+57]V V V D D I E R	2.70	6.57E-03	0.0171	30
P46460	NSF_MOUSE	V K L L I I G T T S R	3.73	6.64E-03	0.0172	30
P46460	NSF_MOUSE	V V L D D G E L L V Q Q T K	2.26	6.68E-03	0.0172	30
P46460	NSF_MOUSE	V C[+57]P T D E L S L S N C[+57]A V V N E K	3.34	6.69E-03	0.0172	30
P46460	NSF_MOUSE	V Y V G E S E A N I R	2.68	6.73E-03	0.0172	30
P46460	NSF_MOUSE	V N I D S N P Y D T D K	2.66	7.61E-03	0.0181	30
P46460	NSF_MOUSE	V L F G L L V K	3.76	7.77E-03	0.0182	30
P46460	NSF_MOUSE	V V V N G P E I L N K	2.38	9.09E-03	0.0197	30
P46460	NSF_MOUSE	V L L I I G T T S R	2.49	1.16E-02	0.0224	30
P46460	NSF_MOUSE	V G H Q L L S A D V D I K	3.20	1.36E-02	0.0244	30
P46460	NSF_MOUSE	V W G D P V T R	2.73	1.58E-02	0.0269	30
Q9Z1G4	VPP1_MOUSE	V Q A E I E N P L E D P V T G D Y V H K	1.88	1.92E-02	0.0306	30
Q93092	TALDO_MOUSE	L F V L F G A E I L K	5.55	2.39E-02	0.0360	30
P12970	RL7A_MOUSE	V N F G I G Q D I Q P K	4.46	2.43E-02	0.0364	30
P63017	HSP7C_MOUSE	R F D D A V V Q S D M K	3.51	2.36E-04	0.0143	30
P63017	HSP7C_MOUSE	C[+57]N E I I S W L D K	1.46	9.53E-04	0.0143	30
P63017	HSP7C_MOUSE	S T A G D T H L G G E D F D N R	1.96	1.27E-03	0.0143	30
P63017	HSP7C_MOUSE	N Q V A M[+16]N P T N T V F D A K	1.86	1.37E-03	0.0143	30
P63017	HSP7C_MOUSE	S I N P D E A V A Y G A A V Q A A I L S G D K	3.09	2.01E-03	0.0143	30
P63017	HSP7C_MOUSE	N S L E S Y A F N M[+16]K	2.18	2.24E-03	0.0143	30
P63017	HSP7C_MOUSE	M V N H F I A E F K R	2.75	2.75E-03	0.0143	30
P63017	HSP7C_MOUSE	D A G T I A G L N V L R	2.22	2.99E-03	0.0143	30
P63017	HSP7C_MOUSE	L L Q D F F N G K	2.31	3.28E-03	0.0143	30
P63017	HSP7C_MOUSE	V Q V E Y K	2.31	3.34E-03	0.0143	30
P63017	HSP7C_MOUSE	F D D A V V Q S D M[+16]K	1.63	3.35E-03	0.0143	30
P63017	HSP7C_MOUSE	F E L T G I P P A P R	2.94	3.84E-03	0.0147	30
P63017	HSP7C_MOUSE	F E E L N A D L F R	2.39	3.95E-03	0.0148	30
P63017	HSP7C_MOUSE	G P A V G I D L G T T Y S C[+57]V G V F Q H G K	3.42	4.05E-03	0.0148	30
P63017	HSP7C_MOUSE	T T P S Y V A F T D T E R	2.21	4.22E-03	0.0149	30
P63017	HSP7C_MOUSE	E I A E A Y L G K	1.74	4.46E-03	0.0151	30
P63017	HSP7C_MOUSE	F D D A V V Q S D M K	2.39	5.21E-03	0.0156	30
P63017	HSP7C_MOUSE	L D K S Q I H D I V L V G G S T R	3.22	5.65E-03	0.0160	30
P63017	HSP7C_MOUSE	S F Y P E E V S S M V L T K	2.58	6.65E-03	0.0172	30
P63017	HSP7C_MOUSE	N S L E S Y A F N M K	2.60	6.79E-03	0.0172	30
P63017	HSP7C_MOUSE	S Q I H D I V L V G G S T R	2.06	7.22E-03	0.0177	30
P63017	HSP7C_MOUSE	Q T Q T F T T Y S D N Q P G V L I Q V Y E G E R	3.49	7.23E-03	0.0177	30
P63017	HSP7C_MOUSE	M K E I A E A Y L G K	2.54	7.65E-03	0.0181	30
P63017	HSP7C_MOUSE	A R F E E L N A D L F R	3.32	8.71E-03	0.0191	30
P63017	HSP7C_MOUSE	H W P F M V V N D A G R P K	4.01	9.34E-03	0.0199	30
P63017	HSP7C_MOUSE	H W P F M[+16]V V N D A G R P K	2.84	9.68E-03	0.0204	30
P63017	HSP7C_MOUSE	T V T N A V V T V P A Y F N D S Q R	2.68	1.11E-02	0.0219	30
P63017	HSP7C_MOUSE	M[+16]V N H F I A E F K	2.42	1.29E-02	0.0237	30
P63017	HSP7C_MOUSE	M V N H F I A E F K	2.39	1.57E-02	0.0268	30
P63017	HSP7C_MOUSE	N Q V A M N P T N T V F D A K	2.19	1.69E-02	0.0281	30

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9QXS6	DREB_MOUSE	EQSIFGDQRDEEEESQM[+16]KK	4.46	1.38E-03	0.0143	26
Q9QXS6	DREB_MOUSE	SPSDSSTASTPIAEQIER	3.64	1.44E-03	0.0143	26
Q9QXS6	DREB_MOUSE	M[+16]APTPIPTR	3.38	1.57E-03	0.0143	26
Q9QXS6	DREB_MOUSE	LREDENAEPVGTTYQK	4.08	1.71E-03	0.0143	26
Q9QXS6	DREB_MOUSE	LKEQSIFGDQRDEEEESQM[+16]K	5.59	1.96E-03	0.0143	26
Q9QXS6	DREB_MOUSE	ASDSGPPSSSSSSSSPPR	6.45	2.90E-03	0.0143	26
Q9QXS6	DREB_MOUSE	TPNLSSSLPC[+57]SHLDSHR	4.02	3.31E-03	0.0143	26
Q9QXS6	DREB_MOUSE	EQFWEQAK	3.90	3.95E-03	0.0148	26
Q9QXS6	DREB_MOUSE	TPFPYITC[+57]HR	4.13	4.16E-03	0.0149	26
Q9QXS6	DREB_MOUSE	SESEVEEAAAIIAQRPDNPR	4.41	4.50E-03	0.0152	26
Q9QXS6	DREB_MOUSE	LAASGEGGLQELSGHFENQK	4.66	4.54E-03	0.0152	26
Q9QXS6	DREB_MOUSE	LELLAAYEEVIR	5.17	4.56E-03	0.0152	26
Q9QXS6	DREB_MOUSE	KSESEVEEAAAIIAQRPDNPR	4.84	4.58E-03	0.0152	26
Q9QXS6	DREB_MOUSE	TDAAVEMK	3.67	4.82E-03	0.0154	26
Q9QXS6	DREB_MOUSE	MAPTPIPTR	4.02	4.84E-03	0.0154	26
Q9QXS6	DREB_MOUSE	KQQSLEAEEAK	4.00	5.12E-03	0.0155	26
Q9QXS6	DREB_MOUSE	EGTQASEGYFSQSQEEFFAQSEEPK[+57]AK	4.95	5.15E-03	0.0155	26
Q9QXS6	DREB_MOUSE	EESAADWALYTYEDGSDDLK	4.61	5.95E-03	0.0163	26
Q9QXS6	DREB_MOUSE	EREQQIEEHR	4.87	8.09E-03	0.0184	26
Q9QXS6	DREB_MOUSE	LKEQSIFGDQRDEEEESQMK	5.60	8.18E-03	0.0186	26
Q9QXS6	DREB_MOUSE	EQSIFGDQRDEEEESQMK	4.75	8.84E-03	0.0193	26
Q9QXS6	DREB_MOUSE	DSQAALPK	3.70	9.10E-03	0.0197	26
Q9QXS6	DREB_MOUSE	YVLINWVGEDVPDARK	4.42	1.16E-02	0.0224	26
Q9QXS6	DREB_MOUSE	YVLINWVGEDVPDAR	5.14	1.25E-02	0.0232	26
Q9QXS6	DREB_MOUSE	VMYGFC[+57]SVK	4.13	1.49E-02	0.0259	26
Q9QXS6	DREB_MOUSE	C[+57]JAC[+57]ASHVAK	4.58	1.57E-02	0.0268	26
Q64331	MYO6_MOUSE	QARPTYATAMLQNLLK	3.49	7.79E-04	0.0143	25
Q64331	MYO6_MOUSE	ALGLNEVDYK	2.98	1.21E-03	0.0143	25
Q64331	MYO6_MOUSE	QREEESQQQAVLAQEC[+57]R	5.58	1.26E-03	0.0143	25
Q64331	MYO6_MOUSE	SSEDLLSALQK	5.06	1.53E-03	0.0143	25
Q64331	MYO6_MOUSE	VNLWLVC[+57]SR	2.92	1.67E-03	0.0143	25
Q64331	MYO6_MOUSE	SAPSLEYC[+57]AELLGLDQDDLK	2.77	1.68E-03	0.0143	25
Q64331	MYO6_MOUSE	IVEANPLLEAFGNAK	4.84	1.70E-03	0.0143	25
Q64331	MYO6_MOUSE	FNEVVSALK	3.52	2.05E-03	0.0143	25
Q64331	MYO6_MOUSE	STGASFIR	5.35	2.07E-03	0.0143	25
Q64331	MYO6_MOUSE	GAEILPR	4.92	2.16E-03	0.0143	25
Q64331	MYO6_MOUSE	LC[+57]AGASEDIR	3.51	2.49E-03	0.0143	25
Q64331	MYO6_MOUSE	LSFISVGNK	4.65	2.72E-03	0.0143	25
Q64331	MYO6_MOUSE	NLEISIDALMAK	5.85	2.78E-03	0.0143	25
Q64331	MYO6_MOUSE	ILKEEQELYQK	6.75	2.78E-03	0.0143	25
Q64331	MYO6_MOUSE	TQLNLLLDK	5.21	2.79E-03	0.0143	25
Q64331	MYO6_MOUSE	LQQFFNER	4.21	2.89E-03	0.0143	25
Q64331	MYO6_MOUSE	IAQNESELISDEAQGDM[+16]ALR	4.85	2.90E-03	0.0143	25
Q64331	MYO6_MOUSE	TVYSHLFDHVVNR	5.35	3.39E-03	0.0143	25
Q64331	MYO6_MOUSE	LVGILDILDEENR	5.67	3.94E-03	0.0147	25
Q64331	MYO6_MOUSE	NLRDDEGFIR	2.02	4.42E-03	0.0151	25
Q64331	MYO6_MOUSE	VQWC[+57]SLSVIK	4.07	4.53E-03	0.0152	25
Q64331	MYO6_MOUSE	NNDALHMSLESLIC[+57]ESR	6.21	6.15E-03	0.0166	25
Q64331	MYO6_MOUSE	C[+57]GGIQYLQSAIESR	2.15	1.51E-02	0.0262	25
Q64331	MYO6_MOUSE	DTINTSC[+57]DIELLAAC[+57]R	6.14	1.58E-02	0.0269	25
Q9ESJ4	SPN90_MOUSE	LLLLLNLR	3.49	1.92E-02	0.0306	25
Q7TSJ2	MAP6_MOUSE	AVAIETQPAQGESDAVAR	3.42	3.32E-04	0.0143	23
Q7TSJ2	MAP6_MOUSE	TEGHEETPLPPAQSQTQEGGPAAGK	4.21	5.17E-04	0.0143	23
Q7TSJ2	MAP6_MOUSE	ATGPAPGPSVDRETVAAPGR	2.80	7.87E-04	0.0143	23
Q7TSJ2	MAP6_MOUSE	SEYQPSDAPFER	3.24	1.42E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	NQDPIIPVPLK	2.81	1.56E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	DQSFPPTAPR	2.39	2.27E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	SQDPIIPALAK	2.76	2.33E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	GQDPLVPAPTK	1.84	2.44E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	ADIAVPLVFTK	3.28	2.51E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	DQGAVLLGPVK	2.39	2.56E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	VQDHIASELLK	2.33	2.62E-03	0.0143	23

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q7TSJ2	MAP6_MOUSE	EEVASTVSSSYR	3.00	2.88E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	NQGLAGPELVK	2.23	3.13E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	DPEGAGGAGVLAAGK	3.79	3.26E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	ATGPAPGPSVDR	2.76	3.27E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	YSEATEHPGAPPQPPAPLQPALAPPSF	4.18	3.30E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	GHDSVFPVAPVK	2.76	3.39E-03	0.0143	23
Q7TSJ2	MAP6_MOUSE	AGPAWM[+16]VTR	2.05	3.88E-03	0.0147	23
Q7TSJ2	MAP6_MOUSE	SGLGLGAASASTSGSGPADSVM[+16]R	3.62	4.65E-03	0.0153	23
Q7TSJ2	MAP6_MOUSE	AGPAWMVR	2.63	6.08E-03	0.0165	23
Q7TSJ2	MAP6_MOUSE	AQSPLLPEPLKNQSPVVPASTK	3.34	1.07E-02	0.0214	23
Q7TSJ2	MAP6_MOUSE	AGPAWMVTR	2.74	1.46E-02	0.0256	23
Q8BPN8	DMXL2_MOUSE	VGC[+57]PVLALEVLSK	2.99	3.10E-02	0.0437	23
P17426	AP2A1_MOUSE	LLGFGSALLDNVDPNPENFVGAGIIQTK	4.14	7.44E-04	0.0143	22
P17426	AP2A1_MOUSE	NSGVLFENQLLQIGVK	2.92	1.39E-03	0.0143	22
P17426	AP2A1_MOUSE	LPVTINK	2.15	1.42E-03	0.0143	22
P17426	AP2A1_MOUSE	FINLFPETK	2.17	1.84E-03	0.0143	22
P17426	AP2A1_MOUSE	IVSSASTDLQDYTYFVPAPWLSVK	4.10	2.07E-03	0.0143	22
P17426	AP2A1_MOUSE	VGGYILGEFGNLIAGDPR	3.74	2.66E-03	0.0143	22
P17426	AP2A1_MOUSE	AC[+57]NQLGQFLQHR	2.14	3.04E-03	0.0143	22
P17426	AP2A1_MOUSE	TSVQFQNFLPTVVHPGDLQTLAVQTK	4.38	3.41E-03	0.0143	22
P17426	AP2A1_MOUSE	NADVELQQR	1.67	9.15E-03	0.0197	22
P17426	AP2A1_MOUSE	ALLLSTYIK	2.10	9.97E-03	0.0206	22
P17426	AP2A1_MOUSE	HLC[+57]JELLAQQF	2.65	1.03E-02	0.0209	22
P17426	AP2A1_MOUSE	VLQIVTNRDDVQGYAAK	1.84	1.18E-02	0.0226	22
P17426	AP2A1_MOUSE	LVEC[+57]LETVLNK	1.73	1.31E-02	0.0239	22
P17426	AP2A1_MOUSE	THIDTVINALK	2.88	1.45E-02	0.0255	22
P17426	AP2A1_MOUSE	IAGDYVSEEVWYR	2.69	1.46E-02	0.0256	22
P17426	AP2A1_MOUSE	GLAVFISDIR	1.75	1.66E-02	0.0277	22
Q8JZQ9	EIF3B_MOUSE	FSHQGVQLIDFSPC[+57]ER	2.95	1.71E-02	0.0283	22
P17183	ENOG_MOUSE	AAVPSGASTGIYEALFLR	1.21	1.76E-02	0.0288	22
Q6ZWN5	RS9_MOUSE	4(LDYILGLK	1.79	2.00E-02	0.0316	22
Q9Z1B3	PLCB1_MOUSE	RLPLEILEFVQEAMK	2.04	2.06E-02	0.0323	22
P63330	PP2AA_MOUSE	ELDQWIEQLNEC[+57]K	3.15	3.13E-02	0.0440	22
P39053	DYN1_MOUSE	LDMLMQFVTK	1.26	3.40E-02	0.0473	22
Q9JHU4	DYHC1_MOUSE	KLVPLLEDGGDAPAALEAALEEK	3.63	8.11E-07	0.0037	21
Q9JHU4	DYHC1_MOUSE	FQSISTEFLALMK	2.85	2.87E-05	0.0143	21
Q9JHU4	DYHC1_MOUSE	LNTQEIFDDWAR	1.90	6.09E-05	0.0143	21
Q9JHU4	DYHC1_MOUSE	ENFIPTIVNFSAAEISDAIR	6.26	9.84E-04	0.0143	21
Q9JHU4	DYHC1_MOUSE	VNFLPEIITLSK	1.96	1.09E-03	0.0143	21
Q9JHU4	DYHC1_MOUSE	ILDDDTIITLENLK	3.05	1.72E-03	0.0143	21
Q9JHU4	DYHC1_MOUSE	LSLSNAISTVPLTQLR	2.60	2.06E-03	0.0143	21
Q9JHU4	DYHC1_MOUSE	LVPILLEDGGDAPAALEAALEEK	2.27	2.89E-03	0.0143	21
Q9JHU4	DYHC1_MOUSE	TYAEPLTAAMVEFYTMSQEF	3.46	3.08E-03	0.0143	21
Q9JHU4	DYHC1_MOUSE	HVPVVYVDYPGPASLTQIYGTFR	2.83	3.19E-03	0.0143	21
Q9JHU4	DYHC1_MOUSE	RAPVIDADKPVSSQLR	1.65	3.21E-03	0.0143	21
Q9JHU4	DYHC1_MOUSE	IFVFEPVPGVK	1.54	3.93E-03	0.0147	21
Q9JHU4	DYHC1_MOUSE	VTDFGDKVEDPTFLNQLQSGVNR	1.93	4.97E-03	0.0155	21
Q9JHU4	DYHC1_MOUSE	VTFVNFTVTR	2.01	5.01E-03	0.0155	21
Q9JHU4	DYHC1_MOUSE	QLQNISQAAASGGAK	1.55	5.20E-03	0.0156	21
Q9JHU4	DYHC1_MOUSE	VLLTTQGVDM[+16]ISK	2.85	5.87E-03	0.0163	21
Q9JHU4	DYHC1_MOUSE	LAETVFNFEK	1.55	1.11E-02	0.0219	21
Q9JHU4	DYHC1_MOUSE	FYFVGDEDLLEIIGNSK	4.86	1.13E-02	0.0221	21
P17427	AP2A2_MOUSE	THIETVINALK	1.09	2.30E-02	0.0350	21
Q61879	MYH10_MOUSE	C[+57]MLQDREDQSILC[+57]TGESGAGK	4.31	2.68E-02	0.0391	21
Q9Z0E0	NCDN_MOUSE	IPISTFLTR	3.88	2.85E-02	0.0409	21
Q8BH44	COR2B_MOUSE	NM[+16]TEALLELHGHSR	5.19	1.50E-03	0.0143	19
Q8BH44	COR2B_MOUSE	VC[+57]GHQGNVLDIK	4.37	1.56E-03	0.0143	19
Q8BH44	COR2B_MOUSE	NVHDNHFC[+57]AVNAR	4.51	1.64E-03	0.0143	19
Q8BH44	COR2B_MOUSE	WNPFDNIIASC[+57]SEDTSVR	5.79	1.97E-03	0.0143	19
Q8BH44	COR2B_MOUSE	VLQEANC[+57]K	4.64	2.37E-03	0.0143	19
Q8BH44	COR2B_MOUSE	YYEISTEKPYLSYLM[+16]EFF	5.31	2.70E-03	0.0143	19
Q8BH44	COR2B_MOUSE	TENELLR	4.28	2.93E-03	0.0143	19

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q8BH44	COR2B_MOUSE	DPVLM[+16]SLK	3.44	3.04E-03	0.0143	19
Q8BH44	COR2B_MOUSE	GLIEPISMIVPR	5.10	3.83E-03	0.0147	19
Q8BH44	COR2B_MOUSE	VLIWNLDIGEPVK	5.81	4.49E-03	0.0151	19
Q8BH44	COR2B_MOUSE	IWEIPDGGLK	4.19	6.46E-03	0.0170	19
Q8BH44	COR2B_MOUSE	QLQLELK	3.91	7.04E-03	0.0175	19
Q8BH44	COR2B_MOUSE	YYEISTEKPYLSYLMEFF	7.51	9.74E-03	0.0204	19
Q8BH44	COR2B_MOUSE	GLIEPISM[+16]IVPR	4.18	1.04E-02	0.0211	19
Q8BH44	COR2B_MOUSE	DPVLMCLK	4.29	1.08E-02	0.0215	19
Q8BH44	COR2B_MOUSE	FLAIVTESAGGGSFLVIPLEQTGR	2.67	1.11E-02	0.0219	19
Q8BH44	COR2B_MOUSE	VGLVEWHPTTNNILFSAGYDYK	6.00	1.69E-02	0.0281	19
P99029	PRDX5_MOUSE	ALNVEPDGTGLTC[+57]SLAPNILSQL	6.64	1.85E-02	0.0298	19
O35643	AP1B1_MOUSE	YNDPIYVK	2.45	2.90E-02	0.0414	19
Q9JKK7	TMOD2_MOUSE	QQLGTAVEM[+16]EIAQM[+16]LEENSR	3.82	2.31E-04	0.0143	19
Q9JKK7	TMOD2_MOUSE	NIDEDELLGK	3.78	2.54E-04	0.0143	19
Q9JKK7	TMOD2_MOUSE	QQLGTAVEMEIAQM[+16]LEENSR	4.00	4.22E-04	0.0143	19
Q9JKK7	TMOD2_MOUSE	AKPVFEEPPNPTNVEASLQQM[+16]K	4.78	6.52E-04	0.0143	19
Q9JKK7	TMOD2_MOUSE	FGYQFTK	4.37	7.56E-04	0.0143	19
Q9JKK7	TMOD2_MOUSE	SNDPVALAFAEMLK	5.14	8.22E-04	0.0143	19
Q9JKK7	TMOD2_MOUSE	ANDPSLQEVNLLNNIK	4.99	9.62E-04	0.0143	19
Q9JKK7	TMOD2_MOUSE	QLENVLDDLDPEATLPAGFR	6.98	1.24E-03	0.0143	19
Q9JKK7	TMOD2_MOUSE	FSLAATR	3.81	1.41E-03	0.0143	19
Q9JKK7	TMOD2_MOUSE	ENDTLTEIK	4.15	1.44E-03	0.0143	19
Q9JKK7	TMOD2_MOUSE	DREDFVPFTGEK	4.36	1.55E-03	0.0143	19
Q9JKK7	TMOD2_MOUSE	LSEEELK	4.81	1.56E-03	0.0143	19
Q9JKK7	TMOD2_MOUSE	QQLGTAVEM[+16]EIAQM[+16]LEENSR	7.39	1.71E-03	0.0143	19
Q9JKK7	TMOD2_MOUSE	AKPVFEEPPNPTNVEASLQQMK	5.08	3.04E-03	0.0143	19
Q9JKK7	TMOD2_MOUSE	QQLGTAVEMEIAQM[+16]LEENSR	4.56	4.20E-03	0.0149	19
Q9JKK7	TMOD2_MOUSE	SNDPVALAFAEM[+16]LK	3.75	5.37E-03	0.0158	19
Q9JKK7	TMOD2_MOUSE	EHLMLYLEK	5.75	6.01E-03	0.0164	19
Q9JKK7	TMOD2_MOUSE	FDEETTNGEGR	4.28	7.65E-03	0.0181	19
Q9JKK7	TMOD2_MOUSE	LSEEELKLENVLDDLDPEATLPAGFR	8.99	8.45E-03	0.0188	19
O08638	MYH11_MOUSE	QLVSNLEK	4.58	1.57E-03	0.0143	19
P05213	TBA1B_MOUSE	LISQIVSSITASLR	3.07	2.82E-03	0.0143	19
O08638	MYH11_MOUSE	KATLQAEQLSNELATER	4.48	3.05E-03	0.0143	19
P05213	TBA1B_MOUSE	AYHEQLSVAEITNAC[+57]FEPANQM[+16]VK	2.42	3.29E-03	0.0143	19
O08638	MYH11_MOUSE	LQNEVESVTGMLNEAEGK	3.59	3.30E-03	0.0143	19
O08638	MYH11_MOUSE	SM[+16]LQDREDQSILC[+57]TGESGAGK	5.18	3.48E-03	0.0144	19
P05213	TBA1B_MOUSE	FDGALNVDLTFEQTNLVYPR	4.07	4.20E-03	0.0149	19
P05213	TBA1B_MOUSE	YM[+16]AC[+57]C[+57]LLYR	1.39	4.21E-03	0.0149	19
P05213	TBA1B_MOUSE	QLFHPEQLITGK	2.29	5.16E-03	0.0155	19
P05213	TBA1B_MOUSE	AVC[+57]MLSNTTAIAEAWAF	2.86	5.17E-03	0.0155	19
P05213	TBA1B_MOUSE	TIGGGDDSFNTFFSETGAGK	2.23	5.86E-03	0.0163	19
O08638	MYH11_MOUSE	KLEGDASDFHEQIADLQAQIAELK	3.75	6.49E-03	0.0170	19
O08638	MYH11_MOUSE	VEDMAELTC[+57]LNEASVLHNLNR	4.46	6.57E-03	0.0171	19
P05213	TBA1B_MOUSE	EIIDLVLDLR	2.18	6.60E-03	0.0171	19
P05213	TBA1B_MOUSE	LDHKFDLMYAK	2.28	6.69E-03	0.0172	19
P05213	TBA1B_MOUSE	AVC[+57]M[+16]LSNTTAIAEAWAF	2.00	6.71E-03	0.0172	19
P05213	TBA1B_MOUSE	NLDIERPTYTNLNR	2.65	6.94E-03	0.0174	19
P05213	TBA1B_MOUSE	VGINYQPPTVVPGGDLAK	2.34	7.47E-03	0.0180	19
P05213	TBA1B_MOUSE	IHFPLATYAPVISA EK	2.40	7.71E-03	0.0181	19
O08638	MYH11_MOUSE	IRELEGHISDLQEDLDSER	3.81	7.72E-03	0.0181	19
O08638	MYH11_MOUSE	ELDEATESNEAMGR	2.68	7.73E-03	0.0182	19
O08638	MYH11_MOUSE	DVASLGSQQLQDTQELLQEETR	4.62	8.97E-03	0.0195	19
P05213	TBA1B_MOUSE	AYHEQLSVAEITNAC[+57]FEPANQMVK	3.10	9.28E-03	0.0199	19
P05213	TBA1B_MOUSE	QLFHPEQLITGKEDAANNYAR	3.09	1.01E-02	0.0207	19
O08638	MYH11_MOUSE	VVSSVLQLGNIVFK	5.44	1.09E-02	0.0216	19
P05213	TBA1B_MOUSE	LADQC[+57]TGLQGFLVFHSGGGTSGGFTSLLM[+16]ER	6.72	1.12E-02	0.0219	19
O08638	MYH11_MOUSE	LDAFLVLEQLR	5.42	1.17E-02	0.0225	19
P05213	TBA1B_MOUSE	YMAC[+57]C[+57]LLYR	2.34	1.19E-02	0.0227	19
O08638	MYH11_MOUSE	SMLQDREDQSILC[+57]TGESGAGK	5.22	1.21E-02	0.0229	19
P05213	TBA1B_MOUSE	EDMAALEK	1.53	1.22E-02	0.0230	19
O08638	MYH11_MOUSE	KLEVQLQDLQSK	4.54	1.25E-02	0.0232	19

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q8BYI9	TENR_MOUSE	VGFGNLEDEFWLGLDNIHR	4.04	1.74E-02	0.0285	19
Q8BPN8	DMXL2_MOUSE	FQLYNWLEK	8.09	2.09E-02	0.0326	19
Q62261	SPTB2_MOUSE	EQWANLEQLSAIR	3.90	2.16E-02	0.0335	19
P62242	RS8_MOUSE	4(ELEFYLR	1.65	2.17E-02	0.0336	19
Q8C0M9	ASGL1_MOUSE	GNLAYATSTGGIVNK	2.81	2.23E-02	0.0343	19
Q571F3	Q571F3_MOUSE	A[+42]AELEYESVLC[+57]VKPDSVYR	1.11	2.55E-02	0.0377	19
P57780	ACTN4_MOUSE	LVSIGAEIIVDGNK	2.46	2.89E-02	0.0414	19
P68033	ACTC_MOUSE	.EITALAPSTM[+16]K	3.38	4.93E-04	0.0143	19
P68033	ACTC_MOUSE	.DLTDYLM[+16]K	3.39	1.27E-03	0.0143	19
P68033	ACTC_MOUSE	.HQGVM[+16]VGMGQK	3.40	2.66E-03	0.0143	19
P68033	ACTC_MOUSE	.AVFPSIVGRPR	4.29	2.75E-03	0.0143	19
P68033	ACTC_MOUSE	.HQGVMVGM[+16]GQK	3.24	2.84E-03	0.0143	19
P68033	ACTC_MOUSE	.S[+42]YELPDGQVITIGNER	4.25	2.98E-03	0.0143	19
P68033	ACTC_MOUSE	.YPIEHGIITNWDDM[+16]EK	3.91	3.09E-03	0.0143	19
P68033	ACTC_MOUSE	.DIKEKLC[+57]YVALDFENEM[+16]ATAASSSSLEK	10.56	3.35E-03	0.0143	19
P68033	ACTC_MOUSE	.E[+42]ITALAPSTM[+16]K	2.45	3.37E-03	0.0143	19
P68033	ACTC_MOUSE	.IWHHTFYNELR	5.33	4.33E-03	0.0150	19
P68033	ACTC_MOUSE	.HQGVMVGMGQK	4.02	4.64E-03	0.0153	19
P68033	ACTC_MOUSE	.DSYVGDEAQSKR	4.33	5.89E-03	0.0163	19
P68033	ACTC_MOUSE	.IIAPPERK	3.91	6.15E-03	0.0166	19
P68033	ACTC_MOUSE	.DLTDYLMK	4.31	6.79E-03	0.0172	19
P68033	ACTC_MOUSE	.EITALAPSTMK	3.64	7.28E-03	0.0177	19
P68033	ACTC_MOUSE	.YPIEHGIITNWDDMEK	5.06	8.40E-03	0.0188	19
P68033	ACTC_MOUSE	.HQGVM[+16]VGM[+16]GQK	3.38	1.24E-02	0.0231	19
Q8CHC4	SYNJ1_MOUSE	VSEQTLQSASSK	3.39	2.28E-02	0.0348	19
Q6ZQ38	CAND1_MOUSE	C[+57]LDAVVSTR	3.70	3.19E-02	0.0447	19
P60710	ACTB_MOUSE	.QEYDESGPSIVHR	3.57	8.73E-04	0.0143	18
P60710	ACTB_MOUSE	.C[+57]PEALFQPSFLGM[+16]ESC[+57]GIHETTFNSIM[+16]K	4.25	1.53E-03	0.0143	18
P60710	ACTB_MOUSE	.KDLYANTVLSGGTTM[+16]YPGIADF	4.17	1.72E-03	0.0143	18
P60710	ACTB_MOUSE	.DLYANTVLSGGTTM[+16]YPGIADF	4.11	1.76E-03	0.0143	18
P60710	ACTB_MOUSE	.C[+57]PEALFQPSFLGMESC[+57]GIHETTFNSIM[+16]K	5.32	1.77E-03	0.0143	18
P60710	ACTB_MOUSE	.C[+57]PEALFQPSFLGM[+16]ESC[+57]GIHETTFNSIMK	5.32	1.80E-03	0.0143	18
P60710	ACTB_MOUSE	.TTGIVM[+16]DSGDGVHTVPIYEGYALPHAILF	5.89	2.01E-03	0.0143	18
P60710	ACTB_MOUSE	.GYSFTTTAER	3.61	2.04E-03	0.0143	18
P60710	ACTB_MOUSE	.C[+57]DVDIR	4.05	2.28E-03	0.0143	18
P60710	ACTB_MOUSE	.EKLC[+57]YVALDFEQEMATAASSSSLEK	4.51	2.52E-03	0.0143	18
P60710	ACTB_MOUSE	.VAPEEHPVLLTEAPLNPK	3.91	3.12E-03	0.0143	18
P60710	ACTB_MOUSE	.C[+57]PEALFQPSFLGMESC[+57]GIHETTFNSIMK	6.16	3.54E-03	0.0144	18
P60710	ACTB_MOUSE	.EKLC[+57]YVALDFEQEM[+16]ATAASSSSLEK	4.11	3.83E-03	0.0147	18
P60710	ACTB_MOUSE	.G[+42]YSFTTTAER	4.08	3.91E-03	0.0147	18
P60710	ACTB_MOUSE	.KDLYANTVLSGGTTMYPGIADF	3.14	4.73E-03	0.0153	18
P60710	ACTB_MOUSE	.DLYANTVLSGGTTMYPGIADF	5.17	5.44E-03	0.0158	18
H3BJD0	H3BJD0_MOUSE	NEPLEDAEANVVGSER	9.94	1.99E-02	0.0314	18
P48962	ADT1_MOUSE	.DFLAGGIAAAVSK	6.07	2.86E-02	0.0410	18
O08553	DPYL2_MOUSE	FQLTDSQIYEVLSVIR	3.53	5.46E-04	0.0143	18
O08553	DPYL2_MOUSE	DHGVNSFLVYMAFK	3.29	6.09E-04	0.0143	18
O08553	DPYL2_MOUSE	DRFQLTDSQIYEVLSVIR	4.99	8.90E-04	0.0143	18
O08553	DPYL2_MOUSE	AALAGGTTM[+16]IIDHVVPEPGTSLAAFDQWF	10.63	9.81E-04	0.0143	18
O08553	DPYL2_MOUSE	ILDLGITGPEGHVLSRPEEVEAEAVNR	2.44	2.16E-03	0.0143	18
O08553	DPYL2_MOUSE	IVNDDQSFYADIYM[+16]JEDGLIK	1.35	3.27E-03	0.0143	18
O08553	DPYL2_MOUSE	ISVGSADLVIWDPDSVK	2.10	3.43E-03	0.0144	18
O08553	DPYL2_MOUSE	AALAGGTTMIIDHVVPEPGTSLAAFDQWF	9.57	3.64E-03	0.0146	18
O08553	DPYL2_MOUSE	DIGAIAQVHAENGDIIEEQQF	1.55	4.61E-03	0.0153	18
O08553	DPYL2_MOUSE	THNSALEYNIFEGMEC[+57]R	2.06	5.58E-03	0.0160	18
O08553	DPYL2_MOUSE	IVNDDQSFYADIYMEDGLIK	3.06	6.13E-03	0.0166	18
O08553	DPYL2_MOUSE	NLHQSGFSLSGAQIDDNIPR	1.33	9.05E-03	0.0196	18
O08553	DPYL2_MOUSE	SITIANQTNK[+57]PLVYTK	1.43	9.33E-03	0.0199	18
O08553	DPYL2_MOUSE	THNSALEYNIFEGM[+16]EC[+57]R	1.17	9.74E-03	0.0204	18
O08553	DPYL2_MOUSE	GLYDGPVC[+57]EVSVTPK	1.18	1.29E-02	0.0237	18
O08553	DPYL2_MOUSE	FQMPDQGM[+16]TSADDFQGTK	1.08	1.49E-02	0.0259	18
P50518	VATE1_MOUSE	LDLIAQQM[+16]M[+16]PEVR	0.88	1.81E-02	0.0294	18
P63330	PP2AA_MOUSE	YSFLQFDPAPR	1.05	2.84E-02	0.0408	18

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9D6F9	TBB4A_MOUSE	EVDEQM[+16]LSVQSK	1.88	1.22E-03	0.0143	17
Q9D6F9	TBB4A_MOUSE	M[+16]REIVHLQAGQC[+57]GNQIGAK	2.53	1.29E-03	0.0143	17
Q9D6F9	TBB4A_MOUSE	GHYTEGAELVDAVLDVVR	4.66	2.22E-03	0.0143	17
Q9D6F9	TBB4A_MOUSE	IM[+16]NTFSVVPSPK	1.68	2.90E-03	0.0143	17
Q9D6F9	TBB4A_MOUSE	ALTVPELTQQM[+16]FDAK	2.15	2.91E-03	0.0143	17
Q9D6F9	TBB4A_MOUSE	ALTVPELTQQMFDAK	2.50	3.40E-03	0.0143	17
Q9D6F9	TBB4A_MOUSE	EIVHLQAGQC[+57]GNQIGAK	2.28	4.11E-03	0.0148	17
Q9D6F9	TBB4A_MOUSE	MAATFIGNSTAIQELFK	3.11	4.73E-03	0.0153	17
Q9D6F9	TBB4A_MOUSE	EVDEQMLSVQSK	2.21	7.45E-03	0.0180	17
Q9D6F9	TBB4A_MOUSE	INVYYNEATGGNYVPR	3.21	7.61E-03	0.0181	17
Q9D6F9	TBB4A_MOUSE	AVLVDLEPGTM[+16]DSVR	1.87	7.91E-03	0.0183	17
Q9D6F9	TBB4A_MOUSE	MREIVHLQAGQC[+57]GNQIGAK	3.06	9.60E-03	0.0203	17
Q9D6F9	TBB4A_MOUSE	IMNTFSVVPSPK	2.38	9.89E-03	0.0205	17
Q9D6F9	TBB4A_MOUSE	AVLVDLEPGTMDSVR	2.74	1.11E-02	0.0219	17
Q9D6F9	TBB4A_MOUSE	EAESC[+57]DC[+57]LQGFQLTHSLGGGTGSGMGTLLISK	3.66	1.13E-02	0.0221	17
Q9D6F9	TBB4A_MOUSE	FWEVISDEHGIDPTGTYHGSDSLQLER	6.20	1.25E-02	0.0232	17
Q9D6F9	TBB4A_MOUSE	YLTVAAVFR	2.84	1.66E-02	0.0277	17
P26039	TLN1_MOUSE	1IPEALAGPPNDFGLFLSDDPKK	3.15	3.15E-04	0.0143	16
P26039	TLN1_MOUSE	1GVAALTSDPAVQAIVLDTASDVLDK	6.26	8.73E-04	0.0143	16
P26039	TLN1_MOUSE	1TLAESALQLLYTAK	4.08	1.65E-03	0.0143	16
P26039	TLN1_MOUSE	1VGDDPAVWQLK	2.39	1.95E-03	0.0143	16
P26039	TLN1_MOUSE	1VAGSVTELIQAAEAMK	4.26	2.26E-03	0.0143	16
P26039	TLN1_MOUSE	1ILAQATSDLVNAIK	4.33	3.03E-03	0.0143	16
P26039	TLN1_MOUSE	1GVGAAATAVTQALNELLQHVK	9.34	3.60E-03	0.0145	16
P26039	TLN1_MOUSE	1LLAALLEDEGGNGRPLLQAAK	2.43	6.34E-03	0.0169	16
P26039	TLN1_MOUSE	1LAQAAQSSVATITR	4.16	9.57E-03	0.0202	16
P26039	TLN1_MOUSE	1AVASAAAALVLK	5.68	1.27E-02	0.0234	16
P26039	TLN1_MOUSE	1LNEAAAAGLNQAATELVQASR	3.22	1.60E-02	0.0271	16
P26039	TLN1_MOUSE	1GSQAQPDSPSAQLALIAASQSFLQPGGK	6.17	1.68E-02	0.0279	16
Q99104	MYO5A_MOUSE	NSLHLLMETLNATTPHYVR	2.63	1.72E-02	0.0284	16
Q62261	SPTB2_MOUSE	LAEISDVWEEMK	5.87	2.07E-02	0.0324	16
P60229	EIF3E_MOUSE	HLVFPILLEFLSVK	4.63	2.20E-02	0.0340	16
Q9CXY6	ILF2_MOUSE	InNQDLAPNSAEQASISLSLVTK	3.51	3.28E-02	0.0458	16
P47757	CAPZB_MOUSE	SGSGTM[+16]NLGGSLTR	3.45	1.13E-03	0.0143	15
P47757	CAPZB_MOUSE	STLNEIYFGK	3.98	1.38E-03	0.0143	15
P47757	CAPZB_MOUSE	DYLLC[+57]DYNR	3.90	1.60E-03	0.0143	15
P47757	CAPZB_MOUSE	LEVEANNAFDQYR	4.57	2.45E-03	0.0143	15
P47757	CAPZB_MOUSE	SPWSNKYDPPLEDGAMPSAR	5.16	2.62E-03	0.0143	15
P47757	CAPZB_MOUSE	RLPPQQIEK	4.39	2.85E-03	0.0143	15
P47757	CAPZB_MOUSE	KLEVEANNAFDQYR	4.35	3.35E-03	0.0143	15
P47757	CAPZB_MOUSE	SGSGTMNLGGSLTR	4.20	3.57E-03	0.0145	15
P47757	CAPZB_MOUSE	LTSTVM[+16]LWLQTNK	6.15	3.94E-03	0.0147	15
P47757	CAPZB_MOUSE	SPWSNKYDPPLEDGAM[+16]PSAR	4.92	4.08E-03	0.0148	15
P47757	CAPZB_MOUSE	GC[+57]WDSIHVVEVQEK	4.86	6.15E-03	0.0166	15
P47757	CAPZB_MOUSE	LVEDM[+16]JENK	3.73	9.29E-03	0.0199	15
P47757	CAPZB_MOUSE	YDPPLEDGAMPSAR	4.63	1.12E-02	0.0219	15
P47757	CAPZB_MOUSE	LTSTVMLWLQTNK	6.84	1.52E-02	0.0263	15
Q8C0C7	SYFA_MOUSE	1SLQALGEVIEAELR	4.87	2.32E-02	0.0352	15
P52480	KPYM_MOUSE	LNFSHGTHEYHAETIK	2.27	8.78E-04	0.0143	15
P52480	KPYM_MOUSE	FGVEQDVDM[+16]VFASFIR	3.04	1.62E-03	0.0143	15
P52480	KPYM_MOUSE	RFDEILEASDGIMVAR	2.17	4.88E-03	0.0155	15
P52480	KPYM_MOUSE	AEGSDVANAVLDGADC[+57]IM[+16]LSGETAK	1.18	4.94E-03	0.0155	15
P52480	KPYM_MOUSE	DAVLNAWAEDVDLR	1.47	5.43E-03	0.0158	15
P52480	KPYM_MOUSE	RFDEILEASDGIM[+16]VAR	1.63	6.30E-03	0.0168	15
P52480	KPYM_MOUSE	FDEILEASDGIM[+16]VAR	2.75	6.32E-03	0.0169	15
P01869	IGH1M_MOUSE	APQVYTIPPPKEQM[+16]AK	2.09	1.84E-02	0.0297	15
Q8VDD5	MYH9_MOUSE	VEEEAAQK	0.73	2.02E-02	0.0318	15
Q91WK2	EIF3H_MOUSE	TAQGSLSLK	5.38	2.06E-02	0.0323	15
P61979	HNRPK_MOUSE	IDEPLEGSEDR	1.88	2.65E-02	0.0388	15
Q8C8N2	SCAI_MOUSE	FTSETSYLNEAFSFSAIR	1.63	2.90E-02	0.0414	15
Q61171	PRDX2_MOUSE	EGGLGPLNIPLADVTK	1.17	3.01E-02	0.0427	15
P26039	TLN1_MOUSE	1NLGTALAEELR	2.13	3.29E-02	0.0460	15

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q8CI94	PYGB_MOUSE	WLLLC[+57]NPGLAEIIVER	1.20	3.56E-02	0.0492	15
Q8BYI9	TENR_MOUSE	ITFTPSSGISSEVTVPR	2.16	9.87E-05	0.0143	14
Q8BYI9	TENR_MOUSE	DKEEDMLEVLLDATKR	3.66	1.47E-03	0.0143	14
Q8BYI9	TENR_MOUSE	LEGLSENTDYTVLLQAAQEATR	3.00	6.40E-03	0.0169	14
Q8BYI9	TENR_MOUSE	AAIENYVLTYSK	2.92	7.23E-03	0.0177	14
Q8BYI9	TENR_MOUSE	DKEEDMLEVLLDATK	4.11	8.44E-03	0.0188	14
Q8BYI9	TENR_MOUSE	SPPTSASVSTVIDGPTQILVR	2.85	8.61E-03	0.0190	14
Q8BYI9	TENR_MOUSE	LYPATEYEISLNSVR	2.47	9.88E-03	0.0205	14
Q8BYI9	TENR_MOUSE	YEVSISAVR	2.15	1.22E-02	0.0230	14
Q8BYI9	TENR_MOUSE	DVSDTVAFVEWTPPR	2.79	1.22E-02	0.0230	14
Q8BYI9	TENR_MOUSE	SSLTSTVFTTGGR	2.06	1.42E-02	0.0251	14
Q8BYI9	TENR_MOUSE	YGLVGGEGGK	1.73	1.51E-02	0.0262	14
D0U286	D0U286_MOUSE	ELLGNVIM[+16]IVLGHHLGK	8.73	1.73E-02	0.0284	14
Q99104	MYO5A_MOUSE	QQQLLAQNLQLPPEAR	2.64	1.82E-02	0.0295	14
Q8C0M9	ASGL1_MOUSE	LQAGIDLC[+57]ETR	3.00	3.36E-02	0.0468	14
P47857	PFKAM_MOUSE	SEWSDLLNDLQK	2.78	2.16E-04	0.0143	14
P47857	PFKAM_MOUSE	GITNLC[+57]VIGGDGSLTGADTFR	2.98	3.29E-04	0.0143	14
P47857	PFKAM_MOUSE	LPLM[+16]EC[+57]VQVTK	1.61	2.30E-03	0.0143	14
P47857	PFKAM_MOUSE	VLVVDHGFEGFLAK	2.04	2.88E-03	0.0143	14
P47857	PFKAM_MOUSE	LNIIIVAEGAIDK	4.51	3.99E-03	0.0148	14
P47857	PFKAM_MOUSE	MGVEAVMALLEGTPDTPAC[+57]VVSLSGNQAVF	5.60	5.54E-03	0.0159	14
P47857	PFKAM_MOUSE	NLEQISANITK	1.65	5.74E-03	0.0161	14
P47857	PFKAM_MOUSE	DLQVNVHLVQK	2.30	6.28E-03	0.0168	14
P47857	PFKAM_MOUSE	ALVFQPVTEK	1.83	8.07E-03	0.0184	14
P47857	PFKAM_MOUSE	VFFVHEGYQGLVDGGEHIR	1.60	9.85E-03	0.0205	14
P47857	PFKAM_MOUSE	VGIFTGAR	1.63	1.18E-02	0.0226	14
P47857	PFKAM_MOUSE	IGLIQGNR	1.65	1.19E-02	0.0227	14
P47857	PFKAM_MOUSE	C[+57]NENYTTDFIFNLYSEEGK	6.13	1.19E-02	0.0227	14
P47857	PFKAM_MOUSE	TFVLEVMGR	2.60	1.34E-02	0.0242	14
Q6A087	Q6A087_MOUSE	SLDDFQAWLGR	2.51	8.52E-04	0.0143	13
Q6A087	Q6A087_MOUSE	VIESTQGLGNDLAGVLALQR	3.64	2.34E-03	0.0143	13
Q6A087	Q6A087_MOUSE	DVEDEILWVTER	5.64	3.01E-03	0.0143	13
Q6A087	Q6A087_MOUSE	LVSQDNFGLELAAVEAAVR	4.52	3.47E-03	0.0144	13
Q6A087	Q6A087_MOUSE	IIGTQEQLNQR	2.51	5.18E-03	0.0156	13
Q6A087	Q6A087_MOUSE	KHEAIETDIVAYSGR	4.36	5.33E-03	0.0158	13
Q6A087	Q6A087_MOUSE	TLGTAAGPELAELQEMWK	5.04	9.49E-03	0.0202	13
Q6A087	Q6A087_MOUSE	VTAVNDIAEQLLK	4.38	1.09E-02	0.0216	13
Q6A087	Q6A087_MOUSE	LTLEQGQQLVAEGHPGANQASTR	3.20	1.13E-02	0.0221	13
Q6A087	Q6A087_MOUSE	LLLNLLELQK	4.44	1.24E-02	0.0231	13
Q6A087	Q6A087_MOUSE	TQTAVASEEGPATLPEAEALLAQHAALF	4.08	1.31E-02	0.0239	13
Q6A087	Q6A087_MOUSE	VGELTQEANALAAGHPAQAPAINTF	3.62	1.45E-02	0.0255	13
P27323	HS901_ARATH_Hc	SLTNDWEDHLAVK	7.14	3.05E-02	0.0431	13
Q8C8N2	SCAI_MOUSE	FNFTNLFGQPLVC[+57]LLSPTAYPK	8.81	2.28E-03	0.0143	13
Q8C8N2	SCAI_MOUSE	F DIAQLLTHSR	4.10	3.14E-03	0.0143	13
Q8C8N2	SCAI_MOUSE	F FSELTVDMFR	3.80	3.29E-03	0.0143	13
Q8C8N2	SCAI_MOUSE	F TVTDFC[+57]YLLDK	5.14	3.46E-03	0.0144	13
Q8C8N2	SCAI_MOUSE	F FSELTVDM[+16]FR	2.12	3.78E-03	0.0147	13
Q8C8N2	SCAI_MOUSE	F KPLFIVVDSSNSVAYK	4.17	5.88E-03	0.0163	13
Q8C8N2	SCAI_MOUSE	F SDGEGPYDFGGVLTNSNR	7.28	8.57E-03	0.0190	13
Q8C8N2	SCAI_MOUSE	F SYYSQVNKEDRPELVVK	7.68	1.04E-02	0.0211	13
Q8C8N2	SCAI_MOUSE	F QWQSYFGR	3.73	1.36E-02	0.0244	13
Q8C8N2	SCAI_MOUSE	F FIVVC[+57]LLLNK	9.14	1.38E-02	0.0247	13
Q8C8N2	SCAI_MOUSE	F IGQLYHYHLYR	3.45	1.55E-02	0.0266	13
Q8C8N2	SCAI_MOUSE	F HILELASILDVR	9.08	1.68E-02	0.0279	13
Q8BH44	COR2B_MOUSE	HGLDVSAC[+57]EVFR	5.19	2.90E-02	0.0414	13
O35643	AP1B1_MOUSE	LASQANIAQVLAELK	1.85	1.73E-03	0.0143	13
O35643	AP1B1_MOUSE	LGAPISSGLSDLFDLTSGVGTLSGSYVAPK	3.62	2.44E-03	0.0143	13
O35643	AP1B1_MOUSE	KPTETQELVQQVLSLATQDSDNPDLR	4.24	3.83E-03	0.0147	13
O35643	AP1B1_MOUSE	LAPPLVTLTSAEPELQYVALR	2.79	4.09E-03	0.0148	13
O35643	AP1B1_MOUSE	LVYLYLMNYAK	2.67	4.63E-03	0.0153	13
O35643	AP1B1_MOUSE	M[+16]EPLNNLQVAVK	4.25	4.91E-03	0.0155	13
O35643	AP1B1_MOUSE	C[+57]VSTLLDLIQTK	2.30	5.87E-03	0.0163	13

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
O35643	AP1B1_MOUSE	EYATEVDVDFVR	3.06	1.23E-02	0.0231	13
O35643	AP1B1_MOUSE	AAMIWIVGEYAER	3.12	1.27E-02	0.0234	13
O35643	AP1B1_MOUSE	LVYLYLM[+16]NYAK	2.00	1.38E-02	0.0247	13
O35643	AP1B1_MOUSE	LSHANSAVVLSAVK	1.44	1.52E-02	0.0263	13
P46460	NSF_MOUSE	VIFSNLVLQALLVLLKK	1.58	2.40E-02	0.0361	13
Q99JY9	ARP3_MOUSE	/DITYFIQQLLR	1.36	2.89E-02	0.0414	13
Q9JJ28	FLII_MOUSE	Pr.LTSLEEFMAANNLELIPESLC[+57]R	7.95	2.14E-03	0.0143	13
Q9JJ28	FLII_MOUSE	Pr.TQSNLPTSLEGLSNLSDVDLSC[+57]NDLTR	5.99	3.06E-03	0.0143	13
Q9JJ28	FLII_MOUSE	Pr.M[+42]EATGVLPFVR	5.16	3.45E-03	0.0144	13
Q9JJ28	FLII_MOUSE	Pr.VGLGLGYLELPQINYK	5.88	4.43E-03	0.0151	13
Q9JJ28	FLII_MOUSE	Pr.LLQSLLDTR	5.32	4.67E-03	0.0153	13
Q9JJ28	FLII_MOUSE	Pr.ADLTALFLPR	5.74	5.26E-03	0.0157	13
Q9JJ28	FLII_MOUSE	Pr.LAEDILNTMFDASYK	5.96	5.88E-03	0.0163	13
Q9JJ28	FLII_MOUSE	Pr.NAEAVLQGQGLSGK	5.64	7.36E-03	0.0178	13
Q9JJ28	FLII_MOUSE	Pr.TGLC[+57]YLPEELAAALQK	3.16	7.74E-03	0.0182	13
Q9JJ28	FLII_MOUSE	Pr.NQLTSLPSAIC[+57]K	2.98	7.97E-03	0.0183	13
Q9JJ28	FLII_MOUSE	Pr.LDFDGLPSGIGK	3.36	8.49E-03	0.0189	13
Q9JJ28	FLII_MOUSE	Pr.VPEC[+57]LYTLPSLR	5.48	8.88E-03	0.0194	13
Q9JJ28	FLII_MOUSE	Pr.LAGASPATVAAAAAVGSGSKDPLAF	6.09	9.42E-03	0.0201	13
P39053	DYN1_MOUSE	IIEGSGDQIDTYELSGGAR	4.20	1.61E-03	0.0143	13
P39053	DYN1_MOUSE	IALLQMVQQFAVDFEK	5.88	4.56E-03	0.0152	13
P39053	DYN1_MOUSE	IIEGSGDQIDTYELSGGAR	1.36	4.78E-03	0.0154	13
P39053	DYN1_MOUSE	IHFALFNTEQR	2.07	5.75E-03	0.0161	13
P39053	DYN1_MOUSE	IQLELAC[+57]ETQEEVDSWK	2.59	8.34E-03	0.0188	13
P39053	DYN1_MOUSE	IC[+57]VDMVISELISTVR	3.91	1.07E-02	0.0214	13
O08638	MYH11_MOUSE	QADLEKEELAEELASSLSGR	2.58	2.16E-02	0.0335	13
A0A0B6VMB;A0A0B6VMB2_MC	NTQPIM[+16]DTDGSYFVYSK		2.00	2.61E-02	0.0384	13
P35980	RL18_MOUSE	€TAVVVGTVTDVDR	1.24	2.64E-02	0.0387	13
Q5SYD0	MYO1D_MOUSE	HQVEYLGLLENVR	0.71	2.72E-02	0.0395	13
Q76MZ3	2AAA_MOUSE	€VLAM[+16]SGDPNYLHR	2.13	3.07E-02	0.0434	13
Q9JMH9	MY18A_MOUSE	TEEQIAAEEAWYETEK	1.05	3.23E-02	0.0452	13
P48036	ANXA5_MOUSE	TPEELSAIK	1.68	3.39E-02	0.0472	13
Q8VDN2	AT1A1_MOUSE	QAADM[+16]ILLDDNFASIVTGVEEGR	2.72	5.34E-04	0.0143	12
Q8VDN2	AT1A1_MOUSE	SPDFTNENPLETR	2.11	7.34E-04	0.0143	12
Q8VDN2	AT1A1_MOUSE	GVGIISEGNETVEDIAAR	3.62	2.59E-03	0.0143	12
Q8VDN2	AT1A1_MOUSE	DGPNALTPPPTTPEWVK	2.87	4.28E-03	0.0150	12
Q8VDN2	AT1A1_MOUSE	AVAGDASESALLK	3.61	4.30E-03	0.0150	12
Q8VDN2	AT1A1_MOUSE	QGAIVAVTGDGVNDSPALKK	2.01	5.07E-03	0.0155	12
Q8VDN2	AT1A1_MOUSE	LNIPVNQVNPR	1.63	5.95E-03	0.0163	12
Q8VDN2	AT1A1_MOUSE	QAADMILLDDNFASIVTGVEEGR	4.00	6.75E-03	0.0172	12
Q8VDN2	AT1A1_MOUSE	NM[+16]VPQQALVIR	1.93	7.26E-03	0.0177	12
Q8VDN2	AT1A1_MOUSE	QGAIVAVTGDGVNDSPALK	2.45	7.84E-03	0.0182	12
Q8VDN2	AT1A1_MOUSE	VDNSSLTGESEPQTR	1.37	8.05E-03	0.0184	12
Q8VDN2	AT1A1_MOUSE	NLEAVETLGGSTSTIC[+57]SDK	2.73	1.38E-02	0.0247	12
Q60875	ARHG2_MOUSE	LGDLLISQFSGSNAEQMR	3.48	1.52E-03	0.0143	12
Q60875	ARHG2_MOUSE	AAVASVTPEK	1.73	2.94E-03	0.0143	12
Q60875	ARHG2_MOUSE	NNTALQSVSLR	3.68	3.18E-03	0.0143	12
Q60875	ARHG2_MOUSE	SVSTTNIAGHFNDESPLGLR	3.78	3.74E-03	0.0147	12
Q60875	ARHG2_MOUSE	YIFTSLDKPSVVSLQNLIVR	8.54	4.11E-03	0.0148	12
Q60875	ARHG2_MOUSE	LQEIYNR	2.58	6.03E-03	0.0164	12
Q60875	ARHG2_MOUSE	ILQNSHGVEEEYQDLASALGLVK	6.82	7.42E-03	0.0179	12
Q60875	ARHG2_MOUSE	FLNQLLER	6.49	9.06E-03	0.0196	12
Q60875	ARHG2_MOUSE	SLPAGDALYLSFNPPQPSR	3.18	1.00E-02	0.0206	12
Q60875	ARHG2_MOUSE	LESFESLR	2.24	1.60E-02	0.0271	12
P02088	HBB1_MOUSE	IVITAFNDGLNHLDSLK	3.88	2.11E-02	0.0329	12
Q61656	DDX5_MOUSE	IENQAINPK	3.25	2.46E-02	0.0367	12
Q8CI94	PYGB_MOUSE	VIPAADLSQQISTAGTEASGTGNM[+16]K	1.74	1.23E-04	0.0143	12
Q8CI94	PYGB_MOUSE	LKQEYFVVAATLQDIIR	4.55	3.90E-03	0.0147	12
Q8CI94	PYGB_MOUSE	LKDFNVGDYIEAVLDR	4.45	4.40E-03	0.0150	12
Q8CI94	PYGB_MOUSE	IGEGFLTDLSQLKK	2.04	4.45E-03	0.0151	12
Q8CI94	PYGB_MOUSE	LLSLVDDEAFIR	1.79	7.44E-03	0.0179	12
Q8CI94	PYGB_MOUSE	GIAGLGDVAEVR	1.53	7.57E-03	0.0180	12

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q8CI94	PYGB_MOUSE	VAIQLNDTHPALSIPELMR	2.07	7.76E-03	0.0182	12
Q8CI94	PYGB_MOUSE	VLYPNDNFFEGK	1.40	1.02E-02	0.0208	12
Q8CI94	PYGB_MOUSE	VIFLENYR	1.48	1.24E-02	0.0231	12
Q8CI94	PYGB_MOUSE	LAAC[+57]FLDSMATGLAAYGYGIF	8.24	1.61E-02	0.0272	12
P07901	HS90A_MOUSE	TLTIVDTGIGMTK	1.24	2.43E-02	0.0364	12
P51410	RL9_MOUSE	60 TGVAC[+57]SVSQAQK	1.86	3.56E-02	0.0492	12
P97427	DPYL1_MOUSE	NLHQS NFSLSGAQIDNNPR	1.37	2.95E-03	0.0143	12
P97427	DPYL1_MOUSE	I AVGSDADVWIWDPDK	3.53	3.31E-03	0.0143	12
P97427	DPYL1_MOUSE	STVEYNIFEGMEC[+57]HGSPLVVISQGK	3.03	4.68E-03	0.0153	12
P97427	DPYL1_MOUSE	GM[+16]YDGPVYEV PATPK	2.28	7.90E-03	0.0183	12
P97427	DPYL1_MOUSE	GLGAVILVHAENGDLIAQEYK	1.76	8.37E-03	0.0188	12
P97427	DPYL1_MOUSE	IINDDQSFYADVYLEGLIK	6.55	9.52E-03	0.0202	12
P97427	DPYL1_MOUSE	DNFTLIPEGVNGIEER	1.50	1.01E-02	0.0207	12
P97427	DPYL1_MOUSE	DLYQMSDSQLYEAF TFLK	5.43	1.23E-02	0.0231	12
P47963	RL13_MOUSE	6 GFSLEELR	1.07	1.82E-02	0.0295	12
Q91V92	ACLY_MOUSE	7 TIAIIAEGIPEALTF	1.37	1.87E-02	0.0300	12
Q6ZQ38	CAND1_MOUSE	LG TLSALDILIK	3.57	3.11E-02	0.0438	12
H3BJD0	H3BJD0_MOUSE	LYDSVSSTDGEDSLER	0.96	3.13E-02	0.0440	12
Q76MZ3	2AAA_MOUSE	3 QLSQSLLPAIVELAEDAK	3.29	1.73E-04	0.0143	11
P58252	EF2_MOUSE	EI ALLELQLEPEELYQTFQR	4.30	2.69E-04	0.0143	11
Q76MZ3	2AAA_MOUSE	3 SALASVIM[+16]GLSPILGK	3.70	3.70E-04	0.0143	11
P58252	EF2_MOUSE	EI EGIPALDNFLDKL	3.02	3.71E-04	0.0143	11
Q76MZ3	2AAA_MOUSE	3 SALASVIMGLSPILGK	2.92	4.18E-04	0.0143	11
P58252	EF2_MOUSE	EI VFDAIMNFR	3.43	9.43E-04	0.0143	11
Q76MZ3	2AAA_MOUSE	3 EFC[+57]ENLSADC[+57]JR	2.15	1.14E-03	0.0143	11
P58252	EF2_MOUSE	EI TFC[+57]QLILDPIFK	2.57	1.73E-03	0.0143	11
Q76MZ3	2AAA_MOUSE	3 LNIISNLDC[+57]VNEVIGIR	2.93	2.16E-03	0.0143	11
P58252	EF2_MOUSE	EI YVEPIEDVPC[+57]GNIVGLVGVDQFLVK	3.23	3.16E-03	0.0143	11
P13020	GELS_MOUSE	3 SEDC[+57]FILDHGR	4.30	3.32E-03	0.0143	11
Q76MZ3	2AAA_MOUSE	3 DNTIEHLLPLFLAQLK	7.56	3.90E-03	0.0147	11
P13020	GELS_MOUSE	3 HVVPNEVVVQR	5.25	4.35E-03	0.0150	11
P58252	EF2_MOUSE	EI WLPAGDALLQMITIHLPSPVTAQK	9.27	4.48E-03	0.0151	11
P13020	GELS_MOUSE	3 DSQEEEKTEALTS AK	3.92	4.59E-03	0.0152	11
Q76MZ3	2AAA_MOUSE	3 YFAQEALTVLSLA	2.31	4.68E-03	0.0153	11
P58252	EF2_MOUSE	EI C[+57]LYASVLT AQPR	1.76	6.00E-03	0.0164	11
P13020	GELS_MOUSE	3 EVQGFESSTFSGYFK	4.97	6.55E-03	0.0171	11
Q76MZ3	2AAA_MOUSE	3 DNTIEHLLPLFLAQLKDEC[+57]PEVR	7.20	6.96E-03	0.0174	11
P13020	GELS_MOUSE	3 YIETDPANR	4.03	7.03E-03	0.0175	11
P13020	GELS_MOUSE	3 SGALNSNDAFVLK	3.23	8.00E-03	0.0183	11
Q76MZ3	2AAA_MOUSE	3 LSTIALALGVER	2.46	8.03E-03	0.0184	11
P13020	GELS_MOUSE	3 VSNAGAGSMSVSLVADENPFAQGALR	6.14	8.32E-03	0.0187	11
P13020	GELS_MOUSE	3 QTQVSVLPEGGETPLFK	4.94	8.64E-03	0.0191	11
P58252	EF2_MOUSE	EI ETVSEESNVLC[+57]LSK	3.98	1.10E-02	0.0217	11
Q76MZ3	2AAA_MOUSE	3 ENVIMTQILPC[+57]IK	2.67	1.26E-02	0.0233	11
P13020	GELS_MOUSE	3 VPVDPATYGFYGGDSYIILYNYF	4.49	1.48E-02	0.0258	11
P58252	EF2_MOUSE	EI STL TDSLVC[+57]K	2.88	1.54E-02	0.0265	11
P58252	EF2_MOUSE	EI STAISLFYELSENDLNFIK	6.53	1.59E-02	0.0270	11
P13020	GELS_MOUSE	3 DGGQTAPASIR	3.49	1.59E-02	0.0270	11
Q8CGF6	WDR47_MOUSE	LIHDTANIHTSTPR	3.26	1.81E-02	0.0294	11
O70194	EIF3D_MOUSE	LGDDIDLIVR	2.04	2.25E-02	0.0345	11
P48453	PP2BB_MOUSE	YENNV MNIR	4.53	3.06E-02	0.0432	11
P16858	G3P_MOUSE	G VIHDNFGIVEGLM[+16]TTVHAITATQK	2.56	2.09E-04	0.0143	11
P16858	G3P_MOUSE	G VIHDNFGIVEGLMTTVHAITATQK	5.88	1.77E-03	0.0143	11
P16858	G3P_MOUSE	G WGEAGAEYVVESTGVFTTMEK	1.87	2.65E-03	0.0143	11
P16858	G3P_MOUSE	G LVINGK PITIFQER	1.69	4.81E-03	0.0154	11
P16858	G3P_MOUSE	G LISWYDNEYGYSNR	2.03	5.36E-03	0.0158	11
P16858	G3P_MOUSE	G RVIISAPSADAPMFVMGVNHEK	2.53	6.25E-03	0.0168	11
P16858	G3P_MOUSE	G RVIISAPSADAPMFVM[+16]GVNHEK	1.53	1.42E-02	0.0251	11
P16858	G3P_MOUSE	G RVIISAPSADAPM[+16]FVMGVNHEK	1.50	1.60E-02	0.0271	11
P97427	DPYL1_MOUSE	IFNLYPR	1.59	1.87E-02	0.0300	11
P17426	AP2A1_MOUSE	EM[+16]GEAFAADIPR	1.41	2.01E-02	0.0317	11
P63101	1433Z_MOUSE	DNLT LWTS D TQGDEAEAGEGGEN	1.02	2.97E-02	0.0422	11

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9JLM8	DCLK1_MOUSE	DASGMLYNLASAIK	5.02	3.79E-04	0.0143	10
Q9JLM8	DCLK1_MOUSE	SFEALLADLTR	4.13	5.43E-04	0.0143	10
Q2QL88	CAZA2_MICMU F-	IVEAAENEYQTAISENYQTM[+16]SDTTFH	4.30	9.14E-04	0.0143	10
Q9ERD7	TBB3_MOUSE	1M[+16]SSTFIGNSTAIQELFK	2.00	1.01E-03	0.0143	10
Q9ERD7	TBB3_MOUSE	1LATPTYGDLNHLVSATM[+16]SGVTTSLF	2.35	1.29E-03	0.0143	10
Q9JLM8	DCLK1_MOUSE	TAHSFEQVLTIDTAIK	6.04	1.45E-03	0.0143	10
Q9ERD7	TBB3_MOUSE	1ISVYYNEASSHK	1.93	1.49E-03	0.0143	10
Q2QL88	CAZA2_MICMU F-	LLLNNNDLLR	4.37	1.62E-03	0.0143	10
Q9ERD7	TBB3_MOUSE	1MSSTFIGNSTAIQELFK	2.80	1.75E-03	0.0143	10
Q2QL88	CAZA2_MICMU F-	IEGYEDQVLITEHGDLGNGK	4.50	1.76E-03	0.0143	10
Q2QL88	CAZA2_MICMU F-	TSVETALR	3.99	1.84E-03	0.0143	10
Q9ERD7	TBB3_MOUSE	1EVDEQM[+16]LAIQSK	1.64	1.96E-03	0.0143	10
Q2QL88	CAZA2_MICMU F-	IQVHYEDGNVQLVSHK	4.74	2.28E-03	0.0143	10
Q2QL88	CAZA2_MICMU F-	EHYPNGVC[+57]TVYGK	4.29	2.29E-03	0.0143	10
Q2QL88	CAZA2_MICMU F-	EATDPRPYEAENAIESWR	4.78	2.54E-03	0.0143	10
Q9JLM8	DCLK1_MOUSE	ISQHGGSSSTLSSTK	2.78	2.87E-03	0.0143	10
Q9JLM8	DCLK1_MOUSE	SPSPSPTSPGSLR	4.40	2.98E-03	0.0143	10
Q2QL88	CAZA2_MICMU F-	FIIHAPPGEFNEVFNDVR	5.70	3.00E-03	0.0143	10
Q9ERD7	TBB3_MOUSE	1LATPTYGDLNHLVSATMSGVTTSLF	3.75	3.15E-03	0.0143	10
Q2QL88	CAZA2_MICMU F-	EGAAHAFQAQYNLDQFTPVK	4.61	3.32E-03	0.0143	10
Q2QL88	CAZA2_MICMU F-	IVEAAENEYQTAISENYQTM[+16]SDTTFH	4.98	3.80E-03	0.0147	10
Q9JLM8	DCLK1_MOUSE	ISSLDQLVEGESYVC[+57]GSIEPFK	5.23	4.04E-03	0.0148	10
Q9JLM8	DCLK1_MOUSE	GIVYAISPDR	2.84	4.32E-03	0.0150	10
Q9JLM8	DCLK1_MOUSE	GGDLFDAITSTSK	3.34	6.74E-03	0.0172	10
Q9JLM8	DCLK1_MOUSE	TLSDNVNLPQGVR	3.24	8.12E-03	0.0185	10
Q9ERD7	TBB3_MOUSE	1FWEVISDEHGIDPSGNYVGSDSLQLER	4.91	8.77E-03	0.0192	10
Q9ERD7	TBB3_MOUSE	1EVDEQMLAIQSK	2.03	9.77E-03	0.0204	10
Q9JLM8	DCLK1_MOUSE	DIKPENLLVYEHQDGSK	4.30	1.62E-02	0.0273	10
P46096	SYT1_MOUSE	9VQVVVTVLDYDK	2.34	1.86E-02	0.0300	10
Q04447	KCRB_MOUSE	RGTGGVDTAAVGGVFDVSNADR	6.43	1.95E-02	0.0309	10
Q8K0U4	HS12A_MOUSE	LDLTGSGGTAVPAR	1.89	6.83E-04	0.0143	10
P61161	ARP2_MOUSE	1HM[+16]VFLGGAVLADIMK	3.68	8.98E-04	0.0143	10
Q8K0U4	HS12A_MOUSE	IFGEDFIEQFK	2.78	1.06E-03	0.0143	10
P61161	ARP2_MOUSE	1HMFVFLGGAVLADIMK	4.55	1.80E-03	0.0143	10
Q8K0U4	HS12A_MOUSE	ATAVDITTSK	1.78	2.08E-03	0.0143	10
Q8K0U4	HS12A_MOUSE	SPLTYGVGVVLR	1.75	2.16E-03	0.0143	10
Q8K0U4	HS12A_MOUSE	1IIPQDVGLTILK	1.75	2.20E-03	0.0143	10
Q99JY9	ARP3_MOUSE	1TLTGTVIDSGDGVTHVIPVAEGYVIGSC[+57]IK	4.32	2.47E-03	0.0143	10
Q99JY9	ARP3_MOUSE	1NIVLSGGSTM[+16]FR	3.46	2.53E-03	0.0143	10
Q8K0U4	HS12A_MOUSE	TNPLNITLPPFSFIDYYK	3.98	2.95E-03	0.0143	10
P61161	ARP2_MOUSE	1ILLTEPPM[+16]NPTK	2.98	3.53E-03	0.0144	10
Q8K0U4	HS12A_MOUSE	VGIDFLNY	1.92	3.63E-03	0.0146	10
P61161	ARP2_MOUSE	1VVVC[+57]DNNGTGFVK	2.34	4.00E-03	0.0148	10
Q99JY9	ARP3_MOUSE	1QYTGVAISK	2.42	4.00E-03	0.0148	10
Q8K0U4	HS12A_MOUSE	FISADQSVALGELVK	2.57	4.05E-03	0.0148	10
Q99JY9	ARP3_MOUSE	1LSEELSGGR	2.48	4.07E-03	0.0148	10
Q99JY9	ARP3_MOUSE	1DYEEIGPSIC[+57]R	2.75	4.08E-03	0.0148	10
P61161	ARP2_MOUSE	1GYAFNHSADFETVR	3.32	4.85E-03	0.0154	10
Q99JY9	ARP3_MOUSE	1LPAC[+57]VVDC[+57]GTGYTK	3.44	6.81E-03	0.0172	10
P61161	ARP2_MOUSE	1LALETTVLVESYTLPDGR	5.68	7.03E-03	0.0175	10
Q99JY9	ARP3_MOUSE	1GVDDLDFFIGDEAIEKPTYATK	4.05	7.35E-03	0.0178	10
P61161	ARP2_MOUSE	1DLMVGDSEASLR	2.55	7.67E-03	0.0181	10
Q99JY9	ARP3_MOUSE	1FMEQVIFK	2.60	7.77E-03	0.0182	10
Q8K0U4	HS12A_MOUSE	GAVLFGLDPAVIK	1.76	8.07E-03	0.0184	10
Q99JY9	ARP3_MOUSE	1NIVLSGGSTMFR	2.98	8.38E-03	0.0188	10
Q9WUM4	COR1C_MOUSE	NDQC[+57]YDDIR	3.83	1.07E-02	0.0214	10
Q9WUM4	COR1C_MOUSE	YFEITDESPYVHYLNTFSSK	5.49	1.10E-02	0.0217	10
Q9WUM4	COR1C_MOUSE	AIFLADGNVFTTGFSR	4.09	1.11E-02	0.0219	10
P61161	ARP2_MOUSE	1KVVC[+57]DNNGTGFVK	3.50	1.32E-02	0.0240	10
P61161	ARP2_MOUSE	1ILLTEPPMNPTK	2.92	1.35E-02	0.0243	10
Q9WUM4	COR1C_MOUSE	NGSLIC[+57]TASK	3.43	1.52E-02	0.0263	10
Q8K0U4	HS12A_MOUSE	ETAPTSTYSSPAR	1.53	1.58E-02	0.0269	10

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9WUM4	COR1C_MOUSE	NADPILISLK	3.31	1.63E-02	0.0274	10
Q9CPV4	GLOD4_MOUSE	VAEGIFETEAPGGYK	3.82	1.73E-02	0.0284	10
P62281	RS11_MOUSE	ΔDVQIGDIVTVGEC[+57]RPLSK	3.31	1.74E-02	0.0285	10
E9QPE7	E9QPE7_MOUSE	QLEEAEEEEESQR	4.26	2.19E-02	0.0338	10
P19253	RL13A_MOUSE	C[+57]EGINISGNFYR	3.27	2.63E-02	0.0386	10
P62830	RL23_MOUSE	εLPAAGVGDMMVATVK	3.30	2.71E-02	0.0394	10
P60710	ACTB_MOUSE	,TTGIVMDSGDGVHTVPIYEGYALPHALF	5.94	2.87E-02	0.0411	10
Q03265	ATPA_MOUSE	,LKEIVTNFLAGFEP	2.38	2.94E-02	0.0419	10
Q9WUA3	PFKAP_MOUSE	M[+16]GVEAVIALLEATPETPAC[+57]VVSLF	3.21	7.23E-04	0.0143	10
Q9WUA3	PFKAP_MOUSE	EWGGLLEELAR	2.16	1.56E-03	0.0143	10
Q9WUA3	PFKAP_MOUSE	WDC[+57]VSSILQVGGTIIGSAR	2.59	1.66E-03	0.0143	10
Q9WUA3	PFKAP_MOUSE	LGITNLC[+57]VIGGDGSLTGANLFR	2.45	2.50E-03	0.0143	10
Q9WUA3	PFKAP_MOUSE	VYFIYEGYQGLVDGGSNIVEAK	3.15	2.74E-03	0.0143	10
Q9WUA3	PFKAP_MOUSE	MGVEAVIALLEATPETPAC[+57]VVSLF	7.33	3.35E-03	0.0143	10
Q9WUA3	PFKAP_MOUSE	NESC[+57]SVNYTTDFIYQLYSEEGK	3.43	5.17E-03	0.0155	10
Q9WUA3	PFKAP_MOUSE	FVSDDSIK[+57]VLGIC[+57]K	1.72	5.37E-03	0.0158	10
Q9WUA3	PFKAP_MOUSE	IIEVVDAIMTTAQSHQF	2.50	8.10E-03	0.0184	10
Q9WUA3	PFKAP_MOUSE	DLLFQPVAELK	1.91	1.05E-02	0.0212	10
P50516	VATA_MOUSE	`ADYAQLLEDMMQNAFR	3.20	7.34E-04	0.0143	10
Q8K1M6	DNM1L_MOUSE	LHDAIVEVVTG[+57]LLR	3.25	8.57E-04	0.0143	10
P17427	AP2A2_MOUSE	TSVSLAVSR	2.14	1.71E-03	0.0143	10
P17427	AP2A2_MOUSE	IIGFGSALLEEVDPNPANFVAGAGIHTK	4.93	2.10E-03	0.0143	10
P50516	VATA_MOUSE	`EILQEEEDLAEIVQLVGK	2.59	2.20E-03	0.0143	10
P50516	VATA_MOUSE	`YSNSDVIIYVGC[+57]GER	2.24	2.23E-03	0.0143	10
Q8K1M6	DNM1L_MOUSE	LQDVFNVTGADIIQLPQIVVGTQSSGK	3.14	2.30E-03	0.0143	10
P17427	AP2A2_MOUSE	LSTVASTDILATVLEEM[+16]PPFPER	3.70	2.82E-03	0.0143	10
Q8K1M6	DNM1L_MOUSE	LYTDFEIRQEIENETER	2.82	2.95E-03	0.0143	10
P17427	AP2A2_MOUSE	ILVAGDTM[+16]DSVK	1.23	3.82E-03	0.0147	10
Q8K1M6	DNM1L_MOUSE	TLESVDPLGGLNTIDILTAIF	2.27	4.29E-03	0.0150	10
P17427	AP2A2_MOUSE	QLSNPQQEVQNIFK	1.87	4.36E-03	0.0150	10
P17427	AP2A2_MOUSE	FVNLFPVEVK	2.06	5.32E-03	0.0158	10
P17427	AP2A2_MOUSE	AVDLLYAMC[+57]DR	2.37	5.34E-03	0.0158	10
Q8K1M6	DNM1L_MOUSE	YIETSELC[+57]GGAR	2.35	5.48E-03	0.0159	10
P50516	VATA_MOUSE	`FSMVQVWPVR	1.76	7.96E-03	0.0183	10
P50516	VATA_MOUSE	`VLDALFPC[+57]VQGGTTAIPGAFGC[+57]GK	1.55	9.78E-03	0.0204	10
P50516	VATA_MOUSE	`EASIYTGITLSEYFF	4.64	1.16E-02	0.0224	10
Q8K1M6	DNM1L_MOUSE	SSLLDDLLTESEDMAQR	3.08	1.16E-02	0.0224	10
P50516	VATA_MOUSE	`VGSHITGGDIYIGVNNENSLIK	1.66	1.17E-02	0.0225	10
Q8K1M6	DNM1L_MOUSE	LGIIQVNR	1.10	1.20E-02	0.0228	10
P50516	VATA_MOUSE	`LIKDDFLQQNGYTPYDR	1.42	1.28E-02	0.0235	10
Q8K1M6	DNM1L_MOUSE	FATEYC[+57]NTIEGTAK	6.30	1.32E-02	0.0240	10
P17427	AP2A2_MOUSE	LSTVASTDILATVLEEMPPFPER	4.30	1.40E-02	0.0249	10
P50516	VATA_MOUSE	`GSVTYIAPPNGYDASDVVLELEFEGVK	5.12	1.55E-02	0.0266	10
P20357	MTAP2_MOUSE	NKDDLTLR	0.83	2.10E-02	0.0328	10
Q80ZK2	Q80ZK2_MOUSE	VPDTAWDGTQSK	2.25	2.29E-02	0.0349	10
Q35643	AP1B1_MOUSE	GLEISGTFTR	8.80	2.40E-02	0.0361	10
Q62261	SPTB2_MOUSE	NDSFTAC[+57]IELGK	0.84	2.50E-02	0.0371	10
P59999	ARPC4_MOUSE	IVAEFLK	1.07	3.09E-02	0.0436	10
P62137	PP1A_MOUSE	§IFC[+57]C[+57]HGGLSPDLQSM[+16]EQIR	3.50	2.13E-04	0.0143	9
Q9WV92	E41L3_MOUSE	VESTSVGSISPGGAK	2.16	2.52E-04	0.0143	9
Q9WV92	E41L3_MOUSE	LM[+16]DGSEILSLLESAR	5.19	2.68E-04	0.0143	9
Q9WV92	E41L3_MOUSE	LMDGSEILSLLESAR	7.22	4.87E-04	0.0143	9
P62137	PP1A_MOUSE	§EIFLSQPILLELEAPLK	5.04	6.15E-04	0.0143	9
P62137	PP1A_MOUSE	§SREIFLSQPILLELEAPLK	6.16	1.46E-03	0.0143	9
P62137	PP1A_MOUSE	§NVQLTENEIR	3.03	2.24E-03	0.0143	9
P62137	PP1A_MOUSE	§TFTDC[+57]FNC[+57]LPAAIVDEK	4.63	2.69E-03	0.0143	9
P62137	PP1A_MOUSE	§LNLDSIIGR	3.81	3.30E-03	0.0143	9
P62137	PP1A_MOUSE	§HDLDLIC[+57]R	3.22	4.51E-03	0.0152	9
P62137	PP1A_MOUSE	§IC[+57]GDIHGQYYDLLR	3.69	7.06E-03	0.0175	9
Q9WV92	E41L3_MOUSE	TEPVEAEVESTPHPQPLSTEK	2.58	7.11E-03	0.0176	9
Q9WV92	E41L3_MOUSE	KPTEFIGGVSSTTQSWVQK	2.98	8.72E-03	0.0191	9
Q9WV92	E41L3_MOUSE	IRPGEFEQFESTIGFK	3.83	9.68E-03	0.0204	9

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9WV92	E41L3_MOUSE	IVITGDADIDHDQALAAIK	3.02	1.55E-02	0.0266	9
Q9WV92	E41L3_MOUSE	GISQTNLITTVTPEK	1.53	1.62E-02	0.0273	9
P16546	SPTN1_MOUSE	SSLSSAQADFNQLAELDR	2.41	2.64E-02	0.0387	9
O35737	HNRH1_MOUSE	EGRPSGEAFVELESEDEVK	5.79	2.76E-02	0.0399	9
Q8BPN8	DMXL2_MOUSE	QLQSPLPLPTTLPLLSASIASTK	5.69	1.05E-04	0.0143	9
P63318	KPCG_MOUSE	LGSGPDGEPTIR	4.54	8.75E-04	0.0143	9
Q60737	CSK21_MOUSE	TPALVFEHVNNTDFK	5.19	2.03E-03	0.0143	9
P42669	PURA_MOUSE	DYLGDFIEHYAQLGPSQPPDLAAQAQDEPR	6.15	2.27E-03	0.0143	9
P42669	PURA_MOUSE	LIDYGVVEEPAELPEGTSLTVDNKR	2.91	2.60E-03	0.0143	9
P42669	PURA_MOUSE	FFFDVGSNK	2.34	3.06E-03	0.0143	9
Q60737	CSK21_MOUSE	GGPNIITLADIVK	4.40	3.48E-03	0.0144	9
Q60737	CSK21_MOUSE	FVHSENQHLVSPEALDFLDK	5.11	4.12E-03	0.0148	9
Q60737	CSK21_MOUSE	VLGTEDLYDYIDKYNIELDPR	6.45	4.17E-03	0.0149	9
Q60737	CSK21_MOUSE	GGPNIITLADIVKDPVSR	5.11	4.79E-03	0.0154	9
Q60737	CSK21_MOUSE	YSEVFEAINITNNEK	3.36	5.40E-03	0.0158	9
P42669	PURA_MOUSE	GPGLGSTQGQTIALPAQGLIEFR	2.39	5.53E-03	0.0159	9
Q60737	CSK21_MOUSE	FNDILGR	4.57	5.58E-03	0.0160	9
Q60737	CSK21_MOUSE	LIDWGLAEFYHPGQEYNVR	5.52	5.63E-03	0.0160	9
P42669	PURA_MOUSE	IAEVGAGGNK	2.21	5.65E-03	0.0160	9
P63318	KPCG_MOUSE	TFC[+57]GTPDYIAPEIIAYQPYGk	3.20	5.76E-03	0.0161	9
Q8BPN8	DMXL2_MOUSE	LVYSQPLDLPEAVEVIR	5.85	6.33E-03	0.0169	9
P42669	PURA_MOUSE	VSEVKPTYR	2.44	6.37E-03	0.0169	9
Q60737	CSK21_MOUSE	QLYQTLTDYDIR	3.89	6.39E-03	0.0169	9
P42669	PURA_MOUSE	NSITVPYK	2.18	7.63E-03	0.0181	9
P42669	PURA_MOUSE	SEFLVR	2.05	1.01E-02	0.0207	9
P63318	KPCG_MOUSE	APTSDEIHITVGEAR	3.78	1.12E-02	0.0219	9
P63318	KPCG_MOUSE	LVLASIDQADFQGFYVNPDPFVHPDAR	8.23	1.32E-02	0.0240	9
Q8BPN8	DMXL2_MOUSE	SIDLVSVDGTPSLPVSLSWVR	6.13	1.55E-02	0.0266	9
P42669	PURA_MOUSE	LIDYGVVEEPAELPEGTSLTVDNK	3.69	1.61E-02	0.0272	9
P63318	KPCG_MOUSE	DVIVQDDDVC[+57]TLVEK	5.37	1.66E-02	0.0277	9
P01869	IGH1M_MOUSE	TTPPSVYPLAPGSAAQTNSMVTLCG[+57]LVk	2.54	1.77E-02	0.0289	9
P47963	RL13_MOUSE	εLATQLTGPVMPPIR	4.27	1.96E-02	0.0310	9
P10126	EF1A1_MOUSE	MDSTEPPEYSQK	6.37	2.04E-02	0.0321	9
Q99KX1	MLF2_MOUSE	I VYQETSEMR	2.21	2.09E-02	0.0326	9
Q3UM45	PP1R7_MOUSE	LQNLDALTNLTVLSVQSNR	3.30	2.28E-02	0.0348	9
P62301	RS13_MOUSE	ζGLAPDLPEDLYHLIK	3.42	2.35E-02	0.0356	9
P17182	ENOA_MOUSE	LAM[+16]QEFM[+16]ILPVGASSFR	2.75	2.82E-02	0.0406	9
P39053	DYN1_MOUSE	I VVPGDQPPDIEFQIR	4.89	3.09E-02	0.0436	9
Q9JMH9	MY18A_MOUSE	I SELTSELTDER	8.52	3.23E-02	0.0452	9
Q9QYR6	MAP1A_MOUSE	SIEEAC[+57]LTLQHLNR	2.37	3.32E-02	0.0463	9
P10126	EF1A1_MOUSE	VETGVLKPGM[+16]VVTFAPVNVTTTEVK	1.40	8.66E-04	0.0143	9
P01837	IGKC_MOUSE	I DSTYSM[+16]SSTLTLTKDEYER	6.36	1.43E-03	0.0143	9
P01837	IGKC_MOUSE	I TSTSPIVK	6.86	2.04E-03	0.0143	9
P10126	EF1A1_MOUSE	THINIVIGHVDVSGK	2.25	2.80E-03	0.0143	9
P10126	EF1A1_MOUSE	DGSASGTTLLEALDC[+57]ILPPTRPTDKPLR	4.02	2.89E-03	0.0143	9
P01837	IGKC_MOUSE	I QNGVLNSWTDQDSKDSTYSM[+16]SSTLTLTK	8.72	3.27E-03	0.0143	9
P10126	EF1A1_MOUSE	VETGVLKPGMVVTFAPVNVTTTEVK	2.02	3.63E-03	0.0146	9
P10126	EF1A1_MOUSE	NM[+16]ITGTSQADC[+57]AVLIVAAGVGEFEAGISk	1.71	5.87E-03	0.0163	9
P01837	IGKC_MOUSE	I RADAAPTYSIFPPSSEQLTSGGASVVC[+57]FLNNFYPK	9.03	6.63E-03	0.0172	9
P10126	EF1A1_MOUSE	YYVTIIDAPGHR	1.42	7.54E-03	0.0180	9
P10126	EF1A1_MOUSE	EHALLAYTLGVK	2.07	7.55E-03	0.0180	9
P01837	IGKC_MOUSE	I DSTYSMSSTLTLTKDEYER	7.00	9.22E-03	0.0198	9
P01837	IGKC_MOUSE	I QNGVLNSWTDQDSKDSTYSMSSTLTLTK	8.33	1.45E-02	0.0255	9
P62270	RS18_MOUSE	ζIAFAITAIK	6.09	2.03E-02	0.0319	9
Q6ZQ38	CAND1_MOUSE	VIRPLDQPSSFDPATPYIK	1.42	2.03E-02	0.0319	9
P62301	RS13_MOUSE	ζLILIESR	6.81	2.33E-02	0.0354	9
P62821	RAB1A_MOUSE	EFADSLGIPFLETSK	7.57	2.39E-02	0.0360	9
P67984	RL22_MOUSE	εITVTSEVPFSK	1.97	2.94E-02	0.0419	9
P62814	VATB2_MOUSE	IYPEEMIQTGISAIDGMNSIAF	3.32	1.32E-03	0.0143	9
P62814	VATB2_MOUSE	AVVGEEALTSDDLLEYFLQK	2.24	1.86E-03	0.0143	9
P62814	VATB2_MOUSE	GPVVAEDFLDIMGQPINPQC[+57]R	4.74	2.18E-03	0.0143	9
P62814	VATB2_MOUSE	HVLVILTMSSYAEALR	4.02	2.93E-03	0.0143	9

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P62814	VATB2_MOUSE	LALTTAEFLAYQC[+57]JEK	2.05	4.42E-03	0.0151	9
P62814	VATB2_MOUSE	IPIFSAAGLPHNEIAAQIC[+57]F	2.11	4.59E-03	0.0152	9
P62814	VATB2_MOUSE	TSC[+57]EFTGDILR	1.29	5.85E-03	0.0163	9
P62814	VATB2_MOUSE	AVVQVFEGTSGIDAK	1.50	6.57E-03	0.0171	9
P62814	VATB2_MOUSE	IPQSTLSEFYPR	2.46	8.93E-03	0.0194	9
Q9DBG3	AP2B1_MOUSE	APEVSQYIYQVYDSILK	3.52	4.04E-04	0.0143	9
Q9DBG3	AP2B1_MOUSE	LAPPLVTLISGEPEVQYVALR	2.73	5.52E-04	0.0143	9
Q9DBG3	AP2B1_MOUSE	KPSETQELVQQVLSLATQDSDNPDLR	3.77	8.81E-04	0.0143	9
P84091	AP2M1_MOUSE	LNYSHDHVIK	3.07	1.36E-03	0.0143	9
Q9DBG3	AP2B1_MOUSE	SQPDMAIMAVNSFVK	3.84	2.31E-03	0.0143	9
P84091	AP2M1_MOUSE	SNIWLAAVTK	3.03	2.61E-03	0.0143	9
P84091	AP2M1_MOUSE	NAVDAFR	2.43	3.17E-03	0.0143	9
P84091	AP2M1_MOUSE	QNVNAAM[+16]VFEFLYK	4.48	4.41E-03	0.0151	9
Q9DBG3	AP2B1_MOUSE	FLELLPK	1.42	5.36E-03	0.0158	9
P84091	AP2M1_MOUSE	EEQSQITSQVTGQIGWR	1.89	5.88E-03	0.0163	9
P84091	AP2M1_MOUSE	QSI AIDDC[+57]TFHQ C[+57]VR	2.23	6.42E-03	0.0169	9
P84091	AP2M1_MOUSE	IPTPLNTSGVQVIC[+57]MK	5.53	7.81E-03	0.0182	9
P84091	AP2M1_MOUSE	MC[+57]DVMAAYFGK	3.47	9.76E-03	0.0204	9
Q9DBG3	AP2B1_MOUSE	LQNNNVYTIK	1.46	1.07E-02	0.0214	9
P84091	AP2M1_MOUSE	ESQISAEIELLPTNDK	3.48	1.28E-02	0.0235	9
Q9DBG3	AP2B1_MOUSE	DIPNENELQFIK	2.30	1.68E-02	0.0279	9
Q9JMH9	MY18A_MOUSE	VASGSDLHLTDIDSDSNR	0.96	2.73E-02	0.0396	9
Q9Z1N5	DX39B_MOUSE	GLAITFVSDENDAK	3.42	3.18E-02	0.0446	9
Q03265	ATPA_MOUSE	/ILGADTSVDLEETGR	2.08	5.28E-04	0.0143	9
Q03265	ATPA_MOUSE	/EVAFAAQFGSDLDAATQQLLSR	3.31	2.16E-03	0.0143	9
Q03265	ATPA_MOUSE	/TSIAIDTIINQK	1.51	2.24E-03	0.0143	9
Q03265	ATPA_MOUSE	/NVQAEEM[+16]VEFSSGLK	5.48	2.67E-03	0.0143	9
Q03265	ATPA_MOUSE	/NVQAEEMVEFSSGLK	2.37	3.69E-03	0.0147	9
Q03265	ATPA_MOUSE	/TGAIVDVPVGEELLGR	1.37	9.87E-03	0.0205	9
Q03265	ATPA_MOUSE	/TGTAEMSSILEER	1.81	1.18E-02	0.0226	9
Q03265	ATPA_MOUSE	/EIVTNFLAGFEP	1.53	1.67E-02	0.0278	9
Q62261	SPTB2_MOUSE	SNAHYNLQNAFNLAEQHLGLTK	3.47	2.93E-02	0.0418	9
P63038	CH60_MOUSE	{VGEVIVTK	2.85	1.25E-03	0.0143	9
P63038	CH60_MOUSE	{GVMLAVDAVIAELKK	2.48	3.23E-03	0.0143	9
P63038	CH60_MOUSE	{ALM[+16]LQGVDLLADAVAVTMGPK	2.24	4.44E-03	0.0151	9
P63038	CH60_MOUSE	{GYISPYFINTSK	3.90	8.47E-03	0.0189	9
P63038	CH60_MOUSE	{C[+57]JEFQDAYVLLSEK	2.97	9.51E-03	0.0202	9
P16546	SPTN1_MOUSE	HQALQAEIAGHEPR	1.63	1.80E-02	0.0293	9
P47911	RL6_MOUSE	6CQLDSGLLLVTGPLVINR	1.58	1.84E-02	0.0297	9
Q9DBJ1	PGAM1_MOUSE	YADLTEDQLPSC[+57]ESLK	1.07	2.36E-02	0.0357	9
P68033	ACTC_MOUSE	.H[+42]QGV M[+16]VGM[+16]GQK	1.08	3.21E-02	0.0450	9
Q99K10	ACON_MOUSE	VAMQDATAQMAMLQFISSGLPK	3.34	2.31E-03	0.0143	9
Q99K10	ACON_MOUSE	NDANPETHAFVTSPEIVTALAIAGTLK	7.49	3.17E-03	0.0143	9
Q99K10	ACON_MOUSE	AKDINQEVYNFLATAGAK	2.21	4.40E-03	0.0150	9
Q99K10	ACON_MOUSE	NAVTQEFQVVPDPTAR	2.52	6.31E-03	0.0169	9
Q99K10	ACON_MOUSE	WVVIQDENYEGESSR	3.85	7.53E-03	0.0180	9
Q99K10	ACON_MOUSE	DVGIVLANAC[+57]GPC[+57]IGQWDR	5.57	9.15E-03	0.0197	9
Q99K10	ACON_MOUSE	GHLDNISNNLLIGAINIENK	1.54	1.28E-02	0.0235	9
Q99K10	ACON_MOUSE	FNPETDFLTGK	1.25	1.51E-02	0.0262	9
Q923T9	KCC2G_MOUSE	IC[+57]DPGLTSFEPEALGNLVEGM[+16]DFHK	1.34	1.88E-02	0.0301	9
P17182	ENOA_MOUSE	SFVQNYPVVSIEDPFDQDDWGAWQK	4.18	4.76E-05	0.0143	9
P17182	ENOA_MOUSE	LAMQEFMILPVGASSFR	2.17	1.81E-03	0.0143	9
P17182	ENOA_MOUSE	AGYTDQVVIGMDVAASEFYR	2.48	2.68E-03	0.0143	9
P17182	ENOA_MOUSE	HIADLAGNPEVILPVPAFNVIINGGSHAGNK	1.85	2.88E-03	0.0143	9
P17182	ENOA_MOUSE	LMIEMDGTENK	1.73	4.22E-03	0.0149	9
P17182	ENOA_MOUSE	FTASAGIQVVGDDTLVTNPK	1.42	8.35E-03	0.0188	9
P17182	ENOA_MOUSE	LAM[+16]QEFMILPVGASSFR	1.86	1.14E-02	0.0222	9
P17182	ENOA_MOUSE	DATNVGDEGGFAPNILENKEALELLK	1.67	1.33E-02	0.0241	9
Q8R071	IP3KA_MOUSE	C[+57]AAVAAAAAAGEPR	1.21	2.81E-02	0.0405	9
Q9D8Y0	EFHD2_MOUSE	SM[+16]IQEVDEDFDSK	4.38	3.38E-04	0.0143	8
Q9D8Y0	EFHD2_MOUSE	FEIEIKAEQEER	4.34	9.94E-04	0.0143	8
P46660	AINX_MOUSE	ALPASDGLDLSQAAAR	2.90	1.13E-03	0.0143	8

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9D8Y0	EFHD2_MOUSE	LSEIDVSTEGVK	4.15	1.39E-03	0.0143	8
Q9D8Y0	EFHD2_MOUSE	RADLNQGIGEPQSPSR	4.69	1.45E-03	0.0143	8
V9GX76	V9GX76_MOUSE	YLTESYGTGQDIDDR	5.74	1.48E-03	0.0143	8
P46660	AINX_MOUSE	A FANLNEQAAR	3.46	1.88E-03	0.0143	8
Q9D8Y0	EFHD2_MOUSE	ADLNQGIGEPQSPSR	4.53	1.94E-03	0.0143	8
Q9D8Y0	EFHD2_MOUSE	SMIQEVDEDFDSK	4.51	1.98E-03	0.0143	8
V9GX76	V9GX76_MOUSE	AGSLKDPDLLDDHGFIR	5.48	1.99E-03	0.0143	8
Q9D8Y0	EFHD2_MOUSE	RVFNPYTEFK	4.90	2.12E-03	0.0143	8
Q3UHD9	AGAP2_MOUSE	YEQLLFLAPLGTTEEPLGR	2.36	2.26E-03	0.0143	8
V9GX76	V9GX76_MOUSE	IQAEEVAQLAR	4.64	2.77E-03	0.0143	8
Q9D8Y0	EFHD2_MOUSE	VFNPYTEFK	2.92	2.88E-03	0.0143	8
P46660	AINX_MOUSE	A VGELFQR	4.91	2.95E-03	0.0143	8
V9GX76	V9GX76_MOUSE	VVAGVLHLGNIDFEEAGSTSGGC[+57]NLK	5.47	3.51E-03	0.0144	8
B9DGT7	TBA2_ARATH Tub	AFVHWYVGEGM[+16]EEGEFSEAR	3.70	3.87E-03	0.0147	8
P46660	AINX_MOUSE	A ALEAELAALR	5.00	4.06E-03	0.0148	8
Q3UHD9	AGAP2_MOUSE	AEEAAVAGLSTPGSLHR	2.60	4.29E-03	0.0150	8
P46660	AINX_MOUSE	A FSTGGLSISGLNPLPNPSYLLPPR	7.67	4.75E-03	0.0154	8
V9GX76	V9GX76_MOUSE	EGLGVNEVHYVDNQDC[+57]IDLIEVK	3.84	5.13E-03	0.0155	8
P46660	AINX_MOUSE	A KVESLLDELAFVR	5.38	5.16E-03	0.0155	8
Q3UHD9	AGAP2_MOUSE	AVVNSQEWTLRS	3.90	5.51E-03	0.0159	8
V9GX76	V9GX76_MOUSE	TFLALINQVFPAAEDSK	8.25	6.13E-03	0.0166	8
B9DGT7	TBA2_ARATH Tub	IDHKFDLMYAK	2.28	6.69E-03	0.0172	8
B9DGT7	TBA2_ARATH Tub	AVFVDLEPTVIDEVR	2.10	6.70E-03	0.0172	8
V9GX76	V9GX76_MOUSE	HFAGAVC[+57]YETTQFVEK	5.16	6.85E-03	0.0173	8
B9DGT7	TBA2_ARATH Tub	FDLM[+16]YAK	1.53	7.16E-03	0.0176	8
P46660	AINX_MOUSE	A SNVASTAAC[+57]SSASSLGLGLAYR	3.24	8.91E-03	0.0194	8
Q3UHD9	AGAP2_MOUSE	ALSTDC[+57]TPSGDLSPLSR	6.19	9.80E-03	0.0204	8
B9DGT7	TBA2_ARATH Tub	AFVHWYVGEGMEEGEFSEAR	4.71	1.02E-02	0.0208	8
B9DGT7	TBA2_ARATH Tub	TIQFVDWC[+57]PTGFK	2.70	1.05E-02	0.0212	8
Q3UHD9	AGAP2_MOUSE	TDSQSEAVAIQAIR	4.63	1.19E-02	0.0227	8
B9DGT7	TBA2_ARATH Tub	LSVDYGKK	2.32	1.27E-02	0.0234	8
Q3UHD9	AGAP2_MOUSE	TTYLISLTLVK	4.28	1.41E-02	0.0250	8
V9GX76	V9GX76_MOUSE	ALFESSTNNNK	6.08	1.46E-02	0.0256	8
Q3UHD9	AGAP2_MOUSE	LGVLGDVR	4.69	1.49E-02	0.0259	8
P46660	AINX_MOUSE	A VESLLDELAFVR	1.96	1.54E-02	0.0265	8
B9DGT7	TBA2_ARATH Tub	FDLMYAK	2.33	1.60E-02	0.0271	8
P06745	G6PI_MOUSE	C EVMQMLVELAK	1.97	2.90E-02	0.0414	8
Q9R1Q8	TAGL3_MOUSE	TTDIFQTVDLWEGK	3.93	2.65E-04	0.0143	8
Q8JZQ9	EIF3B_MOUSE	NLFNVVDC[+57]JK	2.21	2.70E-04	0.0143	8
Q9R1Q8	TAGL3_MOUSE	GFSEEQLR	3.38	7.13E-04	0.0143	8
P62702	RS4X_MOUSE	A TDITYPAGFMDVISIDK	4.80	7.84E-04	0.0143	8
Q8JZQ9	EIF3B_MOUSE	GHPSAGAEIEEGSDGSAAEAEP	5.22	9.57E-04	0.0143	8
P61205	ARF3_MOUSE	A LGEIVTTIPTIGFNVETVEYK	2.59	1.34E-03	0.0143	8
Q61699	HS105_MOUSE	LLTETEDWLYEEGEDQAK	2.83	1.59E-03	0.0143	8
Q61699	HS105_MOUSE	FVVQNVSAQK	2.24	2.45E-03	0.0143	8
Q8R071	IP3KA_MOUSE	GNVQLETSEDVGQK	4.41	2.49E-03	0.0143	8
Q8R071	IP3KA_MOUSE	DTLEISDFFR	5.21	2.68E-03	0.0143	8
Q8R071	IP3KA_MOUSE	MLAVDPEAPTEEEHAQR	5.02	2.72E-03	0.0143	8
P61205	ARF3_MOUSE	A M[+16]LAEDELRDVLLVFANK	2.56	2.85E-03	0.0143	8
Q8JZQ9	EIF3B_MOUSE	IINDYYPEEDGK	4.45	3.07E-03	0.0143	8
Q9R1Q8	TAGL3_MOUSE	LVDWILQC[+57]AEDIEHPPPGR	4.28	3.27E-03	0.0143	8
Q9R1Q8	TAGL3_MOUSE	TLMALGSVAVTK	3.43	3.40E-03	0.0143	8
P61205	ARF3_MOUSE	A ILMVGLDAAGK	1.62	4.03E-03	0.0148	8
Q61699	HS105_MOUSE	SVLDAAQIVGLNC[+57]LR	3.53	4.33E-03	0.0150	8
Q61699	HS105_MOUSE	VVNVELPVEANLVWQLGR	5.11	4.56E-03	0.0152	8
Q61699	HS105_MOUSE	AEDVSAIEIVGGATR	3.10	4.62E-03	0.0153	8
Q9D8E6	RL4_MOUSE	6C GPC[+57]IINYNDNGIIK	4.87	4.69E-03	0.0153	8
Q8R071	IP3KA_MOUSE	GAGPC[+57]SPGLER	4.83	4.98E-03	0.0155	8
P62702	RS4X_MOUSE	A EC[+57]LPLIIFLR	3.71	5.10E-03	0.0155	8
Q61699	HS105_MOUSE	VLGTAFFDPFLGGK	2.66	5.27E-03	0.0157	8
Q61699	HS105_MOUSE	RGPFELEAFYSDPQGVYPPEAK	3.58	5.51E-03	0.0159	8
P61205	ARF3_MOUSE	A MLAEDELRDVLLVFANK	4.37	5.72E-03	0.0161	8

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q8R071	IP3KA_MOUSE	AGVWLIDFGK	4.43	6.03E-03	0.0164	8
Q8JZQ9	EIF3B_MOUSE	AKPAAQSEEEETATSPAASPTQSAEF	6.90	6.36E-03	0.0169	8
P61205	ARF3_MOUSE	INISFTVWDVGGQDK	2.14	6.65E-03	0.0172	8
Q9R1Q8	TAGL3_MOUSE	QMEQISQFLK	3.07	6.75E-03	0.0172	8
Q8R071	IP3KA_MOUSE	AAGTSGILIK	3.32	7.87E-03	0.0183	8
Q9R1Q8	TAGL3_MOUSE	LINSLYPPGQPIPK	3.16	8.24E-03	0.0186	8
P62702	RS4X_MOUSE	HPGSFDVVHVK	3.37	8.29E-03	0.0187	8
Q61699	HS105_MOUSE	SQFEELC[+57]AELLQK	3.82	9.66E-03	0.0203	8
Q8R071	IP3KA_MOUSE	EGISSSTTLGFR	2.11	9.97E-03	0.0206	8
P62702	RS4X_MOUSE	VNDTIQIDLETGK	3.40	1.02E-02	0.0208	8
P62702	RS4X_MOUSE	LREC[+57]LPLIIFLR	6.07	1.05E-02	0.0212	8
Q9D8E6	RL4_MOUSE	60RGPC[+57]IYNEDNGIIK	3.44	1.13E-02	0.0221	8
P62702	RS4X_MOUSE	DANGNSFATR	4.12	1.15E-02	0.0223	8
Q9R1Q8	TAGL3_MOUSE	TLM[+16]JALGSVAVTK	1.54	1.20E-02	0.0228	8
P62702	RS4X_MOUSE	YALTGDEVK	2.35	1.22E-02	0.0230	8
P61205	ARF3_MOUSE	DAVLLVFANK	1.40	1.33E-02	0.0241	8
P61205	ARF3_MOUSE	QDLPNAMNAAEITDK	1.27	1.46E-02	0.0256	8
Q9D8E6	RL4_MOUSE	60KLEAAATALATK	6.01	1.56E-02	0.0267	8
Q9D8E6	RL4_MOUSE	60NIPGITLLNVSK	4.20	1.61E-02	0.0272	8
Q8JZQ9	EIF3B_MOUSE	GYIFLEYASPAHAVDAVK	5.30	1.69E-02	0.0281	8
Q9QY94	GLNA_ACOCA_Gli	RPSANC[+57]DPYAVTEAIVR	4.88	1.72E-02	0.0284	8
O08553	DPYL2_MOUSE	FQM[+16]PDQGM[+16]TSADDFQGTK	3.77	1.81E-02	0.0294	8
Q64331	MYO6_MOUSE	NLEISIDALM[+16]AK	2.65	1.93E-02	0.0307	8
Q9WTM5	RUVB2_MOUSE	FVQC[+57]PDGELQK	1.47	1.94E-02	0.0308	8
P13020	GELS_MOUSE	DPDQTDGPGGLGYLSSHIANVER	5.91	2.26E-02	0.0346	8
P14115	RL27A_MOUSE	NQSFC[+57]PTVNLDK	5.85	2.32E-02	0.0352	8
P01872	IGHM_MOUSE	ISILEGSDEYLVLC[+57]K	5.08	2.54E-02	0.0375	8
O70194	EIF3D_MOUSE	YLEVSEPQDIEC[+57]C[+57]GALEYDYK	6.30	2.69E-02	0.0392	8
P07724	ALBU_MOUSE	AADKDTC[+57]FSTEGPNLVTR	3.02	2.80E-02	0.0404	8
Q8BPN8	DMXL2_MOUSE	FLLQESQQETTVK	8.18	2.83E-02	0.0407	8
Q6PIC6	AT1A3_MOUSE	DFTSEQIDEILQNHTEIFAR	3.16	3.16E-03	0.0143	8
Q6PIC6	AT1A3_MOUSE	M[+16]QVNAAEIVVVDLVEIK	1.91	3.30E-03	0.0143	8
Q6PIC6	AT1A3_MOUSE	IATLASGLEVGK	1.41	6.67E-03	0.0172	8
Q6PIC6	AT1A3_MOUSE	YQLSIHETEDPNDNR	1.87	7.55E-03	0.0180	8
Q6PIC6	AT1A3_MOUSE	LNIPVSQVNPR	1.68	9.22E-03	0.0198	8
Q6PIC6	AT1A3_MOUSE	ADIGVAMGIAGSDVSK	1.46	1.41E-02	0.0250	8
Q6PIC6	AT1A3_MOUSE	C[+57]IELSSGSVK	2.91	1.60E-02	0.0271	8
P49722	PSA2_MOUSE	FLVQIEYALAAVAGGAPSVGIK	1.47	2.21E-02	0.0341	8
P09405	NUCL_MOUSE	GFGFVDFNSEEDAK	3.62	1.93E-03	0.0143	8
P09405	NUCL_MOUSE	SVSLYYTGEK	2.52	3.43E-03	0.0144	8
P09405	NUCL_MOUSE	GLSEDTEETLK	3.31	6.51E-03	0.0171	8
P09405	NUCL_MOUSE	VEGSEPTTFFNLFIGNLNPNK	4.06	7.78E-03	0.0182	8
P09405	NUCL_MOUSE	FAISELFAK	2.88	9.86E-03	0.0205	8
P09405	NUCL_MOUSE	NLSFNITEDELK	2.27	1.03E-02	0.0209	8
P52480	KPYM_MOUSE	LAPITSDPTEAAAVGAVEASFk	3.51	1.84E-02	0.0297	8
Q60875	ARHG2_MOUSE	EVEGLKDLLLGPC[+57]VDLPMTSR	5.88	2.46E-02	0.0367	8
Q04447	KCRB_MOUSE	NYEFM[+16]WNPFLGYILTC[+57]PSNLGTGLR	6.62	2.26E-03	0.0143	8
Q04447	KCRB_MOUSE	LGFSEVELVQMVVDGVK	2.97	2.95E-03	0.0143	8
Q04447	KCRB_MOUSE	NYEFMWNPHLGYILTC[+57]PSNLGTGLR	6.37	3.01E-03	0.0143	8
P08249	MDHM_MOUSE	LTLYDIAHTPGVAADLSHIETR	2.18	3.07E-03	0.0143	8
Q04447	KCRB_MOUSE	FC[+57]TGLTQIETLFK	1.60	8.75E-03	0.0192	8
P08249	MDHM_MOUSE	FVFLVDAMNGK	2.23	9.06E-03	0.0196	8
P08249	MDHM_MOUSE	GYLGPQLPDC[+57]LK	3.24	1.25E-02	0.0232	8
P08249	MDHM_MOUSE	ETEC[+57]TYFSTPLLLGK	1.25	1.57E-02	0.0268	8
P08249	MDHM_MOUSE	GC[+57]DVVVIPAGVPR	1.05	1.62E-02	0.0273	8
P08249	MDHM_MOUSE	VDFPQDQLATLTGR	1.86	1.63E-02	0.0274	8
E9Q912	E9Q912_MOUSE	DQEVLLQTGR	1.23	1.71E-02	0.0283	8
P26039	TLN1_MOUSE	TAGALQC[+57]SPSDVYTK	1.01	1.72E-02	0.0284	8
Q91VR5	DDX1_MOUSE	DQLSVLDNGVDIVVGTGPR	1.05	1.94E-02	0.0308	8
P05202	AATM_MOUSE	ASAELALGENNEVLK	1.06	2.23E-02	0.0343	8
P06151	LDHA_MOUSE	ISADTLWGIQK	1.33	3.03E-02	0.0429	8
Q8BJH1	ZC21A_MOUSE	HINFC[+57]K	1.09	3.51E-02	0.0486	8

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P07724	ALBU_MOUSE	SLPC[+57]VEDYLSAILNR	3.21	1.07E-03	0.0143	8
P17183	ENOG_MOUSE	NYPVVSIEDPFDQDDWAAWSK	2.69	1.21E-03	0.0143	8
O08599	STXB1_MOUSE	AAHVFFTDSC[+57]PDALFNLVVK	2.57	1.68E-03	0.0143	8
P17183	ENOG_MOUSE	FGANAILGVSLAVC[+57]K	2.25	1.83E-03	0.0143	8
O08599	STXB1_MOUSE	DNALLAQLIQDKLDAYK	2.07	2.23E-03	0.0143	8
O08599	STXB1_MOUSE	ISEQTYQLSR	1.47	2.25E-03	0.0143	8
P17183	ENOG_MOUSE	SGETEDTFIADLVVGLC[+57]TGQIK	2.60	3.40E-03	0.0143	8
O08599	STXB1_MOUSE	EVLLDEDDDLWIALR	5.73	4.09E-03	0.0148	8
P07724	ALBU_MOUSE	SDVFLGTFLYEYSR	5.45	4.13E-03	0.0148	8
O08599	STXB1_MOUSE	VLVVDQLSMR	1.73	6.40E-03	0.0169	8
O08599	STXB1_MOUSE	DLSQM[+16]LK	1.77	1.09E-02	0.0216	8
P07724	ALBU_MOUSE	SRHPDYSVSLLLR	1.81	1.24E-02	0.0231	8
P07724	ALBU_MOUSE	SA PQVSTPTLVEAAR	1.70	1.25E-02	0.0232	8
Q9WTM5	RUVB2_MOUSE	TQGFLALFSGDTGEIK	1.12	1.76E-02	0.0288	8
P47963	RL13_MOUSE	ETIGISVDPR	1.11	1.88E-02	0.0301	8
Q8CHC4	SYNJ1_MOUSE	TPGPPSSQGSPVDTQPAAQK	2.31	2.14E-02	0.0333	8
Q8R191	SNG3_MOUSE	STTPGPGTAQAGDAAR	1.13	2.35E-02	0.0356	8
Q61879	MYH10_MOUSE	QEVMSIDLEER	4.83	2.50E-02	0.0371	8
P62242	RS8_MOUSE	4(LDVGNFWSWGSEC[+57]C[+57]TR	0.96	2.67E-02	0.0390	8
Q62261	SPTB2_MOUSE	EIEELQSQAQALSQEGK	0.83	2.80E-02	0.0404	8
O88456	CPNS1_MOUSE	M[+58]FLVNSFLK	1.50	3.06E-02	0.0432	8
P17426	AP2A1_MOUSE	FFQPTEMAAQDFQFR	0.91	3.16E-02	0.0444	8
P97351	RS3A_MOUSE	APAMFNIR	1.43	3.52E-02	0.0487	8
P52480	KPYM_MOUSE	KGVNLPGAAVDLPVASEK	0.91	3.58E-02	0.0494	8
E9Q557	DESP_MOUSE	FGDSNTVM[+16]R	3.39	1.70E-02	0.0282	8
Q9Z2H5	E41L1_MOUSE	IIITGDEDVDQDQALALAIK	2.64	1.81E-03	0.0143	7
Q9Z2H5	E41L1_MOUSE	AETMTVSSLAIR	2.87	2.07E-03	0.0143	7
Q9Z2H5	E41L1_MOUSE	DVLTSTYGATAETLSTSTTHVTI	2.50	2.49E-03	0.0143	7
Q9Z2H5	E41L1_MOUSE	SSPWNFAFTVK	3.50	2.57E-03	0.0143	7
Q6R891	NEB2_MOUSE	IERPGEQSEVAQLIQQTLEQER	6.35	2.66E-03	0.0143	7
Q6R891	NEB2_MOUSE	I LEGYWGEAQSLC[+57]QAVDEHLR	6.22	2.70E-03	0.0143	7
Q80ZK2	Q80ZK2_MOUSE	SAELGC[+57]TVDEVESLIK	3.64	3.50E-03	0.0144	7
Q9Z2H5	E41L1_MOUSE	GQVLFDLVC[+57]JEHLNLEK	6.47	3.75E-03	0.0147	7
Q80ZK2	Q80ZK2_MOUSE	AASAGVPYHGEVPSLAR	2.01	4.94E-03	0.0155	7
Q9Z2H5	E41L1_MOUSE	VTLDDASEYEC[+57]EVEK	3.25	7.17E-03	0.0177	7
Q6R891	NEB2_MOUSE	I ISELEGNLQTLR	3.64	7.88E-03	0.0183	7
Q80ZK2	Q80ZK2_MOUSE	ELDDLEQWIQER	4.76	7.96E-03	0.0183	7
Q9Z2H5	E41L1_MOUSE	YYLC[+57]LQLR	2.86	8.02E-03	0.0184	7
P62242	RS8_MOUSE	4(NC[+57]IVLIDSTPYR	5.38	9.69E-03	0.0204	7
Q6R891	NEB2_MOUSE	I LELFPVELEK	5.06	9.74E-03	0.0204	7
P62242	RS8_MOUSE	4(ISSLLEEQQFQQGK	5.26	1.05E-02	0.0212	7
O70194	EIF3D_MOUSE	IFHTVTTTDDPVIR	3.80	1.12E-02	0.0219	7
P62242	RS8_MOUSE	4(LTPEEEEEILNK	3.72	1.15E-02	0.0223	7
Q80ZK2	Q80ZK2_MOUSE	DLNAAEALQR	2.97	1.20E-02	0.0228	7
Q6R891	NEB2_MOUSE	I SAYEAGIQALKPPDAPGPDEAPK	5.39	1.20E-02	0.0228	7
Q80ZK2	Q80ZK2_MOUSE	LEQSNVPEGPGSGTGDDESSGPR	4.44	1.21E-02	0.0229	7
O70194	EIF3D_MOUSE	NMVQFNLQTLPK	3.29	1.21E-02	0.0229	7
P62242	RS8_MOUSE	4(ADGYVLEGK	3.40	1.21E-02	0.0229	7
O70194	EIF3D_MOUSE	TQGNVFATDAILATLMSC[+57]TF	6.60	1.34E-02	0.0242	7
O70194	EIF3D_MOUSE	TQGNVFATDAILATLM[+16]SC[+57]TF	6.28	1.39E-02	0.0248	7
Q6R891	NEB2_MOUSE	I VFPQPPPPPPAPSGDGATEK	1.70	1.50E-02	0.0261	7
Q8BPN8	DMXL2_MOUSE	IPVAFPSGDANLSK	2.77	1.77E-02	0.0289	7
P39053	DYN1_MOUSE	I ALLQM[+16]VQQFAVDFEK	5.76	2.16E-02	0.0335	7
Q9R1R2	TRIM3_MOUSE	SVLNLGALLTTSATAHETVATGEGFLF	3.18	2.25E-02	0.0345	7
Q8R4U7	LUZP1_MOUSE	VGNSGDAPELSR	3.16	2.29E-02	0.0349	7
P20357	MTAP2_MOUSE	GVVESVVTIEDDFITVVQTTTDEGESGSHSVR	2.86	2.39E-02	0.0360	7
Q9WV92	E41L3_MOUSE	VLQETILVEER	6.11	2.65E-02	0.0388	7
Q6PHZ2	KCC2D_MOUSE	DLINKM[+16]LTINPAK	7.42	2.67E-02	0.0390	7
Q99PU8	DHX30_MOUSE	AVDEAVILLQEIGVLDQR	4.10	2.68E-02	0.0391	7
P17426	AP2A1_MOUSE	DFLTPPLLSVR	3.72	3.43E-02	0.0477	7
P18760	COF1_MOUSE	I NIILEEGKEILVGDVGTVDPPYTTFFVK	3.32	6.86E-04	0.0143	7
P61979	HNRPK_MOUSE	ILSISADIETIGEILK	2.88	9.16E-04	0.0143	7

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9EQH3	VPS35_MOUSE	IPVDTYNNILTVLK	1.61	1.71E-03	0.0143	7
Q9EQH3	VPS35_MOUSE	LFDIFSQQVATVIQSR	2.65	1.85E-03	0.0143	7
P61979	HNRPK_MOUSE	IITITGTQDQIQNAQYLLQNSVK	1.82	1.85E-03	0.0143	7
P18760	COF1_MOUSE	KEDLVFIFWAPENAPLK	2.69	1.88E-03	0.0143	7
Q9EQH3	VPS35_MOUSE	VADLYELVQYAGNIIPR	4.37	2.04E-03	0.0143	7
P18760	COF1_MOUSE	YALYDATYETK	1.19	2.25E-03	0.0143	7
P18760	COF1_MOUSE	HELQANC[+57]YEEVKDR	1.70	2.31E-03	0.0143	7
P61979	HNRPK_MOUSE	GSDFDC[+57]ELR	1.73	2.78E-03	0.0143	7
P61979	HNRPK_MOUSE	LLIHQSLAGGIIGVK	2.04	2.79E-03	0.0143	7
P61979	HNRPK_MOUSE	IILDLISESPIK	1.67	3.02E-03	0.0143	7
P18760	COF1_MOUSE	LGGSAVISLEGKPL	2.13	4.34E-03	0.0150	7
Q9EQH3	VPS35_MOUSE	QIVLTGILEQVVC[+57]R	2.32	4.97E-03	0.0155	7
P18760	COF1_MOUSE	AVLFC[+57]LSEDKK	1.07	5.05E-03	0.0155	7
Q7TPR4	ACTN1_MOUSE	VGWEQLLTTIAR	4.27	5.71E-03	0.0161	7
Q9EQH3	VPS35_MOUSE	LSQLEGVNVER	2.17	6.91E-03	0.0174	7
Q7TPR4	ACTN1_MOUSE	LLETIDQLYLEYAK	6.64	7.65E-03	0.0181	7
Q7TPR4	ACTN1_MOUSE	LASDLLEWIR	2.85	1.06E-02	0.0213	7
Q7TPR4	ACTN1_MOUSE	IDQLEC[+57]DHQLIQEALIFDNK	4.39	1.06E-02	0.0213	7
Q9EQH3	VPS35_MOUSE	IREDLPNLESSEETEQINK	2.07	1.15E-02	0.0223	7
Q7TPR4	ACTN1_MOUSE	TINEVENQILTR	3.28	1.16E-02	0.0224	7
P18760	COF1_MOUSE	EILVGDVGGQTVDDPYTTFFVK	2.03	1.46E-02	0.0256	7
P61979	HNRPK_MOUSE	GSYGDLGGPIITQVTIPK	1.87	1.47E-02	0.0257	7
Q8BP47	SYNC_MOUSE	FLSWILNR	4.20	2.25E-02	0.0345	7
P56480	ATPB_MOUSE	SLQDIIAILGMDELSEEDKLTVSR	3.20	2.42E-02	0.0364	7
P39053	DYN1_MOUSE	INLVDSYMAIVNK	1.70	2.64E-02	0.0387	7
Q8R5C5	ACTY_MOUSE	IVQYTLPDGSTLDVGPAPR	0.94	3.48E-02	0.0483	7
P14869	RLA0_MOUSE	TSFFQALGITTK	2.31	1.09E-03	0.0143	7
Q01853	TERA_MOUSE	AIANEC[+57]QANFISIK	1.92	1.60E-03	0.0143	7
Q8C8R3	ANK2_MOUSE	YGSLDVAK	3.21	2.15E-03	0.0143	7
Q01853	TERA_MOUSE	NAPAIIFIDELDAIAPK	2.11	2.32E-03	0.0143	7
P14869	RLA0_MOUSE	GNVGFVFTK	2.05	2.57E-03	0.0143	7
P14869	RLA0_MOUSE	AGAIAPC[+57]EVTVPAQNTGLGPEK	1.76	2.65E-03	0.0143	7
Q01853	TERA_MOUSE	LDQLIYIPLPEK	1.60	2.81E-03	0.0143	7
P14869	RLA0_MOUSE	GTIEILSDVQLIK	2.15	2.88E-03	0.0143	7
Q01853	TERA_MOUSE	DVDLEFLAK	1.29	4.19E-03	0.0149	7
Q8C8R3	ANK2_MOUSE	EGHVGLVQELLGR	3.32	4.83E-03	0.0154	7
Q8C8R3	ANK2_MOUSE	AGEEEPGEPEIVER	1.52	5.82E-03	0.0162	7
P14869	RLA0_MOUSE	IILQLDDYPK	1.61	6.54E-03	0.0171	7
Q01853	TERA_MOUSE	ELQELVQYPVEHPDK	1.30	7.98E-03	0.0183	7
Q8C8R3	ANK2_MOUSE	SGHDQVVELLER	5.12	8.03E-03	0.0184	7
P14869	RLA0_MOUSE	AFLADPSAFAAAAAPAAAATTAAPAAAAAPA	2.26	1.01E-02	0.0207	7
Q8C8R3	ANK2_MOUSE	VVTEEVTTTTTITEK	5.50	1.09E-02	0.0216	7
Q8C8R3	ANK2_MOUSE	GLVHQAIC[+57]NLNITLPIYAK	5.66	1.09E-02	0.0216	7
Q8C8R3	ANK2_MOUSE	VALLLLEK	3.96	1.14E-02	0.0222	7
Q01853	TERA_MOUSE	AVANETGAFFFLINGPEIMSK	4.67	1.57E-02	0.0268	7
P19253	RL13A_MOUSE	YQAVTATLEEK	3.47	2.16E-02	0.0335	7
P17183	ENOG_MOUSE	VNQIGSVTEAIQAC[+57]K	2.38	3.58E-02	0.0494	7
Q61316	HSP74_MOUSE	SNLAYDIVQLPTGLTGIK	2.32	1.21E-04	0.0143	7
Q61316	HSP74_MOUSE	VLATAFDTTLGGRR	2.23	3.92E-03	0.0147	7
Q61316	HSP74_MOUSE	AFSDPFVEAEK	1.71	4.95E-03	0.0155	7
Q61316	HSP74_MOUSE	SVMDATQIAGLNC[+57]LR	2.55	8.17E-03	0.0185	7
Q61316	HSP74_MOUSE	LMNETTAVALAYGIYK	2.04	1.32E-02	0.0240	7
Q80UX7	Q80UX7_MOUSE	NEAEVINMSEELAQLEGILK	1.71	2.57E-02	0.0379	7
P28652	KCC2B_MOUSE	QTTAPATM[+16]STAASGTTMGLVEQA	2.63	3.27E-02	0.0457	7
Q9Z0E0	NCDN_MOUSE	ILGAWLAEETSSLR	2.45	1.44E-03	0.0143	7
Q9Z0E0	NCDN_MOUSE	LQAGEETASHYR	6.76	2.44E-03	0.0143	7
Q9Z0E0	NCDN_MOUSE	LLLAANVATLGLLMAR	2.35	3.02E-03	0.0143	7
Q9Z0E0	NCDN_MOUSE	FELC[+57]QLLPLFLPPTTVPPEC[+57]HR	6.76	1.17E-02	0.0225	7
Q9WUM4	COR1C_MOUSE	QLALWNP	1.05	1.75E-02	0.0287	7
P09411	PGK1_MOUSE	IVLPGVDALSNV	1.17	2.77E-02	0.0400	7
Q60900	ELAV3_MOUSE	TGQALLTHLYQSSAR	1.07	2.85E-02	0.0409	7
P17710	HXK1_MOUSE	IGAAMVTAVAYR	4.55	1.55E-03	0.0143	7

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P23116	EIF3A_MOUSE	QPALDVLYDVMK	4.55	2.74E-03	0.0143	7
P63101	1433Z_MOUSE	IETELRDIC[+57]NDVLSLLEK	7.49	3.28E-03	0.0143	7
P63101	1433Z_MOUSE	TAFDEAIAELDTLSEESYK	2.41	4.75E-03	0.0154	7
P23116	EIF3A_MOUSE	NQLTAMSSVLAK	4.06	7.25E-03	0.0177	7
P63101	1433Z_MOUSE	DIC[+57]NDVLSLLEK	2.11	7.39E-03	0.0179	7
P17710	HXK1_MOUSE	IGDFIALDLGGSSFR	2.22	9.93E-03	0.0206	7
P17710	HXK1_MOUSE	ILSDEILIDILTR	4.12	1.05E-02	0.0212	7
P17710	HXK1_MOUSE	IIDEAVLITWTK	2.31	1.10E-02	0.0217	7
P23116	EIF3A_MOUSE	LTSLVPFVDAFQLER	6.63	1.13E-02	0.0221	7
P63101	1433Z_MOUSE	GIVDQSQQAYQEAFAFEISK	1.35	1.26E-02	0.0233	7
P23116	EIF3A_MOUSE	FSVLQYVPEVK	6.89	1.28E-02	0.0235	7
P17710	HXK1_MOUSE	IMISGMYLGEIVR	2.10	1.35E-02	0.0243	7
P63101	1433Z_MOUSE	GIVDQSQQAYQEAFAFEISK	1.36	1.40E-02	0.0249	7
P63101	1433Z_MOUSE	YLAEVAAGDDK	0.62	1.44E-02	0.0254	7
P23116	EIF3A_MOUSE	VLLATLSIPITPER	6.83	1.52E-02	0.0263	7
P23116	EIF3A_MOUSE	DIDIEDLEELDPDFIMAK	7.13	1.59E-02	0.0270	7
P17710	HXK1_MOUSE	ISANLVAATLGAILNR	2.13	1.66E-02	0.0277	7
Q8BP67	RL24_MOUSE	εVFQFLNAK	4.75	1.97E-02	0.0311	7
P01837	IGKC_MOUSE	IADAAPTVSIFPPSSEQLTSGGASVVC[+57]FLNNFYPK	2.41	2.39E-02	0.0360	7
P10126	EF1A1_MOUSE	NMITGTSQADC[+57]AVLIVAAGVGEFEAGIS†	1.14	2.95E-02	0.0420	7
P16330	CN37_MOUSE	¿AGQVFLEELGNHK	2.17	9.12E-04	0.0143	6
P47753	CAZA1_MOUSE	EGAAHAFQAQYNMDQFTPVK	3.37	1.11E-03	0.0143	6
P47753	CAZA1_MOUSE	EASDPQPEDVDGGLK	4.86	1.17E-03	0.0143	6
P47753	CAZA1_MOUSE	IEGYDDQVLITEHGDLGNSR	5.00	2.14E-03	0.0143	6
P12382	PFKAL_MOUSE	NEWGSLLEELVK	2.72	2.39E-03	0.0143	6
P16330	CN37_MOUSE	¿AAGAEYYAQQEVVK	2.46	2.45E-03	0.0143	6
P47753	CAZA1_MOUSE	FTITPPSAQVVGVLK	5.57	2.51E-03	0.0143	6
P12382	PFKAL_MOUSE	VFANAPDSAC[+57]VIGLR	2.29	3.00E-03	0.0143	6
P16330	CN37_MOUSE	¿AHVTLGC[+57]AADVQPVQTGLDLLDILQQVK	8.44	3.03E-03	0.0143	6
P47753	CAZA1_MOUSE	FITHAPPGEFNEVFNDVR	4.50	3.33E-03	0.0143	6
P16330	CN37_MOUSE	¿GGSQGEAVGELPR	2.43	5.01E-03	0.0155	6
P16330	CN37_MOUSE	¿LSISALFVTPK	2.50	5.36E-03	0.0158	6
P60229	EIF3E_MOUSE	NALSSLWGK	3.91	8.53E-03	0.0189	6
P12382	PFKAL_MOUSE	AIGVLTSGGDAQGMNAAVR	2.27	9.98E-03	0.0206	6
P47753	CAZA1_MOUSE	ESC[+57]DSALR	4.98	1.01E-02	0.0207	6
P60229	EIF3E_MOUSE	LKETIDNNSVSSPLQSLQQR	4.76	1.17E-02	0.0225	6
P60229	EIF3E_MOUSE	MLFDYLADK	4.65	1.20E-02	0.0228	6
P12382	PFKAL_MOUSE	AIGVLTSGGDAQGM[+16]NAAVR	2.40	1.22E-02	0.0230	6
P12382	PFKAL_MOUSE	LAAAYNLLQHGITNLC[+57]VIGGDGSLTGANIFF	7.91	1.28E-02	0.0235	6
P60229	EIF3E_MOUSE	LASEILMQNWDAAEMDLTR	7.35	1.33E-02	0.0241	6
P60229	EIF3E_MOUSE	LFIFETFC[+57]R	5.53	1.64E-02	0.0275	6
P48036	ANXA5_MOUSE	ETSGNLEQLLLAVVK	7.26	1.87E-02	0.0300	6
P41105	RL28_MOUSE	εTVGVEPAADGK	8.46	2.19E-02	0.0338	6
Q6URW6	MYH14_MOUSE	HEVPPHVVAVTEGAYR	1.75	2.47E-02	0.0368	6
Q60605	MYL6_MOUSE	IILYSQC[+57]GDVMR	5.16	6.53E-04	0.0143	6
P48722	HS74L_MOUSE	EDINSIEIVGGATR	2.60	7.42E-04	0.0143	6
Q60605	MYL6_MOUSE	INKDQGTIEDYVEGLR	5.25	1.36E-03	0.0143	6
Q9R111	GUAD_MOUSE	FTLSC[+57]TETLMSELGNIK	2.01	1.83E-03	0.0143	6
Q9R111	GUAD_MOUSE	GASIAHC[+57]PNSNLSLSSGLLNVLK	3.88	1.90E-03	0.0143	6
Q60605	MYL6_MOUSE	IILYSQC[+57]GDVM[+16]R	5.86	1.91E-03	0.0143	6
Q60605	MYL6_MOUSE	IVLDFEHFLPMLQTVAK	5.69	1.94E-03	0.0143	6
Q60605	MYL6_MOUSE	IEAFQLFDR	4.91	2.24E-03	0.0143	6
P48722	HS74L_MOUSE	EFSTDLVPYSVTLR	3.60	2.43E-03	0.0143	6
Q9QY94	GLNA_ACOCA Gl	RLTGFHETSNINDFSAGVANR	2.03	3.24E-03	0.0143	6
Q9QY94	GLNA_ACOCA Gl	VQAM[+16]YIIVVDGTGEGLR	0.69	3.31E-03	0.0143	6
Q9R111	GUAD_MOUSE	LATLGGSQALGLDSEIGNFEVVK	1.62	3.60E-03	0.0145	6
Q9R111	GUAD_MOUSE	AVMVSNNVLLINK	1.89	3.81E-03	0.0147	6
Q60605	MYL6_MOUSE	IHVLVTLGEK	3.82	4.06E-03	0.0148	6
O54833	CSK22_MOUSE	QLYQILTFDIR	6.97	4.30E-03	0.0150	6
P48722	HS74L_MOUSE	SIDLPIQSSLYR	3.20	5.23E-03	0.0157	6
Q9QY94	GLNA_ACOCA Gl	VQAMYIIVVDGTGEGLR	2.84	5.64E-03	0.0160	6
O54833	CSK22_MOUSE	LIDWGLAEFYHPAQEYNVR	5.09	6.23E-03	0.0167	6

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
O54833	CSK22_MOUSE	VLGTDELYGYLK	3.63	7.41E-03	0.0179	6
P48722	HS74L_MOUSE	VLATTFDPYLGGR	2.37	7.99E-03	0.0183	6
O54833	CSK22_MOUSE	TPALVFHEYINNTDFK	6.08	8.31E-03	0.0187	6
Q9QY94	GLNA_ACOCA_Gli	LTGFHETSININDFSAGVANR	1.43	8.52E-03	0.0189	6
P25444	RS2_MOUSE	4(GC[+57]TATLGNFAK	2.82	8.82E-03	0.0193	6
P25444	RS2_MOUSE	4(C[+57]GSVLVR	3.73	9.22E-03	0.0198	6
P48722	HS74L_MOUSE	LSLTQDPVVK	1.37	1.01E-02	0.0207	6
P25444	RS2_MOUSE	4(GTGIVSAPVVK	3.12	1.01E-02	0.0207	6
O54833	CSK22_MOUSE	HLVSPEALDLLDK	3.33	1.07E-02	0.0214	6
Q9QY94	GLNA_ACOCA_Gli	ITGTNAEVMPAQWFEQIGPC[+57]EGIR	2.43	1.12E-02	0.0219	6
P25444	RS2_MOUSE	4(TSYLTPDLWK	2.42	1.12E-02	0.0219	6
O54833	CSK22_MOUSE	VYAEVNSLR	2.25	1.38E-02	0.0247	6
Q9R111	GUAD_MOUSE	STDVAEEVYTR	1.79	1.42E-02	0.0251	6
Q8R1B4	EIF3C_MOUSE	ELLGQGLLLR	5.76	1.46E-02	0.0256	6
Q8R1B4	EIF3C_MOUSE	GC[+57]ILTLVER	4.82	1.47E-02	0.0257	6
Q8R1B4	EIF3C_MOUSE	DAHALLDIQSSGR	3.73	1.58E-02	0.0269	6
P48722	HS74L_MOUSE	NFDEALVDYFC[+57]DEFK	5.31	1.65E-02	0.0276	6
Q99104	MYO5A_MOUSE	WTYQEFFSR	1.14	1.72E-02	0.0284	6
P20357	MTAP2_MOUSE	ESSKDEEPLKDK	4.46	2.13E-02	0.0331	6
Q61879	MYH10_MOUSE	LQQELDDLTVDLHQR	5.08	2.13E-02	0.0331	6
P07724	ALBU_MOUSE	SRPC[+57]FSALTYDETYVPK	1.07	2.35E-02	0.0356	6
P62259	1433E_MOUSE	VAGM[+16]DVELTVEER	3.17	2.74E-02	0.0397	6
P68404	KPCB_MOUSE	LSVEIWDWDLTSR	5.57	2.76E-02	0.0399	6
Q922U2	K2C5_MOUSE	VDALMDEINFMK	7.68	3.45E-02	0.0479	6
P68510	1433F_MOUSE	ELETVC[+57]NDVLALLDK	2.49	1.72E-03	0.0143	6
Q9R1R2	TRIM3_MOUSE	GRLPQLSAAIALVGGISQQLQER	7.71	2.56E-03	0.0143	6
Q8C1B7	SEP11_MOUSE	LTIVDTVGFQDQINK	1.63	4.48E-03	0.0151	6
Q8C1B7	SEP11_MOUSE	ELEEEVSNFQK	3.35	4.97E-03	0.0155	6
Q9R1R2	TRIM3_MOUSE	LPQLSAAIALVGGISQQLQER	6.41	5.24E-03	0.0157	6
Q9R1R2	TRIM3_MOUSE	TEGDLVLLVLYGQPVPR	4.92	6.35E-03	0.0169	6
Q8C1B7	SEP11_MOUSE	STSQGFC[+57]FNILC[+57]VGETGIGK	2.22	6.55E-03	0.0171	6
P68510	1433F_MOUSE	IEKELETVC[+57]NDVLALLDK	7.29	6.96E-03	0.0174	6
P68510	1433F_MOUSE	QAFDDAIAELDTLNEDSYK	1.75	8.87E-03	0.0194	6
Q8C1B7	SEP11_MOUSE	STLMDTLFNTK	1.31	1.07E-02	0.0214	6
Q9R1R2	TRIM3_MOUSE	LGSAPEVLLVR	1.17	1.24E-02	0.0231	6
P68510	1433F_MOUSE	NC[+57]NDFQYESK	1.25	1.34E-02	0.0242	6
Q9R1R2	TRIM3_MOUSE	QFLVC[+57]SIC[+57]LDR	4.24	1.55E-02	0.0266	6
Q99104	MYO5A_MOUSE	QETDQLVSNLK	0.92	1.78E-02	0.0290	6
Q6PHZ2	KCC2D_MOUSE	IPTGQEYAAK	2.92	2.24E-02	0.0344	6
Q9DBR7	MYPT1_MOUSE	VGQTAFDVADEDILGYLEELQK	1.00	2.26E-02	0.0346	6
P16330	CN37_MOUSE	HFISGDEPK	1.85	2.47E-02	0.0368	6
P16858	G3P_MOUSE	GIVSNASC[+57]TTNC[+57]LAPLAK	3.09	2.98E-02	0.0424	6
E9Q912	E9Q912_MOUSE	M[+16]LIDAQAEAAEQLGK	4.27	2.69E-03	0.0143	6
E9Q912	E9Q912_MOUSE	IPC[+57]VDAGLISPLVQLLNSK	2.81	2.91E-03	0.0143	6
E9Q912	E9Q912_MOUSE	TEGSLEGC[+57]LDC[+57]LLQALAQNNAETSEK	8.40	3.06E-03	0.0143	6
E9Q912	E9Q912_MOUSE	EVQDLAFLDVVSK	1.16	9.54E-03	0.0202	6
Q9CVB6	ARPC2_MOUSE	DTDAAVGDNIGYITFVLFPR	1.47	1.71E-02	0.0283	6
Q61171	PRDX2_MOUSE	QITVNDLPVGR	0.87	2.37E-02	0.0358	6
Q8CHC4	SYNJ1_MOUSE	VLDAYGLLGVLR	2.45	7.59E-04	0.0143	6
Q8CHC4	SYNJ1_MOUSE	NQTLTDWLLDAPK	2.09	8.05E-04	0.0143	6
P62259	1433E_MOUSE	VAGMDVELTVEER	2.63	9.89E-04	0.0143	6
P05202	AATM_MOUSE	HFIEQGINVC[+57]LC[+57]QSYAK	2.75	1.65E-03	0.0143	6
P05202	AATM_MOUSE	DAGMQLQGYR	1.50	1.81E-03	0.0143	6
Q6ZQ38	CAND1_MOUSE	ISGSILNELIGLVR	4.48	2.03E-03	0.0143	6
Q6ZQ38	CAND1_MOUSE	IDLRPVLGEGVPILASFLR	9.18	3.25E-03	0.0143	6
Q8CHC4	SYNJ1_MOUSE	QEADVLLLGNTLNSDLADK	2.03	4.83E-03	0.0154	6
Q8CHC4	SYNJ1_MOUSE	ALLTTGSLR	1.75	5.22E-03	0.0156	6
P05202	AATM_MOUSE	ISVAGVTSGNVGYLAHAHQVTK	2.02	7.19E-03	0.0177	6
P62259	1433E_MOUSE	M[+58]DDREDLVYQAK	1.02	7.57E-03	0.0180	6
P62259	1433E_MOUSE	LIC[+57]C[+57]DILDVLDK	1.84	8.72E-03	0.0191	6
P05202	AATM_MOUSE	TC[+57]GFDGSGALEDISK	1.49	1.24E-02	0.0231	6
P61358	RL27_MOUSE	VVLVLAGR	1.64	1.71E-02	0.0283	6

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P01837	IGKC_MOUSE	I QNGVLNSWTDQDSK	1.31	2.03E-02	0.0319	6
P25444	RS2_MOUSE	4(SLEEIYLFSLPIK	1.11	2.14E-02	0.0333	6
Q71LX4	TLN2_MOUSE	1TYGVSFLLVK	1.28	2.23E-02	0.0343	6
P68510	1433F_MOUSE	YLAEVASGEK	1.26	2.27E-02	0.0347	6
P68033	ACTC_MOUSE	.AGFAGDDAPR	2.69	2.28E-02	0.0348	6
P09405	NUCL_MOUSE	GYAFIEFASFEDAK	1.23	2.46E-02	0.0367	6
Q9WUM4	COR1C_MOUSE	KSDLFQDDLYPDTAGPEAALEAEWFEGK	1.56	2.72E-02	0.0395	6
Q7TMM9	TBB2A_MOUSE	TAVC[+57]DIPPR	0.81	2.74E-02	0.0397	6
Q7TSJ2	MAP6_MOUSE	TTEGPSATKPDDKEQSK	1.12	3.10E-02	0.0437	6
P40142	TKT_MOUSE	Tr TSRPENAIYSNNEFDQVGGQAK	1.55	3.18E-02	0.0446	6
P50396	GDIA_MOUSE	F FDLGQDVIDFTGHALALYR	7.95	3.63E-04	0.0143	6
P06151	LDHA_MOUSE	I DLADELALVDVMEDK	2.22	6.07E-04	0.0143	6
P11499	HS90B_MOUSE	HSQFIGYPITLYLEK	2.37	6.45E-04	0.0143	6
Q61598	GDIB_MOUSE	F FDLGQDVIDFTGHSLALYR	6.63	1.82E-03	0.0143	6
P06745	G6PI_MOUSE	C KIEPELEGSSAVTSHDSSTNGLISFIK	2.04	2.11E-03	0.0143	6
P06745	G6PI_MOUSE	C TLASLSPETSLFIIASK	1.65	2.27E-03	0.0143	6
P06745	G6PI_MOUSE	C ILLANFLAQTEALMK	3.29	2.64E-03	0.0143	6
P06745	G6PI_MOUSE	C ELFEADPER	1.49	3.11E-03	0.0143	6
P06745	G6PI_MOUSE	C SITDIINIGIGGSDLGPLMVTEALKPYSK	8.88	3.65E-03	0.0146	6
P06151	LDHA_MOUSE	I DYC[+57]VTANSK	3.31	5.07E-03	0.0155	6
P06151	LDHA_MOUSE	I LLIVSNPVDILTYVAWK	4.74	5.82E-03	0.0162	6
P50396	GDIA_MOUSE	F MLLYTEVTR	1.40	6.35E-03	0.0169	6
P11499	HS90B_MOUSE	NPDDITQEEYGEFYK	1.32	6.51E-03	0.0171	6
Q61598	GDIB_MOUSE	F VPSTEAEALASSLMGLFEK	3.83	7.58E-03	0.0180	6
P11499	HS90B_MOUSE	APFDLFENK	1.74	8.23E-03	0.0186	6
P11499	HS90B_MOUSE	LVSSPC[+57]C[+57]IVTSTYGWTANMER	1.96	9.47E-03	0.0202	6
P50396	GDIA_MOUSE	F FLVVFANFDENDPK	1.43	9.53E-03	0.0202	6
P06151	LDHA_MOUSE	I VIGSGC[+57]NLDSAR	1.05	1.02E-02	0.0208	6
P50396	GDIA_MOUSE	F FQILEGPPESMGR	1.34	1.07E-02	0.0214	6
P50396	GDIA_MOUSE	F KFDLGQDVIDFTGHALALYR	5.18	1.20E-02	0.0228	6
P06151	LDHA_MOUSE	I DQLIVNLLKEEQAPQNK	2.89	1.34E-02	0.0242	6
Q61598	GDIB_MOUSE	F QLIC[+57]DPSYVK	4.42	1.50E-02	0.0261	6
P50396	GDIA_MOUSE	F VPSTETEALASNLGMFEEK	2.69	1.53E-02	0.0264	6
Q8BFR5	EFTU_MOUSE	I LLDVADTYIPVPTR	6.00	1.87E-02	0.0300	6
Q92111	TRFE_MOUSE	: AVLTSQETLFGGSDC[+57]TGNFC[+57]LFK	1.38	2.29E-02	0.0349	6
P46460	NSF_MOUSE	V: THPSVVPGC[+57]IAFSLPQR	1.30	2.43E-02	0.0364	6
Q9DB20	ATPO_MOUSE	. VSLAVLNPIYK	2.60	2.49E-02	0.0370	6
Q9CQV8	1433B_MOUSE	TAFDEAIAELDTLNEESYK	2.13	2.66E-02	0.0389	6
O88935	SYN1_MOUSE	: VLLVIDEPHTDWAK	1.24	2.90E-02	0.0414	6
Q99104	MYO5A_MOUSE	SHENEAEALRGEIQLSKEENNR	1.62	3.03E-02	0.0429	6
P05201	AATC_MOUSE	. TPGTWSHITEQIGMFSFTGLNPK	3.92	1.12E-03	0.0143	6
P05201	AATC_MOUSE	. IANDNSLNHEYLPIGLAEFR	2.30	3.86E-03	0.0147	6
P05201	AATC_MOUSE	. FLFPFFDSAYQGFASGDLEK	7.27	5.01E-03	0.0155	6
P05201	AATC_MOUSE	. YFVSEGFELFC[+57]AQSFASK	4.34	5.18E-03	0.0156	6
P05201	AATC_MOUSE	. INMC[+57]GLTTK	1.79	5.90E-03	0.0163	6
Q68FD5	CLH1_MOUSE	(AFMTADLPNELIELLEK	1.29	2.49E-02	0.0370	6
P07901	HS90A_MOUSE	HGLEVIYMIPIDEYC[+57]VQQLK	3.51	1.63E-03	0.0143	6
P07901	HS90A_MOUSE	HNDDEQYAWESSAGGSFTVR	3.61	2.19E-03	0.0143	6
P07901	HS90A_MOUSE	HSQFIGYPITLFVEK	1.75	4.98E-03	0.0155	6
P07901	HS90A_MOUSE	HFSVEGQLEFR	2.64	5.04E-03	0.0155	6
Q61879	MYH10_MOUSE	GDEVMI[+16]VELAENGK	1.30	2.43E-02	0.0364	6
O54983	CRYM_MOUSE	SSLLIPPLEAALANFSK	1.45	2.54E-02	0.0375	6
Q8R5C5	ACTY_MOUSE	I TLFSNIVLSGGSTLFLK	2.99	3.62E-04	0.0143	5
P68254	1433T_MOUSE	AVTEQGAELSNEER	2.81	7.05E-04	0.0143	5
Q6P9K8	CSKI1_MOUSE	TLSGPVTGLLATAR	1.38	7.59E-04	0.0143	5
Q8R5C5	ACTY_MOUSE	I IWQYVYSK	1.66	7.76E-04	0.0143	5
P40124	CAP1_MOUSE	. GAVPYVQAFDSSLANPVAEYLK	3.85	7.93E-04	0.0143	5
Q9R0P5	DEST_MOUSE	I C[+57]IVVEEGKEILVGDVGATITDPFK	2.44	8.16E-04	0.0143	5
Q9R0P5	DEST_MOUSE	I LGGSLIVAFEGSPV	2.41	8.51E-04	0.0143	5
Q923G3	Q923G3_MOUSE	SVQTFADK	3.08	1.21E-03	0.0143	5
P59999	ARPC4_MOUSE	ELLLQPVTISR	2.60	1.23E-03	0.0143	5
Q6P9K8	CSKI1_MOUSE	SVSESSPGDSPVKPPEGSSGAAR	5.54	1.27E-03	0.0143	5

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P59999	ARPC4_MOUSE	ATLQAALC[+57]LENFSSQVVER	3.47	1.57E-03	0.0143	5
P68254	1433T_MOUSE	SIC[+57]TTVLELLDK	3.15	1.63E-03	0.0143	5
P59999	ARPC4_MOUSE	AENFFILR	3.29	1.70E-03	0.0143	5
P68254	1433T_MOUSE	TAFDEAIAELDTLNEDSYK	4.21	1.71E-03	0.0143	5
P40124	CAP1_MOUSE	ALLATASQC[+57]QQPAGNK	1.55	1.82E-03	0.0143	5
Q8R5C5	ACTY_MOUSE	IDQLQTFSEEHPVLLTEAPLNPSK	2.54	1.83E-03	0.0143	5
P80317	TCPZ_MOUSE	AQLGVQAFADALLIIPK	4.13	2.01E-03	0.0143	5
P99029	PRDX5_MOUSE	ATDLLLDDSLVSLFGNR	2.46	2.10E-03	0.0143	5
P99029	PRDX5_MOUSE	VGDAIPSVVEFEGEPGK	1.66	2.13E-03	0.0143	5
P80317	TCPZ_MOUSE	NAIDDCG[+57]VVPGAGAVEVALAEALIK	2.50	2.22E-03	0.0143	5
Q9CVB6	ARPC2_MOUSE	ASHTAPQVLFSHR	3.13	2.27E-03	0.0143	5
Q6P9K8	CSK11_MOUSE	NTYSQTALDIVHQFTTSQASK	4.35	2.30E-03	0.0143	5
Q6P9K8	CSK11_MOUSE	GEASAEGPPLAR	4.44	2.40E-03	0.0143	5
Q8BJH1	ZC21A_MOUSE	ASSVNSPLGNKPQTLSPSHR	4.69	2.58E-03	0.0143	5
P80317	TCPZ_MOUSE	VATAQDDITGDGTTSNVLIIGELLK	1.70	2.60E-03	0.0143	5
P80317	TCPZ_MOUSE	GIDPFSLDALAK	1.69	3.10E-03	0.0143	5
Q923G3	Q923G3_MOUSE	QEALKNDLVEALKR	3.59	3.93E-03	0.0147	5
Q923G3	Q923G3_MOUSE	NDLVEALK	3.02	4.00E-03	0.0148	5
Q9R0P5	DEST_MOUSE	HEYQANGPEDLNR	1.47	4.10E-03	0.0148	5
Q9R0Q6	ARC1A_MOUSE	TLESSIQGLR	2.87	4.23E-03	0.0149	5
Q9R0Q6	ARC1A_MOUSE	STVLSLDWHPNVLAAAGSC[+57]DFK	4.64	4.34E-03	0.0150	5
Q9CVB6	ARPC2_MOUSE	VYGSFLVNPEPGYNVSLYDLENLPASK	9.51	4.58E-03	0.0152	5
Q923G3	Q923G3_MOUSE	SKQEALKNDLVEALK	4.51	4.81E-03	0.0154	5
Q8R5C5	ACTY_MOUSE	AGFAGDQIPK	1.58	4.89E-03	0.0155	5
Q923G3	Q923G3_MOUSE	NDLVEALKR	3.12	5.00E-03	0.0155	5
Q9R0Q6	ARC1A_MOUSE	FC[+57]TTGIDGAMTIWDFK	4.96	5.07E-03	0.0155	5
P40124	CAP1_MOUSE	LSDLLAPISEIQEVITFR	5.99	5.46E-03	0.0158	5
Q8BJH1	ZC21A_MOUSE	AIAAPQAGANTK	3.42	5.66E-03	0.0160	5
P99029	PRDX5_MOUSE	THLPGFVEQAGALK	1.76	6.99E-03	0.0175	5
Q9CVB6	ARPC2_MOUSE	MILLEVNNR	3.28	7.21E-03	0.0177	5
P68254	1433T_MOUSE	YLIANATNPESK	2.22	7.67E-03	0.0181	5
P99029	PRDX5_MOUSE	VNLAELFK	2.01	8.41E-03	0.0188	5
Q9R0Q6	ARC1A_MOUSE	LAWVSHDSTVSVADASK	3.43	8.61E-03	0.0190	5
Q6P9K8	CSK11_MOUSE	LLLDGGINAQVR	4.42	9.31E-03	0.0199	5
P59999	ARPC4_MOUSE	VLIEGSINSVR	2.83	1.02E-02	0.0208	5
P40124	CAP1_MOUSE	NSLDC[+57]EIVSAK	1.14	1.06E-02	0.0213	5
Q9R0P5	DEST_MOUSE	EILVGDVGATITDPFK	2.02	1.12E-02	0.0219	5
Q9R0Q6	ARC1A_MOUSE	DGIWKPTLVILR	4.24	1.32E-02	0.0240	5
P68254	1433T_MOUSE	YLAEVAC[+57]GDDRK	2.55	1.41E-02	0.0250	5
Q9R0P5	DEST_MOUSE	IYALYDASFETK	3.82	1.60E-02	0.0271	5
Q8C0M9	ASGL1_MOUSE	GLGGLILVNK	5.83	1.71E-02	0.0283	5
P63038	CH60_MOUSE	ALMLQGVDLLADAVAVTM[+16]GPK	1.73	1.85E-02	0.0298	5
Q9D0F9	PGM1_MOUSE	LSGTGSAGATIR	4.19	1.94E-02	0.0308	5
Q9D8E6	RL4_MOUSE	6C FC[+57]IWTESA FR	2.52	2.32E-02	0.0352	5
Q9D8E6	RL4_MOUSE	6C QPYAVSELAGHQ TSAESWG TGR	1.90	2.70E-02	0.0393	5
P62137	PP1A_MOUSE	IRYPENFFLLR	4.75	2.77E-02	0.0400	5
Q9Z1G3	VATC1_MOUSE	VFVESVLR	0.90	2.92E-02	0.0417	5
P07724	ALBU_MOUSE	ENYGELADC[+57]C[+57]TK	3.34	3.08E-02	0.0435	5
A0A0B6VMB:A0A0B6VMB2_MC	NTQPIMDTDGSYFVYSK		2.56	3.46E-02	0.0480	5
Q6URW6	MYH14_MOUSE	DQADFSVLHYAGK	4.74	3.48E-02	0.0483	5
Q7TQD2	TPPP_MOUSE	LSLESEGANEGATAAPELSALEEAFRR	2.99	4.70E-05	0.0143	5
O08539	BIN1_MOUSE	MLVDQALLTMDTYLGQFPDIK	2.99	5.96E-05	0.0143	5
Q9WV60	GSK3B_MOUSE	VTTVVATPGQGPDPRPQEVSYTDTK	3.80	1.07E-03	0.0143	5
P80314	TCPB_MOUSE	LALVTGGEIASTFDHPELVK	2.33	1.30E-03	0.0143	5
Q8R570	SNP47_MOUSE	NLPLFSEGEAQELTQILSK	5.25	1.58E-03	0.0143	5
P04370	MBP_MOUSE	MYLATASTMDHAF	1.99	1.61E-03	0.0143	5
P04370	MBP_MOUSE	MHRDTGILDSIGR	2.07	1.63E-03	0.0143	5
P80314	TCPB_MOUSE	MLPTIADNAGYDSADLVAQLF	2.76	1.72E-03	0.0143	5
Q8R570	SNP47_MOUSE	TEEVLVGLPLSSIIEIR	6.56	2.07E-03	0.0143	5
Q7TQD2	TPPP_MOUSE	TITFEQFQEALEELAK	4.40	2.10E-03	0.0143	5
Q3THE2	ML12B_MOUSE	DGFIDKEDLHDMLASLGK	5.98	2.51E-03	0.0143	5
Q9WV60	GSK3B_MOUSE	VIGNSGFVVYQAK	3.45	2.58E-03	0.0143	5

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P80314	TCPB_MOUSE	LSSFIGAIAIGDLVK	1.73	2.71E-03	0.0143	5
Q9WV60	GSK3B_MOUSE	DTPALFNFTTQELSSNPPLATILIPPHAF	7.29	2.78E-03	0.0143	5
Q3THE2	ML12B_MOUSE	FTDEEVDELYR	3.63	2.83E-03	0.0143	5
P80314	TCPB_MOUSE	QVLLSAAEAAEVILR	2.43	2.94E-03	0.0143	5
Q9WV60	GSK3B_MOUSE	IQAAASPPANATAASDTNAGDF	3.21	3.09E-03	0.0143	5
Q3THE2	ML12B_MOUSE	ATSNVFAMFDQSQIQEFK	6.12	3.17E-03	0.0143	5
Q3THE2	ML12B_MOUSE	ATSNVFAM[+16]FDQSQIQEFK	3.72	3.18E-03	0.0143	5
Q7TQD2	TPPP_MOUSE	VDLVDESGYVPGYK	1.82	3.55E-03	0.0145	5
O08539	BIN1_MOUSE	MLQAHLVAQTNLLR	1.36	3.80E-03	0.0147	5
Q9QYC0	ADDA_MOUSE	VNLQGDIVDR	2.04	4.29E-03	0.0150	5
Q7TQD2	TPPP_MOUSE	NVTVDVDIVFSK	1.87	4.58E-03	0.0152	5
P04370	MBP_MOUSE	MTQDENPVVHFFK	2.70	5.05E-03	0.0155	5
Q8R570	SNP47_MOUSE	IELLEDALVLR	4.57	5.35E-03	0.0158	5
Q7TQD2	TPPP_MOUSE	LSLESEGANEGATAAPELSALEEAFR	2.33	5.35E-03	0.0158	5
Q8R570	SNP47_MOUSE	DLQQQSEQLDSVLK	2.63	6.02E-03	0.0164	5
O08539	BIN1_MOUSE	MLNQNLNDVLVSLEK	1.58	6.53E-03	0.0171	5
P47963	RL13_MOUSE	ELATQLTGPVM[+16]PIR	6.00	7.34E-03	0.0178	5
Q9QYC0	ADDA_MOUSE	EYQPHVIVSTTGNPNFNTLTDR	3.72	8.27E-03	0.0187	5
O08539	BIN1_MOUSE	MLVQAQHDYTATDTDELQLK	2.61	8.33E-03	0.0187	5
Q8R570	SNP47_MOUSE	FIGKPDVAYQLISAK	3.80	1.02E-02	0.0208	5
Q9QYC0	ADDA_MOUSE	TLASAGGPDNLVLLDPGK	3.79	1.05E-02	0.0212	5
Q9QYC0	ADDA_MOUSE	LADLFGWSQLIYNHITTR	6.08	1.11E-02	0.0219	5
Q3THE2	ML12B_MOUSE	NAFAC[+57]FDEEATGTIQEDYLF	3.49	1.65E-02	0.0276	5
Q8BYI9	TENR_MOUSE	VDFILLK	3.90	1.82E-02	0.0295	5
Q7TMM9	TBB2A_MOUSE	YLTVAEIFR	4.39	1.88E-02	0.0301	5
P17183	ENOG_MOUSE	M[+16]VIGM[+16]DVAASEFYR	9.50	1.88E-02	0.0301	5
Q99104	MYO5A_MOUSE	KTDDDAEAIIC[+57]SMC[+57]NALTTAQIVK	4.40	1.89E-02	0.0302	5
Q9JII6	AK1A1_MOUSE	ALGLSNFNSR	4.90	1.96E-02	0.0310	5
O88935	SYN1_MOUSE	ISQSLTNAFNLPEPAPPRPSLSQDEVK	4.09	2.18E-02	0.0337	5
P97351	RS3A_MOUSE	IVFEVSLADLQNDVAFRK	2.08	2.47E-02	0.0368	5
Q7TQI3	OTUB1_MOUSE	IQQEIAVQNPLVSER	3.59	3.04E-02	0.0430	5
P80315	TCPD_MOUSE	M[+16]PENVASRSGAPTAGPGSR	1.29	3.58E-02	0.0494	5
P20357	MTAP2_MOUSE	SEVQAHSPPSR	1.55	3.58E-02	0.0494	5
P27659	RL3_MOUSE	6C LEQQVPVNQVFGQDEMIDVIGVTK	2.76	2.70E-05	0.0143	5
Q9DBJ1	PGAM1_MOUSE	DAGYEFDIC[+57]FTSVQK	2.92	7.64E-04	0.0143	5
Q9DBJ1	PGAM1_MOUSE	HLEGLSEEAIM[+16]ELNLPTGIPIVYELDK	6.69	1.02E-03	0.0143	5
Q3UHL1	CAMKV_MOUSE	EVFDWILDQGYYSER	5.63	1.08E-03	0.0143	5
Q62167	DDX3X_MOUSE	DLLDLLVEAK	3.93	1.13E-03	0.0143	5
Q62167	DDX3X_MOUSE	SFLDLLLNATGK	4.54	1.31E-03	0.0143	5
P61982	1433G_MOUSE	TAFDDAIAELDTLNEDSYK	2.56	1.93E-03	0.0143	5
Q9DBJ1	PGAM1_MOUSE	ALPFWNEEIVPQIK	1.54	2.06E-03	0.0143	5
Q9D0E1	HNRPM_MOUSE	QGGGGAGGSVPGIER	4.65	2.31E-03	0.0143	5
Q3UHL1	CAMKV_MOUSE	HPNILQLVDVVFVTR	6.58	2.98E-03	0.0143	5
Q9D0E1	HNRPM_MOUSE	GNFGGSFAGSFGGAGGHAPGVAR	4.29	3.13E-03	0.0143	5
P61982	1433G_MOUSE	NVTELNEPLSNEER	1.29	4.22E-03	0.0149	5
Q9D0E1	HNRPM_MOUSE	INEILSNALK	3.85	4.34E-03	0.0150	5
Q9D0E1	HNRPM_MOUSE	AFITNIPFDVK	3.66	5.08E-03	0.0155	5
Q3UHL1	CAMKV_MOUSE	AAATPEPAVAQPDPSTALEGATGQAPPSSK	2.97	5.53E-03	0.0159	5
Q62167	DDX3X_MOUSE	HVINFDLPSDIEEYVHR	4.73	5.56E-03	0.0159	5
P61982	1433G_MOUSE	NC[+57]SETQYESK	1.62	6.27E-03	0.0168	5
P61982	1433G_MOUSE	LGLALNYSVFYIEIQNAPEQAC[+57]HLAK	6.83	6.73E-03	0.0172	5
Q3UHL1	CAMKV_MOUSE	ATPATEESTVPATQSSALPAAK	1.80	7.08E-03	0.0175	5
P27659	RL3_MOUSE	6C HGSLGFLPR	2.57	1.08E-02	0.0215	5
P27659	RL3_MOUSE	6C SINPLGGFVHYGEVTNDFIM[+16]LK	4.01	1.30E-02	0.0238	5
Q9DBJ1	PGAM1_MOUSE	YADLTEDQLPSC[+57]ESLKDTIAR	1.12	1.44E-02	0.0254	5
Q62167	DDX3X_MOUSE	LEQELFSGGNTGINFEK	3.05	1.48E-02	0.0258	5
P61982	1433G_MOUSE	YLAEVATGEK	1.07	1.50E-02	0.0261	5
Q9D0E1	HNRPM_MOUSE	VGEVTVYVLLMDAEGK	7.64	1.60E-02	0.0271	5
P27659	RL3_MOUSE	6C NNASTDYDLSDK	5.12	1.64E-02	0.0275	5
Q3UHL1	CAMKV_MOUSE	ITAEAAISHEWISGNAASDK	3.59	1.64E-02	0.0275	5
P61161	ARP2_MOUSE	SMLEVNYPMENGIVR	6.54	1.73E-02	0.0284	5
P23116	EIF3A_MOUSE	LLQQVAQIQSIEFSR	3.39	1.97E-02	0.0311	5

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P63318	KPCG_MOUSE	LQLEIR	0.99	2.35E-02	0.0356	5
P29341	PABP1_MOUSE	SKVDEAVAVLQAHQAK	2.48	1.20E-03	0.0143	5
P29341	PABP1_MOUSE	ITGMLLEIDNSELLHM[+16]LESPELRL	7.38	4.47E-03	0.0151	5
P29341	PABP1_MOUSE	ITGMLLEIDNSELLHMLESPESLR	5.42	6.22E-03	0.0167	5
P29341	PABP1_MOUSE	ALYDTFSAFGNLSLSC[+57]K	4.67	7.81E-03	0.0182	5
P29341	PABP1_MOUSE	IVATKPLYVALAQR	1.32	1.70E-02	0.0282	5
P56480	ATPB_MOUSE	IGLFGGAGVVK	2.01	2.99E-03	0.0143	5
P56480	ATPB_MOUSE	FTQAGSEVSALLGR	1.44	3.08E-03	0.0143	5
P56480	ATPB_MOUSE	TVLIMELINNVAK	1.72	1.65E-02	0.0276	5
Q9Z2I9	SUCB1_MOUSE	LHGGTPANFLDVGGGATVQQVTEAFK	4.42	2.41E-02	0.0363	5
M7PGV1	M7PGV1_PNEMU	VISNASC[+57]TTNC[+57]LAPLAK	1.20	2.63E-02	0.0386	5
P17751	TPIS_MOUSE	VTNGAFTGEISPGMIK	1.65	1.04E-03	0.0143	5
P17751	TPIS_MOUSE	RHVFGESEDELIGQK	1.51	1.95E-03	0.0143	5
P46096	SYT1_MOUSE	NTLNPPYNEFSFEVFPFEIQIK	3.88	2.48E-03	0.0143	5
P46096	SYT1_MOUSE	LGDIC[+57]FSLR	2.26	3.84E-03	0.0147	5
Q9CQV8	1433B_MOUSE	IEAELQDIC[+57]NDVLELLDK	4.44	4.74E-03	0.0154	5
P17751	TPIS_MOUSE	ELASQPDVDGFLVGGASLKPEFVDIINAK	2.44	5.04E-03	0.0155	5
P17751	TPIS_MOUSE	VSHALAEGLGVIAC[+57]IGEKL	1.67	5.95E-03	0.0163	5
P46096	SYT1_MOUSE	TLNPFVNEQFTFK	1.51	7.03E-03	0.0175	5
Q9CQV8	1433B_MOUSE	YLILNATQAESK	1.49	7.20E-03	0.0177	5
P46096	SYT1_MOUSE	VFVGYNSTGAELR	1.10	8.14E-03	0.0185	5
P17751	TPIS_MOUSE	VVLAYEPVWAIGTGK	1.29	9.47E-03	0.0202	5
Q9CQV8	1433B_MOUSE	VISSIEQK	1.20	1.24E-02	0.0231	5
Q9CQV8	1433B_MOUSE	QTTVSNQQAYQEAFAEISK	1.38	1.26E-02	0.0233	5
P16546	SPTN1_MOUSE	EELYQNLTR	1.76	1.85E-02	0.0298	5
P62242	RS8_MOUSE	IIDVVYNASNNELVR	2.13	2.65E-02	0.0388	5
O35295	PURB_MOUSE	GGGGGGGGPGGEQETQELASK	4.68	2.56E-04	0.0143	5
O35295	PURB_MOUSE	DSLGDFFIEHYAQLGPSSPEQLAAGAEEGGPR	5.58	8.36E-04	0.0143	5
O35295	PURB_MOUSE	GGGGGGGGPGGFQAPAPR	3.21	8.40E-04	0.0143	5
O35295	PURB_MOUSE	GGGGFGGGPGGGLQSGQTIALPAQGLIEFR	3.67	2.43E-03	0.0143	5
O35295	PURB_MOUSE	FGGAFCC[+57]JR	2.51	2.47E-03	0.0143	5
P28652	KCC2B_MOUSE	IC[+57]DPGLTSFEPEALGNLVEGM[+16]DFHR	6.94	1.21E-02	0.0229	5
P28652	KCC2B_MOUSE	QTTAPATM[+16]STAASGTTM[+16]GLVEQA	6.22	1.29E-02	0.0237	5
Q7TPR4	ACTN1_MOUSE	KDDPLTNLNTAFDVAER	4.89	2.26E-02	0.0346	5
P39053	DYN1_MOUSE	VLNQQLTNHIR	6.34	3.25E-02	0.0455	5
Q8BPN8	DMXL2_MOUSE	DGVAVITLPLGGSIK	5.79	3.34E-02	0.0466	5
P09411	PGK1_MOUSE	VNEM[+16]IIGGGM[+16]AFTFLK	1.51	8.42E-03	0.0188	5
P09411	PGK1_MOUSE	IDC[+57]VGPEVENAC[+57]ANPAAGTVILLENLR	1.74	1.07E-02	0.0214	5
P09411	PGK1_MOUSE	IQIWNPGVGVFEWEAFAR	7.58	1.35E-02	0.0243	5
P09411	PGK1_MOUSE	IALESPERPFLAILGGAK	1.38	1.59E-02	0.0270	5
Q8R1B4	EIF3C_MOUSE	TEPTAQNLALQLAEK	2.08	2.76E-02	0.0399	5
P14152	MDHC_MOUSE	EVGVYEALKDDSWLK	1.82	6.17E-03	0.0166	5
P14152	MDHC_MOUSE	AIADHIR	3.77	6.39E-03	0.0169	5
P14152	MDHC_MOUSE	NVWGNHSSSTQYPDVNHAK	1.37	1.08E-02	0.0215	5
P14152	MDHC_MOUSE	DLDAVAVLVGSMR	1.55	1.18E-02	0.0226	5
Q9DBG3	AP2B1_MOUSE	VNYVVQEAVVIR	0.79	3.19E-02	0.0447	5
P05064	ALDOA_MOUSE	C[+57]PLLKPWALTFSYGR	2.32	4.68E-03	0.0153	5
P05064	ALDOA_MOUSE	FSNEEIAMATVTALR	1.35	1.23E-02	0.0231	5
P05064	ALDOA_MOUSE	TVPPAVTGVTFVLSGGQSEEEASINLNAINK	1.49	1.31E-02	0.0239	5
Q9JHU4	DYHC1_MOUSE	LLNTFLER	1.30	2.31E-02	0.0352	5
Q8CGF6	WDR47_MOUSE	LILDFLNSK	1.37	2.81E-02	0.0405	5
A0A0G2JDN7	A0A0G2JDN7_MOUSE	LSAGELASLSASQVPTALTFEETPAK	3.53	3.72E-04	0.0143	4
P49813	TMOD1_MOUSE	SNPVAFALAEMLK	7.54	5.58E-04	0.0143	4
A0A0G2JDN7	A0A0G2JDN7_MOUSE	EIEVTATQSIPSLLEETPR	4.60	6.14E-04	0.0143	4
A0A0G2JDN7	A0A0G2JDN7_MOUSE	VDSC[+57]PFIC[+57]LGGEK	3.49	1.11E-03	0.0143	4
P80316	TCPE_MOUSE	LGFAVVQEISFGTTK	1.91	1.29E-03	0.0143	4
Q8C0M9	ASGL1_MOUSE	TVEEAAQLALDYMK	2.55	1.43E-03	0.0143	4
Q7TMB8	CYFP1_MOUSE	DFVSEAYLITLTK	2.88	1.44E-03	0.0143	4
Q61768	KINH_MOUSE	TGAEGAVLDEAK	2.19	1.47E-03	0.0143	4
P49813	TMOD1_MOUSE	LADLTGPIPK	4.99	1.50E-03	0.0143	4
Q9QZ83	Q9QZ83_MOUSE	KDLYANTVLSGGTTM[+16]YPGLADF	4.17	1.72E-03	0.0143	4
Q9QZ83	Q9QZ83_MOUSE	DLYANTVLSGGTTM[+16]YPGLADF	4.11	1.76E-03	0.0143	4

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9CYT6	CAP2_MOUSE	/LINSMVAEFLK	2.00	1.90E-03	0.0143	4
P08553	NFM_MOUSE	NEYQDLLNVK	4.08	2.00E-03	0.0143	4
P47754	CAZA2_MOUSE	DIQDSLTVSNEVQTAK	4.59	2.05E-03	0.0143	4
Q5SYD0	MYO1D_MOUSE	VVSVIAELLSTK	4.60	2.06E-03	0.0143	4
Q63844	MK03_MOUSE	IIC[+57]DFGLAR	1.72	2.45E-03	0.0143	4
P47754	CAZA2_MOUSE	VDGQQTIIAC[+57]IESHQFQAK	4.94	2.47E-03	0.0143	4
P49813	TMOD1_MOUSE	TLENELDELDPDNALLPAGLR	6.64	2.49E-03	0.0143	4
P47754	CAZA2_MOUSE	FTVTPSTTQVVGILK	4.88	2.58E-03	0.0143	4
P63330	PP2AA_MOUSE	GAGYTFGQDISETFNHANGLTLVSR	3.41	2.62E-03	0.0143	4
Q61768	KINH_MOUSE	K EVLQALEELAVNYDQK	2.75	2.71E-03	0.0143	4
P15105	GLNA_MOUSE	TC[+57]LLNETGDEPFQYKN	1.67	2.73E-03	0.0143	4
Q63844	MK03_MOUSE	I GTAGVVPVVPGEVEVVK	2.18	2.76E-03	0.0143	4
Q8K183	PDXK_MOUSE	DIEDPEIVVQATVL	2.13	3.08E-03	0.0143	4
Q6PIE5	AT1A2_MOUSE	SPEFTHENPLETR	1.96	3.08E-03	0.0143	4
Q9CYT6	CAP2_MOUSE	/SALFAQLNQGEAITK	2.67	3.16E-03	0.0143	4
P51863	VA0D1_MOUSE	FC[+57]TLLGGTTADAMC[+57]PILEFEADRF	6.37	3.29E-03	0.0143	4
P80318	TCPG_MOUSE	AVAQALEVIPR	1.63	3.45E-03	0.0144	4
Q91V92	ACLY_MOUSE	/DLVSSLTSGLLTIGDR	2.72	3.48E-03	0.0144	4
P60335	PCBP1_MOUSE	AITIAGVPQSVTEC[+57]VK	1.92	3.51E-03	0.0144	4
Q9Z1D1	EIF3G_MOUSE	ETDLQELFRPFGSISR	6.32	3.63E-03	0.0146	4
P10630	IF4A2_MOUSE	I VLIITDLLAR	1.84	3.74E-03	0.0147	4
Q61768	KINH_MOUSE	K ISFLENNLEQLTK	2.35	3.82E-03	0.0147	4
P10630	IF4A2_MOUSE	I QFYINVER	1.50	3.97E-03	0.0148	4
Q9Z1D1	EIF3G_MOUSE	LPGELEPVQAAQSK	3.61	3.97E-03	0.0148	4
Q5SYD0	MYO1D_MOUSE	TLFTLEELR	4.39	4.04E-03	0.0148	4
P80318	TCPG_MOUSE	I VLLDSSLEYK	1.87	4.20E-03	0.0149	4
Q641P0	ARP3B_MOUSE	DYEEYGPSIC[+57]R	3.32	4.57E-03	0.0152	4
Q9QZ83	Q9QZ83_MOUSE	KDLYANTVLSGGTTMYPGLADR	3.14	4.73E-03	0.0153	4
Q9Z1D1	EIF3G_MOUSE	VTNLSEDTR	5.66	4.76E-03	0.0154	4
Q61768	KINH_MOUSE	K LYLVDLAGSEK	1.95	4.80E-03	0.0154	4
P08553	NFM_MOUSE	N VQSLQDEVAFLR	4.12	4.92E-03	0.0155	4
P62908	RS3_MOUSE	4(AELNEFLTR	2.54	5.03E-03	0.0155	4
P47754	CAZA2_MOUSE	KVDGQQTIIAC[+57]IESHQFQAK	3.63	5.06E-03	0.0155	4
P80316	TCPE_MOUSE	WVVGPEIELIAIATGGR	5.87	5.07E-03	0.0155	4
P63330	PP2AA_MOUSE	NVVTIFSAPNYC[+57]YR	2.60	5.10E-03	0.0155	4
Q641P0	ARP3B_MOUSE	GVDDLDFFIGDEAIDKPTYATK	4.41	5.37E-03	0.0158	4
Q9QZ83	Q9QZ83_MOUSE	DLYANTVLSGGTTMYPGLADR	5.17	5.44E-03	0.0158	4
P49813	TMOD1_MOUSE	TLNVESNFISGAGILR	4.62	5.51E-03	0.0159	4
Q8K183	PDXK_MOUSE	DKSFLAMVVDIVR	4.02	5.87E-03	0.0163	4
Q92111	TRFE_MOUSE	S DFASC[+57]HLAQAPNHVVVSR	3.64	6.10E-03	0.0166	4
P10630	IF4A2_MOUSE	I GFKDQIYEIFQK	2.56	6.13E-03	0.0166	4
Q9Z1D1	EIF3G_MOUSE	ELAEQLGLSTGEK	6.74	6.27E-03	0.0168	4
Q9CYT6	CAP2_MOUSE	/LEQLSAGLDGPPR	1.57	6.32E-03	0.0169	4
Q641P0	ARP3B_MOUSE	NVVLSSGGSTMFR	3.05	6.61E-03	0.0171	4
Q6PIE5	AT1A2_MOUSE	GIVIATGDR	4.20	6.91E-03	0.0174	4
Q92111	TRFE_MOUSE	S DFQLFSSPLGK	2.14	7.34E-03	0.0178	4
P15105	GLNA_MOUSE	L VLC[+57]EVFK	1.36	7.47E-03	0.0180	4
P80318	TCPG_MOUSE	EMMLSIINSSITTK	2.69	7.81E-03	0.0182	4
Q5SYD0	MYO1D_MOUSE	IGELVGLVNHFK	4.36	7.88E-03	0.0183	4
Q61937	NPM_MOUSE	N M[+16]SVQPTVSLGGFEITPPVVLR	6.53	7.88E-03	0.0183	4
P60335	PCBP1_MOUSE	L VVPATQC[+57]GSLIGK	1.37	7.95E-03	0.0183	4
P80316	TCPE_MOUSE	I ADGYEQAAR	2.18	8.93E-03	0.0194	4
P51863	VA0D1_MOUSE	LLFEGAGSNPGDK	1.57	9.34E-03	0.0199	4
Q8K183	PDXK_MOUSE	AEAGEGQKPSPAQLELR	5.75	9.61E-03	0.0203	4
P62908	RS3_MOUSE	4(GGKPEPPAMPQPVPPTA	3.57	1.02E-02	0.0208	4
Q61937	NPM_MOUSE	N GPSSVEDIK	2.75	1.06E-02	0.0213	4
P15105	GLNA_MOUSE	TC[+57]LLNETGDEPFQYK	1.37	1.09E-02	0.0216	4
P08553	NFM_MOUSE	NEIEAEIQALR	2.60	1.15E-02	0.0223	4
P10630	IF4A2_MOUSE	I GYDVIAQAQSGTGK	1.80	1.18E-02	0.0226	4
P62908	RS3_MOUSE	4(GFGPEGSVELYAEK	3.65	1.18E-02	0.0226	4
A0A0G2JDN7	A0A0G2JDN7_MOUSE	LGFFEGK	2.31	1.19E-02	0.0227	4
Q91V92	ACLY_MOUSE	/LGLVGVNLSLDGVK	1.53	1.21E-02	0.0229	4

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P62908	RS3_MOUSE	4(TTEIILATR	2.06	1.21E-02	0.0229	4
Q92111	TRFE_MOUSE	3(SAGWVIPIGLLFC[+57]K	3.02	1.22E-02	0.0230	4
Q9CYT6	CAP2_MOUSE	7(FGLVFDHVVGIVEVINSK	2.96	1.25E-02	0.0232	4
Q61937	NPM_MOUSE	NMSVQPTVSLGGFEITPPVVLR	6.54	1.31E-02	0.0239	4
P62301	RS13_MOUSE	2(GLSQSALPYR	3.68	1.33E-02	0.0241	4
P80318	TCPG_MOUSE	TAVETAVLLLR	3.00	1.39E-02	0.0248	4
Q63844	MK03_MOUSE	IDVYIVQDLMETDLYK	3.08	1.39E-02	0.0248	4
Q7TMB8	CYFP1_MOUSE	LGTPQQIAIAR	1.30	1.43E-02	0.0253	4
Q6PIE5	AT1A2_MOUSE	AGQENISVSK	1.37	1.45E-02	0.0255	4
P60335	PCBP1_MOUSE	IANPVEGSSGR	1.22	1.47E-02	0.0257	4
Q7TMB8	CYFP1_MOUSE	FINMFAVLDELK	5.33	1.52E-02	0.0263	4
P80316	TCPE_MOUSE	QMAEIAVNAVLTVADMER	4.63	1.57E-02	0.0268	4
P51863	VA0D1_MOUSE	AGVLSQADYLNLVQC[+57]ETLEDLK	3.30	1.62E-02	0.0273	4
P51410	RL9_MOUSE	6(CDFNHINVELSLLGK	3.88	1.62E-02	0.0273	4
P62301	RS13_MOUSE	2(KGLTPSQIGVILR	4.32	1.65E-02	0.0276	4
Q91V92	ACLY_MOUSE	7(YIC[+57]TTSAIQNR	2.56	1.65E-02	0.0276	4
P17426	AP2A1_MOUSE	ALQVGC[+57]LLR	1.37	1.71E-02	0.0283	4
Q7TMM9	TBB2A_MOUSE	IMNTFSVMPSPK	2.34	1.73E-02	0.0284	4
O08638	MYH11_MOUSE	LQQELDDLVDLDNQR	2.00	1.74E-02	0.0285	4
P16546	SPTN1_MOUSE	GAC[+57]AGSEDAVK	2.56	1.80E-02	0.0293	4
P28651	CAH8_MOUSE	1(GAELVEGC[+57]DGILGDNFRPTQPLSDR	1.40	1.84E-02	0.0297	4
Q6URW6	MYH14_MOUSE	MLIAALESK	1.37	1.87E-02	0.0300	4
P16858	G3P_MOUSE	G VVDLMAYMASKE	3.24	1.88E-02	0.0301	4
Q9QYC0	ADDA_MOUSE	VNSEQEHFLVPPFGLLYSEVTASSLVK	5.03	1.88E-02	0.0301	4
Q9JMH9	MY18A_MOUSE	TC[+57]WLILASIHGAAGATK	2.61	2.05E-02	0.0322	4
Q7TMK9	HNRPQ_MOUSE	AIEALKEFNEDGALAVLQQFK	3.30	2.17E-02	0.0336	4
P48318	DCE1_MOUSE	1(MVISNPAATQSDIDFLIEEIEF	1.19	2.22E-02	0.0342	4
Q6ZQ38	CAND1_MOUSE	TYIQC[+57]IAAISR	2.38	2.28E-02	0.0348	4
P20357	MTAP2_MOUSE	VSEGPRPFAPVFFQSDDKVSLQDPSALATSK	3.62	2.32E-02	0.0352	4
P01837	IGKC_MOUSE	I DSTYSMSSTLTLTK	2.62	2.34E-02	0.0355	4
Q6ZWN5	RS9_MOUSE	4(LIGEYGLR	0.84	2.51E-02	0.0372	4
Q9JMH9	MY18A_MOUSE	TTSFQHLVQYLATIAGTSGTK	6.65	2.71E-02	0.0394	4
Q8BJH1	ZC21A_MOUSE	LPPPPPSYDPDIQC[+57]PYC[+57]QR	1.73	2.77E-02	0.0400	4
Q9CPR4	RL17_MOUSE	6(YSLDPENPTK	2.37	2.83E-02	0.0407	4
P97427	DPYL1_MOUSE	IVFEDGNISVSK	1.69	3.13E-02	0.0440	4
P14152	MDHC_MOUSE	DLDVAVLVGSM[+16]PR	2.78	3.19E-02	0.0447	4
P28652	KCC2B_MOUSE	LTQYIDGQGRPR	3.60	3.35E-02	0.0467	4
Q501J6	DDX17_MOUSE	STC[+57]IYGGAPK	1.55	3.37E-02	0.0469	4
O08599	STXB1_MOUSE	LAEQIATLC[+57]ATLK	3.87	3.53E-02	0.0489	4
Q9QYG0	NDRG2_MOUSE	GIIQHAPNLENIELYWNSYNNR	5.40	2.07E-04	0.0143	4
Q922F4	TBB6_MOUSE	1M[+16]ASTFIGNSTAIQELFK	2.45	2.35E-04	0.0143	4
O54983	CRYM_MOUSE	SLGMAVEDLVAAK	1.88	5.18E-04	0.0143	4
Q9QXS1	PLEC_MOUSE	IIISLETYNLFR	2.95	5.48E-04	0.0143	4
Q61548	AP180_MOUSE	GLGSDLSSLASLVGNLIGISGTTSK	4.26	6.45E-04	0.0143	4
Q61361	PGCB_MOUSE	C[+57]EVQHGIDDSSDAVEVK	1.26	7.35E-04	0.0143	4
Q9QYJ0	DNJA2_MOUSE	ITFTGEADQAPGVEPGDIVLLLQEK	4.37	9.04E-04	0.0143	4
Q922F4	TBB6_MOUSE	1MASTFIGNSTAIQELFK	2.64	1.11E-03	0.0143	4
P99024	TBB5_MOUSE	1M[+16]AVTFIGNSTAIQELFK	2.25	1.18E-03	0.0143	4
F7B0R9	F7B0R9_MOUSE	SPEQPGTKPPLPR	5.13	1.58E-03	0.0143	4
Q9QYJ0	DNJA2_MOUSE	VIPEGC[+57]VR	2.78	1.66E-03	0.0143	4
Q9QYG0	NDRG2_MOUSE	FGDMQEIIQNFVR	2.80	1.98E-03	0.0143	4
P68368	TBA4A_MOUSE	AVFVDLEPTVIDEIR	2.34	2.15E-03	0.0143	4
Q61548	AP180_MOUSE	DPLADLNIKDFL	1.81	2.19E-03	0.0143	4
F7B0R9	F7B0R9_MOUSE	KPLLPSTLTPYPPTGLDTSPGESER	5.40	2.27E-03	0.0143	4
Q922F4	TBB6_MOUSE	1LHFFM[+16]PGFAPLTAR	2.80	2.58E-03	0.0143	4
F7B0R9	F7B0R9_MOUSE	LIPVILPPEPR	4.71	2.69E-03	0.0143	4
P08551	NFL_MOUSE	N6IDSLMDEIAFLK	6.00	2.82E-03	0.0143	4
Q61548	AP180_MOUSE	ATNSSWVVVFK	1.92	2.90E-03	0.0143	4
Q9QYJ0	DNJA2_MOUSE	NVLC[+57]SAC[+57]SGQQGK	4.08	2.93E-03	0.0143	4
Q61656	DDX5_MOUSE	ITGTAYFFFTPNNIK	2.93	3.10E-03	0.0143	4
F7B0R9	F7B0R9_MOUSE	DEQSHVGAAPALR	3.39	3.14E-03	0.0143	4
Q9QYG0	NDRG2_MOUSE	YALNHPDTEGLVLINIDPNAK	2.42	3.52E-03	0.0144	4

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9QYG0	NDRG2_MOUSE	TASLTSAAIDGSR	1.83	3.57E-03	0.0145	4
P08551	NFL_MOUSE	NKLAEDATNEK	4.16	3.76E-03	0.0147	4
P08551	NFL_MOUSE	NKFAFIER	2.26	3.76E-03	0.0147	4
Q9QXS1	PLEC_MOUSE	ILSVAQAQEAAR	4.56	3.90E-03	0.0147	4
H3BJD0	H3BJD0_MOUSE	TEAVSPTVSQLSAVFENSEPPGALTS GK	5.33	3.97E-03	0.0148	4
Q922F4	TBB6_MOUSE	TLHFFMPGFAPLTAR	3.97	4.43E-03	0.0151	4
Q8C0P5	COR2A_MOUSE	WNPFNDFEIASC[+57]SEDATIK	7.12	4.68E-03	0.0153	4
P50518	VATE1_MOUSE	DDLITDLLNEAK	2.24	4.79E-03	0.0154	4
Q9JI91	ACTN2_MOUSE	C[+57]QLEINFNTLQTK	4.76	5.41E-03	0.0158	4
Q9JI91	ACTN2_MOUSE	LVSIGAEIIVDGNVK	4.18	6.17E-03	0.0166	4
P99024	TBB5_MOUSE	TALVPELTQQVFD AK	2.56	6.65E-03	0.0172	4
Q61656	DDX5_MOUSE	LIDFLEC[+57]GK	2.74	7.22E-03	0.0177	4
P08551	NFL_MOUSE	NKLEIEAC[+57]R	2.94	7.29E-03	0.0177	4
Q9JI91	ACTN2_MOUSE	GYEEWLLNEIR	1.42	7.82E-03	0.0182	4
Q9QXS1	PLEC_MOUSE	IGFFDPNTHENLTYLQLLER	5.12	8.33E-03	0.0187	4
P99024	TBB5_MOUSE	TMAVTFIGNSTAIQELFK	3.85	8.38E-03	0.0188	4
P68368	TBA4A_MOUSE	EIIDPV LDR	1.79	8.40E-03	0.0188	4
Q501J6	DDX17_MOUSE	LIQLMEEIMAEK	3.40	8.44E-03	0.0188	4
P68368	TBA4A_MOUSE	TIGGGDDSF TFFFC[+57]ETGAGK	2.65	9.58E-03	0.0203	4
Q501J6	DDX17_MOUSE	APILIATDVASR	2.22	9.59E-03	0.0203	4
O54983	CRYM_MOUSE	FASTVQGDVR	2.36	9.60E-03	0.0203	4
Q8C0P5	COR2A_MOUSE	GLDVSSC[+57]EIFR	3.19	9.96E-03	0.0206	4
Q9QXS1	PLEC_MOUSE	IDGHNLISLLEVLSGDSLPR	5.06	9.99E-03	0.0206	4
Q9JI91	ACTN2_MOUSE	FAIQDISVEETSAK	3.93	1.00E-02	0.0206	4
Q8C0P5	COR2A_MOUSE	ENC[+57]YDSVPITR	4.48	1.08E-02	0.0215	4
P68368	TBA4A_MOUSE	DVNAAIAAIK	1.74	1.10E-02	0.0217	4
P50518	VATE1_MOUSE	ARDDLITDLLNEAK	1.94	1.13E-02	0.0221	4
Q61548	AP180_MOUSE	IAAAQYSVTGSAVAF	1.33	1.16E-02	0.0224	4
Q61361	PGCB_MOUSE	SWEEAESQC[+57]R	1.63	1.16E-02	0.0224	4
P12970	RL7A_MOUSE	KAGVNTVTTLVENK	5.83	1.32E-02	0.0240	4
Q61656	DDX5_MOUSE	ILLQLVEDR	1.94	1.37E-02	0.0246	4
Q9QYJ0	DNJA2_MOUSE	IGLVEALC[+57]GFQFTFK	6.44	1.43E-02	0.0253	4
Q501J6	DDX17_MOUSE	GVEIC[+57]IATPGR	2.56	1.66E-02	0.0277	4
P58252	EF2_MOUSE	EIAYL P VNESFGFTADLR	0.90	1.81E-02	0.0294	4
Q8K183	PDXK_MOUSE	VVPVADIITPNQFEALLSGR	1.84	1.84E-02	0.0297	4
Q9DCL9	PUR6_MOUSE	IASILNTWISLK	1.84	1.90E-02	0.0303	4
P99024	TBB5_MOUSE	TISVYYNEATGGK	1.44	1.90E-02	0.0303	4
Q8VDD5	MYH9_MOUSE	LTEM[+16]ETM[+16]QSQLMAEK	4.36	1.92E-02	0.0306	4
Q9CVB6	ARPC2_MOUSE	VMVSISLK	5.07	1.94E-02	0.0308	4
P61021	RAB5B_MOUSE	LVLLGESAVGK	6.28	1.98E-02	0.0313	4
P17427	AP2A2_MOUSE	VVHLLNDQHLGVVTAATSLITTLAQK	1.71	2.42E-02	0.0364	4
Q8QZY1	EIF3L_MOUSE	LHSLLDGYYQAIK	2.79	2.43E-02	0.0364	4
Q9CZM2	RL15_MOUSE	KSLQSVAEER	2.50	2.45E-02	0.0366	4
Q62261	SPTB2_MOUSE	LLTQHENIKNEIDNYEEDYQK	1.74	2.53E-02	0.0374	4
Q9CZ04	CSN7A_MOUSE	VTTAAAAAATSQDPEQH L TELF	4.85	2.61E-02	0.0384	4
P07356	ANXA2_MOUSE	TPAQYDASELK	4.33	2.70E-02	0.0393	4
P05064	ALDOA_MOUSE	FSNEEIAMATVTALRR	2.55	2.82E-02	0.0406	4
Q61879	MYH10_MOUSE	MQAHIQDLEEQ L DEEEGAR	3.53	3.11E-02	0.0438	4
Q8BZ98	DYN3_MOUSE	IRPLVLQLVTSK	1.27	3.35E-02	0.0467	4
Q9Z1G3	VATC1_MOUSE	VQENLLASGVDLV TYITR	3.25	1.59E-03	0.0143	4
Q60932	VDAC1_MOUSE	VTQSNFAVG YK	2.08	1.65E-03	0.0143	4
Q60932	VDAC1_MOUSE	EHINLGC[+57]DVDFDIAGPSIR	2.99	2.93E-03	0.0143	4
Q9Z1G3	VATC1_MOUSE	VGTL DVLVGLSDELAK	2.28	3.64E-03	0.0146	4
Q6PHZ2	KCC2D_MOUSE	STVASMHR	3.79	4.31E-03	0.0150	4
Q60932	VDAC1_MOUSE	TDEFQLHTNVNDGTEFGGSIYQK	2.57	4.70E-03	0.0153	4
P14131	RS16_MOUSE	KGPLQSVQVFGR	3.40	5.31E-03	0.0158	4
Q61171	PRDX2_MOUSE	KEGGLGPLNIPL LADVTK	1.81	5.63E-03	0.0160	4
P14131	RS16_MOUSE	KFAGVDIR	3.05	5.71E-03	0.0161	4
P48036	ANXA5_MOUSE	GLGTDEDSILNLLTSR	1.97	7.14E-03	0.0176	4
P14131	RS16_MOUSE	KLLEPV LLLGK	4.10	1.01E-02	0.0207	4
Q6PHZ2	KCC2D_MOUSE	IC[+57]DPGLTAFEPEALGNLVEGM[+16]DFHR	7.38	1.02E-02	0.0208	4
P48036	ANXA5_MOUSE	GTVTDFPGFDGR	1.14	1.08E-02	0.0215	4

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9Z1G3	VATC1_MOUSE	FNIPDLK	1.27	1.10E-02	0.0217	4
Q60932	VDAC1_MOUSE	GYGFGLIK	1.64	1.14E-02	0.0222	4
P97351	RS3A_MOUSE	AC[+57]QSIYPLHDVFVR	3.01	1.21E-02	0.0229	4
P97351	RS3A_MOUSE	VFEVSLADLQNDVAFR	3.37	1.55E-02	0.0266	4
P14131	RS16_MOUSE	EIKDILIQYDR	4.20	1.64E-02	0.0275	4
Q61598	GDIB_MOUSE	FNTNDANSC[+57]QIIIPQNQVNR	1.44	1.87E-02	0.0300	4
Q8K1M6	DNM1L_MOUSE	DTLQSELVGQLYK	1.32	2.12E-02	0.0330	4
Q04447	KCRB_MOUSE	VLTPELYAELR	4.37	2.24E-02	0.0344	4
Q547J4	Q547J4_MOUSE	AEEAGIGDTPNQEDQAAGHVTAQAF	0.86	2.37E-02	0.0358	4
Q8QZY1	EIF3L_MOUSE	IVYELQASR	3.34	2.47E-02	0.0368	4
P52480	KPYM_MOUSE	C[+57]DENILWLDYK	5.14	2.66E-02	0.0389	4
Q3UHD9	AGAP2_MOUSE	STAGTGASAAAAGGGGSAAVTTSGGVBGAGAGTF	1.11	2.91E-02	0.0416	4
Q8H156	RAN3_ARATH GTI	LVIVGDGGTGK	1.02	3.00E-02	0.0426	4
Q8BYI9	TENR_MOUSE	LDSSVVPNTVTEFAITR	1.23	3.39E-02	0.0472	4
Q9EQH3	VPS35_MOUSE	LLDEAIQAVK	2.39	3.50E-02	0.0485	4
O08709	PRDX6_MOUSE	DLAILLGM[+16]LDPVEK	2.43	1.51E-03	0.0143	4
Q91VR5	DDX1_MOUSE	DLGLAFEIPAHIK	2.58	3.01E-03	0.0143	4
O08709	PRDX6_MOUSE	DLAILLGMLDPVEK	2.51	3.22E-03	0.0143	4
Q91VR5	DDX1_MOUSE	GHVDVLAPTQELAALEK	2.32	3.75E-03	0.0147	4
Q91VR5	DDX1_MOUSE	FLVLDEADGLLSQGYSDFINR	4.50	6.79E-03	0.0172	4
O08709	PRDX6_MOUSE	VVDSLQLTGTKPVATPVDWK	1.19	1.42E-02	0.0251	4
P12970	RL7A_MOUSE	HWGGNVLGPK	2.12	1.94E-02	0.0308	4
Q9WUM4	COR1C_MOUSE	ETIC[+57]SQDER	0.59	2.94E-02	0.0419	4
Q64332	SYN2_MOUSE	VENHYDFQDIASVVALTQTYATAEPFIDAF	6.91	1.72E-03	0.0143	4
Q64332	SYN2_MOUSE	QHAFGMAENEDFR	1.67	4.49E-03	0.0151	4
Q64332	SYN2_MOUSE	SFRPDFVLIR	1.42	9.75E-03	0.0204	4
Q9ERD7	TBB3_MOUSE	M[+16]SM[+16]KEVDEQM[+16]LAIQSK	1.26	1.86E-02	0.0300	4
Q61781	K1C14_MOUSE	YC[+57]M[+16]QLAQIQEM[+16]IGSVEEQLAQLF	8.60	4.16E-04	0.0143	4
P40142	TKT_MOUSE	Tr NMAEQIIQEISQVQSK	3.52	3.75E-03	0.0147	4
Q61781	K1C14_MOUSE	ADLEM[+16]QIESLKEELAYLK	4.65	4.25E-03	0.0149	4
P40142	TKT_MOUSE	Tr ILTVEDHYYEGGIGEAVSAAVVGEPGVTVTF	2.07	4.43E-03	0.0151	4
Q61781	K1C14_MOUSE	GQVGGDVNVEM[+16]DAAPGVDLRSR	2.11	6.64E-03	0.0172	4
Q61781	K1C14_MOUSE	ADLEMQIESLKEELAYLK	6.39	8.62E-03	0.0190	4
P40142	TKT_MOUSE	Tr LDNLVAIFDINR	1.49	1.15E-02	0.0223	4
Q8QZY1	EIF3L_MOUSE	LAGFLDLTEQEFR	4.86	1.35E-02	0.0243	4
Q8C0P5	COR2A_MOUSE	DSVIAGPVK	4.54	2.42E-02	0.0364	4
P11499	HS90B_MOUSE	TLTLVDTGIGMTK	3.92	2.43E-02	0.0364	4
Q9CPR4	RL17_MOUSE	GLDVDSLVIHIVQVVK	1.56	2.46E-02	0.0367	4
P19001	K1C19_MOUSE	LSVEADINGLR	1.13	3.18E-02	0.0446	4
Q02053	UBA1_MOUSE	LAYVAAGDLAPINAFIAGGLAAQEVMT[+16]K	2.12	3.21E-03	0.0143	4
Q02053	UBA1_MOUSE	LAYVAAGDLAPINAFIAGGLAAQEVMTK	3.36	3.37E-03	0.0143	4
Q02053	UBA1_MOUSE	LAGTQPLEVLEAVQR	1.85	4.67E-03	0.0153	4
Q02053	UBA1_MOUSE	YFLVGAGAIGC[+57]JELLK	1.61	9.69E-03	0.0204	4
Q9JMH9	MY18A_MOUSE	WQALSTLLEAFGNSPTIMNGSATR	7.76	1.77E-02	0.0289	4
P97427	DPYL1_MOUSE	QIGENLIVPGGVK	6.60	1.82E-02	0.0295	4
Q61361	PGCB_MOUSE	FKDLEALEEEK	7.08	1.84E-02	0.0297	4
Q2M3X8	PHAR1_MOUSE	LSQRPTAEELEQR	6.98	3.15E-02	0.0443	4
P05063	ALDOC_MOUSE	GILAADESVMGSMK	2.02	5.15E-03	0.0155	4
P05063	ALDOC_MOUSE	YASIC[+57]QQNGIVPIVEPEILPDGDHDLK	1.77	1.02E-02	0.0208	4
P05063	ALDOC_MOUSE	TVPPAVPGVTFLSGGQSEEEASLNLNAINR	1.60	1.14E-02	0.0222	4
P05063	ALDOC_MOUSE	LSQIGVENTEENR	2.45	1.21E-02	0.0229	4
O88935	SYN1_MOUSE	QLIVELVVNK	1.35	1.15E-02	0.0223	4
O88935	SYN1_MOUSE	LGTEEFPLIDQTFYPNHK	1.41	1.20E-02	0.0228	4
O08638	MYH11_MOUSE	IAQLEEQVEQEAR	1.11	2.17E-02	0.0336	4
O08638	MYH11_MOUSE	ALEEALAKEELER	1.07	2.90E-02	0.0414	4
Q8BFR5	EFTU_MOUSE	IDLDKPFLLPVESVYSIPGR	3.06	2.42E-04	0.0143	3
P28663	SNAB_MOUSE	VAAYAAQLEQYQK	2.02	3.67E-04	0.0143	3
P29515	TBB7_ARATH Tub	EVDEQMLNVQNK	2.24	3.72E-04	0.0143	3
Q2PFD7	PSD3_MOUSE	IELLTTDGNPEVGLK	2.62	4.92E-04	0.0143	3
P14094	AT1B1_MOUSE	SYEAYVLNIIR	2.03	6.12E-04	0.0143	3
Q8K0S0	PHYIP_MOUSE	M[+42]JELLSTPHSIEINNITC[+57]DSFR	4.24	7.04E-04	0.0143	3
P29515	TBB7_ARATH Tub	EVDEQM[+16]LNVQNK	1.76	7.20E-04	0.0143	3

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
O08788	DCTN1_MOUSE	AFLQGGQEATDIALLLR	3.21	8.31E-04	0.0143	3
Q5PR73	DIRA2_MOUSE	ELFQELLNLEK	2.63	8.41E-04	0.0143	3
P68404	KPCB_MOUSE	C[+57]SLNPEWNETFR	2.76	8.69E-04	0.0143	3
Q9Z2X1	HNRPF_MOUSE	ATENDIYNFFSPLNPVR	2.84	1.24E-03	0.0143	3
Q91YR1	TWF1_MOUSE	INEVQTDVSVDTK	2.54	1.39E-03	0.0143	3
P48318	DCE1_MOUSE	TETDFSNLFAQDLLPAK	3.28	1.42E-03	0.0143	3
Q8R429	AT2A1_MOUSE	TASEM[+16]VLADDNFSTIVAAVEEGF	3.09	1.57E-03	0.0143	3
A2N1N1	A2N1N1_MOUSE	ESGVPDR	7.79	1.62E-03	0.0143	3
Q9D4J1	EFHD1_MOUSE	DGFIDLM[+16]ELK	3.36	1.69E-03	0.0143	3
Q8R429	AT2A1_MOUSE	VDQSILTGESVSVIK	2.15	1.76E-03	0.0143	3
P63037	DNJA1_MOUSE	NVVHQLSVTLEDLYNGATR	7.59	1.96E-03	0.0143	3
A2N1N1	A2N1N1_MOUSE	NYLAWYQKQKPGQSPK	6.93	2.39E-03	0.0143	3
P63276	RS17_MOUSE	LDFGSLSNLQVTQPTVGMNFK	3.41	2.57E-03	0.0143	3
P14094	AT1B1_MOUSE	VAPPGLTQIPQIQK	2.17	2.67E-03	0.0143	3
Q6PGN3	DCLK2_MOUSE	SLSDNVNLPQGVV	4.78	2.75E-03	0.0143	3
O08788	DCTN1_MOUSE	GPPPSGIATLVSGIAGEEPQR	2.58	2.80E-03	0.0143	3
Q9JM76	ARPC3_MOUSE	LIGNM[+16]ALLPLR	2.71	2.86E-03	0.0143	3
Q9D4J1	EFHD1_MOUSE	LGAPQTHLGLK	4.28	2.86E-03	0.0143	3
Q91YR1	TWF1_MOUSE	SPLLEIVER	4.34	3.00E-03	0.0143	3
Q91YR1	TWF1_MOUSE	YLLSQSSPAPLTAEEEEELR	3.30	3.10E-03	0.0143	3
Q60930	VDAC2_MOUSE	VNNSLIGVGYTQTLRPGVK	3.31	3.24E-03	0.0143	3
P62880	GBB2_MOUSE	LIWDSYTTNK	2.14	3.32E-03	0.0143	3
P63276	RS17_MOUSE	LDFGSLSNLQVTQPTVGM[+16]NFK	2.21	3.33E-03	0.0143	3
P62631	EF1A2_MOUSE	VETGILRPGMVVTFAPVNITTEVK	2.17	3.45E-03	0.0144	3
O70172	PI42A_MOUSE	DVEFLAQLK	2.87	3.49E-03	0.0144	3
O70172	PI42A_MOUSE	FLDFIGHIL	5.93	3.51E-03	0.0144	3
Q9Z2X1	HNRPF_MOUSE	VHIEIGPDGR	2.62	3.69E-03	0.0147	3
P62880	GBB2_MOUSE	LLVSASQDGK	2.57	3.73E-03	0.0147	3
Q6PGN3	DCLK2_MOUSE	GGDLFDAITSSTK	3.24	3.77E-03	0.0147	3
Q9WTM5	RUVB2_MOUSE	AVLIAGQPGTGK	2.17	4.09E-03	0.0148	3
P63037	DNJA1_MOUSE	ITFHGEGDQEPGLEPGDIIIIVLDQK	6.72	4.09E-03	0.0148	3
Q68FG2	Q68FG2_MOUSE	LLDPEDVNVDPQDEK	2.42	4.11E-03	0.0148	3
P48318	DCE1_MOUSE	M[+16]VISNPAATQSDIDFLIEEIER	4.94	4.36E-03	0.0150	3
Q8R429	AT2A1_MOUSE	TASEMVLADDNFSTIVAAVEEGF	3.61	4.37E-03	0.0150	3
Q2PFD7	PSD3_MOUSE	IIGSTTNPFLDIPHPNAAVYK	2.18	4.63E-03	0.0153	3
Q68FG2	Q68FG2_MOUSE	VPTLEQHYEELQAR	1.82	4.90E-03	0.0155	3
Q60930	VDAC2_MOUSE	LTL SALVDGK	2.04	4.92E-03	0.0155	3
Q8K0S0	PHYIP_MOUSE	FLTC[+57]SVEDGELIFR	2.15	4.97E-03	0.0155	3
P28663	SNAB_MOUSE	LDQWLTTMLLR	3.65	5.16E-03	0.0155	3
Q9JM76	ARPC3_MOUSE	LIGNMALLPLR	3.81	5.28E-03	0.0157	3
Q8K0S0	PHYIP_MOUSE	TEYSVAVQTAVK	1.80	5.42E-03	0.0158	3
Q9JM76	ARPC3_MOUSE	DTDIVDEAIYYFK	4.17	5.55E-03	0.0159	3
Q99KX1	MLF2_MOUSE	IQDYINLDESEAAAFDDEWRR	5.31	5.89E-03	0.0163	3
Q2PFD7	PSD3_MOUSE	IGTVLYLQK	1.59	6.16E-03	0.0166	3
Q2M3X8	PHAR1_MOUSE	ISFNLGAAEEVER	2.81	6.27E-03	0.0168	3
Q9JIS5	SV2A_MOUSE	DREELAQQYETILR	4.19	6.61E-03	0.0171	3
Q68FG2	Q68FG2_MOUSE	QLANSLSGVQNQLQSFNSYR	1.10	7.00E-03	0.0175	3
Q9CR57	RL14_MOUSE	AAIAAAAAAAAAA	5.75	7.41E-03	0.0179	3
P28663	SNAB_MOUSE	AALC[+57]HFIVDELNAK	1.98	7.54E-03	0.0180	3
P61358	RL27_MOUSE	YSVDIPLDK	1.14	7.64E-03	0.0181	3
A0A0B6VMB;A0A0B6VMB2_MC	DDPEVQFSWFVDDVEVHTAQTKPR		3.84	7.74E-03	0.0182	3
P14094	AT1B1_MOUSE	YNPNVLPVQC[+57]TGK	1.69	7.75E-03	0.0182	3
P62281	RS11_MOUSE	C[+57]PFTGNVSIR	3.51	7.80E-03	0.0182	3
Q9D4J1	EFHD1_MOUSE	DGFIDLMELK	4.55	8.50E-03	0.0189	3
P29515	TBB7_ARATH Tub	NSSYFVEWIPNNVK	3.05	8.97E-03	0.0195	3
Q99KX1	MLF2_MOUSE	MLSGGFGYSPFLSITDGNMPATRPASF	4.49	9.56E-03	0.0202	3
Q60930	VDAC2_MOUSE	LTFDITTFSPNTGK	2.51	9.71E-03	0.0204	3
P62245	RS15A_MOUSE	IVVNLTR	2.70	9.81E-03	0.0204	3
A2N1N1	A2N1N1_MOUSE	LLLYFASTR	4.05	9.86E-03	0.0205	3
P63037	DNJA1_MOUSE	QISQAYEVLADSK	1.93	1.01E-02	0.0207	3
P63276	RS17_MOUSE	DNYVPEVSALDQEIIIVDPDTK	4.62	1.07E-02	0.0214	3
Q99PT1	GDIR1_MOUSE	AEEYEFLTPMEEAPK	1.74	1.07E-02	0.0214	3

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P62245	RS15A_MOUSE	HGYIGEFEIIDDHR	2.70	1.08E-02	0.0215	3
Q99PT1	GDIR1_MOUSE	SIQEIQELDKDDESLRK	1.08	1.10E-02	0.0217	3
Q9JIS5	SV2A_MOUSE	SGGLSDGEGPPGGR	1.40	1.12E-02	0.0219	3
Q5PR73	DIRA2_MOUSE	EVQSSEAEALAR	1.52	1.16E-02	0.0224	3
Q99KK2	NEUA_MOUSE	LAGVPLIGWVLR	3.55	1.18E-02	0.0226	3
P62245	RS15A_MOUSE	QFGFIVLTTSAGIMDHEEAR	2.72	1.22E-02	0.0230	3
P61358	RL27_MOUSE	ENIDDGTSRDPYSHALVAGIDR	6.51	1.24E-02	0.0231	3
P62631	EF1A2_MOUSE	VETGILRPGM[+16]VVTFAPVNITTEVK	1.05	1.25E-02	0.0232	3
Q6PGN3	DCLK2_MOUSE	VIGDGNFAVVK	2.45	1.25E-02	0.0232	3
Q99KK2	NEUA_MOUSE	GLEKPPHLAALVLAR	2.25	1.26E-02	0.0233	3
P62631	EF1A2_MOUSE	YYITIIDAPGHR	1.40	1.26E-02	0.0233	3
P62889	RL30_MOUSE	ELVILANNC[+57]PALR	4.66	1.33E-02	0.0241	3
Q5PR73	DIRA2_MOUSE	VAVFGAGGVGK	1.46	1.34E-02	0.0242	3
P62889	RL30_MOUSE	ELVC[+57]TLAIIDPGDSDIIR	4.53	1.43E-02	0.0253	3
Q8BFR5	EFTU_MOUSE	IGITINAAHVEYSTAAF	1.66	1.53E-02	0.0264	3
Q9JIS5	SV2A_MOUSE	SAAPILFASAALALGSSLALK	3.15	1.56E-02	0.0267	3
P62880	GBB2_MOUSE	ITFVSGAC[+57]DASIK	1.80	1.59E-02	0.0270	3
Q9Z2X1	HNRPF_MOUSE	ITGEAFVQFASQELAEK	5.72	1.66E-02	0.0277	3
Q04447	KCRB_MOUSE	TDLNPDNLQGGDDLDPNYVLSSR	5.11	1.71E-02	0.0283	3
Q88544	CSN4_MOUSE	IVISFEEQVASIR	2.55	1.74E-02	0.0285	3
P68404	KPCB_MOUSE	EVLIVVVR	4.20	1.74E-02	0.0285	3
Q9Z0E0	NCDN_MOUSE	IFDAVGFTFPNR	5.51	1.75E-02	0.0287	3
P63038	CH60_MOUSE	ENAGVEGSLIVEK	1.49	1.81E-02	0.0294	3
Q64332	SYN2_MOUSE	SFPLIEQTYYPNHR	4.55	1.87E-02	0.0300	3
P12658	CALB1_MOUSE	LLPVQENFLK	3.72	1.93E-02	0.0307	3
P16125	LDHB_MOUSE	IMVVD SAYEVIK	2.39	1.95E-02	0.0309	3
P60335	PCBP1_MOUSE	QVTITGSAASISLAQYLINAF	1.10	2.05E-02	0.0322	3
Q9D8N0	EF1G_MOUSE	ITFLVGER	2.38	2.07E-02	0.0324	3
E9PV24	FIBA_MOUSE	FGLIDEANQDFTNR	6.81	2.08E-02	0.0325	3
Q6PIC6	AT1A3_MOUSE	KYNTDC[+57]VQGLTHSK	6.66	2.21E-02	0.0341	3
Q9Z1N5	DX39B_MOUSE	ILVATNLFGR	3.06	2.23E-02	0.0343	3
P11499	HS90B_MOUSE	YHTSQSGDEMTSLSEYVSR	3.33	2.30E-02	0.0350	3
P63038	CH60_MOUSE	ENAAVEEGIVLGGGC[+57]ALLR	5.66	2.36E-02	0.0357	3
P62962	PROF1_MOUSE	DSLQDGEFTMDLR	6.59	2.59E-02	0.0381	3
P61021	RAB5B_MOUSE	TAMNVNDLFLAIK	6.81	2.75E-02	0.0398	3
P14873	MAP1B_MOUSE	IAELEER	6.29	2.75E-02	0.0398	3
Q3UH68	LIMC1_MOUSE	TGLENGILLC[+57]JELNNAIKPGLVK	2.24	2.81E-02	0.0405	3
Q8VDD5	MYH9_MOUSE	DLGEELEALKTELEDTLDSTAAQQELR	2.10	2.97E-02	0.0422	3
P48774	GSTM5_MOUSE	SMVLGYWDIR	3.80	3.13E-02	0.0440	3
P52480	KPYM_MOUSE	EKGADFLVTEVENGGSLGSK	6.46	3.30E-02	0.0461	3
Q6R891	NEB2_MOUSE	IETQAQYQALER	5.83	3.44E-02	0.0478	3
Q01853	TERA_MOUSE	WALSQSNPSALR	4.42	3.58E-02	0.0494	3
Q9Z1N5	DX39B_MOUSE	C[+57]IALAQLLVEQNFPAAIHR	4.69	2.06E-04	0.0143	3
P27546	MAP4_MOUSE	GMVSLSEIEEALAK	4.37	3.36E-04	0.0143	3
P43006	EAA2_MOUSE	INDEVSSLDNFLDLIR	3.22	3.94E-04	0.0143	3
E9PV24	FIBA_MOUSE	FSQLQEAPPEWK	3.35	1.22E-03	0.0143	3
Q8R4U7	LUZP1_MOUSE	GQVPGHASQGTQAVESSC[+57]SK	5.41	1.37E-03	0.0143	3
Q9DBR7	MYPT1_MOUSE	STQGVTLTDLQAEK	2.39	1.55E-03	0.0143	3
P43006	EAA2_MOUSE	INDEVSSLDNFLDLIR	3.95	1.64E-03	0.0143	3
P80313	TCPH_MOUSE	SQDAEVGDGTTSVTLAAEFLK	2.33	1.76E-03	0.0143	3
Q9D394	RUFY3_MOUSE	LTEELAVANNR	2.60	1.85E-03	0.0143	3
P62754	RS6_MOUSE	CDIPGLTDTTVPR	4.48	1.89E-03	0.0143	3
Q8R4U7	LUZP1_MOUSE	IEDGISSTLSSK	2.55	1.91E-03	0.0143	3
P27546	MAP4_MOUSE	SPATTLPK	2.01	2.01E-03	0.0143	3
P62082	RS7_MOUSE	CDTLTAVHDAILEDLVFPSEIVGK	3.38	2.24E-03	0.0143	3
P19096	FAS_MOUSE	FELLLPEDPLISGLLNSQALK	2.63	2.27E-03	0.0143	3
P80313	TCPH_MOUSE	IALLNVELELK	3.92	2.52E-03	0.0143	3
P62962	PROF1_MOUSE	DSLQDGEFTM[+16]DLR	4.02	2.88E-03	0.0143	3
P63085	MK01_MOUSE	IFRHENIIGINDIIR	3.84	3.00E-03	0.0143	3
P63085	MK01_MOUSE	IVADPDHDHTGFLTEYVATR	3.04	3.04E-03	0.0143	3
P27546	MAP4_MOUSE	ATSPSTLVSTGPSSR	2.96	3.61E-03	0.0145	3
P19096	FAS_MOUSE	FESYIITGGLGGFGLLELAR	4.86	3.71E-03	0.0147	3

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P80315	TCPD_MOUSE	ALIAGGGAPEIELALR	1.64	3.85E-03	0.0147	3
Q9D394	RUFY3_MOUSE	LVPEAAEITASVK	2.08	4.37E-03	0.0150	3
E9PV24	FIBA_MOUSE	F GDFANANNFDNTYQVSEDLR	2.09	4.46E-03	0.0151	3
P62270	RS18_MOUSE	4VLNTNIDGR	3.43	4.65E-03	0.0153	3
Q8K310	MATR3_MOUSE	DLSAAGIGLLAAATQSLSM[+16]PASLGF	4.97	4.66E-03	0.0153	3
P62082	RS7_MOUSE	4(DVNFEPFPEFQL	2.70	4.66E-03	0.0153	3
P80315	TCPD_MOUSE	IIGLIQFC[+57]LSAPK	2.02	4.73E-03	0.0153	3
Q64531	HPRT_MUSSP Hy	FFADLLDYIK	2.60	4.98E-03	0.0155	3
Q62420	SH3G2_MOUSE	GPGYPQAEALLAEAMLK	1.85	5.07E-03	0.0155	3
Q62420	SH3G2_MOUSE	ALYDFEPENEGELGFK	2.15	5.27E-03	0.0157	3
Q62420	SH3G2_MOUSE	QAVQILQQVTVR	1.48	5.46E-03	0.0158	3
Q64531	HPRT_MUSSP Hy	TM[+16]QTLLSLVK	1.93	5.49E-03	0.0159	3
P63325	RS10_MOUSE	4IAIYELLFK	2.53	5.67E-03	0.0160	3
Q9JII6	AK1A1_MOUSE	GLEVTAYSPLGSSDR	1.94	5.74E-03	0.0161	3
Q8BRT1	CLAP2_MOUSE	VLNTGSDVEEAVADALLLGDIR	7.18	5.79E-03	0.0162	3
Q64531	HPRT_MUSSP Hy	NVLVEDIIDTGK	1.35	7.33E-03	0.0178	3
Q9DBR7	MYPT1_MOUSE	TGSYGALAEISASK	3.31	7.38E-03	0.0178	3
Q8K310	MATR3_MOUSE	YQLLQLVEPFGVISNHLILNK	8.25	7.63E-03	0.0181	3
Q8BRT1	CLAP2_MOUSE	EGLLGLQNLLK	4.67	7.71E-03	0.0181	3
P35979	RL12_MOUSE	6HSGNITFDEIVNIAR	3.36	9.01E-03	0.0196	3
P62270	RS18_MOUSE	4IPDWFLNR	4.37	9.14E-03	0.0197	3
P63325	RS10_MOUSE	4AEAGAGSATEFQFR	3.09	1.02E-02	0.0208	3
P80313	TCPH_MOUSE	EGTDSSQGIPQLVSNISAC[+57]QVIAEAVF	6.51	1.12E-02	0.0219	3
Q9DCH4	EIF3F_MOUSE	VIGLSSDLQQVGGASAR	4.52	1.20E-02	0.0228	3
Q9DCH4	EIF3F_MOUSE	VIGTLLGTVDK	4.66	1.21E-02	0.0229	3
P43006	EAA2_MOUSE	I NLFPENLVQAC[+57]FQQIQVTVK	2.36	1.22E-02	0.0230	3
Q8BRT1	CLAP2_MOUSE	TILLLLETLGDKKEPTIR	6.59	1.25E-02	0.0232	3
P62082	RS7_MOUSE	4(CIIIFVVPVQLK	2.09	1.26E-02	0.0233	3
P35979	RL12_MOUSE	6EILGTAQSVGC[+57]NVDGR	3.12	1.40E-02	0.0249	3
P62754	RS6_MOUSE	4(LIEVDDER	3.32	1.44E-02	0.0254	3
P63085	MK01_MOUSE	ILKELIFEETAR	2.20	1.48E-02	0.0258	3
P62962	PROF1_MOUSE	TFVSITPAEVGVLVGK	1.45	1.50E-02	0.0261	3
Q9D394	RUFY3_MOUSE	IITLQEEMER	3.88	1.55E-02	0.0266	3
Q9JII6	AK1A1_MOUSE	HPDEPVLLEEPVVLALAEK	1.51	1.61E-02	0.0272	3
Q2M3X8	PHAR1_MOUSE	LLDVESAQR	1.42	1.96E-02	0.0310	3
P52480	KPYM_MOUSE	VNLAM[+16]DVGK	3.57	2.02E-02	0.0318	3
Q8VDD5	MYH9_MOUSE	M[+16]QQNIQELEEQLLEEEESAR	4.35	2.03E-02	0.0319	3
P26039	TLN1_MOUSE	1TEDSGLQTQVIAAATQC[+57]ALSTSQLVAC[+57]Tf	3.18	2.07E-02	0.0324	3
Q9JMH9	MY18A_MOUSE	VVHFAEPGAGTK	1.22	2.22E-02	0.0342	3
P28652	KCC2B_MOUSE	NLINQM[+16]LTINPAK	8.06	2.26E-02	0.0346	3
P63318	KPCG_MOUSE	FEAC[+57]NYPLELYER	3.98	2.28E-02	0.0348	3
P17710	HXK1_MOUSE	IM[+16]PLGFTFSFPC[+57]K	2.27	2.40E-02	0.0361	3
P07901	HS90A_MOUSE	VILHLKEDQTEYLEER	0.97	2.54E-02	0.0375	3
Q62261	SPTB2_MOUSE	FESLEPEMNNQASR	3.65	2.58E-02	0.0380	3
P12970	RL7A_MOUSE	6(TC[+57]TTVAFTQVNSKDGALAK	3.98	2.61E-02	0.0384	3
Q99104	MYO5A_MOUSE	RAATIVIQSYLR	6.03	2.79E-02	0.0403	3
P52480	KPYM_MOUSE	EATESFASDPILYRPVAVALDTK	4.27	3.02E-02	0.0428	3
Q71LX4	TLN2_MOUSE	1VMVTNVTSLLK	1.29	3.18E-02	0.0446	3
P84099	RL19_MOUSE	6VWLDPNETNEIANANSR	1.33	3.58E-02	0.0494	3
Q5SQX6	CYFP2_MOUSE	DFVSEAYLLTLGK	2.88	1.44E-03	0.0143	3
Q5SQX6	CYFP2_MOUSE	NTIYAALQDFAQVTLR	3.39	2.46E-03	0.0143	3
Q5SQX6	CYFP2_MOUSE	NVLISVLQAIR	2.64	2.95E-03	0.0143	3
P17742	PPIA_MOUSE	F IIPGFM[+16]C[+57]QGDFTR	1.67	4.35E-03	0.0150	3
P02088	HBB1_MOUSE	IYFDSFGDLSSASAIMGNAK	1.88	4.42E-03	0.0151	3
P17742	PPIA_MOUSE	F VSFELFADK	1.25	1.00E-02	0.0206	3
Q6ZWN5	RS9_MOUSE	4(LFEGNALLR	2.71	1.25E-02	0.0232	3
P47963	RL13_MOUSE	6STESLQANVQR	1.52	1.89E-02	0.0302	3
P60710	ACTB_MOUSE	,DIKEKLC[+57]YVALDFEQEMATAASSSSLEK	1.14	1.99E-02	0.0314	3
P17742	PPIA_MOUSE	FKITISDC[+57]GQL	4.64	2.00E-02	0.0316	3
P20357	MTAP2_MOUSE	ADQGLDFAATK	1.32	2.10E-02	0.0328	3
O08599	STXB1_MOUSE	MTDIMTEGIVEDINK	2.11	2.51E-02	0.0372	3
P28660	NCKP1_MOUSE	NLITDIC[+57]TEQC[+57]TJLSDQLLPK	3.05	2.55E-04	0.0143	3

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
A2AJI0	MA7D1_MOUSE	TAEGLLPFAEAEAFLEK	6.66	2.40E-03	0.0143	3
P28660	NCKP1_MOUSE	AINQIAAALFTIHK	2.71	5.91E-03	0.0163	3
A2AJI0	MA7D1_MOUSE	ETAANNNGPDPVK	5.24	7.01E-03	0.0175	3
P48453	PP2BB_MOUSE	SQTTGFPSLITIFSAPNYLDVYNNK	2.94	8.76E-03	0.0192	3
P48453	PP2BB_MOUSE	YLFLGDYVDR	1.48	9.72E-03	0.0204	3
P00920	CAH2_MOUSE	SIVNNGHSFNVEFDDSQDNAVLK	1.74	1.34E-02	0.0242	3
Q99104	MYO5A_MOUSE	KTDDDAEAIC[+57]SM[+16]C[+57]NALTTAQIVK	1.45	2.19E-02	0.0338	3
Q68FD5	CLH1_MOUSE	(QNLQIC[+57]VQVASK	2.44	2.56E-02	0.0377	3
A0A0N5DP62	A0A0N5DP62_TRI	GAILTTM[+16]IATF	1.44	2.62E-02	0.0385	3
Q61598	GDIB_MOUSE	FVPSTEAALASSLM[+16]GLFEK	2.69	2.67E-02	0.0390	3
Q9WV60	GSK3B_MOUSE	DIKPQNLLLDPTAVLK	1.26	3.05E-02	0.0431	3
P20029	BIP_MOUSE	En ITPSYVAFTPEGER	2.30	1.79E-03	0.0143	3
Q8VEK3	HNRPU_MOUSE	YNILGTNTIMDK	1.50	1.88E-03	0.0143	3
Q8VEK3	HNRPU_MOUSE	EKPYFPIPEDC[+57]TFIQNVPLEDR	2.99	4.72E-03	0.0153	3
P20029	BIP_MOUSE	En IINEPTAAAIAYGLDK	2.50	6.64E-03	0.0172	3
P20029	BIP_MOUSE	En VEIANDQGNR	1.89	6.69E-03	0.0172	3
Q8VEK3	HNRPU_MOUSE	NFILDQTNVSAQAQR	4.69	6.76E-03	0.0172	3
Q80TJ1	CAPS1_MOUSE	LDALQTFIR	1.55	7.93E-03	0.0183	3
Q80TJ1	CAPS1_MOUSE	FVTILEGLVAK	1.60	9.72E-03	0.0204	3
Q80TJ1	CAPS1_MOUSE	DVLGSAASGAR	2.15	1.04E-02	0.0211	3
P63011	RAB3A_MOUSE	YADDSFTPAFVSTVGIDFK	2.36	1.30E-03	0.0143	3
P61922	GABT_MOUSE	TLLTGLLDLQAQYPQFISR	5.04	2.48E-03	0.0143	3
P61922	GABT_MOUSE	NLLLAEVINIIK	2.73	2.65E-03	0.0143	3
P63011	RAB3A_MOUSE	QLADHLGFEFFEASAK	2.11	3.08E-03	0.0143	3
P61922	GABT_MOUSE	M[+16]LDLYSQISSVPIGYNHPALAK	2.32	7.06E-03	0.0175	3
P02088	HBB1_MOUSE	IKVITAFNDGLNHLDSLK	1.48	1.89E-02	0.0302	3
P16125	LDHB_MOUSE	IITVVGVGQVGMAC[+57]JAISILGK	1.67	3.53E-03	0.0144	3
P16125	LDHB_MOUSE	IGMYGIENEVFLSLPC[+57]ILNAR	4.77	1.35E-02	0.0243	3
Q9ERD7	TBB3_MOUSE	ISGAFGHLFRPDNFIFGQSGAGNNWAK	1.21	1.95E-02	0.0309	3
P11798	KCC2A_MOUSE	MC[+57]DPGM[+16]TAFEPEALGNLVEGLDFHR	7.09	5.48E-03	0.0159	3
P11798	KCC2A_MOUSE	VTEQLIEAISNGDFESYTK	4.53	8.55E-03	0.0190	3
P35979	RL12_MOUSE	ε HPHDIIDDINSGAVEC[+57]PAS	4.53	2.62E-02	0.0385	3
Q8CBE3	WDR37_MOUSE	YAGHVGSVNSIK	2.81	7.91E-05	0.0143	2
P32067	LA_MOUSE	Lup LTTDFNVIVQALS	2.32	8.52E-05	0.0143	2
Q9QZX7	SRR_MOUSE	S DLVDDVFTVTEDEIK	3.46	1.38E-04	0.0143	2
Q9DCD0	6PGD_MOUSE	INPELQNLDDDFK	3.01	2.20E-04	0.0143	2
P13707	GPDA_MOUSE	LGLMEMIAFAK	2.71	3.05E-04	0.0143	2
P29516	TBB8_ARATH	Tub EVDEQMINVQNK	2.24	3.72E-04	0.0143	2
A0A0N5DKY8	A0A0N5DKY8_TRI	AFM[+16]TADLPNELIEILEK	4.22	5.52E-04	0.0143	2
P29516	TBB8_ARATH	Tub EVDEQM[+16]INVQNK	1.76	7.20E-04	0.0143	2
Q8H156	RAN3_ARATH	GTIVC[+57]ENIPIVLC[+57]GNK	2.16	7.93E-04	0.0143	2
O88456	CPNS1_MOUSE	ILGGVISAISEAAAQYNPEPPPPF	4.07	7.95E-04	0.0143	2
Q7TPW1	NEXN_MOUSE	LEINFEQLLR	7.01	8.30E-04	0.0143	2
F8VPU2	FARP1_MOUSE	LGAPENSGISTLER	2.72	8.41E-04	0.0143	2
Q8C845	Q8C845_MOUSE	AAAGELQEDSGLHVLAR	4.24	9.13E-04	0.0143	2
P61027	RAB10_MOUSE	LQIWDTAGQER	2.11	1.06E-03	0.0143	2
Q7TPW1	NEXN_MOUSE	NTSVVDSEPV	2.44	1.10E-03	0.0143	2
P62827	RAN_MOUSE	G SNYNFEKPFLWLAR	3.48	1.22E-03	0.0143	2
P11983	TCPA_MOUSE	SLLVIPNTLAVNAAQDSTDLVAK	1.97	1.25E-03	0.0143	2
Q9ESN6	TRIM2_MOUSE	ASLQVQLDAVNK	2.97	1.29E-03	0.0143	2
P49615	CDK5_MOUSE	IDLQNLLK	2.14	1.40E-03	0.0143	2
G3UZJ2	G3UZJ2_MOUSE	KTTASGDLAQAPGAFK	6.14	1.43E-03	0.0143	2
P31938	MP2K1_MOUSE	LC[+57]DFGVSGQLIDSMANSFVGT	3.24	1.53E-03	0.0143	2
Q80VD1	FA98B_MOUSE	NSEIC[+57]QEVQAVC[+57]DALGVPK	3.31	1.58E-03	0.0143	2
Q84W47	Q84W47_ARATH	IAPNM[+16]ETITESLEK	5.15	1.60E-03	0.0143	2
Q6P8J7	KCRS_MOUSE	GWEFMWNERLGYILTC[+57]PSNLGTGLR	5.96	1.66E-03	0.0143	2
Q8CIE6	COPA_MOUSE	SILLSVPLLVDN	2.64	1.76E-03	0.0143	2
Q8BP47	SYNC_MOUSE	NLMFLVLR	2.08	1.78E-03	0.0143	2
Q9QXY6	EHD3_MOUSE	IFVC[+57]AQLPNAVLESISVIDTPGILSGEK	4.26	1.79E-03	0.0143	2
A0A178UNP6	A0A178UNP6_AR	M[+16]ATPPLTPR	3.06	1.90E-03	0.0143	2
Q9DCL9	PUR6_MOUSE	IITSC[+57]IFQLLQEAGIK	3.08	1.91E-03	0.0143	2
P60867	RS20_MOUSE	TPVEPEVAIHR	2.68	1.95E-03	0.0143	2

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P53994	RAB2A_MOUSE	GAAGALLVYDITR	1.29	1.97E-03	0.0143	2
Q9CPV4	GLOD4_MOUSE	VTLAVSDLQK	3.29	1.99E-03	0.0143	2
O54946	DNJB6_MOUSE	QVAEAYEVLSDAK	4.39	2.11E-03	0.0143	2
Q9CZ04	CSN7A_MOUSE	QLEDLVIEAVYADVLR	4.97	2.24E-03	0.0143	2
G3UZJ2	G3UZJ2_MOUSE	TTASGDLAQAPGAFK	6.18	2.25E-03	0.0143	2
Q8CBY8	DCTN4_MOUSE	AGASISTLAGLSLR	4.35	2.31E-03	0.0143	2
A0A0N5DFM1	A0A0N5DFM1_TR	NAPAILFIDEIDAIAPK	2.11	2.32E-03	0.0143	2
Q9CQE8	RTRAF_MOUSE	HILGFDTGDAVLNEAAQILR	8.32	2.38E-03	0.0143	2
Q80Y86	MK15_MOUSE	ILC[+57]DFGLAR	1.72	2.45E-03	0.0143	2
Q8CBE3	WDR37_MOUSE	STLLELFGQIER	4.57	2.46E-03	0.0143	2
P53994	RAB2A_MOUSE	TASNVEEAFINTAK	1.52	2.50E-03	0.0143	2
Q8C0E9	Q8C0E9_MOUSE	ISNSSEFSAK	2.64	2.57E-03	0.0143	2
Q9QZE5	COPG1_MOUSE	SIATLAITTLK	2.50	2.60E-03	0.0143	2
P51881	ADT2_MOUSE	YFPTQALNFQAFK	2.13	2.61E-03	0.0143	2
Q80Y86	MK15_MOUSE	ILLDVIPAK	5.15	2.65E-03	0.0143	2
Q9QXY6	EHD3_MOUSE	LFEEAEQDLFR	4.86	2.76E-03	0.0143	2
P48484	PP14_ARATH_Seri	IYGFYDEC[+57]K	3.44	2.76E-03	0.0143	2
P49615	CDK5_MOUSE	SFLFQLLK	2.84	2.85E-03	0.0143	2
O88685	PRS6A_MOUSE	VDILDPELLR	2.01	2.87E-03	0.0143	2
P58771	TPM1_MOUSE	KLVIIESDLR	5.14	2.89E-03	0.0143	2
O88685	PRS6A_MOUSE	TMLELLNQLDGFQPNQVVK	3.47	2.90E-03	0.0143	2
Q9Z204	HNRPC_MOUSE	GFQVYVNER	2.07	2.94E-03	0.0143	2
P01831	THY1_MOUSE	VTSLTAC[+57]LVNQNLK	3.11	3.01E-03	0.0143	2
Q9EPU0	RENT1_MOUSE	LVLGIRPIR	2.25	3.07E-03	0.0143	2
Q5SV64	Q5SV64_MOUSE	ASFYDSVSGLHEPPVDR	4.88	3.07E-03	0.0143	2
P21107	TPM3_MOUSE	KLVIIEGDLR	2.50	3.10E-03	0.0143	2
Q9Z1G4	VPP1_MOUSE	FTHGFQNIVDAYGIGTYR	3.33	3.13E-03	0.0143	2
Q91WQ3	SYYC_MOUSE	QVEHPLLSGLLYPGLQALDEEYLK	5.96	3.19E-03	0.0143	2
P70248	MYO1F_MOUSE	DIILQSNPLLEAFGNAK	5.86	3.20E-03	0.0143	2
D3Z4J3	D3Z4J3_MOUSE	LTNENLDLM[+16]EQLEK	3.94	3.24E-03	0.0143	2
P0CG50	UBC_MOUSE	PTLSDYNIQK	2.38	3.24E-03	0.0143	2
Q80VD1	FA98B_MOUSE	GPLLEEQALSK	2.49	3.45E-03	0.0144	2
Q9QZX7	SRR_MOUSE	SLLIPTAGVALAAVLSQHFQTVSPEVK	4.41	3.48E-03	0.0144	2
Q91WQ3	SYYC_MOUSE	IDVGAEPR	1.90	3.60E-03	0.0145	2
Q91Z69	SRGP1_MOUSE	VQLLQDLQDFFR	7.07	3.78E-03	0.0147	2
Q6P1F6	2ABA_MOUSE	SFFSEIISISDVK	5.67	3.86E-03	0.0147	2
P61027	RAB10_MOUSE	AFLTLAEDILR	2.13	3.92E-03	0.0147	2
P0CG50	UBC_MOUSE	PTITLEVEPSDTIENVK	3.17	4.08E-03	0.0148	2
Q6NS52	DGKB_MOUSE	DIVC[+57]YLSLLER	5.75	4.13E-03	0.0148	2
Q91Z69	SRGP1_MOUSE	VSGSQVEVNDIK	3.98	4.36E-03	0.0150	2
P60867	RS20_MOUSE	LIDLHSPSEIVK	2.85	4.40E-03	0.0150	2
Q9SIP7	RS31_ARATH_40S	ELAEDGYSGVEVR	1.78	4.40E-03	0.0150	2
Q9EPN1	NBEA_MOUSE	ATDAQLC[+57]LESSPK	4.38	4.68E-03	0.0153	2
P70248	MYO1F_MOUSE	ISNFLLEK	4.55	4.77E-03	0.0154	2
A0A178UNP6	A0A178UNP6_AR	MATPPLTPR	3.98	5.10E-03	0.0155	2
A0A0N5DF32	A0A0N5DF32_TRI	EC[+57]LPLILFIR	3.71	5.10E-03	0.0155	2
Q9EPU0	RENT1_MOUSE	NVFLLGFIK	4.41	5.11E-03	0.0155	2
Q9Z1W8	AT12A_MOUSE	LIIVEGC[+57]QR	1.67	5.13E-03	0.0155	2
P51881	ADT2_MOUSE	DFLAGGVAAAISK	1.92	5.23E-03	0.0157	2
P11983	TCPA_MOUSE	LGVQVVITDPEKLDQIR	2.95	5.32E-03	0.0158	2
Q84W47	Q84W47_ARATH	LVVDGDFGR	1.37	5.33E-03	0.0158	2
Q9ESN6	TRIM2_MOUSE	VLQSQLDILLQGESIK	2.40	5.40E-03	0.0158	2
P31938	MP2K1_MOUSE	LPSGVFSLEFQDFVNK	4.80	5.72E-03	0.0161	2
Q9DBZ5	EIF3K_MOUSE	YNPENLATLER	3.94	6.07E-03	0.0165	2
P38647	GRP75_MOUSE	AQFEGIVTDLIK	1.81	6.28E-03	0.0168	2
Q6P1F6	2ABA_MOUSE	VVIFQQEQENK	1.90	6.37E-03	0.0169	2
F8VPU2	FARP1_MOUSE	SLVSQPTAPNSEVVK	2.48	6.37E-03	0.0169	2
P48486	PP16_ARATH_Seri	AHQVVEDGYEFFAK	3.33	6.47E-03	0.0170	2
P01872	IGHM_MOUSE	ILVESGFTTDPVTIENK	2.20	6.53E-03	0.0171	2
P42932	TCPQ_MOUSE	FAEAFEAIK	1.46	6.57E-03	0.0171	2
M7NIQ0	M7NIQ0_PNEMU	YPENFFILR	3.97	6.81E-03	0.0172	2
P48482	PP12_ARATH_Seri	YPENFFLLR	3.97	6.81E-03	0.0172	2

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P58389	PTPA_MOUSE	QVDDQVAIVFK	1.31	6.91E-03	0.0174	2
E9Q634	MYO1E_MOUSE	VDFFLVDSINK	4.60	6.96E-03	0.0174	2
P21107	TPM3_MOUSE	IQLVVEELDR	3.75	7.21E-03	0.0177	2
P32067	LA_MOUSE	LupGSIFAVFDSIQSAK	3.79	7.21E-03	0.0177	2
M7NIQ0	M7NIQ0_PNEMU	QIKYPENFFILR	4.76	7.21E-03	0.0177	2
P48482	PP12_ARATH_Seri	QIKYPENFFLLR	4.76	7.21E-03	0.0177	2
P49722	PSA2_MOUSE	QYNEDLELEDIAHTAILTLK	3.97	7.31E-03	0.0178	2
P46638	RB11B_MOUSE	QAVGALLVYDIAK	1.42	7.33E-03	0.0178	2
P48484	PP14_ARATH_Seri	QSQLETIC[+57]LLLAYK	4.33	7.34E-03	0.0178	2
P48486	PP16_ARATH_Seri	QSIETIC[+57]LLLAYK	4.33	7.34E-03	0.0178	2
Q9ESJ4	SPN90_MOUSE	QVIGAEELMELVR	5.83	7.57E-03	0.0180	2
P67871	CSK2B_MOUSE	QYQQGDFGYC[+57]PR	6.77	7.63E-03	0.0181	2
Q91ZU6	DYST_MOUSE	QITREEQVDGATEK	2.96	7.72E-03	0.0181	2
P62264	RS14_MOUSE	QTPGPGAQSALR	2.97	7.72E-03	0.0181	2
P01831	THY1_MOUSE	QVTLSNQPYIK	2.48	8.01E-03	0.0184	2
Q8C1B1	CAMP2_MOUSE	QSDANNFLILFR	3.82	8.08E-03	0.0184	2
Q3UGR5	HDHD2_MOUSE	QVFFLEALR	1.31	8.35E-03	0.0188	2
O88544	CSN4_MOUSE	QLYNNITFEELGALLEIPAAK	7.43	8.41E-03	0.0188	2
Q8C854	MYEF2_MOUSE	QVGEVTVYVELFK	2.25	8.59E-03	0.0190	2
Q91VA7	Q91VA7_MOUSE	QNIANPTAMLLSATNMLR	3.82	8.64E-03	0.0191	2
Q9ERK4	XPO2_MOUSE	QVILLQAFLEK	3.01	8.65E-03	0.0191	2
Q6NS52	DGKB_MOUSE	QHPPVAILPLGTGNDLAR	3.88	8.72E-03	0.0191	2
Q571F3	Q571F3_MOUSE	QVSGELFAQAPVEQYPGIAVETVTDSSR	2.24	8.77E-03	0.0192	2
P14106	C1QB_MOUSE	QVITNANENYEPR	3.93	8.84E-03	0.0193	2
P61294	RAB6B_MOUSE	QDSTVAVVVYDITNLNSFQQTSK	2.51	9.22E-03	0.0198	2
Q5SV64	Q5SV64_MOUSE	QVFAELWKDEIQTIR	5.88	9.26E-03	0.0198	2
Q8C1B1	CAMP2_MOUSE	QDGTGDC[+57]ALAALIHFYC[+57]PAVVR	6.99	9.29E-03	0.0199	2
Q9DB20	ATPO_MOUSE	QVLGNTQGIIAFSTIMSVHR	3.54	9.30E-03	0.0199	2
Q9Z1W8	AT12A_MOUSE	QVAEIPFNSTNK	1.23	9.41E-03	0.0201	2
E9Q634	MYO1E_MOUSE	QVLQVSIQGPLPK	6.41	9.51E-03	0.0202	2
Q9DCD0	6PGD_MOUSE	QVILFVSGVSGGEEGAR	1.58	9.69E-03	0.0204	2
P12960	CNTN1_MOUSE	QIFNIQLEDEGLYEC[+57]EAENIR	4.80	9.77E-03	0.0204	2
Q9DB72	BTBDH_MOUSE	QLVVTPASSGGDAAGVSFQK	5.43	1.00E-02	0.0206	2
D3Z4J3	D3Z4J3_MOUSE	QLTNENLDLMEQLEK	5.38	1.02E-02	0.0208	2
P58389	PTPA_MOUSE	QLVALLDTLDR	1.22	1.03E-02	0.0209	2
A0A0N5DF32	A0A0N5DF32_TRI	QLREC[+57]LPLILFIR	6.07	1.05E-02	0.0212	2
Q8C854	MYEF2_MOUSE	QLGSTIFVANLDFK	5.27	1.08E-02	0.0215	2
P62264	RS14_MOUSE	QVIEDVTPIPSDSTR	2.41	1.10E-02	0.0217	2
O35737	HNRH1_MOUSE	QHTGPNSPDTANDGFVR	1.76	1.12E-02	0.0219	2
Q60676	PPP5_MOUSE	QVAFLEENQLDYIIR	2.55	1.12E-02	0.0219	2
P38647	GRP75_MOUSE	QQAASSLQQASLK	1.90	1.15E-02	0.0223	2
P12960	CNTN1_MOUSE	QVQVTSQEYSAR	2.93	1.17E-02	0.0225	2
P62717	RL18A_MOUSE	QLTTAGAVTQC[+57]YR	5.18	1.22E-02	0.0230	2
P62267	RS23_MOUSE	QVANVSLALYK	4.38	1.23E-02	0.0231	2
Q60676	PPP5_MOUSE	QVTEC[+57]YGYALGDATR	3.70	1.32E-02	0.0240	2
Q8CBY8	DCTN4_MOUSE	QLIEYYQQLAQK	2.50	1.34E-02	0.0242	2
Q8C845	Q8C845_MOUSE	QKAAAGELQEDSGLHVLAR	4.19	1.35E-02	0.0243	2
P62855	RS26_MOUSE	QVDISEASVFDAVYVLPK	3.60	1.35E-02	0.0243	2
O54946	DNJB6_MOUSE	QVVEEDGQLK	2.06	1.38E-02	0.0247	2
P62267	RS23_MOUSE	QVITAFVPNDGC[+57]LNFIEENDEVLVAGFGR	3.56	1.38E-02	0.0247	2
Q9CXY6	ILF2_MOUSE	QVILPTLEAVAALGNK	4.62	1.41E-02	0.0250	2
P13707	GPDA_MOUSE	QLGIPMSVLMGANIASEVAEEK	2.70	1.42E-02	0.0251	2
Q9DB72	BTBDH_MOUSE	QITWNVLFSPR	3.62	1.43E-02	0.0253	2
Q9ERK4	XPO2_MOUSE	QVIFLESVEGNQNYPLLLTLLEK	4.96	1.45E-02	0.0255	2
P42932	TCPQ_MOUSE	QVAIAGTGANVIVTGGK	1.56	1.55E-02	0.0266	2
P41105	RL28_MOUSE	QVQTYSTEPNNLK	5.17	1.55E-02	0.0266	2
A0A0N5DFM1	A0A0N5DFM1_TR	QVANETGAFFLLNGPEIMSK	4.67	1.57E-02	0.0268	2
Q9EPN1	NBEA_MOUSE	QVAVLEQFLSFAK	1.19	1.58E-02	0.0269	2
P46638	RB11B_MOUSE	QVSTIGVEFATR	2.02	1.59E-02	0.0270	2
Q8CIE6	COPA_MOUSE	QVVGQSIAYLQK	2.73	1.59E-02	0.0270	2
P62855	RS26_MOUSE	QVNIVEAAAVR	3.52	1.60E-02	0.0271	2
P14106	C1QB_MOUSE	QVINSPLRPNQVIR	3.19	1.60E-02	0.0271	2

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P84099	RL19_MOUSE	εLLADQAEAR	2.73	1.67E-02	0.0278	2
Q9SIP7	RS31_ARATH	40SGLC[+57]AIAQAESLR	3.31	1.67E-02	0.0278	2
P67871	CSK2B_MOUSE	RPANQFVPR	4.08	1.67E-02	0.0278	2
Q9D051	ODPB_MOUSE	VFLLGEEVAQYDGAYK	3.25	1.73E-02	0.0284	2
P08553	NFM_MOUSE	NLRDDTEAAIR	1.85	1.74E-02	0.0285	2
P20357	MTAP2_MOUSE	QSTEPSIVMPSIGLSAEPPAPK	1.38	1.78E-02	0.0290	2
P68510	1433F_MOUSE	NSVVEASEAAIK	1.89	1.79E-02	0.0292	2
Q99104	MYO5A_MOUSE	GDDFETVSFWSNTC[+57]R	2.92	1.83E-02	0.0296	2
Q9CZT8	RAB3B_MOUSE	TYSWDNAQVILVGNK	2.44	1.90E-02	0.0303	2
Q8CAA7	PGM2L_MOUSE	LIDALIENFLEPSK	2.66	1.92E-02	0.0306	2
P46460	NSF_MOUSE	VLDIEAM[+16]DPSILK	4.68	1.92E-02	0.0306	2
P27659	RL3_MOUSE	6CVAFSVAR	1.17	1.97E-02	0.0311	2
P16858	G3P_MOUSE	G VVDLMAYMASK	6.97	2.01E-02	0.0317	2
P17183	ENOG_MOUSE	LAMQEFMILPVGAESFR	1.58	2.15E-02	0.0334	2
Q6P8J7	KCRS_MOUSE	LG YILTC[+57]PSNLGTGLR	4.83	2.16E-02	0.0335	2
Q9WUM4	COR1C_MOUSE	VTWSSFC[+57]AVNPR	5.14	2.19E-02	0.0338	2
P00920	CAH2_MOUSE	AVQQPDGLAVLGIFLK	1.37	2.19E-02	0.0338	2
O70172	PI42A_MOUSE	FGIDDQDFQNSLTR	5.89	2.23E-02	0.0343	2
P33175	KIF5A_MOUSE	SLSALGNVISALAEGTK	2.30	2.24E-02	0.0344	2
Q8CGF6	WDR47_MOUSE	AAYADLLTPLISK	5.25	2.30E-02	0.0350	2
P47757	CAPZB_MOUSE	QMEKDET VSDC[+57]SPHIANIGR	1.44	2.34E-02	0.0355	2
Q9CR57	RL14_MOUSE	εC[+57]MQLTDFILK	1.56	2.37E-02	0.0358	2
Q8CI94	PYGB_MOUSE	TC[+57]AYTNHTVLPEALER	3.71	2.44E-02	0.0365	2
Q9D051	ODPB_MOUSE	TYMSAGLQVPVIVFR	2.40	2.45E-02	0.0366	2
Q91VA7	Q91VA7_MOUSE	KLDLFANVVHVK	3.93	2.45E-02	0.0366	2
Q9QZE5	COPG1_MOUSE	AIVDC[+57]IISIIIEENSESK	1.17	2.45E-02	0.0366	2
P04370	MBP_MOUSE	MDTGILDSIGR	2.86	2.48E-02	0.0369	2
Q8C1B7	SEP11_MOUSE	SYELQESNVR	1.50	2.48E-02	0.0369	2
Q61598	GDIB_MOUSE	FSPYLYPLYGLGELPQGFAR	7.49	2.49E-02	0.0370	2
P15105	GLNA_MOUSE	C[+57]IEEAIDK	1.31	2.53E-02	0.0374	2
Q8JZQ9	EIF3B_MOUSE	VDNAYWLWTFQGR	2.15	2.54E-02	0.0375	2
P14873	MAP1B_MOUSE	MSISEGTVSDK	1.54	2.59E-02	0.0381	2
P00920	CAH2_MOUSE	QSPVDIDTATAQHDPALQPLLI SYDK	3.80	2.63E-02	0.0386	2
Q9JHU4	DYHC1_MOUSE	DFPLNDLLSATELDK	4.31	2.68E-02	0.0391	2
P25444	RS2_MOUSE	4CLSI PVPR	4.33	2.75E-02	0.0398	2
P62281	RS11_MOUSE	4RDYLHYIR	2.14	2.75E-02	0.0398	2
Q9WV54	ASAH1_MOUSE	ESLDVYELDPK	3.97	2.85E-02	0.0409	2
Q92019	WDR7_MOUSE	LNIWNIADIAEK	1.09	2.93E-02	0.0418	2
Q8C1B7	SEP11_MOUSE	STLM[+16]DTL FNTK	1.14	2.99E-02	0.0425	2
Q9R0Y5	KAD1_MOUSE	7KVNAEGTVDTVFSEVC[+57]TYLDSLK	1.14	2.99E-02	0.0425	2
Q6A087	Q6A087_MOUSE	VATLEQSYEALC[+57]ELAATR	3.23	3.05E-02	0.0431	2
Q8BPN8	DMXL2_MOUSE	NFFPIAGLEFSELPVTSPLGIAVIK	4.53	3.26E-02	0.0456	2
Q61316	HSP74_MOUSE	NFTTEQVTAMLLSK	1.18	3.28E-02	0.0458	2
Q99L45	IF2B_MOUSE	ETSFVNFTDIC[+57]K	2.86	3.42E-02	0.0475	2
P08249	MDHM_MOUSE	IFGVTTLDIVR	1.23	3.52E-02	0.0487	2
Q8BL97	SRSF7_MOUSE	NPPGF AFVEFEDPR	3.96	3.56E-02	0.0492	2
O08749	DLDH_MOUSE	RPFTQNLGLEELGIELDPK	2.99	1.51E-04	0.0143	2
P54609	CD48A_ARATH	CεGVLFYGP PGC[+57]GK	3.04	4.81E-04	0.0143	2
P28651	CAH8_MOUSE	AVTEILQDIQYK	2.35	4.92E-04	0.0143	2
D3YVF0	AKAP5_MOUSE	VTVDHAE EATVGQAE EATVGQAEK	2.11	7.51E-04	0.0143	2
P97315	CSR P1_MOUSE	GFGFGQGAGALVHSE	1.77	1.03E-03	0.0143	2
P35279	RAB6A_MOUSE	LQLWDTAGQER	2.11	1.06E-03	0.0143	2
P97315	CSR P1_MOUSE	GLESTTLADKDGEIYC[+57]K	3.90	1.13E-03	0.0143	2
Q7M6Y3	PICAL_MOUSE	NTLFNLSNFLDK	1.68	1.48E-03	0.0143	2
Q3UM45	PP1R7_MOUSE	A IENIDTLTNLES LFLGK	3.37	1.51E-03	0.0143	2
A0A0J9YUN4	A0A0J9YUN4_MOUSE	C[+57]VDMVVSELTSTIR	2.06	1.78E-03	0.0143	2
Q61644	PACN1_MOUSE	GPQYGS LER	2.99	1.92E-03	0.0143	2
P14824	ANXA6_MOUSE	DQAQEDAQVAEILEIADTPSGDK	2.57	2.01E-03	0.0143	2
P62852	RS25_MOUSE	4AALQELLSK	2.20	2.64E-03	0.0143	2
P48962	ADT1_MOUSE	7EQGFLSFWR	2.27	2.77E-03	0.0143	2
Q9CZ30	OLA1_MOUSE	IPAFLN VVDIAGLVK	1.99	2.92E-03	0.0143	2
A0A0J9YUN4	A0A0J9YUN4_MOUSE	TGLFTPD LAF EATVK	1.61	3.08E-03	0.0143	2

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P54609	CD48A_ARATH	CεIVSQLLTLMDGLK	2.26	3.16E-03	0.0143	2
O70435	PSA3_MOUSE	FHVGMVAVAGLLADAR	1.75	3.28E-03	0.0143	2
P55066	NCAN_MOUSE	AALAEVLVALPC[+57]FFTLQPR	4.05	3.36E-03	0.0143	2
O08749	DLDH_MOUSE	EANLAAAFGKPINF	2.25	3.39E-03	0.0143	2
P46735	MYO1B_MOUSE	IFLLTNNNLLLADQK	7.14	3.82E-03	0.0147	2
D3YVF0	AKAP5_MOUSE	TSEQYETLLIETASSLVK	6.07	3.88E-03	0.0147	2
P55066	NCAN_MOUSE	ELGGEVFYVGPARG	2.10	4.18E-03	0.0149	2
Q91WK2	EIF3H_MOUSE	HYQEEGQGTEVVQGVLLGLVVEDR	5.32	4.38E-03	0.0150	2
P62743	AP2S1_MOUSE	QLLMLQSLE	2.06	4.43E-03	0.0151	2
Q9SZN1	VATB2_ARATH	V-IPLFSAAGLPHNEIAAQIC[+57]F	2.11	4.59E-03	0.0152	2
G5E8R0	G5E8R0_MOUSE	ETAEADVASLNR	3.76	4.71E-03	0.0153	2
Q61553	FSCN1_MOUSE	YWTLTATGGVQSTASTK	6.83	5.03E-03	0.0155	2
P48774	GSTM5_MOUSE	LVFVDFLTYDVLVDQNR	5.35	5.32E-03	0.0158	2
P07356	ANXA2_MOUSE	SALSGHLETVILGLLK	5.91	5.33E-03	0.0158	2
P35279	RAB6A_MOUSE	LVFLGEQSVGK	1.51	5.34E-03	0.0158	2
Q7M6Y3	PICAL_MOUSE	FIQYLASR	1.55	6.08E-03	0.0165	2
Q61553	FSCN1_MOUSE	VGKDELFALEQSC[+57]AQVVLQAANER	1.98	6.10E-03	0.0166	2
Q9SZN1	VATB2_ARATH	V-QIYPPINVLPSLSR	1.55	6.17E-03	0.0166	2
P08113	ENPL_MOUSE	IGVVDSDDLPLNVSR	1.76	6.38E-03	0.0169	2
Q812A2	SRGP3_MOUSE	VPGSQVEVNDIK	4.02	6.39E-03	0.0169	2
Q812A2	SRGP3_MOUSE	TYLSAEYNLETSR	4.31	6.54E-03	0.0171	2
Q8R4E6	PURG_MOUSE	DALVQLIEDYGEEDIEER	5.31	6.72E-03	0.0172	2
Q62188	DPYL3_MOUSE	IAVGSDSDLVIWDPDALK	1.97	6.99E-03	0.0175	2
Q9CZ30	OLA1_MOUSE	(NYIVEDGDIIFFK	2.34	7.53E-03	0.0180	2
P14824	ANXA6_MOUSE	DAFVAIVQSVK	3.95	7.55E-03	0.0180	2
O70435	PSA3_MOUSE	FSNFGYNIPLK	1.58	7.79E-03	0.0182	2
P57722	PCBP3_MOUSE	INISEGNC[+57]PER	1.17	7.96E-03	0.0183	2
Q9JJK2	LANC2_MOUSE	IKDLLQQMEEGLK	2.87	8.56E-03	0.0190	2
P62852	RS25_MOUSE	4LITPAVVSER	2.30	9.26E-03	0.0198	2
P61089	UBE2N_MOUSE	TNEAQAIETAR	2.25	9.51E-03	0.0202	2
P08113	ENPL_MOUSE	IFAFQAEVNR	1.82	9.67E-03	0.0204	2
Q9JJK2	LANC2_MOUSE	SGNYPPSSLSNETDR	2.38	1.01E-02	0.0207	2
P61089	UBE2N_MOUSE	YFHVVIAGPQDSPFEGGTFK	1.93	1.02E-02	0.0208	2
Q9WUB3	PYGM_MOUSE	VAIQLNDTHPSLAPELMR	2.13	1.03E-02	0.0209	2
P46735	MYO1B_MOUSE	LFSWLVR	3.21	1.03E-02	0.0209	2
Q61701	ELAV4_MOUSE	ILVDQVTGVSR	2.74	1.06E-02	0.0213	2
P57722	PCBP3_MOUSE	LVVPASQC[+57]GSLIGK	1.28	1.07E-02	0.0214	2
Q8VDM4	PSMD2_MOUSE	AVPLALALISVSNPR	3.89	1.14E-02	0.0222	2
P51150	RAB7A_MOUSE	DPENFPFVVLGNK	1.49	1.21E-02	0.0229	2
Q9CZM2	RL15_MOUSE	εVLNSYWVGEDSTYK	3.01	1.26E-02	0.0233	2
Q9WUB3	PYGM_MOUSE	VHINPNSLFDVQVK	2.32	1.31E-02	0.0239	2
G5E8R0	G5E8R0_MOUSE	SLQEQADAAEER	5.35	1.31E-02	0.0239	2
Q8R4E6	PURG_MOUSE	FGENFIK	1.13	1.32E-02	0.0240	2
Q61701	ELAV4_MOUSE	LDNLLNMAYGVK	1.38	1.43E-02	0.0253	2
P62830	RL23_MOUSE	εISLGLPVGAVINC[+57]ADNTGAK	3.67	1.57E-02	0.0268	2
Q61644	PACN1_MOUSE	AYAQLTDWAK	1.42	1.61E-02	0.0272	2
Q62188	DPYL3_MOUSE	SAADLISQAR	1.08	1.61E-02	0.0272	2
P35980	RL18_MOUSE	εTNRPPLSLSR	3.57	1.68E-02	0.0279	2
Q62261	SPTB2_MOUSE	FLQDC[+57]QELSLWINEK	2.54	1.73E-02	0.0284	2
O54774	AP3D1_MOUSE	NYLSLAPLFFK	6.05	1.78E-02	0.0290	2
P62702	RS4X_MOUSE	4LSNIFVIGK	3.86	1.81E-02	0.0294	2
Q8C0E9	Q8C0E9_MOUSE	M[+42]IGVNSVQSASK	2.19	1.83E-02	0.0296	2
P09405	NUCL_MOUSE	QKVEGSEPTTFFNLFIGNLNPNK	5.90	1.84E-02	0.0297	2
Q8VEM8	MPCP_MOUSE	IQTQPGYANTLR	2.49	1.91E-02	0.0305	2
P63318	KPCG_MOUSE	LLNQEEGEYYNVPVADADNC[+57]SLLQK	5.26	1.96E-02	0.0310	2
Q99PT1	GDIR1_MOUSE	VAVSADPNVNPVIVTR	2.19	2.06E-02	0.0323	2
P20357	MTAP2_MOUSE	RLSNVSSSGSINLLESPQLATLAEDVTAALAK	2.68	2.06E-02	0.0323	2
Q8JZQ9	EIF3B_MOUSE	VTLMQLPTR	1.63	2.26E-02	0.0346	2
Q8VDD5	MYH9_MOUSE	TEM[+16]JEDLM[+16]SSK	1.57	2.28E-02	0.0348	2
P05064	ALDOA_MOUSE	IGEHTPSALAIMENANVLAF	4.61	2.32E-02	0.0352	2
Q8QZY1	EIF3L_MOUSE	IYGDFFIR	2.02	2.44E-02	0.0365	2
F6ZIA4	F6ZIA4_MOUSE	GAYDAQGTLSK	4.66	2.45E-02	0.0366	2

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q99JX4	EIF3M_MOUSE	VAASC[+57]GAIQYIPTELDQVR	4.86	2.46E-02	0.0367	2
P56480	ATPB_MOUSE	VALTGLTVAEYFR	3.39	2.64E-02	0.0387	2
P58771	TPM1_MOUSE	C[+57]JAELEELK	1.19	2.70E-02	0.0393	2
P40124	CAP1_MOUSE	VENQENVSNLVIDDTELK	2.76	2.70E-02	0.0393	2
O54983	CRYM_MOUSE	SLGM[+16]AVEDLVAAK	1.84	2.83E-02	0.0407	2
P14115	RL27A_MOUSE	TGVAPIIDVVR	1.28	2.85E-02	0.0409	2
P62827	RAN_MOUSE	GLVLVGDGGTGK	5.05	2.99E-02	0.0425	2
Q6ZWW3	RL10_MOUSE	FNADEFEDMVAEK	1.28	3.03E-02	0.0429	2
P97427	DPYL1_MOUSE	GVNSFQVYMAYK	3.16	3.13E-02	0.0440	2
P04370	MBP_MOUSE	YLATASTM[+16]DHAF	1.15	3.60E-02	0.0496	2
O54774	AP3D1_MOUSE	GVPVAEEVSALFAGELNPVAPK	3.73	1.55E-03	0.0143	2
Q8QZT1	THIL_MOUSE	AQEQDTYALSSYTR	4.37	1.63E-03	0.0143	2
Q99JX4	EIF3M_MOUSE	QQWQQLYDTLNAWK	4.83	2.02E-03	0.0143	2
Q99K85	SERC_MOUSE	ASLYNAVTTEDVEK	1.38	2.34E-03	0.0143	2
Q8K0T0	RTN1_MOUSE	ILFLVQDLVDSLK	4.53	2.36E-03	0.0143	2
Q8BVE3	VATH_MOUSE	LLEVSDDPQVLAVAAHDVGEYVR	1.76	3.02E-03	0.0143	2
O70161	PI51C_MOUSE	GAIQLGIGYTVGNLSSKPER	3.06	3.21E-03	0.0143	2
P63044	VAMP2_MOUSE	LSELDDRADALQAGASQFETSAAK	1.76	3.61E-03	0.0145	2
Q99K85	SERC_MOUSE	VIFVQGGGSGQFSAVPLNLIGLK	2.78	3.65E-03	0.0146	2
Q92019	WDR7_MOUSE	FRPPLLEMLAR	4.51	4.75E-03	0.0154	2
Q8BVE3	VATH_MOUSE	YNIIPVLSDILQESVK	2.44	4.85E-03	0.0154	2
O70161	PI51C_MOUSE	ITVQVEPVC[+57]GVGVPK	1.47	6.12E-03	0.0166	2
P35700	PRDX1_MOUSE	QITINDLPVGR	1.22	6.34E-03	0.0169	2
P35700	PRDX1_MOUSE	LVQAFQFTDK	2.35	7.12E-03	0.0176	2
P63044	VAMP2_MOUSE	LQQTQAQVDEVVDIMR	2.06	8.59E-03	0.0190	2
Q8QZT1	THIL_MOUSE	IAAFADAAVDPIDFPLAPAYAVPK	1.69	9.14E-03	0.0197	2
Q8K0T0	RTN1_MOUSE	IHQAVDQYLGLVR	1.27	1.26E-02	0.0233	2
Q80ZK2	Q80ZK2_MOUSE	VVNAAIATASSAPGESEEPVPSASF	2.82	1.78E-02	0.0290	2
P16546	SPTN1_MOUSE	ALINADELANDVAGAEALLDF	1.30	1.94E-02	0.0308	2
B9EKR1	PTPRZ_MOUSE	AIIDGTESVSR	4.79	2.46E-02	0.0367	2
P50516	VATA_MOUSE	LPANHPLLTGQR	1.37	2.50E-02	0.0371	2
Q6URW6	MYH14_MOUSE	LQQLFNHTM[+16]FVLEQEEYQR	1.84	2.93E-02	0.0418	2
O55131	SEPT7_MOUSE	STLINSFLTDLYSPEYGPSPHR	2.80	1.13E-03	0.0143	2
Q3UHJ0	AAK1_MOUSE	VAEDEFDPIPVLTIK	3.78	1.62E-03	0.0143	2
Q3UHJ0	AAK1_MOUSE	LQTGFTENEVLQIFC[+57]DTC[+57]EAVAR	6.29	1.95E-03	0.0143	2
O55131	SEPT7_MOUSE	NLEGYVGFANLPNQVYR	1.82	8.71E-03	0.0191	2
Q91V12	BACH_MOUSE	ATLWYVPLSLK	1.40	9.42E-03	0.0201	2
Q921M7	FA49B_MOUSE	GLLGALTSTPYSPQHLER	1.70	1.04E-02	0.0211	2
Q11011	PSA_MOUSE	PiATFDISLVVPK	1.26	1.24E-02	0.0231	2
Q921M7	FA49B_MOUSE	DQPPNSVEGLLNLR	1.99	1.49E-02	0.0259	2
Q11011	PSA_MOUSE	PiYAAVTQFEATDAF	1.39	1.65E-02	0.0276	2
Q91V12	BACH_MOUSE	VLEVPPIVYLR	1.16	1.69E-02	0.0281	2
Q7TMB8	CYFP1_MOUSE	QLQVVPLFGDMQIELAR	6.54	1.88E-02	0.0301	2
Q9CR57	RL14_MOUSE	LVAIVDVIDQNR	5.79	3.32E-02	0.0463	2
A0A0N5E063	A0A0N5E063_TRII	EKLC[+57]FVALDFEQEM[+16]JATAASSSSLEK	4.51	2.39E-03	0.0143	2
Q9Z2T6	KRT85_MOUSE	LC[+57]JEGVGSVNVVC[+57]VSSSR	2.00	2.85E-03	0.0143	2
Q7TMK9	HNRPQ_MOUSE	EFNEDGALAVLQQFK	4.28	2.90E-03	0.0143	2
Q9CZX8	RS19_MOUSE	RVLQALEGLK	1.99	5.73E-03	0.0161	2
Q9D6R2	IDH3A_MOUSE	ENTEGEYSGIEHVVDGVVQSIK	1.65	7.83E-03	0.0182	2
Q9Z2T6	KRT85_MOUSE	SDLEANVEALVEESSFLK	3.25	9.83E-03	0.0205	2
Q9CZX8	RS19_MOUSE	LKVPEWVDTVK	1.64	1.45E-02	0.0255	2
Q9D6R2	IDH3A_MOUSE	TPIAAGHPSMNLLLR	1.53	1.47E-02	0.0257	2
B9EKR1	PTPRZ_MOUSE	FAVLYQPLAGNDQAK	3.75	1.79E-02	0.0292	2
P14869	RLA0_MOUSE	VLALSVETEYTFPLTEK	4.61	2.17E-02	0.0336	2
O08638	MYH11_MOUSE	YEILAANAIPK	4.43	2.23E-02	0.0343	2
P01869	IGH1M_MOUSE	DVLTITLTPK	3.04	3.17E-02	0.0445	2
Q7TQF7	AMPH_MOUSE	LVDGSLTLDTYLGQFPDIK	2.88	4.34E-04	0.0143	2
Q7TQF7	AMPH_MOUSE	VETLHDFEAANSDELNLQR	1.34	3.02E-03	0.0143	2
Q61765	K1H1_MOUSE	ETM[+16]QFLNDR	1.88	3.99E-03	0.0148	2
Q9R111	GUAD_MOUSE	TPPLALVFR	5.15	2.36E-02	0.0357	2
P10649	GSTM1_MOUSE	VTYVDFLAYDILDQYR	3.65	6.81E-03	0.0172	2
P10649	GSTM1_MOUSE	LGLDFPNLPYLIDGSHK	2.05	9.10E-03	0.0197	2

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q922U2	K2C5_MOUSE	†TTAENEFVMLK	2.50	7.68E-03	0.0181	2
Q9DBZ5	EIF3K_MOUSE	FIC[+57]HVVGITYQHIDR	3.70	3.44E-02	0.0478	2
Q9ERE2	KRT81_MOUSE	LLEGEEQR	3.55	5.60E-03	0.0160	2
Q9ERE2	KRT81_MOUSE	FAAFIDKVR	2.49	5.67E-03	0.0160	2
P51150	RAB7A_MOUSE	EAINVEQAFQTIAR	1.15	3.60E-02	0.0496	2
Q3TLQ0	Q3TLQ0_MOUSE	HSAGGGNVQIVTK	4.60	1.15E-05	0.0143	1
Q8C153	Q8C153_MOUSE	ALLELQLEPEEIIYQTFQR	4.30	2.69E-04	0.0143	1
P18872	GNAO_MOUSE	IGAGDYQPTEQDILR	2.00	3.05E-04	0.0143	1
E9PVU0	E9PVU0_MOUSE	SVTDYAQQNPAAQLPAR	4.48	4.76E-04	0.0143	1
Q5SVJ0	Q5SVJ0_MOUSE	ISDILNSVR	1.96	6.32E-04	0.0143	1
P62874	GBB1_MOUSE	†LFVSGAC[+57]DASAK	1.67	1.06E-03	0.0143	1
Q99L75	Q99L75_MOUSE	TSTVDLPIESQLLWQLDR	2.58	1.29E-03	0.0143	1
P28738	KIF5C_MOUSE	ATEILNLLK	2.26	1.35E-03	0.0143	1
Q8CG29	Q8CG29_MOUSE	RPLPLTFSDLLQFR	5.38	1.72E-03	0.0143	1
M7NKU9	M7NKU9_PNEMU	LIAQVSSITASLR	2.78	1.86E-03	0.0143	1
P15508	SPTB1_MOUSE	FLDLLEPLGR	3.72	1.97E-03	0.0143	1
Q3UJV2	Q3UJV2_MOUSE	DVQDSVTVSNEIQTTK	5.04	1.99E-03	0.0143	1
Q3THH8	Q3THH8_MOUSE	SKDAEVDGTTSVTLAAEFLK	2.26	2.05E-03	0.0143	1
Q9CWF2	TBB2B_MOUSE	INVYYNEATGNK	2.29	2.08E-03	0.0143	1
Q3U804	Q3U804_MOUSE	IRIIAPPER	3.79	2.22E-03	0.0143	1
P84104	SRSF3_MOUSE	AFGYYGPLR	3.81	2.23E-03	0.0143	1
P68369	TBA1A_MOUSE	LIGQIVSSITASLR	2.96	2.33E-03	0.0143	1
Q8BFZ3	ACTBL_MOUSE	VAPDEHPILLTEAPLNPK	3.90	2.90E-03	0.0143	1
A0A0S2UN46	A0A0S2UN46_9CF	YVGDEAQSQR	3.84	2.92E-03	0.0143	1
P17156	HSP72_MOUSE	SINPDEAVAYGAAVQAAILIGDK	5.29	3.45E-03	0.0144	1
P61164	ACTZ_MOUSE	†DQLQTFSEEHPVLLTEAPLNPR	2.88	3.52E-03	0.0144	1
Q8C7C3	Q8C7C3_MOUSE	EQAEAEVASLNR	3.53	4.16E-03	0.0149	1
Q56WH1	TBA3_ARATH_Tub	FDGAINVDITEFQTNLVPYPR	4.07	4.20E-03	0.0149	1
P61750	ARF4_MOUSE	†IQEGAAVLQK	1.67	4.22E-03	0.0149	1
Q61990	PCBP2_MOUSE	QVTITGSAASISLAQYLINVF	1.67	4.40E-03	0.0150	1
A0A0N5DS75	A0A0N5DS75_TRI	DLIGVQNLIK	2.66	4.53E-03	0.0152	1
M7P3Y2	M7P3Y2_PNEMU	†LPIFSAAGLPHNEIAAQIC[+57]FR	2.11	4.59E-03	0.0152	1
Q9D1G1	RAB1B_MOUSE	EFADSLGVPFLETSK	3.18	4.59E-03	0.0152	1
P45591	COF2_MOUSE	†LGGSVVVSLEGKPL	3.15	4.73E-03	0.0153	1
A0A087WQ31	A0A087WQ31_MC	VLSTSTDLEAAVADALLLGDAR	7.22	5.09E-03	0.0155	1
B2RXX6	B2RXX6_MOUSE	LQTASDES YKDP TNIQLSK	2.87	5.11E-03	0.0155	1
A0A158UT74	A0A158UT74_TRA	KFDEILEVSDGIMVAR	2.08	5.68E-03	0.0161	1
Q91Z67	SRGP2_MOUSE	GASLLLYQR	2.79	5.89E-03	0.0163	1
A3QM89	A3QM89_MOUSE	SQAIDL L YWR	1.57	5.92E-03	0.0163	1
M7NI55	M7NI55_PNEMU	CVEILANDQGNR	1.89	6.69E-03	0.0172	1
P68372	TBB4B_MOUSE	INVYYNEATGGK	2.08	7.01E-03	0.0175	1
Q3U561	Q3U561_MOUSE	FSVC[+57]VLGDQQHC[+57]DEAK	2.79	7.04E-03	0.0175	1
A0A0N5DMQ1	A0A0N5DMQ1_TR	DLYANTVLSGGSTM[+16]YPGIADF	2.73	8.09E-03	0.0184	1
D3Z2H9	D3Z2H9_MOUSE	IQVLQQQADDAEER	2.60	8.09E-03	0.0184	1
F6VME3	F6VME3_MOUSE	FSWGAEGQKPGFGYGGR	3.31	8.56E-03	0.0190	1
A0A0C5PUT3	A0A0C5PUT3_PEI	†VAEALATAAGHLDDLPGALSALSDLHAHK	6.88	1.05E-02	0.0212	1
Q3UX10	TBAL3_MOUSE	SFGGGTSGSFTSLLMER	4.14	1.19E-02	0.0227	1
A0A0N5DXG6	A0A0N5DXG6_TR	VPTPDVSVVDLTC[+57]R	1.22	1.19E-02	0.0227	1
O55143	AT2A2_MOUSE	IGIFGQDEDVTSK	2.37	1.21E-02	0.0229	1
O70456	1433S_MOUSE	VLSSIEQK	1.20	1.24E-02	0.0231	1
P46097	SYT2_MOUSE	†IFVGSNATGTELR	1.55	1.36E-02	0.0244	1
B2RRE2	B2RRE2_MOUSE	EPADLDPEAASPAYSQAK	5.73	1.61E-02	0.0272	1
Q641P0	ARP3B_MOUSE	NVVLSSGGSTM[+16]FR	1.70	1.73E-02	0.0284	1
P63011	RAB3A_MOUSE	TYSWDNAQVLLVGNK	1.48	1.89E-02	0.0302	1
Q8R1B4	EIF3C_MOUSE	FEELTNLIR	8.27	2.14E-02	0.0333	1
P51410	RL9_MOUSE	6C TILSNQTVDIPENVEITLK	5.06	2.18E-02	0.0337	1
Q61879	MYH10_MOUSE	RHEMPPHIYAISESAYR	1.20	2.24E-02	0.0344	1
Q61765	K1H1_MOUSE	†LNVEVDAAPTVDLNR	1.04	2.36E-02	0.0357	1
Q9Z204	HNRPC_MOUSE	VFIGNLNTLVVK	2.52	2.44E-02	0.0365	1
Q8CGP0	H2B3B_MOUSE	AMGIMNSFVNDIFER	3.71	2.56E-02	0.0377	1
P11798	KCC2A_MOUSE	GAILTTM[+16]LATR	1.04	2.62E-02	0.0385	1
Q9D8E6	RL4_MOUSE	6C YAIC[+57]SALAASALPALVMSK	6.66	2.83E-02	0.0407	1

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
Q9JMH9	MY18A_MOUSE	GASFEELC[+57]HNYAQDR	3.36	2.86E-02	0.0410	1
Q8K310	MATR3_MOUSE	ITPENLPQILLQLK	5.52	3.03E-02	0.0429	1
Q923T9	KCC2G_MOUSE	ITEQLIEAINNGDFEAYTK	1.40	3.34E-02	0.0466	1
Q63844	MK03_MOUSE	IAPEIMLNSK	4.17	3.39E-02	0.0472	1
Q80TL0	PPM1E_MOUSE	ETDGTEGTVEIETVK	2.73	5.31E-04	0.0143	1
Q8BK64	AHSA1_MOUSE	VFTTQELVQAFTHAPAALEADR	2.68	5.49E-04	0.0143	1
P61255	RL26_MOUSE	εDDEVQVVR	2.81	6.73E-04	0.0143	1
Q9QW16	SRCN1_MOUSE	QIASLTGLVQSALLR	5.63	7.16E-04	0.0143	1
P28661	SEPT4_MOUSE	STLVNSLFLTDLYR	3.35	8.20E-04	0.0143	1
Q6PER3	MARE3_MOUSE	VLQAAFK	2.62	1.05E-03	0.0143	1
Q8K386	RAB15_MOUSE	IQIWDTAGQER	2.11	1.06E-03	0.0143	1
P39054	DYN2_MOUSE	IVYSPHVLNLTLDLPGITK	2.67	1.14E-03	0.0143	1
Q9Z1W9	STK39_MOUSE	DAYELQEVIQSGATAVVQAALC[+57]KPF	4.75	1.16E-03	0.0143	1
Q9CPU0	LGUL_MOUSE	IGLAFIQDPDGYWIEILNPNK	6.54	1.23E-03	0.0143	1
S4R2F3	S4R2F3_MOUSE	FLGPPVIVEIPHFAALR	3.12	1.49E-03	0.0143	1
Q9JJV2	PROF2_MOUSE	SQGGEPTYNVAVGR	2.26	1.74E-03	0.0143	1
Q8R081	HNRPL_MOUSE	VFNVFC[+57]LYGNVEK	3.01	1.77E-03	0.0143	1
Q05512	MARK2_MOUSE	VPVASPSAHNISSSSGAPDR	3.83	2.02E-03	0.0143	1
Q8BGQ7	SYAC_MOUSE	NVGC[+57]LQEALQLATSFAQLR	5.28	2.53E-03	0.0143	1
Q920Q6	MSI2H_MOUSE	GFGFVTFADPASVDK	2.54	2.79E-03	0.0143	1
F8VQC1	F8VQC1_MOUSE	DIHTLAQLISAYSLVDPEK	5.23	3.09E-03	0.0143	1
P35922	FMR1_MOUSE	SFLEFAEDVIQVPR	2.99	3.93E-03	0.0147	1
Q7TNM2	TRI46_MOUSE	LLTELSFLR	1.83	4.01E-03	0.0148	1
P49312	ROA1_MOUSE	LFIGGLSFETTDESLR	3.22	4.82E-03	0.0154	1
P62141	PP1B_MOUSE	IVQMTEAEVR	3.60	4.89E-03	0.0155	1
O65719	HSP7C_ARATH_HUMAN	IIINEPTAAAIAYGLDKK	2.62	5.61E-03	0.0160	1
O08807	PRDX4_MOUSE	QITLNDLPVGR	1.22	6.34E-03	0.0169	1
Q9Z0R4	ITSN1_MOUSE	TPIFLNEVLVK	2.34	6.40E-03	0.0169	1
P57776	EF1D_MOUSE	IGVVQDLQQAISK	1.85	6.69E-03	0.0172	1
P20444	KPCA_MOUSE	LTDFNFLMVLGK	6.33	7.08E-03	0.0175	1
Q9Z2U0	PSA7_MOUSE	FALLEVVQSGGK	1.33	7.28E-03	0.0177	1
P97384	ANX11_MOUSE	GTITAASGFDPLR	1.16	7.49E-03	0.0180	1
Q0KK55	KNDC1_MOUSE	NAGLLGQLEDFISSK	7.15	7.58E-03	0.0180	1
Q8CGY8	OGT1_MOUSE	VPNSVLWLLR	3.25	8.77E-03	0.0192	1
Q9Z0H8	CLIP2_MOUSE	AQELEGLDVEYR	3.35	9.76E-03	0.0204	1
Q8BYR5	CAPS2_MOUSE	LFTSTGVLALEDKELGR	1.85	1.04E-02	0.0211	1
A0A0N5E1B9	A0A0N5E1B9_TRI	AIDALHR	4.42	1.05E-02	0.0212	1
Q9D1A2	CNDP2_MOUSE	LGGSVELVDIGK	2.37	1.05E-02	0.0212	1
Q8BGT8	PHIPL_MOUSE	TEYTVAVQTASK	1.83	1.08E-02	0.0215	1
Q9DC51	GNAI3_MOUSE	LLLLGAGESGK	1.27	1.10E-02	0.0217	1
Q6IFX2	K1C42_MOUSE	ALEEANADLEVK	1.31	1.15E-02	0.0223	1
Q8BH66	ATLA1_MOUSE	SM[+16]LQATAEANNLAAVATAK	2.93	1.15E-02	0.0223	1
Q64467	G3PT_MOUSE	VPTPNVSVVDLTC[+57]R	1.21	1.16E-02	0.0224	1
O55100	SNG1_MOUSE	DNPLNEGTDAAAR	1.29	1.39E-02	0.0248	1
P48320	DCE2_MOUSE	IGAAALGIGTDSVILIK	1.51	1.42E-02	0.0251	1
Q91WC3	ACSL6_MOUSE	LPELSDLGQFFR	3.85	1.42E-02	0.0251	1
A0A0N5DZK1	A0A0N5DZK1_TRI	QDLPNAMNAAELTDK	1.27	1.46E-02	0.0256	1
P62849	RS24_MOUSE	LTTPDVIVFVFGFR	6.40	1.46E-02	0.0256	1
O35098	DPYL4_MOUSE	QIGENLIVPGGIK	1.19	1.47E-02	0.0257	1
P19157	GSTP1_MOUSE	YVTLIYTNYENK	1.35	1.57E-02	0.0268	1
Q8C2E7	WASC5_MOUSE	LSEFIPAVFLK	5.74	1.66E-02	0.0277	1
P62806	H4_MOUSE	His ISGLIYEETR	3.92	1.70E-02	0.0282	1
P62259	1433E_MOUSE	AAFDDAIAELDTLSEESYK	1.67	1.71E-02	0.0283	1
A0A0N5E063	A0A0N5E063_TRII	LC[+57]FVALDFEQEM[+16]ATAASSSSLEK	1.60	1.79E-02	0.0292	1
Q61361	PGCB_MOUSE	ALGAHLTSIC[+57]TPEEQDFVNDR	1.06	1.91E-02	0.0305	1
H3BJD0	H3BJD0_MOUSE	VFNTYSNEDYDR	2.53	1.92E-02	0.0306	1
Q9R1Q8	TAGL3_MOUSE	AAEVYGVV	1.40	1.93E-02	0.0307	1
Q8VDD5	MYH9_MOUSE	INFVNGYIVGANIETYLLEK	1.06	2.39E-02	0.0360	1
O70194	EIF3D_MOUSE	SVYSWDIVVQR	3.70	2.39E-02	0.0360	1
P05201	AATC_MOUSE	NLDYVATSIHEAVTK	1.97	2.50E-02	0.0371	1
P19096	FAS_MOUSE	FεVLEALLPLK	5.70	2.55E-02	0.0377	1
Q64436	ATP4A_MOUSE	NAADM[+16]ILLDDNFASIVTGVEQGR	7.22	2.56E-02	0.0377	1

Protein Accession	Protein Description	Modified Peptide Sequence	co-IP:Ctrl	p value	q value	Sig Peptide Count
P07724	ALBU_MOUSE	TC[+57]VADESAANC[+57]DK	6.92	2.68E-02	0.0391	1
Q9DCH4	EIF3F_MOUSE	FLMSLVNQVPK	8.50	2.80E-02	0.0404	1
Q8BWH8	Q8BWH8_MOUSE	SSLYLLM[+16]ETLNATTPHYVR	4.94	2.83E-02	0.0407	1
Q9JHU4	DYHC1_MOUSE	VAEVLFDAAADANAIEEVNLAYENVK	3.37	2.85E-02	0.0409	1
P62743	AP2S1_MOUSE	VYTVVDEM[+16]FLAGEIR	2.17	3.01E-02	0.0427	1
A0A0N5DZTC	A0A0N5DZT0_TRI	LLLPGELSK	3.32	3.40E-02	0.0473	1
Q3UGR5	HDHD2_MOUSE	LLLDGAPLIAHK	3.00	3.54E-02	0.0490	1
P97807	FUMH_MOUSE	ETAIELGYLTAEQFDEWVKPK	5.04	7.01E-04	0.0143	1
Q6ZPE2	MTMR5_MOUSE	ISVQTPVDQLLQDGLQLR	5.37	1.39E-03	0.0143	1
P15532	NDKA_MOUSE	EISLWFQPEELVEYK	3.85	1.42E-03	0.0143	1
Q8R1Q8	DC1L1_MOUSE	AGATSEGVLNFFNSLLSK	5.28	1.91E-03	0.0143	1
P28740	KIF2A_MOUSE	IDILTELK	2.78	2.63E-03	0.0143	1
P19246	NFH_MOUSE	NKLLEGEEC[+57]R	3.78	3.62E-03	0.0146	1
P27773	PDIA3_MOUSE	ELNDFISYLQR	4.64	3.92E-03	0.0147	1
Q80U49	C170B_MOUSE	LGDASDTEAVDGER	4.83	4.64E-03	0.0153	1
O88569	ROA2_MOUSE	LFIGGLSFETTEESLR	2.78	5.07E-03	0.0155	1
Q9QZD9	EIF3I_MOUSE	ESYSSGGEDGYVR	2.59	8.78E-03	0.0192	1
O54781	SRPK2_MOUSE	LKPWSLFDVLVEK	2.93	9.12E-03	0.0197	1
Q8BG05	ROA3_MOUSE	LFIGGLSFETDDSLR	2.26	1.03E-02	0.0209	1
P51174	ACADL_MOUSE	AQDTAELFFEDVR	1.93	1.04E-02	0.0211	1
Q60865	CAPR1_MOUSE	LNQDQLDAVSK	3.15	1.07E-02	0.0214	1
Q62277	SYPH_MOUSE	LHQVYFDAPSC[+57]VK	1.55	1.10E-02	0.0217	1
Q9Z2Q6	SEPT5_MOUSE	ESAPFAVIGSNTVVEAK	1.61	1.53E-02	0.0264	1
Q8BJH1	ZC21A_MOUSE	FNENAADR	3.12	2.32E-02	0.0352	1
P63325	RS10_MOUSE	DYLHLPPEIVPATLR	5.61	2.40E-02	0.0361	1
P39053	DYN1_MOUSE	IKGWLTINNIGIMK	4.53	2.62E-02	0.0385	1
O08553	DPYL2_MOUSE	IVLEDGTLHVTEGSGR	3.32	2.85E-02	0.0409	1
P08249	MDHM_MOUSE	AGAGSATLSMAYAGAF	1.99	3.03E-02	0.0429	1
Q9R0P9	UCHL1_MOUSE	MPFPVNHGASSEDSSLQDAAK	1.41	5.63E-03	0.0160	1
P42644	14333_ARATH	14-DSTLIMQLLR	1.78	7.91E-03	0.0183	1
P11758	HBB_MYOVE_Herr	GTFASLSELHC[+57]DK	1.75	1.46E-02	0.0256	1
P63328	PP2BA_MOUSE	QTLQSATVEAIEADEAIK	4.63	1.57E-02	0.0268	1
P17426	AP2A1_MOUSE	LLQC[+57]YPPPEDAAVK	1.76	2.06E-02	0.0323	1
Q99KK2	NEUA_MOUSE	VGLSAVPADAC[+57]SGAQK	1.76	2.98E-02	0.0424	1
P70168	IMB1_MOUSE	IGALQYLVPILTQTLTK	3.01	8.97E-04	0.0143	1
P26369	U2AF2_MOUSE	NFAFLEFR	3.29	1.85E-03	0.0143	1
Q9CZU6	CISY_MOUSE	CALGVLAQLIWSR	3.95	2.90E-03	0.0143	1
P17183	ENOG_MOUSE	DATNVGDEGGFAPNILENSEALELVK	2.89	3.18E-02	0.0446	1
E9Q557	DESP_MOUSE	LLQLQEQM[+16]R	1.69	7.54E-04	0.0143	1
P26443	DHE3_MOUSE	IVYNEAGVTFT	1.77	1.11E-02	0.0219	1