Table S1 Information of peptides identified in IEC MHCII immunopeptidome (related to Fig.2d)

H2Ab1f f-CAD Peptide	-10LgP	Mass	Length	ppm	m/z	z	RT	Area ZKD_1	Intensity ZKD_1	Source File	Accession	PTM	AScore	Decoy
A(+42.01)AGVEAAAEVAATEPKME	47.14	1785.85	18	-2.8	893.928	2	42.043			ZKD_1.raw	Q9D0E1|HNRPM	Acetylation (N-term)		FALSE
A(+42.01)ASAIKGLSALR	45.33	1198.7	12	-2.1	600.358	2	35.8232	5.20E+05	7.67E+06	ZKD_1.raw	Q9D8T7|SLIRP_M	Acetylation (N-term)		FALSE
A(+42.01)EGQVLVLDGRGHLLG	26.44	1674.91	16	-1.4	838.459	2	40.7899			ZKD_1.raw	P19253|RL13A_M	Acetylation (N-term)		FALSE
A(+42.01)EVEQKKKRTFR	35.77	1560.87	12	0.1	391.226	4	11.1525	7.77E+05	2.72E+07	ZKD_1.raw	P62843|RS15_MO	Acetylation (N-term)		FALSE
A(+42.01)GYEYVSPEQLSGFDK	47.45	1830.83	16	-0.1	916.423	2	42.4485	1.96E+05	3.40E+06	ZKD_1.raw	Q80TA1|EPT1_MO	Acetylation (N-term)		FALSE
A(+42.01)LKRINKELSDLARD	43.52	1783	15	0.9	595.34	3	33.7822	1.14E+06	1.46E+07	ZKD_1.raw	P61079|UB2D3_M	Acetylation (N-term)		FALSE
A(+42.01)SASGAMAKHEQILVLD	41.54	1781.9	17	1	891.957	2	34.8681	3.22E+05	6.03E+06	ZKD_1.raw	Q9WV55|VAPA_M	Acetylation (N-term)		FALSE
AAKPKVAKAKKVAAKKK	50.69	1764.18	17	-0.8	589.068	3	7.0989	4.25E+06	8.50E+07	ZKD_1.raw	P15864|H12_MOUSE			FALSE
AALQELLSKGLIKLVSKHR	41.77	2103.29	19	2.4	526.831	4	39.6915			ZKD_1.raw	P62852|RS25_MOUSE			FALSE
AAYLWVGAGASEAEK	41.82	1521.75	15	5	761.884	2	31.5961	2.47E+05	5.46E+06	ZKD_1.raw	P13020|GELS_MOUSE;#CONTAM#Q3SX14			FALSE
AAYLWVGAGASEAEKT	47.27	1622.79	16	-0.2	812.404	2	32.2156	4.35E+06	5.31E+07	ZKD_1.raw	P13020|GELS_MOUSE;#CONTAM#Q3SX14			FALSE
ADFHYAASKALRVPA	59.25	1615.85	15	2.3	539.624	3	25.5986	6.53E+05	1.12E+07	ZKD_1.raw	Q80TA9|EPG5_MOUSE			FALSE
ADGYEPPVQESV	25.24	1289.58	12	-0.2	645.796	2	26.6434	4.40E+05	1.00E+07	ZKD_1.raw	P97351|RS3A_MOUSE			FALSE
AFRVPTPNVSVVD	38.27	1399.75	13	-2.3	700.879	2	35.2806	1.25E+06	9.34E+06	ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
AGIEGPLLASEVERDK	24.76	1682.88	16	0.8	561.969	3	29.3766	1.67E+05	3.86E+06	ZKD_1.raw	Q9QX47|SON_MOUSE			FALSE
AGKVRGQTPKVAKQEKK	24.43	1852.1	17	-0.2	618.374	3	8.1561	8.96E+04	2.13E+06	ZKD_1.raw	P62862|RS30_MOUSE			FALSE
AGKVRGQTPKVAKQEKKK	48.08	1980.2	18	-0.2	496.056	4	7.6288	1.26E+07	1.22E+08	ZKD_1.raw	P62862|RS30_MOUSE			FALSE
AGKVRGQTPKVAKQEKKKK	32.83	2108.29	19	-0.1	703.771	3	7.2913	1.98E+06	2.25E+07	ZKD_1.raw	P62862|RS30_MOUSE			FALSE
AIFARGPQAHLVHG	39.7	1472.8	14	1.7	491.942	3	24.0376	1.89E+06	2.66E+07	ZKD_1.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
AKGLFRAAVPSGAST	21.88	1431.78	15	-0.7	478.268	3	22.6371	2.35E+05	7.65E+06	ZKD_1.raw	P17183|ENOG_MOUSE;P17182|ENOA_MOUSE			FALSE
AKIKARDLRGKKKEELLKQL	36.05	2364.47	20	0.1	592.125	4	16.6636	1.13E+06	2.26E+07	ZKD_1.raw	Q6ZWV7|RL35_MOUSE			FALSE
AKKGGEKKKGRSAINEVVTR	32.25	2155.25	20	0.1	432.058	5	10.7266	2.91E+06	8.78E+07	ZKD_1.raw	P62900|RL31_MOUSE			FALSE
AKPKVAKAKKVAAKKK	38.46	1693.15	16	-1.1	339.636	5	6.7695	1.52E+06	5.44E+07	ZKD_1.raw	P15864|H12_MOUSE			FALSE
AKPVSQMRM(+15.99)ATPLLMRPM	31.77	2073.07	18	1	692.032	3	28.4877	4.81E+05	8.55E+06	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M)	9:Oxidation (M):0.0	FALSE
AKPVSQMRMATPLLM(+15.99)RPM(+15.99)	21.25	2089.07	18	1.3	697.364	3	26.4111	5.97E+05	1.11E+07	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M); Oxid	M):19.48;M18:Oxid	FALSE
AKPVSQMRMATPLLMRPM	40.24	2057.08	18	0.5	686.7	3	32.9253	4.88E+06	6.48E+07	ZKD_1.raw	P04441|HG2A_MOUSE			FALSE
AKPVSQMRMATPLLMRPM(+15.99)	39.79	2073.07	18	1	692.032	3	29.5857	2.73E+06	2.63E+07	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M)	8:Oxidation (M):19	FALSE
ALKAKKAVLKGVHSHKK	45.1	1842.17	17	-1.1	615.063	3	9.6559	1.08E+05	3.53E+06	ZKD_1.raw	P62751|RL23A_MOUSE			FALSE
ALYSFKAARALLDHR	24.86	1730.96	15	-1.2	433.746	4	29.8709			ZKD_1.raw	Q9WTN3|SRBP1_MOUSE			FALSE
AMGIMNSFVNDIFER	53.03	1742.81	15	1.5	872.415	2	51.3111	2.27E+05	4.47E+06	ZKD_1.raw	Q8CGP2|H2B1P_MOUSE;Q64525|H2B2B_MOUSE;Q6			FALSE
AMLQVLGPKPALPEG	38.67	1519.84	15	1.1	760.93	2	37.4826			ZKD_1.raw	P13020|GELS_MOUSE			FALSE
APDTRFVAPGALG	39.63	1270.67	13	-2.2	636.339	2	29.3923	6.94E+05	9.08E+06	ZKD_1.raw	Q3U2C5|RN149_MOUSE			FALSE
APDTRFVAPGALGNAPW	53.12	1738.88	17	4.4	870.451	2	40.908	2.07E+06	1.93E+07	ZKD_1.raw	Q3U2C5|RN149_MOUSE			FALSE
APGGYVAPKAVWLPA	44.14	1495.82	15	0.2	748.917	2	38.3196	2.52E+06	2.66E+07	ZKD_1.raw	Q9DBG3|AP2B1_MOUSE			FALSE
APM(+15.99)YYRGAQAAIVV	35.75	1524.78	14	-1.1	763.394	2	29.9404	1.33E+06	9.63E+06	ZKD_1.raw	P61021|RAB5B_M	Oxidation (M)		FALSE
APM(+15.99)YYRGAQAAIVVY	36.85	1687.84	15	-0.4	844.927	2	32.2139	1.43E+07	9.89E+07	ZKD_1.raw	P61021|RAB5B_M	Oxidation (M)		FALSE
APM(+15.99)YYRGAQAAIVVYD	43.24	1802.87	16	0.4	902.441	2	31.1583	2.36E+07	1.51E+08	ZKD_1.raw	P61021|RAB5B_M	Oxidation (M)		FALSE
APMYYRGAQAAIVV	40.58	1508.78	14	0.8	755.398	2	32.8356	2.38E+06	3.39E+07	ZKD_1.raw	P61021|RAB5B_MOUSE;Q9CQD1|RAB5A_MOUSE;P3			FALSE
APMYYRGAQAAIVVY	43.14	1671.84	15	-0.5	836.929	2	34.8395	2.27E+07	2.40E+08	ZKD_1.raw	P61021|RAB5B_MOUSE;Q9CQD1|RAB5A_MOUSE;P3			FALSE
APMYYRGAQAAIVVYD	47.97	1786.87	16	0.3	894.443	2	33.7511	3.44E+07	3.45E+08	ZKD_1.raw	P61021|RAB5B_MOUSE;Q9CQD1|RAB5A_MOUSE;P3			FALSE
APMYYRGSAAAIIVYD	30.57	1759.86	16	1.1	880.938	2	35.9451	2.82E+05	7.42E+06	ZKD_1.raw	P35285|RB22A_MOUSE			FALSE
APPLPIKTPIPTPS	39.82	1427.84	14	1.7	714.928	2	38.0883			ZKD_1.raw	Q7TQH7|LRP10_MOUSE			FALSE
APPLPIKTPIPTPST	55.86	1528.89	15	-1.5	765.449	2	38.1006	1.99E+06	1.69E+07	ZKD_1.raw	Q7TQH7|LRP10_MOUSE			FALSE
APPLPIKTPIPTPSTLP	44.84	1739.02	17	-0.3	870.519	2	44.6847	6.92E+05	5.59E+06	ZKD_1.raw	Q7TQH7|LRP10_MOUSE			FALSE
APPLPIKTPIPTPSTLPA	47.08	1810.06	18	1.5	906.039	2	43.7188	4.83E+05	5.60E+06	ZKD_1.raw	Q7TQH7|LRP10_MOUSE			FALSE
APQ(+0.98)GSLGEYLFERLTLKHD	28.48	2174.1	19	8.9	544.537	4	42.4784	3.33E+05	5.51E+06	ZKD_1.raw	P29391|FRIL1_MO	Deamidation (NQ)		FALSE
APQGSLGEYLFERLTLKHD	42.11	2173.12	19	6.7	544.29	4	42.4838			ZKD_1.raw	P29391|FRIL1_MOUSE			FALSE
APSNYLNN(+0.98)PYVRKALHIPE	22.05	2196.13	19	9.3	733.058	3	36.2086			ZKD_1.raw	P16675|PPGB_MO	Deamidation (NQ)	Deamidation (NQ):(	FALSE
APSNYLNNPYVRKALHIPE	39.31	2195.15	19	0.8	732.724	3	36.2223	3.61E+06	3.32E+07	ZKD_1.raw	P16675|PPGB_MOUSE			FALSE
ARTKQTARKSTGGKAPRK	43.27	1941.13	18	0.8	486.291	4	6.1898	4.54E+05	1.08E+07	ZKD_1.raw	P68433|H31_MOUSE;P84244|H33_MOUSE;P84228|H3			FALSE
ASKPKATKAKKAAPR	37.96	1551.96	15	0.6	518.327	3	6.5634	5.44E+04	1.63E+06	ZKD_1.raw	P43277|H13_MOUSE			FALSE
ASKPKATKAKKAAPRKK	41.41	1808.15	17	-0.5	453.044	4	6.1389	2.78E+06	4.76E+07	ZKD_1.raw	P43277|H13_MOUSE			FALSE
ASLVYENASAIMAHE	50.57	1604.75	15	-0.8	803.382	2	34.3184	4.32E+05	7.56E+06	ZKD_1.raw	E9Q0N2|PTPRH_MOUSE			FALSE
ASLVYENASAIMAHES	45.65	1691.78	16	0.9	846.899	2	33.6599			ZKD_1.raw	E9Q0N2|PTPRH_MOUSE			FALSE
ATDDVFSPSHAIPIET	35.5	1698.81	16	-0.4	850.412	2	37.3927	1.34E+05	2.92E+06	ZKD_1.raw	Q91ZH7|ABHD3_MOUSE			FALSE
ATLEIKGPQADLIDA	33.27	1553.83	15	1.2	777.923	2	35.564	4.59E+05	6.63E+06	ZKD_1.raw	Q8CAS9|PARP9_MOUSE			FALSE
ATLEIKGPQADLIDAV	37.61	1652.9	16	0.1	827.457	2	40.4736	6.63E+05	8.27E+06	ZKD_1.raw	Q8CAS9|PARP9_MOUSE			FALSE
ATNPIITPVAQENQ	48.4	1494.77	14	0.6	748.392	2	29.4577	1.25E+06	1.30E+07	ZKD_1.raw	P08226|APOE_MOUSE			FALSE
AVGKNKRLTKGGKKGA	23.99	1611.99	16	0.4	404.005	4	6.7517	2.92E+05	9.95E+06	ZKD_1.raw	P97351|RS3A_MOUSE			FALSE
AVGKNKRLTKGGKKGAK	31.63	1740.08	17	-0.2	436.028	4	6.2388	5.31E+06	1.13E+08	ZKD_1.raw	P97351|RS3A_MOUSE			FALSE
AYVRLAPDYDALDVANK	54.3	1892.96	17	0.3	631.995	3	32.6837			ZKD_1.raw	P62751|RL23A_MOUSE			FALSE
CADAVLLELRKHLPKYYGV	21.34	2187.19	19	6.6	547.808	4	34.5775			ZKD_1.raw	Q7TT16|IPMK_MOUSE			FALSE
DALDVANKIGII	41.15	1240.7	12	-0.1	621.359	2	43.4145	2.02E+06	2.11E+07	ZKD_1.raw	P62751|RL23A_MOUSE			FALSE
DARSYTAAVANRAK	45.16	1492.77	14	-0.2	498.599	3	16.1112	8.57E+05	1.59E+07	ZKD_1.raw	Q91XS1|MTMR4_MOUSE			FALSE
DARSYTAAVANRAKGGG	48.27	1663.84	17	-0.9	555.62	3	17.433	3.07E+06	4.38E+07	ZKD_1.raw	Q91XS1|MTMR4_MOUSE			FALSE
DEATRYLAPTILTDVDPN	47.42	2002.98	18	1.6	1002.5	2	43.7782	5.72E+05	7.66E+06	ZKD_1.raw	P47740|AL3A2_MOUSE			FALSE
DEGERYIAPTVLVDVQ	43.91	1802.91	16	-1.1	902.459	2	40.6104	1.76E+05	2.79E+06	ZKD_1.raw	Q80VQ0|AL3B1_MOUSE;E9Q3E1|AL3B2_MOUSE;J3Q			FALSE
DEGERYIAPTVLVDVQE	48.75	1931.95	17	0.6	966.982	2	40.6897	1.19E+06	1.64E+07	ZKD_1.raw	Q80VQ0|AL3B1_MOUSE;E9Q3E1|AL3B2_MOUSE;J3Q			FALSE
DEVAASAILTAQL	42.03	1300.69	13	1.6	651.352	2	46.7485	5.97E+05	6.97E+06	ZKD_1.raw	P13020|GELS_MOUSE;#CONTAM#Q3SX14			FALSE
DFLAGGVAAAISK	43.76	1218.66	13	-1.5	610.337	2	37.3915	6.86E+04	2.16E+06	ZKD_1.raw	P51881|ADT2_MOUSE			FALSE
DGDSYRSPWSNKYDPP	46.61	1882.81	16	-0.1	628.611	3	26.3258	1.67E+06	2.30E+07	ZKD_1.raw	P47757|CAPZB_MOUSE			FALSE
DGDSYRSPWSNKYDPPL	42.6	1995.9	17	0.4	666.306	3	32.8386	8.76E+06	5.62E+07	ZKD_1.raw	P47757|CAPZB_MOUSE			FALSE
DLLYSFPVVIKNKT	36.48	1635.92	14	-2.8	546.314	3	40.6267	3.02E+05	2.78E+06	ZKD_1.raw	P14152|MDHC_MOUSE			FALSE
DLSSGLGVTRQELGQVT	45.21	1758.91	17	1.4	880.464	2	36.0244	1.15E+05	3.88E+06	ZKD_1.raw	P04441|HG2A_MOUSE			FALSE
DLSSGLGVTRQELGQVTL	51.54	1872	18	-0.5	937.004	2	43.4451	1.12E+06	1.46E+07	ZKD_1.raw	P04441|HG2A_MOUSE			FALSE
DLSYQSSLASWNYN	27.02	1646.72	14	-4.8	824.364	2	40.8612	7.66E+04	2.62E+06	ZKD_1.raw	Q8R0I0|ACE2_MOUSE			FALSE
DLTGGYRYPRALEEEV	22.86	1866.91	16	0.3	934.463	2	32.5942			ZKD_1.raw	Q8K3K8|OPTN_MOUSE			FALSE
DLTGGYRYPRALEEEVE	24.2	1995.95	17	1	666.326	3	32.0369			ZKD_1.raw	Q8K3K8|OPTN_MOUSE			FALSE
DNDNIFLSPLSIST	26.99	1534.75	14	-3.8	768.38	2	54.23			ZKD_1.raw	P32261|ANT3_MOUSE			FALSE
DNDNIFLSPLSISTA	37.44	1605.79	15	-0.6	803.901	2	54.6118	3.07E+05	6.46E+06	ZKD_1.raw	P32261|ANT3_MOUSE			FALSE
DPIQKYLTPQM(+15.99)ATSIT	34.57	1821.92	16	-4	911.963	2	34.8861			ZKD_1.raw	Q6P9J9|ANO6_M	Oxidation (M)		FALSE
DPIQKYLTPQMATSIT	54.91	1805.92	16	-1	903.968	2	40.2547	1.94E+06	1.56E+07	ZKD_1.raw	Q6P9J9|ANO6_MOUSE			FALSE
DPSLGIYNSPYIIPGSK	47.99	1819.94	17	2	910.977	2	40.7066	8.00E+04	2.65E+06	ZKD_1.raw	P18894|OXDA_MOUSE			FALSE
DPTFHTPLDLYAYAR	49.28	1778.86	15	0.8	593.962	3	41.0891	8.67E+05	8.28E+06	ZKD_1.raw	Q07797|LG3BP_MOUSE			FALSE
DPTTAFQAPDVGQAL	30.13	1529.74	15	0.2	765.876	2	41.9495			ZKD_1.raw	A2ASQ1|AGRIN_MOUSE			FALSE
DRKIVYEGPELNHAFG	52.28	1843.92	16	-0.6	615.648	3	28.2078	3.13E+07	2.45E+08	ZKD_1.raw	Q91ZX7|LRP1_MOUSE			FALSE
DSHGAIVDGPVPITIEVK	49.97	1845.98	18	1.9	616.336	3	37.8649	1.30E+05	2.72E+06	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
DSHGAIVDGPVPITIEVKD	51.35	1961.01	19	-1.6	654.676	3	37.9764	3.13E+05	6.42E+06	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
DSPNKLYTLVTYVPVTTFK	52.4	2185.17	19	-0.2	729.396	3	46.7485	1.66E+06	1.89E+07	ZKD_1.raw	P62900|RL31_MOUSE			FALSE
DSRLVLEVAQHLGESTVRT	33.32	2109.12	19	-1.3	704.046	3	38.9593			ZKD_1.raw	P56480|ATPB_MOUSE			FALSE
DTEGRLEVVTDPTTNAGYVK	33.9	2164.06	20	2.3	722.364	3	27.5963			ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
DTIEFRGPNGLLVYQ	44.17	1720.88	15	0.8	861.447	2	41.5745	2.66E+06	3.57E+07	ZKD_1.raw	Q9DCN2|NB5R3_MOUSE			FALSE
DTIEFRGPNGLLVYQG	39.81	1777.9	16	0.4	889.958	2	41.5745	1.59E+07	1.72E+08	ZKD_1.raw	Q9DCN2|NB5R3_MOUSE			FALSE
DTIEFRGPNGLLVYQGK	50.69	1905.99	17	0.5	636.339	3	35.9787	1.54E+06	2.53E+07	ZKD_1.raw	Q9DCN2|NB5R3_MOUSE			FALSE
DTKVVFLSPAVPEEPE	54.78	1755.89	16	2.4	878.956	2	39.6828	6.05E+05	8.48E+06	ZKD_1.raw	B2RXS4|PLXB2_MOUSE			FALSE
DVAIFARGPQAHLVH	25.56	1629.87	15	-4.8	544.296	3	28.4065			ZKD_1.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
DVAIFARGPQAHLVHG	36.3	1686.9	16	-0.4	563.306	3	28.3655	2.73E+06	2.63E+07	ZKD_1.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
DVAIFARGPQAHLVHGVQ	45.57	1914.02	18	-0.2	639.015	3	29.8021	3.51E+06	3.37E+07	ZKD_1.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
DVYKIGGIGTVPVG	24.01	1373.76	14	0.7	687.886	2	37.4842	8.81E+04	3.42E+06	ZKD_1.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
EDLSYQSSLASWNYN	52.93	1775.76	15	0.9	888.89	2	39.035	4.02E+06	4.73E+07	ZKD_1.raw	Q8R0I0|ACE2_MOUSE			FALSE
EDVAIFARGPQAHLVHGVQ	43.27	2043.06	19	1.1	682.03	3	29.3923	9.10E+05	1.13E+07	ZKD_1.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
EFQAWKSPGASLLPV	41.96	1628.86	15	0.4	815.436	2	44.5349	8.14E+05	1.22E+07	ZKD_1.raw	Q8VC30|TKFC_MOUSE			FALSE
EFYSASVAEDATLG	33.97	1458.65	14	0.4	730.333	2	35.5975	8.92E+05	1.20E+07	ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
EGERYIAPTVLVDVQ	39.34	1687.88	15	-0.5	844.946	2	38.1759			ZKD_1.raw	Q80VQ0|AL3B1_MOUSE;E9Q3E1|AL3B2_MOUSE;J3Q			FALSE
EGERYIAPTVLVDVQE	46.27	1816.92	16	0.3	909.468	2	38.2904	3.10E+05	8.49E+06	ZKD_1.raw	Q80VQ0|AL3B1_MOUSE;E9Q3E1|AL3B2_MOUSE;J3Q			FALSE
EGRLRFHGSGALRVGSQ	28.21	1825.97	17	0.3	457.499	4	18.6803			ZKD_1.raw	Q99JB7|AMNLS_MOUSE			FALSE
EKPVPAAPVPSPVAPAPV	36.58	1721.97	18	1.4	861.994	2	34.069			ZKD_1.raw	P97825|JUPI1_MOUSE			FALSE
EKPVPAAPVPSPVAPAPVP	49.79	1819.02	19	-0.4	910.519	2	35.5316	6.66E+05	7.38E+06	ZKD_1.raw	P97825|JUPI1_MOUSE			FALSE
EKPVPAAPVPSPVAPAPVPS	24.63	1906.06	20	0	954.035	2	33.6005			ZKD_1.raw	P97825|JUPI1_MOUSE			FALSE
ELEEQLGPVAEETR	44.94	1598.78	14	0.9	800.397	2	26.6127	1.52E+06	2.24E+07	ZKD_1.raw	P08226|APOE_MOUSE			FALSE
ELEEQLGPVAEETRA	45.69	1669.82	15	1	835.916	2	28.0542	3.25E+06	3.57E+07	ZKD_1.raw	P08226|APOE_MOUSE			FALSE
ENIWKAPEPVEIR	43.26	1579.84	13	-0.1	527.619	3	30.7909	7.15E+05	1.19E+07	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
ENIWKAPEPVEIRE	38	1708.88	14	1.2	570.634	3	31.0944	5.80E+06	7.12E+07	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
EPPPAYEPPAPAPAPLPP	40.09	1806.92	18	0.9	904.468	2	38.1973	5.29E+06	2.29E+07	ZKD_1.raw	O35609|SCAM3_MOUSE			FALSE
EPPPAYEPPAPAPAPLPPP	44.11	1903.97	19	-0.1	635.665	3	39.2801	6.73E+07	5.78E+08	ZKD_1.raw	O35609|SCAM3_MOUSE			FALSE
EPYGARYVGSMVADVHR	45.62	1905.92	17	-2.4	636.311	3	27.7418	6.30E+05	7.36E+06	ZKD_1.raw	P70695|F16P2_MOUSE			FALSE
ERASFITPVPGGVG	39.11	1385.73	14	2.3	693.874	2	32.4877	1.79E+05	4.04E+06	ZKD_1.raw	Q922D8|C1TC_MOUSE			FALSE
ERASFITPVPGGVGP	32.76	1482.78	15	5.3	742.403	2	34.9297	4.13E+05	5.03E+06	ZKD_1.raw	Q922D8|C1TC_MOUSE			FALSE
ERASFITPVPGGVGPM	38.01	1613.82	16	-0.4	807.919	2	38.7711			ZKD_1.raw	Q922D8|C1TC_MOUSE			FALSE
ESEPYTFSHPNKGEIG	53.96	1790.81	16	0	896.413	2	21.6003	4.58E+05	1.47E+07	ZKD_1.raw	Q5U462|CDCP1_MOUSE			FALSE
EVPAVGIVPPPPILS	26.94	1483.87	15	4.7	742.943	2	52.1006	1.27E+05	2.24E+06	ZKD_1.raw	O70133|DHX9_MOUSE			FALSE
EVSLADLQNDEVAFR	37.82	1704.83	15	2.4	853.425	2	38.8286			ZKD_1.raw	P97351|RS3A_MOUSE			FALSE
EVSSVEAPSVSPAR	42.18	1413.71	14	-4.8	707.859	2	20.2187	1.85E+06	3.03E+07	ZKD_1.raw	Q8BUJ9|LRP12_MOUSE			FALSE
EVSSVEAPSVSPARHQ	49.44	1678.83	16	-1.2	560.616	3	17.4776			ZKD_1.raw	Q8BUJ9|LRP12_MOUSE			FALSE
EWKDYKAGFGNLERE	54.58	1840.87	15	-0.8	614.632	3	25.4986	6.80E+05	1.20E+07	ZKD_1.raw	P12804|FGL2_MOUSE			FALSE
FAKLVRPPVQVY	27.23	1415.83	12	0	472.95	3	30.2014			ZKD_1.raw	Q9DB20|ATPO_MOUSE			FALSE
FAKLVRPPVQVYG	47.9	1472.85	13	0	491.957	3	29.4242	2.58E+06	2.09E+07	ZKD_1.raw	Q9DB20|ATPO_MOUSE			FALSE
FAKLVRPPVQVYGIEGR	39.93	1928.1	17	0.8	643.708	3	30.3507			ZKD_1.raw	Q9DB20|ATPO_MOUSE			FALSE
FGPYYTEPVIAGLDPK	48.29	1765.89	16	-0.7	883.953	2	41.3412			ZKD_1.raw	Q9R1P1|PSB3_MOUSE			FALSE
FIEKVIPSTANSNNL	23.24	1645.87	15	0.7	823.942	2	31.8618			ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
FIREFYSASVAEDATL	42.71	1817.88	16	0.2	909.949	2	38.742	9.76E+04	2.37E+06	ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
FIREFYSASVAEDATLG	50.42	1874.91	17	1	938.461	2	37.5965	1.02E+06	1.41E+07	ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
FPKPPSYNVATTLPSYD	31.57	1895.93	17	1.8	948.974	2	36.6015	1.55E+06	1.39E+07	ZKD_1.raw	Q8R0W6|NFIP1_MOUSE			FALSE
FPKPPSYNVATTLPSYDE	41.39	2024.97	18	0.5	1013.49	2	36.2482	2.75E+07	1.82E+08	ZKD_1.raw	Q8R0W6|NFIP1_MOUSE			FALSE
FPKPPSYNVATTLPSYDEA	46.62	2096.01	19	-0.5	1049.01	2	36.8803	7.80E+06	5.52E+07	ZKD_1.raw	Q8R0W6|NFIP1_MOUSE			FALSE
FPTDYPFKPPKVAFTTR	28.26	2011.06	17	-0.8	503.771	4	35.0102			ZKD_1.raw	P61079|UB2D3_MOUSE			FALSE
FPYVTPAPHEPV	50.71	1352.68	12	-0.9	677.345	2	32.0018	1.61E+06	2.61E+07	ZKD_1.raw	Q9D074|MGRN1_MOUSE			FALSE
FPYVTPAPHEPVK	51.44	1480.77	13	0.1	494.598	3	25.0511	1.74E+07	1.65E+08	ZKD_1.raw	Q9D074|MGRN1_MOUSE			FALSE

FPYVTPAPHEPVKT	53.09	1581.82	14	1.1	528.281	3	26.0381	1.52E+06	2.19E+07	ZKD_1.raw	Q9D074|MGRN1_MOUSE		FALSE
FRPAHQAPMAQTTIH	43.94	1704.85	15	0.3	569.291	3	16.7149	2.82E+05	9.00E+06	ZKD_1.raw	O08573|LEG9_MOUSE		FALSE
FRVNFVDPAASSSADD	54.77	1696.77	16	-1.2	849.391	2	34.8395	3.53E+06	3.33E+07	ZKD_1.raw	P55012|S12A2_MOUSE		FALSE
FTAQWIAPSVQLTGYR	24.97	1836.95	16	1.7	919.485	2	42.4345	4.93E+04	1.74E+06	ZKD_1.raw	P11276|FINC_MOUSE		FALSE
FTYQQPQPLSVEPR	52.87	1688.85	14	1.3	845.435	2	29.5227	7.93E+05	1.36E+07	ZKD_1.raw	B2RXS4|PLXB2_MOUSE		FALSE
FVAPAVTPVKGVL	51.75	1296.78	13	1.2	649.398	2	38.2597	3.31E+05	6.10E+06	ZKD_1.raw	P70158|ASM3A_MOUSE		FALSE
GAIVDGPVPITIEVKD	51.08	1621.89	16	0.5	811.954	2	40.3013	9.38E+04	3.22E+06	ZKD_1.raw	Q9R100|CAD17_MOUSE		FALSE
GDLEYQMSTTARAK	47.64	1569.75	14	0.5	524.256	3	18.74	4.96E+05	1.62E+07	ZKD_1.raw	Q02257|PLAK_MOUSE		FALSE
GDLEYQMSTTARAKR	38.42	1725.85	15	-0.6	576.289	3	16.9257	1.10E+06	2.47E+07	ZKD_1.raw	Q02257|PLAK_MOUSE		FALSE
GDLSQHATPLPTPAVLPG	47.66	1769.93	18	-0.2	885.973	2	37.8495	3.36E+06	2.91E+07	ZKD_1.raw	O88746|TOM1_MOUSE		FALSE
GDTIEFRGPNGLLVYQG	52.36	1834.92	17	0.4	918.468	2	40.1978	1.32E+06	1.71E+07	ZKD_1.raw	Q9DCN2|NB5R3_MOUSE		FALSE
GDTIEFRGPNGLLVYQGK	46.94	1963.02	18	1.8	655.347	3	34.8993	1.40E+06	1.86E+07	ZKD_1.raw	Q9DCN2|NB5R3_MOUSE		FALSE
GEDVAIFARGPQAHLVHGVQ	39.54	2100.09	20	-1	701.035	3	29.4086	2.02E+05	6.61E+06	ZKD_1.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE		FALSE
GERFEAPEALFQPH	41.28	1626.78	14	-1.1	543.266	3	32.837	4.16E+05	7.22E+06	ZKD_1.raw	P61161|ARP2_MOUSE		FALSE
GGEDVAIFARGPQAHLVHG	30.69	1929.98	19	0.4	644.335	3	28.4563	1.94E+05	3.60E+06	ZKD_1.raw	P24822|PPBI_MOUSE		FALSE
GGLPDYSAPNPIKVTH	45.6	1664.85	16	1.8	555.959	3	28.3033	1.51E+06	2.47E+07	ZKD_1.raw	Q8CFG0|SULF2_MOUSE		FALSE
GGLPDYSAPNPIKVTHR	59.68	1820.95	17	-0.9	456.245	4	25.0529	2.17E+06	3.76E+07	ZKD_1.raw	Q8CFG0|SULF2_MOUSE		FALSE
GGVAAGVAVLDNPYPV	44.04	1497.78	16	1.1	749.9	2	43.7633	7.03E+04	2.56E+06	ZKD_1.raw	P51855|GSHB_MOUSE		FALSE
GHEVVVIAPEASIHIK	32.83	1697.95	16	-1.9	566.988	3	28.5131			ZKD_1.raw	Q63886|UD11_MOUSE		FALSE
GIDPYDQPNAIYIER	53.01	1762.85	15	0.4	882.434	2	32.6801	1.24E+06	1.86E+07	ZKD_1.raw	O88307|SORL_MOUSE		FALSE
GIYVSEKGTVQQADE	46.55	1622.78	15	2.7	812.399	2	19.9718			ZKD_1.raw	P51410|RL9_MOUSE		FALSE
GKLTGMAFRVPTPNVSVVD	47.16	1987.06	19	1.3	663.36	3	37.7866	2.99E+06	2.19E+07	ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE		FALSE
GKNKRLTKGGKKGAK	36.57	1569.98	15	-0.7	393.502	4	6.2442			ZKD_1.raw	P97351|RS3A_MOUSE		FALSE
GKQKKTRKYATMKR	26.05	1723	14	0.4	431.758	4	7.2737	1.44E+05	4.36E+06	ZKD_1.raw	Q9CTH6|FCF1_MOUSE		FALSE
GKTAWVGSLASGVGL	29.93	1401.76	15	3.1	701.89	2	40.0621	6.01E+04	2.00E+06	ZKD_1.raw	Q7TM99|MOT9_MOUSE		FALSE
GKVRGQTPKVAKQEKKK	49.21	1909.16	17	1	637.394	3	7.4211	3.60E+05	5.63E+06	ZKD_1.raw	P62862|RS30_MOUSE		FALSE
GKYTYGKPVPGHVK	46.21	1529.84	14	0.2	383.466	4	12.528	1.05E+06	1.02E+07	ZKD_1.raw	P28665|MUG1_MOUSE		FALSE
GKYTYGKPVPGHVKI	57.11	1642.92	15	1.2	411.738	4	18.1624	1.96E+06	2.15E+07	ZKD_1.raw	P28665|MUG1_MOUSE		FALSE
GLKGRVFEVSLA	32.49	1274.73	12	0.3	638.375	2	29.925	6.48E+05	1.28E+07	ZKD_1.raw	P97351|RS3A_MOUSE		FALSE
GLKGRVFEVSLADLQN	21.27	1744.95	16	1.8	582.657	3	35.564	1.19E+05	2.68E+06	ZKD_1.raw	P97351|RS3A_MOUSE		FALSE
GLPDYSAPNPIKVT	44.32	1470.77	14	0.2	736.393	2	32.5864	2.68E+05	5.52E+06	ZKD_1.raw	Q8CFG0|SULF2_MOUSE		FALSE
GLPDYSAPNPIKVTH	51.24	1607.83	15	-0.8	536.95	3	28.1442	2.59E+06	3.26E+07	ZKD_1.raw	Q8CFG0|SULF2_MOUSE		FALSE
GLVPIVEPEVLPDGDH	46.54	1684.87	16	0.3	843.441	2	43.4733	4.12E+05	7.90E+06	ZKD_1.raw	Q91Y97|ALDOB_MOUSE		FALSE
GLVPIVEPEVLPDGDHD	47.08	1799.89	17	0	900.954	2	43.6048			ZKD_1.raw	Q91Y97|ALDOB_MOUSE		FALSE
GM(+15.99)AFRVPTPNVSVVD	43.3	1603.8	15	1.4	802.91	2	35.8224	1.39E+07	8.35E+07	ZKD_1.raw	P16858|G3P_MOU	Oxidation (M)	FALSE
GMAFRVPTPNVSVV	45	1472.78	14	-0.7	737.397	2	41.0891	4.88E+05	4.83E+06	ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE		FALSE
GMAFRVPTPNVSVVD	53.34	1587.81	15	0.4	794.912	2	39.6166	2.13E+07	1.21E+08	ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE		FALSE
GNMIVIVLGHHLGK	20.46	1486.84	14	-1.5	496.621	3	34.3156			ZKD_1.raw	P02088|HBB1_MOUSE		FALSE
GNPLNSVFVAPAVTPVK	48.08	1708.95	17	0.5	855.483	2	41.4342	9.06E+04	2.21E+06	ZKD_1.raw	P70158|ASM3A_MOUSE		FALSE
GPDGRFVM(+15.99)GPTVAPSQ	33.16	1630.78	16	-1	816.395	2	23.7063			ZKD_1.raw	Q05BQ1|TUTLA_M	Oxidation (M)	FALSE
GPDGRFVM(+15.99)GPTVAPSQEK	41.4	1887.91	18	3.1	630.314	3	20.3568	2.51E+05	9.98E+06	ZKD_1.raw	Q05BQ1|TUTLA_M	Oxidation (M)	FALSE
GPDGRFVM(+15.99)GPTVAPSQEKL	36.77	2001	19	5.7	668.011	3	26.4844	9.10E+05	1.58E+07	ZKD_1.raw	Q05BQ1|TUTLA_M	Oxidation (M)	FALSE
GPDGRFVMGPTVAPSQ	42.52	1614.78	16	0.3	808.399	2	28.9871	2.17E+06	3.14E+07	ZKD_1.raw	Q05BQ1|TUTLA_MOUSE		FALSE
GPDGRFVMGPTVAPSQEK	47.01	1871.92	18	0.6	624.981	3	24.587	1.05E+06	2.32E+07	ZKD_1.raw	Q05BQ1|TUTLA_MOUSE		FALSE
GPDGRFVMGPTVAPSQEKL	56.99	1985	19	-3.7	662.673	3	30.4972	2.32E+06	3.75E+07	ZKD_1.raw	Q05BQ1|TUTLA_MOUSE		FALSE
GPKPFSAPKPQTSPS	56.64	1524.79	15	0.6	763.405	2	16.957	3.74E+06	4.65E+07	ZKD_1.raw	P40124|CAP1_MOUSE		FALSE
GPKPFSAPKPQTSPSP	58.76	1621.85	16	1.3	811.932	2	18.8524	8.75E+06	9.39E+07	ZKD_1.raw	P40124|CAP1_MOUSE		FALSE
GPKPFSAPKPQTSPSPK	59.74	1749.94	17	-3.2	584.319	3	15.7748	3.32E+06	6.85E+07	ZKD_1.raw	P40124|CAP1_MOUSE		FALSE
GPKPFSAPKPQTSPSPKP	52.27	1846.99	18	0.1	616.672	3	17.3701	2.09E+07	1.84E+08	ZKD_1.raw	P40124|CAP1_MOUSE		FALSE
GPTYRGPVPWHTIN	41.51	1593.81	14	-0.3	532.276	3	28.2078	5.80E+06	5.38E+07	ZKD_1.raw	Q9WV54|ASAH1_MOUSE		FALSE
GQNAWFLPAQADIVATK	53.03	1828.95	17	0.5	915.481	2	42.9153	2.87E+05	5.84E+06	ZKD_1.raw	P10852|4F2_MOUSE		FALSE
GSDMFKASLVIPSKD	44.58	1593.81	15	0.4	532.277	3	32.5504	4.74E+05	8.09E+06	ZKD_1.raw	Q8BJD1|ITIH5_MOUSE		FALSE
GSILWSQPLPSLPGGPP	48.57	1701.91	17	-0.2	851.962	2	52.323	2.46E+06	2.30E+07	ZKD_1.raw	Q8C0Z1|F234A_MOUSE		FALSE
GSILWSQPLPSLPGGPPS	47.7	1788.94	18	3.6	895.481	2	50.93	4.93E+05	6.74E+06	ZKD_1.raw	Q8C0Z1|F234A_MOUSE		FALSE
GSVLWERPVAQDVAL	47.31	1638.87	15	-1	820.443	2	39.8708			ZKD_1.raw	Q8C0Z1|F234A_MOUSE		FALSE
GTPEYLAPEIILSK	39.16	1529.83	14	-1.9	765.923	2	40.9696	1.34E+05	2.42E+06	ZKD_1.raw	P68181|KAPCB_MOUSE;P05132|KAPCA_MOUSE		FALSE
GTPEYLAPEIILSKG	50.8	1586.86	15	0.9	794.436	2	41.5745	1.78E+06	1.94E+07	ZKD_1.raw	P68181|KAPCB_MOUSE;P05132|KAPCA_MOUSE		FALSE
GVYTYGKPVPGLVT	39.55	1449.79	14	1.3	725.902	2	31.8292	2.03E+05	4.29E+06	ZKD_1.raw	Q61838|PZP_MOUSE		FALSE
GYAVYETPTAHNGAKNPR	54.6	1944.94	18	3.2	649.324	3	15.5328	4.58E+05	7.99E+06	ZKD_1.raw	Q9QZ06|TOLIP_MOUSE		FALSE
HDTSYKPPAGRTAAPE	36.41	1696.82	16	-0.1	849.416	2	12.8901	6.43E+05	9.44E+06	ZKD_1.raw	Q69ZQ1|MYORG_MOUSE		FALSE
HEAGDMMGGHAIRILG	43.24	1663.79	16	-5.4	555.602	3	27.8427			ZKD_1.raw	P10605|CATB_MOUSE		FALSE
HEVVVIAPEASIHIK	52.56	1640.92	15	-1.4	547.982	3	28.4261	1.24E+06	1.72E+07	ZKD_1.raw	Q63886|UD11_MOUSE		FALSE
HGAIVDGPVPITIEV	38.09	1515.83	15	1	758.923	2	44.1588	1.20E+05	2.86E+06	ZKD_1.raw	Q9R100|CAD17_MOUSE		FALSE
HGLYEKKKTSRKQ	40.41	1601.9	13	-0.2	401.482	4	6.9595	1.43E+05	4.59E+06	ZKD_1.raw	P62849|RS24_MOUSE		FALSE
HINIVVIGHVDSGK	50.95	1486.83	14	0.1	496.616	3	24.8932	7.91E+05	1.71E+07	ZKD_1.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE		FALSE
HLKIVYRRFRHGFR	27	1884.09	14	0.6	472.029	4	17.2788	1.92E+07	3.58E+08	ZKD_1.raw	Q9D823|RL37_MOUSE		FALSE
HLKIVYRRFRHGFREG	22.25	2070.15	16	-2.5	518.544	4	17.3701	4.07E+06	3.05E+07	ZKD_1.raw	Q9D823|RL37_MOUSE		FALSE
HNYEGPETHTSLR	44.49	1539.71	13	-0.5	514.243	3	13.2778	1.82E+06	2.51E+07	ZKD_1.raw	P14483|HB2A_MOUSE		FALSE
HRNGIKKPRSQR	38.26	1475.85	12	0.6	369.971	4	6.9732	5.47E+05	8.13E+06	ZKD_1.raw	P47915|RL29_MOUSE		FALSE
HVSHGHGRIGKH	28.23	1320.69	12	-0.6	331.18	4	6.1711	4.56E+05	7.16E+06	ZKD_1.raw	P14115|RL27A_MOUSE		FALSE
IAIYYHASRAIPFG	37.29	1577.84	14	1.6	526.953	3	34.1564	1.98E+05	4.76E+06	ZKD_1.raw	Q9ET30|TM9S3_MOUSE		FALSE
IEFRGPNGLLVYQG	34.56	1561.83	14	0.2	781.92	2	38.6067	2.67E+05	4.51E+06	ZKD_1.raw	Q9DCN2|NB5R3_MOUSE		FALSE
IEKVIPSTANSNNL	42.85	1498.8	14	1.5	750.408	2	24.7508	4.46E+05	1.65E+07	ZKD_1.raw	E9Q7P9|CDHR2_MOUSE		FALSE
IEVSSPITLQAL	44.87	1269.72	12	-0.3	635.866	2	47.277	3.40E+06	3.85E+07	ZKD_1.raw	E9Q414|APOB_MOUSE;#CONTAM#ENSEMBL:ENSBT		FALSE
IEVSSPITLQALVQ	42.29	1496.85	14	1.9	749.431	2	50.0418	1.63E+06	2.26E+07	ZKD_1.raw	E9Q414|APOB_MOUSE		FALSE
IFARGPQAHLVHG	43.06	1401.76	13	-0.4	468.261	3	24.1058	9.24E+06	9.58E+07	ZKD_1.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE		FALSE
IGDSNFGAPSASVAAAPAP	35.31	1698.82	19	-0.5	850.418	2	33.4956	4.07E+05	1.03E+07	ZKD_1.raw	O35643|AP1B1_MOUSE		FALSE
IGDTIEFRGPN(+0.98)GLLVYQGK	41.13	2077.08	19	9.1	693.375	3	36.9592			ZKD_1.raw	Q9DCN2|NB5R3	Deamidation (NQ)	Deamidation (NQ):1	FALSE
IGDTIEFRGPNGLLVYQG	53.17	1948.01	18	0	975.01	2	42.2993	4.94E+05	9.20E+06	ZKD_1.raw	Q9DCN2|NB5R3_MOUSE			FALSE
IGDTIEFRGPNGLLVYQGK	48.56	2076.1	19	-0.5	693.04	3	36.9697	1.18E+06	1.83E+07	ZKD_1.raw	Q9DCN2|NB5R3_MOUSE			FALSE
INIVVIGHVDSGK	44.42	1349.77	13	-0.1	450.929	3	29.0485	3.74E+06	5.33E+07	ZKD_1.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
INIVVIGHVDSGKSTTTGHL	42.59	2047.11	20	1.9	683.377	3	29.4725	1.52E+05	5.11E+06	ZKD_1.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
IPFYTPIPNGLYPS	44.01	1577.81	14	0.2	789.914	2	51.2825	4.97E+06	3.23E+07	ZKD_1.raw	O08573|LEG9_MOUSE			FALSE
IPGTNM(+15.99)YNTDRANPVLD	54.85	1905.89	17	1	953.953	2	26.1375	2.83E+06	2.53E+07	ZKD_1.raw	E9Q7P9|CDHR2_	Oxidation (M)		FALSE
IPGTNM(+15.99)YNTDRANPVLDLP	47.74	2116.03	19	-0.6	1059.02	2	37.755	7.11E+06	3.68E+07	ZKD_1.raw	E9Q7P9|CDHR2_	Oxidation (M)		FALSE
IPGTNM(+15.99)YNTDRANPVLDLPT	41.75	2217.07	20	-3.7	1109.54	2	36.7096	3.65E+05	4.98E+06	ZKD_1.raw	E9Q7P9|CDHR2_	Oxidation (M)		FALSE
IPGTNMYNTDRANPV	50.42	1661.78	15	0.4	831.899	2	25.3389	4.32E+05	7.47E+06	ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IPGTNMYNTDRANPVL	53.72	1774.87	16	1.4	888.442	2	31.5734			ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IPGTNMYNTDRANPVLD	59.99	1889.89	17	0.1	945.955	2	30.1193	1.01E+07	8.32E+07	ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IPGTNMYNTDRANPVLDLP	57.75	2100.03	19	0	1051.02	2	40.6569	1.27E+07	6.68E+07	ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IPGTNMYNTDRANPVLDLPT	51.57	2201.08	20	1.6	1101.55	2	39.5564	1.49E+06	1.55E+07	ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IPIRWTAPEAIAH	30.18	1473.81	13	0.6	492.277	3	32.3366	3.26E+05	5.51E+06	ZKD_1.raw	Q60750|EPHA1_MOUSE			FALSE
IPIRWTAPEAIAHR	27.67	1629.91	14	8	544.315	3	28.8382			ZKD_1.raw	Q60750|EPHA1_MOUSE			FALSE
IPIRWTAPEAISYR	31.84	1671.91	14	-4.3	558.308	3	33.9976	1.15E+06	1.17E+07	ZKD_1.raw	Q03145|EPHA2_MOUSE			FALSE
IPIRWTAPEAISYRK	22.87	1800	15	0.3	451.009	4	29.646	1.35E+06	1.66E+07	ZKD_1.raw	Q03145|EPHA2_MOUSE			FALSE
IPSRYSSPTTIATVM	25.07	1622.83	15	4.4	812.428	2	32.9351			ZKD_1.raw	Q9DBM2|ECHP_MOUSE			FALSE
IQEPYTFPAILKS	35.33	1505.81	13	2.1	753.915	2	40.7862	1.03E+05	2.24E+06	ZKD_1.raw	Q8BFR4|GNS_MOUSE			FALSE
IREFYSASVAEDA	39.89	1456.68	13	-0.2	729.349	2	26.5961	2.49E+05	8.32E+06	ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IREFYSASVAEDAT	43.7	1557.73	14	0.9	779.874	2	26.5472	1.08E+06	2.02E+07	ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IREFYSASVAEDATL	46.63	1670.82	15	-0.4	836.415	2	33.9682	1.86E+07	1.83E+08	ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IREFYSASVAEDATLG	49.96	1727.84	16	1	864.926	2	32.7755	1.44E+07	1.58E+08	ZKD_1.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IRENIWKAPEPVEIR	35.06	1849.02	15	0.9	617.348	3	28.366	2.23E+05	5.02E+06	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
IRENIWKAPEPVEIRE	46.79	1978.06	16	1.1	660.363	3	28.7358	1.67E+06	2.68E+07	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
ISQIFSQAMAARSINR	21.11	1791.94	16	-1.3	598.32	3	29.925	3.92E+05	7.08E+06	ZKD_1.raw	P34914|HYES_MOUSE			FALSE
ISQIFSQAMAARSINRP	22.16	1888.99	17	0.7	630.672	3	31.2227	5.42E+06	6.60E+07	ZKD_1.raw	P34914|HYES_MOUSE			FALSE
ITNQYNSPTGLYSSEN	52.73	1786.8	16	0.9	894.409	2	25.879	3.46E+06	5.01E+07	ZKD_1.raw	O70400|PDLI1_MOUSE			FALSE
ITPSYVAFTPEGER	32.64	1565.77	14	-1.2	783.893	2	31.2358	1.28E+05	4.47E+06	ZKD_1.raw	P20029|BIP_MOUSE			FALSE
ITPSYVAFTPEGERL	38.93	1678.86	15	7.1	840.442	2	37.1883	4.41E+05	6.28E+06	ZKD_1.raw	P20029|BIP_MOUSE			FALSE
ITQVQWNDPGAQYSLVN	45.32	1931.94	17	-0.2	966.976	2	39.1875	2.27E+06	3.05E+07	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
ITQVQWNDPGAQYSLVNK	57.68	2060.03	18	3	687.687	3	33.5101	1.67E+05	5.63E+06	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
ITTDYNSPEAGNIF	39.99	1540.7	14	0.6	771.36	2	36.848	9.66E+05	1.16E+07	ZKD_1.raw	B2RXV4|FLVC1_MOUSE			FALSE
IVSHDYKGSTSHSLPY	33.61	1789.86	16	1.1	597.629	3	18.2026			ZKD_1.raw	E9Q414|APOB_MOUSE			FALSE
K(+42.01)AAKPKKTAAKKK	23.36	1438.93	13	-6.1	480.649	3	10.4538			ZKD_1.raw	P43274|H14_MOU	Acetylation (N-term)		FALSE
K(+42.01)KAKKPAAAGVKKVAKSPKK	22.84	2104.36	20	9.4	421.883	5	9.419	2.13E+06	2.46E+07	ZKD_1.raw	P43276|H15_MOU	Acetylation (N-term)		FALSE
KAAKPKTS(+79.97)KPKAAKP	22.06	1629.93	15	4.9	815.978	2	7.4825			ZKD_1.raw	P43274|H14_MOU	Phosphorylation (S	sphorylation (STY)	FALSE
KAGAAKAKKPAGAAKKPKK	45.06	1848.18	19	-0.2	617.067	3	6.3643	3.90E+05	4.99E+06	ZKD_1.raw	P15864|H12_MOUSE;P43277|H13_MOUSE			FALSE
KARLQHQVT(+79.97)EDGEFW	23.65	1922.87	15	-7	481.721	4	23.5358			ZKD_1.raw	Q64691|CAN3_M	Phosphorylation (STY)		FALSE
KASKPKATKAKKAAPRK	21.5	1808.15	17	-0.1	603.723	3	6.1373	1.84E+06	3.25E+07	ZKD_1.raw	P43277|H13_MOUSE			FALSE
KEGKKPRTKAPKIQRLVTPR	40.3	2330.44	20	1.6	389.414	6	12.9874	1.98E+06	3.07E+07	ZKD_1.raw	P62754|RS6_MOUSE			FALSE
KELEEQLGPVAEETR	47.86	1726.87	15	-0.4	576.632	3	22.6209	2.32E+06	2.86E+07	ZKD_1.raw	P08226|APOE_MOUSE			FALSE
KELEEQLGPVAEETRA	41.28	1797.91	16	3.1	600.313	3	23.8825	7.59E+05	1.34E+07	ZKD_1.raw	P08226|APOE_MOUSE			FALSE
KFTYRGVDLDQLLD	36.91	1681.87	14	-0.9	561.629	3	39.0663	2.51E+06	3.01E+07	ZKD_1.raw	P62843|RS15_MOUSE			FALSE
KFYKGKKYKPLDLRPKKT	65.52	2237.34	18	-0.1	560.343	4	14.3714	5.98E+07	1.29E+09	ZKD_1.raw	Q6ZWV7|RL35_MOUSE			FALSE
KFYKGKKYKPLDLRPKKTR	62.04	2393.44	19	-0.8	479.695	5	13.7617	8.59E+06	2.29E+08	ZKD_1.raw	Q6ZWV7|RL35_MOUSE			FALSE
KHKRKKVKLAVLK	35.2	1575.08	13	0.9	394.778	4	10.9231	6.84E+05	1.79E+07	ZKD_1.raw	P62983|RS27A_MOUSE			FALSE
KHKRKKVKLAVLKYYK	31.49	2029.3	16	0.4	508.334	4	14.3714	6.30E+05	1.29E+07	ZKD_1.raw	P62983|RS27A_MOUSE			FALSE
KIVYEGPELNHAFG	52.06	1572.79	14	1.5	525.273	3	29.4577	4.04E+06	3.15E+07	ZKD_1.raw	Q91ZX7|LRP1_MOUSE			FALSE
KKAAGAGKVTKSAQKAQKAK	37.28	1998.21	20	0.5	667.076	3	7.2733	1.25E+05	4.00E+06	ZKD_1.raw	P10126|EF1A1_MOUSE			FALSE
KKAKAKGKGQPQARVTVNR	29.66	2064.24	19	2.9	689.089	3	8.7666			ZKD_1.raw	Q9D6S7|RRFM_MOUSE			FALSE
KKIEDNNT(+79.97)LVFIVDVKANK	20.7	2267.19	19	-3	567.804	4	31.1745			ZKD_1.raw	P62751|RL23A_M	Phosphorylation (STY)		FALSE
KKKKKKKKPFM(+15.99)L	20.97	1547.01	12	-0.6	387.76	4	10.5457	1.06E+06	9.11E+06	ZKD_1.raw	Q99L45|IF2B_MO	Oxidation (M)		FALSE
KKKKKKKKPFMLD	25.85	1646.04	13	-0.7	412.518	4	11.5892	1.66E+06	1.75E+07	ZKD_1.raw	Q99L45|IF2B_MOUSE			FALSE
KKKKRFSFKKSFK	25.69	1686.05	13	-1.2	422.518	4	11.2501	3.98E+05	1.39E+07	ZKD_1.raw	P26645|MARCS_MOUSE			FALSE
KKKRFSFKKSFK	25.18	1557.95	12	0.8	390.495	4	11.7356	3.50E+05	1.11E+07	ZKD_1.raw	P26645|MARCS_MOUSE			FALSE
KKKWSKGKVRDK	27.1	1486.91	12	0.6	372.735	4	6.5796	3.90E+05	7.00E+06	ZKD_1.raw	P62852|RS25_MOUSE			FALSE
KKLRNKQRRAQKK	19.92	1681.07	13	-5.8	421.272	4	8.8781			ZKD_1.raw	Q80UM3|NAA15_MOUSE			FALSE
KKPAKAAAPRKKP	21.26	1389.89	13	-5	464.303	3	9.2684	8.20E+05	8.94E+06	ZKD_1.raw	P43275|H11_MOUSE			FALSE
KKQKQNRPIPQWIRMK	26.94	2078.2	16	4.5	520.561	4	18.5798			ZKD_1.raw	P62892|RL39_MOUSE			FALSE
KKTPKKAKKPAAAAVTKK	20.58	1893.23	18	1.1	379.653	5	7.192	2.99E+05	2.96E+06	ZKD_1.raw	P15864|H12_MOUSE			FALSE
KKVRGTAKANVGAGKKPKE	48.66	1966.18	19	0.4	492.552	4	7.8065	6.69E+05	1.08E+07	ZKD_1.raw	P62849|RS24_MOUSE			FALSE
KKYKPLDLRPKKTRAM(+15.99)RR	26.3	2300.37	18	-1.9	384.402	6	11.0074	7.18E+05	1.38E+07	ZKD_1.raw	Q6ZWV7|RL35_M	Oxidation (M)		FALSE
KLTGKDVNFEFPEFQL	38.46	1910.98	16	0.2	638	3	43.9007	3.37E+05	6.72E+06	ZKD_1.raw	P62082|RS7_MOUSE			FALSE

KLTGM(+15.99)AFRVPTPNVSVVD	27.59	1946.03	18	2.2	649.685	3	34.0757	2.39E+05	3.21E+06	ZKD_1.raw	P16858|G3P_MOU	Oxidation (M)		FALSE
KLTGMAFRVPTPNVSVVD	30.76	1930.03	18	1.4	644.353	3	37.7869	1.34E+06	1.18E+07	ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
KNLDYVATSIHEAVT	52.69	1659.85	15	-0.2	554.289	3	28.1772	6.50E+05	1.16E+07	ZKD_1.raw	P05201|AATC_MOUSE			FALSE
KPAAAKKTKKPAKA	20.51	1436.92	14	-0.7	479.98	3	9.677			ZKD_1.raw	P43275|H11_MOUSE			FALSE
KPFQNPVPNQSPS	29.74	1438.72	13	4.1	720.37	2	19.3092			ZKD_1.raw	P16382|IL4RA_MOUSE			FALSE
KPKTPAKPKKAAPKKK	33.79	1745.14	16	0.4	582.721	3	6.9143	2.16E+05	5.36E+06	ZKD_1.raw	P43275|H11_MOUSE			FALSE
KPKTSKPKAAKPKKTAAKKK	45.98	2163.39	20	0	722.139	3	6.221	1.03E+05	3.34E+06	ZKD_1.raw	P43274|H14_MOUSE			FALSE
KPPSYNVATTLPSYDE	43.03	1780.85	16	1.9	891.435	2	29.6777	3.63E+05	6.71E+06	ZKD_1.raw	Q8R0W6|NFIP1_MOUSE			FALSE
KPRGEFHTPVTVAGPH	45.34	1728.91	16	0.7	433.234	4	17.7808	7.81E+05	1.47E+07	ZKD_1.raw	Q8JZQ5|AOC1_MOUSE			FALSE
KPVSQM(+15.99)RM(+15.99)ATPLLM(+15.99)RPM	31.03	2034.02	17	-3.9	509.512	4	20.9803	4.91E+06	4.44E+07	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M); Oxi	3:Oxidation (M):46.	FALSE
KPVSQM(+15.99)RM(+15.99)ATPLLMRPM	41.59	2018.03	17	1.9	505.516	4	24.8242	6.41E+06	7.66E+07	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M); Oxi	M):89.48;M8:Oxida	FALSE
KPVSQM(+15.99)RM(+15.99)ATPLLMRPM(+15.99)	39.57	2034.02	17	-3.9	509.512	4	20.9803	4.91E+06	8.87E+07	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M); Oxi	:Oxidation (M):78.1	FALSE
KPVSQM(+15.99)RMATPLLM(+15.99)RPM	34.88	2018.03	17	-0.9	673.683	3	24.8278	1.52E+07	8.54E+07	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M); Oxi	M):18.53;M14:Oxid	FALSE
KPVSQM(+15.99)RMATPLLM(+15.99)RPM(+15.99)	20.86	2034.02	17	-2	679.014	3	20.9472	9.66E+06	8.44E+07	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M); Oxi	:Oxidation (M):17.2	FALSE
KPVSQM(+15.99)RMATPLLMRPM	29.82	2002.03	17	-0.1	501.516	4	27.8345	6.87E+06	8.40E+07	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M)	6:Oxidation (M):0.0	FALSE
KPVSQMRM(+15.99)ATPLLM(+15.99)RPM	33.47	2018.03	17	0.5	673.684	3	24.0376	2.13E+07	1.21E+08	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M); Oxi	M):5.47;M14:Oxida	FALSE
KPVSQMRM(+15.99)ATPLLM(+15.99)RPM(+15.99)	26.73	2034.02	17	-0.2	679.015	3	21.5851	6.63E+06	6.76E+07	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M); Oxi	:Oxidation (M):63.6	FALSE
KPVSQMRM(+15.99)ATPLLMRPM	38.93	2002.03	17	0.6	668.353	3	27.8363	1.64E+07	1.88E+08	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M)	8:Oxidation (M):5.9	FALSE
KPVSQMRMATPLLM(+15.99)RPM	31.48	2002.03	17	0.1	501.516	4	28.6732	1.34E+08	5.83E+08	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M)	14:Oxidation (M):0.	FALSE
KPVSQMRMATPLLM(+15.99)RPM(+15.99)	29.07	2018.03	17	0.9	673.684	3	25.7852	2.90E+07	2.01E+08	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M); Oxi	M):66.64;M17:Oxid	FALSE
KPVSQMRMATPLLMRP	35.29	1855	16	3.3	619.343	3	29.6126	1.99E+06	2.42E+07	ZKD_1.raw	P04441|HG2A_MOUSE			FALSE
KPVSQMRMATPLLMRPM	43.81	1986.04	17	0.3	663.021	3	32.3943	6.30E+07	5.56E+08	ZKD_1.raw	P04441|HG2A_MOUSE			FALSE
KPVSQMRMATPLLMRPM(+15.99)	33.35	2002.03	17	0	501.516	4	28.9841	9.24E+07	5.89E+08	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M)	7:Oxidation (M):19	FALSE
KPYHKKRKYELGRPA	24.25	1870.07	15	-0.9	468.524	4	10.3828	2.51E+05	4.66E+06	ZKD_1.raw	P62242|RS8_MOUSE			FALSE
KRKYSAAKTKVEKK	36.83	1664.01	14	0.7	417.01	4	7.0507	1.66E+05	5.68E+06	ZKD_1.raw	P47911|RL6_MOUSE			FALSE
KRKYSAAKTKVEKKK	23.98	1792.1	15	0.4	449.034	4	6.8274	8.86E+05	2.02E+07	ZKD_1.raw	P47911|RL6_MOUSE			FALSE
KSFVQNYPVVSIEDPF	43.08	1867.94	16	1.3	934.976	2	45.0015	1.08E+05	2.52E+06	ZKD_1.raw	P17182|ENOA_MOUSE			FALSE
KSPKKAKVTKPKKVK	46.8	1694.13	15	-0.6	424.539	4	6.9291	1.10E+06	1.90E+07	ZKD_1.raw	P15864|H12_MOUSE			FALSE
KTPESFLGPNAALVDLD	23.67	1785.91	17	1.9	893.966	2	42.7662			ZKD_1.raw	Q80VP1|EPN1_MOUSE			FALSE
KTSKPKAAKPKKTAAKK	36.18	1810.15	17	-0.1	604.391	3	2.9729	1.61E+07	1.75E+07	ZKD_1.raw	P43274|H14_MOUSE			FALSE
KVAKSPKKAKVTKPKKVK	21.44	1992.33	18	-1.4	665.116	3	7.5477			ZKD_1.raw	P15864|H12_MOUSE			FALSE
KVRGQTPKVAKQEKKK	46.08	1852.14	16	0.2	618.386	3	7.2576	6.56E+05	8.85E+06	ZKD_1.raw	P62862|RS30_MOUSE			FALSE
KVRGQTPKVAKQEKKKKK	51.8	2108.33	18	0.8	703.783	3	6.7377	1.96E+05	2.65E+06	ZKD_1.raw	P62862|RS30_MOUSE			FALSE
KVRGQTPKVAKQEKKKKKTG	68.45	2266.4	20	0.4	756.473	3	6.9112	1.80E+05	3.93E+06	ZKD_1.raw	P62862|RS30_MOUSE			FALSE
KYDS(+79.97)FSDHIQLVGAEQT	20.29	2016.88	17	-3.5	505.226	4	32.5563			ZKD_1.raw	Q8BLQ7|CTR4_M	Phosphorylation (S	osphorylation (STY	FALSE
KYTYGKPVPGHVK	50.9	1472.81	13	0.7	491.946	3	12.3345	4.30E+06	3.97E+07	ZKD_1.raw	P28665|MUG1_MOUSE			FALSE
KYTYGKPVPGHVKI	34.41	1585.9	14	0.7	397.482	4	17.9984	8.49E+05	9.31E+06	ZKD_1.raw	P28665|MUG1_MOUSE			FALSE
LAPDYDALDVANK	51.41	1403.69	13	1.1	702.855	2	29.1121	1.43E+07	1.46E+08	ZKD_1.raw	P62751|RL23A_MOUSE			FALSE
LAPDYDALDVANKIG	51.17	1573.8	15	-0.1	787.907	2	36.7543	5.40E+05	1.04E+07	ZKD_1.raw	P62751|RL23A_MOUSE			FALSE
LAPDYDALDVANKIGII	38.12	1799.97	17	-0.9	900.99	2	49.4738	9.30E+04	2.09E+06	ZKD_1.raw	P62751|RL23A_MOUSE			FALSE
LAPM(+15.99)YYRGAQAAIVVYD	34.82	1915.95	17	5.2	958.987	2	34.0771	1.79E+05	5.97E+06	ZKD_1.raw	P61021|RAB5B_M	Oxidation (M)		FALSE
LAPMYYRGAQAAIVVYD	40.75	1899.96	17	0.8	950.986	2	37.6293	3.45E+05	6.71E+06	ZKD_1.raw	P61021|RAB5B_MOUSE;Q9CQD1|RAB5A_MOUSE;P3			FALSE
LDQLFSGPLPGRLPV	46.6	1607.9	15	-1.1	804.958	2	47.277	5.51E+05	7.63E+06	ZKD_1.raw	Q60805|MERTK_MOUSE			FALSE
LEISYTGSRPASNMV	43.89	1623.79	15	3.2	812.906	2	29.9941			ZKD_1.raw	P28666|MUG2_MOUSE;P28665|MUG1_MOUSE			FALSE
LERAFRGATVLPANPPG	27.89	1764.96	17	0.7	589.329	3	27.2057	6.08E+05	5.92E+06	ZKD_1.raw	Q3B7Z2|OSBP1_MOUSE			FALSE
LHLRFSAPQIENEP	38.02	1649.85	14	1.1	550.959	3	31.2838	4.63E+05	1.04E+07	ZKD_1.raw	Q61190|I10R2_MOUSE			FALSE
LHLRFSAPQIENEPE	40.24	1778.9	15	1.4	593.973	3	30.9781	1.16E+07	9.37E+07	ZKD_1.raw	Q61190|I10R2_MOUSE			FALSE
LHLRFSAPQIENEPET	48.37	1879.94	16	0.4	627.655	3	31.0954	1.94E+06	2.05E+07	ZKD_1.raw	Q61190|I10R2_MOUSE			FALSE
LLILLILCFIKRS(+79.97)KG	20.94	1809.07	15	-1.9	453.274	4	38.9547			ZKD_1.raw	P11627|L1CAM_M	Phosphorylation (STY)		FALSE
LNFRNPAVQEEIK	33.3	1556.83	13	3.9	519.953	3	25.3909			ZKD_1.raw	Q91WV7|SLC31_MOUSE			FALSE
LPAAAQAPDALPAGWE	39.51	1576.79	16	-1.4	789.401	2	40.3779	3.49E+05	4.95E+06	ZKD_1.raw	Q9DBH0|WWP2_MOUSE			FALSE
LPPASLPESTPVPSSSPPP	33.81	1855.96	19	-3.4	928.983	2	35.8714			ZKD_1.raw	Q6PB44|PTN23_MOUSE			FALSE
LPPHVYSTPQPSLPP	38.75	1628.86	15	2.6	815.438	2	30.7023			ZKD_1.raw	Q3UPH1|PRRC1_MOUSE			FALSE
LPPHVYSTPQPSLPPV	39.69	1727.92	16	-1.5	864.968	2	35.3775	9.08E+06	3.72E+07	ZKD_1.raw	Q3UPH1|PRRC1_MOUSE			FALSE
LPPHVYSTPQPSLPPVQ	27.43	1855.98	17	0.6	928.999	2	32.6805	1.53E+05	3.75E+06	ZKD_1.raw	Q3UPH1|PRRC1_MOUSE			FALSE
LPPYDDATAVPSTAKEPPPP	44.17	2062.03	20	1.1	688.35	3	29.5857	3.96E+07	2.20E+08	ZKD_1.raw	Q91XQ6|LAP4B_MOUSE			FALSE
LPQDPTFHTPLDLYAYAR	50.15	2117.06	18	0.8	706.694	3	41.7829	1.69E+06	1.61E+07	ZKD_1.raw	Q07797|LG3BP_MOUSE			FALSE
LPSIPAWTGPEIPESGPS	20.25	1833.91	18	-1	917.964	2	47.6346			ZKD_1.raw	Q8K4G1|LTBP4_MOUSE			FALSE
LPSPLIM(+15.99)SPGPIYAVDG	53.24	1741.9	17	2.4	871.957	2	46.9358	2.09E+05	2.53E+06	ZKD_1.raw	Q8VHF2|CDHR5_	Oxidation (M)		FALSE
LPSPLIM(+15.99)SPGPIYAVDGD	58.96	1856.92	18	-0.4	929.468	2	46.9971	5.42E+05	5.12E+06	ZKD_1.raw	Q8VHF2|CDHR5_	Oxidation (M)		FALSE
LPSPLIM(+15.99)SPGPIYAVDGDQ	54.18	1984.98	19	1.4	993.499	2	45.9802			ZKD_1.raw	Q8VHF2|CDHR5_	Oxidation (M)		FALSE
LPSPLIMSPGPIYAVDG	49.9	1725.9	17	-1.3	863.957	2	52.2912	1.77E+05	3.37E+06	ZKD_1.raw	Q8VHF2|CDHR5_MOUSE			FALSE
LPSPLIMSPGPIYAVDGD	58.03	1840.93	18	0.4	921.472	2	52.433	8.72E+04	2.83E+06	ZKD_1.raw	Q8VHF2|CDHR5_MOUSE			FALSE
LPSPLIMSPGPIYAVDGDQ	57.32	1968.99	19	3	985.504	2	51.4044	2.13E+05	3.04E+06	ZKD_1.raw	Q8VHF2|CDHR5_MOUSE			FALSE
LPSTWSDPSVNISLDN	46.67	1743.83	16	0.6	872.924	2	42.4801	1.87E+06	2.12E+07	ZKD_1.raw	Q99KN9|EPN4_MOUSE			FALSE
LQDEIDAALPNKAP	41.92	1493.77	14	0.7	747.894	2	29.7061	4.49E+05	8.07E+06	ZKD_1.raw	Q64464|CP3AD_MOUSE			FALSE
LQDEIDAALPNKAPA	51.58	1564.81	15	0.1	783.412	2	29.1464	1.45E+06	1.56E+07	ZKD_1.raw	Q64464|CP3AD_MOUSE			FALSE
LQDEIDAALPNKAPAT	50.84	1665.86	16	0.6	833.936	2	29.0799	6.36E+05	9.05E+06	ZKD_1.raw	Q64464|CP3AD_MOUSE			FALSE
LSLLYNVPAVAEEIQ	20.27	1657.89	15	0.1	829.954	2	51.6598	7.16E+05	8.11E+06	ZKD_1.raw	P12023|A4_MOUSE			FALSE
LSLLYNVPAVAEEIQD	26.35	1772.92	16	-4.7	887.463	2	51.5327	2.48E+05	3.29E+06	ZKD_1.raw	P12023|A4_MOUSE			FALSE
LSQEYSGSVANEANVY	52.44	1729.78	16	0.5	865.898	2	27.8035	1.36E+06	2.71E+07	ZKD_1.raw	E9Q414|APOB_MOUSE			FALSE
LTGGYRYPRALEEEV	25.84	1751.88	15	1.8	584.97	3	27.5283	2.53E+06	3.96E+07	ZKD_1.raw	Q8K3K8|OPTN_MOUSE			FALSE
LTGM(+15.99)AFRVPTPNVSVVD	46.19	1817.93	17	0.8	909.975	2	38.1983	2.36E+06	1.72E+07	ZKD_1.raw	P16858|G3P_MOU	Oxidation (M)		FALSE
LTGMAFRVPTPNVS	24.41	1488.78	14	0.7	745.396	2	37.3716	4.52E+05	4.10E+06	ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
LTGMAFRVPTPNVSVVD	57.18	1801.94	17	-0.7	901.976	2	42.5077	4.56E+06	3.51E+07	ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
LVPIVEPEVLPDGDH	45.93	1627.85	15	-1.3	814.929	2	40.4097	6.07E+05	8.30E+06	ZKD_1.raw	Q91Y97|ALDOB_MOUSE			FALSE
LVRYTQKAPQVSTPTLV	31.5	1900.08	17	1.8	634.368	3	28.2264			ZKD_1.raw	P07724|ALBU_MOUSE			FALSE
LVTLPVSFAQLK	39.15	1314.79	12	1	658.404	2	44.1716	1.46E+06	1.78E+07	ZKD_1.raw	Q922Q8|LRC59_MOUSE			FALSE
LYTLVTYVPVTTFK	47.28	1643.92	14	-0.4	822.966	2	45.638	1.81E+05	3.50E+06	ZKD_1.raw	P62900|RL31_MOUSE			FALSE
M(+15.99)AFRVPTPNVSVVD	49.94	1546.78	14	0.7	774.399	2	35.8232	1.87E+06	1.41E+07	ZKD_1.raw	P16858|G3P_MOU	Oxidation (M)		FALSE
M(+42.01)(+15.99)FSSSAKIVKPNGEKPDEFE	20.77	2297.09	20	0.9	766.704	3	27.0586			ZKD_1.raw	P62082|RS7_MOU	Acetylation (N-term); Oxidation (M)		FALSE
M(+42.01)(+15.99)NDTVTIRTRKFMTNR	22.67	2041.02	16	1.5	681.348	3	21.4916			ZKD_1.raw	P62849|RS24_MC	Acetylation (N-term	-term):22.74;)1:Ox	FALSE
M(+42.01)DETSPLVSPERAQPP	49.17	1794.85	16	0	898.43	2	36.5657	2.14E+05	2.43E+06	ZKD_1.raw	Q2TBE6|P4K2A_M	Acetylation (N-term)		FALSE
M(+42.01)FSSSAKIVKPNGEKPDEFE	49.22	2281.09	20	-0.5	761.371	3	31.8133	9.88E+05	1.57E+07	ZKD_1.raw	P62082|RS7_MOU	Acetylation (N-term)		FALSE
M(+42.01)NDTVTIRTRKFMTNR	43.38	2025.02	16	-0.2	676.015	3	25.6281	2.30E+06	5.08E+07	ZKD_1.raw	P62849|RS24_MC	Acetylation (N-term)		FALSE
MAFRVPTPNVSVVD	43.53	1530.79	14	0.7	766.401	2	39.2186	5.36E+06	3.54E+07	ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
MGGLQISSFKLE	49.07	1308.67	12	-0.4	655.344	2	39.3691	3.98E+05	7.38E+06	ZKD_1.raw	Q9CQW5|LEG2_MOUSE			FALSE
NGLVPIVEPEVLPDG	25.54	1546.82	15	-1.2	774.419	2	49.2264	2.45E+05	3.43E+06	ZKD_1.raw	Q91Y97|ALDOB_MOUSE			FALSE
NGLVPIVEPEVLPDGDH	48.69	1798.91	17	0	900.462	2	43.2986	2.24E+05	3.82E+06	ZKD_1.raw	Q91Y97|ALDOB_MOUSE			FALSE
NGLVPIVEPEVLPDGDHD	49.12	1913.94	18	-1.5	957.974	2	43.4153	1.95E+05	3.69E+06	ZKD_1.raw	Q91Y97|ALDOB_MOUSE			FALSE
NHLRFNYPEVQ(+0.98)KVMPR	47.09	2028.04	16	8.2	508.021	4	26.7387	1.61E+06	1.13E+07	ZKD_1.raw	Q6XQH0|G3ST2_	Deamidation (NQ)	Deamidation (NQ):	FALSE
NHLRFNYPEVQKVMPR	50.15	2027.05	16	-2.1	507.769	4	26.6434	3.31E+06	1.82E+07	ZKD_1.raw	Q6XQH0|G3ST2_MOUSE			FALSE
NIYDLVAPFPSAPN	35.95	1516.76	14	0.7	759.386	2	49.0424	1.20E+05	2.17E+06	ZKD_1.raw	P09470|ACE_MOUSE			FALSE
NIYVPAHAHEGSNL	26.98	1520.74	14	3.1	761.378	2	20.8371			ZKD_1.raw	Q8BK48|EST2E_MOUSE			FALSE
NMIVIVLGHHLGK	26.19	1429.82	13	1.1	477.615	3	33.2852			ZKD_1.raw	P02088|HBB1_MOUSE			FALSE
NNQAYHSPATALAIVD	32.23	1683.82	16	-1.2	842.917	2	32.2711	1.60E+06	1.53E+07	ZKD_1.raw	Q8R420|ABCA3_MOUSE			FALSE
NPHVNPLPTGYE	46.63	1336.64	12	-3	669.326	2	25.2141	7.95E+05	1.46E+07	ZKD_1.raw	P43023|CX6A2_MOUSE;P43024|CX6A1_MOUSE			FALSE
NPLNSVFVAPAVTPV	44.82	1523.83	15	-0.3	762.924	2	49.4435	2.60E+06	2.34E+07	ZKD_1.raw	P70158|ASM3A_MOUSE			FALSE
NPLNSVFVAPAVTPVK	60.38	1651.93	16	0.6	826.973	2	40.1667	6.34E+07	4.87E+08	ZKD_1.raw	P70158|ASM3A_MOUSE			FALSE
NPLNSVFVAPAVTPVKG	59.8	1708.95	17	0.3	855.483	2	39.9539	4.84E+07	5.15E+08	ZKD_1.raw	P70158|ASM3A_MOUSE			FALSE
NPLNSVFVAPAVTPVKGV	60.98	1808.02	18	1.2	905.018	2	43.4145	1.70E+06	2.08E+07	ZKD_1.raw	P70158|ASM3A_MOUSE			FALSE
NPLNSVFVAPAVTPVKGVL	61.72	1921.1	19	-0.6	961.559	2	48.3529	2.52E+06	2.41E+07	ZKD_1.raw	P70158|ASM3A_MOUSE			FALSE
NPPSYYTQPVPVPN	40.51	1571.76	14	-0.7	786.888	2	32.4877	2.87E+06	3.36E+07	ZKD_1.raw	Q9JLJ0|LITAF_MOUSE			FALSE
NPPSYYTQPVPVPNA	47.95	1642.8	15	-0.3	822.407	2	34.0638	1.38E+06	1.89E+07	ZKD_1.raw	Q9JLJ0|LITAF_MOUSE			FALSE
NPPSYYTQPVPVPNAN	52.48	1756.84	16	0.7	879.429	2	32.1238	1.35E+07	1.32E+08	ZKD_1.raw	Q9JLJ0|LITAF_MOUSE			FALSE
NPPSYYTQPVPVPNANA	44.53	1827.88	17	1	914.948	2	33.1545			ZKD_1.raw	Q9JLJ0|LITAF_MOUSE			FALSE
NPVVIPEPPNPIPSYSE	40.86	1847.93	17	1.4	924.974	2	43.5798			ZKD_1.raw	Q99N10|M4A8_MOUSE			FALSE
NQAYHSPATALAIVD	30.09	1569.78	15	1.2	785.898	2	32.2452	3.54E+05	4.24E+06	ZKD_1.raw	Q8R420|ABCA3_MOUSE			FALSE
NSIIGDHKRWPHTIPYVLE	35.37	2274.19	19	0.2	759.071	3	33.4034	3.40E+06	3.85E+07	ZKD_1.raw	Q61847|MEP1B_MOUSE			FALSE
NTKGGDAPAAGEDA	39.82	1272.56	14	1.7	637.288	2	10.2533	2.29E+05	8.10E+06	ZKD_1.raw	P62852|RS25_MOUSE			FALSE
NVLRIINEPTAAAIAYG	51.42	1784.98	17	1.2	893.498	2	40.0124	4.59E+05	9.41E+06	ZKD_1.raw	P17879|HS71B_MOUSE;P16627|HS71L_MOUSE;P171			FALSE
NVQFNYPQASVTDVT	35.99	1681.79	15	0.7	841.905	2	35.8847	5.56E+06	7.25E+07	ZKD_1.raw	Q61703|ITIH2_MOUSE			FALSE
PGKGILAADESTGSI	22.69	1414.73	15	-9	708.366	2	39.7473			ZKD_1.raw	P05064|ALDOA_MOUSE			FALSE
PKRKAEGDAKGDKTKVK	33.93	1855.06	17	-0.8	464.773	4	6.3702			ZKD_1.raw	P09602|HMGN2_MOUSE			FALSE
PLNSVFVAPAVTPVK	47.37	1537.89	15	2.3	769.953	2	38.1149			ZKD_1.raw	P70158|ASM3A_MOUSE			FALSE
PLNSVFVAPAVTPVKG	55.3	1594.91	16	-4.4	798.458	2	37.9012			ZKD_1.raw	P70158|ASM3A_MOUSE			FALSE
PLPPLPEYGGKVRLG	39.39	1591.91	15	0.6	531.644	3	34.156	4.06E+05	5.40E+06	ZKD_1.raw	Q9CQQ7|AT5F1_MOUSE			FALSE
PPHVQFTYQQPQPLSVEPR	45.77	2247.14	19	-2.7	750.053	3	31.3241			ZKD_1.raw	B2RXS4|PLXB2_MOUSE			FALSE
PPPAYEPPAPAPAPLPPP	38.22	1774.93	18	1	592.651	3	38.8826	2.56E+05	3.03E+06	ZKD_1.raw	O35609|SCAM3_MOUSE			FALSE
PRKIEEIKDFLLT	38.22	1600.92	13	0	534.647	3	33.2751	7.18E+05	9.92E+06	ZKD_1.raw	Q9JJI8|RL38_MOUSE			FALSE
PVVVPPFLQPEVM(+15.99)GVSK	26.19	1838	17	-2	920.006	2	50.6629			ZKD_1.raw	P02666	Oxidation (M)		FALSE
QASIYSPPAAAAAAA	48.66	1358.68	15	1.6	680.35	2	29.4302			ZKD_1.raw	P70297|STAM1_MOUSE			FALSE
QEYSGSVANEANVY	46.93	1529.66	14	-1.2	765.838	2	24.7443			ZKD_1.raw	E9Q414|APOB_MOUSE			FALSE
QNAWFLPAQADIVATK	52.21	1771.93	16	-0.4	886.97	2	43.0877	2.55E+05	4.56E+06	ZKD_1.raw	P10852|4F2_MOUSE			FALSE
QPDLNFRNPAVQEEIK	40.26	1896.97	16	2.4	633.332	3	28.4567	5.66E+06	3.13E+07	ZKD_1.raw	Q91WV7|SLC31_MOUSE			FALSE
QPGPLEPLGGPG	21.3	1117.58	12	4.6	559.798	2	41.5745	2.34E+07	1.65E+08	ZKD_1.raw	Q91YJ2|SNX4_MOUSE			FALSE
QPSTSSLAAPTVEAAA	24.12	1499.75	16	-0.7	750.88	2	28.4877	2.79E+05	5.01E+06	ZKD_1.raw	Q91ZP6|NFIP2_MOUSE			FALSE
QPSTSSLAAPTVEAAAS	27.98	1586.78	17	1.9	794.398	2	27.6199	7.74E+06	7.48E+07	ZKD_1.raw	Q91ZP6|NFIP2_MOUSE			FALSE
QPSTSSLAAPTVEAAASA	27.55	1657.82	18	0.2	829.915	2	30.1796	7.80E+06	8.06E+07	ZKD_1.raw	Q91ZP6|NFIP2_MOUSE			FALSE
QPSTSSLAAPTVEAAASAP	28.94	1754.87	19	3.5	878.445	2	31.783	7.99E+06	7.06E+07	ZKD_1.raw	Q91ZP6|NFIP2_MOUSE			FALSE
QPSTSSLAAPTVEAAASAPA	37.41	1825.91	20	0.3	913.96	2	31.2826	1.35E+07	1.30E+08	ZKD_1.raw	Q91ZP6|NFIP2_MOUSE			FALSE
QQLAFKQPSSAYAAFN	46.55	1769.87	16	-0.7	885.944	2	31.8134	8.95E+05	1.66E+07	ZKD_1.raw	P01027|CO3_MOUSE			FALSE
QSINFLGGQPAAAPYPG	38.79	1686.84	17	-0.4	844.425	2	40.562	2.68E+05	5.61E+06	ZKD_1.raw	Q8K419|LEG4_MOUSE			FALSE
QVQWNDPGAQYSLVN	56.95	1717.81	15	0.4	859.911	2	36.632	1.01E+06	1.47E+07	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
RENIWKAPEPVEIR	47.81	1735.94	14	0.1	579.653	3	26.4214	1.63E+06	2.46E+07	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
RENIWKAPEPVEIRE	46	1864.98	15	0.4	622.667	3	26.8598	2.53E+07	2.91E+08	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
RHNYEGPETHTSL	24.04	1539.71	13	0.7	514.243	3	14.4451			ZKD_1.raw	P14483|HB2A_MOUSE			FALSE
RHNYEGPETHTSLR	52.79	1695.81	14	-0.7	424.959	4	12.0454	1.04E+07	8.30E+07	ZKD_1.raw	P14483|HB2A_MOUSE			FALSE
RHNYEGPETHTSLRR	40.24	1851.91	15	-0.9	463.984	4	11.2397			ZKD_1.raw	P14483|HB2A_MOUSE			FALSE
RIALAFTGIGLLV	27.37	1342.83	13	5.8	672.428	2	58.9523			ZKD_1.raw	Q8K2C8|GPAT4_MOUSE			FALSE
RKDAKSVKIKKNKDNVKFK	61.01	2273.37	19	0.2	758.797	3	9.9697	2.79E+06	6.36E+07	ZKD_1.raw	Q9JJI8|RL38_MOUSE			FALSE
RKEVRYGSLKYKVKKRP	50.61	2134.29	17	-0.9	534.578	4	12.0131	3.50E+06	3.66E+07	ZKD_1.raw	Q99KK1|REEP3_MOUSE			FALSE

RKEVRYGSLKYKVKKRPQ	57.16	2262.34	18	-2.7	566.592	4	11.628	1.29E+07	1.98E+08	ZKD_1.raw	Q99KK1|REEP3_MOUSE		FALSE
RKEVRYGSLKYKVKKRPQV	53.69	2361.41	19	-0.6	788.144	3	13.951	4.46E+06	6.71E+07	ZKD_1.raw	Q99KK1|REEP3_MOUSE		FALSE
RKEVRYGSLKYKVKKRPQVY	54.95	2524.48	20	-0.8	632.126	4	14.982	6.82E+05	1.22E+07	ZKD_1.raw	Q99KK1|REEP3_MOUSE		FALSE
RKIVYEGPELNHAFG	53.24	1728.89	15	0.3	577.306	3	25.5313	3.25E+07	2.49E+08	ZKD_1.raw	Q91ZX7|LRP1_MOUSE		FALSE
RKKAKTTKKIVLR	43.41	1569.06	13	0.5	393.272	4	8.8631	2.47E+05	7.81E+06	ZKD_1.raw	P83882|RL36A_MOUSE		FALSE
RKPYHKKRKYELGRPA	45.79	2026.17	16	0	507.55	4	10.1278	4.61E+06	7.97E+07	ZKD_1.raw	P62242|RS8_MOUSE		FALSE
RKTRKLRGHVSHGHGR	35.19	1881.08	16	0	314.52	6	7.0345	4.99E+05	9.67E+06	ZKD_1.raw	P14115|RL27A_MOUSE		FALSE
RKTRKLRGHVSHGHGRIGKH	30.35	2316.34	20	-0.1	773.12	3	8.1292	1.90E+06	2.63E+07	ZKD_1.raw	P14115|RL27A_MOUSE		FALSE
RNVQFNYPQASVTDVT	52.21	1837.9	16	0.1	919.955	2	30.0216	1.01E+06	1.55E+07	ZKD_1.raw	Q61703|ITIH2_MOUSE		FALSE
RPDAEYWNSQPEILE	45.85	1845.85	15	0.4	923.934	2	34.187	9.07E+05	9.35E+06	ZKD_1.raw	P14483|HB2A_MOUSE;P01921|HB2D_MOUSE;P0634		FALSE
RPDAEYWNSQPEILER	55.99	2001.95	16	0.4	668.326	3	29.6764	3.66E+06	4.02E+07	ZKD_1.raw	P14483|HB2A_MOUSE;P01921|HB2D_MOUSE;P0634		FALSE
RPGAIGGSKPRQ	21.01	1222.69	12	-1.2	408.57	3	14.0601			ZKD_1.raw	P47239|PAX7_MOUSE		FALSE
RPVQFPYVTPAPH	30.71	1507.79	13	-6.1	503.602	3	28.4818			ZKD_1.raw	Q9D074|MGRN1_MOUSE		FALSE
RPVQFPYVTPAPHEPV	40.9	1832.96	16	2.8	611.995	3	31.8141	1.53E+06	1.91E+07	ZKD_1.raw	Q9D074|MGRN1_MOUSE		FALSE
RPVQFPYVTPAPHEPVK	52.3	1961.05	17	-0.7	654.691	3	26.2937	1.71E+07	1.85E+08	ZKD_1.raw	Q9D074|MGRN1_MOUSE		FALSE
RPVQFPYVTPAPHEPVKT	54.12	2062.1	18	2.7	688.376	3	27.0284	2.50E+05	8.68E+06	ZKD_1.raw	Q9D074|MGRN1_MOUSE		FALSE
RRAAWRRRNTLQLHRYR	25.45	2308.31	17	-0.9	578.085	4	13.4709	3.15E+06	5.67E+07	ZKD_1.raw	Q9CZM2|RL15_MOUSE		FALSE
RYFDVWGTGTTVTVSS	50.15	1774.85	16	0.9	888.434	2	38.0071	1.88E+05	4.36E+06	ZKD_1.raw	P06329|HVM50_MOUSE		FALSE
S(+42.01)GRGKQGGKARAKAKSR	28.05	1784.02	17	-0.1	447.013	4	6.2693	2.70E+06	5.99E+07	ZKD_1.raw	Q8BFU2|H2A3_M	Acetylation (N-term)	FALSE
S(+42.01)GRGKQGGKARAKAKTR	45.1	1798.04	17	-1.3	360.615	5	6.4546	7.13E+06	1.20E+08	ZKD_1.raw	C0HKE3|H2A1D_I	Acetylation (N-term)	FALSE
S(+42.01)ILRIHAREIFD	42.39	1510.83	12	-2.6	504.615	3	36.8173	2.27E+05	4.64E+06	ZKD_1.raw	P17182|ENOA_M	Acetylation (N-term)	FALSE
S(+42.01)IRVTQKSYKM(+15.99)S	41.41	1484.77	12	-3.8	495.927	3	15.5008	6.06E+05	1.11E+07	ZKD_1.raw	P11679|K2C8_MC	Acetylation (N-term); Oxidation (M)	FALSE
S(+42.01)IRVTQKSYKM(+15.99)STSGPR	44.62	1983.02	17	1.4	662.015	3	15.1253			ZKD_1.raw	P11679|K2C8_MC	Acetylation (N-term); Oxidation (M)	FALSE
S(+42.01)IRVTQKSYKMS	43.88	1468.77	12	-0.9	490.597	3	19.1666	7.20E+05	1.32E+07	ZKD_1.raw	P11679|K2C8_MC	Acetylation (N-term)	FALSE
S(+42.01)IRVTQKSYKMSTSGPR	48.25	1967.03	17	0.3	656.683	3	18.5286			ZKD_1.raw	P11679|K2C8_MC	Acetylation (N-term)	FALSE
S(+42.01)IRVTQKSYKMSTSGPRA	44.45	2038.06	18	5.4	680.365	3	19.2143	8.15E+05	2.35E+07	ZKD_1.raw	P11679|K2C8_MC	Acetylation (N-term)	FALSE
S(+42.01)LVIPEKFQHILR	41.06	1620.94	13	0.2	541.319	3	41.3373	1.01E+07	7.92E+07	ZKD_1.raw	P62270|RS18_MC	Acetylation (N-term)	FALSE
S(+42.01)SKKAKTKTTKKRPQR	30.42	1914.15	16	-0.5	639.057	3	6.2871	1.40E+05	2.68E+06	ZKD_1.raw	Q3THE2|ML12B_M	Acetylation (N-term)	FALSE
S(+42.01)SVAVLTQESFAEHR	23.02	1701.83	15	0	851.923	2	35.6393			ZKD_1.raw	Q8VDJ3|VIGLN_M	Acetylation (N-term)	FALSE
S(+42.01)VQVVSAAAAAKVPEV	47.8	1566.86	16	3.7	784.441	2	43.0863	6.25E+05	7.84E+06	ZKD_1.raw	Q68FL4|SAHH3_M	Acetylation (N-term)	FALSE
S(+42.01)VQVVSAAAAAKVPEVE	49.64	1695.9	17	0.1	848.96	2	41.2127	5.77E+05	8.03E+06	ZKD_1.raw	Q68FL4|SAHH3_M	Acetylation (N-term)	FALSE
SAFSYVDPVITSISPR	53.73	1737.89	16	0.3	869.954	2	43.3564	7.37E+05	7.41E+06	ZKD_1.raw	P16056|MET_MOUSE		FALSE
SAKPVSQMRMATPLLM(+15.99)RPM	22.34	2160.1	19	2	721.043	3	29.5875	1.01E+06	1.28E+07	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M)	16:Oxidation (M):9.	FALSE
SAKPVSQMRMATPLLM(+15.99)RPM(+15.99)	23.7	2176.1	19	0	726.374	3	26.7659	7.64E+05	7.26E+06	ZKD_1.raw	P04441|HG2A_MO	Oxidation (M); Oxic	(M):8.28;M19:Oxic	FALSE
SAKPVSQMRMATPLLMRPM	45.06	2144.11	19	0.5	715.711	3	33.1785	3.58E+06	4.47E+07	ZKD_1.raw	P04441|HG2A_MOUSE			FALSE
SEEEYSAPLPTPAPS	32.85	1573.71	15	4	787.868	2	31.272			ZKD_1.raw	P97467|AMD_MOUSE			FALSE
SFFWNVAPGAESAVAS	22.21	1638.77	16	-4.7	820.387	2	47.4298	6.51E+05	3.36E+06	ZKD_1.raw	P57716|NICA_MOUSE			FALSE
SGGKAKKKKWSKGKVRDK	22.34	2015.21	18	-0.6	504.81	4	6.6379	1.69E+05	3.56E+06	ZKD_1.raw	P62852|RS25_MOUSE			FALSE
SGGKAKKKKWSKGKVRDKLN	36.68	2242.34	20	0.4	748.454	3	8.9251	9.39E+04	3.02E+06	ZKD_1.raw	P62852|RS25_MOUSE			FALSE
SGNFRPANPNWGVF	38.75	1561.74	14	-0.8	781.878	2	36.8788	1.84E+05	3.89E+06	ZKD_1.raw	E9PV24|FIBA_MOUSE			FALSE
SGNFRPANPNWGVFS	47.15	1648.77	15	-0.5	825.394	2	35.2506	8.65E+05	1.08E+07	ZKD_1.raw	E9PV24|FIBA_MOUSE			FALSE
SGPKPFSAPKPQTSPSPK	59.24	1836.97	18	1.1	460.251	4	16.0767	5.27E+06	6.29E+07	ZKD_1.raw	P40124|CAP1_MOUSE			FALSE
SGPKPFSAPKPQTSPSPKP	47.01	1934.03	19	3.1	484.515	4	17.7214	1.22E+07	9.13E+07	ZKD_1.raw	P40124|CAP1_MOUSE			FALSE
SGPKPFSAPKPQTSPSPKPA	43.37	2005.06	20	-1.6	669.361	3	17.3237	6.75E+05	2.13E+07	ZKD_1.raw	P40124|CAP1_MOUSE			FALSE
SIASFKDPKISTSLPV	47.41	1688.93	16	-0.5	845.474	2	34.6123	1.42E+05	4.86E+06	ZKD_1.raw	Q61233|PLSL_MOUSE			FALSE
SILWSQPLPSLPGGPP	54.45	1644.89	16	-1.5	823.45	2	52.5429	7.42E+05	7.60E+06	ZKD_1.raw	Q8C0Z1|F234A_MOUSE			FALSE
SINFLGGQPAAAPYPG	47.88	1558.78	16	-2.1	780.395	2	41.2146	8.23E+05	9.28E+06	ZKD_1.raw	Q8K419|LEG4_MOUSE			FALSE
SLHLRFSAPQIENEPE	33.64	1865.93	16	-0.5	622.983	3	31.7833	1.09E+06	9.94E+06	ZKD_1.raw	Q61190|I10R2_MOUSE			FALSE
SLHLRFSAPQIENEPET	27.93	1966.97	17	-6.4	656.661	3	31.9785			ZKD_1.raw	Q61190|I10R2_MOUSE			FALSE
SLQAFSNPSAGISVDVK	52.19	1718.88	17	4.8	860.453	2	34.1039			ZKD_1.raw	Q8BG07|PLD4_MOUSE			FALSE
SLVSKGTLVQTK	48.69	1259.74	12	-0.8	630.879	2	18.2995			ZKD_1.raw	P43276|H15_MOUSE;P43274|H14_MOUSE;P43277|H1			FALSE
SLVYPFPGPIPN	40.62	1299.69	12	2.9	650.852	2	48.1145	3.56E+05	3.79E+06	ZKD_1.raw	P02666			FALSE
SPARSHLYHPSSPWPIG	40.61	1887.94	17	0.5	630.32	3	26.9225	4.07E+05	7.63E+06	ZKD_1.raw	P97798|NEO1_MOUSE			FALSE
SPATRKEYHTGKAVTSKGDK	34.03	2160.13	20	2.5	721.052	3	8.8191			ZKD_1.raw	E9PV24|FIBA_MOUSE			FALSE
SPGYNPPQMNTLPV	33.55	1513.72	14	-1.3	757.868	2	38.5537			ZKD_1.raw	Q8K419|LEG4_MOUSE			FALSE
SPNKLYTLVTYVPVTTFK	48.97	2070.14	18	2.4	691.056	3	43.1162	3.53E+05	5.53E+06	ZKD_1.raw	P62900|RL31_MOUSE			FALSE
SPPHVQFTYQQPQPLSVEPR	71.28	2334.18	20	0.3	1168.1	2	31.3992	2.32E+07	2.14E+08	ZKD_1.raw	B2RXS4|PLXB2_MOUSE			FALSE
SPPPGGYGQPSVLPGGYP	24.35	1725.84	18	-0.7	863.925	2	36.6335	1.97E+06	8.53E+06	ZKD_1.raw	Q8BJZ3|LFG3_MOUSE			FALSE
SPPPYAAYATPTPEVYG	54.04	1779.84	17	-0.4	890.925	2	36.9115	2.66E+06	2.88E+07	ZKD_1.raw	Q9QZC7|PKHB2_MOUSE			FALSE
SSEVYTFPVPERHLE	33.53	1788.87	15	-4.9	597.294	3	30.5383			ZKD_1.raw	P09803|CADH1_MOUSE			FALSE
SSHKTFRIKRFL	30.22	1518.88	12	-0.9	380.727	4	19.2974	1.23E+06	2.29E+07	ZKD_1.raw	P62892|RL39_MOUSE			FALSE
SSHKTFRIKRFLA	35.6	1589.92	13	0.9	530.98	3	18.9825	2.51E+06	5.58E+07	ZKD_1.raw	P62892|RL39_MOUSE			FALSE
SSHKTFRIKRFLAKKQ	38.93	1974.16	16	-1.1	494.548	4	14.7288	4.67E+06	6.85E+07	ZKD_1.raw	P62892|RL39_MOUSE			FALSE
SSHKTFRIKRFLAKKQKQ	40.18	2230.32	18	-0.4	558.586	4	13.5283	1.02E+06	2.52E+07	ZKD_1.raw	P62892|RL39_MOUSE			FALSE
SSM(+15.99)NYTGPRTNLGYL	29.63	1688.78	15	4.3	845.402	2	29.7875			ZKD_1.raw	Q32NZ6|TMC5_M	Oxidation (M)		FALSE
SSMNYTGPRTNLGYL	48.1	1672.79	15	1.6	837.403	2	32.6279	5.90E+05	9.58E+06	ZKD_1.raw	Q32NZ6|TMC5_MOUSE			FALSE
STIAVNSPVISVSINK	46.04	1627.91	16	1.1	814.965	2	35.0297			ZKD_1.raw	Q8JZZ7|AGRL2_MOUSE			FALSE
SVATNPIITPVAQENQ	44.2	1680.87	16	1	841.442	2	32.9606			ZKD_1.raw	P08226|APOE_MOUSE			FALSE
SVFVAPAVTPVK	52.83	1213.71	12	0.5	607.861	2	31.7837	5.68E+07	6.12E+08	ZKD_1.raw	P70158|ASM3A_MOUSE			FALSE
SVFVAPAVTPVKG	47.69	1270.73	13	-0.3	636.371	2	31.6579	5.06E+07	4.67E+08	ZKD_1.raw	P70158|ASM3A_MOUSE			FALSE
SVFVAPAVTPVKGV	50.63	1369.8	14	1.3	685.907	2	36.2524	6.11E+05	1.12E+07	ZKD_1.raw	P70158|ASM3A_MOUSE			FALSE
SVFVAPAVTPVKGVL	54.58	1482.88	15	-0.2	742.448	2	42.1716	1.16E+06	1.65E+07	ZKD_1.raw	P70158|ASM3A_MOUSE			FALSE
SVNVDYSKLKKEGPDF	47.93	1824.93	16	-1	609.315	3	25.4667	1.61E+06	2.10E+07	ZKD_1.raw	Q62425|NDUA4_MOUSE			FALSE
SYRSIEAPEVAIDVDG	45.87	1719.83	16	0	860.923	2	33.6883	7.93E+05	1.44E+07	ZKD_1.raw	Q3UVU3|ZNT10_MOUSE			FALSE
TAKPKAAKAKKAVSKKK	34.7	1782.16	17	-0.5	446.546	4	6.3985	5.30E+06	6.62E+07	ZKD_1.raw	P43276|H15_MOUSE			FALSE
TDAPSFSDIPNPI	30.4	1372.65	13	1.4	687.334	2	43.5933	3.78E+06	3.23E+07	ZKD_1.raw	P02662			FALSE
TDDVFSPSHAIPIET	41.52	1627.77	15	0.1	814.894	2	37.2957	7.91E+04	2.62E+06	ZKD_1.raw	Q91ZH7|ABHD3_MOUSE			FALSE
TGGYRYPRALEEEV	39.68	1638.8	14	1.3	820.408	2	25.3093	8.77E+05	1.68E+07	ZKD_1.raw	Q8K3K8|OPTN_MOUSE			FALSE
TGM(+15.99)AFRVPTPNVSV	49.41	1490.76	14	-0.9	746.384	2	34.894	4.08E+05	4.11E+06	ZKD_1.raw	P16858|G3P_MOU	Oxidation (M)		FALSE
TGM(+15.99)AFRVPTPNVSVV	51.17	1589.82	15	-0.1	795.919	2	37.4392	4.23E+06	2.42E+07	ZKD_1.raw	P16858|G3P_MOU	Oxidation (M)		FALSE
TGM(+15.99)AFRVPTPNVSVVD	50.84	1704.85	16	-0.3	853.432	2	35.9455	1.15E+08	6.28E+08	ZKD_1.raw	P16858|G3P_MOU	Oxidation (M)		FALSE
TGM(+15.99)AFRVPTPNVSVVDL	28.12	1817.93	17	0.2	909.975	2	43.687	1.57E+05	2.20E+06	ZKD_1.raw	P16858|G3P_MOU	Oxidation (M)		FALSE
TGMAFRVPTPNVS	46.98	1375.69	13	3.2	688.855	2	34.1321			ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
TGMAFRVPTPNVS(+79.97)V	24.04	1554.73	14	-0.6	778.37	2	39.9527			ZKD_1.raw	P16858|G3P_MOU	Phosphorylation (S	osphorylation (STY	FALSE
TGMAFRVPTPNVSV	50.64	1474.76	14	-0.8	738.387	2	39.035	1.33E+06	1.03E+07	ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
TGMAFRVPTPNVSVV	54.36	1573.83	15	-0.1	787.922	2	41.3949	7.27E+06	4.47E+07	ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
TGMAFRVPTPNVSVVD	52.77	1688.86	16	-0.1	845.435	2	39.9252	1.63E+08	1.04E+09	ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
TGMAFRVPTPNVSVVDL	47.25	1801.94	17	-1.1	901.976	2	47.0916	2.93E+05	3.66E+06	ZKD_1.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
THDLYIQSHISENREE	38.25	1969.91	16	0.9	657.646	3	19.1819			ZKD_1.raw	Q9R111|GUAD_MOUSE			FALSE
THINIVVIGHVDSG	52.37	1459.78	14	-1.3	730.896	2	29.7754	1.22E+06	7.92E+06	ZKD_1.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
THINIVVIGHVDSGK	54.46	1587.87	15	-0.4	530.298	3	25.656	4.22E+07	4.12E+08	ZKD_1.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
THINIVVIGHVDSGKST	53.32	1775.95	17	0.6	592.992	3	25.5313	1.18E+06	2.06E+07	ZKD_1.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
THINIVVIGHVDSGKSTT	35.52	1877	18	0.6	626.675	3	25.6043			ZKD_1.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
THINIVVIGHVDSGKSTTT	56.62	1978.05	19	-0.6	660.356	3	25.6281	5.13E+06	8.33E+07	ZKD_1.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
TIEFRGPNGLLVYQG	48.53	1662.87	15	-1	832.443	2	39.4958	4.78E+05	8.64E+06	ZKD_1.raw	Q9DCN2|NB5R3_MOUSE			FALSE
TLVTRTQGTKIASDGLKGR	45.86	2001.13	19	1.3	501.291	4	17.0566	4.93E+06	7.56E+07	ZKD_1.raw	P97351|RS3A_MOUSE			FALSE
TLVTYVPVTTFK	41.56	1367.77	12	-0.3	684.892	2	37.7244	5.05E+06	5.60E+07	ZKD_1.raw	P62900|RL31_MOUSE			FALSE
TNTAYVGSAILSEET	39.58	1554.74	15	-2.2	778.376	2	35.2184	1.06E+06	1.27E+07	ZKD_1.raw	Q9QZC7|PKHB2_MOUSE			FALSE
TPAYTIPFYTPIPNG	47.67	1650.83	15	0.5	826.422	2	49.5398	2.61E+06	2.15E+07	ZKD_1.raw	O08573|LEG9_MOUSE			FALSE
TPESFLGPNAALVD	28.32	1429.71	14	2	715.863	2	41.6838			ZKD_1.raw	Q80VP1|EPN1_MOUSE			FALSE
TPESFLGPNAALVDL	25.76	1542.79	15	-1	772.403	2	51.9178			ZKD_1.raw	Q80VP1|EPN1_MOUSE			FALSE
TPESFLGPNAALVDLD	41.27	1657.82	16	1.7	829.919	2	49.4134	4.15E+05	6.04E+06	ZKD_1.raw	Q80VP1|EPN1_MOUSE			FALSE
TPEYVAPEVILNKG	44.97	1528.81	14	-1.6	765.413	2	34.1553	2.46E+05	4.41E+06	ZKD_1.raw	Q61410|KGP2_MOUSE			FALSE
TPFQFRAASPVEE	49.53	1477.72	13	0.3	739.868	2	31.2219	1.64E+06	2.27E+07	ZKD_1.raw	Q3UKC1|TAXB1_MOUSE			FALSE
TPFQFRAASPVEEL	54.1	1590.8	14	-1.3	796.408	2	38.9741	7.93E+05	1.18E+07	ZKD_1.raw	Q3UKC1|TAXB1_MOUSE			FALSE
TPFQFRAASPVEELL	33.16	1703.89	15	1.9	852.953	2	46.4396	7.09E+04	1.68E+06	ZKD_1.raw	Q3UKC1|TAXB1_MOUSE			FALSE
TPPSPKVTYKAPVPTGEVY	24.37	2030.07	19	-6.4	677.694	3	28.1824			ZKD_1.raw	P35564|CALX_MOUSE			FALSE
TPSAAYLWVGAGASEAEK	54.5	1806.88	18	3.2	904.45	2	35.1524	6.54E+05	9.84E+06	ZKD_1.raw	P13020|GELS_MOUSE;#CONTAM#Q3SX14			FALSE
TPSAAYLWVGAGASEAEKT	60.4	1907.93	19	0.3	954.971	2	35.9169	6.46E+06	7.88E+07	ZKD_1.raw	P13020|GELS_MOUSE;#CONTAM#Q3SX14			FALSE
TPSAAYLWVGAGASEAEKTG	55.06	1964.95	20	5.3	983.487	2	35.9155	4.57E+05	6.65E+06	ZKD_1.raw	P13020|GELS_MOUSE;#CONTAM#Q3SX14			FALSE
TPVFVHAGPFANIAHGN	44.12	1747.88	17	-0.2	583.634	3	33.1785	3.25E+05	5.01E+06	ZKD_1.raw	Q922D8|C1TC_MOUSE;Q3V3R1|C1TM_MOUSE			FALSE
TPVFVHAGPFANIAHGNS	54.58	1834.91	18	1	612.645	3	32.8652	2.29E+06	1.75E+07	ZKD_1.raw	Q922D8|C1TC_MOUSE;Q3V3R1|C1TM_MOUSE			FALSE
TPVVVPPFLQPEV	27.9	1420.8	13	1.8	711.407	2	53.5819			ZKD_1.raw	P02666			FALSE
TPVVVPPFLQPEVM(+15.99)GVSK	46.57	1939.05	18	-0.9	970.531	2	51.9491	1.29E+06	7.79E+06	ZKD_1.raw	P02666	Oxidation (M)		FALSE
TQSLVYPFPGPIPNS	40.59	1615.82	15	-3	808.917	2	52.9781			ZKD_1.raw	P02666			FALSE
TQVQWNDPGAQYSLV	31.33	1704.81	15	2.8	853.415	2	40.1806			ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
TQVQWNDPGAQYSLVN	46.34	1818.85	16	0	910.434	2	36.7216	7.52E+06	7.95E+07	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
TRKEYHTGKAVTSKG	38.7	1661.88	15	0.6	416.479	4	8.0014	6.90E+04	2.37E+06	ZKD_1.raw	E9PV24|FIBA_MOUSE			FALSE
TSKPKAAKPKKTAAKK	39.02	1682.06	16	-0.3	561.693	3	6.1907	1.30E+05	2.37E+06	ZKD_1.raw	P43274|H14_MOUSE			FALSE
TSKPKAAKPKKTAAKKK	29.07	1810.15	17	-0.1	604.391	3	2.9729	1.61E+07	8.73E+06	ZKD_1.raw	P43274|H14_MOUSE			FALSE
TSSYSNPTIGYENR	42.32	1587.72	14	1.3	794.867	2	19.9771			ZKD_1.raw	Q07797|LG3BP_MOUSE			FALSE
TSWTYNPAAVSKVAPA	22.46	1661.84	16	1	831.929	2	32.2863			ZKD_1.raw	Q80SY4|MIB1_MOUSE			FALSE
TVKPKAAKPKTSKPKAAKPK	25.3	2103.33	20	1.2	702.117	3	8.4606			ZKD_1.raw	P43274|H14_MOUSE			FALSE
VADKEFHAPLIIDENG	23.22	1766.88	16	0.1	589.969	3	31.9095	4.21E+05	6.34E+06	ZKD_1.raw	Q91YN5|UAP1_MOUSE			FALSE
VAIFARGPQAHLVH	40.66	1514.85	14	-1	505.956	3	24.1264	2.28E+07	2.56E+08	ZKD_1.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
VAIFARGPQAHLVHG	33.59	1571.87	15	-0.3	524.963	3	24.0672	1.87E+08	1.65E+09	ZKD_1.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
VAIFARGPQAHLVHGV	52.24	1670.94	16	3	836.478	2	27.154	2.28E+06	4.04E+07	ZKD_1.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
VAIFARGPQAHLVHGVQ	25.15	1799	17	1.4	450.757	4	25.7225	2.54E+07	2.23E+08	ZKD_1.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
VAKSPKKAKVTKPKKVK	34.43	1864.23	17	0	622.419	3	7.6863			ZKD_1.raw	P15864|H12_MOUSE			FALSE
VARYRPRAPIIAVTRNP	36.94	1949.14	17	-2.4	488.292	4	20.7387	1.03E+06	1.64E+07	ZKD_1.raw	P52480|KPYM_MOUSE			FALSE
VARYRPRAPIIAVTRNPQ	49.95	2077.2	18	-0.8	520.307	4	20.1879	5.54E+06	7.04E+07	ZKD_1.raw	P52480|KPYM_MOUSE			FALSE
VATNPIITPVAQENQ	49.69	1593.84	15	1.6	797.927	2	31.7833	5.20E+05	7.37E+06	ZKD_1.raw	P08226|APOE_MOUSE			FALSE
VDFDFAGPAIHGSAV	29.06	1501.72	15	-0.5	751.867	2	39.2302			ZKD_1.raw	Q60930|VDAC2_MOUSE			FALSE
VDFNTPRPSTVEA	46.04	1431.7	13	0	716.857	2	25.5646	7.08E+05	1.14E+07	ZKD_1.raw	G3X939|SL9A3_MOUSE			FALSE
VDLRFSTSQSLPASQT	34.01	1735.87	16	-0.8	868.944	2	31.1029			ZKD_1.raw	P28665|MUG1_MOUSE			FALSE
VDVFYSSGIPATARP	44.86	1578.8	15	-0.2	790.409	2	34.288			ZKD_1.raw	Q91VN0|LRP5_MOUSE			FALSE
VDVFYSSGIPATARPY	53.16	1741.87	16	0.4	871.941	2	36.8957	2.10E+05	4.68E+06	ZKD_1.raw	Q91VN0|LRP5_MOUSE			FALSE
VEYAVRGPIVQRALEL	42.2	1812.03	16	-0.6	605.016	3	36.5367	1.23E+06	1.15E+07	ZKD_1.raw	Q8QZR5|ALAT1_MOUSE			FALSE
VFDVTAPNTFKTLD	31.18	1566.79	14	-3.2	784.401	2	37.4841			ZKD_1.raw	P51150|RAB7A_MOUSE			FALSE
VFEVSLADLQNDEVAFR	45.07	1950.97	17	-0.3	976.491	2	46.7602			ZKD_1.raw	P97351|RS3A_MOUSE			FALSE
VFVAPAVTPVKG	46.66	1183.7	12	0.9	592.856	2	29.6146	5.25E+05	8.91E+06	ZKD_1.raw	P70158|ASM3A_MOUSE			FALSE
VGGERFEAPEALFQPH	46.49	1782.87	16	1	595.298	3	33.904	1.76E+06	2.01E+07	ZKD_1.raw	P61161|ARP2_MOUSE			FALSE

VGTKRYMAPEVLDETIN	36.54	1934.98	17	0.9	646	3	29.6146	1.57E+06	2.63E+07	ZKD_1.raw	Q61271|ACV1B_MOUSE			FALSE
VIGHALGPSPIPA	38.86	1227.7	13	0.9	614.857	2	29.6915	1.95E+05	3.32E+06	ZKD_1.raw	Q9WV38|GTR5_MOUSE			FALSE
VITNQYNSPTGLYSSEN	29.06	1885.87	17	-0.1	943.942	2	28.4931			ZKD_1.raw	O70400|PDLI1_MOUSE			FALSE
VKVTFNSALAQKEAKK	53.12	1761.01	16	3.1	441.262	4	17.9371	1.20E+06	2.08E+07	ZKD_1.raw	O89051|ITM2B_MOUSE			FALSE
VLLPKKTESHHKAKGK	22.32	1800.07	16	-0.1	451.026	4	9.0102			ZKD_1.raw	C0HKE3|H2A1D_MOUSE;C0HKE7|H2A1N_MOUSE;Q8			FALSE
VLTVINQTQKENLR	44.68	1654.94	14	2.5	552.654	3	22.1574	1.51E+06	3.49E+07	ZKD_1.raw	Q6ZWV7|RL35_MOUSE			FALSE
VLVTWTPPRARIAGYR	29.01	1855.06	16	0.6	464.772	4	29.7688	7.32E+05	8.93E+06	ZKD_1.raw	P11276|FINC_MOUSE			FALSE
VNPGGWAPASVLRAVAK	23.14	1691.95	17	-1.3	564.989	3	37.3281			ZKD_1.raw	Q9EQG9|CERT_MOUSE			FALSE
VNVDFNTPRPSTVEA	46.62	1644.81	15	1.3	823.414	2	28.767	3.26E+06	4.17E+07	ZKD_1.raw	G3X939|SL9A3_MOUSE			FALSE
VPDDLLYSFPVVIKNK	54.78	1846.02	16	-3.7	616.346	3	43.2099	7.43E+05	8.44E+06	ZKD_1.raw	P14152|MDHC_MOUSE			FALSE
VPDDLLYSFPVVIKNKT	53.49	1947.07	17	-1.4	650.03	3	43.2084	6.25E+05	7.98E+06	ZKD_1.raw	P14152|MDHC_MOUSE			FALSE
VPFETRGPHINNSVH	37.82	1702.85	15	0.2	426.721	4	19.2307	4.89E+05	8.05E+06	ZKD_1.raw	Q8K296|MTMR3_MOUSE			FALSE
VPIVEPEVLPDG	37.14	1262.68	12	3.2	632.347	2	40.2285	5.68E+05	5.93E+06	ZKD_1.raw	Q91Y97|ALDOB_MOUSE			FALSE
VPIVEPEVLPDGDHD	44.12	1629.79	15	-2.5	815.9	2	34.846			ZKD_1.raw	Q91Y97|ALDOB_MOUSE			FALSE
VPLPVSLGPPLP	25.63	1184.72	12	5.9	593.369	2	59.0901			ZKD_1.raw	Q62406|IRAK1_MOUSE			FALSE
VPPDQYYWAPLAQHERG	31.53	2025.97	17	9.7	676.337	3	32.4633			ZKD_1.raw	P30999|CTND1_MOUSE			FALSE
VPPFLQPEVM(+15.99)GVSK	42.44	1542.81	14	-2	772.412	2	34.7808	3.67E+05	7.58E+05	ZKD_1.raw	P02666	Oxidation (M)		FALSE
VPPVQVSPLIKFGR	43.44	1535.92	14	-1.6	512.979	3	36.0403	1.17E+05	2.70E+06	ZKD_1.raw	Q06185|ATP5I_MOUSE			FALSE
VPTVPLLPPQVNQSL	20.97	1600.92	15	-0.1	801.467	2	50.1681	1.65E+05	1.96E+06	ZKD_1.raw	Q99JX3|GORS2_MOUSE			FALSE
VPVSVPIPVPGP	27.23	1156.69	12	8.8	579.355	2	57.0815			ZKD_1.raw	Q9JMC2|INSM2_MOUSE			FALSE
VPWNFHEPQPGQYE	36.27	1726.77	14	0.9	864.395	2	32.7165			ZKD_1.raw	P23780|BGAL_MOUSE			FALSE
VQWNDPGAQYSLVN	43.39	1589.75	14	-0.2	795.881	2	36.5355	1.54E+05	2.69E+06	ZKD_1.raw	Q9R100|CAD17_MOUSE			FALSE
VRTDM(+15.99)AGPKATKSPEE	22.93	1731.85	16	1.3	578.29	3	10.5216			ZKD_1.raw	P48758|CBR1_MO	Oxidation (M)		FALSE
VRTDMAGPKATKSPEE	36.17	1715.85	16	2.2	572.959	3	12.4661			ZKD_1.raw	P48758|CBR1_MOUSE			FALSE
VSHDYKGSTSHSLPY	30.89	1676.78	15	0	559.934	3	16.5024	6.09E+06	4.02E+07	ZKD_1.raw	E9Q414|APOB_MOUSE			FALSE
VSLADLQNDEVAFR	50.17	1575.79	14	-0.1	788.902	2	37.8168	2.53E+06	3.14E+07	ZKD_1.raw	P97351|RS3A_MOUSE			FALSE
VTIAQGGVLPNIQAVLLPK	49.65	1930.16	19	1	966.089	2	50.5465	1.79E+05	4.01E+06	ZKD_1.raw	C0HKE3|H2A1D_MOUSE;C0HKE8|H2A1O_MOUSE;Q8			FALSE
VTKPKTPAKPKKAAPKKK	44.09	1945.26	18	0.8	649.427	3	8.089	9.75E+04	1.47E+06	ZKD_1.raw	P43275|H11_MOUSE			FALSE
VTPEYTTANVISVGSG	32.56	1593.79	16	2.5	797.904	2	33.4743			ZKD_1.raw	Q8K177|KCP3_MOUSE			FALSE
VTQFHPPHIEIQ	33.59	1444.75	12	0	482.589	3	29.2996	1.11E+06	9.80E+06	ZKD_1.raw	P01887|B2MG_MOUSE			FALSE
VTQFHPPHIEIQM	27.87	1575.79	13	0.2	526.27	3	35.1524	2.12E+05	2.17E+06	ZKD_1.raw	P01887|B2MG_MOUSE			FALSE
VTQFHPPHIEIQM(+15.99)L	29.96	1704.87	14	-2.2	569.295	3	35.5324	7.81E+05	5.54E+06	ZKD_1.raw	P01887|B2MG_M	Oxidation (M)		FALSE
VTYVPVTTFKNLQTVNVDEN	36.6	2280.16	20	-1.1	761.061	3	39.2186	9.30E+05	1.51E+07	ZKD_1.raw	P62900|RL31_MOUSE			FALSE
VVPPFLQPEVM(+15.99)GVSK	49.34	1641.88	15	0.2	821.947	2	40.1353			ZKD_1.raw	P02666	Oxidation (M)		FALSE
WVRTDM(+15.99)AGPKATKSPEE	44.11	1917.93	17	-0.5	640.315	3	13.9918	1.27E+06	1.94E+07	ZKD_1.raw	P48758|CBR1_M	Oxidation (M)		FALSE
WVRTDMAGPKATKSPE	20.61	1772.89	16	-2.6	591.968	3	16.6813	1.42E+05	4.55E+06	ZKD_1.raw	P48758|CBR1_MOUSE			FALSE
WVRTDMAGPKATKSPEE	45.88	1901.93	17	3.2	634.986	3	17.0554	1.42E+06	2.57E+07	ZKD_1.raw	P48758|CBR1_MOUSE			FALSE
YAVRGPIVQRALEL	49.87	1583.91	14	1.2	528.98	3	33.593	9.68E+05	9.69E+06	ZKD_1.raw	Q8QZR5|ALAT1_MOUSE			FALSE
YDALDVANKIGII	48.1	1403.77	13	1.3	702.891	2	45.4794	3.14E+05	4.63E+06	ZKD_1.raw	P62751|RL23A_MOUSE			FALSE
YFDVWGTGTTVTVSS	39	1618.75	15	1.2	810.384	2	44.3858	1.08E+06	1.38E+07	ZKD_1.raw	P06329|HVM50_MOUSE			FALSE
YFQINQDEEEEEDED	41.11	1930.72	15	-3.1	966.366	2	27.2864	6.44E+05	1.48E+07	ZKD_1.raw	P67984|RL22_MOUSE			FALSE
YLNIYVPAHAHEG	40.81	1482.73	13	0.4	495.249	3	26.1851	3.24E+05	8.00E+06	ZKD_1.raw	Q8BK48|EST2E_MOUSE			FALSE
YLNIYVPAHAHEGSN	46.95	1683.8	15	-0.1	562.274	3	25.8803	5.23E+06	7.05E+07	ZKD_1.raw	Q8BK48|EST2E_MOUSE			FALSE
YLNIYVPAHAHEGSNL	43.94	1796.88	16	1.6	599.97	3	29.9587	2.20E+06	3.79E+07	ZKD_1.raw	Q8BK48|EST2E_MOUSE			FALSE
YLNIYVPAHAHEGSNLPV	25.7	1993.01	18	-1.6	665.341	3	34.6567	2.77E+06	4.58E+07	ZKD_1.raw	Q8BK48|EST2E_MOUSE			FALSE
YPDKKVTFSSGYVNLSPEN	38.58	2144.04	19	0	715.688	3	29.6934			ZKD_1.raw	P06684|CO5_MOUSE			FALSE
YPNTPYISPVASYSGQP	29.3	1839.87	17	-0.3	920.941	2	37.3801			ZKD_1.raw	Q3UPL0|SC31A_MOUSE			FALSE
YPSQASIYSPPAAAAAAA	33.59	1705.83	18	0.6	853.923	2	33.0041	1.80E+05	3.29E+06	ZKD_1.raw	P70297|STAM1_MOUSE			FALSE
YPSQASIYSPPAAAAAAAA	48.5	1776.87	19	0.2	889.442	2	34.3818	1.25E+06	1.16E+07	ZKD_1.raw	P70297|STAM1_MOUSE			FALSE
YPTPAYTIPFYTPIPNG	42.67	1910.95	17	2.3	956.482	2	52.3248	5.55E+05	8.18E+06	ZKD_1.raw	O08573|LEG9_MOUSE			FALSE
YTIPFYTPIPNG	39.77	1381.69	12	0	691.853	2	47.9343	6.88E+06	5.89E+07	ZKD_1.raw	O08573|LEG9_MOUSE			FALSE
YVTQFHPPHIEIQ	52.64	1607.81	13	0.3	804.912	2	32.1554	3.58E+07	5.34E+08	ZKD_1.raw	P01887|B2MG_MOUSE			FALSE
YVTQFHPPHIEIQM	35.31	1738.85	14	0.7	580.624	3	37.4392	3.83E+06	2.37E+07	ZKD_1.raw	P01887|B2MG_MOUSE			FALSE
YVTQFHPPHIEIQM(+15.99)L	25.9	1867.93	15	0.5	623.651	3	37.6927	1.87E+07	8.11E+07	ZKD_1.raw	P01887|B2MG_M	Oxidation (M)		FALSE
YVTQFHPPHIEIQM(+15.99)LK	51.75	1996.02	16	0.8	666.349	3	32.3407	9.46E+05	6.54E+06	ZKD_1.raw	P01887|B2MG_M	Oxidation (M)		FALSE
YVTQFHPPHIEIQML	50.74	1851.93	15	0.3	926.975	2	41.906	1.20E+07	6.51E+07	ZKD_1.raw	P01887|B2MG_MOUSE			FALSE
YVTQFHPPHIEIQMLK	56.86	1980.03	16	0.6	661.017	3	36.252	1.39E+07	5.73E+07	ZKD_1.raw	P01887|B2MG_MOUSE			FALSE
YVTQFHPPHIEIQMLKN	41.53	2094.07	17	2.9	699.033	3	35.5968	8.20E+05	1.18E+07	ZKD_1.raw	P01887|B2MG_MOUSE			FALSE
YVTQFHPPHIEIQMLKNGK	57.21	2279.19	19	-0.9	760.736	3	32.471	1.01E+06	8.05E+06	ZKD_1.raw	P01887|B2MG_MOUSE			FALSE

H2Ab1DIEC-CAD														
Peptide	-10LgP	Mass	Length	ppm	m/z	z	RT	Area ZKD_3	Intensity ZKD_3	Source File	Accession	PTM	AScore	Decoy
A(+42.01)LKRINKELSDLARD	25.41	1783	15	-2.7	595.337	3	32.0743	7.53E+05	1.08E+07	ZKD_3.raw	P61079|UB2D3_M	Acetylation (N-term)		FALSE
ADGYEPPVQESV	48.52	1289.58	12	0.3	645.796	2	25.7669	1.12E+06	1.53E+07	ZKD_3.raw	P97351|RS3A_MOUSE			FALSE
AGIEGPLLASEVERDK	37.38	1682.88	16	4.9	561.971	3	27.5871	3.90E+05	6.77E+06	ZKD_3.raw	Q9QX47|SON_MOUSE			FALSE
AGKVRGQTPKVAKQEKKK	41.94	1980.2	18	0.4	661.073	3	4.3536	3.11E+06	1.25E+07	ZKD_3.raw	P62862|RS30_MOUSE			FALSE
AGNLGGGVVTIER	40.17	1241.67	13	-1.8	621.843	2	22.9019	2.75E+05	9.65E+06	ZKD_3.raw	P67984|RL22_MOUSE			FALSE
AKIKARDLRGKKKEELLKQL	38.78	2364.47	20	-4.7	592.122	4	12.4077			ZKD_3.raw	Q6ZWV7|RL35_MOUSE			FALSE
AKKGGEKKKGRSAINEVVTR	62.84	2155.25	20	-0.2	539.821	4	7.1363	2.78E+06	5.81E+07	ZKD_3.raw	P62900|RL31_MOUSE			FALSE
APM(+15.99)YYRGAQAAIVVYD	34.31	1802.87	16	0.1	902.44	2	29.7975			ZKD_3.raw	P61021|RAB5B_M	Oxidation (M)		FALSE
APMYYRGAQAAIVVY	41.14	1671.84	15	-0.1	836.929	2	33.3421	6.13E+05	1.19E+07	ZKD_3.raw	P61021|RAB5B_MOUSE;Q9CQD1|RAB5A_MOUSE;P3			FALSE
APMYYRGAQAAIVVYD	43.16	1786.87	16	-0.7	894.442	2	32.4788			ZKD_3.raw	P61021|RAB5B_MOUSE;Q9CQD1|RAB5A_MOUSE;P3			FALSE
ASALIDRPAPYFER	46.55	1604.83	14	-0.6	535.951	3	26.1379	1.68E+05	5.58E+06	ZKD_3.raw	Q9WV92|E41L3_MOUSE			FALSE
AVVGVVAGGGRIDKPILK	46.31	1748.07	18	-1	438.024	4	23.6121	5.09E+05	7.79E+06	ZKD_3.raw	P62918|RL8_MOUSE			FALSE
AYVRLAPDYDALDVANK	55.73	1892.96	17	0.6	631.995	3	31.3146	3.27E+06	4.26E+07	ZKD_3.raw	P62751|RL23A_MOUSE			FALSE
DRKIVYEGPELNHAFG	54.31	1843.92	16	-3	615.646	3	26.3715	1.21E+06	3.63E+07	ZKD_3.raw	Q91ZX7|LRP1_MOUSE			FALSE
DSPNKLYTLVTYVPVTTFK	49.17	2185.17	19	2.2	729.398	3	45.9474	4.69E+05	8.77E+06	ZKD_3.raw	P62900|RL31_MOUSE			FALSE
EERERRDNYVPEVSAL	33.71	1960.96	16	0.2	654.661	3	23.7988	1.60E+06	2.22E+07	ZKD_3.raw	P63276|RS17_MOUSE			FALSE
ELEEQLGPVAEETRA	41.59	1669.82	15	-0.3	835.915	2	26.7837	7.81E+05	8.84E+06	ZKD_3.raw	P08226|APOE_MOUSE			FALSE
ENIWKAPEPVEIRE	30.65	1708.88	14	1.1	570.634	3	29.5734	3.49E+05	5.20E+06	ZKD_3.raw	Q9R100|CAD17_MOUSE			FALSE
EPPPAYEPPAPAPAPLPPP	42.66	1903.97	19	0.8	952.994	2	38.6233	9.55E+05	1.01E+07	ZKD_3.raw	O35609|SCAM3_MOUSE			FALSE
FAKLVRPPVQVYG	49.33	1472.85	13	-1.3	491.957	3	27.4553	4.07E+06	6.00E+07	ZKD_3.raw	Q9DB20|ATPO_MOUSE			FALSE
FAKLVRPPVQVYGIEGR	57.69	1928.1	17	0.3	483.032	4	28.4425	1.62E+06	1.28E+07	ZKD_3.raw	Q9DB20|ATPO_MOUSE			FALSE
FPKPPSYNVATTLPSYDE	43.39	2024.97	18	0	1013.49	2	35.18	1.34E+06	1.44E+07	ZKD_3.raw	Q8R0W6|NFIP1_MOUSE			FALSE
FPYVTPAPHEPVK	49.11	1480.77	13	0	494.598	3	22.8251	1.90E+06	1.91E+07	ZKD_3.raw	Q9D074|MGRN1_MOUSE			FALSE
GEKKAYVRLAPDYDALD	45.13	1922.97	17	0	641.999	3	23.645	6.70E+05	1.33E+07	ZKD_3.raw	P62751|RL23A_MOUSE			FALSE
GFVKVVKNKAYFKRYQVRFR	59	2532.46	20	-1	634.122	4	18.7238	1.05E+07	1.12E+08	ZKD_3.raw	P47962|RL5_MOUSE			FALSE
GIYVSEKGTVQQADE	55.15	1622.78	15	2.1	812.398	2	18.0255	5.92E+05	1.77E+07	ZKD_3.raw	P51410|RL9_MOUSE			FALSE
GLKGRVFEVSLA	25.25	1274.73	12	-1.1	638.374	2	27.7473			ZKD_3.raw	P97351|RS3A_MOUSE			FALSE
GM(+15.99)AFRVPTPNVSVVD	37.78	1603.8	15	-0.6	802.908	2	34.6448			ZKD_3.raw	P16858|G3P_MOU	Oxidation (M)		FALSE
GMAFRVPTPNVSVVD	47.97	1587.81	15	2.4	794.913	2	38.6363			ZKD_3.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
GPDGRFVMGPTVAPSQEK	42.36	1871.92	18	3.3	624.983	3	22.6773	2.45E+05	5.99E+06	ZKD_3.raw	Q05BQ1|TUTLA_MOUSE			FALSE
GSDMFKASLVIPSKD	44	1593.81	15	0.8	532.277	3	31.1509	1.47E+05	5.04E+06	ZKD_3.raw	Q8BJD1|ITIH5_MOUSE			FALSE
GVPLDATEDSKKNEPIFK	48.97	1987.03	18	-2	663.348	3	21.4225	9.52E+05	1.54E+07	ZKD_3.raw	Q6NV83|SR140_MOUSE			FALSE
HINIVVIGHVDSGK	53.57	1486.83	14	1.9	496.617	3	22.1576	7.73E+05	1.62E+07	ZKD_3.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
HLKIVYRRFRHG	28.08	1580.92	12	0.5	396.237	4	10.8226	7.58E+06	1.54E+08	ZKD_3.raw	Q9D823|RL37_MOUSE			FALSE
HLKIVYRRFRHGF	23.77	1727.98	13	1	433.004	4	14.2691			ZKD_3.raw	Q9D823|RL37_MOUSE			FALSE
IIGGDTVVPHSRPYMALLK	36.23	2066.13	19	-0.1	517.541	4	31.0238	2.54E+05	4.40E+06	ZKD_3.raw	P11032|GRAA_MOUSE			FALSE
IKIAWESPQGQVSR	48.17	1597.86	14	-0.5	533.626	3	23.7982	2.61E+05	4.94E+06	ZKD_3.raw	P11276|FINC_MOUSE			FALSE
INIVVIGHVDSGK	48.8	1349.77	13	0.2	450.93	3	27.1679	1.91E+06	2.42E+07	ZKD_3.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
INIVVIGHVDSGKSTTT	27.43	1739.94	17	4.3	580.99	3	27.0784			ZKD_3.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
IREFYSASVAEDATL	39.3	1670.82	15	-0.5	836.414	2	32.7332			ZKD_3.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IREFYSASVAEDATLG	45.43	1727.84	16	0.1	864.926	2	31.5653			ZKD_3.raw	E9Q7P9|CDHR2_MOUSE			FALSE
KAYVRLAPDYDALDVANK	51.02	2021.06	18	0.2	674.694	3	26.8323	1.96E+05	6.44E+06	ZKD_3.raw	P62751|RL23A_MOUSE			FALSE
KFTYRGVDLDQLLD	27.06	1681.87	14	0.1	561.63	3	37.8714	1.85E+06	2.92E+07	ZKD_3.raw	P62843|RS15_MOUSE			FALSE
KFYKGKKYKPLDLRPKKT	66	2237.34	18	0.7	746.788	3	10.7954	1.11E+07	1.94E+08	ZKD_3.raw	Q6ZWV7|RL35_MOUSE			FALSE
KFYKGKKYKPLDLRPKKTR	64.01	2393.44	19	-2.6	479.695	5	10.1753	2.57E+07	4.23E+08	ZKD_3.raw	Q6ZWV7|RL35_MOUSE			FALSE
KISRNPTFKVLKDRVKLLK	29.23	2282.43	19	-5.6	571.612	4	18.7532			ZKD_3.raw	Q08288|LYAR_MOUSE			FALSE
KKAKAKGKGQPQARVTVNR	48.11	2064.24	19	0	413.855	5	6.2445	1.39E+06	5.51E+07	ZKD_3.raw	Q9D6S7|RRFM_MOUSE			FALSE
KKKKKKKKPFMLD	27.44	1646.04	13	-0.1	412.518	4	6.721	3.00E+06	2.67E+07	ZKD_3.raw	Q99L45|IF2B_MOUSE			FALSE
KKKKRFSFKKSFK	26.2	1686.05	13	0.5	422.519	4	6.9981	7.52E+05	2.53E+07	ZKD_3.raw	P26645|MARCS_MOUSE			FALSE
KKNS(+79.97)KVRRQQRKKKPPA	24.02	2156.25	17	-5.9	540.067	4	47.7388			ZKD_3.raw	Q8CFW7|C2D2A	Phosphorylation (STY)		FALSE
KKPAAAAGAKKVS(+79.97)KS(+79.97)	25.85	1600.81	15	1.4	401.21	4	6.6163			ZKD_3.raw	P43277|H13_MOU	Phosphorylation (STY); Phosphorylati		FALSE
KLLEPVDHGKIEYEPFR	36.61	2069.09	17	0.1	518.281	4	25.3026			ZKD_3.raw	Q569Z5|DDX46_MOUSE			FALSE
KPLQPKQ(+0.98)PTLTGKKITEK	24.21	2035.2	18	0.5	509.809	4	18.8686			ZKD_3.raw	Q9CQJ7|PTTG1_I	Deamidation (NQ)	Q7:Deamidation (N	FALSE
KPVSQ(+0.98)M(+15.99)RMATPLLMRPM	29.16	2003.02	17	9	501.767	4	25.21			ZKD_3.raw	P04441|HG2A_MO	Deamidation (NQ)	Q5:Deamidation (N	FALSE
KPVSQM(+15.99)RMATPLLMRPM	39	2002.03	17	2.8	501.517	4	26.0916	8.48E+05	1.35E+07	ZKD_3.raw	P04441|HG2A_MO	Oxidation (M)	M6:Oxidation (M):9	FALSE
KPVSQMRM(+15.99)ATPLLMRPM	38.08	2002.03	17	-0.6	668.352	3	25.2049	4.51E+05	6.68E+06	ZKD_3.raw	P04441|HG2A_MO	Oxidation (M)	M8:Oxidation (M):0	FALSE
KPVSQMRMATPLLM(+15.99)RPM(+15.99)	35.92	2018.03	17	0.9	505.515	4	23.1655	1.83E+06	4.49E+07	ZKD_3.raw	P04441|HG2A_MO	Oxidation (M); Oxi	M14:Oxidation (M)	FALSE
KPVSQMRMATPLLMRP	36	1855	16	3.1	464.759	4	27.138	5.46E+05	7.96E+06	ZKD_3.raw	P04441|HG2A_MOUSE			FALSE
KPVSQMRMATPLLMRPM	45.38	1986.04	17	2.1	663.022	3	30.2637	4.05E+06	5.13E+07	ZKD_3.raw	P04441|HG2A_MOUSE			FALSE
KQPVIVKAKFFS	39.63	1390.83	12	-9	696.418	2	27.1988	5.65E+05	1.04E+07	ZKD_3.raw	P14115|RL27A_MOUSE			FALSE
LAPDYDALDVANK	52.06	1403.69	13	-0.4	702.854	2	27.8995	1.85E+07	2.11E+08	ZKD_3.raw	P62751|RL23A_MOUSE			FALSE
LAPDYDALDVANKIG	37.53	1573.8	15	1.7	787.908	2	35.8175	3.97E+05	8.80E+06	ZKD_3.raw	P62751|RL23A_MOUSE			FALSE
LLILLILCFIKRS(+79.97)KG	25.16	1809.07	15	6.6	453.278	4	35.7826			ZKD_3.raw	P11627|L1CAM_M	Phosphorylation (STY)		FALSE
LVTLPVSFAQLK	39.77	1314.79	12	-0.4	658.403	2	43.105	7.06E+05	1.50E+07	ZKD_3.raw	Q922Q8|LRC59_MOUSE			FALSE
M(+15.99)GGLQISSFKLE	40.97	1324.67	12	-0.7	663.342	2	35.4512	1.18E+05	3.92E+06	ZKD_3.raw	Q9CQW5|LEG2_M	Oxidation (M)		FALSE
M(+42.01)(+15.99)NDTVTIRTRKFMTNR	35.62	2041.02	16	-2.1	511.261	4	18.7083	1.41E+06	2.91E+07	ZKD_3.raw	P62849|RS24_MO	Acetylation (N-term	M1:Acetylation (N-	FALSE
M(+42.01)FSSSAKIVKPNGEKPDEFE	51.5	2281.09	20	3.1	761.374	3	30.3253	8.29E+05	1.49E+07	ZKD_3.raw	P62082|RS7_MOU	Acetylation (N-term)		FALSE
M(+42.01)NDTVTIRTRKFMTNR	33.91	2025.02	16	0	507.264	4	23.2976	9.92E+06	1.09E+08	ZKD_3.raw	P62849|RS24_MO	Acetylation (N-term)		FALSE
NPHVNPLPTGYE	48.84	1336.64	12	-0.5	669.328	2	23.2965	1.22E+06	2.16E+07	ZKD_3.raw	P43023|CX6A2_MOUSE;P43024|CX6A1_MOUSE			FALSE
NPHVNPLPTGYEDE	51.76	1580.71	14	0.5	791.363	2	23.6932	1.58E+05	5.73E+06	ZKD_3.raw	P43024|CX6A1_MOUSE			FALSE
NPLNSVFVAPAVTPVK	57.92	1651.93	16	0.1	826.972	2	39.0788	7.04E+05	1.77E+07	ZKD_3.raw	P70158|ASM3A_MOUSE			FALSE
NPLNSVFVAPAVTPVKG	60.66	1708.95	17	5.1	855.487	2	38.8948	8.39E+05	1.37E+07	ZKD_3.raw	P70158|ASM3A_MOUSE			FALSE
NPPSYYTQPVPVPNAN	47.34	1756.84	16	3.3	879.431	2	31.3476	2.61E+05	5.51E+06	ZKD_3.raw	Q9JLJ0|LITAF_MOUSE			FALSE
NSIIGDHKRWPHTIPYVLE	31.12	2274.19	19	-1.4	569.554	4	31.8585	2.10E+06	2.63E+07	ZKD_3.raw	Q61847|MEP1B_MOUSE			FALSE
NVQFNYPQASVTDVT	31.17	1681.79	15	3.8	841.908	2	35.1741			ZKD_3.raw	Q61703|ITIH2_MOUSE			FALSE
PGVTVKDVNQQEFVR	55.46	1714.9	15	-3.3	572.639	3	21.4549	1.54E+06	1.27E+07	ZKD_3.raw	Q9CZX8|RS19_MOUSE			FALSE
PGVTVKDVNQQEFVRALA	56.79	1970.06	18	4.3	657.696	3	31.7345	4.13E+05	1.00E+07	ZKD_3.raw	Q9CZX8|RS19_MOUSE			FALSE
PRKIEEIKDFLLT	28.69	1600.92	13	-1.2	534.646	3	31.5715	5.87E+05	9.97E+06	ZKD_3.raw	Q9JJI8|RL38_MOUSE			FALSE
PRKIEEIKDFLLTARRKD	27.35	2227.28	18	2.2	557.829	4	25.1857	9.58E+05	9.01E+06	ZKD_3.raw	Q9JJI8|RL38_MOUSE			FALSE
PSSRPQSSGTKKLRLVGPT	26.02	1995.12	19	1.7	499.789	4	31.0339			ZKD_3.raw	Q924C6|LOXL4_MOUSE			FALSE
QYAKDIGFIKLD	25.15	1409.76	12	-0.8	470.925	3	31.3146	5.16E+06	5.04E+07	ZKD_3.raw	P62274|RS29_MOUSE			FALSE
RENIWKAPEPVEIRE	46.31	1864.98	15	-0.6	622.667	3	24.7198	6.03E+05	1.48E+07	ZKD_3.raw	Q9R100|CAD17_MOUSE			FALSE
RKDAKSVKIKKNKDNVKFK	63.54	2273.37	19	-1.9	569.349	4	6.8024	1.56E+06	4.93E+07	ZKD_3.raw	Q9JJI8|RL38_MOUSE			FALSE
RKEVRYGSLKYKVKKRP	50.53	2134.29	17	-0.3	534.578	4	9.0868			ZKD_3.raw	Q99KK1|REEP3_MOUSE			FALSE
RKEVRYGSLKYKVKKRPQ(+0.98)V	37.36	2362.4	19	9.3	473.491	5	10.6836	1.86E+06	3.73E+07	ZKD_3.raw	Q99KK1|REEP3_I	Deamidation (NQ)		FALSE
RKEVRYGSLKYKVKKRPQV	36.6	2361.41	19	-1.3	394.575	6	10.6697	4.26E+06	5.95E+07	ZKD_3.raw	Q99KK1|REEP3_MOUSE			FALSE
RKIVYEGPELNHAFG	55.89	1728.89	15	-0.8	577.305	3	22.9483	2.03E+06	2.72E+07	ZKD_3.raw	Q91ZX7|LRP1_MOUSE			FALSE
RKPYHKKRKYELGRPA	51.54	2026.17	16	5.8	507.553	4	6.6588	7.03E+06	1.37E+08	ZKD_3.raw	P62242|RS8_MOUSE			FALSE
RKTRKLRGHVSHGHGRIGKH	25.36	2316.34	20	0	464.275	5	1.1287	1.06E+07	2.22E+07	ZKD_3.raw	P14115|RL27A_MOUSE			FALSE
RPDAEYWNSQPEILER	54.35	2001.95	16	-1.2	668.325	3	28.1565	1.31E+06	1.58E+07	ZKD_3.raw	P14483|HB2A_MOUSE;P01921|HB2D_MOUSE;P0634			FALSE
RPVQFPYVTPAPHEPVK	50.5	1961.05	17	1.4	654.692	3	23.872	1.67E+05	5.66E+06	ZKD_3.raw	Q9D074|MGRN1_MOUSE			FALSE
RTQ(+0.98)GTKIASDGLKGRVFE	33.9	1963.05	18	7.9	491.773	4	15.8161			ZKD_3.raw	P97351|RS3A_MO	Deamidation (NQ)		FALSE
RTQGTKIASDGLKGRVFE	45.49	1962.06	18	-2.7	491.522	4	15.7796	1.18E+06	2.64E+07	ZKD_3.raw	P97351|RS3A_MOUSE			FALSE
S(+42.01)GDHLHNDSQIEADFR	31.31	1881.82	16	1.6	628.283	3	21.2969			ZKD_3.raw	Q04750|TOP1_MO	Acetylation (N-term)		FALSE
S(+42.01)IRVTQKSYKM(+15.99)STSGPRA	51.31	2054.06	18	-0.1	514.522	4	12.9142	8.09E+05	1.14E+07	ZKD_3.raw	P11679|K2C8_MO	Acetylation (N-term); Oxidation (M)		FALSE
S(+42.01)IRVTQKSYKMS	26.73	1468.77	12	0	490.598	3	16.5006			ZKD_3.raw	P11679|K2C8_MO	Acetylation (N-term)		FALSE
S(+42.01)IRVTQKSYKMSTSGP	26.27	1810.92	16	-0.4	604.649	3	19.1684	4.31E+05	1.37E+07	ZKD_3.raw	P11679|K2C8_MO	Acetylation (N-term)		FALSE
S(+42.01)IRVTQKSYKMSTSGPRA	47.17	2038.06	18	0.7	680.362	3	16.1665			ZKD_3.raw	P11679|K2C8_MO	Acetylation (N-term)		FALSE
S(+42.01)IRVTQKSYKMSTSGPRAF	60.88	2185.13	19	-0.1	547.29	4	22.0945	2.73E+06	5.62E+07	ZKD_3.raw	P11679|K2C8_MO	Acetylation (N-term)		FALSE
S(+42.01)LVIPEKFQHILR	44.71	1620.94	13	-2.4	541.318	3	40.1281	6.14E+06	5.75E+07	ZKD_3.raw	P62270|RS18_MO	Acetylation (N-term)		FALSE
SDGLKGRVFEVSLA	23.39	1476.79	14	0.7	493.272	3	30.3252	2.14E+05	5.20E+06	ZKD_3.raw	P97351|RS3A_MOUSE			FALSE
SGKIEVEKPFAIAKE	47.51	1644.91	15	-0.7	412.234	4	21.095	6.22E+05	8.38E+06	ZKD_3.raw	P24369|PPIB_MOUSE			FALSE
SLQAFSNPSAGISVDVK	35.04	1718.88	17	0.6	860.45	2	32.9269			ZKD_3.raw	Q8BG07|PLD4_MOUSE			FALSE
SLVSKGTLVQTK	47.78	1259.74	12	-0.6	420.922	3	15.1312	2.10E+06	3.81E+07	ZKD_3.raw	P43276|H15_MOUSE;P43274|H14_MOUSE;P43277|H1			FALSE
SPNKLYTLVTYVPVTTFK	46.77	2070.14	18	4.2	691.057	3	41.9004			ZKD_3.raw	P62900|RL31_MOUSE			FALSE
SPPHVQFTYQQPQPLSVEPR	58.57	2334.18	20	-0.6	779.065	3	29.9197	1.75E+06	2.91E+07	ZKD_3.raw	B2RXS4|PLXB2_MOUSE			FALSE
SSAASSGGDSGV	26.12	980.405	12	-1.5	491.209	2	22.3895			ZKD_3.raw	Q80TF6|STAR9_MOUSE			FALSE
SSHKTFRIKRFL	37.12	1518.88	12	-2	380.726	4	14.2622	3.95E+06	5.09E+07	ZKD_3.raw	P62892|RL39_MOUSE			FALSE
SSHKTFRIKRFLA	44.9	1589.92	13	-1.6	398.486	4	14.1019	2.99E+06	5.75E+07	ZKD_3.raw	P62892|RL39_MOUSE			FALSE
SSHKTFRIKRFLAKKQ	37.07	1974.16	16	-1.3	494.548	4	10.3275	5.07E+06	8.10E+07	ZKD_3.raw	P62892|RL39_MOUSE			FALSE
SVFVAPAVTPVK	52.8	1213.71	12	-2	607.86	2	30.1976	1.52E+06	3.00E+07	ZKD_3.raw	P70158|ASM3A_MOUSE			FALSE
SVFVAPAVTPVKG	47.46	1270.73	13	1.1	636.372	2	30.0745	2.38E+06	3.40E+07	ZKD_3.raw	P70158|ASM3A_MOUSE			FALSE
SVNVDYSKLKKEGPDF	34.75	1824.93	16	0.4	609.316	3	23.5614	1.96E+06	3.22E+07	ZKD_3.raw	Q62425|NDUA4_MOUSE			FALSE
T(+79.97)LVT(+79.97)RTQ(+0.98)GTKIASDGLKGR	29.68	2162.05	19	4.2	541.522	4	32.1891			ZKD_3.raw	P97351|RS3A_MO	Phosphorylation (S	T1:Phosphorylatio	FALSE
TGM(+15.99)AFRVPTPNVSVVD	56.41	1704.85	16	0.9	853.433	2	34.7008	7.63E+06	3.99E+07	ZKD_3.raw	P16858|G3P_MOU	Oxidation (M)		FALSE
TGMAFRVPTPNVSVVD	51.75	1688.86	16	0.9	845.436	2	38.8981	8.38E+06	6.05E+07	ZKD_3.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
TGNKIRYNSKRRHWR	25.59	1971.08	15	-0.9	493.776	4	6.998	7.08E+05	1.77E+07	ZKD_3.raw	P62892|RL39_MOUSE			FALSE
THINIVVIGHVDSGK	53.86	1587.87	15	0.9	530.299	3	23.015	3.55E+07	2.56E+08	ZKD_3.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
THINIVVIGHVDSGKST	56.09	1775.95	17	-0.9	592.991	3	22.95	1.18E+06	2.04E+07	ZKD_3.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
THINIVVIGHVDSGKSTTT	60.15	1978.05	19	3.7	660.359	3	23.0763	3.09E+06	3.67E+07	ZKD_3.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE			FALSE
TLVTRTQGTKIASDGLKGR	42.24	2001.13	19	-2.6	401.233	5	14.0099	1.05E+07	2.02E+08	ZKD_3.raw	P97351|RS3A_MOUSE			FALSE
TLVTYVPVTTFK	43.15	1367.77	12	0.1	684.892	2	36.4155	3.97E+06	5.38E+07	ZKD_3.raw	P62900|RL31_MOUSE			FALSE
TPSAAYLWVGAGASEAEKT	52.93	1907.93	19	-1	954.97	2	34.6207	1.18E+05	3.75E+06	ZKD_3.raw	P13020|GELS_MOUSE;#CONTAM#Q3SX14			FALSE
VAIFARGPQAHLVH	34.3	1514.85	14	-0.7	379.719	4	21.3594	1.85E+06	2.36E+07	ZKD_3.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
VAIFARGPQAHLVHG	32.48	1571.87	15	0.4	524.964	3	21.2593	9.36E+06	9.18E+07	ZKD_3.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
VAIFARGPQAHLVHGVQ	29.14	1799	17	-0.6	450.756	4	23.0477	5.34E+06	6.17E+07	ZKD_3.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
VLTVINQTQKENLR	47.98	1654.94	14	0	552.653	3	19.5654	1.27E+07	1.38E+08	ZKD_3.raw	Q6ZWV7|RL35_MOUSE			FALSE
VLTVINQTQKENLRKFYK	38.03	2221.26	18	2.7	556.323	4	22.5096			ZKD_3.raw	Q6ZWV7|RL35_MOUSE			FALSE
VNVDYSKLKKEGPDF	27.29	1737.89	15	2.7	580.307	3	22.9256			ZKD_3.raw	Q62425|NDUA4_MOUSE			FALSE
VSLADLQNDEVAFR	40.43	1575.79	14	0	788.902	2	36.9478	2.25E+06	3.40E+07	ZKD_3.raw	P97351|RS3A_MOUSE			FALSE
YFQINQDEEEEEDED	35.41	1930.72	15	1	966.37	2	26.7195	1.86E+06	4.62E+07	ZKD_3.raw	P67984|RL22_MOUSE			FALSE
YLNIYVPAHAHEGSN	45.68	1683.8	15	5.1	562.277	3	23.7113			ZKD_3.raw	Q8BK48|EST2E_MOUSE			FALSE
YVPVTTFKNLQTVNVDEN	46.55	2080.05	18	0.8	1041.03	2	34.3613	2.38E+06	3.30E+07	ZKD_3.raw	P62900|RL31_MOUSE			FALSE
YVTQFHPPHIEIQMLK	25.39	1980.03	16	-1.2	496.014	4	34.654			ZKD_3.raw	P01887|B2MG_MOUSE			FALSE

H2Ab1f f-AAD														
Peptide	-10LgP	Mass	Length	ppm	m/z	z	RT	Area ZKD_5	Intensity ZKD_5	Source File	Accession	PTM	AScore	Decoy
A(+42.01)AKKTKKPAKAAAPRKK	26.37	1834.16	17	-9.7	459.544	4	6.1509			ZKD_5.raw	P43275|H11_MOU	Acetylation (N-term)		FALSE
A(+42.01)SLVPLKEKKLME	33.31	1526.87	13	0.4	509.966	3	29.3839	2.42E+05	5.78E+06	ZKD_5.raw	P56135|ATPK_MO	Acetylation (N-term)		FALSE
AAYLWVGAGASEAEK	42.66	1521.75	15	3.1	761.883	2	29.6659	3.06E+05	6.58E+06	ZKD_5.raw	P13020|GELS_MOUSE;#CONTAM#Q3SX14			FALSE
AAYLWVGAGASEAEKT	44.53	1622.79	16	0.8	812.405	2	30.3784	3.36E+06	4.90E+07	ZKD_5.raw	P13020|GELS_MOUSE;#CONTAM#Q3SX14			FALSE
ADFHYAASKALRVPA	49.3	1615.85	15	-4.5	539.621	3	23.3127	5.33E+05	1.07E+07	ZKD_5.raw	Q80TA9|EPG5_MOUSE			FALSE
ADGYEPPVQESV	43.38	1289.58	12	-0.6	645.796	2	25.6783	7.05E+05	1.05E+07	ZKD_5.raw	P97351|RS3A_MOUSE			FALSE
AIFARGPQAHLVHG	41.89	1472.8	14	-1.5	491.94	3	21.4232	3.14E+06	3.71E+07	ZKD_5.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
AKIKARDLRGKKKEELLKQL	36.15	2364.47	20	0.5	592.125	4	13.0782	2.15E+06	3.72E+07	ZKD_5.raw	Q6ZWV7|RL35_MOUSE			FALSE
AKKAPKS(+79.97)PAKAKT(+79.97)	21.98	1484.75	13	1.9	495.925	3	6.558			ZKD_5.raw	P43274|H14_MOU	Phosphorylation (STY); Phosphorylati		FALSE
AKKGGEKKKGRSAINEVVTR	25.69	2155.25	20	-1.8	432.058	5	7.4307	7.36E+05	1.22E+07	ZKD_5.raw	P62900|RL31_MOUSE			FALSE
AKPVSQ(+0.98)MRMATPLLMRPM	32.84	2058.06	18	8.2	515.527	4	30.5179			ZKD_5.raw	P04441|HG2A_MO	Deamidation (NQ)		FALSE
AKPVSQMRM(+15.99)ATPLLMRPM	33.24	2073.07	18	-0.6	519.275	4	25.9941	1.21E+06	2.29E+07	ZKD_5.raw	P04441|HG2A_MO	Oxidation (M)	M9:Oxidation (M):(	FALSE
AKPVSQMRMATPLLM(+15.99)RPM	24.46	2073.07	18	-0.9	519.275	4	26.8781	1.07E+06	1.13E+07	ZKD_5.raw	P04441|HG2A_MO	Oxidation (M)	M15:Oxidation (M)	FALSE
AKPVSQMRMATPLLMRPM	36.76	2057.08	18	-0.6	515.276	4	30.533	6.94E+06	9.95E+07	ZKD_5.raw	P04441|HG2A_MOUSE			FALSE
AKPVSQMRMATPLLMRPM(+15.99)	40.9	2073.07	18	0.3	692.031	3	27.222	9.79E+05	1.31E+07	ZKD_5.raw	P04441|HG2A_MO	Oxidation (M)	M18:Oxidation (M)	FALSE
ALAVAGAPIALSAVG	36.29	1279.75	15	0.8	640.883	2	44.3617	6.62E+05	8.41E+06	ZKD_5.raw	Q8VC49|IF27B_MOUSE			FALSE
APAAPAAPAPAEKTPVKK	23.26	1713.98	18	-8.6	572.328	3	47.3037			ZKD_5.raw	P43274|H14_MOUSE			FALSE
APAAPAAPAPAEKTPVKKKA	30.37	1913.11	20	-9.9	479.28	4	51.0965			ZKD_5.raw	P43274|H14_MOUSE			FALSE
APFFIVRHQLLKK	22.12	1595.97	13	-1.5	399.998	4	22.5915	3.65E+05	5.45E+06	ZKD_5.raw	P17665|COX7C_MOUSE			FALSE
APGGYVAPKAVWLPA	43.04	1495.82	15	3.2	748.919	2	36.7155	1.38E+06	1.84E+07	ZKD_5.raw	Q9DBG3|AP2B1_MOUSE			FALSE
APGILPPPPPTPYHFT	22.19	1700.89	16	4.5	567.974	3	52.1412			ZKD_5.raw	Q6PB44|PTN23_MOUSE			FALSE
APISSHTAPRPNPTPA	27.3	1612.83	16	-2.7	538.617	3	13.2563	1.09E+06	3.85E+07	ZKD_5.raw	Q6PB44|PTN23_MOUSE			FALSE
APM(+15.99)YYRGAQAAIVV	27.44	1524.78	14	0.3	763.395	2	27.9272			ZKD_5.raw	P61021|RAB5B_M	Oxidation (M)		FALSE
APM(+15.99)YYRGAQAAIVVY	36.3	1687.84	15	-0.2	844.927	2	30.316	8.43E+06	5.60E+07	ZKD_5.raw	P61021|RAB5B_M	Oxidation (M)		FALSE
APM(+15.99)YYRGAQAAIVVYD	37.97	1802.87	16	1.7	902.442	2	29.3839	1.43E+07	9.18E+07	ZKD_5.raw	P61021|RAB5B_M	Oxidation (M)		FALSE
APMYYRGAQAAIVV	40.5	1508.78	14	1.3	755.399	2	30.8768	1.24E+06	1.64E+07	ZKD_5.raw	P61021|RAB5B_MOUSE;Q9CQD1|RAB5A_MOUSE;P3			FALSE
APMYYRGAQAAIVVY	40.29	1671.84	15	0	836.929	2	33.0264	1.23E+07	1.46E+08	ZKD_5.raw	P61021|RAB5B_MOUSE;Q9CQD1|RAB5A_MOUSE;P3			FALSE
APMYYRGAQAAIVVYD	43.24	1786.87	16	0.2	894.443	2	32.0731	2.20E+07	2.54E+08	ZKD_5.raw	P61021|RAB5B_MOUSE;Q9CQD1|RAB5A_MOUSE;P3			FALSE
APPLPIKTPIPTPST	51.58	1528.89	15	0.7	765.451	2	36.749	6.42E+05	9.20E+06	ZKD_5.raw	Q7TQH7|LRP10_MOUSE			FALSE
APSNYLNNPYVRKALHIPE	30.92	2195.15	19	0.6	549.795	4	34.3424	6.65E+06	1.57E+08	ZKD_5.raw	P16675|PPGB_MOUSE			FALSE
APYGARYVGSMVADIHR	38.02	1861.93	17	0	466.489	4	26.4395	5.20E+05	6.93E+06	ZKD_5.raw	Q9QXD6|F16P1_MOUSE			FALSE
ATNPIITPVAQENQ	44.3	1494.77	14	0.1	748.391	2	28.3083	1.16E+06	1.48E+07	ZKD_5.raw	P08226|APOE_MOUSE			FALSE
AVS(+79.97)PAAAAKAAA	20.96	1077.52	12	-7.5	539.764	2	43.2758			ZKD_5.raw	P54320|ELN_MOU	Phosphorylation (STY)		FALSE
AYVRLAPDYDALDVANK	47.32	1892.96	17	0.1	631.995	3	30.9762			ZKD_5.raw	P62751|RL23A_MOUSE			FALSE
DGDSYRSPWSNKYDPP	38.99	1882.81	16	-0.7	628.611	3	24.6521	2.22E+06	2.46E+07	ZKD_5.raw	P47757|CAPZB_MOUSE			FALSE
DGDSYRSPWSNKYDPPL	37.74	1995.9	17	0.6	666.306	3	31.1637	4.43E+06	3.77E+07	ZKD_5.raw	P47757|CAPZB_MOUSE			FALSE
DGNHTLFHNPHVNPLPTGYE	45.88	2258.05	20	-3.4	753.688	3	28			ZKD_5.raw	P43023|CX6A2_MOUSE;P43024|CX6A1_MOUSE			FALSE
DLEYQMSTTARAK	40.37	1512.72	13	2.1	505.25	3	17.6387	3.47E+05	5.74E+06	ZKD_5.raw	Q02257|PLAK_MOUSE			FALSE
DLNFFNQKKKKKKTKK	42.91	2022.21	16	4.2	506.562	4	8.6526			ZKD_5.raw	Q99L45|IF2B_MOUSE			FALSE
DPTPDPNTAYASYPSASVEN	41.74	2094.9	20	2.8	1048.46	2	28.4837	3.25E+05	6.82E+06	ZKD_5.raw	O55101|SNG2_MOUSE			FALSE
DRKIVYEGPELNHAFG	47.08	1843.92	16	0.8	615.648	3	26.2492	3.39E+07	2.61E+08	ZKD_5.raw	Q91ZX7|LRP1_MOUSE			FALSE
DRPHTYFGPETSASKF	36.99	1838.86	16	3.9	613.963	3	21.6154			ZKD_5.raw	P70277|SIA7B_MOUSE			FALSE
DRPHTYFGPETSASKFK	47.49	1966.95	17	0	492.746	4	16.4476	7.99E+05	1.17E+07	ZKD_5.raw	P70277|SIA7B_MOUSE			FALSE
DTEGRLEVVTDPTTNAGYVK	43.23	2164.06	20	5.7	722.366	3	26.1914			ZKD_5.raw	Q9R100|CAD17_MOUSE			FALSE
DTIEFRGPNGLLVYQ	43.89	1720.88	15	4.9	861.451	2	40.6307	1.14E+06	1.85E+07	ZKD_5.raw	Q9DCN2|NB5R3_MOUSE			FALSE
DTIEFRGPNGLLVYQG	45.54	1777.9	16	1.4	889.958	2	40.6834	6.97E+06	9.28E+07	ZKD_5.raw	Q9DCN2|NB5R3_MOUSE			FALSE
DTIEFRGPNGLLVYQGK	34.69	1905.99	17	0.2	636.339	3	34.5881			ZKD_5.raw	Q9DCN2|NB5R3_MOUSE			FALSE
DVAIFARGPQAHLVH	36.38	1629.87	15	-1.7	544.298	3	26.3798	8.93E+05	1.25E+07	ZKD_5.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
DVAIFARGPQAHLVHG	32.32	1686.9	16	0.7	563.306	3	26.3427	2.76E+06	2.97E+07	ZKD_5.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
DVAIFARGPQAHLVHGVQ	43.7	1914.02	18	-0.6	639.014	3	27.8281	2.28E+06	4.08E+07	ZKD_5.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
EDLSYQSSLASWNYN	47.68	1775.76	15	1.1	888.89	2	38.3183	8.36E+05	1.81E+07	ZKD_5.raw	Q8R0I0|ACE2_MOUSE			FALSE
EDRRYNPPIIHQGFQ	34.22	1868.93	15	2.7	623.985	3	21.2785	1.03E+05	3.32E+06	ZKD_5.raw	P27784|CCL6_MOUSE			FALSE
EDVAIFARGPQAHLVHG	32.97	1815.94	17	-0.9	606.319	3	26.0318			ZKD_5.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
EDVAIFARGPQAHLVHGVQ	26.52	2043.06	19	5.7	511.776	4	27.5007			ZKD_5.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
EFQAWKSPGASLLPV	41.37	1628.86	15	0.5	815.436	2	43.3574	1.84E+05	6.47E+06	ZKD_5.raw	Q8VC30|TKFC_MOUSE			FALSE
EHCQYVS(+79.97)EKVLAAVYK	47.49	1945.9	16	-6.6	649.637	3	31.1357			ZKD_5.raw	Q91Y97|ALDOB_I	Phosphorylation (S	S7:Phosphorylatio	FALSE
ELEEQLGPVAEETR	43.74	1598.78	14	-1.6	800.395	2	25.242	1.58E+06	2.14E+07	ZKD_5.raw	P08226|APOE_MOUSE			FALSE
ELEEQLGPVAEETRA	41.89	1669.82	15	-0.4	835.915	2	26.6295	2.28E+06	2.53E+07	ZKD_5.raw	P08226|APOE_MOUSE			FALSE
ENIWKAPEPVEIR	42.72	1579.84	13	-2.3	527.618	3	28.8193	5.74E+05	1.33E+07	ZKD_5.raw	Q9R100|CAD17_MOUSE			FALSE
ENIWKAPEPVEIRE	42.76	1708.88	14	0.2	570.634	3	29.2323	6.14E+06	7.31E+07	ZKD_5.raw	Q9R100|CAD17_MOUSE			FALSE
ENPIYKSAVTTVVNPK	41.63	1758.95	16	2.5	587.326	3	24.9611	3.39E+05	5.87E+06	ZKD_5.raw	P09055|ITB1_MOUSE			FALSE
EPGRYRFMGAEASAESIE	31.86	1998.91	18	-1.4	667.31	3	25.1159	1.66E+06	2.17E+07	ZKD_5.raw	Q91WV7|SLC31_MOUSE			FALSE
EPPPAYEPPAPAPAPLPP	37.7	1806.92	18	0.2	904.467	2	37.3618	2.61E+06	1.14E+07	ZKD_5.raw	O35609|SCAM3_MOUSE			FALSE
EPPPAYEPPAPAPAPLPPP	35.49	1903.97	19	1.2	635.665	3	38.3744	2.82E+07	1.08E+08	ZKD_5.raw	O35609|SCAM3_MOUSE			FALSE
EPYGARYVGSMVADVHR	35.71	1905.92	17	-1.5	636.312	3	25.8696	4.07E+06	4.81E+07	ZKD_5.raw	P70695|F16P2_MOUSE			FALSE
EPYGARYVGSMVADVHRT	39.44	2006.96	18	-0.8	669.995	3	25.9807			ZKD_5.raw	P70695|F16P2_MOUSE			FALSE
ERASFITPVPGGVG	42.84	1385.73	14	0.2	693.873	2	30.7323	1.28E+05	4.14E+06	ZKD_5.raw	Q922D8|C1TC_MOUSE			FALSE
ESEPYTFSHPNKGEIG	28.83	1790.81	16	0.4	597.945	3	19.5193	2.75E+06	4.95E+07	ZKD_5.raw	Q5U462|CDCP1_MOUSE			FALSE
EVSSVEAPSVSPAR	41	1413.71	14	0.1	707.862	2	18.6436	3.28E+06	4.12E+07	ZKD_5.raw	Q8BUJ9|LRP12_MOUSE			FALSE
EWKDYKAGFGNLERE	29.96	1840.87	15	-1.9	461.225	4	23.5659	7.30E+05	1.15E+07	ZKD_5.raw	P12804|FGL2_MOUSE			FALSE
FAAPFFIVRHQLLKK	45.88	1814.07	15	0.3	454.525	4	31.9407	9.60E+05	9.86E+06	ZKD_5.raw	P17665|COX7C_MOUSE			FALSE
FAKLVRPPVQ(+0.98)VYGIEGRYA	36.89	2163.18	19	8.9	541.808	4	30.5018	4.06E+05	8.50E+06	ZKD_5.raw	Q9DB20|ATPO_M	Deamidation (NQ)		FALSE
FAKLVRPPVQVY	41.05	1415.83	12	1	472.951	3	27.9223	8.28E+05	8.91E+06	ZKD_5.raw	Q9DB20|ATPO_MOUSE			FALSE
FAKLVRPPVQVYG	42.69	1472.85	13	0.5	491.958	3	27.25	9.95E+06	1.27E+08	ZKD_5.raw	Q9DB20|ATPO_MOUSE			FALSE
FAKLVRPPVQVYGIEGR	51.92	1928.1	17	1.1	483.033	4	28.2115	1.29E+06	1.20E+07	ZKD_5.raw	Q9DB20|ATPO_MOUSE			FALSE
FAKLVRPPVQVYGIEGRYA	46.71	2162.2	19	0.4	541.558	4	30.5466			ZKD_5.raw	Q9DB20|ATPO_MOUSE			FALSE
FPKPPSYNVATTLPSYD	30.18	1895.93	17	1.3	948.974	2	35.2541	3.42E+05	6.09E+06	ZKD_5.raw	Q8R0W6|NFIP1_MOUSE			FALSE
FPKPPSYNVATTLPSYDE	39.79	2024.97	18	0.2	1013.49	2	34.8752	2.17E+07	1.51E+08	ZKD_5.raw	Q8R0W6|NFIP1_MOUSE			FALSE
FPKPPSYNVATTLPSYDEA	38.82	2096.01	19	1.1	1049.01	2	35.5654	7.34E+06	5.71E+07	ZKD_5.raw	Q8R0W6|NFIP1_MOUSE			FALSE
FPYVTPAPHEPV	47.61	1352.68	12	0.3	677.346	2	30.1187	2.52E+05	8.24E+06	ZKD_5.raw	Q9D074|MGRN1_MOUSE			FALSE
FPYVTPAPHEPVK	44.53	1480.77	13	-0.2	494.598	3	22.9053	2.21E+07	2.07E+08	ZKD_5.raw	Q9D074|MGRN1_MOUSE			FALSE
FPYVTPAPHEPVKT	46.15	1581.82	14	0.9	528.281	3	23.9392	2.38E+06	2.30E+07	ZKD_5.raw	Q9D074|MGRN1_MOUSE			FALSE
FRVNFVDPAASSSADD	47.69	1696.77	16	-0.2	849.392	2	33.4169	4.92E+05	1.09E+07	ZKD_5.raw	P55012|S12A2_MOUSE			FALSE
FTYQQPQPLSVEPR	45.87	1688.85	14	1.7	845.435	2	27.9373	2.35E+05	7.40E+06	ZKD_5.raw	B2RXS4|PLXB2_MOUSE			FALSE
FVAPAVTPVKGVL	39.58	1296.78	13	4.5	649.401	2	36.7206			ZKD_5.raw	P70158|ASM3A_MOUSE			FALSE
FYSKYSAPRLPAAL	21.1	1582.85	14	-1.5	528.623	3	30.4237	9.95E+04	3.29E+06	ZKD_5.raw	P97432|NBR1_MOUSE			FALSE
GDLEYQM(+15.99)STTARAK	40.94	1585.74	14	-5	529.585	3	11.7927	2.53E+05	7.63E+06	ZKD_5.raw	Q02257|PLAK_MO	Oxidation (M)		FALSE
GDLEYQMSTTARAK	43.62	1569.75	14	1.4	524.257	3	16.3529	1.88E+06	4.00E+07	ZKD_5.raw	Q02257|PLAK_MOUSE			FALSE
GDLEYQMSTTARAKR	34.44	1725.85	15	-1	576.289	3	14.3902	6.56E+05	2.60E+07	ZKD_5.raw	Q02257|PLAK_MOUSE			FALSE
GDLSQHATPLPTPAVLPG	36.03	1769.93	18	-0.7	885.972	2	36.6628			ZKD_5.raw	O88746|TOM1_MOUSE			FALSE
GDTIEFRGPNGLLVYQG	31.85	1834.92	17	0	918.468	2	39.1408			ZKD_5.raw	Q9DCN2|NB5R3_MOUSE			FALSE
GDTIEFRGPNGLLVYQGK	38.44	1963.02	18	1.9	655.347	3	33.3454			ZKD_5.raw	Q9DCN2|NB5R3_MOUSE			FALSE
GEKKAYVRLAPDYDALD	33.32	1922.97	17	0.6	641.999	3	23.6942			ZKD_5.raw	P62751|RL23A_MOUSE			FALSE
GERFEAPEALFQPH	39.52	1626.78	14	0	543.267	3	30.9421	3.76E+05	4.99E+06	ZKD_5.raw	P61161|ARP2_MOUSE			FALSE
GFVKVVKNKAYFKRYQVRF	47.81	2376.36	19	0.6	476.279	5	21.6085	4.06E+06	5.04E+07	ZKD_5.raw	P47962|RL5_MOUSE			FALSE
GGLPDYSAPNPIKVTH	45.32	1664.85	16	0.2	555.958	3	26.6617	1.81E+06	2.75E+07	ZKD_5.raw	Q8CFG0|SULF2_MOUSE			FALSE
GGLPDYSAPNPIKVTHR	41.65	1820.95	17	1.2	456.246	4	23.0321	3.41E+06	4.19E+07	ZKD_5.raw	Q8CFG0|SULF2_MOUSE			FALSE
GIDPYDQPNAIYIER	47.06	1762.85	15	1.1	882.435	2	31.2116	2.51E+05	8.14E+06	ZKD_5.raw	O88307|SORL_MOUSE			FALSE
GIYVSEKGTVQQADE	48.96	1622.78	15	-2.6	812.395	2	18.1545	1.10E+06	2.44E+07	ZKD_5.raw	P51410|RL9_MOUSE			FALSE
GKLTGMAFRVPTPNVSVVD	46.37	1987.06	19	1.4	663.36	3	36.1762	1.57E+06	1.30E+07	ZKD_5.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
GKYTYGKPVPGHVK	48.4	1529.84	14	-0.4	383.466	4	10.3263	1.26E+06	2.50E+07	ZKD_5.raw	P28665|MUG1_MOUSE			FALSE
GKYTYGKPVPGHVKI	44.99	1642.92	15	0.8	411.738	4	14.7126	3.39E+06	3.48E+07	ZKD_5.raw	P28665|MUG1_MOUSE			FALSE
GLPDYSAPNPIK	38.22	1270.66	12	3.9	636.338	2	26.097			ZKD_5.raw	Q8CFG0|SULF2_MOUSE			FALSE
GLPDYSAPNPIKVT	37.9	1470.77	14	0.3	736.393	2	31.0824			ZKD_5.raw	Q8CFG0|SULF2_MOUSE			FALSE
GLPDYSAPNPIKVTH	48.63	1607.83	15	0.8	536.951	3	26.503	3.42E+06	4.18E+07	ZKD_5.raw	Q8CFG0|SULF2_MOUSE			FALSE
GLPDYSAPNPIKVTHR	46.77	1763.93	16	-0.5	588.984	3	22.8282	3.06E+05	1.05E+07	ZKD_5.raw	Q8CFG0|SULF2_MOUSE			FALSE
GM(+15.99)AFRVPTPNVSVVD	48.35	1603.8	15	0.9	802.909	2	34.3116	6.35E+06	4.73E+07	ZKD_5.raw	P16858|G3P_MOU	Oxidation (M)		FALSE
GMAFRVPTPNVSVVD	44.46	1587.81	15	-1.8	794.91	2	38.3446	9.53E+06	7.65E+07	ZKD_5.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
GPDGRFVM(+15.99)GPTVAPSQ	33.87	1630.78	16	2.2	816.398	2	22.3433			ZKD_5.raw	Q05BQ1|TUTLA_I	Oxidation (M)		FALSE
GPDGRFVM(+15.99)GPTVAPSQEK	49.15	1887.91	18	-2.1	630.311	3	18.4483	3.50E+06	2.83E+07	ZKD_5.raw	Q05BQ1|TUTLA_I	Oxidation (M)		FALSE
GPDGRFVM(+15.99)GPTVAPSQEKL	43.68	2001	19	-3.4	668.005	3	24.6238	2.05E+06	2.02E+07	ZKD_5.raw	Q05BQ1|TUTLA_I	Oxidation (M)		FALSE
GPDGRFVMGPTVAPSQ	40.86	1614.78	16	-2.6	808.396	2	27.5282	8.71E+05	2.02E+07	ZKD_5.raw	Q05BQ1|TUTLA_MOUSE			FALSE
GPDGRFVMGPTVAPSQEK	46.69	1871.92	18	-0.3	624.98	3	22.7176	9.05E+06	1.14E+08	ZKD_5.raw	Q05BQ1|TUTLA_MOUSE			FALSE
GPDGRFVMGPTVAPSQEKL	49.41	1985	19	-0.5	662.675	3	28.5949	3.31E+06	4.79E+07	ZKD_5.raw	Q05BQ1|TUTLA_MOUSE			FALSE
GPKPFSAPKPQTSPS	34.89	1524.79	15	-1.2	509.271	3	14.4986	2.87E+06	5.25E+07	ZKD_5.raw	P40124|CAP1_MOUSE			FALSE
GPKPFSAPKPQTSPSP	42.37	1621.85	16	-1.2	541.622	3	16.1307	7.64E+06	7.46E+07	ZKD_5.raw	P40124|CAP1_MOUSE			FALSE
GPKPFSAPKPQTSPSPK	43.32	1749.94	17	1.7	584.322	3	13.2082	1.31E+07	1.51E+08	ZKD_5.raw	P40124|CAP1_MOUSE			FALSE
GPKPFSAPKPQTSPSPKP	47.65	1846.99	18	-0.4	616.672	3	14.5896	1.89E+07	1.69E+08	ZKD_5.raw	P40124|CAP1_MOUSE			FALSE
GPLIVSGPDGAPAKGDG	45.01	1506.77	17	-0.1	754.391	2	22.6542	8.17E+05	1.25E+07	ZKD_5.raw	Q8VBW1|SC6A8_MOUSE			FALSE
GPPPYHESLAGASQPP	38.78	1603.76	16	2.6	802.891	2	20.7256	1.23E+06	1.28E+07	ZKD_5.raw	Q9D7I0|SHSA5_MOUSE			FALSE
GPTYRGPVPWHTIN	46.88	1593.81	14	0.4	532.276	3	26.0562	7.69E+06	7.69E+07	ZKD_5.raw	Q9WV54|ASAH1_MOUSE			FALSE
GRCVKVDLSEKYKKLVLR	23.92	2133.25	18	-3.4	534.317	4	12.2475			ZKD_5.raw	Q8K310|MATR3_MOUSE			FALSE
GREFGNLARIRHVIS	31.7	1723.96	15	0.9	431.998	4	21.7629	7.96E+05	1.35E+07	ZKD_5.raw	Q9CQ69|QCR8_MOUSE			FALSE
GRFTYQNAAAQPETGPG	23.24	1763.82	17	2.5	882.921	2	18.2312			ZKD_5.raw	Q9QZM4|TR10B_MOUSE			FALSE
GRFVMGPTVAPSQEK	41.37	1602.82	15	-2.2	535.279	3	19.8666	4.96E+05	1.07E+07	ZKD_5.raw	Q05BQ1|TUTLA_MOUSE			FALSE
GRLEVVTDPTTNAGYVK	44.06	1818.95	17	-4	607.321	3	22.5258	6.82E+05	1.48E+07	ZKD_5.raw	Q9R100|CAD17_MOUSE			FALSE
GSDMFKASLVIPSKD	30.41	1593.81	15	-2.1	532.275	3	30.7948	9.14E+04	2.94E+06	ZKD_5.raw	Q8BJD1|ITIH5_MOUSE			FALSE
GSILWSQPLPSLPGGPP	46.62	1701.91	17	-0.6	851.961	2	51.6843	1.78E+06	1.75E+07	ZKD_5.raw	Q8C0Z1|F234A_MOUSE			FALSE
GSILWSQPLPSLPGGPPS	43.67	1788.94	18	5.5	895.483	2	50.19	1.61E+05	3.78E+06	ZKD_5.raw	Q8C0Z1|F234A_MOUSE			FALSE
GTPEYLAPEIILSKG	45.03	1586.86	15	1.1	794.436	2	40.3074	3.41E+05	9.22E+06	ZKD_5.raw	P68181|KAPCB_MOUSE;P05132|KAPCA_MOUSE			FALSE
GYAVYETPTAHNGAKNPR	43.22	1944.94	18	2.7	649.324	3	13.0821			ZKD_5.raw	Q9QZ06|TOLIP_MOUSE			FALSE
GYKPFQNPVPNQSPS	41.16	1658.81	15	3.8	830.413	2	22.7471	1.34E+06	1.47E+07	ZKD_5.raw	P16382|IL4RA_MOUSE			FALSE
HDLRHAFSPVASVESA	40.83	1721.85	16	0	574.957	3	23.6275	1.20E+06	2.10E+07	ZKD_5.raw	P29699|FETUA_MOUSE			FALSE
HDLRHAFSPVASVESAS	37.93	1808.88	17	-1.6	603.967	3	23.3117	1.35E+06	2.72E+07	ZKD_5.raw	P29699|FETUA_MOUSE			FALSE
HEVVVIAPEASIHIK	47.72	1640.92	15	-0.6	547.982	3	26.3174	7.86E+05	1.42E+07	ZKD_5.raw	Q63886|UD11_MOUSE			FALSE
HLKIVYRRFRHG	26.94	1580.92	12	2.7	396.237	4	11.1135			ZKD_5.raw	Q9D823|RL37_MOUSE			FALSE
HLKIVYRRFRHGF	28.75	1727.98	13	-1.7	433.003	4	14.5896	2.45E+06	2.76E+07	ZKD_5.raw	Q9D823|RL37_MOUSE			FALSE
HLKIVYRRFRHGFR	35.22	1884.09	14	1.6	377.825	5	13.1453	4.56E+07	7.00E+08	ZKD_5.raw	Q9D823|RL37_MOUSE			FALSE
HLRFNYPEVQKVMPR	44.98	1913.01	15	-0.7	479.259	4	24.6394			ZKD_5.raw	Q6XQH0|G3ST2_MOUSE			FALSE
HNYEGPETHTSLR	38.18	1539.71	13	4.6	514.245	3	11.1739	1.22E+06	2.26E+07	ZKD_5.raw	P14483|HB2A_MOUSE			FALSE
IEDIEVAPPKAHEVR	45.86	1701.9	15	1.4	426.484	4	18.0408			ZKD_5.raw	P00329|ADH1_MOUSE			FALSE
IEKVIPSTANSNNL	42.11	1498.8	14	-4.8	750.403	2	22.9228	4.93E+05	1.12E+07	ZKD_5.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IEVSSPITLQAL	41.35	1269.72	12	1.3	635.867	2	46.3579	2.67E+06	3.44E+07	ZKD_5.raw	E9Q414|APOB_MOUSE;#CONTAM#ENSEMBL:ENSBT			FALSE
IEVSSPITLQALVQ	43.73	1496.85	14	-0.3	749.43	2	49.2419	6.21E+05	9.60E+06	ZKD_5.raw	E9Q414|APOB_MOUSE			FALSE
IFARGPQAHLVH	31.16	1344.74	12	6.3	449.257	3	21.5586			ZKD_5.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
IFARGPQAHLVHG	41.87	1401.76	13	1	468.262	3	21.4232	2.67E+06	3.01E+07	ZKD_5.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE			FALSE
IGDTIEFRGPNGLLVYQGK	46.65	2076.1	19	1.7	693.042	3	35.4697	9.62E+05	2.44E+07	ZKD_5.raw	Q9DCN2|NB5R3_MOUSE			FALSE

IIGGDTVVPHSRPYMALLK	23.04	2066.13	19	0.6	517.541	4	30.7532			ZKD_5.raw	P11032|GRAA_MOUSE			FALSE
IIGGHEVKPHSRPYM	27.6	1719.89	15	-2.3	430.978	4	12.9207			ZKD_5.raw	P13366|GRAG_MOUSE;P04187|GRAB_MOUSE;P0888			FALSE
IKIAWESPQGQVSR	38.58	1597.86	14	3.4	533.628	3	23.8885			ZKD_5.raw	P11276|FINC_MOUSE			FALSE
IPFYTPIPNGLYPS	40.35	1577.81	14	2.6	789.916	2	50.5103	2.90E+06	2.26E+07	ZKD_5.raw	O08573|LEG9_MOUSE			FALSE
IPGTNM(+15.99)YNTDRANPVLD	50.41	1905.89	17	0.6	953.952	2	24.6201	2.24E+06	2.46E+07	ZKD_5.raw	E9Q7P9|CDHR2_	Oxidation (M)		FALSE
IPGTNM(+15.99)YNTDRANPVLDLP	47.57	2116.03	19	1.9	1059.02	2	36.2732	4.48E+06	2.58E+07	ZKD_5.raw	E9Q7P9|CDHR2_	Oxidation (M)		FALSE
IPGTNMYNTDRANPV	44.11	1661.78	15	3	831.901	2	23.6738	2.09E+05	6.72E+06	ZKD_5.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IPGTNMYNTDRANPVLD	48.14	1889.89	17	0.4	945.955	2	28.5649	6.56E+06	7.21E+07	ZKD_5.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IPGTNMYNTDRANPVLDLP	50.41	2100.03	19	-1.2	1051.02	2	39.4278	8.78E+06	5.48E+07	ZKD_5.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IPIRWTAPEAIAH	27.99	1473.81	13	-2.4	492.276	3	30.4043			ZKD_5.raw	Q60750|EPHA1_MOUSE			FALSE
IPIRWTAPEAIAHR	25.99	1629.91	14	0.7	408.485	4	26.5867			ZKD_5.raw	Q60750|EPHA1_MOUSE			FALSE
IPIRWTAPEAISYRK	20.83	1800	15	2.4	451.01	4	27.4173	1.53E+06	2.23E+07	ZKD_5.raw	Q03145|EPHA2_MOUSE			FALSE
IPSRYSSPTTIATVM	23.24	1622.83	15	1.5	812.425	2	30.9909	9.29E+04	2.75E+06	ZKD_5.raw	Q9DBM2|ECHP_MOUSE			FALSE
IREFYSASVAEDA	27.05	1456.68	13	1.5	729.35	2	24.8849			ZKD_5.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IREFYSASVAEDAT	43.49	1557.73	14	1.7	779.874	2	24.8694	1.55E+06	2.90E+07	ZKD_5.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IREFYSASVAEDATL	43.18	1670.82	15	-0.1	836.415	2	32.2941	1.33E+07	1.42E+08	ZKD_5.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IREFYSASVAEDATLG	46.24	1727.84	16	0.1	864.926	2	31.1334	1.23E+07	1.38E+08	ZKD_5.raw	E9Q7P9|CDHR2_MOUSE			FALSE
IREN(+0.98)IWKAPEPVEIRE	31.21	1979.05	16	8.2	660.695	3	26.6653			ZKD_5.raw	Q9R100|CAD17_M	Deamidation (NQ)		FALSE
IRENIWKAPEPVEIR	41.57	1849.02	15	1	463.263	4	26.1523	3.62E+05	6.53E+06	ZKD_5.raw	Q9R100|CAD17_MOUSE			FALSE
IRENIWKAPEPVEIRE	38.9	1978.06	16	3.9	660.364	3	26.6964			ZKD_5.raw	Q9R100|CAD17_MOUSE			FALSE
ISQIFSQAMAARSINRP	25.98	1888.99	17	0	630.672	3	29.1384	3.82E+06	6.11E+07	ZKD_5.raw	P34914|HYES_MOUSE			FALSE
ISTPEELGLDKV	25.99	1299.69	12	3.3	650.856	2	31.425			ZKD_5.raw	P12787|COX5A_MOUSE			FALSE
ITNQYNSPTGLYSSEN	46.32	1786.8	16	0.5	894.408	2	24.8705	3.43E+06	4.61E+07	ZKD_5.raw	O70400|PDLI1_MOUSE			FALSE
ITPSYVAFTPEGERL	30.58	1678.86	15	0.8	840.436	2	35.6617	2.41E+05	5.50E+06	ZKD_5.raw	P20029|BIP_MOUSE			FALSE
ITQVQWNDPGAQYSLVN	50.3	1931.94	17	0.7	966.977	2	38.2885	1.48E+06	2.81E+07	ZKD_5.raw	Q9R100|CAD17_MOUSE			FALSE
K(+42.01)AAKPKTS(+79.97)KPKAAKPKK	30.92	1928.13	17	-9.2	483.036	4	8.2358			ZKD_5.raw	P43274|H14_MOU	Acetylation (N-tern	K1:Acetylation (N-t	FALSE
KDAKSVKIKKNKDNVKFK	32.71	2117.27	18	-0.2	706.763	3	7.2092	1.80E+06	3.41E+07	ZKD_5.raw	Q9JJI8|RL38_MOUSE			FALSE
KEGKKPRTKAPKIQRLVTPR	41.63	2330.44	20	-0.7	389.413	6	9.7818	9.24E+05	1.57E+07	ZKD_5.raw	P62754|RS6_MOUSE			FALSE
KELEEQLGPVAEETR	43.96	1726.87	15	0.6	576.632	3	20.7893			ZKD_5.raw	P08226|APOE_MOUSE			FALSE
KELEEQLGPVAEETRA	44.85	1797.91	16	0	600.311	3	22.0846	8.32E+05	2.09E+07	ZKD_5.raw	P08226|APOE_MOUSE			FALSE
KFTYRGVDLDQLLD	37.27	1681.87	14	1.1	561.63	3	37.6415	1.44E+06	1.92E+07	ZKD_5.raw	P62843|RS15_MOUSE			FALSE
KFYKGKKYKPLDLRPKKT	53.38	2237.34	18	-0.4	560.342	4	11.0229	4.50E+06	1.19E+08	ZKD_5.raw	Q6ZWV7|RL35_MOUSE			FALSE
KIVYEGPELNHAFG	45.74	1572.79	14	3.6	525.274	3	27.45	3.98E+06	4.83E+07	ZKD_5.raw	Q91ZX7|LRP1_MOUSE			FALSE
KKAKAKGKGQPQARVTVNR	47.16	2064.24	19	-0.7	413.855	5	6.3286	1.20E+07	5.79E+08	ZKD_5.raw	Q9D6S7|RRFM_MOUSE			FALSE
KKKKKKKKPFMLD	34.07	1646.04	13	-0.7	412.518	4	7.0767	9.70E+05	2.39E+07	ZKD_5.raw	Q99L45|IF2B_MOUSE			FALSE
KKKKRFSFKKSFK	28.16	1686.05	13	0.5	422.519	4	7.3315	3.18E+05	7.50E+06	ZKD_5.raw	P26645|MARCS_MOUSE			FALSE
KKKRFSFKKSFK	28.44	1557.95	12	0.4	390.495	4	7.8559	1.20E+06	2.33E+07	ZKD_5.raw	P26645|MARCS_MOUSE			FALSE
KKQKQNRPIPQWIRMK	39.67	2078.2	16	-0.6	520.558	4	14.333			ZKD_5.raw	P62892|RL39_MOUSE			FALSE
KLTGMAFRVPTPNVSVVD	35.42	1930.03	18	1.6	644.353	3	36.1762	4.87E+05	6.14E+06	ZKD_5.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
KNLDYVATSIHEAVT	48.73	1659.85	15	-2	554.289	3	26.2508	5.87E+05	1.13E+07	ZKD_5.raw	P05201|AATC_MOUSE			FALSE
KPAAKKAGSDAA	23.03	1113.61	12	-1.7	557.813	2	42.8896			ZKD_5.raw	P47911|RL6_MOUSE			FALSE
KPKAAKPKT(+79.97)S(+79.97)KPKAAKPK	21.88	2063.14	18	4.6	516.795	4	9.6282			ZKD_5.raw	P43274|H14_MOU	Phosphorylation (STY); Phosphorylati		FALSE
KPKASKAKVT(+79.97)KP	21.54	1361.78	12	1.7	454.935	3	7.3315	4.18E+05	9.39E+06	ZKD_5.raw	P43275|H11_MOU	Phosphorylation (S	T10:Phosphorylatio	FALSE
KPPSYNVATTLPSYDE	39.78	1780.85	16	5.5	891.438	2	28.0831	3.40E+05	7.43E+06	ZKD_5.raw	Q8R0W6|NFIP1_MOUSE			FALSE
KPRGEFHTPVTVAGPH	41.77	1728.91	16	-0.7	433.234	4	14.6082			ZKD_5.raw	Q8JZQ5|AOC1_MOUSE			FALSE
KPVSQM(+15.99)RMATPLLM(+15.99)RPM	35.85	2018.03	17	-1	505.514	4	22.0849	2.13E+07	9.75E+07	ZKD_5.raw	P04441|HG2A_MO	Oxidation (M); Oxid	M6:Oxidation (M):(	FALSE
KPVSQM(+15.99)RMATPLLM(+15.99)RPM(+15.99)	35.92	2034.02	17	2.5	509.515	4	18.0922	2.60E+06	5.00E+07	ZKD_5.raw	P04441|HG2A_MO	Oxidation (M); Oxid	M6:Oxidation (M):(	FALSE
KPVSQM(+15.99)RMATPLLMRPM	38.9	2002.03	17	-0.3	501.516	4	26.0252	2.73E+07	1.31E+08	ZKD_5.raw	P04441|HG2A_MO	Oxidation (M)	M6:Oxidation (M):(	FALSE
KPVSQMRM(+15.99)ATPLLM(+15.99)RPM	30.05	2018.03	17	-1.8	673.683	3	21.4522	1.53E+07	7.98E+07	ZKD_5.raw	P04441|HG2A_MO	Oxidation (M); Oxid	M8:Oxidation (M):4	FALSE
KPVSQMRM(+15.99)ATPLLMRPM	42.22	2002.03	17	-1	501.516	4	25.1136	3.71E+07	3.78E+08	ZKD_5.raw	P04441|HG2A_MO	Oxidation (M)	M8:Oxidation (M):5	FALSE
KPVSQMRM(+15.99)ATPLLMRPM(+15.99)	42.27	2018.03	17	-1.8	505.514	4	21.4522	9.30E+06	5.37E+07	ZKD_5.raw	P04441|HG2A_MO	Oxidation (M); Oxid	M8:Oxidation (M):(	FALSE
KPVSQMRMATPLLM(+15.99)RPM(+15.99)	38.9	2018.03	17	-0.3	505.515	4	23.2481	1.46E+07	1.06E+08	ZKD_5.raw	P04441|HG2A_MO	Oxidation (M); Oxid	M14:Oxidation (M)	FALSE
KPVSQMRMATPLLMRP	34.22	1855	16	-0.9	619.34	3	27.0332	1.55E+06	1.99E+07	ZKD_5.raw	P04441|HG2A_MOUSE			FALSE
KPVSQMRMATPLLMRPM	34.93	1986.04	17	-0.3	497.517	4	29.9789	6.50E+07	5.99E+08	ZKD_5.raw	P04441|HG2A_MOUSE			FALSE
KPVSQMRMATPLLMRPM(+15.99)	40.25	2002.03	17	0.5	501.516	4	26.2822	6.32E+07	3.89E+08	ZKD_5.raw	P04441|HG2A_MO	Oxidation (M)	M17:Oxidation (M)	FALSE
KSAVGTLS(+79.97)GN(+0.98)SSN(+0.98)VIQLIID	21.24	2097.02	20	8.1	525.268	4	12.8104	1.58E+06	1.70E+07	ZKD_5.raw	P09055|ITB1_MOU	Phosphorylation (S	S8:Phosphorylatio	FALSE
KVAKS(+79.97)PKKAKVT(+79.97)KPKK	21.08	1925.1	16	3.9	482.284	4	7.4015			ZKD_5.raw	P15864|H12_MOU	Phosphorylation (STY); Phosphorylati		FALSE
KVLIPS(+79.97)Y(+79.97)AAGSII	21	1490.72	13	-3.5	497.912	3	46.3772			ZKD_5.raw	Q9JKN6|NOVA1_	Phosphorylation (S	S6:Phosphorylatio	FALSE
KVTFNSALAQKEAKK	51.26	1661.95	15	-0.2	416.494	4	12.1352	1.64E+06	2.87E+07	ZKD_5.raw	O89051|ITM2B_MOUSE			FALSE
KYTYGKPVPGHVK	43.98	1472.81	13	-0.5	369.211	4	10.0406	2.02E+07	2.11E+08	ZKD_5.raw	P28665|MUG1_MOUSE			FALSE
LAPDYDALDVANK	46.18	1403.69	13	0	702.854	2	27.6715	4.42E+06	6.02E+07	ZKD_5.raw	P62751|RL23A_MOUSE			FALSE
LAPMYYRGAQAAIVVYD	36.12	1899.96	17	0.3	950.985	2	36.1923	1.18E+05	3.67E+06	ZKD_5.raw	P61021|RAB5B_MOUSE;Q9CQD1|RAB5A_MOUSE;P3			FALSE
LDQLFSGPLPGRLPV	39.35	1607.9	15	-1.6	804.958	2	46.2364	5.57E+05	9.66E+06	ZKD_5.raw	Q60805|MERTK_MOUSE			FALSE
LEISYTGSRPASNMV	43.15	1623.79	15	-1.3	812.903	2	28.228	2.54E+05	8.02E+06	ZKD_5.raw	P28666|MUG2_MOUSE;P28665|MUG1_MOUSE			FALSE
LERAFRGATVLPANPPG	28.15	1764.96	17	-2.1	589.327	3	25.1152	1.13E+06	1.32E+07	ZKD_5.raw	Q3B7Z2|OSBP1_MOUSE			FALSE
LHLRFSAPQIENEP	36.79	1649.85	14	0.6	550.958	3	29.2924	7.52E+05	1.03E+07	ZKD_5.raw	Q61190|I10R2_MOUSE			FALSE
LHLRFSAPQIENEPE	44.57	1778.9	15	0.8	593.973	3	29.0101	8.82E+06	7.39E+07	ZKD_5.raw	Q61190|I10R2_MOUSE			FALSE
LHLRFSAPQIENEPET	44.46	1879.94	16	1.8	627.656	3	29.2008	1.21E+06	1.92E+07	ZKD_5.raw	Q61190|I10R2_MOUSE			FALSE
LLLLLLS(+79.97)LLRLLRRRSCLLA	29.12	2427.5	20	-7.2	405.588	6	29.7705	6.84E+06	2.16E+07	ZKD_5.raw	Q8K1S7|KREM2_	Phosphorylation (S	S7:Phosphorylatio	FALSE
LLLLT(+79.97)CDCGS(+79.97)GPIGGAATG	21.73	1877.77	19	-5.8	470.447	4	16.5948			ZKD_5.raw	O35902|DSG3_M	Phosphorylation (S	T5:Phosphorylatio	FALSE
LNFRNPAVQEEIK	40.64	1556.83	13	0.6	519.951	3	23.2307			ZKD_5.raw	Q91WV7|SLC31_MOUSE			FALSE
LPDYSAPNPIKVTH	46	1550.81	14	0.1	517.944	3	25.212	1.42E+06	2.53E+07	ZKD_5.raw	Q8CFG0|SULF2_MOUSE			FALSE
LPDYSAPNPIKVTHR	25.42	1706.91	15	1.3	427.735	4	21.644			ZKD_5.raw	Q8CFG0|SULF2_MOUSE			FALSE
LPPHVYSTPQPSLPP	39.61	1628.86	15	1.1	815.436	2	28.4682	4.83E+05	6.30E+06	ZKD_5.raw	Q3UPH1|PRRC1_MOUSE			FALSE
LPPHVYSTPQPSLPPV	43.69	1727.92	16	-2.4	864.968	2	33.7733	1.42E+06	1.11E+07	ZKD_5.raw	Q3UPH1|PRRC1_MOUSE			FALSE
LPPYDDATAVPSTAKEPPP	39.68	1964.97	19	1.7	655.999	3	27.1912	5.76E+05	2.21E+07	ZKD_5.raw	Q91XQ6|LAP4B_MOUSE			FALSE
LPPYDDATAVPSTAKEPPPP	44.91	2062.03	20	2.8	688.351	3	28.2115	3.98E+07	2.26E+08	ZKD_5.raw	Q91XQ6|LAP4B_MOUSE			FALSE
LPQDPTFHTPLDLYAYAR	46.7	2117.06	18	-1.5	706.692	3	40.6495			ZKD_5.raw	Q07797|LG3BP_MOUSE			FALSE
LPSTWSDPSVNISLDN	22.59	1743.83	16	-0.1	872.923	2	41.7742			ZKD_5.raw	Q99KN9|EPN4_MOUSE			FALSE
LPVKWTAPEAIRT	25.15	1480.84	13	0.8	494.621	3	28.529			ZKD_5.raw	Q922K9|FRK_MOUSE			FALSE
LSLLYNVPAVAEEIQ	27.35	1657.89	15	-0.4	829.953	2	50.8879	4.53E+05	7.23E+06	ZKD_5.raw	P12023|A4_MOUSE			FALSE
LSQEYSGSVANEANVY	49.57	1729.78	16	-0.2	865.897	2	26.6616	1.15E+06	2.11E+07	ZKD_5.raw	E9Q414|APOB_MOUSE			FALSE
LTGGYRYPRALEEEV	20.98	1751.88	15	-0.7	584.968	3	25.3946	4.06E+06	5.78E+07	ZKD_5.raw	Q8K3K8|OPTN_MOUSE			FALSE
LTGM(+15.99)AFRVPTPNVSVVD	47.42	1817.93	17	0.5	909.975	2	36.8456	1.45E+06	1.20E+07	ZKD_5.raw	P16858|G3P_MOU	Oxidation (M)		FALSE
LTGMAFRVPTPNVSVVD	52.52	1801.94	17	0.5	901.978	2	41.3601	2.51E+06	2.25E+07	ZKD_5.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
LVRYTQKAPQVSTPTL	39.8	1801.01	16	-1	601.343	3	24.0089			ZKD_5.raw	P07724|ALBU_MOUSE			FALSE
LVTLPVSFAQLK	35.49	1314.79	12	-5	658.4	2	42.9514			ZKD_5.raw	Q922Q8|LRC59_MOUSE			FALSE
M(+42.01)(+15.99)FSSSAKIVKPNGEKPDEFE	44.97	2297.09	20	2.1	766.705	3	25.274	3.41E+05	6.86E+06	ZKD_5.raw	P62082|RS7_MOU	Acetylation (N-term); Oxidation (M)		FALSE
M(+42.01)FSSSAKIVKPNGEKPDEFE	50.7	2281.09	20	3.7	761.375	3	30.0111	9.95E+05	1.88E+07	ZKD_5.raw	P62082|RS7_MOU	Acetylation (N-term)		FALSE
M(+42.01)N(+0.98)DTVTIRTRKFMTNR	37.36	2026.01	16	9.2	507.514	4	23.3479			ZKD_5.raw	P62849|RS24_MC	Acetylation (N-tern	M1:Acetylation (N-	FALSE
M(+42.01)NDTVTIRTRKFMTNR	32.13	2025.02	16	1.8	507.264	4	23.3445	2.38E+06	2.70E+07	ZKD_5.raw	P62849|RS24_MC	Acetylation (N-term)		FALSE
MAFRVPTPNVSVVD	42.76	1530.79	14	0	766.401	2	37.9083	2.63E+06	2.19E+07	ZKD_5.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
NHLRFNYPEVQKVMPR	47.79	2027.05	16	-0.5	507.77	4	24.1556	4.57E+06	7.93E+07	ZKD_5.raw	Q6XQH0|G3ST2_MOUSE			FALSE
NIYVPAHAHEGSNL	32.85	1520.74	14	-2.7	507.918	3	18.1873	2.21E+06	3.22E+07	ZKD_5.raw	Q8BK48|EST2E_MOUSE			FALSE
NNQAYHSPATALAIVD	28.97	1683.82	16	-1.8	842.917	2	30.4245	2.77E+05	6.44E+06	ZKD_5.raw	Q8R420|ABCA3_MOUSE			FALSE
NPHVNPLPTGYE	45.13	1336.64	12	0.6	669.328	2	23.344	1.63E+06	3.09E+07	ZKD_5.raw	P43023|CX6A2_MOUSE;P43024|CX6A1_MOUSE			FALSE
NPHVNPLPTGYEDE	41.87	1580.71	14	1.9	791.364	2	23.7516			ZKD_5.raw	P43024|CX6A1_MOUSE			FALSE
NPLNSVFVAPAVTPV	43.55	1523.83	15	1.8	762.926	2	48.5652	9.93E+05	1.05E+07	ZKD_5.raw	P70158|ASM3A_MOUSE			FALSE
NPLNSVFVAPAVTPVK	51.55	1651.93	16	0.1	826.972	2	38.8338	2.49E+07	2.48E+08	ZKD_5.raw	P70158|ASM3A_MOUSE			FALSE
NPLNSVFVAPAVTPVKG	51.91	1708.95	17	-0.4	855.483	2	38.6686	1.44E+07	1.32E+08	ZKD_5.raw	P70158|ASM3A_MOUSE			FALSE
NPLNSVFVAPAVTPVKGV	50.99	1808.02	18	2.9	905.02	2	42.1831	4.86E+05	8.15E+06	ZKD_5.raw	P70158|ASM3A_MOUSE			FALSE
NPLNSVFVAPAVTPVKGVL	53.71	1921.1	19	0.6	961.56	2	47.2518	2.04E+06	2.25E+07	ZKD_5.raw	P70158|ASM3A_MOUSE			FALSE
NPPSYYTQPVPVPN	43.96	1571.76	14	-2.6	786.886	2	31.2261	5.94E+05	1.07E+07	ZKD_5.raw	Q9JLJ0|LITAF_MOUSE			FALSE
NPPSYYTQPVPVPNA	27.31	1642.8	15	1.2	822.408	2	32.9364			ZKD_5.raw	Q9JLJ0|LITAF_MOUSE			FALSE
NPPSYYTQPVPVPNAN	43.2	1756.84	16	0.3	879.429	2	30.9731	7.42E+06	7.66E+07	ZKD_5.raw	Q9JLJ0|LITAF_MOUSE			FALSE
NSEEFAAAMSRYELK	23.45	1744.81	15	0.3	582.611	3	29.3901			ZKD_5.raw	E9Q414|APOB_MOUSE			FALSE
NSIIGDHKRWPHTIPYVLE	24.59	2274.19	19	-1.5	569.554	4	31.4459	2.40E+06	2.45E+07	ZKD_5.raw	Q61847|MEP1B_MOUSE			FALSE
NVQFNYPQASVTDVT	30.47	1681.79	15	-1.4	841.903	2	34.8146	2.98E+06	3.97E+07	ZKD_5.raw	Q61703|ITIH2_MOUSE			FALSE
PDYSAPNPIKVTH	39.58	1437.73	13	-1.6	480.248	3	26.518	5.48E+04	3.67E+06	ZKD_5.raw	Q8CFG0|SULF2_MOUSE			FALSE
PGVTVKDVNQQEFVRALA	53.8	1970.06	18	0.6	657.694	3	31.3522	2.79E+06	5.03E+07	ZKD_5.raw	Q9CZX8|RS19_MOUSE			FALSE
PKKAKT(+79.97)VKPKAKS(+79.97)	21.33	1569.84	13	6.6	524.291	3	9.6709			ZKD_5.raw	P10922|H10_MOU	Phosphorylation (STY); Phosphorylati		FALSE
PPSYYTQPVPVPNAN	46.49	1642.8	15	0	822.407	2	30.9512			ZKD_5.raw	Q9JLJ0|LITAF_MOUSE			FALSE
QEYSGSVANEANVY	43.95	1529.66	14	1.1	765.84	2	23.6581	4.09E+05	9.24E+06	ZKD_5.raw	E9Q414|APOB_MOUSE			FALSE
QPDLNFRNPAVQEEIK	44.83	1896.97	16	2.4	633.332	3	26.6914	4.21E+06	2.65E+07	ZKD_5.raw	Q91WV7|SLC31_MOUSE			FALSE
QPDLNFRNPAVQEEIKE	21.53	2026.01	17	-1.8	676.343	3	27.319	1.10E+06	1.02E+07	ZKD_5.raw	Q91WV7|SLC31_MOUSE			FALSE
QPGPLEPLGGPG	23.59	1117.58	12	1.6	559.797	2	40.5282	9.07E+06	7.45E+07	ZKD_5.raw	Q91YJ2|SNX4_MOUSE			FALSE
QPSTSSLAAPTVEAAAS	29.59	1586.78	17	0.1	794.397	2	26.5345	6.72E+06	7.37E+07	ZKD_5.raw	Q91ZP6|NFIP2_MOUSE			FALSE
QPSTSSLAAPTVEAAASAP	32.9	1754.87	19	-0.5	878.441	2	30.5622	5.71E+06	5.66E+07	ZKD_5.raw	Q91ZP6|NFIP2_MOUSE			FALSE
QPSTSSLAAPTVEAAASAPA	34.33	1825.91	20	1	913.961	2	30.1032	1.35E+07	1.35E+08	ZKD_5.raw	Q91ZP6|NFIP2_MOUSE			FALSE
QQLAFKQPSSAYAAF	34.44	1655.83	15	-1.2	828.922	2	32.2162	1.35E+05	4.58E+06	ZKD_5.raw	P01027|CO3_MOUSE			FALSE
QQLAFKQPSSAYAAFN	39.67	1769.87	16	0	885.944	2	30.1706			ZKD_5.raw	P01027|CO3_MOUSE			FALSE
QVQWNDPGAQYSLVN	48.35	1717.81	15	0.7	859.911	2	35.5955	3.75E+05	8.90E+06	ZKD_5.raw	Q9R100|CAD17_MOUSE			FALSE
QYAKDIGFIKLD	27.09	1409.76	12	0.7	470.926	3	30.9421	5.01E+06	5.85E+07	ZKD_5.raw	P62274|RS29_MOUSE			FALSE
REFYSASVAEDATLG	24.6	1614.75	15	0.9	808.384	2	28.057			ZKD_5.raw	E9Q7P9|CDHR2_MOUSE			FALSE
RENIWKAPEPVEIR	43.14	1735.94	14	-2.4	579.652	3	24.0019	1.80E+06	3.24E+07	ZKD_5.raw	Q9R100|CAD17_MOUSE			FALSE
RENIWKAPEPVEIRE	45.26	1864.98	15	-0.1	622.667	3	24.6201	2.96E+07	3.48E+08	ZKD_5.raw	Q9R100|CAD17_MOUSE			FALSE
RFTYQNAAAQPETGPG	42.26	1706.8	16	0	854.408	2	18.0763	3.52E+05	1.16E+07	ZKD_5.raw	Q9QZM4|TR10B_MOUSE			FALSE
RFVNVVPTFGKKKGPNANS	41.31	2059.13	19	-1	515.79	4	18.0638			ZKD_5.raw	P62862|RS30_MOUSE			FALSE
RHNYEGPETHTSLR	46.36	1695.81	14	-0.7	424.959	4	9.9741	1.05E+07	9.31E+07	ZKD_5.raw	P14483|HB2A_MOUSE			FALSE
RKDAKSVKIKKNKDNVKFK	46.62	2273.37	19	-1.4	569.349	4	6.9793	3.46E+07	5.30E+08	ZKD_5.raw	Q9JJI8|RL38_MOUSE			FALSE
RKEVRYGSLKYKVKKRPQ	50.12	2262.34	18	-0.4	453.476	5	9.0601	3.66E+06	9.84E+07	ZKD_5.raw	Q99KK1|REEP3_MOUSE			FALSE
RKEVRYGSLKYKVKKRPQV	42.29	2361.41	19	-4.5	473.288	5	10.8943	3.09E+06	7.95E+07	ZKD_5.raw	Q99KK1|REEP3_MOUSE			FALSE
RKIVYEGPELNHAFG	47.76	1728.89	15	2	577.307	3	23.0292	4.00E+07	3.07E+08	ZKD_5.raw	Q91ZX7|LRP1_MOUSE			FALSE
RKPYHKKRKYELG	35.29	1701.98	13	-0.5	426.502	4	6.2895	5.22E+05	2.51E+07	ZKD_5.raw	P62242|RS8_MOUSE			FALSE
RKPYHKKRKYELGRP	38.53	1955.13	15	0	392.034	5	6.8203	5.33E+06	6.29E+07	ZKD_5.raw	P62242|RS8_MOUSE			FALSE
RKPYHKKRKYELGRPA	42.51	2026.17	16	1.4	507.551	4	6.8503	7.66E+06	1.24E+08	ZKD_5.raw	P62242|RS8_MOUSE			FALSE
RKWHRNGIKKPRSQ	40.1	1790.03	14	3.9	359.014	5	6.5155	8.16E+05	1.75E+07	ZKD_5.raw	P47915|RL29_MOUSE			FALSE
RNVQFNYPQASVTDVT	38.9	1837.9	16	0.4	919.956	2	28.4392			ZKD_5.raw	Q61703|ITIH2_MOUSE			FALSE
RPDAEYWNSQPEILE	37.42	1845.85	15	2.5	923.936	2	32.7877			ZKD_5.raw	P14483|HB2A_MOUSE;P01921|HB2D_MOUSE;P0634			FALSE
RPDAEYWNSQPEILER	47.83	2001.95	16	0.2	668.326	3	27.8892	5.03E+06	5.36E+07	ZKD_5.raw	P14483|HB2A_MOUSE;P01921|HB2D_MOUSE;P0634			FALSE
RPVQFPYVTPAPHEPV	40.7	1832.96	16	-1.8	611.992	3	29.7315	4.59E+05	1.04E+07	ZKD_5.raw	Q9D074|MGRN1_MOUSE			FALSE
RPVQFPYVTPAPHEPVK	48.06	1961.05	17	-0.7	654.691	3	23.8771	1.15E+07	1.44E+08	ZKD_5.raw	Q9D074|MGRN1_MOUSE			FALSE
RRAAWRRRNTLQLHRYR	42.91	2308.31	17	-2.3	462.669	5	9.9741	1.97E+07	2.58E+08	ZKD_5.raw	Q9CZM2|RL15_MOUSE			FALSE
RVPTPNVSVVDLT	30.72	1395.77	13	-1	698.893	2	32.8432			ZKD_5.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE			FALSE
RYMAPEVLDETIN	39.33	1549.74	13	-0.3	775.879	2	31.305	1.29E+05	4.43E+06	ZKD_5.raw	Q61271|ACV1B_MOUSE			FALSE
S(+42.01)IRVTQ(+0.98)KSYKMSTSGPRA	28.64	2039.05	18	8.8	680.696	3	16.305	4.09E+05	1.32E+07	ZKD_5.raw	P11679|K2C8_MC	Acetylation (N-term); Deamidation (N		FALSE
S(+42.01)IRVTQ(+0.98)KSYKMSTSGPRAF	46.83	2186.12	19	8.6	547.541	4	22.1509			ZKD_5.raw	P11679|K2C8_MC	Acetylation (N-term); Deamidation (N		FALSE
S(+42.01)IRVTQKSYKM(+15.99)S	41.66	1484.77	12	-0.3	495.929	3	13.3701			ZKD_5.raw	P11679|K2C8_MC	Acetylation (N-term); Oxidation (M)		FALSE
S(+42.01)IRVTQKSYKM(+15.99)STSGPR	37.18	1983.02	17	1.7	496.763	4	12.7317			ZKD_5.raw	P11679|K2C8_MC	Acetylation (N-term); Oxidation (M)		FALSE

S(+42.01)IRVTQKSYKMSTSGPRA	48.6	2038.06	18	2.1	510.524	4	16.3211	1.17E+06	2.32E+07	ZKD_5.raw	P11679|K2C8_MC	Acetylation (N-term)	FALSE
S(+42.01)LVIPEKFQHILR	41.25	1620.94	13	0	541.319	3	39.953	6.81E+06	6.82E+07	ZKD_5.raw	P62270|RS18_MC	Acetylation (N-term)	FALSE
SAKPVSQMRM(+15.99)ATPLLMRPM	37.15	2160.1	19	0.3	541.033	4	26.503	8.35E+05	1.04E+07	ZKD_5.raw	P04441|HG2A_M(	Oxidation (M)	M10:Oxidation (M) FALSE
SAKPVSQMRMATPLLMRPM	45.27	2144.11	19	0.9	715.711	3	30.8443	4.19E+06	5.27E+07	ZKD_5.raw	P04441|HG2A_MOUSE		FALSE
SGFAAPFFIVRHQLLKK	25.58	1958.13	17	0.5	490.539	4	34.2941			ZKD_5.raw	P17665|COX7C_MOUSE		FALSE
SGKIEVEKPFAIAKE	37.64	1644.91	15	8.2	549.315	3	21.2709			ZKD_5.raw	P24369|PPIB_MOUSE		FALSE
SGNFRPANPNWG	25.85	1315.61	12	-2	658.809	2	20.8877			ZKD_5.raw	E9PV24|FIBA_MOUSE		FALSE
SGNFRPANPNWGVF	38.87	1561.74	14	3.7	781.882	2	35.1328	3.25E+05	8.52E+06	ZKD_5.raw	E9PV24|FIBA_MOUSE		FALSE
SGNFRPANPNWGVFS	44.63	1648.77	15	-4.6	825.391	2	33.465	1.58E+06	2.94E+07	ZKD_5.raw	E9PV24|FIBA_MOUSE		FALSE
SGPKPFSAPKPQTSPSPKP	48.63	1934.03	19	0.6	645.683	3	14.9353	2.93E+07	2.76E+08	ZKD_5.raw	P40124|CAP1_MOUSE		FALSE
SGPKPFSAPKPQTSPSPKPA	30.03	2005.06	20	-1.3	502.272	4	14.6203	9.80E+05	1.39E+07	ZKD_5.raw	P40124|CAP1_MOUSE		FALSE
SILWSQPLPSLPGGPP	46.55	1644.89	16	-0.6	823.451	2	51.8753	3.66E+05	5.72E+06	ZKD_5.raw	Q8C0Z1|F234A_MOUSE		FALSE
SLVSKGTLVQTK	37.6	1259.74	12	1.5	420.923	3	15.3886	3.46E+05	1.64E+07	ZKD_5.raw	P43276|H15_MOUSE;P43274|H14_MOUSE;P43277|H1		FALSE
SPARSHLYHPSSPWPIG	28.48	1887.94	17	3.2	630.322	3	24.232			ZKD_5.raw	P97798|NEO1_MOUSE		FALSE
SPPHVQFTYQQPQPLSVEPR	52.61	2334.18	20	0.3	779.066	3	29.6028	3.66E+07	3.54E+08	ZKD_5.raw	B2RXS4|PLXB2_MOUSE		FALSE
SPPPGGYGQPSVLPGGYP	24.98	1725.84	18	2.2	863.927	2	35.5654	6.41E+05	5.51E+06	ZKD_5.raw	Q8BJZ3|LFG3_MOUSE		FALSE
SPPPYAAYATPTPEVYG	47.98	1779.84	17	-1.4	890.924	2	35.8475	1.34E+06	1.59E+07	ZKD_5.raw	Q9QZC7|PKHB2_MOUSE		FALSE
SPRPGSDSGNFRPANPNWG	28.56	2011.92	19	1.2	671.65	3	20.1081	4.00E+05	1.25E+07	ZKD_5.raw	E9PV24|FIBA_MOUSE		FALSE
SSEVYTFPVPERHLE	41.62	1788.87	15	-0.5	597.296	3	28.5318	6.68E+05	2.18E+07	ZKD_5.raw	P09803|CADH1_MOUSE		FALSE
SSGAHGEEGSARMWKALT	33.52	1873.87	18	-1.2	625.631	3	19.0665			ZKD_5.raw	P43024|CX6A1_MOUSE		FALSE
SSHKTFRIKRFL	40.51	1518.88	12	0.5	380.727	4	14.7126	2.63E+06	3.56E+07	ZKD_5.raw	P62892|RL39_MOUSE		FALSE
SSHKTFRIKRFLA	29.91	1589.92	13	-0.6	398.486	4	14.4986	2.56E+06	4.88E+07	ZKD_5.raw	P62892|RL39_MOUSE		FALSE
SSPGRKKFPLKIFKKPLKK	39.63	2226.41	19	-9	446.285	5	11.7475	4.61E+06	5.45E+07	ZKD_5.raw	P70302|STIM1_MOUSE		FALSE
SVFVAPAVTPVK	47.65	1213.71	12	1	607.861	2	29.9158	2.33E+07	2.59E+08	ZKD_5.raw	P70158|ASM3A_MOUSE		FALSE
SVFVAPAVTPVKG	45.27	1270.73	13	-0.1	636.372	2	29.8247	2.84E+07	2.84E+08	ZKD_5.raw	P70158|ASM3A_MOUSE		FALSE
SVFVAPAVTPVKGV	40.03	1369.8	14	-0.1	685.906	2	34.5954	1.30E+05	5.17E+06	ZKD_5.raw	P70158|ASM3A_MOUSE		FALSE
SVNVDYSKLKKEGPDF	43.1	1824.93	16	-1.7	457.238	4	23.5677	2.82E+06	3.76E+07	ZKD_5.raw	Q62425|NDUA4_MOUSE		FALSE
SYRSIEAPEVAIDVDG	42.38	1719.83	16	2.2	860.925	2	32.1703	2.18E+05	4.88E+06	ZKD_5.raw	Q3UVU3|ZNT10_MOUSE		FALSE
T(+79.97)KAPKIQRLVTPR	32.35	1586.9	13	8.3	529.979	3	21.9909	1.99E+06	3.13E+07	ZKD_5.raw	P62754|RS6_MOU	Phosphorylation (S	T1:Phosphorylation FALSE
TGM(+15.99)AFRVPTPNVSVV	48.69	1589.82	15	-1.7	795.918	2	35.9425	1.40E+06	1.18E+07	ZKD_5.raw	P16858|G3P_MOU	Oxidation (M)	FALSE
TGM(+15.99)AFRVPTPNVSVVD	46.91	1704.85	16	0.6	853.433	2	34.4526	7.07E+07	3.49E+08	ZKD_5.raw	P16858|G3P_MOU	Oxidation (M)	FALSE
TGMAFRVPTPNVS	44.03	1375.69	13	-2	688.852	2	32.494			ZKD_5.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE		FALSE
TGMAFRVPTPNVSVV	48.72	1573.83	15	0.2	787.922	2	40.1085	3.29E+06	3.49E+07	ZKD_5.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE		FALSE
TGMAFRVPTPNVSVVD	47.49	1688.86	16	0.1	845.435	2	38.643	1.06E+08	5.75E+08	ZKD_5.raw	P16858|G3P_MOUSE;Q64467|G3PT_MOUSE		FALSE
THDLYIQSHISENREE	43.56	1969.91	16	0.3	657.645	3	16.3852	5.51E+05	1.18E+07	ZKD_5.raw	Q9R111|GUAD_MOUSE		FALSE
THINIVVIGHVDSGK	48.82	1587.87	15	0.7	530.299	3	23.1538	1.88E+07	1.99E+08	ZKD_5.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE		FALSE
THINIVVIGHVDSGKSTTT	51.63	1978.05	19	1.4	660.358	3	23.188	1.18E+06	2.35E+07	ZKD_5.raw	P62631|EF1A2_MOUSE;P10126|EF1A1_MOUSE		FALSE
TKAGSKGGNLRDKLD	31.11	1558.84	15	0.3	390.718	4	8.6096	5.64E+05	1.13E+07	ZKD_5.raw	Q922Q8|LRC59_MOUSE		FALSE
TKAPKIQRLVTPR	24.11	1506.94	13	-0.4	377.741	4	13.0461	1.41E+05	2.60E+06	ZKD_5.raw	P62754|RS6_MOUSE		FALSE
TLVTYVPVTTFK	37.8	1367.77	12	0.5	684.893	2	36.1762	1.30E+06	2.03E+07	ZKD_5.raw	P62900|RL31_MOUSE		FALSE
TNTAYVGSAILSEET	43.58	1554.74	15	-2.4	778.376	2	33.9898	8.05E+05	1.60E+07	ZKD_5.raw	Q9QZC7|PKHB2_MOUSE		FALSE
TPAYTIPFYTPIPNG	40.99	1650.83	15	1.1	826.423	2	48.722	1.34E+06	1.30E+07	ZKD_5.raw	O08573|LEG9_MOUSE		FALSE
TPESFLGPNAALVDLD	22.1	1657.82	16	-0.2	829.917	2	48.6733	2.00E+05	5.14E+06	ZKD_5.raw	Q80VP1|EPN1_MOUSE		FALSE
TPFQFRAASPVEE	46.03	1477.72	13	0	739.867	2	29.3839	1.45E+06	2.67E+07	ZKD_5.raw	Q3UKC1|TAXB1_MOUSE		FALSE
TPFQFRAASPVEEL	46.23	1590.8	14	0.5	796.41	2	37.5018	2.23E+05	7.37E+06	ZKD_5.raw	Q3UKC1|TAXB1_MOUSE		FALSE
TPSAAYLWVGAGASEAEK	45.8	1806.88	18	0.4	904.447	2	33.4487	2.06E+05	6.80E+06	ZKD_5.raw	P13020|GELS_MOUSE;#CONTAM#Q3SX14		FALSE
TPSAAYLWVGAGASEAEKT	52.03	1907.93	19	1.4	954.972	2	34.3108	3.70E+06	4.74E+07	ZKD_5.raw	P13020|GELS_MOUSE;#CONTAM#Q3SX14		FALSE
TPSAAYLWVGAGASEAEKTG	46.36	1964.95	20	-1.2	983.48	2	34.3635			ZKD_5.raw	P13020|GELS_MOUSE;#CONTAM#Q3SX14		FALSE
TPVFVHAGPFANIAHGNS	37.14	1834.91	18	1.6	612.645	3	30.8768	8.11E+05	6.06E+06	ZKD_5.raw	Q922D8|C1TC_MOUSE;Q3V3R1|C1TM_MOUSE		FALSE
TQVQWNDPGAQYSLVN	47.52	1818.85	16	1	910.435	2	35.725	6.49E+06	7.34E+07	ZKD_5.raw	Q9R100|CAD17_MOUSE		FALSE
TSSYSNPTIGYENR	47.79	1587.72	14	3.8	794.869	2	18.2195	4.83E+05	9.83E+06	ZKD_5.raw	Q07797|LG3BP_MOUSE		FALSE
TTGAWKNPHVQQAAQ	35.73	1635.81	15	-0.6	546.278	3	12.9777	5.00E+05	6.99E+06	ZKD_5.raw	Q9JKD3|SCAM5_MOUSE		FALSE
VAIFARGPQAHLVH	25.87	1514.85	14	-0.9	379.719	4	21.512	4.06E+07	3.86E+08	ZKD_5.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE		FALSE
VAIFARGPQAHLVHG	33.89	1571.87	15	0.7	393.975	4	21.4204	1.26E+08	1.13E+09	ZKD_5.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE		FALSE
VAIFARGPQAHLVHGVQ	31.47	1799	17	0.1	450.756	4	23.1559	3.45E+07	2.99E+08	ZKD_5.raw	P24823|PPBN_MOUSE;P24822|PPBI_MOUSE		FALSE
VANVS(+79.97)LLALYKGKKERPRS	38.85	2208.21	19	-0.2	553.061	4	31.4281			ZKD_5.raw	P62267|RS23_MC	Phosphorylation (S	S5:Phosphorylatio FALSE
VARYRPRAPIIAVTRNPQ	37.55	2077.2	18	-1.5	520.307	4	16.7941	6.77E+06	9.25E+07	ZKD_5.raw	P52480|KPYM_MOUSE		FALSE
VATNPIITPVAQENQ	21.27	1593.84	15	2.3	797.927	2	30.6709			ZKD_5.raw	P08226|APOE_MOUSE		FALSE
VDFNTPRPSTVEA	39.03	1431.7	13	-2.6	716.855	2	24.0964			ZKD_5.raw	G3X939|SL9A3_MOUSE		FALSE
VDLRFSTSQSLPASQT	37.76	1735.87	16	-3.2	868.942	2	29.6982	3.64E+05	7.65E+06	ZKD_5.raw	P28665|MUG1_MOUSE		FALSE
VEYAVRGPIVQRALE	22.2	1698.94	15	0	567.321	3	26.2515			ZKD_5.raw	Q8QZR5|ALAT1_MOUSE		FALSE
VEYAVRGPIVQRALEL	38.69	1812.03	16	-1.2	605.015	3	34.638	6.84E+05	8.82E+06	ZKD_5.raw	Q8QZR5|ALAT1_MOUSE		FALSE
VGTKRYMAPEVLDETIN	37.62	1934.98	17	1.9	646.001	3	27.6123			ZKD_5.raw	Q61271|ACV1B_MOUSE		FALSE
VGTRRYMAPEVLEGAIN	22.73	1874.97	17	0.3	625.997	3	28.4667	6.43E+05	1.52E+07	ZKD_5.raw	P27038|AVR2A_MOUSE;P27040|AVR2B_MOUSE		FALSE
VKVTFNSALAQKEAKK	49	1761.01	16	0.2	441.261	4	14.6522	1.79E+06	2.83E+07	ZKD_5.raw	O89051|ITM2B_MOUSE		FALSE
VLTVINQTQKENLR	42.34	1654.94	14	0.8	552.653	3	19.8013	9.93E+05	1.85E+07	ZKD_5.raw	Q6ZWV7|RL35_MOUSE		FALSE
VLVTWTPPRARIAGYR	27.09	1855.06	16	0.4	464.772	4	27.6093			ZKD_5.raw	P11276|FINC_MOUSE		FALSE
VPFETRGPHINNSVH	34.09	1702.85	15	-1	426.72	4	16.3532	1.10E+06	1.25E+07	ZKD_5.raw	Q8K296|MTMR3_MOUSE		FALSE
VPLPVSLGPPLP	29.92	1184.72	12	6.2	593.369	2	55.7635	4.32E+05	2.42E+06	ZKD_5.raw	Q62406|IRAK1_MOUSE		FALSE
VPWNFHEPQPGQYE	42.37	1726.77	14	1.6	864.396	2	31.0173	4.74E+05	6.95E+06	ZKD_5.raw	P23780|BGAL_MOUSE		FALSE
VRYTQKAPQVSTPTL	35.16	1687.93	15	1.1	563.65	3	21.6049	8.18E+05	1.55E+07	ZKD_5.raw	P07724|ALBU_MOUSE		FALSE
VSHDYKGSTSHSLPY	29.23	1676.78	15	-4.7	559.931	3	13.8802	1.89E+06	3.46E+07	ZKD_5.raw	E9Q414|APOB_MOUSE		FALSE
VSLADLQNDEVAFR	45.55	1575.79	14	1	788.903	2	36.6851	2.35E+06	3.33E+07	ZKD_5.raw	P97351|RS3A_MOUSE		FALSE
VTQFHPPHIEIQ	28.96	1444.75	12	0.5	482.59	3	27.222	1.64E+06	1.24E+07	ZKD_5.raw	P01887|B2MG_MOUSE		FALSE
VTQPTVGMNFKTPRGAV	41.31	1801.95	17	-0.3	601.657	3	25.3954	3.62E+05	9.73E+06	ZKD_5.raw	P63276|RS17_MOUSE		FALSE
WVRTDM(+15.99)AGPKATKSPEE	41.24	1917.93	17	-3.4	640.314	3	11.81	4.56E+05	9.93E+06	ZKD_5.raw	P48758|CBR1_M(	Oxidation (M)	FALSE
WVRTDMAGPKATKSPEE	37.4	1901.93	17	-0.5	476.49	4	14.5896	3.03E+06	4.93E+07	ZKD_5.raw	P48758|CBR1_MOUSE		FALSE
YAVRGPIVQRALEL	45.12	1583.91	14	-0.2	528.979	3	31.3839	7.33E+05	7.15E+06	ZKD_5.raw	Q8QZR5|ALAT1_MOUSE		FALSE
YDPIVNKKVLFVEQKKIRSL	28.42	2416.42	20	0.6	605.113	4	26.2009	2.47E+05	5.81E+06	ZKD_5.raw	Q9CQP0|RM33_MOUSE		FALSE
YLNIYTPAHAHEGSN	34.96	1685.78	15	0.4	562.934	3	20.3768	1.29E+06	1.26E+07	ZKD_5.raw	Q91WG0|EST2C_MOUSE		FALSE
YLNIYVPAHAHEG	40.42	1482.73	13	0.2	495.249	3	23.9067	3.86E+05	9.69E+06	ZKD_5.raw	Q8BK48|EST2E_MOUSE		FALSE
YLNIYVPAHAHEGSN	46.71	1683.8	15	2	842.909	2	23.7387	7.58E+06	1.01E+08	ZKD_5.raw	Q8BK48|EST2E_MOUSE		FALSE
YLNIYVPAHAHEGSNL	42.23	1796.88	16	-0.1	599.969	3	27.8294	1.34E+06	2.59E+07	ZKD_5.raw	Q8BK48|EST2E_MOUSE		FALSE
YLNIYVPAHAHEGSNLPV	24.51	1993.01	18	1.3	665.343	3	32.8315	2.28E+06	4.23E+07	ZKD_5.raw	Q8BK48|EST2E_MOUSE		FALSE
YPDKKVTFSSGYVNLSPEN	28.63	2144.04	19	6.3	715.693	3	28.1222			ZKD_5.raw	P06684|CO5_MOUSE		FALSE
YPSQASIYSPPAAAAAAAA	42.55	1776.87	19	-0.9	889.441	2	33.1822	3.74E+05	7.05E+06	ZKD_5.raw	P70297|STAM1_MOUSE		FALSE
YTIPFYTPIPNG	41.33	1381.69	12	0.3	691.853	2	47.0647	2.78E+06	2.95E+07	ZKD_5.raw	O08573|LEG9_MOUSE		FALSE
YVPVTTFKNLQTVNVDEN	41.45	2080.05	18	-1.3	1041.03	2	34.0504	2.66E+06	3.96E+07	ZKD_5.raw	P62900|RL31_MOUSE		FALSE
YVTQFHPPHIEIQ	48.07	1607.81	13	0.6	804.913	2	30.1341	3.67E+07	3.66E+08	ZKD_5.raw	P01887|B2MG_MOUSE		FALSE
YVTQFHPPHIEIQM(+15.99)L	33.25	1867.93	15	-0.2	623.65	3	36.0353	1.59E+07	8.72E+07	ZKD_5.raw	P01887|B2MG_M(	Oxidation (M)	FALSE
YVTQFHPPHIEIQML	46.32	1851.93	15	2.3	618.32	3	40.4287	1.20E+07	8.21E+07	ZKD_5.raw	P01887|B2MG_MOUSE		FALSE
YVTQFHPPHIEIQMLK	49.46	1980.03	16	-0.4	661.017	3	34.3108	9.06E+06	6.17E+07	ZKD_5.raw	P01887|B2MG_MOUSE		FALSE
YVTQFHPPHIEIQMLKNGK	44.57	2279.19	19	1.8	570.805	4	30.4012			ZKD_5.raw	P01887|B2MG_MOUSE		FALSE

Table S1 Information of peptides identified in IEC MHCII immunopeptidome (related to Fig.2d)

Table S2 Information of peptides identified in IEC MHCII immunopeptidome (related to Supplementary Fig. S7e)

	Peptide	X.10LgP	Mass	Tag.Length	CAA....	Length	Delta.RT	MS2.Correlation	ppm	m.z	z	RT	Accession	PTM	AScore	Positional.Confide	tag...0.0..	Found.By	Area.Sample.1	Clean_Sequence	share
	H2Ab1ff_GBD																				
1	KPVSQMRMATPLLMRPM	40.12	1986.04	17	11.8	17	0.0284	0.24	-1.6	663.0211	3	18.6677	P04441|HG2A_MOUSE:Q545Y5|Q545Y5_MOUSE:Q3			5 2 1 0 0 0 0 0 0	KPVSQMRMATPL	DB Search	47000	KPVSQMRMATPL	3
2	VAIFARGPQAHLVHG	40.12	1571.868	15	26.7	15	0.3915	0.35	-0.2	786.9432	2	14.4539	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:			0 0 0 0 0 0 0 0 0	VAIFARGPQAHL	DB Search	30900	VAIFARGPQAHL	3
3	GDAEMAIYGPAAIYLR	40.12	1691.675	16	47.1	17	0.5692	0.76	4	921.4557	2	24.8633	A0ABD1KMS1|A0ABD1KMS1_9TELE			0 0 0 1 2 12 12 45	MGDAEMAIYGP	DB Search	23700	GDAEMAIYGPAA	1
4	LPPYDDATAVPSTAKEPPPP	40.12	2062.026	20	50	20	-0.1034	0.73	-0.2	688.3507	3	16.5699	B2CZK6|B2CZK6_MOUSE:Q91XQ6|LAP4B_MOUSE			0 0 0 0 0 0 0 0 12	LPPYDDATAVPS	DB Search	17800	LPPYDDATAVPS	3
5	LGEYGFQNAILVR	40.12	1478.788	13	84.6	13	0.1735	0.78	4.4	740.4064	2	21.3774	Q546G4|Q546G4_MOUSE:P07724|ALBU_MOUSE			5 8 8 44 27 27 29	LGEYGFQNAILV	DB Search	17700	LGEYGFQNAILV	3
6	GKFMKPGKVVLVLAGRYSGRKAVIVKNID	39.71	3142.853	29	3.4	29	-2.8076	0.27	3.9	786.7236	4	17.5508	P61358|RL27_MOUSE:Q5BLJ9|Q5BLJ9_MOUSE			0 0 0 0 0 0 0 0 0	GKFMKPGKVVLV	DB Search	16400	GKFMKPGKVVLV	3
7	SVFVAPAVTPVKG	40.12	1270.729	13	53.8	13	0.1448	0.7	-1	636.3724	2	18.0278	P70158|ASM3A_MOUSE			0 0 28 28 69 2 2	SVFVAPAVTPVK	DB Search	14200	SVFVAPAVTPVK	3
8	SVFVAPAVTPVK	40.12	1213.707	12	58.3	12	0.7595	0.71	1.7	607.8632	2	18.097	P70158|ASM3A_MOUSE			0 0 22 38 89 6 6	SVFVAPAVTPVK	DB Search	13900	SVFVAPAVTPVK	3
9	VAIFARGPQAHLVHGVQ	40.12	1798.995	17	41.2	17	0.4095	0.31	1.4	600.6747	3	15.2954	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:			5 52 0 0 0 0 0 0 0	VAIFARGPQAHL	DB Search	13800	VAIFARGPQAHL	3
10	DAEMAIYGPAAIYLR	40.12	1652.823	15	46.7	15	0.7976	0.83	3.4	827.4237	2	24.8311	A0ABD1KMS1|A0ABD1KMS1_9TELE			0 0 0 12 12 40 95	DAEMAIYGPAAI	DB Search	13200	DAEMAIYGPAAI	1
11	KPVSQMRMATPLLMRPM(+15.99)	36.61	2002.035	17	23.5	17	0.2602	0.7	-2.1	501.5161	4	16.8461	P04441|HG2A_M	Oxidation (M)	M17:Oxidation (M	0 0 0 3 0 0 1 0 0	KPVSQMRMATPL	DB Search	13000	KPVSQMRMATPL	2
12	APMYYRGAQAAIVVYD	40.12	1786.871	16	50	16	-0.9109	0.44	3.2	894.4479	2	18.9079	Q3TCT9|Q3TCT9_MOUSE:P61021|RAB5B_MOUSE:			0 0 0 0 1 1 1 1 3	APMYYRGAQAAI	DB Search	9980	APMYYRGAQAAI	3
13	RKIVYEGPELNHAFG	40.12	1728.895	15	73.3	15	0.4843	0.52	-3.8	577.3047	3	15.1327	A0A0R4J0I9|A0A0R4J0I9_MOUSE:Q91ZX7|LRP1_MO			0 0 2 5 9 9 42 13	RKIVYEGPELNH	DB Search	8760	RKIVYEGPELNH	3
14	DLYANTVLSGGTTMYPGLADR	40.12	2214.063	21	42.9	21	-0.2222	0.57	6.9	1108.049	2	22.8085	Q9QZ83|Q9QZ83_MOUSE			0 0 0 1 1 1 8 6 7	DLYANTVLSGGT	DB Search	8030	DLYANTVLSGGT	3
15	DLYANTVLSGGTTMYPGIADR	40.12	2214.063	21	42.9	21	0.0052	0.58	6.9	1108.049	2	22.8085	P63260|ACTG_MOUSE:Q3U5R4|Q3U5R4_MOUSE:P			0 0 0 1 1 1 8 6 7	DLYANTVLSGGT	DB Search	8030	DLYANTVLSGGT	3
16	DRKIVYEGPELNHAFG	40.12	1843.922	16	43.8	16	0.241	0.45	-3.2	615.6473	3	16.3955	A0A0R4J0I9|A0A0R4J0I9_MOUSE:Q91ZX7|LRP1_MO			0 0 0 0 0 2 4 8 0	DRKIVYEGPELN	DB Search	7720	DRKIVYEGPELN	3
17	VAIFARGPQAHLVH	39.62	1514.847	14	28.6	14	0.5874	0.49	-0.9	758.4301	2	14.4896	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:			0 0 0 0 0 0 0 0 0	VAIFARGPQAHL	DB Search	6690	VAIFARGPQAHL	3
18	LAPITSDPTEAAAVGAVEASFK	40.12	2144.1	22	4.5	22	-0.6855	0.5	1.7	1073.062	2	24.0592	P52480|KPYM_MOUSE			0 0 0 0 0 0 1 0 0	LAPITSDPTEAAA	DB Search	5380	LAPITSDPTEAAA	1
19	YVTQFHPPHIEIQML	40.12	1851.934	15	26.7	15	0.3769	0.62	-0.4	926.9762	2	23.4417	Q9D239|Q9D239_MOUSE:P01887|B2MG_MOUSE:Q			0 0 0 0 0 1 0 0 0	YVTQFHPPHIEIQ	DB Search	5320	YVTQFHPPHIEIQ	3
20	GFGSAGGSNTFSRTTKAVVVKKIETRDGKLVS	39.16	3296.784	32	6.2	32	-6.2169	NA	1.2	660.3665	5	14.7285	P11679|K2C8_MOUSE			0 0 0 1 58 11 0 0	GFGSAGGSNTF	DB Search	5230	GFGSAGGSNTF	2
21	IPGTNMYNTDRANPVLD	40.12	1889.894	17	17.6	17	0.1339	0.37	2	945.9585	2	17.1733	Q8K066|Q8K066_MOUSE:E9Q7P9|CDHR2_MOUSE			5 0 0 0 0 0 0 0 0	IPGTNMYNTDRA	DB Search	5100	IPGTNMYNTDRA	3
22	NPPSYYTQPVPVPNAN	40.12	1756.842	16	43.8	16	-0.0804	0.73	1.7	879.4319	2	17.8937	Q9JLJ0|LITAF_MOUSE:E0CYR5|E0CYR5_MOUSE			0 0 0 0 0 3 2 4 2	NPPSYYTQPVPV	DB Search	4670	NPPSYYTQPVPV	3
23	AGLQFPVGR	39.28	943.5239	9	77.8	9	-0.4117	0.83	0.6	472.7695	2	17.0545	Q8BFU2|H2A3_MOUSE:A0AUV1|A0AUV1_MOUSE:Q			4 4 7 71 63 2 2 0	AGLQFPVGR	DB Search	4520	AGLQFPVGR	3
24	SPPHVQFTYQQPQPLSVEPR	40.12	2334.176	20	50	20	0.2442	0.55	2.6	779.0697	3	17.6781	B2RXS4|PLXB2_MOUSE			0 0 0 0 1 1 3 3 5	SPPHVQFTYQQP	DB Search	4520	SPPHVQFTYQQP	3
25	TVKPKAAKPKTSKPKAAKPKKTAAKKK	40.12	2858.827	27	29.6	27	-0.6836	0.58	-1.4	477.4789	6	1.9044	P43274|H14_MOUSE			0 0 0 6 0 0 0 0 0	TVKPKAAKPKTS	DB Search	4470	TVKPKAAKPKTS	3
26	FPKPPSYNVATTLPSYDE	40.12	2024.973	18	5.6	18	-0.3534	0.92	3.3	1013.5	2	20.0365	A0A494BAA4|A0A494BAA4_MOUSE:Q8R0W6|NFIP1			0 0 0 0 0 0 0 0 0	FPKPPSYNVATT	DB Search	4350	FPKPPSYNVATT	3
27	FPYVTPAPHEPVK	40.12	1480.771	13	53.8	13	-0.5944	0.52	-1.5	494.5982	3	14.5551	Q9D074|MGRN1_MOUSE			0 0 0 20 63 2 2 1	FPYVTPAPHEPV	DB Search	4060	FPYVTPAPHEPV	3
28	EITALAPSTM(+15.99)K	39.78	1176.606	11	45.5	11	0.6739	0.8	-0.9	589.3112	2	12.4084	P63260|ACTG_M	Oxidation (M)	M10:Oxidation (M	0 0 19 19 69 96 0	EITALAPSTM(+1	DB Search	4030	EITALAPSTMK	3
29	VYLIQGTQVYVFLTK	40.12	1770.992	15	66.7	15	-0.0056	0.36	4.4	886.5093	2	26.1866	Q91X72|HEMO_MOUSE			0 0 0 3 63 12 10	VYLIQGTQVYVFL	DB Search	3950	VYLIQGTQVYVFL	3
30	TGMAFRVPTPNVSVVD	40.12	1688.856	16	56.2	16	0.9822	0.44	4.2	845.4406	2	22.1628	S4R257|S4R257_MOUSE:Q3V2I5|Q3V2I5_MOUSE:S			0 0 0 1 1 3 5 2 2	TGMAFRVPTPNV	DB Search	3740	TGMAFRVPTPNV	3
31	HNYEGPETHTSLR	40.12	1539.707	13	76.9	13	0.257	0.62	-1.5	514.2432	3	5.1748	P14483|HB2A_MOUSE:Q5XQL0|Q5XQL0_MOUSE:Q			5 13 2 2 2 0 2 4 5	HNYEGPETHTSL	DB Search	3410	HNYEGPETHTSL	3
32	ALEEQLQQIRAE	40.12	1426.742	12	66.7	12	0.2418	0.77	2.6	714.3816	2	16.275	P02535|K1C10_MOUSE:A2A513|A2A513_MOUSE			0 0 42 19 19 67 8	ALEEQLQQIRAE	DB Search	3270	ALEEQLQQIRAE	3
33	WGEAGAEYVVESTGVFTTMEK	40.12	2290.046	21	0	21	-1.4416	0.55	0.9	1146.034	2	24.8541	A0A1D5RLD8|A0A1D5RLD8_MOUSE:S4R257|S4R25			0 0 0 0 0 0 0 0 0	WGEAGAEYVVE	DB Search	3270	WGEAGAEYVVE	3
34	EMEENFALEAANYQDTIGR	40.12	2199.974	19	36.8	19	-1.5716	0.73	8.2	1101.006	2	20.8411	P20152|VIME_MOUSE:Q5FWJ3|Q5FWJ3_MOUSE:Q			0 0 0 0 0 1 2 2 3	EMEENFALEAAN	DB Search	2960	EMEENFALEAAN	3
35	KPVSQMRMATPLLM(+15.99)RPM	38.73	2002.035	17	41.2	17	0.4206	0.6	-2.1	501.5161	4	16.8461	P04441|HG2A_M	Oxidation (M)	M14:Oxidation (M	0 0 0 0 0 0 0 0 2	KPVSQMRMATPL	DB Search	2920	KPVSQMRMATPL	3
36	KPVSQM(+15.99)RMATPLLMRPM	27	2002.035	17	5.9	17	-0.7031	0.38	-0.9	668.3516	3	16.3164	P04441|HG2A_M	Oxidation (M)	M6:Oxidation (M):	5 1 0 0 0 0 0 0 0	KPVSQM(+15.99)	DB Search	2920	KPVSQMRMATPL	2
37	GQVGGDVNVEM(+15.99)DAAPGVDLSR	40.12	2100.975	21	4.8	21	-0.4423	0.85	1.4	1051.499	2	16.2738	Q6IFX2|K1C42_M	Oxidation (M)	M11:Oxidation (M	0 0 0 0 0 0 0 0 0	GQVGGDVNVEM	DB Search	2910	GQVGGDVNVEM	1
38	IPGTNMYNTDRANPVLDLP	39.46	2100.031	19	10.5	19	1.028	0.57	5.7	1051.031	2	22.6021	Q8K066|Q8K066_MOUSE:E9Q7P9|CDHR2_MOUSE			0 0 0 0 0 0 0 0 0	IPGTNMYNTDRA	DB Search	2760	IPGTNMYNTDRA	3
39	LLLPGELAK	34.87	952.5957	9	66.7	9	0.0729	0.55	-0.5	477.3049	2	19.1451	B2RTK3|B2RTK3_MOUSE:P70696|H2B1A_MOUSE:A			5 12 44 10 3 2 0	LLLPGELAK	DB Search	2730	LLLPGELAK	3
40	APMYYRGAQAAIVVY	40.1	1671.844	15	40	15	-0.3773	0.64	4.1	836.9348	2	19.5028	Q3TCT9|Q3TCT9_MOUSE:P61021|RAB5B_MOUSE:			0 0 0 1 0 0 0 1 1	APMYYRGAQAAI	DB Search	2710	APMYYRGAQAAI	3
41	G(+42.01)KEKTHINIVVIGHVDSGKSTTTGHLIYK	40.12	3173.72	29	3.4	29	-3.436	0.34	15	635.7622	5	13.9974	Q58E64|Q58E64_	Acetylation (N-ter	G1:Acetylation (N	0 0 0 0 0 0 0 0 0	G(+42.01)KEKTH	DB Search	2480	GKEKTHINIVVIG	2
42	NPTIYPLTLPRALSSDPV	40.12	1953.057	18	11.1	18	-0.0785	0.8	3.2	977.5412	2	25.4623	Q99KA4|Q99KA4_MOUSE:Q58E61|Q58E61_MOUSE:			5 0 0 1 4 1 1 1 1	NPTIYPLTLPRAL	DB Search	2340	NPTIYPLTLPRAL	3
43	APM(+15.99)YYRGAQAAIVVYD	39.94	1802.866	16	25	16	-0.5476	0.33	2.2	902.4445	2	17.609	Q3TCT9|Q3TCT9	Oxidation (M)	M3:Oxidation (M):	0 0 0 0 0 0 0 0 0	APM(+15.99)YYR	DB Search	2310	APMYYRGAQAAI	3
44	PKGKKAKGKKVAPAPAVVKKQEAKKVVNPLFE	40.1	3412.081	32	6.2	32	-5.2287	NA	4.3	683.428	5	9.66	Q5EBG5|Q5EBG5_MOUSE:Q80UT7|Q80UT7_MOUSE			0 0 0 0 0 0 0 0 0	PKGKKAKGKKV	DB Search	2300	PKGKKAKGKKV	2
45	DSYVGDEAQSK	40.08	1197.515	11	45.5	11	-1.064	0.86	-0.9	599.7656	2	4.9059	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:A0			0 0 3 30 6 3 3 0 0	DSYVGDEAQSK	DB Search	2270	DSYVGDEAQSK	3
46	AGGSNTFSRTTKAVVVKKIETRDGKLVS	37.39	2948.641	28	0	28	-2.3728	0.21	5.5	738.1715	4	12.8796	P11679|K2C8_MOUSE			0 0 0 0 0 0 0 0 0	AGGSNTFSRTTK	DB Search	2220	AGGSNTFSRTTK	2
47	RPVQFPYVTPAPHEPVK	40.12	1961.052	17	52.9	17	-0.5976	0.79	-1.4	654.692	3	15.2431	Q9D074|MGRN1_MOUSE			0 0 0 0 7 23 23 27	RPVQFPYVTPAP	DB Search	2080	RPVQFPYVTPAP	3
48	G(+42.01)DAEMAIYGPAAIYLR	40.12	1733.686	16	47.1	17	0.1495	0.8	1.4	929.4508	2	23.8901	A0ABD1KMS1|A0	Oxidation (M)	M1:Oxidation (M):	0 0 0 1 3 9 9 20 4	M(+15.99)GDAE	DB Search	2080	GDAEMAIYGPAA	1
49	YEDIAQKSKAEAE	40.12	1480.705	13	23.1	13	0.8131	0.66	-2.5	741.3594	2	6.2709	Q3UV17|K22O_MOUSE			0 0 0 0 2 1 1 0 0	YEDIAQKSKAEA	DB Search	2030	YEDIAQKSKAEA	2
50	ELEEQLGPVAEETRA	40.12	1669.816	15	66.7	15	-0.267	0.89	2.6	835.9193	2	16.3066	G3UZM8|G3UZM8_MOUSE:G3UWN5|G3UWN5_MO			0 0 10 10 12 22 4	ELEEQLGPVAEE	DB Search	2020	ELEEQLGPVAEE	3
51	ERYKTGKNKWFFQKLRF	40.09	2275.238	17	17.6	17	4.3564	0.6	-1.9	569.817	4	20.618	A2A4Q0|A2A4Q0_MOUSE:P61358|RL27_MOUSE:Q5			0 0 0 0 0 0 0 0 0	ERYKTGKNKWF	DB Search	1970	ERYKTGKNKWF	2
52	EVSSVEAPSVSPAR	40.12	1413.71	14	57.1	14	0.1827	0.89	-2.5	707.8621	2	12.1677	Q8BUJ9|LRP12_MOUSE			0 0 2 4 12 39 39 2	EVSSVEAPSVSP	DB Search	1910	EVSSVEAPSVSP	3
53	GGLPDYSAPNPIKVTHR	40.12	1820.953	17	5.9	17	-0.6255	0.41	-0.3	607.993	3	14.6301	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			0 0 0 14 0 0 1 0 0	GGLPDYSAPNPI	DB Search	1900	GGLPDYSAPNPI	3
54	GPDGRFVMGPTVAPSQEK	40.12	1871.92	18	50	18	-0.5854	0.76	-4.3	624.9794	3	14.3922	Q05BQ1|TUTLA_MOUSE			0 0 0 0 0 5 6 17 1	GPDGRFVMGPT	DB Search	1900	GPDGRFVMGPT	3
55	QPSTSSLAAPTVEAAASAPA	39.94	1825.906	20	30	20	-0.3417	0.64	1.8	913.9639	2	17.7114	A0AAQ4VMX1|A0AAQ4VMX1_MOUSE:A0AAQ4VMV3			0 0 0 0 0 3 0 0 9 1	QPSTSSLAAPTV	DB Search	1890	QPSTSSLAAPTV	3
56	GFGSAGGSNTFSRTTKAVVVKKIETRDGKLVSE	40.12	3425.827	33	9.1	33	-6.4368	NA	-1.1	686.1735	5	14.7886	P11679|K2C8_MOUSE			0 0 0 0 47 19 3 0	GFGSAGGSNTF	DB Search	1790	GFGSAGGSNTF	1
57	SQVFSTAADGQTQVEIK	40.12	1807.895	17	64.7	17	-0.3677	0.58	2.3	904.9591	2	15.5771	P38647|HSPA9_MOUSE			0 0 0 8 6 8 8 13 1	SQVFSTAADGQT	DB Search	1780	SQVFSTAADGQT	3
58	AKPVSQMRMATPLLMRPM	39.7	2057.077	18	16.7	18	0.1631	0.7	1.3	686.7005	3	18.9634	P04441|HG2A_MOUSE:Q545Y5|Q545Y5_MOUSE:Q3			0 0 2 2 0 0 0 0 0	AKPVSQMRMAT	DB Search	1780	AKPVSQMRMAT	3
59	ITNQYNSPTGLYSSEN	40.12	1786.801	16	56.2	16	-0.7957	0.71	5.2	894.4145	2	15.1625	O70400|PDLI1_MOUSE:S4R1V0|S4R1V0_MOUSE:Q			0 0 0 4 19 19 54 0	ITNQYNSPTGLYS	DB Search	1650	ITNQYNSPTGLYS	3
60	VFENYEASKAYSSVD	40.12	1707.763	15	73.3	15	-0.1764	0.65	1.9	854.8923	2	14.8079	Q9D306|MGT4C_MOUSE			0 0 4 5 13 20 20 1	VFENYEASKAYS	DB Search	1530	VFENYEASKAYS	3
61	SVGDGETVEFDVVEGEK	40.12	1794.816	17	35.3	17	-1.4288	0.76	5.7	898.4224	2	18.1441	Q9JKB3|YBOX3_MOUSE:Q60951|Q60951_MOUSE:A			0 0 0 0 0 0 3 3 7 5	SVGDGETVEFDV	DB Search	1520	SVGDGETVEFDV	1
62	VFENYEASKAYSSVDE	40.12	1836.805	16	68.8	16	-0.2938	0.61	1.6	919.4136	2	14.9751	Q9D306|MGT4C_MOUSE			0 0 0 2 6 16 12 0	VFENYEASKAYS	DB Search	1460	VFENYEASKAYS	3
63	DVDAAYM(+15.99)NKVELEAK	40.12	1710.813	15	6.7	15	-0.8955	0.56	1.6	856.4174	2	13.1367	Q148Q7|Q148Q7	Oxidation (M)	M7:Oxidation (M):	0 0 2 0 1 0 0 0 0	DVDAAYM(+15.9	DB Search	1460	DVDAAYMNKVEL	1
64	YVTQFHPPHIEIQ	40.12	1607.81	13	30.8	13	0.008	0.37	3.2	804.9165	2	18.3418	Q9D239|Q9D239_MOUSE:P01887|B2MG_MOUSE:Q			0 0 1 0 0 2 0 0 0	YVTQFHPPHIEIQ	DB Search	1450	YVTQFHPPHIEIQ	3
65	VEKNNSRIKLGLK	40.05	1497.899	13	7.7	13	-0.1321	0.54	4.8	749.9622	2	8.2813	P15864|H12_MOUSE:P43276|H15_MOUSE:P43275|H			0 0 0 0 0 0 0 0 0	VEKNNSRIKLGL	DB Search	1420	VEKNNSRIKLGL	1
66	NPLNSVFVAPAVTPVK	40.12	1651.93	16	50	16	0.2788	0.72	3.8	826.9772	2	22.3594	P70158|ASM3A_MOUSE			5 0 0 3 5 5 10 10	NPLNSVFVAPAV	DB Search	1410	NPLNSVFVAPAV	3
67	IREFYSASVAEDATLG	40.12	1727.837	16	62.5	16	-0.0465	0.51	1	864.9285	2	18.6604	E9Q7P9|CDHR2_MOUSE			0 0 0 1 2 5 5 5 5 1	IREFYSASVAED	DB Search	1400	IREFYSASVAED	3
68	RHNYEGPETHTSLR	40.12	1695.808	14	21.4	14	-1.3161	0.65	1.6	566.2788	3	2.3703	P14483|HB2A_MOUSE:Q5XQL0|Q5XQL0_MOUSE:Q			0 0 0 1 1 3 1 1 5 4	RHNYEGPETHTS	DB Search	1340	RHNYEGPETHTS	3
69	VAPEEHPVLLTEAPLNPK	40.12	1953.057	18	33.3	18	0.0416	0.58	-4.1	652.0252	3	17.906	P63260|ACTG_MOUSE:E9Q5F4|E9Q5F4_MOUSE:G3			0 0 4 0 0 0 0 0 2 3	VAPEEHPVLLTE	DB Search	1330	VAPEEHPVLLTE	3
70	SGPKPFSAPKPQTSPSPKP	40.12	1934.026	19	5.3	19	0.9942	0.57	2.1	645.6856	3	10.3903	Q3TC53|Q3TC53_MOUSE:P40124|CAP1_MOUSE:Q3			0 0 0 0 0 0 1 1 0 0	SGPKPFSAPKPQ	DB Search	1310	SGPKPFSAPKPQ	3
71	QPSTSSLAAPTVEAAASA	40.11	1657.816	18	61.1	18	-1.0578	0.65	3	829.9196	2	17.3081	A0AAQ4VMX1|A0AAQ4VMX1_MOUSE:A0AAQ4VMV3			0 0 0 0 1 0 0 8 16	QPSTSSLAAPTV	DB Search	1310	QPSTSSLAAPTV	2
72	AKASKPKASKPKATKAKKAAPRKK	38.42	2518.591	24	25	24	18.3682	0.65	-5	420.7713	6	20.8129	Q149Z9|Q149Z9_MOUSE:P43277|H13_MOUSE:Q3U			0 0 0 0 0 0 0 0 0	AKASKPKASKPK	DB Search	1290	AKASKPKASKPK	1
73	VSHVSTGGGASLELLEGK	40.12	1739.905	18	66.7	18	-0.3945	0.71	-2.2	580.9758	3	16.308	P09041|PGK2_MOUSE:P09411|PGK1_MOUSE			0 0 0 2 2 2 4 5 11	VSHVSTGGGASL	DB Search	1290	VSHVSTGGGASL	1
74	EEQLQQIRAE	39.7	1242.62	10	80	10	-0.2836	0.89	-2.9	622.3171	2	11.2446	P02535|K1C10_MOUSE:A2A513|A2A513_MOUSE			0 0 29 60 70 34 3	EEQLQQIRAE	DB Search	1290	EEQLQQIRAE	2
75	MRYVASYLLAALGGNSSPSAKDIKKIL	40.12	2865.579	27	29.6	27	-0.1673	0.35	5.8	717.4078	4	25.0343	A0A5F8MPY2|A0A5F8MPY2_MOUSE:P99027|RLA2_			0 0 0 0 0 0 5 20 3	MRYVASYLLAAL	DB Search	1280	MRYVASYLLAAL	3
76	GPKPFSAPKPQTSPSPKP	40.12	1846.994	18	11.1	18	0.8943	0.45	3.2	616.6754	3	10.2271	Q3TC53|Q3TC53_MOUSE:P40124|CAP1_MOUSE:Q3			0 0 4 1 0 0 0 0 0	GPKPFSAPKPQT	DB Search	1210	GPKPFSAPKPQT	3
77	GYSFTTTAER	39.32	1131.52	10	50	10	0.0585	0.8	1.2	566.7691	2	11.8015	P63260|ACTG_MOUSE:E9Q5F4|E9Q5F4_MOUSE:Q6			0 0 52 52 41 9 3 0	GYSFTTTAER	DB Search	1200	GYSFTTTAER	3
78	AM(+15.99)GIM(+15.99)NSFVNDIFER	40.12	1774.802	15	33.3	15	0.1726	0.68	6.5	888.4161	2	23.2139	B2RTK3|B2RTK3_	Oxidation (M);Oxi	M2:Oxidation (M):	0 0 0 0 2 2 2 2 3 1	AM(+15.99)GIM(+	DB Search	1200	AMGIMNSFVNDI	3
79	AVFPSIVGRPR	40.1	1197.698	11	18.2	11	-0.3674	0.7	-2.7	599.8561	2	16.0117	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:A0			0 0 14 3 0 0 1 0 0	AVFPSIVGRPR	DB Search	1160	AVFPSIVGRPR	3
80	QQLSAEELDAQLDAYNAR	40.12	2033.965	18	11.1	18	-0.6548	0.64	1.9	1017.994	2	19.2369	G3X9I4|G3X9I4_MOUSE:Q9JJW6|ALRF2_MOUSE:O			0 0 0 0 0 0 0 0 1 1	QQLSAEELDAQL	DB Search	1150	QQLSAEELDAQL	3
81	NPLNSVFVAPAVTPVKGVL	40.12	1921.104	19	42.1	19	0.3327	0.78	1.6	961.5629	2	26.4632	P70158|ASM3A_MOUSE			0 0 0 2 2 2 4 4 6	NPLNSVFVAPAV	DB Search	1140	NPLNSVFVAPAV	3
82	AVFPSIVGR	38.81	944.5443	9	44.4	9	0.1893	0.89	-1.7	473.2798	2	18.4342	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:A0			2 2 39 38 1 1 0 0	AVFPSIVGR	DB Search	1120	AVFPSIVGR	3
83	PKGKKAKGKKVAPAPAVVKKQEAKKVVNPLF	39.71	3283.038	31	3.2	31	-4.7805	NA	2.4	821.7688	4	9.5821	Q5EBG5|Q5EBG5_MOUSE:Q80UT7|Q80UT7_MOUSE			0 0 0 0 0 0 0 0 0	PKGKKAKGKKV	DB Search	1110	PKGKKAKGKKV	2
84	YEDIAQKS	36.54	952.4501	8	75	8	-2.6544	0.81	-1.7	477.2327	2	3.7572	Q3UV17|K22O_MOUSE			5 71 4 2 7 4 0 0	YEDIAQKS	DB Search	1110	YEDIAQKS	1
85	ISGLIYEETR	36.72	1179.614	10	60	10	-0.6501	0.79	0.9	590.8146	2	15.5164	P62806|H4_MOUSE:B2RTM0|B2RTM0_MOUSE:Q6B			5 54 14 14 74 21	ISGLIYEETR	DB Search	1110	ISGLIYEETR	3
86	VAIFARGPQAHLLHG	40.09	1585.884	15	53.3	15	0.2118	0.08	0.1	529.6366	3	16.0427	F8VQM0|F8VQM0_MOUSE:Q1LZM2|Q1LZM2_MOUS			5 87 66 22 0 0 0	VAIFARGPQAHLL	DB Search	1100	VAIFARGPQAHLL	3
87	ELEEQLGPVAEETR	40.12	1598.779	14	42.9	14	-0.4666	0.88	-1.6	800.3972	2	15.6036	G3UZM8|G3UZM8_MOUSE:G3UWN5|G3UWN5_MO			0 0 0 4 14 34 46 1	ELEEQLGPVAEE	DB Search	1080	ELEEQLGPVAEE	3
88	NVFENYEASKAYSSVDE	40.12	1950.848	17	70.6	17	-0.986	0.62	3.8	976.4374	2	16.9485	Q9D306|MGT4C_MOUSE			0 0 1 3 4 5 5 5 4 6	NVFENYEASKAY	DB Search	1060	NVFENYEASKAY	3
89	HNYEGPETHTSL	40.12	1383.606	12	41.7	12	-0.096	0.59	3.4	692.814	2	9.4937	P14483|HB2A_MOUSE:Q5XQL0|Q5XQL0_MOUSE:Q			0 0 0 0 2 0 0 1 2 4	HNYEGPETHTSL	DB Search	1050	HNYEGPETHTSL	3
90	YTPSGQSGAAASESLFISNHAY	40.09	2257.029	22	0	22	-1.0276	0.38	-2.5	1129.521	2	19.066	Q6NY00|Q6NY00_MOUSE:P05064|ALDOA_MOUSE:			0 0 0 0 0 0 0 0 0	YTPSGQSGAAAS	DB Search	1040	YTPSGQSGAAAS	1
91	IIAPPERK	26.8	922.56	8	62.5	8	0.6661	0.72	-0.5	462.287	2	5.2645	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:Q3			5 13 97 21 3 0 0	IIAPPERK	DB Search	1020	IIAPPERK	3
92	GLPDYSAPNPIKVTHR	40.12	1763.932	16	37.5	16	-0.7502	0.36	-1.6	588.985	3	14.5474	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			0 0 18 15 9 3 3 1	GLPDYSAPNPIK	DB Search	1010	GLPDYSAPNPIK	3
93	VFLENVIR	33.97	988.5706	8	50	8	0.6352	0.84	-1.1	495.292	2	19.6776	Q61667|Q61667_MOUSE:P62806|H4_MOUSE:B2RT			5 24 45 18 1 1 0 0	VFLENVIR	DB Search	996	VFLENVIR	3
94	GDLEYQMSTTARAK	40.12	1569.746	14	42.9	14	-0.6525	0.77	3.1	785.8844	2	11.2684	Q02257|PLAK_MOUSE			0 0 4 4 8 8 9 2 1 1	GDLEYQMSTTA	DB Search	988	GDLEYQMSTTA	3
95	LPKSAKPVSQMRMATPLLMRPM	40.12	2482.341	22	27.3	22	-0.1789	0.48	-1.9	621.5928	4	18.2567	P04441|HG2A_MOUSE:Q545Y5|Q545Y5_MOUSE:Q3			5 0 0 0 0 2 0 0 0	LPKSAKPVSQMR	DB Search	943	LPKSAKPVSQMR	3
96	DVAIFARGPQAHLVHG	38.81	1686.895	16	18.8	16	-0.136	0.24	5.2	844.4594	2	16.5534	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:			1 0 0 0 0 0 0 0 0	DVAIFARGPQAH	DB Search	935	DVAIFARGPQAH	3
97	TFSRTTKAVVVKKIETRDGKLVS	40.11	2562.486	23	0	23	-2.4155	0.35	6.1	641.6341	4	11.4719	P11679|K2C8_MOUSE			0 0 0 0 0 0 1 1 0 0	TFSRTTKAVVVK	DB Search	928	TFSRTTKAVVVK	3
98	EVSFQATGDSEWR	40.11	1510.669	13	69.2	13	-0.7975	0.82	3.9	756.3464	2	15.8717	Q8R5L1|Q8R5L1_MOUSE:O35658|C1QBP_MOUSE			0 0 21 21 63 89 6	EVSFQATGDSEV	DB Search	902	EVSFQATGDSEV	1
99	LGDLYEEEMR	34.5	1253.56	10	70	10	-1.0493	0.63	1.6	627.7882	2	15.3246	P20152|VIME_MOUSE:A4IF59|A4IF59_MOUSE:Q3TF			5 22 22 29 75 12	LGDLYEEEMR	DB Search	868	LGDLYEEEMR	3
100	SAGGSNTFSRTTKAVVVKKIETRDGKLVSE	35.55	3164.715	30	6.7	30	-3.6075	0.3	-1.2	633.9511	5	13.0974	P11679|K2C8_MOUSE			5 8 0 0 0 0 0 0 0	SAGGSNTFSRTT	DB Search	867	SAGGSNTFSRTT	1
101	IGGIGTVPVGR	39.63	1024.603	11	63.6	11	-0.0909	0.73	-1.7	513.3079	2	14.9226	Q58E64|Q58E64_MOUSE:Q3UZQ3|Q3UZQ3_MOUSE			5 13 10 10 17 15	IGGIGTVPVGR	DB Search	852	IGGIGTVPVGR	3
102	YQSKYEEL	38.04	1058.492	8	100	8	-1.2652	0.73	0.4	530.2535	2	11.3806	P04104|K2C1_MOUSE			5 12 6 5 4 13 19 5	YQSKYEEL	DB Search	847	YQSKYEEL	3
103	GQTVPQVNNAVSALAK	40.12	1595.863	16	12.5	16	0.0053	0.69	2.6	798.9428	2	17.3194	A0ABD1KMS1|A0ABD1KMS1_9TELE			0 0 0 8 1 1 2 1 1	GQTVPQVNNAVS	DB Search	816	GQTVPQVNNAVS	1
104	FVAPAVTPVKG	40.1	1084.628	11	63.6	11	0.3245	0.65	-5.4	543.3196	2	15.4134	P70158|ASM3A_MOUSE			2 2 88 16 9 7 6 0	FVAPAVTPVKG	DB Search	808	FVAPAVTPVKG	3
105	RKRSRKESYSVYVYKVLKQVHPD	39.69	2864.577	23	8.7	23	0.5419	0.44	1.3	717.1525	4	15.442	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:			0 0 0 0 0 0 0 0 0	RKRSRKESYSVY	DB Search	801	RKRSRKESYSVY	3
106	VSHDYKGSTSHSLPY	32.51	1676.779	15	13.3	15	0.1291	0.39	1.1	839.3999	2	9.4573	E9Q1Y3|E9Q1Y3_MOUSE:E9Q414|APOB_MOUSE			0 0 0 0 0 0 0 0 0	VSHDYKGSTSHS	DB Search	791	VSHDYKGSTSHS	3
107	GIDPYDQPNAIYIER	40.12	1762.853	15	33.3	15	-0.3513	0.33	5.3	882.4403	2	18.3527	Q3U2X9|Q3U2X9_MOUSE:O88307|SORL_MOUSE			0 0 31 0 1 3 7 0 0	GIDPYDQPNAIYI	DB Search	774	GIDPYDQPNAIYI	3
108	ASGPPVSELITK	40.12	1197.661	12	66.7	12	-0.1532	0.58	-0.9	599.8384	2	16.438	P15864|H12_MOUSE:Q149Z9|Q149Z9_MOUSE:P432			5 18 18 98 11 11	ASGPPVSELITK	DB Search	763	ASGPPVSELITK	3
109	TVPQVNNAVSALAK	40.12	1410.783	14	21.4	14	0.1953	0.24	3	706.4026	2	16.9777	A0ABD1KMS1|A0ABD1KMS1_9TELE			2 2 1 1 5 1 1 0 0	TVPQVNNAVSAL	DB Search	761	TVPQVNNAVSAL	1
110	KELEEQLGPVAEETR	40.12	1726.874	15	60	15	-0.3873	0.82	-2.7	576.6317	3	13.5227	G3UZM8|G3UZM8_MOUSE:G3UWN5|G3UWN5_MO			0 0 1 4 5 15 30 72	KELEEQLGPVAE	DB Search	759	KELEEQLGPVAE	3
111	VEKNNSRIKLGLKSLVSKGTLVQT	40.12	2611.538	24	12.5	24	-0.4277	0.14	-5	653.8901	4	16.286	P43276|H15_MOUSE:P43274|H14_MOUSE:Q149Z9|Q			1 0 0 0 0 0 0 0 0	VEKNNSRIKLGL	DB Search	740	VEKNNSRIKLGL	1
112	R(+42.01)KRGRKESYSIYVYKVLKQVHPD	30.84	2890.593	23	17.4	23	-4.1958	0.38	19.1	723.671	4	12.3293	Q8CGP0|H2B3B_	Acetylation (N-ter	R1:Acetylation (N	0 0 0 0 0 0 0 0 0	R(+42.01)KRGRK	DB Search	731	RKRGRKESYSIY	1
113	YLNIYVPAHAHEGSN	40.12	1683.801	15	46.7	15	-0.9051	0.7	2.1	842.9113	2	15.1339	Q8BK48|EST2E_MOUSE			0 0 2 14 14 14 2 2	YLNIYVPAHAHE	DB Search	731	YLNIYVPAHAHE	3
114	SLDLDSIIAEVK	40.11	1301.708	12	66.7	12	-0.0073	0.55	-0.7	651.8622	2	25.9394	Q0VDR7|Q0VDR7_MOUSE:Q9Z331|K2C6B_MOUSE:			0 0 42 42 47 13 1	SLDLDSIIAEVK	DB Search	720	SLDLDSIIAEVK	3
115	APM(+15.99)YYRGAQAAIVVY	39.65	1687.839	15	33.3	15	-0.2517	0.55	2.8	844.9312	2	18.1742	Q3TCT9|Q3TCT9	Oxidation (M)	M3:Oxidation (M):	0 0 0 0 0 0 0 0 1 1	APM(+15.99)YYR	DB Search	718	APMYYRGAQAAI	3
116	GRDKYEPAAVSEHGDKKGKKAKKERDM	40.12	3057.578	27	7.4	27	-0.8011	0.46	-0.6	612.5239	5	2.1781	Q8VDN2|AT1A1_MOUSE:Q3TXF9|Q3TXF9_MOUSE			0 0 0 0 0 0 1 1 6 0	GRDKYEPAAVSE	DB Search	711	GRDKYEPAAVSE	1
117	A(+42.01)EAKAEAKAEAKAE	34.31	1457.736	14	35.7	14	3.3347	0.52	-3.2	486.9189	3	10.0085	Q7TNL7|Q7TNL7_	Acetylation (N-ter	A1:Acetylation (N-	5 75 34 0 0 0 10 1	A(+42.01)EAKAE	DB Search	709	AEAKAEAKAEAK	1
118	D(+42.01)DDIAALVVDNGSGMCKA	40.12	1834.808	18	72.2	18	-1.6082	0.74	2.7	918.4157	2	24.5805	E9Q5F4|E9Q5F4_	Acetylation (N-ter	D1:Acetylation (N	0 0 2 22 50 91 52	D(+42.01)DDIAAL	DB Search	686	DDDIAALVVDNG	3
119	ALEEQLQQIR	39.96	1226.662	10	60	10	0.0735	0.89	-1.6	614.3387	2	15.0453	P02535|K1C10_MOUSE:A2A513|A2A513_MOUSE			0 0 86 86 92 85 3	ALEEQLQQIR	DB Search	683	ALEEQLQQIR	2
120	GPKPFSAPKPQTSPSPK	40.12	1749.941	17	29.4	17	0.448	0.54	1.7	584.3234	3	9.0481	Q3TC53|Q3TC53_MOUSE:P40124|CAP1_MOUSE:Q3			0 0 0 5 5 1 1 2 2 0	GPKPFSAPKPQT	DB Search	679	GPKPFSAPKPQT	3
121	FLEQQNQVLQTK	40.12	1474.778	12	83.3	12	0.0066	0.71	0.8	738.3986	2	14.2332	Q6NXH9|K2C73_MOUSE:P04104|K2C1_MOUSE:Q08			5 30 44 35 35 19	FLEQQNQVLQTK	DB Search	677	FLEQQNQVLQTK	2
122	AGFAGDDAPR	39.63	975.441	10	80	10	-0.7674	0.77	2.4	488.7289	2	8.3021	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:A0			5 8 9 81 17 17 3 3	AGFAGDDAPR	DB Search	676	AGFAGDDAPR	3
123	EIAQDFKTDLR	40.12	1334.683	11	63.6	11	-0.007	0.64	1.2	668.3511	2	14.0105	A1L0U3|A1L0U3_MOUSE:A1L0V4|A1L0V4_MOUSE:P			3 3 8 8 5 5 4 1 1 0	EIAQDFKTDLR	DB Search	675	EIAQDFKTDLR	3
124	DVAIFARGPQAHLVHGVQ	40.12	1914.022	18	27.8	18	0.5053	0.33	-0.5	639.0159	3	17.218	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:			0 0 35 35 1 0 1 0	DVAIFARGPQAH	DB Search	672	DVAIFARGPQAH	3
125	NPPSYYTQPVPVPN	39.56	1571.762	14	35.7	14	0.1962	0.6	4.8	786.892	2	18.1479	Q9JLJ0|LITAF_MOUSE:E0CYR5|E0CYR5_MOUSE			0 0 0 0 1 5 2 3 1 1	NPPSYYTQPVPV	DB Search	665	NPPSYYTQPVPV	3
126	TSSYSNPTIGYENR	40.12	1587.717	14	64.3	14	0.0618	0.9	-0.7	794.8668	2	11.9144	Q07797|LG3BP_MOUSE			0 0 12 12 15 27 1	TSSYSNPTIGYEN	DB Search	657	TSSYSNPTIGYEN	2
127	NPLNSVFVAPAVTPVKG	40.12	1708.951	17	47.1	17	0.126	0.71	-0.9	855.4841	2	22.2545	P70158|ASM3A_MOUSE			4 1 1 3 4 4 6 6 10	NPLNSVFVAPAV	DB Search	646	NPLNSVFVAPAV	3
128	VRDMRQTVAVGVIKAVDKKAAGAGKVTK	40.12	2895.68	28	21.4	28	-2.9454	0.49	7.3	580.1489	5	14.3495	Q58E64|Q58E64_MOUSE:Q3UZQ3|Q3UZQ3_MOUSE			0 0 0 0 0 0 0 0 0	VRDMRQTVAVG	DB Search	645	VRDMRQTVAVG	3
129	FQNAILVR	39.26	959.5552	8	75	8	-0.1679	0.86	-1	480.7844	2	16.0009	Q546G4|Q546G4_MOUSE:P07724|ALBU_MOUSE			5 19 25 12 12 2 0	FQNAILVR	DB Search	639	FQNAILVR	3
130	KYTYGKPVPGHVK	40.12	1472.814	13	69.2	13	-1.611	0.75	-1.6	491.9456	3	2.3405	P28665|MUG1_MOUSE			0 0 12 7 2 15 8 8	KYTYGKPVPGHV	DB Search	639	KYTYGKPVPGHV	3
131	DARSYTAAVANRAKGGG	40.12	1663.839	17	29.4	17	0.9972	0.86	2.5	555.623	3	10.5936	Q91XS1|MTMR4_MOUSE:Q6PE02|Q6PE02_MOUSE			5 0 0 0 0 0 3 5 5 3	DARSYTAAVANR	DB Search	630	DARSYTAAVANR	3
132	GDAEM(+15.99)AIYGPAAIYLR	40.12	1707.67	16	29.4	17	-0.1641	0.84	5.6	929.4547	2	22.8319	A0ABD1KMS1|A0	Oxidation (M)	M6:Oxidation (M):	0 0 0 0 0 1 3 6 15	MGDAEM(+15.99	DB Search	621	GDAEMAIYGPAA	1
133	FVAPAVTPVK	40.09	1027.607	10	50	10	0.5302	0.53	-5.4	514.809	2	15.4336	P70158|ASM3A_MOUSE			0 0 96 12 8 3 3 0	FVAPAVTPVK	DB Search	620	FVAPAVTPVK	3
134	GLPDYSAPNPIKVTH	40.12	1607.831	15	46.7	15	-0.5581	0.53	-2.3	536.9509	3	16.1556	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			0 0 19 18 2 2 3 2	GLPDYSAPNPIK	DB Search	619	GLPDYSAPNPIK	3
135	DARSYTAAVANRAK	39.7	1492.775	14	50	14	0.7225	0.82	-0.1	498.5988	3	9.604	Q91XS1|MTMR4_MOUSE:Q6PE02|Q6PE02_MOUSE			0 0 0 0 11 11 58 5	DARSYTAAVANR	DB Search	612	DARSYTAAVANR	3
136	NFILDQTNVSAAAQR	40.12	1646.838	15	73.3	15	-0.5643	0.64	4.5	824.4317	2	17.8164	Q3TVV6|Q3TVV6_MOUSE:Q8C290|Q8C290_MOUSE			0 0 21 32 24 24 4	NFILDQTNVSAA	DB Search	607	NFILDQTNVSAA	1
137	VLNNMEIGTSLYDEEGAK	40.12	1981.93	18	16.7	18	-0.5992	0.75	6.8	991.9815	2	19.188	P09411|PGK1_MOUSE			0 0 0 0 1 3 6 1 1 1	VLNNMEIGTSLY	DB Search	604	VLNNMEIGTSLY	1
138	IFARGPQAHLVHG	40.12	1401.763	13	53.8	13	0.311	0.23	-1	468.2622	3	11.0292	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:			5 42 4 0 0 0 0 4 7	IFARGPQAHLVH	DB Search	599	IFARGPQAHLVH	3
139	APMYYRGAQAAIVV	40.1	1508.781	14	42.9	14	-0.0948	0.68	-1.7	755.3983	2	18.6251	Q3TCT9|Q3TCT9_MOUSE:P61021|RAB5B_MOUSE:			0 0 0 0 0 0 1 1 2 1	APMYYRGAQAAI	DB Search	596	APMYYRGAQAAI	3
140	NLQEAEEWYK	39.76	1308.599	10	50	10	-0.5713	0.63	-1.2	655.3073	2	15.8015	P20152|VIME_MOUSE:G3X981|G3X981_MOUSE:G5E			0 0 66 47 16 16 7	NLQEAEEWYK	DB Search	593	NLQEAEEWYK	1
141	GPDGRFVMGPTVAPSQ	39.28	1614.782	16	25	16	-0.1713	0.63	3.7	808.4015	2	16.6922	Q05BQ1|TUTLA_MOUSE			0 0 0 0 0 0 0 7 3 0	GPDGRFVMGPT	DB Search	591	GPDGRFVMGPT	3
142	TPAYTIPFYTPIPNG	40.12	1650.829	15	53.3	15	0.3729	0.64	3.7	826.4269	2	26.6087	O08573|LEG9_MOUSE:B1AQR8|B1AQR8_MOUSE:G			0 0 0 0 0 19 6 6 3	TPAYTIPFYTPIPN	DB Search	591	TPAYTIPFYTPIPN	3
143	RHNYEGPETHTSL	40.12	1539.707	13	53.8	13	0.5004	0.59	-1.7	514.2432	3	7.8266	P14483|HB2A_MOUSE:Q5XQL0|Q5XQL0_MOUSE:Q			0 0 6 29 37 37 16	RHNYEGPETHTS	DB Search	578	RHNYEGPETHTS	3
144	KELEEQLGPVAEETRA	39.7	1797.911	16	50	16	-0.5855	0.86	-6.2	600.3072	3	14.2852	G3UZM8|G3UZM8_MOUSE:G3UWN5|G3UWN5_MO			0 0 0 0 2 2 15 48	KELEEQLGPVAE	DB Search	575	KELEEQLGPVAE	3
145	APDTRFVAPGALG	36.48	1270.667	13	38.5	13	-0.3577	0.61	-0.9	636.3402	2	17.0213	Q3U2C5|RN149_MOUSE			0 0 0 0 0 1 3 18 0	APDTRFVAPGAL	DB Search	574	APDTRFVAPGAL	2
146	DTIEFRGPNGLLVYQG	40.12	1777.9	16	75	16	-0.1877	0.76	6.1	889.9647	2	22.809	F2Z456|F2Z456_MOUSE:Q9DCN2|NB5R3_MOUSE:			0 0 3 3 4 4 4 1 1 5	DTIEFRGPNGLL	DB Search	574	DTIEFRGPNGLL	3
147	SM(+15.99)DNNRSLDLD	40.12	1294.546	11	54.5	11	0.4216	0.56	1.7	648.2829	2	10.7842	Q4L0E7|Q4L0E7_	Oxidation (M)	M2:Oxidation (M):	0 0 4 2 1 0 0 5 14	SM(+15.99)DNNR	DB Search	567	SMDNNRSLDLD	2
148	VGKARGFFKKGDVVIVLTG	39.87	1990.173	19	26.3	19	0.1353	0.15	-3.5	664.3974	3	16.8498	P52480|KPYM_MOUSE			0 0 0 0 0 0 0 0 1 0	VGKARGFFKKGD	DB Search	564	VGKARGFFKKGD	3
149	GYSFVTTAER	39.41	1129.54	10	50	10	-0.1465	0.83	2.9	565.7791	2	13.9408	Q3UJ36|Q3UJ36_MOUSE:A0A494B9T3|A0A494B9T3			0 0 52 52 84 11 5	GYSFVTTAER	DB Search	563	GYSFVTTAER	3
150	KIVYEGPELNHAFG	40.12	1572.794	14	42.9	14	0.4926	0.62	-3.7	525.2711	3	17.1575	A0A0R4J0I9|A0A0R4J0I9_MOUSE:Q91ZX7|LRP1_MO			0 0 0 6 18 25 29 2	KIVYEGPELNHA	DB Search	560	KIVYEGPELNHA	3
151	DNIQGITKPAIR	40.12	1324.746	12	41.7	12	-0.6335	0.59	3.4	663.3842	2	12.6771	P62806|H4_MOUSE:B2RTM0|B2RTM0_MOUSE			0 0 0 10 5 5 2 2 1	DNIQGITKPAIR	DB Search	558	DNIQGITKPAIR	3
152	IPFYTPIPNGLYPS	40.12	1577.813	14	35.7	14	0.7809	0.65	6	789.9204	2	27.1438	O08573|LEG9_MOUSE:B1AQR8|B1AQR8_MOUSE:G			0 0 0 1 3 16 25 0	IPFYTPIPNGLYP	DB Search	558	IPFYTPIPNGLYP	3
153	A(+42.01)SGVAVSDGVIK	40.12	1143.614	12	66.7	12	0.7507	0.55	-0.6	572.8151	2	17.1403	P18760|COF1_M	Acetylation (N-ter	A1:Acetylation (N-	3 3 8 13 43 36 7 3	A(+42.01)SGVAV	DB Search	555	ASGVAVSDGVIK	3
154	LYIAVGISGAIQHLAGMKDSKTIVAINK	40.12	2910.637	28	25	28	-1.7264	0.53	3.6	728.6707	4	24.4378	Q99LC5|ETFA_MOUSE			0 0 26 31 31 13 1	LYIAVGISGAIQH	DB Search	551	LYIAVGISGAIQH	3
155	GGLPDYSAPNPIKVTH	40.12	1664.852	16	12.5	16	-0.4741	0.21	2.2	833.4372	2	16.2337	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			0 0 0 0 0 1 2 2 0 0	GGLPDYSAPNPI	DB Search	551	GGLPDYSAPNPI	3
156	IREFYSASVAEDAT	40.12	1557.731	14	57.1	14	-0.0289	0.58	1.8	779.876	2	15.5619	E9Q7P9|CDHR2_MOUSE			0 0 0 0 6 16 16 26	IREFYSASVAED	DB Search	548	IREFYSASVAED	3
157	FPYVTPAPHEPVKT	40.12	1581.819	14	35.7	14	-0.1849	0.74	0.6	791.9192	2	15.0503	Q9D074|MGRN1_MOUSE			5 1 1 3 5 1 1 0 0 1	FPYVTPAPHEPV	DB Search	529	FPYVTPAPHEPV	3
158	GDRRWPGVYTFLSDKHLNWIKKIMKG	31.9	3144.681	26	0	26	0.3672	0.33	-1.1	629.9442	5	23.632	P11032|GRAA_MOUSE:Q3UK79|Q3UK79_MOUSE:Q			0 0 0 0 0 0 0 0 0	GDRRWPGVYTF	DB Search	499	GDRRWPGVYTF	1
159	GSDMFKASLVIPSKDK	40.12	1721.902	16	37.5	16	-0.2047	0.87	-2.3	574.9747	3	16.3961	Q8BK33|Q8BK33_MOUSE:Q8BJD1|ITIH5_MOUSE			0 0 0 0 1 0 0 3 18	GSDMFKASLVIP	DB Search	487	GSDMFKASLVIP	3
160	EVSSVEAPSVSPARHQ	39.69	1678.827	16	12.5	16	0.0737	0.89	5.4	840.4255	2	10.4764	Q8BUJ9|LRP12_MOUSE			0 0 0 0 0 2 3 1 0 0	EVSSVEAPSVSP	DB Search	486	EVSSVEAPSVSP	3
161	FPKPPSYNVATTLPSYDEA	40.12	2096.01	19	10.5	19	-0.3124	0.85	6	1049.021	2	20.3572	A0A494BAA4|A0A494BAA4_MOUSE:Q8R0W6|NFIP1			0 0 0 0 0 0 0 0 0	FPKPPSYNVATT	DB Search	476	FPKPPSYNVATT	3
162	ESEPYTFSHPNKGEIG	40.12	1790.811	16	6.2	16	-0.7317	0.46	3.2	896.4178	2	12.8375	Q5U462|CDCP1_MOUSE			0 0 1 0 0 0 0 0 0	ESEPYTFSHPNK	DB Search	473	ESEPYTFSHPNK	3
163	AVFVDLEPTVIDEVR	40.12	1700.898	15	60	15	0.2529	0.85	1.6	851.4598	2	24.6385	P68369|TBA1A_MOUSE:P68373|TBA1C_MOUSE:A0			0 0 7 7 10 14 30 4	AVFVDLEPTVIDE	DB Search	466	AVFVDLEPTVIDE	2
164	DAVTYTEHAK	40.04	1133.535	10	50	10	-1.3016	0.8	0.5	567.7766	2	2.9665	Q61667|Q61667_MOUSE:P62806|H4_MOUSE:B2RT			0 0 35 52 23 6 6 1	DAVTYTEHAK	DB Search	463	DAVTYTEHAK	3
165	RENIWKAPEPVEIREN(+15.00)ST	40.1	2182.102	18	0	18	-0.3511	0.49	1.6	728.3774	3	15.0097	Q3TAN0|Q3TAN0	Deamidation follo	N16:Deamidation	0 0 0 0 0 1 1 0 0	RENIWKAPEPVE	DB Search	456	RENIWKAPEPVE	2
166	NVQFNYPQASVTDVT	40.12	1681.795	15	53.3	15	0.0432	0.6	5.7	841.9114	2	20.006	G3X977|G3X977_MOUSE:Q8K016|Q8K016_MOUSE:			0 0 0 0 0 11 11 6	NVQFNYPQASVT	DB Search	454	NVQFNYPQASVT	3
167	RPGSGFTNTMRVVPVP	27.44	1713.898	16	31.2	16	0.6982	0.1	0.9	572.3073	3	18.3754	P52480|KPYM_MOUSE			0 0 0 0 0 0 0 0 0	RPGSGFTNTMR	DB Search	447	RPGSGFTNTMR	3
168	VAIFARGPQAHLVHGV	40.05	1670.937	16	31.2	16	0.6207	0.32	-2.7	557.986	3	16.1259	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:			0 0 55 17 7 1 0 0	VAIFARGPQAHL	DB Search	435	VAIFARGPQAHL	3
169	EYQDLLNVK	40.01	1120.576	9	77.8	9	0.0492	0.68	-0.2	561.2967	2	16.7514	P03995|GFAP_MOUSE:P20152|VIME_MOUSE:Q5FW			5 9 60 34 31 8 3 0	EYQDLLNVK	DB Search	435	EYQDLLNVK	3
170	AAIAAAAAAAAAK	40.1	1040.598	13	84.6	13	-1.2935	0.62	-3.3	521.3057	2	12.3136	Q9CWK0|Q9CWK0_MOUSE:Q9CR57|RL14_MOUSE			4 4 13 96 44 41 1	AAIAAAAAAAAA	DB Search	430	AAIAAAAAAAAA	1
171	SGGTTM(+15.99)YPGLADR	39.71	1340.603	13	38.5	13	-0.6219	0.9	3.2	671.3109	2	11.1442	Q9QZ83|Q9QZ83	Oxidation (M)	M6:Oxidation (M):	1 0 0 0 22 26 58	SGGTTM(+15.99)	DB Search	429	SGGTTMYPGLAD	3
172	SGGTTM(+15.99)YPGIADR	39.71	1340.603	13	38.5	13	-0.2763	0.9	3.2	671.3109	2	11.1442	P63260|ACTG_M	Oxidation (M)	M6:Oxidation (M):	1 0 0 0 22 26 58	SGGTTM(+15.99)	DB Search	429	SGGTTMYPGIAD	3
173	HSVLTGDGYILSIHRIPRGRK	40.12	2374.335	21	38.1	21	-0.602	0.27	8.3	594.5972	4	14.5171	Q9Z0M5|LICH_MOUSE:Q3TEL5|Q3TEL5_MOUSE:Q6			5 16 16 4 4 0 0 2	HSVLTGDGYILSI	DB Search	412	HSVLTGDGYILSI	1
174	DGDSYRSPWSNKYDPPL	40.12	1995.896	17	17.6	17	-0.1307	0.48	-2	666.3063	3	18.5697	F6YHZ8|F6YHZ8_MOUSE:Q923G3|Q923G3_MOUSE			0 0 0 3 0 0 0 0 4 1	DGDSYRSPWSN	DB Search	412	DGDSYRSPWSN	2
175	VELQELNDR	38.01	1114.562	9	55.6	9	-0.5862	0.62	0.1	558.2896	2	12.8772	P20152|VIME_MOUSE:A4IF59|A4IF59_MOUSE:Q5FV			5 37 90 75 11 1 1	VELQELNDR	DB Search	410	VELQELNDR	3
176	TEAPLNPK	36.54	868.4654	8	62.5	8	0.5165	0.57	-1.9	435.2392	2	6.6325	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:A0			5 25 59 6 6 1 0 0	TEAPLNPK	DB Search	409	TEAPLNPK	2
177	LVRYTQKAPQVSTPTL	40.11	1801.01	16	12.5	16	0.3566	0.4	-2	601.3441	3	15.3474	Q546G4|Q546G4_MOUSE:P07724|ALBU_MOUSE			0 0 0 0 0 1 1 2 0 0	LVRYTQKAPQVS	DB Search	406	LVRYTQKAPQVS	3
178	HVPTLQVLRPGLVVVH	40.12	1763.057	16	6.2	16	0.0677	0.14	-6.6	588.6904	3	19.9678	D3Z7S4|D3Z7S4_MOUSE:Q9D3D9|ATPD_MOUSE:Q			0 0 0 0 0 1 1 2 1 0	HVPTLQVLRPGL	DB Search	401	HVPTLQVLRPGL	3
179	ETTSTTTTTHITKTVKGGISETRIEKRIVITG	35.44	3458.894	32	12.5	32	-4.0351	NA	1.4	692.7888	5	14.9003	A0A3B2WD96|A0A3B2WD96_MOUSE:A0A3B2WBE1			0 0 74 67 67 22 0	ETTSTTTTTHITK	DB Search	400	ETTSTTTTTHITK	2
180	GMAFRVPTPNVSVVD	40.12	1587.808	15	80	15	1.1026	0.48	6.1	794.9179	2	22.0558	S4R257|S4R257_MOUSE:Q3V2I5|Q3V2I5_MOUSE:S			0 0 0 3 2 11 4 4 5	GMAFRVPTPNVS	DB Search	393	GMAFRVPTPNVS	3
181	HLQLAIRNDEELNK	39.71	1691.896	14	7.1	14	0.0026	0.5	0.8	846.9557	2	12.997	Q8BFU2|H2A3_MOUSE:A0AUV1|A0AUV1_MOUSE:Q			1 1 0 0 0 0 0 0 0	HLQLAIRNDEEL	DB Search	388	HLQLAIRNDEEL	3
182	SINPDEAVAYGAAVQAAILSGDK	40.12	2259.138	23	8.7	23	-0.1537	0.58	4.4	1130.584	2	26.6498	Q3KQJ4|Q3KQJ4_MOUSE:Q3U9L2|Q3U9L2_MOUSE			0 0 0 0 0 0 1 1 3 3	SINPDEAVAYGA	DB Search	386	SINPDEAVAYGA	2
183	LHTKGALPLDTVTFYKVIPKSKFVLVKF	40.12	3188.873	28	14.3	28	-0.5306	0.62	4.6	798.231	4	23.6837	P57759|ERP29_MOUSE:A8C1V9|A8C1V9_MOUSE			0 0 0 1 0 0 0 1 1 1	LHTKGALPLDTV	DB Search	385	LHTKGALPLDTV	3
184	PKGKKAKGKKVAPAPAVVKKQEAKKVVNPLFEK	39.71	3540.176	33	24.2	33	-6.0556	NA	2.5	591.0381	6	8.6993	Q5EBG5|Q5EBG5_MOUSE:Q80UT7|Q80UT7_MOUSE			0 0 0 0 0 0 0 0 0	PKGKKAKGKKV	DB Search	376	PKGKKAKGKKV	3

185	VEVERDNLAEDIMR	40.12	1687.82	14	57.1	14	0.3215	0.29	4.6	563.6178	3	17.0254	P20152|VIME_MOUSE:Q5FWJ3|Q5FWJ3_MOUSE:A			5 100 6 0 0 0 4 10	VEVERDNLAEDII	DB Search	376	VEVERDNLAEDII	1
186	ALAAAGYDVEK	40.1	1106.561	11	45.5	11	0.11	0.73	-0.5	554.2887	2	11.8567	P15864|H12_MOUSE:P43274|H14_MOUSE:Q149Z9|Q			0 0 42 42 61 6 6 0	ALAAAGYDVEK	DB Search	376	ALAAAGYDVEK	3
187	RENIWKAPEPVEIRE	40.11	1864.98	15	13.3	15	-0.1373	0.64	2.5	622.6701	3	15.7312	Q3TAN0|Q3TAN0_MOUSE:A2AKS7|A2AKS7_MOUSE			0 0 0 0 1 2 2 0 0	RENIWKAPEPVE	DB Search	374	RENIWKAPEPVE	2
188	RKESYSVYVYKVLKQVHPD	39.97	2337.248	19	26.3	19	1.0918	0.45	-2	585.3195	4	18.0562	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:Q			0 0 0 0 0 5 18 19	RKESYSVYVYKV	DB Search	373	RKESYSVYVYKV	3
189	KESYSVYVYK	40.12	1264.634	10	50	10	-0.0856	0.75	0.5	633.3261	2	11.7107	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:Q			3 3 2 1 1 1 3 3 1 1	KESYSVYVYK	DB Search	372	KESYSVYVYK	3
190	ITQVQWNDPGAQYSLVNK	40.12	2060.033	18	22.2	18	0.0965	0.82	4.7	1031.031	2	18.8069	Q3TAN0|Q3TAN0_MOUSE:A2AKS7|A2AKS7_MOUSE			0 0 0 1 3 4 2 2 0 0	ITQVQWNDPGA(	DB Search	369	ITQVQWNDPGA(	3
191	DVDAAYMNKVELEAK	40.12	1694.819	15	20	15	-1.1609	0.64	1.6	848.4199	2	15.9662	Q148Q7|Q148Q7_MOUSE:Q8BIS2|Q8BIS2_MOUSE:I			0 0 0 1 3 3 3 0 0 1	DVDAAYMNKVEL	DB Search	369	DVDAAYMNKVEL	1
192	M(+42.01)MLGAEGGEGFVVK	40.12	1465.695	14	78.6	14	1.7848	0.64	1.9	733.8576	2	25.7431	Q811L7|Q811L7_	Acetylation (N-ter	M1:Acetylation (N	5 8 27 33 33 58 2	M(+42.01)MLGAE	DB Search	367	MMLGAEGGEGF	1
193	GLSEDTTEETLKESFEGSVR	40.12	2213.033	20	0	20	-1.0612	0.45	1.2	738.6877	3	18.5278	P09405|NUCL_MOUSE:Q3TT41|Q3TT41_MOUSE:Q8			0 0 0 0 0 0 0 0 0 0	GLSEDTTEETLKI	DB Search	364	GLSEDTTEETLKI	1
194	YLNIYVPAHAHEGSNLPV	40.09	1993.006	18	22.2	18	-0.313	0.3	-6	665.3401	3	19.5139	Q8BK48|EST2E_MOUSE			0 0 0 2 2 3 0 0 0 1	YLNIYVPAHAHE(	DB Search	363	YLNIYVPAHAHE(	2
195	VNVDFNTPRPSTVEA	40.12	1644.811	15	53.3	15	0.1289	0.55	2.2	823.4164	2	16.5684	A0A286YD40|A0A286YD40_MOUSE:G3X939|SL9A3			1 0 2 5 8 12 17 0	VNVDFNTPRPST	DB Search	363	VNVDFNTPRPST	2
196	QSGEAFVELESEDDVK	40.12	1780.8	16	37.5	16	-0.894	0.74	4.1	891.4132	2	17.4837	Q9Z2X1|HNRPF_MOUSE:J3QM80|J3QM80_MOUSE:.			0 0 0 0 2 3 6 8 5 5	QSGEAFVELESE	DB Search	361	QSGEAFVELESE	1
197	DGKKRKRSRKESYSVYVYKVLKQVHPD	39	3292.816	27	25.9	27	3.4306	0.61	-0.7	549.8095	6	14.7658	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:Q			0 0 0 0 0 0 0 0 0 0	DGKKRKRSRKES	DB Search	359	DGKKRKRSRKES	2
198	IPGTNMYNTDRANPVLDLPT	38.18	2201.079	20	0	20	0.531	0.2	5.6	1101.553	2	21.9272	Q8K066|Q8K066_MOUSE:E9Q7P9|CDHR2_MOUSE			0 0 0 0 0 0 0 0 0 0	IPGTNMYNTDRA	DB Search	356	IPGTNMYNTDRA	2
199	EDVAIFARGPQAHLVHG	37.38	1815.938	17	17.6	17	-0.0541	0.14	4.2	606.3225	3	16.3585	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:Q			0 0 0 70 70 13 0 0	EDVAIFARGPQA	DB Search	356	EDVAIFARGPQA	3
200	QSLEASLAETEGR	39.86	1389.674	13	69.2	13	0.0063	0.86	0.1	695.8458	2	14.8584	P02535|K1C10_MOUSE:A2A513|A2A513_MOUSE			2 2 14 16 30 12 1	QSLEASLAETEG	DB Search	356	QSLEASLAETEG	1
201	YYTSASGDEMVSLK	39.96	1549.697	14	64.3	14	-0.382	0.67	2.7	775.8597	2	15.3742	P07901|HS90A_MOUSE:Q3TKA2|Q3TKA2_MOUSE:Q			1 1 37 37 44 13 6	YYTSASGDEMVS	DB Search	355	YYTSASGDEMVS	1
202	YLNIYVPAHAHEGSNL	40.08	1796.885	16	31.2	16	-0.7025	0.7	0.7	899.4523	2	17.2466	Q8BK48|EST2E_MOUSE			0 0 2 4 5 7 0 0 2 0	YLNIYVPAHAHE(	DB Search	354	YLNIYVPAHAHE(	3
203	LQEEMLQREEAESTLQSFR	40.12	2323.111	19	42.1	19	-1.8595	0.19	3.4	775.3822	3	18.1696	P20152|VIME_MOUSE:Q5FWJ3|Q5FWJ3_MOUSE:A			0 0 0 1 0 0 2 1 2 2	LQEEMLQREEAE	DB Search	354	LQEEMLQREEAE	1
204	A(+42.01)EAKAEAKAEAKAEAK	39.87	1656.868	16	56.2	16	1.3809	0.53	6	553.3013	3	10.069	Q7TNL7|Q7TNL7	Acetylation (N-ter	A1:Acetylation (N-	5 27 27 0 0 0 2 2	A(+42.01)EAKAE/	DB Search	350	AEAKAEAKAEAK	3
205	GSDMFKASLVIPSKD	40.12	1593.807	15	6.7	15	0.0542	0.79	1.4	797.9139	2	18.5858	Q8BK33|Q8BK33_MOUSE:Q8BJD1|ITIH5_MOUSE			0 0 0 0 0 1 1 0 0 1	GSDMFKASLVIPS	DB Search	348	GSDMFKASLVIPS	1
206	SLHTLFGDK	40.02	1016.529	9	66.7	9	-0.249	0.59	-2.1	509.2719	2	14.0548	K7R066|K7R066_MOUSE:Q546G4|Q546G4_MOUSE:			5 9 69 4 0 5 0 0 5	SLHTLFGDK	DB Search	344	SLHTLFGDK	3
207	DLYANTVLSGGTTM(+15.99)YPGLADR	40.12	2230.058	21	23.8	21	0.0197	0.66	2.9	1116.042	2	20.9041	Q9QZ83|Q9QZ83	Oxidation (M)	M14:Oxidation (M	0 0 0 1 1 1 4 6 5 2	DLYANTVLSGGT	DB Search	341	DLYANTVLSGGT	2
208	DLYANTVLSGGTTM(+15.99)YPGIADR	40.12	2230.058	21	23.8	21	0.4012	0.66	2.9	1116.042	2	20.9041	P63260|ACTG_M	Oxidation (M)	M14:Oxidation (M	0 0 0 1 1 1 4 6 5 2	DLYANTVLSGGT	DB Search	341	DLYANTVLSGGT	2
209	SLVSKGTLVQT	39.97	1131.65	11	63.6	11	0.4361	0.83	1.8	566.8346	2	14.0998	P43276|H15_MOUSE:P43274|H14_MOUSE:Q149Z9|Q			0 0 40 9 4 0 0 35	SLVSKGTLVQT	DB Search	341	SLVSKGTLVQT	1
210	EEQLQQIR	35.31	1042.541	8	75	8	-0.6127	0.85	1.3	522.2795	2	9.5118	P02535|K1C10_MOUSE:A2A513|A2A513_MOUSE:Q3			5 5 87 95 41 4 0 0	EEQLQQIR	DB Search	338	EEQLQQIR	1
211	IREFYSASVAEDATL	40.12	1670.815	15	66.7	15	-0.3692	0.4	2.2	836.4186	2	19.3186	E9Q7P9|CDHR2_MOUSE			0 0 0 1 4 8 8 13 1	IREFYSASVAED/	DB Search	332	IREFYSASVAED/	3
212	GIVDQSQQAYQEAFEISK	40.12	2039.98	18	22.2	18	-0.6841	0.8	3.7	1021.003	2	20.7067	Q3UA58|Q3UA58_MOUSE:A0A2I3BQ03|A0A2I3BQ03			0 0 2 1 0 1 1 1 1 2	GIVDQSQQAYQE	DB Search	329	GIVDQSQQAYQE	1
213	ILGADTSVDLEETGR	40.12	1574.779	15	46.7	15	0.279	0.79	-1.1	788.3976	2	16.9793	D3Z6F5|D3Z6F5_MOUSE:Q03265|ATPA_MOUSE:D6			0 0 1 1 2 2 6 6 4 4	ILGADTSVDLEET	DB Search	324	ILGADTSVDLEET	1
214	LQDEIQNMKEEMAR	40.12	1733.808	14	64.3	14	0.0156	0.4	-0.9	578.944	3	14.918	P20152|VIME_MOUSE:Q3TFD9|Q3TFD9_MOUSE:Q5			5 27 12 11 9 2 2 2	LQDEIQNMKEEM	DB Search	321	LQDEIQNMKEEM	1
215	S(+42.01)IRVTQKSYKMSTSGPRAFSSR	40.09	2515.297	22	13.6	22	-1.0441	0.39	-1.9	504.0668	5	12.8182	P11679|K2C8_M	Acetylation (N-ter	S1:Acetylation (N-	0 0 0 8 0 0 9 0 0 0	S(+42.01)IRVTQK	DB Search	321	SIRVTQKSYKMS	2
216	KNLDYVATSIHEAVTK	40.12	1787.942	16	37.5	16	-0.5537	0.69	0.4	596.9895	3	15.4453	P05201|AATC_MOUSE			0 0 0 2 1 4 2 1 6 6	KNLDYVATSIHE/	DB Search	321	KNLDYVATSIHE/	3
217	KPVSQMRM(+15.99)ATPLLMRPM	40.04	2002.035	17	35.3	17	-0.3809	0.69	-1	501.5167	4	16.3294	P04441|HG2A_M	Oxidation (M)	M8:Oxidation (M):	0 0 0 0 0 0 0 0 4 2	KPVSQMRM(+15	DB Search	319	KPVSQMRMATPL	3
218	RPDAEYWNSQPELLER	40.12	2001.955	16	50	16	-0.8282	0.85	6.6	668.3314	3	17.0377	Q5XQL0|Q5XQL0_MOUSE			0 0 0 0 0 10 15 7	RPDAEYWNSQP	DB Search	318	RPDAEYWNSQP	2
219	RPDAEYWNSQPEILER	40.12	2001.955	16	50	16	-0.4445	0.85	6.6	668.3314	3	17.0377	P14483|HB2A_MOUSE:Q5XQJ9|Q5XQJ9_MOUSE:Q3			0 0 0 0 0 10 15 7	RPDAEYWNSQP	DB Search	318	RPDAEYWNSQP	2
220	VFVAPAVTPVK	40.07	1126.675	11	72.7	11	0.3357	0.55	-1.4	564.3453	2	17.0313	P70158|ASM3A_MOUSE			3 3 43 43 7 7 5 5	VFVAPAVTPVK	DB Search	316	VFVAPAVTPVK	3
221	FTYQQPQPLSVEPR	40.12	1688.852	14	28.6	14	0.1195	0.89	3	845.4379	2	16.8341	B2RXS4|PLXB2_MOUSE			0 0 8 6 6 1 1 1 1 2	FTYQQPQPLSVE	DB Search	315	FTYQQPQPLSVE	3
222	LPDYSAPNPIKVTHR	40.12	1706.91	15	20	15	-0.3515	0.53	-1.3	569.978	3	13.904	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			5 55 0 0 0 0 1 1 1	LPDYSAPNPIKVT	DB Search	310	LPDYSAPNPIKVT	3
223	VGTRRYMAPEVLEGAIN	26.86	1874.967	17	29.4	17	-0.6731	0.13	-3.8	625.9954	3	17.7066	P27038|AVR2A_MOUSE:A2AI38|A2AI38_MOUSE:P27			0 0 0 0 0 0 1 0 0 0	VGTRRYMAPEVL	DB Search	309	VGTRRYMAPEVL	1
224	EPYGARYVGSMVADVHR	40.12	1905.916	17	35.3	17	-0.1714	0.83	-1	636.3133	3	16.2402	P70695|F16P2_MOUSE:Q3TH92|Q3TH92_MOUSE:Q:			0 0 0 0 0 0 0 0 2 2	EPYGARYVGSM\	DB Search	305	EPYGARYVGSM\	2
225	IEKVIPSTANSNNL	40.12	1498.799	14	57.1	14	0.0225	0.75	1	750.4094	2	14.7453	E9Q7P9|CDHR2_MOUSE			0 0 1 6 41 3 3 4 4	IEKVIPSTANSNN	DB Search	302	IEKVIPSTANSNN	3
226	VRFLEQQNK	40.08	1160.63	9	55.6	9	-0.0521	0.67	-2	581.3226	2	9.4698	P03995|GFAP_MOUSE:P20152|VIME_MOUSE:P9786			0 0 1 1 3 5 5 2 2	VRFLEQQNK	DB Search	301	VRFLEQQNK	3
227	NLDLDSIIAEVK	40.08	1328.719	12	58.3	12	-0.0168	0.6	-0.5	665.3679	2	25.8687	Q8VED5|K2C79_MOUSE			1 1 40 40 45 14 1	NLDLDSIIAEVK	DB Search	300	NLDLDSIIAEVK	3
228	EM(+15.99)EENFALEAANYQDTIGR	40.12	2215.969	19	5.3	19	-0.7034	0.67	4.2	1108.999	2	19.6219	P20152|VIME_M	Oxidation (M)	M2:Oxidation (M):	0 0 0 0 0 0 1 1 2 1	EM(+15.99)EENF	DB Search	294	EMEENFALEAAN	1
229	GSAGGSNTFSRTTKAVVVKKIETRDGKLVS	40.04	3092.694	30	3.3	30	-3.739	0.4	0.5	774.183	4	13.0361	P11679|K2C8_MOUSE			0 0 1 1 0 0 0 0 0 0	GSAGGSNTFSRT	DB Search	293	GSAGGSNTFSRT	1
230	DLEM(+15.99)QIESL	31.18	1092.501	9	66.7	9	2.5636	0.56	-5.1	547.2562	2	23.6064	P02535|K1C10_M	Oxidation (M)	M4:Oxidation (M):	0 0 1 11 29 75 29	DLEM(+15.99)QIE	DB Search	290	DLEMQIESL	1
231	FSPDGELYASGSEDGTLR	40.12	1899.849	18	16.7	18	0.0011	0.76	2.3	950.936	2	16.7733	Q9Z1Z2|STRAP_MOUSE:B2RUC7|B2RUC7_MOUSE			0 0 0 0 0 0 2 4 5 0	FSPDGELYASGS	DB Search	284	FSPDGELYASGS	1
232	EREQIKTL	26	1015.566	8	62.5	8	-1.4639	0.76	-0.8	508.7912	2	7.7139	Q08EK4|Q08EK4_MOUSE:Q9DCV7|K2C7_MOUSE:Q			0 0 0 7 34 50 39 5	EREQIKTL	DB Search	284	EREQIKTL	2
233	ALEESNYELEGK	40.12	1380.641	12	75	12	-1.212	0.74	2.8	691.3312	2	12.3203	P02535|K1C10_MOUSE:A2A513|A2A513_MOUSE			5 29 93 93 33 33	ALEESNYELEGK	DB Search	284	ALEESNYELEGK	1
234	GPDGRFVMGPTVAPSQEKL	40.12	1985.004	19	36.8	19	0.3962	0.89	0.5	662.6772	3	17.388	Q05BQ1|TUTLA_MOUSE			0 0 0 0 0 0 0 29 4	GPDGRFVMGPT\	DB Search	281	GPDGRFVMGPT\	3
235	RLWWLDLK	36.93	1128.644	8	62.5	8	-0.3782	0.9	-1.3	565.3287	2	23.1577	Q91X72|HEMO_MOUSE			0 0 1 2 9 10 12 5	RLWWLDLK	DB Search	273	RLWWLDLK	2
236	LKGEATVSFDDPPSAK	36.74	1660.831	16	43.8	16	-0.6446	0.57	-2.3	554.6176	3	12.7221	Q8CFQ9|Q8CFQ9_MOUSE:P56959|FUS_MOUSE:Q3			0 0 0 0 0 25 25 28	LKGEATVSFDDP	DB Search	273	LKGEATVSFDDP	1
237	ERIFYHKTYINEALK	40.12	1924.021	15	53.3	15	-0.4976	0.65	-3	482.0121	4	13.2427	Q3TZ78|Q3TZ78_MOUSE:F8VPT3|F8VPT3_MOUSE			0 0 0 0 7 19 19 22	ERIFYHKTYINEA	DB Search	272	ERIFYHKTYINEA	2
238	TSSVTLQTITAQNAAVQAVK	40.12	2030.101	20	25	20	0.0304	0.76	-1.6	1016.058	2	18.737	Q3U7N2|Q3U7N2_MOUSE:A0A1B0GX08|A0A1B0GX0			0 0 0 0 0 1 2 3 3 1	TSSVTLQTITAQN	DB Search	271	TSSVTLQTITAQN	1
239	AAVPSGASTGIYEALELR	40.12	1803.937	18	5.6	18	-0.9198	0.34	5.7	902.9829	2	22.383	Q545V3|Q545V3_MOUSE:P17183|ENOG_MOUSE:Q5			0 0 13 0 0 0 0 0 1 1	AAVPSGASTGIYI	DB Search	268	AAVPSGASTGIYI	1
240	FEDENFILK	38.26	1153.566	9	66.7	9	-0.2357	0.74	0.5	577.7903	2	18.7423	Q3TE63|Q3TE63_MOUSE:Q5SVY2|Q5SVY2_MOUSE			5 38 23 11 4 4 1 0	FEDENFILK	DB Search	267	FEDENFILK	3
241	QPSTSSLAAPTVEAAASAP	39.71	1754.869	19	36.8	19	-0.0182	0.6	8	878.4486	2	18.0378	A0AAQ4VMX1|A0AAQ4VMX1_MOUSE:A0AAQ4VMV3			0 0 0 0 0 1 1 2 5 1	QPSTSSLAAPTVI	DB Search	267	QPSTSSLAAPTVI	3
242	LQYVEDGVYSMQVASAR	40.12	1914.915	17	64.7	17	-1.1162	0.61	3.1	958.4697	2	18.5576	Q8BMK4|CKAP4_MOUSE			0 0 3 8 4 4 4 4 12	LQYVEDGVYSM(	DB Search	263	LQYVEDGVYSM(	1
243	AQYEDIAQKSKAEAE	40.12	1679.8	15	13.3	15	0.1067	0.56	-4.1	840.9059	2	9.7029	Q3UV17|K22O_MOUSE			0 0 0 0 0 1 1 1 0 0	AQYEDIAQKSKA	DB Search	263	AQYEDIAQKSKA	2
244	RNVQFNYPQASVTDVT	40.12	1837.896	16	81.2	16	-0.2201	0.68	5.4	919.9623	2	17.1931	G3X977|G3X977_MOUSE:Q8K016|Q8K016_MOUSE:Q			0 0 0 3 14 16 28 2	RNVQFNYPQAS\	DB Search	262	RNVQFNYPQAS\	2
245	EDVAIFARGPQAHLVHGVQ	40.09	2043.065	19	36.8	19	0.0124	0.39	0.5	682.0309	3	16.9741	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:Q			0 0 42 40 40 0 0 0	EDVAIFARGPQA	DB Search	261	EDVAIFARGPQA	2
246	VFVAPAVTPVKG	40.12	1183.696	12	50	12	0.2048	0.55	2.5	592.8584	2	16.973	P70158|ASM3A_MOUSE			4 4 51 56 0 0 3 11	VFVAPAVTPVKG	DB Search	256	VFVAPAVTPVKG	3
247	LVIIESDLER	37.18	1185.661	10	70	10	-0.3034	0.65	-0.1	593.8375	2	18.3435	A0A2R2Y2P8|A0A2R2Y2P8_MOUSE:E9Q456|E9Q45			4 4 88 88 28 6 6 1	LVIIESDLER	DB Search	254	LVIIESDLER	3
248	VTIAQGGVLPNIQAVLLPK	40.12	1930.162	19	36.8	19	0.5276	0.85	8.9	966.0989	2	27.2237	Q8BFU2|H2A3_MOUSE:A0AUV1|A0AUV1_MOUSE:Q			0 0 0 11 17 4 4 8	VTIAQGGVLPNI(	DB Search	253	VTIAQGGVLPNI(	1
249	FPYVTPAPHEPV	40.12	1352.676	12	66.7	12	-0.3259	0.57	2.8	677.349	2	18.0592	Q9D074|MGRN1_MOUSE			5 11 10 10 20 3 3	FPYVTPAPHEPV	DB Search	251	FPYVTPAPHEPV	3
250	TDMDNQIVVSDYAQMDR	35.87	1999.862	17	29.4	17	-1.551	0.67	-1.6	1000.939	2	18.1109	G5E839|G5E839_MOUSE:Q3UJZ8|Q3UJZ8_MOUSE:			0 0 0 0 1 1 4 14 8	TDMDNQIVVSDY	DB Search	250	TDMDNQIVVSDY	1
251	NPDDITQEEYGEFYK	40.12	1846.79	15	6.7	15	-1.5735	0.65	-3.6	924.401	2	17.1351	E9Q3D6|E9Q3D6_MOUSE:P11499|HS90B_MOUSE:Q			0 0 0 0 2 1 1 1 1 1	NPDDITQEEYGE	DB Search	249	NPDDITQEEYGE	1
252	ELAEDGYSGVEVR	40.12	1422.663	13	84.6	13	-0.3195	0.75	-6.1	712.3359	2	13.7974	D3YV43|D3YV43_MOUSE:Q9D0A2|Q9D0A2_MOUSE			3 3 49 49 66 39 3	ELAEDGYSGVE\	DB Search	248	ELAEDGYSGVE\	1
253	EGRPSGEAFVELESEDEVK	40.1	2105.975	19	47.4	19	-1.3426	0.66	-5.2	702.997	3	16.6237	Q811L7|Q811L7_MOUSE:Q3UR26|Q3UR26_MOUSE:			0 0 0 0 0 0 0 10 4	EGRPSGEAFVEL	DB Search	246	EGRPSGEAFVEL	1
254	LVQDVANNTNEEAGDGTTTATVLAR	40.12	2559.241	25	0	25	-0.7651	0.68	-0.8	1280.63	2	15.6723	D3Z2F2|D3Z2F2_MOUSE:D3Z7J9|D3Z7J9_MOUSE:F			0 0 0 0 0 1 0 0 0 0	LVQDVANNTNEE	DB Search	245	LVQDVANNTNEE	2
255	NPPSYYTQPVPVPNANA	40.12	1827.879	17	5.9	17	-0.0132	0.75	-0.9	914.9482	2	18.3745	Q9JLJ0|LITAF_MOUSE:E0CYR5|E0CYR5_MOUSE			0 0 0 0 0 2 1 1 1 1	NPPSYYTQPVPV	DB Search	241	NPPSYYTQPVPV	2
256	NNQAYHSPATALAIVD	36.88	1683.822	16	37.5	16	0.0407	0.62	4.5	842.9219	2	18.5887	Q8R420|ABCA3_MOUSE:Q80XT2|Q80XT2_MOUSE			0 0 0 1 0 0 0 0 2 2	NNQAYHSPATAL	DB Search	238	NNQAYHSPATAL	2
257	GGSKSISIS	26.41	834.4447	9	55.6	9	-1.7766	0.65	-1.2	418.2291	2	7.5452	Q3UV17|K22O_MOUSE			0 0 1 0 2 11 17 9	GGSKSISIS	DB Search	234	GGSKSISIS	3
258	MGLAMGGAGGASFDR	39.91	1396.623	15	53.3	15	-0.2121	0.71	0	699.3203	2	16.9886	Q3TW40|Q3TW40_MOUSE:B8JK33|B8JK33_MOUSE			0 0 0 26 26 10 3 3	MGLAMGGAGGA	DB Search	234	MGLAMGGAGGA	1
259	QTVAVGVIK	39.88	913.5596	9	88.9	9	0.5541	0.82	-0.4	457.788	2	13.1126	Q58E64|Q58E64_MOUSE:Q3UZQ3|Q3UZQ3_MOUSE			5 12 62 24 24 3 2	QTVAVGVIK	DB Search	233	QTVAVGVIK	3
260	YVTQFHPPHIEIQMLK	39.71	1980.029	16	31.2	16	0.0579	0.42	3.8	661.0195	3	20.421	Q9D239|Q9D239_MOUSE:P01887|B2MG_MOUSE			5 11 0 1 5 5 2 0 0	YVTQFHPPHIEIQ	DB Search	231	YVTQFHPPHIEIQ	3
261	NAGVEGSLIVEK	39.94	1214.651	12	58.3	12	0.1365	0.59	2.6	608.3356	2	14.3923	P63038|CH60_MOUSE			2 2 5 5 65 3 0 0 0	NAGVEGSLIVEK	DB Search	231	NAGVEGSLIVEK	2
262	SGPKPFSAPKPQTSPSPK	39.56	1836.973	18	22.2	18	0.921	0.67	3.2	613.3337	3	9.3086	Q3TC53|Q3TC53_MOUSE:P40124|CAP1_MOUSE:Q3			0 0 0 0 0 0 0 2 1 2	SGPKPFSAPKPQ	DB Search	229	SGPKPFSAPKPQ	1
263	ELISNASDALDK	40.09	1274.635	12	50	12	0.557	0.66	-0.4	638.3262	2	14.7535	D3Z1R1|D3Z1R1_MOUSE:Q91V38|Q91V38_MOUSE:			0 0 47 44 27 27 5	ELISNASDALDK	DB Search	229	ELISNASDALDK	3
264	DPIQNTDEETKTE	40.12	1518.669	13	53.8	13	0.059	0.38	1	760.3441	2	8.2288	Q5G866|DFA23_MOUSE:Q64016|DFA17_MOUSE:P5			0 0 3 5 2 2 2 1 1 2	DPIQNTDEETKTI	DB Search	227	DPIQNTDEETKTI	2
265	GSSGVGLTAAVTTDQETGER	40.12	1934.918	20	20	20	-0.6794	0.66	1.3	968.4699	2	14.4886	Q3ULD6|Q3ULD6_MOUSE:P25206|MCM3_MOUSE:Q			0 0 0 0 0 1 1 1 2 2	GSSGVGLTAAVT	DB Search	227	GSSGVGLTAAVT	1
266	VSSVEAPSVSPAR	39.53	1284.667	13	53.8	13	0.2524	0.88	0.3	643.3411	2	11.4568	Q8BUJ9|LRP12_MOUSE			5 4 3 3 34 38 1 1	VSSVEAPSVSPAI	DB Search	224	VSSVEAPSVSPAI	3
267	VCRHNYEGPET(+79.97)HTSLR	36.65	1977.852	16	0	16	0.946	0.44	-1.6	660.2916	3	8.0132	P14483|HB2A_M	Phosphorylation (	T11:Phosphorylat	0 0 0 0 0 0 0 0 0 0	VCRHNYEGPET(	DB Search	223	VCRHNYEGPETH	1
268	DGDSYRSPWSNKYDPP	40.12	1882.812	16	18.8	16	-0.6257	0.32	2.4	628.6143	3	15.2598	F6YHZ8|F6YHZ8_MOUSE:Q923G3|Q923G3_MOUSE			0 0 0 1 1 1 1 4 5 5	DGDSYRSPWSN	DB Search	221	DGDSYRSPWSN	2
269	VENPEYLAPRAGTASQPHP	37.24	2032.997	19	42.1	19	-0.0025	0.24	1.8	678.6756	3	13.3207	P70424|ERBB2_MOUSE:Q8R2X1|Q8R2X1_MOUSE:Q			5 18 50 4 4 10 7 7	VENPEYLAPRAG	DB Search	220	VENPEYLAPRAG	3
270	DVAIFARGPQAHLVH	24.84	1629.874	15	33.3	15	0.2282	0.18	-7	544.2961	3	16.5786	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:Q			0 0 52 52 3 0 0 0	DVAIFARGPQAH	DB Search	219	DVAIFARGPQAH	2
271	HNDDEQYAWESSAGGSFTVR	40.12	2254.951	20	55	20	-1.1324	0.72	-2.5	752.6577	3	16.8743	P07901|HS90A_MOUSE:B7ZC50|B7ZC50_MOUSE:Q			0 0 0 1 1 4 12 12	HNDDEQYAWES	DB Search	219	HNDDEQYAWES	1
272	KTQYISPNLNPND	38.9	1502.737	13	30.8	13	0.6853	0.74	0.5	752.3759	2	13.9224	P97499|TEP1_MOUSE:Q5XKB2|Q5XKB2_MOUSE			0 0 0 1 9 22 0 0 1	KTQYISPNLNPNI	DB Search	218	KTQYISPNLNPNI	2
273	NPLNSVFVAPAVTPVKGV	40.12	1808.02	18	44.4	18	0.7701	0.74	5.2	905.0239	2	23.9557	P70158|ASM3A_MOUSE			5 0 0 2 4 4 4 4 10	NPLNSVFVAPAV	DB Search	218	NPLNSVFVAPAV	2
274	FADLSEAANR	33.86	1092.52	10	70	10	-0.7765	0.71	-2.3	547.2673	2	12.2154	P20152|VIME_MOUSE:Q3TFD9|Q3TFD9_MOUSE:Q5			5 38 51 51 34 9 9	FADLSEAANR	DB Search	218	FADLSEAANR	3
275	EEAESTLQSFR	40.11	1295.599	11	63.6	11	-0.3311	0.78	3.7	648.8109	2	13.8118	P20152|VIME_MOUSE:Q5FWJ3|Q5FWJ3_MOUSE:A			0 0 52 52 48 33 3	EEAESTLQSFR	DB Search	214	EEAESTLQSFR	1
276	LPPYDDATAVPSTAKEPPP	26.76	1964.973	19	0	19	-0.3525	0.64	3.3	983.497	2	16.0716	B2CZK6|B2CZK6_MOUSE:Q91XQ6|LAP4B_MOUSE			0 0 0 0 0 0 0 0 0 0	LPPYDDATAVPS	DB Search	213	LPPYDDATAVPS	2
277	DIIAILGM(+15.99)DELSEEDK	40.12	1805.861	16	62.5	16	0.9735	0.6	-3.6	903.9364	2	24.8159	P56480|ATPB_M	Oxidation (M)	M8:Oxidation (M):	0 0 26 17 57 47 2	DIIAILGM(+15.99	DB Search	212	DIIAILGMDELSE	1
278	LSQEYSGSVANEANVY	40.12	1729.78	16	68.8	16	-0.6695	0.67	-0.5	865.8986	2	16.0349	E9Q1Y3|E9Q1Y3_MOUSE:E9Q414|APOB_MOUSE			0 0 0 0 6 13 2 0 7	LSQEYSGSVANE	DB Search	212	LSQEYSGSVANE	2
279	ITGEAFVQFASQELAEK	40.12	1866.936	17	58.8	17	0.2958	0.78	4.4	934.4818	2	25.1758	Q9Z2X1|HNRPF_MOUSE:J3QM80|J3QM80_MOUSE:.			0 0 0 1 2 5 14 25	ITGEAFVQFASQI	DB Search	211	ITGEAFVQFASQI	1
280	AIILLLLLI	39.87	993.7202	9	11.1	9	-7.4489	0	1.6	994.7313	1	20.0418	Q544T2|Q544T2_MOUSE:G3UXE5|G3UXE5_MOUSE			5 0 0 0 0 0 0 0 0	AIILLLLLI	DB Search	210	AIILLLLLI	3
281	QQLAFKQPSSAYAAFN	40.12	1769.874	16	56.2	16	-0.3342	0.51	7.4	885.9527	2	18.0914	P01027|CO3_MOUSE:E1APH6|E1APH6_MOUSE:Q20			0 0 0 1 5 4 4 0 0 0	QQLAFKQPSSAY	DB Search	210	QQLAFKQPSSAY	2
282	ALLLLLLLL	39.87	993.7202	9	11.1	9	-7.1517	0	1.6	994.7313	1	20.0418	G3UXY8|G3UXY8_MOUSE:Q9JJS0|SCUB2_MOUSE:			5 0 0 0 0 0 0 0 0	ALLLLLLLL	DB Search	210	ALLLLLLLL	3
283	ALLLLLLIL	39.87	993.7202	9	11.1	9	-7.0557	0	1.6	994.7313	1	20.0418	D3Z7F6|D3Z7F6_MOUSE:E9PWV0|E9PWV0_MOUSE			5 0 0 0 0 0 0 0 0	ALLLLLLIL	DB Search	210	ALLLLLLIL	3
284	AIILLLLIL	39.87	993.7202	9	11.1	9	-7.1952	0	1.6	994.7313	1	20.0418	A2AFG7|A2AFG7_MOUSE:Q6PGJ3|Q6PGJ3_MOUSE			5 0 0 0 0 0 0 0 0	AIILLLLIL	DB Search	210	AIILLLLIL	3
285	ALLLLLLLI	39.87	993.7202	9	11.1	9	-7.278	0	1.6	994.7313	1	20.0418	A0A2I3BPJ2|A0A2I3BPJ2_MOUSE			5 0 0 0 0 0 0 0 0	ALLLLLLLI	DB Search	210	ALLLLLLLI	2
286	ALLILILLI	39.87	993.7202	9	11.1	9	-7.1148	0	1.6	994.7313	1	20.0418	A0A1W2P7Y9|A0A1W2P7Y9_MOUSE:Q810U4|NRCA			5 0 0 0 0 0 0 0 0	ALLILILLI	DB Search	210	ALLILILLI	3
287	ALLILILLL	39.87	993.7202	9	11.1	9	-7.0177	0	1.6	994.7313	1	20.0418	A0A0R4IZW5|A0A0R4IZW5_MOUSE:P09803|CADH1			5 0 0 0 0 0 0 0 0	ALLILILLL	DB Search	210	ALLILILLL	3
288	TGM(+15.99)AFRVPTPNVSVVD	40.12	1704.851	16	43.8	16	0.3178	0.4	1.6	853.4359	2	20.1105	S4R257|S4R257_	Oxidation (M)	M3:Oxidation (M):	0 0 0 0 1 2 7 0 0 1	TGM(+15.99)AFR	DB Search	208	TGMAFRVPTPNV	3
289	DIIFFKFNTPQQPKKK	40.12	1978.104	16	12.5	16	0.5821	0.35	2.5	660.3785	3	18.595	Q9CZ30|OLA1_MOUSE:Q3TW21|Q3TW21_MOUSE:Q			0 0 17 1 0 0 0 1 1	DIIFFKFNTPQQP	DB Search	207	DIIFFKFNTPQQP	3
290	ESTLHLVLR	39.38	1066.614	9	100	9	0.2634	0.79	0	534.314	2	15.6042	P0CG50|UBC_MOUSE:E9Q5F6|E9Q5F6_MOUSE:Q3			5 12 13 17 35 3 3	ESTLHLVLR	DB Search	207	ESTLHLVLR	3
291	LHLRFSAPQIENEPE	39.69	1778.895	15	13.3	15	-0.1464	0.3	-2.1	593.9711	3	17.9241	Q61190|I10R2_MOUSE:Q8VHM7|Q8VHM7_MOUSE:Q			0 0 0 0 0 3 25 0 0	LHLRFSAPQIENE	DB Search	206	LHLRFSAPQIENE	3
292	LPQDPTFHTPLDLYAYAR	40.12	2117.058	18	22.2	18	-0.6011	0.56	-4	706.6922	3	22.96	Q07797|LG3BP_MOUSE			5 4 4 3 0 0 0 1 1 0	LPQDPTFHTPLDI	DB Search	205	LPQDPTFHTPLDI	2
293	LAETQEEISAEVAAK	40.12	1587.799	15	53.3	15	-1.0956	0.78	2.4	794.9106	2	14.1655	E9Q715|E9Q715_MOUSE:Q3UZ17|Q3UZ17_MOUSE:			2 0 0 10 10 15 14	LAETQEEISAEVA	DB Search	205	LAETQEEISAEVA	1
294	DGQVINETSQHHDDLE	39.71	1835.792	16	6.2	16	-0.2578	0.42	0.8	918.9041	2	10.5174	P20152|VIME_MOUSE:Q5FWJ3|Q5FWJ3_MOUSE:Q			0 0 0 1 1 0 1 1 0 0	DGQVINETSQHH	DB Search	203	DGQVINETSQHH	2
295	IQLVEEELDR	36.96	1242.646	10	70	10	-0.3253	0.65	3.4	622.3322	2	17.0903	D3Z6I8|D3Z6I8_MOUSE:Q9D1R6|Q9D1R6_MOUSE:Q			4 4 58 38 13 2 2 0	IQLVEEELDR	DB Search	200	IQLVEEELDR	3
296	MRYVASYLLAALGGNSSPSAKDIKK	40.12	2639.41	25	40	25	0.0165	0.25	5.7	660.8652	4	21.285	A0A5F8MPY2|A0A5F8MPY2_MOUSE:P99027|RLA2_			0 0 0 0 0 0 5 10 16	MRYVASYLLAAL	DB Search	200	MRYVASYLLAAL	3
297	TTPSYVAFTDTER	39.17	1486.694	13	61.5	13	-0.4503	0.28	-0.6	744.3555	2	15.8578	A1E2B8|A1E2B8_MOUSE:B2CSK2|B2CSK2_MOUSE			5 5 4 3 3 7 10 4 1	TTPSYVAFTDTEI	DB Search	196	TTPSYVAFTDTEI	2
298	DNIQGITKPAIRR	39.7	1480.847	13	53.8	13	-0.3763	0.11	3.4	494.6247	3	10.7853	P62806|H4_MOUSE:B2RTM0|B2RTM0_MOUSE			0 0 30 59 4 4 3 3	DNIQGITKPAIRR	DB Search	192	DNIQGITKPAIRR	2
299	PPSYYTQPVPVPNAN	39.86	1642.799	15	13.3	15	-0.4171	0.77	-2.8	822.4064	2	17.8922	Q9JLJ0|LITAF_MOUSE:E0CYR5|E0CYR5_MOUSE			0 0 0 0 0 0 0 4 4 0	PPSYYTQPVPVPI	DB Search	190	PPSYYTQPVPVPI	3
300	A(+42.01)AAAAAAAAAGAAGGR	39.95	1239.632	16	62.5	16	-0.233	0.63	4.7	620.8276	2	18.1448	G3UY42|G3UY42	Acetylation (N-ter	A1:Acetylation (N-	0 0 2 18 66 66 90	A(+42.01)AAAAA/	DB Search	185	AAAAAAAAAAGA	1
301	GGEDVAIFARGPQAHLVHG	40.05	1929.981	19	31.6	19	-0.1676	0.22	-1.8	644.3346	3	16.5329	F8VPQ6|F8VPQ6_MOUSE:P24822|PPBI_MOUSE:Q0			0 0 7 20 20 42 39	GGEDVAIFARGP	DB Search	185	GGEDVAIFARGP	3
302	SYELPDGQVITIGNER	40.12	1789.885	16	56.2	16	0.721	0.64	3.1	895.9545	2	20.5045	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:Q6			0 0 4 16 2 2 1 2 7	SYELPDGQVITIG	DB Search	181	SYELPDGQVITIG	3
303	SAKPVSQMRMATPLLMRPM	40.12	2144.109	19	15.8	19	-0.5999	0.47	0	715.712	3	19.0014	P04441|HG2A_MOUSE:Q545Y5|Q545Y5_MOUSE:Q3			0 0 20 5 5 1 1 0 0	SAKPVSQMRMA	DB Search	180	SAKPVSQMRMA	3
304	VSDLTQAANK	37.59	1045.54	10	60	10	0.0116	0.66	7.5	523.7814	2	6.1058	Q3V1K9|Q3V1K9_MOUSE:P31001|DESM_MOUSE:Q3			5 54 16 16 17 14	VSDLTQAANK	DB Search	176	VSDLTQAANK	2
305	GPTYRGPVPWHTIN	39.52	1593.805	14	21.4	14	-0.2504	0.53	-1.7	532.2748	3	16.3797	Q78P93|Q78P93_MOUSE:Q9WV54|ASAH1_MOUSE:Q			0 0 0 0 0 4 0 0 17	GPTYRGPVPWH	DB Search	175	GPTYRGPVPWH	3
306	YHSKYEEL	39.83	1067.492	8	100	8	-0.8685	0.5	2.1	534.7559	2	8.8707	Q3TTY5|K22E_MOUSE:B2RTP7|B2RTP7_MOUSE			5 56 7 3 3 3 12 5	YHSKYEEL	DB Search	175	YHSKYEEL	2
307	GQVGGEINVEM(+15.99)DAAPGVDLSR	40.1	2129.006	21	9.5	21	-0.5864	0.83	-3.9	1065.509	2	17.5982	Q9QWL7|K1C17_	Oxidation (M)	M11:Oxidation (M	0 0 0 0 0 0 2 0 0 1	GQVGGEINVEM(	DB Search	174	GQVGGEINVEMD	1
308	VITNQYNSPTGLYSSEN	40.12	1885.869	17	47.1	17	-0.3341	0.65	4	943.948	2	16.3701	O70400|PDLI1_MOUSE:S4R1V0|S4R1V0_MOUSE:Q3			0 0 0 0 0 25 20 20	VITNQYNSPTGLY	DB Search	172	VITNQYNSPTGLY	3
309	LVSIGAEEIVDGNAK	40.12	1513.799	15	60	15	-0.1168	0.68	1	757.9092	2	18.0869	D3Z761|D3Z761_MOUSE:Q1A602|Q1A602_MOUSE:/			0 0 5 0 32 32 33 2	LVSIGAEEIVDGN	DB Search	171	LVSIGAEEIVDGN	1
310	IREFYSASVAEDA	40.12	1456.683	13	69.2	13	0.447	0.63	4.4	729.3539	2	15.6216	E9Q7P9|CDHR2_MOUSE			0 0 0 0 4 6 6 20 3	IREFYSASVAED/	DB Search	170	IREFYSASVAED/	3
311	GEDVAIFARGPQAHLVHGVQ	40.1	2100.086	20	20	20	-0.6966	0.51	2	701.0391	3	16.9922	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:Q			0 0 0 1 61 3 0 0 0	GEDVAIFARGPQ	DB Search	168	GEDVAIFARGPQ	2
312	AQYEDIAQK	40.06	1064.514	9	77.8	9	-0.8666	0.67	1.5	533.2662	2	8.4187	Q3UV17|K22O_MOUSE			5 7 27 15 5 5 2 1	AQYEDIAQK	DB Search	166	AQYEDIAQK	1
313	TIGGGDDSFNTFFSETGAGK	40.12	2006.886	20	5	20	-0.5649	0.31	2.4	1004.455	2	21.8526	P68369|TBA1A_MOUSE:P68373|TBA1C_MOUSE:A0/			0 0 1 0 0 0 0 0 1 1	TIGGGDDSFNTF	DB Search	165	TIGGGDDSFNTF	1
314	AAIDWFDGK	31.71	1021.487	9	66.7	9	-0.807	0.7	-3.1	511.7503	2	19.4591	Q8BQ46|Q8BQ46_MOUSE:Q8CFQ9|Q8CFQ9_MOUS			5 11 62 63 22 4 0	AAIDWFDGK	DB Search	164	AAIDWFDGK	1
315	LFIGGLNTETNEK	39.57	1434.736	13	69.2	13	-0.1011	0.55	1.9	718.3763	2	18.001	A0A2I3BRL8|A0A2I3BRL8_MOUSE:Q9WV02|RBMX_			5 15 98 34 9 9 12	LFIGGLNTETNEK	DB Search	164	LFIGGLNTETNEK	1
316	QITVNDLPVGR	39.87	1210.667	11	63.6	11	0.1124	0.74	-1.1	606.3415	2	16.8138	Q61171|PRDX2_MOUSE:Q5M9N9|Q5M9N9_MOUSE			5 5 11 11 13 13 2	QITVNDLPVGR	DB Search	162	QITVNDLPVGR	2
317	TNAENEFVTIK	40.11	1264.63	11	81.8	11	0.0812	0.56	0.5	633.324	2	14.9988	P04104|K2C1_MOUSE			2 2 71 71 28 21 1	TNAENEFVTIK	DB Search	162	TNAENEFVTIK	1
318	APAAAATTAAPAAAAAPAK	40.12	1562.842	19	31.6	19	0.1681	0.65	7.7	782.4359	2	10.3437	Q5M8R8|Q5M8R8_MOUSE:P14869|RLA0_MOUSE:Q			0 0 0 0 2 3 6 5 5 8	APAAAATTAAPA/	DB Search	159	APAAAATTAAPA/	3
319	SGRFTYQNAAAQPETGPG	40.12	1850.855	18	16.7	18	-0.0014	0.71	2.5	926.4391	2	11.9574	Q9QZM4|TR10B_MOUSE			0 0 0 0 0 0 0 0 1 4	SGRFTYQNAAA(	DB Search	158	SGRFTYQNAAA(	2
320	NVQFNYPQASVTD	40.12	1481.679	13	69.2	13	0.0595	0.6	-2.8	741.8463	2	17.9426	G3X977|G3X977_MOUSE:Q8K016|Q8K016_MOUSE:Q			0 0 0 4 4 31 8 2 2	NVQFNYPQASVT	DB Search	158	NVQFNYPQASVT	2
321	NVFENYEASKAYSSVD	40.12	1821.806	16	75	16	-0.9624	0.81	-0.4	911.9119	2	16.882	Q9D306|MGT4C_MOUSE			0 0 3 7 7 9 8 10 8	NVFENYEASKAY	DB Search	157	NVFENYEASKAY	2
322	GPKPFSAPKPQTSPSP	40.06	1621.846	16	6.2	16	0.2343	0.69	2	811.934	2	11.1478	Q3TC53|Q3TC53_MOUSE:P40124|CAP1_MOUSE:Q3			0 0 0 0 0 0 0 0 0 0	GPKPFSAPKPQT	DB Search	157	GPKPFSAPKPQT	2
323	ISVYYNEATGGK	40.1	1300.63	12	66.7	12	-0.5888	0.71	-2.3	651.3223	2	12.7428	P99024|TBB5_MOUSE			5 11 11 69 41 5 5	ISVYYNEATGGK	DB Search	157	ISVYYNEATGGK	1
324	NALESYAFNM(+15.99)K	39.65	1302.591	11	63.6	11	-0.641	0.71	-0.2	652.3044	2	15.4058	A1E2B8|A1E2B8	Oxidation (M)	M10:Oxidation (M	0 0 73 75 67 67 9	NALESYAFNM(+1	DB Search	157	NALESYAFNMK	3
325	SVDETTQAMAFDGIIFQGQSLK	40.12	2385.152	22	36.4	22	-1.0478	0.63	6.2	1193.594	2	25.2213	Q80XR5|Q80XR5_MOUSE:P26369|U2AF2_MOUSE:Q			0 0 0 0 0 0 1 3 3 3	SVDETTQAMAFD	DB Search	156	SVDETTQAMAFD	1
326	VGTKRYMAPEVLDETIN	38.96	1934.977	17	17.6	17	-0.8918	0.34	7.7	968.5033	2	17.2061	Q61271|ACV1B_MOUSE:Q3TZF1|Q3TZF1_MOUSE			0 0 0 0 0 0 0 1 0 0	VGTKRYMAPEVL	DB Search	156	VGTKRYMAPEVL	3
327	A(+42.01)SKRALVILAKGAE	37.26	1467.877	14	50	14	0.658	0.72	-1	490.3004	3	16.4279	A2A815|A2A815_	Acetylation (N-ter	A1:Acetylation (N-	5 0 0 0 0 3 8 20 1	A(+42.01)SKRAL\	DB Search	150	ASKRALVILAKG/	3
328	DAEM(+15.99)AIYGPAAIYLR	40.12	1668.818	15	53.3	15	0.2044	0.88	2.1	835.42	2	22.8592	A0ABD1KMS1|A0	Oxidation (M)	M4:Oxidation (M):	0 0 0 2 9 46 84 33	DAEM(+15.99)AI\	DB Search	147	DAEMAIYGPAAI\	1
329	LVQAFQFTDK	39.42	1195.624	10	60	10	-0.0875	0.64	-2.3	598.8178	2	17.8581	B1AXW5|B1AXW5_MOUSE:P35700|PRDX1_MOUSE:			5 10 86 86 0 0 3 3	LVQAFQFTDK	DB Search	147	LVQAFQFTDK	2
330	VFLENVIRDAVTYTEHAK	40.12	2104.095	18	50	18	0.5905	0.36	3.8	702.3767	3	25.6057	Q61667|Q61667_MOUSE:P62806|H4_MOUSE:B2RTM			5 25 38 17 0 0 6 1	VFLENVIRDAVTY	DB Search	145	VFLENVIRDAVTY	2
331	DGEGTSPADKVVKKGKKDKKTKKTFF	37.4	2866.592	26	7.7	26	4.4116	0.29	6.5	717.6615	4	8.1187	Q6P542|ABCF1_MOUSE:Q5RL55|Q5RL55_MOUSE			0 0 0 3 3 0 0 0 0 0	DGEGTSPADKV\	DB Search	143	DGEGTSPADKV\	1
332	GLQFPVGR	36.19	872.4868	8	50	8	-0.5273	0.85	-2.6	437.2495	2	16.463	Q8BFU2|H2A3_MOUSE:A0AUV1|A0AUV1_MOUSE:Q			0 0 70 77 5 2 0 0	GLQFPVGR	DB Search	142	GLQFPVGR	2
333	EPYGARYVGSMVADVHRT	39.43	2006.963	18	27.8	18	-0.3069	0.74	0.4	669.9968	3	16.3303	P70695|F16P2_MOUSE:Q3TH92|Q3TH92_MOUSE:Q:			0 0 0 0 0 0 0 0 1 1	EPYGARYVGSM\	DB Search	142	EPYGARYVGSM\	1
334	GSNTFSRTTKAVVVKKIETRDGKLVS	33.57	2820.582	26	3.8	26	-1.7118	0.5	4.2	706.1558	4	12.5127	P11679|K2C8_MOUSE			0 0 0 0 0 0 0 0 0 0	GSNTFSRTTKAV	DB Search	140	GSNTFSRTTKAV	1
335	IIFFKFNTPQQPKKK	39.71	1863.077	15	6.7	15	0.1549	0.37	3.1	622.0349	3	16.356	Q9CZ30|OLA1_MOUSE:Q3TW21|Q3TW21_MOUSE:Q			0 0 17 0 0 0 1 1 1	IIFFKFNTPQQPK	DB Search	139	IIFFKFNTPQQPK	3
336	LVRYTQKAPQVSTPTLV	39.68	1900.078	17	11.8	17	0.1379	0.42	3.2	634.3687	3	16.3406	Q546G4|Q546G4_MOUSE:P07724|ALBU_MOUSE			0 0 0 0 0 1 1 1 0 0	LVRYTQKAPQVS	DB Search	138	LVRYTQKAPQVS	2
337	DVWGIEGPIDAAFTR	40.06	1645.81	15	53.3	15	0.2812	0.85	3.8	823.9174	2	26.518	P29788|VTNC_MOUSE			0 0 15 11 30 88 4	DVWGIEGPIDAA	DB Search	138	DVWGIEGPIDAA	1
338	A(+42.01)ETLSGLGDASAAGAAAVSSAASETGTR	40.12	2520.194	28	64.3	28	-0.2039	0.72	3.2	841.0765	3	23.8876	S4R1M2|S4R1M2	Acetylation (N-ter	A1:Acetylation (N-	0 0 8 32 33 9 9 13	A(+42.01)ETLSGI	DB Search	135	AETLSGLGDASA	1
339	KKKKKKKKPFML	38.36	1531.016	12	16.7	12	-0.1933	0.62	-2	511.3461	3	2.2515	Q3ULL5|Q3ULL5_MOUSE:Q99L45|IF2B_MOUSE:E0C			0 0 0 0 3 4 0 0 0 0	KKKKKKKKPFML	DB Search	133	KKKKKKKKPFML	1
340	ESTGAQVQVAGDMLPNSTER	40.12	2088.975	20	5	20	-0.5347	0.63	1.3	1045.498	2	16.4635	A0A2R8VHP9|A0A2R8VHP9_MOUSE:A0A2R8VHN3|A			0 0 0 0 0 0 1 1 1 3	ESTGAQVQVAGI	DB Search	133	ESTGAQVQVAGI	1
341	QDHPSSMGVYGQESGGFSGPGENR	40.12	2479.046	24	50	24	-0.6193	0.86	-0.6	827.3574	3	13.2104	Q3UI30|Q3UI30_MOUSE:Q61545|EWS_MOUSE:Q3U			0 0 0 0 1 1 0 0 4 3	QDHPSSMGVYG(	DB Search	131	QDHPSSMGVYG(	1
342	AVLDVAETGTEAAAATGVK	40.12	1772.916	19	63.2	19	0.1677	0.61	6.6	887.473	2	18.1294	Q91WP6|SPA3N_MOUSE:A2RTV1|A2RTV1_MOUSE:			0 0 0 6 18 26 36 4	AVLDVAETGTEA	DB Search	130	AVLDVAETGTEA	1
343	VPENPPSM(+15.99)VFK	34.53	1259.622	11	54.5	11	-0.6197	0.32	-3.6	630.8175	2	13.224	P37804|TAGL_M	Oxidation (M)	M8:Oxidation (M):	5 3 3 16 4 0 0 0 0	VPENPPSM(+15.9	DB Search	129	VPENPPSMVFK	1
344	DIQDSLTVSNEVQTAK	40.11	1746.864	16	56.2	16	-0.494	0.83	2.4	874.4432	2	16.2162	Q3U7G3|Q3U7G3_MOUSE:P47754|CAZA2_MOUSE:Q			0 0 12 15 21 13 4	DIQDSLTVSNEV(	DB Search	127	DIQDSLTVSNEV(	1
345	VATNPIITPVAQENQ	40.12	1593.836	15	26.7	15	-0.1326	0.69	-4.8	797.9235	2	18.1257	Q3UEE7|Q3UEE7_MOUSE:Q3TX45|Q3TX45_MOUSE			0 0 0 0 0 0 20 63	VATNPIITPVAQEI	DB Search	126	VATNPIITPVAQEI	1
346	GDIIFFKFNTPQQPKKK	39.71	2035.126	17	17.6	17	0.3356	0.41	6.5	679.3868	3	17.7627	Q9CZ30|OLA1_MOUSE:Q3TW21|Q3TW21_MOUSE:Q			0 0 8 13 0 0 0 0 0	GDIIFFKFNTPQQ	DB Search	125	GDIIFFKFNTPQQ	3
347	ISGLIYEETRGVLK	39.71	1576.882	14	21.4	14	0.2356	0.51	3.4	789.4512	2	18.6306	P62806|H4_MOUSE:B2RTM0|B2RTM0_MOUSE:Q6B			5 3 0 0 1 2 1 1 1 0	ISGLIYEETRGVL	DB Search	124	ISGLIYEETRGVL	2
348	DNNRSLDLD	32.54	1060.479	9	88.9	9	-0.1131	0.9	-7.8	531.2437	2	11.3824	Q4L0E7|Q4L0E7_MOUSE:Q08EK4|Q08EK4_MOUSE:			3 3 3 0 7 7 22 14	DNNRSLDLD	DB Search	123	DNNRSLDLD	3
349	AGIALNDNFVK	37.16	1160.619	11	54.5	11	0.2195	0.62	-3.7	581.316	2	17.5892	A0A1D5RLD8|A0A1D5RLD8_MOUSE:S4R257|S4R25			0 0 5 56 37 12 5 4	AGIALNDNFVK	DB Search	123	AGIALNDNFVK	1
350	LFIGGLSFETTDESLR	40.12	1783.899	16	56.2	16	0.2631	0.39	-1.5	892.9576	2	24.9312	P49312|ROA1_MOUSE:Q3TIK8|Q3TIK8_MOUSE:Q5E			3 3 3 1 1 8 6 6 8 3	LFIGGLSFETTDE	DB Search	122	LFIGGLSFETTDE	2
351	NPPSYYTQPVPVPNA	40.12	1642.799	15	26.7	15	0.2731	0.55	-1.6	822.4075	2	18.8915	Q9JLJ0|LITAF_MOUSE:E0CYR5|E0CYR5_MOUSE			0 0 0 0 3 3 0 0 12	NPPSYYTQPVPV	DB Search	118	NPPSYYTQPVPV	2
352	T(+42.01)SRKKVLLKVIILG	40.12	1609.065	14	42.9	14	-0.5159	0.24	-1.3	537.363	3	19.1845	P51150|RAB7A_N	Acetylation (N-ter	T1:Acetylation (N-	0 0 0 0 0 1 3 3 0 0	T(+42.01)SRKKVI	DB Search	118	TSRKKVLLKVIIL(	2
353	IEKVIPSTANSN	40.08	1271.672	12	50	12	0.0927	0.7	-3.9	636.8424	2	11.0378	E9Q7P9|CDHR2_MOUSE			4 0 0 6 27 0 0 3 7	IEKVIPSTANSN	DB Search	116	IEKVIPSTANSN	2
354	THINIVVIGHVDSGK	39.91	1587.873	15	26.7	15	0.1837	0.58	-0.6	794.9453	2	15.1845	Q58E64|Q58E64_MOUSE:Q3UZQ3|Q3UZQ3_MOUSE			0 0 2 1 1 6 3 3 1 0	THINIVVIGHVDS(	DB Search	115	THINIVVIGHVDS(	1
355	VEIIANDQGNR	37.58	1227.621	11	63.6	11	0.4406	0.59	3.6	614.8199	2	10.4995	Q3TKF8|Q3TKF8_MOUSE:Q3U6V3|Q3U6V3_MOUSE			5 5 50 69 48 13 8	VEIIANDQGNR	DB Search	114	VEIIANDQGNR	2
356	RSRKESYSVYVYKVLKQVHPD	40.12	2580.381	21	14.3	21	0.3701	0.54	-1.6	646.1031	4	17.0534	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:Q			0 0 0 0 0 0 0 0 0 0	RSRKESYSVYVY	DB Search	112	RSRKESYSVYVY	2
357	KESYSIYVYK	39.71	1278.65	10	40	10	-0.2595	0.78	4.7	640.3351	2	13.1916	Q8CGP0|H2B3B_MOUSE:Q64524|H2B2E_MOUSE:Q			4 4 1 1 1 1 2 2 1 1	KESYSIYVYK	DB Search	111	KESYSIYVYK	3
358	SM(+15.99)DNNRSLDLDSIIA	39.59	1678.783	15	46.7	15	0.5231	0.27	2.1	840.4027	2	21.2544	Q0VDR7|Q0VDR7	Oxidation (M)	M2:Oxidation (M):	0 0 0 1 1 1 0 0 6 7	SM(+15.99)DNNR	DB Search	109	SMDNNRSLDLDS	2
359	ISEQFTAM(+15.99)FR	40.08	1244.586	10	90	10	-0.3377	0.81	-2.3	623.3003	2	16.3668	Q9CWF2|TBB2B	Oxidation (M)	M8:Oxidation (M):	5 8 8 36 71 19 4 4	ISEQFTAM(+15.9	DB Search	108	ISEQFTAMFR	1
360	RPVQFPYVTPAPHEPVKT	39.67	2062.1	18	27.8	18	-0.3526	0.62	0.8	688.3761	3	15.6077	Q9D074|MGRN1_MOUSE			0 0 0 0 5 0 0 25 2	RPVQFPYVTPAP	DB Search	107	RPVQFPYVTPAP	2
361	FFTGQITAAGK	35.15	1139.598	11	36.4	11	0.3659	0.68	-3	570.8057	2	15.352	E9Q8F4|E9Q8F4_MOUSE:Q3TGH1|Q3TGH1_MOUSE			5 6 41 1 1 5 1 0 0	FFTGQITAAGK	DB Search	107	FFTGQITAAGK	1
362	EPDLDPRFIREFYSASVAEDATLG	40.09	2697.292	24	16.7	24	-0.0767	0.24	4.8	900.1111	3	26.3354	E9Q7P9|CDHR2_MOUSE			0 0 0 0 0 0 0 0 0 0	EPDLDPRFIREF\	DB Search	107	EPDLDPRFIREF\	1
363	GQVGGDVNVEMDAAPGVDLSR	40.11	2084.98	21	4.8	21	-1.1442	0.7	3.4	1043.503	2	18.5509	Q6IFX2|K1C42_MOUSE:Q9CWC9|Q9CWC9_MOUSE			0 0 0 0 0 0 1 1 1 1	GQVGGDVNVEM	DB Search	106	GQVGGDVNVEM	1
364	SIQADGLVWGSSK	40.12	1346.683	13	69.2	13	-0.3939	0.53	0.2	674.3505	2	17.7733	A0A087WS46|A0A087WS46_MOUSE:O70251|EF1B_			0 0 84 50 38 10 1	SIQADGLVWGSS	DB Search	105	SIQADGLVWGSS	1
365	ALTVPELTQQVFDAK	40.12	1658.888	15	26.7	15	0.1999	0.65	6	830.4582	2	24.1108	P99024|TBB5_MOUSE:Q80ZV2|Q80ZV2_MOUSE			0 0 0 5 2 2 3 0 0 1	ALTVPELTQQVFI	DB Search	104	ALTVPELTQQVFI	1
366	APIIAVTR	36.08	839.5229	8	75	8	0.063	0.84	-6.1	420.7661	2	13.5179	P52480|KPYM_MOUSE			5 39 77 38 9 2 0 0	APIIAVTR	DB Search	103	APIIAVTR	2
367	DYEEVGVDSVEGEGEEEGEEY	40.12	2347.898	21	66.7	21	-0.1172	0.53	4.6	1174.964	2	18.6033	P68369|TBA1A_MOUSE:P05213|TBA1B_MOUSE:Q9			0 0 8 15 48 11 11	DYEEVGVDSVE(	DB Search	101	DYEEVGVDSVE(	1
368	STGEAFVQFASQEIAEK	40.12	1840.884	17	47.1	17	-1.3112	0.89	7.6	921.4586	2	22.2048	Q811L7|Q811L7_MOUSE:Q3UR26|Q3UR26_MOUSE:			0 0 0 1 2 5 11 17	STGEAFVQFASQ	DB Search	100	STGEAFVQFASQ	1
369	ANNVLSGGTTM(+15.99)YPGIADR	40.12	1851.879	18	44.4	18	-0.3408	0.64	2.1	926.9506	2	15.9855	Q3UJ36|Q3UJ36	Oxidation (M)	M11:Oxidation (M	0 0 0 7 7 3 3 2 0 0	ANNVLSGGTTM(	DB Search	99.5	ANNVLSGGTTMY	3
370	TVTAM(+15.99)DVVYALKR	40.12	1481.791	13	69.2	13	-0.2683	0.44	-0.7	741.9041	2	17.569	Q61667|Q61667	Oxidation (M)	M5:Oxidation (M):	4 4 5 5 9 9 9 13 2	TVTAM(+15.99)D	DB Search	99.2	TVTAMDVVYALK	3
371	TNDRYVASLAARNKV	39.65	1676.896	15	40	15	-0.5084	0.75	2.9	559.9742	3	11.633	Q00560|IL6RB_MOUSE:Q6PDI9|Q6PDI9_MOUSE:V9			0 0 0 0 1 2 7 2 2 4	TNDRYVASLAAR	DB Search	98.3	TNDRYVASLAAR	2
372	ESYSVYVYK	40.04	1136.539	9	77.8	9	-0.7956	0.82	1.2	569.2788	2	14.1616	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:Q			5 6 31 53 50 14 8	ESYSVYVYK	DB Search	98.2	ESYSVYVYK	2

373	TAVVVGTVTDDVR	39.73	1330.709	13	53.8	13	0.2658	0.71	3.2	666.3656	2	15.1803	A0A1B0GSA8|A0A1B0GSA8_MOUSE:Q0QEW9|Q0Q	0 0 4 27 60 13 6 6	TAVVVGTVTDDV	DB Search	97.7	TAVVVGTVTDDV	1
374	AETECQ(+15.00)N(+15.00)AEYQQLLDIK	40.11	2024.925	17	35.3	17	11.1162	0.77	4.7	1013.477	2	22.2369	P02535|K1C10_M	Deamidation (N	Q6:Deamidation (N	0 0 1 0 1 0 0 0 2 2	AETECQ(+15.00)	DB Search	95.7	AETECQNAEYQ	1
375	GQTGGDVNVEM(+15.99)DAAPGVDLSR	40.06	2102.954	21	0	21	-0.9553	0.78	-0.9	1052.486	2	15.3114	Q3SYP5|Q3SYP5_MOUSE	Oxidation (M)	M11:Oxidation (M	0 0 0 0 0 0 0 0 1 0	GQTGGDVNVEM	DB Search	94.8	GQTGGDVNVEM	1
376	KKELEEQLGPVAEETR	39.97	1854.969	16	31.2	16	-0.7114	0.75	2.9	619.3334	3	11.934	G3UZM8|G3UZM8_MOUSE:G3UWN5|G3UWN5_MOU			0 0 0 0 0 0 1 6 15	KKELEEQLGPVA	DB Search	94.8	KKELEEQLGPVA	2
377	S(+42.01)GSFYFVIVGHH	40.12	1390.667	12	75	12	0.0606	0.53	-0.3	696.3422	2	25.0411	Q9CQP2|TPPC2_	Acetylation (N-ter	S1:Acetylation (N	5 2 2 20 49 68 52	S(+42.01)GSFYF	DB Search	94.3	SGSFYFVIVGHH	1
378	ENVRYSFSTVNLSPEN	40.12	1854.875	16	50	16	0.1096	0.71	2.4	928.449	2	18.5571	Q8BWN9|Q8BWN9_MOUSE:Q8BW		S8|Q8BWS8_MO	0 0 0 0 0 5 4 4 4 3	ENVRYSFSTVNL	DB Search	93.5	ENVRYSFSTVNL	2
379	M(+15.99)SVQPTVSLGGFEITPPVVLR	40.12	2242.203	21	4.8	21	0.844	0.62	5.7	1122.118	2	27.1514	Q3UDA7|Q3UDA7	Oxidation (M)	M1:Oxidation (M)	0 0 0 0 0 0 1 1 1 0	M(+15.99)SVQPT	DB Search	90.3	MSVQPTVSLGGF	1
380	LPDYSAPNPIKVTH	40.12	1550.809	14	7.1	14	-0.8383	0.75	-1.1	776.4128	2	15.5111	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			5 0 0 1 1 1 0 0 1 1	LPDYSAPNPIKVT	DB Search	87.8	LPDYSAPNPIKVT	2
381	IEVIEIM(+15.99)TDR	25.68	1233.627	10	70	10	-0.5791	0.66	-0.9	617.8204	2	17.0008	P49312|ROA1_M	Oxidation (M)	M7:Oxidation (M)	5 8 65 74 52 5 5 0	IEVIEIM(+15.99)T	DB Search	87.5	IEVIEIMTDR	2
382	PTVDQVDDTSIVVR	37.79	1542.789	14	7.1	14	-0.6875	0.64	3.5	772.4063	2	15.9614	Q3TCF1|Q3TCF1_MOUSE:B7ZNJ1|B7ZNJ1_MOUSE			0 0 0 0 1 2 1 1 0 0	PTVDQVDDTSIVV	DB Search	87.4	PTVDQVDDTSIVV	1
383	VDFNTPRPSTVEA	40.1	1431.699	13	46.2	13	0.1539	0.73	-1.5	716.8575	2	15.0125	A0A286YD40|A0A286YD40_MOUSE:G3X939|SL9A3			0 0 8 34 34 0 0 2	VDFNTPRPSTVE	DB Search	87.1	VDFNTPRPSTVE	1
384	GHAYSVTGAEEVESSGSLQK	40.12	2034.949	20	55	20	-1.1524	0.79	-1.7	679.3242	3	12.3811	Q3U8S5|Q3U8S5_MOUSE:Q8R486|Q8R486_MOUSE			0 0 0 0 0 0 40 5 5	GHAYSVTGAEEV	DB Search	86.1	GHAYSVTGAEEV	1
385	AQYEDIAQKS	40.1	1151.546	10	50	10	-0.5887	0.72	1.4	576.7824	2	8.8286	Q3UV17|K22O_MOUSE			0 0 34 16 13 6 3 1	AQYEDIAQKS	DB Search	86	AQYEDIAQKS	1
386	TLSDYNIQK	36.25	1080.545	9	44.4	9	-0.5475	0.73	-3.6	541.2792	2	11.1227	P0CG50|UBC_MOUSE:E9Q5F6|E9Q5F6_MOUSE:B0			5 5 11 11 1 1 1 0	TLSDYNIQK	DB Search	86	TLSDYNIQK	1
387	SVFVAPAVTPVKGVL	40.12	1482.881	15	40	15	0.5217	0.64	2.3	742.4512	2	23.4335	P70158|ASM3A_MOUSE			0 0 0 6 37 2 2 4 1	SVFVAPAVTPVK	DB Search	84.8	SVFVAPAVTPVK	2
388	EITALAPSTMK	38.35	1160.611	11	63.6	11	0.1824	0.66	-6.7	581.3103	2	15.1348	Q3UJ36|Q3UJ36_MOUSE:P63260|ACTG_MOUSE:Q3			0 0 49 49 73 44 5	EITALAPSTMK	DB Search	83.6	EITALAPSTMK	1
389	LAVNM(+15.99)VPFPR	40.02	1158.622	10	60	10	-0.187	0.9	-4.9	580.3168	2	18.2488	Q9CRT0|Q9CRT0	Oxidation (M)	M5:Oxidation (M)	5 8 29 13 13 33 1	LAVNM(+15.99)VI	DB Search	83.5	LAVNMVPFPR	3
390	YLNIYVPAHAHEG	40.12	1482.726	13	53.8	13	-1.1185	0.73	3.7	742.3745	2	15.2958	Q8BK48|EST2E_MOUSE			0 0 6 10 32 32 2 2	YLNIYVPAHAHEG	DB Search	83.5	YLNIYVPAHAHEG	1
391	TYQSYSSPSPRVSRFK	39.57	1888.943	16	31.2	16	-0.6498	0.03	2.3	630.6579	3	10.3432	E9QPG8|E9QPG8_MOUSE:A0A140LI59|A0A140LI59			0 0 99 22 22 11 3	TYQSYSSPSPRV	DB Search	83.2	TYQSYSSPSPRV	1
392	EQVANSAFVER	39.88	1248.61	11	63.6	11	-0.2974	0.74	0.1	625.3137	2	11.5282	E9Q0C3|E9Q0C3_MOUSE:Q80YC2|Q80YC2_MOUSE			0 0 33 62 31 20 1	EQVANSAFVER	DB Search	81.3	EQVANSAFVER	2
393	IVSHDYKGSTSHSLP	28.57	1626.8	15	40	15	3.2783	0.32	3.5	543.2759	3	8.8202	E9Q1Y3|E9Q1Y3_MOUSE:E9Q414|APOB_MOUSE			0 0 0 0 2 7 0 4 0 0	IVSHDYKGSTSHS	DB Search	81.1	IVSHDYKGSTSHS	2
394	AAYLWVGAGASEAEKT	40.12	1622.794	16	50	16	-0.2111	0.69	2.4	812.4081	2	18.4536	Q3U9Q8|Q3U9Q8_MOUSE:P13020|GELS_MOUSE:Q			0 0 8 19 32 57 16	AAYLWVGAGASE	DB Search	80.5	AAYLWVGAGASE	3
395	YPSQASIYSPPAAAAAAA	40.12	1705.831	18	33.3	18	-0.0209	0.26	3.8	853.9281	2	18.3568	Q3TQ49|Q3TQ49_MOUSE:P70297|STAM1_MOUSE:C			0 0 0 0 0 0 0 0 16	YPSQASIYSPPAA	DB Search	80.3	YPSQASIYSPPAA	2
396	GEDVAIFARGPQAHLVHG	40	1872.96	18	33.3	18	-0.343	0.29	-1.2	625.3278	3	16.3506	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:C			0 0 21 21 50 50 9	GEDVAIFARGPQ	DB Search	80.2	GEDVAIFARGPQ	2
397	DNLIDDLQR	34.49	1100.546	9	55.6	9	1.2432	0.55	-5.9	551.2784	2	19.5509	Q3V1K9|Q3V1K9_MOUSE:P31001|DESM_MOUSE:Q			3 3 27 99 23 1 1 0	DNLIDDLQR	DB Search	79.4	DNLIDDLQR	3
398	VGGTSDVEVNEK	40.05	1232.588	12	66.7	12	-0.1399	0.66	-4.4	617.3002	2	7.2888	P63038|CH60_MOUSE			5 33 0 0 33 14 4 4	VGGTSDVEVNEK	DB Search	79.2	VGGTSDVEVNEK	1
399	YM(+15.99)NKVELEAK	37.63	1239.617	10	40	10	-0.9188	0.59	2.2	620.8185	2	8.0252	A0A6B9SLG6|A0A	Oxidation (M)	M2:Oxidation (M)	3 3 0 0 0 0 2 0 0 5	YM(+15.99)NKVE	DB Search	76.5	YMNKVELEAK	1
400	LISWYDNEYGYSNR	40.12	1778.79	14	42.9	14	-0.6847	0.67	5.5	890.4092	2	18.8178	A0A1D5RLD8|A0A1D5RLD8_MOUSE:S4R257|S4R25			0 0 1 1 8 2 2 4 7 2	LISWYDNEYGYS	DB Search	76.3	LISWYDNEYGYS	1
401	LHTKGALPLDTVTFYKVIPKSKFVLVKFD	40.12	3303.9	29	34.5	29	-0.7656	0.53	-1.7	661.7877	5	23.5197	P57759|ERP29_MOUSE:A8C1V9|A8C1V9_MOUSE			0 0 5 0 0 8 44 13	LHTKGALPLDTVT	DB Search	75.7	LHTKGALPLDTVT	1
402	ASLENSLEETK	33.76	1219.593	11	54.5	11	0.8122	0.78	-4.7	610.8024	2	12.3765	Q3SYP5|Q3SYP5_MOUSE:Q9EQD6|Q9EQD6_MOUS			0 0 42 77 15 10 7	ASLENSLEETK	DB Search	74.3	ASLENSLEETK	2
403	VRYTQKAPQVSTPTL	38.45	1687.926	15	0	15	0.1695	0.42	5.6	844.9769	2	14.1422	Q546G4|Q546G4_MOUSE:P07724|ALBU_MOUSE			0 0 0 0 0 1 0 0 0 0	VRYTQKAPQVST	DB Search	73.7	VRYTQKAPQVST	3
404	TSGGAGGLGSLR	39.66	1031.536	12	83.3	12	-0.3444	0.76	1.9	516.7763	2	11.047	Q3V1K9|Q3V1K9_MOUSE:P31001|DESM_MOUSE:Q			5 6 26 11 11 24 2	TSGGAGGLGSLR	DB Search	73	TSGGAGGLGSLR	2
405	YFDSFGDLSSASAIM(+15.99)GNAK	40.12	1995.888	19	21.1	19	-0.458	0.65	14.8	998.9686	2	20.633	B1Q450|B1Q450_	Oxidation (M)	M15:Oxidation (M	0 0 0 2 2 0 0 2 0 0	YFDSFGDLSSAS	DB Search	72.9	YFDSFGDLSSAS	1
406	A(+42.01)SNVTNKTDPR	37.29	1243.616	11	27.3	11	3.9355	0.84	-0.4	622.8149	2	6.4322	A0A2I3BQH3|A0A	Acetylation (N-ter	A1:Acetylation (N	0 0 0 2 6 1 0 0 6 0	A(+42.01)SNVTN	DB Search	72.2	ASNVTNKTDPR	2
407	S(+42.01)ETAPAAPAAPAPVEKTPVK	39.82	1973.047	20	0	20	-0.0585	0.67	-6.6	987.5266	2	13.8906	Q149Z9|Q149Z9_	Acetylation (N-ter	S1:Acetylation (N	0 0 0 0 0 0 1 0 0 0	S(+42.01)ETAPA	DB Search	71.4	SETAPAAPAAPA	1
408	GYAVYETPTAHNGAKNPR	40.1	1944.944	18	27.8	18	-0.4515	0.37	-0.8	649.323	3	8.7653	A9JEI5|A9JEI5_MOUSE:Q8C5G6|Q8C5G6_MOUSE:F			0 0 2 4 56 0 0 0 0	GYAVYETPTAHN	DB Search	70.9	GYAVYETPTAHN	2
409	TLM(+15.99)ALGSLAVTK	39.35	1219.685	12	41.7	12	-0.2265	0.65	-5.2	610.8478	2	18.2836	P37804|TAGL_M	Oxidation (M)	M3:Oxidation (M)	0 0 88 48 48 21 0	TLM(+15.99)ALG	DB Search	70.2	TLMALGSLAVTK	3
410	IINEPTAAAIAYGLDKK	39.7	1786.983	17	23.5	17	0.0415	0.74	5.7	894.5038	2	18.4502	Q3KQJ4|Q3KQJ4_MOUSE:Q3U9L2|Q3U9L2_MOUSE			3 0 0 2 0 0 0 0 0 0	IINEPTAAAIAYGL	DB Search	69.4	IINEPTAAAIAYGL	1
411	DVDAAYM(+15.99)NKVELQAK	40.12	1709.829	15	6.7	15	-1.071	0.54	3.3	855.9268	2	12.6246	P50446|K2C6A_M	Oxidation (M)	M7:Oxidation (M)	2 0 0 1 0 0 0 0 0 0	DVDAAYM(+15.9	DB Search	68.2	DVDAAYMNKVEL	1
412	TLTLVDTGIGM(+15.99)TK	39.7	1364.722	13	53.8	13	0.1693	0.59	5.8	683.3723	2	18.0196	P11499|HS90B_M	Oxidation (M)	M11:Oxidation (M	0 0 27 27 72 33 1	TLTLVDTGIGM(+	DB Search	66	TLTLVDTGIGMTK	2
413	TLTIVDTGIGM(+15.99)TK	39.7	1364.722	13	53.8	13	0.4732	0.58	5.8	683.3723	2	18.0196	P07901|HS90A_M	Oxidation (M)	M11:Oxidation (M	0 0 27 27 72 33 1	TLTIVDTGIGM(+1	DB Search	66	TLTIVDTGIGMTK	2
414	TAKGLFRAAVPSGAST	40.12	1532.831	16	6.2	16	-0.1327	0.85	-0.8	767.424	2	14.1847	Q545V3|Q545V3_MOUSE:P17183|ENOG_MOUSE:D3			0 0 1 1 1 0 0 0 0 1	TAKGLFRAAVPS	DB Search	65.9	TAKGLFRAAVPS	1
415	TSSYSNPTIGYENRV	40.12	1686.785	15	20	15	-0.3793	0.88	3.3	844.4045	2	14.2799	Q07797|LG3BP_MOUSE			0 0 0 0 3 4 1 0 6 1	TSSYSNPTIGYEN	DB Search	65.9	TSSYSNPTIGYEN	2
416	AMEVFIQPTPIITYR	40.11	1777.944	15	46.7	15	-0.4248	0.77	7.1	889.9876	2	24.3026	B5THE3|B5THE3_MOUSE:F8VQM5|F8VQM5_MOUSE			0 0 0 5 8 28 55 5	AMEVFIQPTPIITY	DB Search	61.7	AMEVFIQPTPIITY	1
417	A(+42.01)AQGEPQVQFK	40.07	1243.62	11	36.4	11	0.0866	0.75	-0.5	622.8183	2	15.12	P62827|RAN_MO	Acetylation (N-ter	A1:Acetylation (N	0 0 1 5 5 0 0 8 3 0	A(+42.01)AQGEP	DB Search	60.6	AAQGEPQVQFK	2
418	RVPTPNVSVVD	38.78	1181.64	11	45.5	11	0.0247	0.76	-4	591.8251	2	14.9124	S4R257|S4R257_MOUSE:Q3V2I5|Q3V2I5_MOUSE:S			0 0 0 0 0 0 19 19	RVPTPNVSVVD	DB Search	60.1	RVPTPNVSVVD	3
419	TPFQFRAASPVEE	40.12	1477.72	13	38.5	13	-0.0632	0.68	6.2	739.8737	2	17.9	D3Z715|D3Z715_MOUSE:D3Z213|D3Z213_MOUSE:C			3 2 0 0 0 1 1 1 7 0	TPFQFRAASPVE	DB Search	59.8	TPFQFRAASPVE	1
420	YAVYETPTAHNGAK	40.03	1520.726	14	28.6	14	-0.4441	0.54	1.5	761.3732	2	9.1699	A9JEI5|A9JEI5_MOUSE:Q8C5G6|Q8C5G6_MOUSE:F			0 0 3 3 5 14 0 0 0	YAVYETPTAHNG	DB Search	59.5	YAVYETPTAHNG	1
421	NQVAM(+15.99)NPTNTVFDAK	39.71	1664.783	15	40	15	0.0593	0.55	3	833.4012	2	14.1468	Q3U9L2|Q3U9L2_	Oxidation (M)	M5:Oxidation (M)	0 0 2 5 5 14 0 0 0	NQVAM(+15.99)N	DB Search	57.6	NQVAMNPTNTVF	2
422	DVQDSVTVSNEIQTTK	40.12	1762.859	16	62.5	16	-0.5991	0.73	4.7	882.4428	2	14.2472	Q5RKN9|Q5RKN9_MOUSE:Q3UJV2|Q3UJV2_MOUSE			0 0 4 3 13 14 20 1	DVQDSVTVSNEI	DB Search	57.4	DVQDSVTVSNEI	1
423	S(+42.01)LKIQTSNVTNKND	33.96	1602.821	14	7.1	14	1.4407	0.54	0.7	802.4204	2	13.2375	Q3U3F6|Q3U3F6	Acetylation (N-ter	S1:Acetylation (N	0 0 0 0 0 0 0 0 0 2	S(+42.01)LKIQTS	DB Search	55.6	SLKIQTSNVTNKN	1
424	AVKSKYKASIAALEAKI	39.7	1790.067	17	11.8	17	-0.2565	0.42	-3.2	597.6942	3	15.5983	Q7TQJ6|Q7TQJ6_MOUSE:Q811J9|Q811J9_MOUSE:C			0 0 4 0 0 0 0 0 0 0	AVKSKYKASIAAL	DB Search	54	AVKSKYKASIAAL	2
425	KPTVTVVSPLPNDSINPQ	40.11	1905.021	18	22.2	18	-0.1	0.6	2.4	953.5222	2	18.3976	Q8VD58|EVI2B_MOUSE			0 0 0 0 0 0 2 3 0 0	KPTVTVVSPLPND	DB Search	51.4	KPTVTVVSPLPND	1
426	KYDEELEER	35.7	1209.551	9	44.4	9	-0.2716	0.85	-0.3	605.7842	2	7.0309	P37804|TAGL_MOUSE:A0A1L1STN8|A0A1L1STN8_M			5 12 2 2 1 1 0 0 0	KYDEELEER	DB Search	51.4	KYDEELEER	2
427	LDQLFSGPLPGRLPV	40.12	1607.903	15	53.3	15	-0.1248	0.73	-5.6	804.9564	2	25.9763	Q60805|MERTK_MOUSE			1 1 1 16 16 49 49	LDQLFSGPLPGR	DB Search	51.2	LDQLFSGPLPGR	1
428	DPKFEVIDKPQS	40.12	1401.714	12	66.7	12	-0.4767	0.7	1.7	701.8671	2	13.4855	P97450|ATP5J_MOUSE			5 7 4 4 4 4 5 1 2 0	DPKFEVIDKPQS	DB Search	50.9	DPKFEVIDKPQS	2
429	ENIWKAPEPVEIRE	40.12	1708.878	14	35.7	14	0.1379	0.55	-1.8	570.6337	3	17.7525	Q3TAN0|Q3TAN0_MOUSE:A2AKS7|A2AKS7_MOUSE			0 0 0 4 1 7 0 0 33	ENIWKAPEPVEIF	DB Search	49.5	ENIWKAPEPVEIF	2
430	ASPYSGAFPSTPVK	40.12	1407.703	14	57.1	14	-0.23	0.3	-1.2	704.8598	2	15.6557	A0A0J9YVJ0|A0A0J9YVJ0_MOUSE:A0A571BF69|A0A			5 9 6 6 18 3 3 12	ASPYSGAFPSTP	DB Search	49	ASPYSGAFPSTP	1
431	GKYTYGKPVPGHVKI	40.12	1642.919	15	46.7	15	0.6995	0.79	-4.5	548.6459	3	10.5668	P28665|MUG1_MOUSE			5 8 0 4 4 0 0 5 5 3	GKYTYGKPVPGH	DB Search	48.6	GKYTYGKPVPGH	1
432	GTPEYLAPEIILSKG	40.12	1586.856	15	20	15	0.4678	0.75	4.4	794.4404	2	23.1496	P68181|KAPCB_MOUSE:P05132|KAPCA_MOUSE			0 0 0 0 4 5 18 1 1	GTPEYLAPEIILSK	DB Search	48.5	GTPEYLAPEIILSK	2
433	IDPYDQPNAIYIER	40.12	1705.831	14	21.4	14	-0.5991	0.82	-1.8	853.9233	2	17.6247	Q3U2X9|Q3U2X9_MOUSE:O88307|SORL_MOUSE			0 0 0 1 2 4 0 0 0 0	IDPYDQPNAIYIE	DB Search	46.9	IDPYDQPNAIYIE	2
434	NYEGPETHTSLR	40.11	1402.648	12	16.7	12	-0.4711	0.35	5.8	702.3369	2	8.5387	P14483|HB2A_MOUSE:Q5XQL0|Q5XQL0_MOUSE:Q5			0 0 0 3 0 0 0 3 0 0	NYEGPETHTSLR	DB Search	45.3	NYEGPETHTSLR	2
435	ASLVYENASAIMAHESE	40.12	1820.825	17	58.8	17	-0.7431	0.59	-0.7	911.4213	2	19.3183	E9Q0N2|PTPRH_MOUSE			0 0 0 3 7 6 3 3 9 5	ASLVYENASAIM	DB Search	41.9	ASLVYENASAIM	2
436	VVLAAADLGTEAGVQR	38.1	1568.852	16	31.2	16	-0.0756	0.63	1.6	785.4365	2	17.57	G3UXX3|G3UXX3_MOUSE:Q91XH5|Q91XH5_MOUSE			0 0 0 13 15 0 0 19	VVLAAADLGTEA	DB Search	38.1	VVLAAADLGTEA	1
437	HEVVVIAPEASIHIK	40.12	1640.925	15	53.3	15	-0.1473	0.65	0.4	547.9838	3	16.4531	Q9R0A4|Q9R0A4_MOUSE:J7HWK0|J7HWK0_MOUS			0 0 2 13 32 38 15	HEVVVIAPEASIH	DB Search	35.3	HEVVVIAPEASIH	1
438	DIVVQETMEDIDK	36.15	1533.723	13	38.5	13	-0.5379	0.42	-4.7	767.8671	2	19.1856	G3UWR0|G3UWR0_MOUSE:Q6XLQ8|Q6XLQ8_MOU			0 0 0 3 7 10 6 2 0	DIVVQETMEDIDK	DB Search	34.6	DIVVQETMEDIDK	1
439	TNAENEFVTIKK	40.12	1392.725	12	58.3	12	0.3676	0.49	1	697.3721	2	11.9029	P04104|K2C1_MOUSE			5 8 9 9 5 5 1 1 2 0	TNAENEFVTIKK	DB Search	33.3	TNAENEFVTIKK	1
440	VFSDEVQQQAQLSTIR	40.12	1847.938	16	50	16	-0.8507	0.74	1.1	924.9794	2	16.8376	Q8QZY1|EIF3L_MOUSE			0 0 0 0 1 2 5 5 3 3	VFSDEVQQQAQL	DB Search	33	VFSDEVQQQAQL	2
441	FTASAGIQVVGDDLTVTNPK	40.12	2032.048	20	15	20	0.0717	0.79	2.1	1017.036	2	20.9394	Q6PHC1|Q6PHC1_MOUSE:Q5FW97|Q5FW97_MOUS			0 0 0 0 0 1 1 3 3 4	FTASAGIQVVGD	DB Search	32.1	FTASAGIQVVGD	1
442	NVVWDYFTQLSNNAKE	40.12	1926.911	16	50	16	-0.0394	0.44	-0.5	964.4646	2	26.1202	P06728|APOA4_MOUSE:Q810I7|Q810I7_MOUSE:Q9			0 0 0 6 3 0 4 10 1	NVVWDYFTQLSN	DB Search	30.6	NVVWDYFTQLSN	1
443	EAGVEMDDEEDLSTPNEK	39.98	2006.826	18	11.1	18	-0.4302	0.7	-1.5	1004.421	2	13.8327	Q922B2|SYDC_MOUSE:Q3UJQ3|Q3UJQ3_MOUSE:C			0 0 0 0 0 0 1 1 1 1	EAGVEMDDEEDL	DB Search	27.8	EAGVEMDDEEDL	1
444	VQVEYKGETK	39.91	1179.614	10	70	10	-1.3109	0.52	-8.3	590.8106	2	3.0555	Q3KQJ4|Q3KQJ4_MOUSE:Q3U9L2|Q3U9L2_MOUSE			3 3 11 5 1 1 2 0 2	VQVEYKGETK	DB Search	26.9	VQVEYKGETK	1

	H2Ab1DIEC-GBD																				
	Peptide	X.10LgP	Mass	Tag.Length	CAA....	Length	Delta.RT	MS2.Correlation	ppm	m.z	z	RT	Accession	PTM	AScore	ositional.Confidenc	tag...0.0..	Found.By	Area.Sample.2	Clean_Sequence	share
1	DIIFFKFNTPQQPKKK	40.12	1978.104	16	12.5	16	0.5821	0.35	2.5	660.3785	3	18.595	Q9CZ30|OLA1_MOUSE:Q3TW21|Q3TW21_MOUSE:(			0 0 17 1 0 0 0 1 1	DIIFFKFNTPQQP	DB Search	541	DIIFFKFNTPQQP	3
2	FADLSEAANR	33.86	1092.52	10	70	10	-0.7765	0.71	-2.3	547.2673	2	12.2154	P20152|VIME_MOUSE:Q3TFD9|Q3TFD9_MOUSE:Q5			5 38 51 51 34 9 9	FADLSEAANR	DB Search	124	FADLSEAANR	3
3	IFARGPQAHLVHG	40.12	1401.763	13	53.8	13	0.311	0.23	-1	468.2622	3	11.0292	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:(			5 42 4 0 0 0 0 4 7	IFARGPQAHLVH(	DB Search	1090	IFARGPQAHLVH(	3
4	HLQLAIRNDEELNK	39.71	1691.896	14	7.1	14	0.0026	0.5	0.8	846.9557	2	12.997	Q8BFU2|H2A3_MOUSE:A0AUV1|A0AUV1_MOUSE:Q			1 1 0 0 0 0 0 0 0 (	HLQLAIRNDEELN	DB Search	339	HLQLAIRNDEELN	3
5	RPGSGFTNTMRVVPVP	27.44	1713.898	16	31.2	16	0.6982	0.1	0.9	572.3073	3	18.3754	P52480|KPYM_MOUSE			0 0 0 0 0 0 0 0 0 (	RPGSGFTNTMR\	DB Search	1400	RPGSGFTNTMR\	3
6	AIILLLLLI	39.87	993.7202	9	11.1	9	-7.4489	0	1.6	994.7313	1	20.0418	Q544T2|Q544T2_MOUSE:G3UXE5|G3UXE5_MOUSE			5 0 0 0 0 0 0 0 0	AIILLLLLI	DB Search	112	AIILLLLLI	3
7	VELQELNDR	38.01	1114.562	9	55.6	9	-0.5862	0.62	0.1	558.2896	2	12.8772	P20152|VIME_MOUSE:A4IF59|A4IF59_MOUSE:Q5FV			5 37 90 75 11 1 1	VELQELNDR	DB Search	435	VELQELNDR	3
8	EVSSVEAPSVSPARHQ	39.69	1678.827	16	12.5	16	0.0737	0.89	5.4	840.4255	2	10.4764	Q8BUJ9|LRP12_MOUSE			0 0 0 0 0 2 3 1 0 (	EVSSVEAPSVSP/	DB Search	1080	EVSSVEAPSVSP/	3
9	AKPVSQMRMATPLLMRPM	39.7	2057.077	18	16.7	18	0.1631	0.7	1.3	686.7005	3	18.9634	P04441|HG2A_MOUSE:Q545Y5|Q545Y5_MOUSE:Q3			0 0 2 2 0 0 0 0 0 (	AKPVSQMRMATI	DB Search	4330	AKPVSQMRMATI	3
10	KYTYGKPVPGHVK	40.12	1472.814	13	69.2	13	-1.611	0.75	-1.6	491.9456	3	2.3405	P28665|MUG1_MOUSE			0 0 12 7 2 15 8 8	KYTYGKPVPGHV	DB Search	1380	KYTYGKPVPGHV	3
11	ASGPPVSELITK	40.12	1197.661	12	66.7	12	-0.1532	0.58	-0.9	599.8384	2	16.438	P15864|H12_MOUSE:Q149Z9|Q149Z9_MOUSE:P432			5 18 18 98 11 11	ASGPPVSELITK	DB Search	849	ASGPPVSELITK	3
12	LHTKGALPLDTVTFYKVIPKSKFVLVKF	40.12	3188.873	28	14.3	28	-0.5306	0.62	4.6	798.231	4	23.6837	P57759|ERP29_MOUSE:A8C1V9|A8C1V9_MOUSE			0 0 0 1 0 0 0 1 1	LHTKGALPLDTV1	DB Search	944	LHTKGALPLDTV1	3
13	KPVSQMRMATPLLM(+15.99)RPM	38.73	2002.035	17	41.2	17	0.4206	0.6	-2.1	501.5161	4	16.8461	P04441|HG2A_M(	Oxidation (M)	M14:Oxidation (M	0 0 0 0 0 0 0 0 2 1	KPVSQMRMATPI	DB Search	28000	KPVSQMRMATPI	3
14	ALEEQLQQIRAE	40.12	1426.742	12	66.7	12	0.2418	0.77	2.6	714.3816	2	16.275	P02535|K1C10_MOUSE:A2A513|A2A513_MOUSE			0 0 42 19 19 67 8	ALEEQLQQIRAE	DB Search	795	ALEEQLQQIRAE	3
15	SQVFSTAADGQTQVEIK	40.12	1807.895	17	64.7	17	-0.3677	0.58	2.3	904.9591	2	15.5771	P38647|HSPA9_MOUSE			0 0 0 8 6 8 8 13 1	SQVFSTAADGQT	DB Search	330	SQVFSTAADGQT	3
16	VAIFARGPQAHLVHGVQ	40.12	1798.995	17	41.2	17	0.4095	0.31	1.4	600.6747	3	15.2954	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:(			5 52 0 0 0 0 0 0 0	VAIFARGPQAHL\	DB Search	19300	VAIFARGPQAHL\	3
17	SLDLDSIIAEVK	40.11	1301.708	12	66.7	12	-0.0073	0.55	-0.7	651.8622	2	25.9394	Q0VDR7|Q0VDR7_MOUSE:Q9Z331|K2C6B_MOUSE:			0 0 42 42 47 13 1	SLDLDSIIAEVK	DB Search	110	SLDLDSIIAEVK	3
18	KESYSVYVYK	40.12	1264.634	10	50	10	-0.0856	0.75	0.5	633.3261	2	11.7107	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:(			3 3 2 1 1 1 3 3 1 1	KESYSVYVYK	DB Search	104	KESYSVYVYK	3
19	GGLPDYSAPNPIKVTH	40.12	1664.852	16	12.5	16	-0.4741	0.21	2.2	833.4372	2	16.2337	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			0 0 0 0 0 1 2 2 0 (	GGLPDYSAPNPII	DB Search	962	GGLPDYSAPNPII	3
20	FPYVTPAPHEPVKT	40.12	1581.819	14	35.7	14	-0.1849	0.74	0.6	791.9192	2	15.0503	Q9D074|MGRN1_MOUSE			5 1 1 3 5 1 1 0 0 1	FPYVTPAPHEPVI	DB Search	1120	FPYVTPAPHEPVI	3
21	APAAAATTAAPAAAAAPAK	40.12	1562.842	19	31.6	19	0.1681	0.65	7.7	782.4359	2	10.3437	Q5M8R8|Q5M8R8_MOUSE:P14869|RLA0_MOUSE:Q			0 0 0 0 2 3 6 5 5 8	APAAAATTAAPA/	DB Search	294	APAAAATTAAPA/	3
22	QPSTSSLAAPTVEAAASAPA	39.94	1825.906	20	30	20	-0.3417	0.64	1.8	913.9639	2	17.7114	A0AAQ4VMX1|A0AAQ4VMX1_MOUSE:A0AAQ4VMV3			0 0 0 0 0 3 0 0 9 1	QPSTSSLAAPTVI	DB Search	4420	QPSTSSLAAPTVI	3
23	HNYEGPETHTSL	40.12	1383.606	12	41.7	12	-0.096	0.59	3.4	692.814	2	9.4937	P14483|HB2A_MOUSE:Q5XQL0|Q5XQL0_MOUSE:Q5			0 0 0 0 2 0 0 1 2 4	HNYEGPETHTSL	DB Search	1040	HNYEGPETHTSL	3
24	YVTQFHPPHIEIQMLK	39.71	1980.029	16	31.2	16	0.0579	0.42	3.8	661.0195	3	20.421	Q9D239|Q9D239_MOUSE:P01887|B2MG_MOUSE			5 11 0 1 5 5 2 0 0	YVTQFHPPHIEIQ	DB Search	1290	YVTQFHPPHIEIQ	3
25	NPPSYYTQPVPVPN	39.56	1571.762	14	35.7	14	0.1962	0.6	4.8	786.892	2	18.1479	Q9JLJ0|LITAF_MOUSE:E0CYR5|E0CYR5_MOUSE			0 0 0 0 1 5 2 3 1 1	NPPSYYTQPVPV	DB Search	976	NPPSYYTQPVPV	3
26	YQSKYEEL	38.04	1058.492	8	100	8	-1.2652	0.73	0.4	530.2535	2	11.3806	P04104|K2C1_MOUSE			5 12 6 5 4 13 19 5	YQSKYEEL	DB Search	1020	YQSKYEEL	3
27	ALLLLLLLL	39.87	993.7202	9	11.1	9	-7.1517	0	1.6	994.7313	1	20.0418	G3UXY8|G3UXY8_MOUSE:Q9JJS0|SCUB2_MOUSE:			5 0 0 0 0 0 0 0 0	ALLLLLLLL	DB Search	112	ALLLLLLLL	3
28	DTIEFRGPNGLLVYQG	40.12	1777.9	16	75	16	-0.1877	0.76	6.1	889.9647	2	22.809	F2Z456|F2Z456_MOUSE:Q9DCN2|NB5R3_MOUSE:(			0 0 3 3 4 4 4 1 1 5	DTIEFRGPNGLL\	DB Search	751	DTIEFRGPNGLL\	3
29	APMYYRGAQAAIVV	40.1	1508.781	14	42.9	14	-0.0948	0.68	-1.7	755.3983	2	18.6251	Q3TCT9|Q3TCT9_MOUSE:P61021|RAB5B_MOUSE:(			0 0 0 0 0 0 1 1 2 1	APMYYRGAQAAI	DB Search	1230	APMYYRGAQAAI	3
30	TFSRTTKAVVVKKIETRDGKLVS	40.11	2562.486	23	0	23	-2.4155	0.35	6.1	641.6341	4	11.4719	P11679|K2C8_MOUSE			0 0 0 0 0 0 1 1 0 (	TFSRTTKAVVVKI	DB Search	603	TFSRTTKAVVVKI	3
31	AVFPSIVGRPR	40.1	1197.698	11	18.2	11	-0.3674	0.7	-2.7	599.8561	2	16.0117	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:A0.			0 0 14 3 0 0 1 0 0	AVFPSIVGRPR	DB Search	2150	AVFPSIVGRPR	3
32	SGGTTM(+15.99)YPGLADR	39.71	1340.603	13	38.5	13	-0.6219	0.9	3.2	671.3109	2	11.1442	Q9QZ83|Q9QZ83	Oxidation (M)	M6:Oxidation (M):	1 0 0 0 22 26 58 9	SGGTTM(+15.99)	DB Search	541	SGGTTMYPGLAD	3
33	GKFMKPGKVVLVLAGRYSGRKAVIVKNID	39.71	3142.853	29	3.4	29	-2.8076	0.27	3.9	786.7236	4	17.5508	P61358|RL27_MOUSE:Q5BLJ9|Q5BLJ9_MOUSE			0 0 0 0 0 0 0 0 0 (	GKFMKPGKVVLV	DB Search	22000	GKFMKPGKVVLV	3
34	HVPTLQVLRPGLVVVH	40.12	1763.057	16	6.2	16	0.0677	0.14	-6.6	588.6904	3	19.9678	D3Z7S4|D3Z7S4_MOUSE:Q9D3D9|ATPD_MOUSE:Q			0 0 0 0 0 1 1 2 1 (	HVPTLQVLRPGL\	DB Search	1180	HVPTLQVLRPGL\	3
35	VRDMRQTVAVGVIKAVDKKAAGAGKVTK	40.12	2895.68	28	21.4	28	-2.9454	0.49	7.3	580.1489	5	14.3495	Q58E64|Q58E64_MOUSE:Q3UZQ3|Q3UZQ3_MOUSE			0 0 0 0 0 0 0 0 0 (	VRDMRQTVAVG\	DB Search	234	VRDMRQTVAVG\	3
36	YLNIYVPAHAHEGSN	40.12	1683.801	15	46.7	15	-0.9051	0.7	2.1	842.9113	2	15.1339	Q8BK48|EST2E_MOUSE			0 0 2 14 14 14 2 2	YLNIYVPAHAHE(	DB Search	562	YLNIYVPAHAHE(	3
37	TLM(+15.99)ALGSLAVTK	39.35	1219.685	12	41.7	12	-0.2265	0.65	-5.2	610.8478	2	18.2836	P37804|TAGL_M(	Oxidation (M)	M3:Oxidation (M):	0 0 88 48 48 21 0	TLM(+15.99)ALG	DB Search	115	TLMALGSLAVTK	3
38	GPDGRFVMGPTVAPSQEKL	40.12	1985.004	19	36.8	19	0.3962	0.89	0.5	662.6772	3	17.388	Q05BQ1|TUTLA_MOUSE			0 0 0 0 0 0 0 29 4	GPDGRFVMGPT\	DB Search	531	GPDGRFVMGPT\	3
39	DARSYTAAVANRAK	39.7	1492.775	14	50	14	0.7225	0.82	-0.1	498.5988	3	9.604	Q91XS1|MTMR4_MOUSE:Q6PE02|Q6PE02_MOUSE			0 0 0 0 11 11 58 5	DARSYTAAVANR	DB Search	1010	DARSYTAAVANR	3
40	D(+42.01)DDIAALVVDNGSGMCKA	40.12	1834.808	18	72.2	18	-1.6082	0.74	2.7	918.4157	2	24.5805	E9Q5F4|E9Q5F4	Acetylation (N-ter	D1:Acetylation (N	0 0 2 22 50 91 52	D(+42.01)DDIAAL	DB Search	62	DDDIAALVVDNG	3
41	FPKPPSYNVATTLPSYDEA	40.12	2096.01	19	10.5	19	-0.3124	0.85	6	1049.021	2	20.3572	A0A494BAA4|A0A494BAA4_MOUSE:Q8R0W6|NFIP1			0 0 0 0 0 0 0 0 0 1	FPKPPSYNVATTI	DB Search	1170	FPKPPSYNVATTI	3
42	VSSVEAPSVSPAR	39.53	1284.667	13	53.8	13	0.2524	0.88	0.3	643.3411	2	11.4568	Q8BUJ9|LRP12_MOUSE			5 4 3 3 34 38 1 1	VSSVEAPSVSPAI	DB Search	604	VSSVEAPSVSPAI	3
43	EITALAPSTM(+15.99)K	39.78	1176.606	11	45.5	11	0.6739	0.8	-0.9	589.3112	2	12.4084	P63260|ACTG_M(	Oxidation (M)	M10:Oxidation (M	0 0 19 19 69 96 0	EITALAPSTM(+1!	DB Search	3400	EITALAPSTMK	3
44	LGDLYEEEMR	34.5	1253.56	10	70	10	-1.0493	0.63	1.6	627.7882	2	15.3246	P20152|VIME_MOUSE:A4IF59|A4IF59_MOUSE:Q3TF			5 22 22 29 75 12	LGDLYEEEMR	DB Search	168	LGDLYEEEMR	3
45	GGLPDYSAPNPIKVTHR	40.12	1820.953	17	5.9	17	-0.6255	0.41	-0.3	607.993	3	14.6301	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			0 0 0 14 0 0 1 0 0	GGLPDYSAPNPII	DB Search	4080	GGLPDYSAPNPII	3
46	KELEEQLGPVAEETRA	39.7	1797.911	16	50	16	-0.5855	0.86	-6.2	600.3072	3	14.2852	G3UZM8|G3UZM8_MOUSE:G3UWN5|G3UWN5_MOU			0 0 0 0 2 2 15 48	KELEEQLGPVAE	DB Search	1040	KELEEQLGPVAE	3
47	YLNIYVPAHAHEGSNL	40.08	1796.885	16	31.2	16	-0.7025	0.7	0.7	899.4523	2	17.2466	Q8BK48|EST2E_MOUSE			0 0 2 4 5 7 0 0 2 (	YLNIYVPAHAHE(	DB Search	335	YLNIYVPAHAHE(	3
48	DLYANTVLSGGTTMYPGLADR	40.12	2214.063	21	42.9	21	-0.2222	0.57	6.9	1108.049	2	22.8085	Q9QZ83|Q9QZ83_MOUSE			0 0 0 1 1 1 8 6 7 3	DLYANTVLSGGT	DB Search	610	DLYANTVLSGGT	3
49	GMAFRVPTPNVSVVD	40.12	1587.808	15	80	15	1.1026	0.48	6.1	794.9179	2	22.0558	S4R257|S4R257_MOUSE:Q3V2I5|Q3V2I5_MOUSE:S			0 0 0 3 2 11 4 4 5	GMAFRVPTPNVS	DB Search	716	GMAFRVPTPNVS	3
50	VSHDYKGSTSHSLPY	32.51	1676.779	15	13.3	15	0.1291	0.39	1.1	839.3999	2	9.4573	E9Q1Y3|E9Q1Y3_MOUSE:E9Q414|APOB_MOUSE			0 0 0 0 0 0 0 0 0 (	VSHDYKGSTSHS	DB Search	1450	VSHDYKGSTSHS	3
51	YVTQFHPPHIEIQML	40.12	1851.934	15	26.7	15	0.3769	0.62	-0.4	926.9762	2	23.4417	Q9D239|Q9D239_MOUSE:P01887|B2MG_MOUSE:Q:			0 0 0 0 0 1 0 0 0 1	YVTQFHPPHIEIQ	DB Search	10900	YVTQFHPPHIEIQ	3
52	ESEPYTFSHPNKGEIG	40.12	1790.811	16	6.2	16	-0.7317	0.46	3.2	896.4178	2	12.8375	Q5U462|CDCP1_MOUSE			0 0 1 0 0 0 0 0 0 (	ESEPYTFSHPNK	DB Search	717	ESEPYTFSHPNK	3
53	GYSFTTTAER	39.32	1131.52	10	50	10	0.0585	0.8	1.2	566.7691	2	11.8015	P63260|ACTG_MOUSE:E9Q5F4|E9Q5F4_MOUSE:Q6			0 0 52 52 41 9 3 (	GYSFTTTAER	DB Search	821	GYSFTTTAER	3
54	AVFPSIVGR	38.81	944.5443	9	44.4	9	0.1893	0.89	-1.7	473.2798	2	18.4342	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:A0.			2 2 39 38 1 1 0 0	AVFPSIVGR	DB Search	2020	AVFPSIVGR	3
55	IGMLGILVKTGKYKAA	37.14	1661.99	16	37.5	16	0.1463	0.34	3.5	555.0059	3	18.9212	Q3UGR5|HDHD2_MOUSE			5 0 0 8 0 0 14 5 5	IGMLGILVKTGKY	DB Search	96.7	IGMLGILVKTGKY	1
56	LVRYTQKAPQVSTPTLV	39.68	1900.078	17	11.8	17	0.1379	0.42	3.2	634.3687	3	16.3406	Q546G4|Q546G4_MOUSE:P07724|ALBU_MOUSE			0 0 0 0 0 1 1 1 0 (	LVRYTQKAPQVS	DB Search	47.5	LVRYTQKAPQVS	2
57	DNNTLVFIVDVKANKHQIKQAVKKLY	39.96	3025.708	26	15.4	26	-3.5963	0.22	-3.5	757.4333	4	18.402	Q91YK6|Q91YK6_MOUSE:P62751|RL23A_MOUSE:Q			0 0 0 58 91 54 8 (	DNNTLVFIVDVK/	DB Search	372	DNNTLVFIVDVK/	1
58	ASLVYENASAIMAHES	39.71	1691.783	16	68.8	16	-1.0415	0.58	2.2	846.9003	2	19.2061	E9Q0N2|PTPRH_MOUSE			0 0 0 24 42 42 25	ASLVYENASAIM/	DB Search	184	ASLVYENASAIM/	2
59	KPVSQMRM(+15.99)ATPLLMRPM(+15.99)	26.07	2018.03	17	5.9	17	-0.0326	0.31	1.2	673.6847	3	14.6346	P04441|HG2A_M(	Oxidation (M);Oxi(	M8:Oxidation (M):	3 1 0 0 0 0 0 0 0 (	KPVSQMRM(+15	DB Search	805	KPVSQMRMATPI	1
60	VAPEEHPV	30.66	876.4341	8	75	8	-2.2448	0.72	1.8	439.2251	2	6.1777	P63260|ACTG_MOUSE:E9Q5F4|E9Q5F4_MOUSE:G:			5 8 6 6 2 2 0 0	VAPEEHPV	DB Search	85.7	VAPEEHPV	2
61	DARSYAAAVANRAK	35.22	1462.764	14	35.7	14	0.4239	0.84	3.5	488.597	3	11.4794	Q8K296|MTMR3_MOUSE:R4GML8|R4GML8_MOUSE			0 0 0 0 0 0 0 76 73	DARSYAAAVANF	DB Search	62.2	DARSYAAAVANF	1
62	GFGSAGGSNTFSRTTKAVVVKKIETRDGKLVS	39.16	3296.784	32	6.2	32	-6.2169	NA	1.2	660.3665	5	14.7285	P11679|K2C8_MOUSE			0 0 0 1 58 11 0 0	GFGSAGGSNTFS	DB Search	7440	GFGSAGGSNTFS	2
63	IIGGHEVKPHSRPYMAL	39.04	1904.009	17	41.2	17	0.9464	0.48	5.3	635.6803	3	12.7682	Q3TZH4|Q3TZH4_MOUSE:Q3TIP3|Q3TIP3_MOUSE:(			5 46 5 5 3 1 1 1 3	IIGGHEVKPHSRF	DB Search	3760	IIGGHEVKPHSRF	1
64	VQFLEQQNK	35.38	1132.588	9	77.8	9	0.1136	0.57	0.5	567.3014	2	12.2762	A0A2R8VHP3|A0A2R8VHP3_MOUSE:Q6IFZ8|Q6IFZ8			4 4 29 26 3 3 2 0	VQFLEQQNK	DB Search	170	VQFLEQQNK	2
65	SSGAHGEEGSARMWKALTY	31.05	2036.937	19	10.5	19	-0.3517	0.2	3	679.9885	3	15.3585	Q9DCW5|Q9DCW5_MOUSE:P43024|CX6A1_MOUSE			0 0 0 0 0 0 0 0 0 (	SSGAHGEEGSAI	DB Search	455	SSGAHGEEGSAI	1
66	KPVSQM(+15.99)RMATPLLMRPM	27	2002.035	17	5.9	17	-0.7031	0.38	-0.9	668.3516	3	16.3164	P04441|HG2A_M(	Oxidation (M)	M6:Oxidation (M):	5 1 0 0 0 0 0 0 0 (	KPVSQM(+15.99)	DB Search	6790	KPVSQMRMATPI	2
67	LAPMYYRGAQAAIVVYD	39.7	1899.955	17	47.1	17	-0.9711	0.35	7	950.9916	2	20.8116	Q3TCT9|Q3TCT9_MOUSE:P61021|RAB5B_MOUSE:(			0 0 0 0 0 2 2 2 2 1	LAPMYYRGAQA/	DB Search	121	LAPMYYRGAQA/	2
68	TFSRTTKAVVVKKIETRDGKLVSESS	26.58	2865.592	26	0	26	-2.8796	0.52	4.1	717.4083	4	11.4749	P11679|K2C8_MOUSE			0 0 0 0 0 0 0 0 0 (	TFSRTTKAVVVKI	DB Search	560	TFSRTTKAVVVKI	1
69	PKGKKAKGKKVAPAPAVVKKQEAKKVVNPLFE	40.1	3412.081	32	6.2	32	-5.2287	NA	4.3	683.428	5	9.66	Q5EBG5|Q5EBG5_MOUSE:Q80UT7|Q80UT7_MOUSI			0 0 0 0 0 0 0 0 0 (	PKGKKAKGKKVA	DB Search	3220	PKGKKAKGKKVA	2
70	ATKKKKKKK	23.74	1086.76	9	22.2	9	12.271	0	-3	1087.764	1	13.6768	Q9ESX4|ZCC17_MOUSE:Q3TG23|Q3TG23_MOUSE			5 2 0 0 0 0 0 0 0	ATKKKKKKK	DB Search	94.4	ATKKKKKKK	1
71	LVILEGELER	38.83	1169.666	10	70	10	-0.1004	0.67	0.2	585.8402	2	19.3969	Q9D1R6|Q9D1R6_MOUSE:P58774|TPM2_MOUSE:Q:			5 19 96 96 49 3 2	LVILEGELER	DB Search	316	LVILEGELER	2
72	A(+42.01)NTALSGGTTM(+15.99)YPGIADR	39.04	1852.863	18	50	18	-0.9449	0.75	7.2	927.4452	2	16.4759	Q3UAA9|Q3UAA9	Acetylation (N-ter	A1:Acetylation (N-	0 0 0 3 11 12 2 2	A(+42.01)NTALS(	DB Search	53.4	ANTALSGGTTMY	1
73	SM(+15.99)DNNRSLDL	36.36	1179.519	10	60	10	-0.4882	0.52	-1.7	590.7658	2	11.8222	Q4L0E7|Q4L0E7	Oxidation (M)	M2:Oxidation (M):	0 0 15 13 0 0 2 16	SM(+15.99)DNNF	DB Search	122	SMDNNRSLDL	1
74	DLTDYLM(+15.99)K	36.6	1013.474	8	50	8	-0.5423	0.56	1	507.7448	2	17.5011	P63260|ACTG_M(	Oxidation (M)	M7:Oxidation (M):	0 0 35 18 7 4 0 0	DLTDYLM(+15.99	DB Search	763	DLTDYLMK	2
75	ENIWKAPEPVEIRE	40.12	1708.878	14	35.7	14	0.1379	0.55	-1.8	570.6337	3	17.7525	Q3TAN0|Q3TAN0_MOUSE:A2AKS7|A2AKS7_MOUSE			0 0 0 4 1 7 0 0 33	ENIWKAPEPVEIF	DB Search	205	ENIWKAPEPVEIF	2
76	L(+42.01)LLLLLPPAL	26.91	1116.752	10	0	10	0.6257	0.24	14.9	559.3917	2	28.8149	A2A5D9|A2A5D9	Acetylation (N-ter	L1:Acetylation (N-	0 0 0 0 0 0 0 0 0 (	L(+42.01)LLLLPI	DB Search	749	LLLLLLPPAL	1
77	RLWWLDLK	36.93	1128.644	8	62.5	8	-0.3782	0.9	-1.3	565.3287	2	23.1577	Q91X72|HEMO_MOUSE			0 0 1 2 9 10 12 5	RLWWLDLK	DB Search	157	RLWWLDLK	2
78	VKVDPEIQ	29.83	926.5073	8	62.5	8	0.024	0.75	-0.8	464.2606	2	11.4182	Q3TTY5|K22E_MOUSE:B2RTP7|B2RTP7_MOUSE			0 0 0 6 6 9 39 5	VKVDPEIQ	DB Search	503	VKVDPEIQ	1
79	VAPEEHPTLLTEAPLNPK	39.66	1955.036	18	16.7	18	0.0395	0.56	1.2	652.6868	3	17.2968	Q3UJ36|Q3UJ36_MOUSE:A0A494B9T3|A0A494B9T3			0 0 0 0 0 0 0 0 0 1	VAPEEHPTLLTE/	DB Search	916	VAPEEHPTLLTE/	2
80	DMRQTVAVGVIKAVDKKAAGAGKVTKSAQKAQK	39.71	3381.924	33	3	33	-1.8835	NA	11.3	677.3997	5	14.3481	Q58E64|Q58E64_MOUSE:Q3UZQ3|Q3UZQ3_MOUSE			0 0 0 0 1 1 1 0 0 (	DMRQTVAVGVIK	DB Search	254	DMRQTVAVGVIK	1
81	ILVRYTQKAPQVSTPTLV	26.81	2013.162	18	11.1	18	0.3533	0.26	4	672.064	3	18.1649	Q546G4|Q546G4_MOUSE:P07724|ALBU_MOUSE			0 0 0 0 0 0 0 1 0 (	ILVRYTQKAPQV!	DB Search	142	ILVRYTQKAPQV!	1
82	AALRPLVKPKIVKKRTKKFIRHQSDRYVKIKRN	39.04	4014.48	33	6.1	33	-8.1764	NA	10.3	670.0942	6	10.2302	Q5PR09|Q5PR09_MOUSE:P62911|RL32_MOUSE			0 0 0 0 0 0 1 3 0 2	AALRPLVKPKIVK	DB Search	792	AALRPLVKPKIVK	1
83	KRSRKESYSVYVYKVLKQVHPD	39.71	2708.476	22	22.7	22	0.0014	0.42	3.7	678.1289	4	16.1453	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:(			0 0 0 0 0 0 0 0 0 (	KRSRKESYSVYV	DB Search	1210	KRSRKESYSVYV	2
84	AMDYWGQGTSVTVSS	40.12	1587.688	15	20	15	-0.4032	0.55	3.1	794.8554	2	19.3786	X5J5A3|X5J5A3_MOUSE:X5J523|X5J523_MOUSE:K7			0 0 0 2 4 0 0 2 0 (	AMDYWGQGTS\	DB Search	216	AMDYWGQGTS\	2
85	IPIRWTAPEAISYRK	40.12	1800.005	15	53.3	15	0.264	0.58	2.2	601.0115	3	16.9956	Q03145|EPHA2_MOUSE			5 0 0 0 1 2 2 7 7 9	IPIRWTAPEAISY	DB Search	175	IPIRWTAPEAISY	1
86	RVAPEEHPVL	27.02	1145.619	10	30	10	-0.5194	0.82	1.2	573.8176	2	11.0625	P63260|ACTG_MOUSE:E9Q5F4|E9Q5F4_MOUSE:G:			0 0 0 0 0 6 16 0 0	RVAPEEHPVL	DB Search	271	RVAPEEHPVL	1
87	FLEQQNQVLQTK	40.12	1474.778	12	83.3	12	0.0066	0.71	0.8	738.3986	2	14.2332	Q6NXH9|K2C73_MOUSE:P04104|K2C1_MOUSE:Q08			5 30 44 35 35 19	FLEQQNQVLQTK	DB Search	114	FLEQQNQVLQTK	2
88	DLPSPIER	26.8	925.4869	8	25	8	-0.1954	0.76	-1.9	463.7498	2	14.2673	A0A4V6JA63|A0A4V6JA63_MOUSE:Q569X1|Q569X1			0 0 32 32 1 1 0 0	DLPSPIER	DB Search	212	DLPSPIER	1
89	GEDVAIFARGPQAHLVHGVQ	40.1	2100.086	20	20	20	-0.6966	0.51	2	701.0391	3	16.9922	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:(			0 0 0 1 61 3 0 0 0	GEDVAIFARGPQ	DB Search	226	GEDVAIFARGPQ	2
90	GPDGRFVM(+15.99)GPTVAPSQEK	39.24	1887.915	18	33.3	18	-0.1741	0.68	-0.7	630.3118	3	12.1213	Q05BQ1|TUTLA_I	Oxidation (M)	M8:Oxidation (M):	0 0 0 0 0 0 0 2 8 8	GPDGRFVM(+15.	DB Search	223	GPDGRFVMGPT\	1
91	TRLEQEIATYR	39.55	1378.721	11	0	11	0.297	0.53	4.8	690.3708	2	13.549	Q3SYP5|Q3SYP5_MOUSE:Q9QWL7|K1C17_MOUSE			0 0 0 0 0 0 0 0 0 (	TRLEQEIATYR	DB Search	213	TRLEQEIATYR	2
92	LSDKHLNWIKKIMKG	39.04	1810.029	15	26.7	15	-0.3164	0.32	1.4	604.351	3	16.4539	P11032|GRAA_MOUSE:Q3UK79|Q3UK79_MOUSE:Q:			5 2 0 0 0 0 1 0 1 1	LSDKHLNWIKKIN	DB Search	351	LSDKHLNWIKKIN	1
93	KTFRIKRF	27.04	1094.671	8	37.5	8	-0.1944	0.01	-2.7	365.8967	3	8.1142	Q9CQD0|RL39L_MOUSE:P62892|RL39_MOUSE:Q50			5 14 1 1 3 1 0 0	KTFRIKRF	DB Search	790	KTFRIKRF	1
94	IVDVKANKHQIKQAVKKLY	39.04	2222.326	19	15.8	19	-0.3094	0.64	1.9	556.5899	4	11.2868	Q91YK6|Q91YK6_MOUSE:P62751|RL23A_MOUSE:Q			5 59 0 0 0 0 0 0 0	IVDVKANKHQIK(	DB Search	231	IVDVKANKHQIK(	1
95	KPVSQMRMATPLLMRP	27.71	1854.999	16	18.8	16	0.1419	0.15	6.8	619.3446	3	17.2631	P04441|HG2A_MOUSE:Q545Y5|Q545Y5_MOUSE:Q3			5 8 7 0 0 0 0 0 0 (	KPVSQMRMATPI	DB Search	732	KPVSQMRMATPI	1
96	STGDVNVEM(+15.99)NAAPGVDLT	39.95	1804.815	18	22.2	18	-0.2694	0.87	-3.3	903.4139	2	17.6402	P02535|K1C10_M	Oxidation (M)	M9:Oxidation (M):	0 0 0 0 0 1 4 0 0 (	STGDVNVEM(+1!	DB Search	223	STGDVNVEMNA/	1
97	LALKQSLEAS	36.7	1058.597	10	90	10	0.398	0.7	-0.2	530.3057	2	13.5481	P02535|K1C10_MOUSE:A2A513|A2A513_MOUSE			5 14 24 0 10 17 5	LALKQSLEAS	DB Search	108	LALKQSLEAS	1
98	NDKKKGPKVTVKVY	31.48	1602.946	14	0	14	0.9234	0.36	-0.2	535.3224	3	3.9334	Q9DCY1|Q9DCY1_MOUSE:Q6ZQM2|Q6ZQM2_MOU			0 0 0 0 1 0 0 0 0 1	NDKKKGPKVTVK	DB Search	474	NDKKKGPKVTVK	1
99	M(+15.99)ELQEIQLK	27.03	1146.596	9	33.3	9	-0.999	0.54	-0.2	574.3049	2	14.6442	Q8K0Z5|Q8K0Z5	Oxidation (M)	M1:Oxidation (M):	0 0 54 22 17 0 0 (	M(+15.99)ELQEI(	DB Search	101	MELQEIQLK	2
100	VARNPPGFAF	35.03	1074.561	10	60	10	-0.3674	0.62	-2.2	538.2866	2	17.7518	Q9D6W4|Q9D6W4_MOUSE:P84104|SRSF3_MOUSE			3 2 1 1 6 0 0 46 4	VARNPPGFAF	DB Search	198	VARNPPGFAF	1
101	GGEDVAIFARGPQAHLVHGVQ	39.66	2157.108	21	19	21	-0.7916	0.3	4	720.0461	3	17.2001	F8VPQ6|F8VPQ6_MOUSE:P24822|PPBI_MOUSE:Q0\			0 0 0 0 7 44 44 0	GGEDVAIFARGP	DB Search	180	GGEDVAIFARGP	1
102	YVRLAPDY	31.96	995.5076	8	87.5	8	-0.5096	0.88	-1.7	498.7602	2	14.8931	Q91YK6|Q91YK6_MOUSE:P62751|RL23A_MOUSE:Q			5 16 0 4 17 2 2 5	YVRLAPDY	DB Search	852	YVRLAPDY	1
103	LVRYTQKAPQVSTPT	28.01	1687.926	15	0	15	0.3013	0.35	-1.6	563.6483	3	11.4226	Q546G4|Q546G4_MOUSE:P07724|ALBU_MOUSE			0 0 0 0 0 0 0 0 0 (	LVRYTQKAPQVS	DB Search	145	LVRYTQKAPQVS	1
104	IEKVIPSTANSN	40.08	1271.672	12	50	12	0.0927	0.7	-3.9	636.8424	2	11.0378	E9Q7P9|CDHR2_MOUSE			4 0 0 6 27 0 0 3 7	IEKVIPSTANSN	DB Search	63.3	IEKVIPSTANSN	2
105	LHVDPENFR	38.28	1125.557	9	55.6	9	0.1327	0.67	-1.3	563.7849	2	13.0391	B1Q450|B1Q450_MOUSE:A8DV41|A8DV41_MOUSE:			2 2 54 54 0 0 2 0	LHVDPENFR	DB Search	894	LHVDPENFR	2
106	EEAENNLAAFR	40.1	1262.589	11	54.5	11	-0.9554	0.76	3.7	632.3057	2	14.007	Q3V1K9|Q3V1K9_MOUSE:P31001|DESM_MOUSE:Q:			0 0 15 15 67 37 3	EEAENNLAAFR	DB Search	83.5	EEAENNLAAFR	1
107	GFVKVVKNKAYFKRYQVRFR	39.01	2532.459	20	30	20	0.1221	0.24	2.8	507.5006	5	13.7212	Q58EU6|Q58EU6_MOUSE:P47962|RL5_MOUSE:Q3T			0 0 0 61 3 0 54 54	GFVKVVKNKAYF	DB Search	228	GFVKVVKNKAYF	1
108	GSPPRAFTKVSSFLSWIKKTMKS	27.49	2582.404	23	8.7	23	-1.0776	0.5	-0.8	646.6079	4	24.5604	Q3TZH4|Q3TZH4_MOUSE:Q3TIP3|Q3TIP3_MOUSE:(			0 0 0 0 0 0 0 2 0 (	GSPPRAFTKVSS	DB Search	78.7	GSPPRAFTKVSS	1
109	ASLVYENASAIMAHESE	40.12	1820.825	17	58.8	17	-0.7431	0.59	-0.7	911.4213	2	19.3183	E9Q0N2|PTPRH_MOUSE			0 0 0 3 7 6 3 3 9 5	ASLVYENASAIM/	DB Search	117	ASLVYENASAIM/	2
110	S(+42.01)DAAVDTSSEITTK	39.71	1465.678	14	64.3	14	-0.0209	0.77	4.6	733.8499	2	13.6699	Q0VGU2|Q0VGU2	Acetylation (N-ter	S1:Acetylation (N-	0 0 3 53 52 41 31	S(+42.01)DAAVD	DB Search	160	SDAAVDTSSEITT	2
111	GDTEGRLEVVTDPTTNAGYVK	40.09	2221.086	21	42.9	21	-0.8317	0.67	-0.9	741.3704	3	15.3548	Q3TAN0|Q3TAN0_MOUSE:A2AKS7|A2AKS7_MOUSE			0 0 0 0 0 0 0 2 11	GDTEGRLEVVTD	DB Search	604	GDTEGRLEVVTD	2
112	FIEKVIPSTANSNNL	40.12	1645.868	15	46.7	15	1.0212	0.73	3	823.9454	2	18.1871	E9Q7P9|CDHR2_MOUSE			0 0 0 0 3 26 0 0 4	FIEKVIPSTANSNI	DB Search	44.9	FIEKVIPSTANSNI	1
113	VAPEEHPVL	36.04	989.5182	9	44.4	9	-0.8286	0.72	0.4	495.7666	2	12.9027	P63260|ACTG_MOUSE:E9Q5F4|E9Q5F4_MOUSE:G:			5 5 9 6 0 0 0 0 0	VAPEEHPVL	DB Search	42.1	VAPEEHPVL	1
114	GFVKVVKNKAYFKRY	39.04	1846.062	15	46.7	15	1.1486	0.73	1.6	462.5234	4	11.4797	Q58EU6|Q58EU6_MOUSE:P47962|RL5_MOUSE:Q3T			0 0 0 0 0 32 9 9 9	GFVKVVKNKAYF	DB Search	280	GFVKVVKNKAYF	1
115	YVRYDSDVGEHRAVTELGRPDAEY	23.83	2796.31	24	8.3	24	-0.6363	0.58	2.6	700.0867	4	14.055	Q7YQ02|Q7YQ02_MOUSE:O19455|O19455_MOUSE:			0 0 0 0 0 0 0 0 0 (	YVRYDSDVGEHF	DB Search	361	YVRYDSDVGEHF	1

	H2Ab1_ff-AAD																				
	Peptide	X.10LgP	Mass	Tag.Length	CAA....	Length	Delta.RT	MS2.Correlation	ppm	m.z	z	RT	Accession	PTM	AScore	ositional.Confidenc	tag...0.0..	Found.By	Area.Sample.1	Clean_Sequence	share
1	KPVSQMRMATPLLMRPM	40.12	1986.04	17	11.8	17	0.0284	0.24	-1.6	663.0211	3	18.6677	P04441|HG2A_MOUSE:Q545Y5|Q545Y5_MOUSE:Q3			5 2 1 0 0 0 0 0 0 (	KPVSQMRMATPL	DB Search	47000	KPVSQMRMATPL	3
2	VAIFARGPQAHLVHG	40.12	1571.868	15	26.7	15	0.3915	0.35	-0.2	786.9432	2	14.4539	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:(			0 0 0 0 0 0 0 0 0 (	VAIFARGPQAHL\	DB Search	30900	VAIFARGPQAHL\	3
4	LPPYDDATAVPSTAKEPPPP	40.12	2062.026	20	50	20	-0.1034	0.73	-0.2	688.3507	3	16.5699	B2CZK6|B2CZK6_MOUSE:Q91XQ6|LAP4B_MOUSE			0 0 0 0 0 0 0 0 12	LPPYDDATAVPS	DB Search	17800	LPPYDDATAVPS	3
5	LGEYGFQNAILVR	40.12	1478.788	13	84.6	13	0.1735	0.78	4.4	740.4064	2	21.3774	Q546G4|Q546G4_MOUSE:P07724|ALBU_MOUSE			5 8 8 44 27 27 29	LGEYGFQNAILVI	DB Search	17700	LGEYGFQNAILVI	3
6	GKFMKPGKVVLVLAGRYSGRKAVIVKNID	39.71	3142.853	29	3.4	29	-2.8076	0.27	3.9	786.7236	4	17.5508	P61358|RL27_MOUSE:Q5BLJ9|Q5BLJ9_MOUSE			0 0 0 0 0 0 0 0 0 (	GKFMKPGKVVLV	DB Search	16400	GKFMKPGKVVLV	3
7	SVFVAPAVTPVKG	40.12	1270.729	13	53.8	13	0.1448	0.7	-1	636.3724	2	18.0278	P70158|ASM3A_MOUSE			0 0 28 28 69 2 2 3	SVFVAPAVTPVK(	DB Search	14200	SVFVAPAVTPVK(	3
8	SVFVAPAVTPVK	40.12	1213.707	12	58.3	12	0.7595	0.71	1.7	607.8632	2	18.097	P70158|ASM3A_MOUSE			0 0 22 38 89 6 6 6	SVFVAPAVTPVK	DB Search	13900	SVFVAPAVTPVK	3
9	VAIFARGPQAHLVHGVQ	40.12	1798.995	17	41.2	17	0.4095	0.31	1.4	600.6747	3	15.2954	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:(			5 52 0 0 0 0 0 0 0	VAIFARGPQAHL\	DB Search	13800	VAIFARGPQAHL\	3
12	APMYYRGAQAAIVVYD	40.12	1786.871	16	50	16	-0.9109	0.44	3.2	894.4479	2	18.9079	Q3TCT9|Q3TCT9_MOUSE:P61021|RAB5B_MOUSE:(			0 0 0 0 1 1 1 1 3 7	APMYYRGAQAAI	DB Search	9980	APMYYRGAQAAI	3
13	RKIVYEGPELNHAFG	40.12	1728.895	15	73.3	15	0.4843	0.52	-3.8	577.3047	3	15.1327	A0A0R4J0I9|A0A0R4J0I9_MOUSE:Q91ZX7|LRP1_MC			0 0 2 5 9 9 42 13	RKIVYEGPELNH/	DB Search	8760	RKIVYEGPELNH/	3
14	DLYANTVLSGGTTMYPGLADR	40.12	2214.063	21	42.9	21	-0.2222	0.57	6.9	1108.049	2	22.8085	Q9QZ83|Q9QZ83_MOUSE			0 0 0 1 1 1 8 6 7 3	DLYANTVLSGGT	DB Search	8030	DLYANTVLSGGT	3
15	DLYANTVLSGGTTMYPGIADR	40.12	2214.063	21	42.9	21	0.0052	0.58	6.9	1108.049	2	22.8085	P63260|ACTG_MOUSE:Q3U5R4|Q3U5R4_MOUSE:P(			0 0 0 1 1 1 8 6 7 3	DLYANTVLSGGT	DB Search	8030	DLYANTVLSGGT	3
16	DRKIVYEGPELNHAFG	40.12	1843.922	16	43.8	16	0.241	0.45	-3.2	615.6473	3	16.3955	A0A0R4J0I9|A0A0R4J0I9_MOUSE:Q91ZX7|LRP1_MC			0 0 0 0 0 2 4 8 0 (	DRKIVYEGPELNI	DB Search	7720	DRKIVYEGPELNI	3
17	VAIFARGPQAHLVH	39.62	1514.847	14	28.6	14	0.5874	0.49	-0.9	758.4301	2	14.4896	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:(			0 0 0 0 0 0 0 0 0 1	VAIFARGPQAHL\	DB Search	6690	VAIFARGPQAHL\	3
19	YVTQFHPPHIEIQML	40.12	1851.934	15	26.7	15	0.3769	0.62	-0.4	926.9762	2	23.4417	Q9D239|Q9D239_MOUSE:P01887|B2MG_MOUSE:Q3			0 0 0 0 0 1 0 0 0 1	YVTQFHPPHIEIQ	DB Search	5320	YVTQFHPPHIEIQ	3
21	IPGTNMYNTDRANPVLD	40.12	1889.894	17	17.6	17	0.1339	0.37	2	945.9585	2	17.1733	Q8K066|Q8K066_MOUSE:E9Q7P9|CDHR2_MOUSE			5 0 0 0 0 0 0 0 0 (	IPGTNMYNTDRA	DB Search	5100	IPGTNMYNTDRA	3
22	NPPSYYTQPVPVPNAN	40.12	1756.842	16	43.8	16	-0.0804	0.73	1.7	879.4319	2	17.8937	Q9JLJ0|LITAF_MOUSE:E0CYR5|E0CYR5_MOUSE			0 0 0 0 0 3 2 4 2 2	NPPSYYTQPVPV	DB Search	4670	NPPSYYTQPVPV	3
23	AGLQFPVGR	39.28	943.5239	9	77.8	9	-0.4117	0.83	0.6	472.7695	2	17.0545	Q8BFU2|H2A3_MOUSE:A0AUV1|A0AUV1_MOUSE:Q			4 4 7 71 63 2 2 0	AGLQFPVGR	DB Search	4520	AGLQFPVGR	3
24	SPPHVQFTYQQPQPLSVEPR	40.12	2334.176	20	50	20	0.2442	0.55	2.6	779.0697	3	17.6781	B2RXS4|PLXB2_MOUSE			0 0 0 0 1 1 3 3 5 5	SPPHVQFTYQQF	DB Search	4520	SPPHVQFTYQQF	3
25	TVKPKAAKPKTSKPKAAKPKKTAAKKK	40.12	2858.827	27	29.6	27	-0.6836	0.58	-1.4	477.4789	6	1.9044	P43274|H14_MOUSE			0 0 0 6 0 0 0 0 0 (	TVKPKAAKPKTSI	DB Search	4470	TVKPKAAKPKTSI	3
26	FPKPPSYNVATTLPSYDE	40.12	2024.973	18	5.6	18	-0.3534	0.92	3.3	1013.5	2	20.0365	A0A494BAA4|A0A494BAA4_MOUSE:Q8R0W6|NFIP1			0 0 0 0 0 0 0 0 0 1	FPKPPSYNVATTI	DB Search	4350	FPKPPSYNVATTI	3
27	FPYVTPAPHEPVK	40.12	1480.771	13	53.8	13	-0.5944	0.52	-1.5	494.5982	3	14.5551	Q9D074|MGRN1_MOUSE			0 0 0 20 63 2 2 10	FPYVTPAPHEPVI	DB Search	4060	FPYVTPAPHEPVI	3
28	EITALAPSTM(+15.99)K	39.78	1176.606	11	45.5	11	0.6739	0.8	-0.9	589.3112	2	12.4084	P63260|ACTG_M	Oxidation (M)	M10:Oxidation (M	0 0 19 19 69 96 0	EITALAPSTM(+15	DB Search	4030	EITALAPSTMK	3
29	VYLIQGTQVYVFLTK	40.12	1770.992	15	66.7	15	-0.0056	0.36	4.4	886.5093	2	26.1866	Q91X72|HEMO_MOUSE			0 0 0 3 63 12 10 1	VYLIQGTQVYVFL	DB Search	3950	VYLIQGTQVYVFL	3
30	TGMAFRVPTPNVSVVD	40.12	1688.856	16	56.2	16	0.9822	0.44	4.2	845.4406	2	22.1628	S4R257|S4R257_MOUSE:Q3V2I5|Q3V2I5_MOUSE:S			0 0 0 1 1 3 5 2 2 1	TGMAFRVPTPNV	DB Search	3740	TGMAFRVPTPNV	3
31	HNYEGPETHTSLR	40.12	1539.707	13	76.9	13	0.257	0.62	-1.5	514.2432	3	5.1748	P14483|HB2A_MOUSE:Q5XQL0|Q5XQL0_MOUSE:Q5			5 13 2 2 2 0 2 4 5	HNYEGPETHTSL	DB Search	3410	HNYEGPETHTSL	3
32	ALEEQLQQIRAE	40.12	1426.742	12	66.7	12	0.2418	0.77	2.6	714.3816	2	16.275	P02535|K1C10_MOUSE:A2A513|A2A513_MOUSE			0 0 42 19 19 67 8	ALEEQLQQIRAE	DB Search	3270	ALEEQLQQIRAE	3
33	WGEAGAEYVVESTGVFTTMEK	40.12	2290.046	21	0	21	-1.4416	0.55	0.9	1146.034	2	24.8541	A0A1D5RLD8|A0A1D5RLD8_MOUSE:S4R257|S4R25			0 0 0 0 0 0 0 0 0 (	WGEAGAEYVVE	DB Search	3270	WGEAGAEYVVE	3
34	EMEENFALEAANYQDTIGR	40.12	2199.974	19	36.8	19	-1.5716	0.73	8.2	1101.006	2	20.8411	P20152|VIME_MOUSE:Q5FWJ3|Q5FWJ3_MOUSE:Q			0 0 0 0 0 1 2 2 3 4	EMEENFALEAAN	DB Search	2960	EMEENFALEAAN	3
35	KPVSQMRMATPLLM(+15.99)RPM	38.73	2002.035	17	41.2	17	0.4206	0.6	-2.1	501.5161	4	16.8461	P04441|HG2A_M	Oxidation (M)	M14:Oxidation (M	0 0 0 0 0 0 0 0 2 1	KPVSQMRMATPL	DB Search	2920	KPVSQMRMATPL	3
38	IPGTNMYNTDRANPVLDLP	39.46	2100.031	19	10.5	19	1.028	0.57	5.7	1051.031	2	22.6021	Q8K066|Q8K066_MOUSE:E9Q7P9|CDHR2_MOUSE			0 0 0 0 0 0 0 0 0 (	IPGTNMYNTDRA	DB Search	2760	IPGTNMYNTDRA	3
39	LLLPGELAK	34.87	952.5957	9	66.7	9	0.0729	0.55	-0.5	477.3049	2	19.1451	B2RTK3|B2RTK3_MOUSE:P70696|H2B1A_MOUSE:A			5 12 44 10 3 2 0 (	LLLPGELAK	DB Search	2730	LLLPGELAK	3
40	APMYYRGAQAAIVVY	40.1	1671.844	15	40	15	-0.3773	0.64	4.1	836.9348	2	19.5028	Q3TCT9|Q3TCT9_MOUSE:P61021|RAB5B_MOUSE:(			0 0 0 1 0 0 0 1 1 9	APMYYRGAQAAI	DB Search	2710	APMYYRGAQAAI	3
41	G(+42.01)KEKTHINIVVIGHVDSGKSTTTGHLIYK	40.12	3173.72	29	3.4	29	-3.436	0.34	15	635.7622	5	13.9974	Q58E64|Q58E64	Acetylation (N-ter	G1:Acetylation (N	0 0 0 0 0 0 0 0 0 (	G(+42.01)KEKTH	DB Search	2480	GKEKTHINIVVIGH	2
42	NPTIYPLTLPRALSSDPV	40.12	1953.057	18	11.1	18	-0.0785	0.8	3.2	977.5412	2	25.4623	Q99KA4|Q99KA4_MOUSE:Q58E61|Q58E61_MOUSE:			5 0 0 1 4 1 1 1 1 (	NPTIYPLTLPRAL	DB Search	2340	NPTIYPLTLPRAL	3
43	APM(+15.99)YYRGAQAAIVVYD	39.94	1802.866	16	25	16	-0.5476	0.33	2.2	902.4445	2	17.609	Q3TCT9|Q3TCT9	Oxidation (M)	M3:Oxidation (M):	0 0 0 0 0 0 0 0 0 (	APM(+15.99)YYR	DB Search	2310	APMYYRGAQAAI	3
45	DSYVGDEAQSK	40.08	1197.515	11	45.5	11	-1.064	0.86	-0.9	599.7656	2	4.9059	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:A0			0 0 3 30 6 3 3 0 0	DSYVGDEAQSK	DB Search	2270	DSYVGDEAQSK	3
46	AGGSNTFSRTTKAVVVKKIETRDGKLVS	37.39	2948.641	28	0	28	-2.3728	0.21	5.5	738.1715	4	12.8796	P11679|K2C8_MOUSE			0 0 0 0 0 0 0 0 0 (	AGGSNTFSRTTK	DB Search	2220	AGGSNTFSRTTK	2
47	RPVQFPYVTPAPHEPVK	40.12	1961.052	17	52.9	17	-0.5976	0.79	-1.4	654.692	3	15.2431	Q9D074|MGRN1_MOUSE			0 0 0 0 7 23 23 27	RPVQFPYVTPAP	DB Search	2080	RPVQFPYVTPAP	3
50	ELEEQLGPVAEETRA	40.12	1669.816	15	66.7	15	-0.267	0.89	2.6	835.9193	2	16.3066	G3UZM8|G3UZM8_MOUSE:G3UWN5|G3UWN5_MOU			0 0 10 10 12 22 4	ELEEQLGPVAEE	DB Search	2020	ELEEQLGPVAEE	3
52	EVSSVEAPSVSPAR	40.12	1413.71	14	57.1	14	0.1827	0.89	-2.5	707.8621	2	12.1677	Q8BUJ9|LRP12_MOUSE			0 0 2 4 12 39 39 2	EVSSVEAPSVSP/	DB Search	1910	EVSSVEAPSVSP/	3
53	GGLPDYSAPNPIKVTHR	40.12	1820.953	17	5.9	17	-0.6255	0.41	-0.3	607.993	3	14.6301	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			0 0 0 14 0 0 1 0 0	GGLPDYSAPNPII	DB Search	1900	GGLPDYSAPNPII	3
54	GPDGRFVMGPTVAPSQEK	40.12	1871.92	18	50	18	-0.5854	0.76	-4.3	624.9794	3	14.3922	Q05BQ1|TUTLA_MOUSE			0 0 0 0 0 5 6 17 1	GPDGRFVMGPT\	DB Search	1900	GPDGRFVMGPT\	3
55	QPSTSSLAAPTVEAAASAPA	39.94	1825.906	20	30	20	-0.3417	0.64	1.8	913.9639	2	17.7114	A0AAQ4VMX1|A0AAQ4VMX1_MOUSE:A0AAQ4VMV3			0 0 0 0 0 3 0 0 9 1	QPSTSSLAAPTVI	DB Search	1890	QPSTSSLAAPTVI	3
57	SQVFSTAADGQTQVEIK	40.12	1807.895	17	64.7	17	-0.3677	0.58	2.3	904.9591	2	15.5771	P38647|HSPA9_MOUSE			0 0 0 8 6 8 8 13 1	SQVFSTAADGQT	DB Search	1780	SQVFSTAADGQT	3
58	AKPVSQMRMATPLLMRPM	39.7	2057.077	18	16.7	18	0.1631	0.7	1.3	686.7005	3	18.9634	P04441|HG2A_MOUSE:Q545Y5|Q545Y5_MOUSE:Q3			0 0 2 2 0 0 0 0 0 (	AKPVSQMRMATI	DB Search	1780	AKPVSQMRMATI	3
59	ITNQYNSPTGLYSSEN	40.12	1786.801	16	56.2	16	-0.7957	0.71	5.2	894.4145	2	15.1625	O70400|PDLI1_MOUSE:S4R1V0|S4R1V0_MOUSE:Q3			0 0 0 4 19 19 54 0	ITNQYNSPTGLYS	DB Search	1650	ITNQYNSPTGLYS	3
60	VFENYEASKAYSSVD	40.12	1707.763	15	73.3	15	-0.1764	0.65	1.9	854.8923	2	14.8079	Q9D306|MGT4C_MOUSE			0 0 4 5 13 20 20 1	VFENYEASKAYS	DB Search	1530	VFENYEASKAYS	3
62	VFENYEASKAYSSVDE	40.12	1836.805	16	68.8	16	-0.2938	0.61	1.6	919.4136	2	14.9751	Q9D306|MGT4C_MOUSE			0 0 0 2 6 16 12 0	VFENYEASKAYS	DB Search	1460	VFENYEASKAYS	3
64	YVTQFHPPHIEIQ	40.12	1607.81	13	30.8	13	0.008	0.37	3.2	804.9165	2	18.3418	Q9D239|Q9D239_MOUSE:P01887|B2MG_MOUSE:Q3			0 0 1 0 0 2 0 0 0 (	YVTQFHPPHIEIQ	DB Search	1450	YVTQFHPPHIEIQ	3
66	NPLNSVFVAPAVTPVK	40.12	1651.93	16	50	16	0.2788	0.72	3.8	826.9772	2	22.3594	P70158|ASM3A_MOUSE			5 0 0 3 5 5 10 10	NPLNSVFVAPAV	DB Search	1410	NPLNSVFVAPAV	3
67	IREFYSASVAEDATLG	40.12	1727.837	16	62.5	16	-0.0465	0.51	1	864.9285	2	18.6604	E9Q7P9|CDHR2_MOUSE			0 0 0 1 2 5 5 5 5 1	IREFYSASVAED/	DB Search	1400	IREFYSASVAED/	3
68	RHNYEGPETHTSLR	40.12	1695.808	14	21.4	14	-1.3161	0.65	1.6	566.2788	3	2.3703	P14483|HB2A_MOUSE:Q5XQL0|Q5XQL0_MOUSE:Q5			0 0 0 1 1 3 1 1 5 4	RHNYEGPETHTS	DB Search	1340	RHNYEGPETHTS	3
69	VAPEEHPVLLTEAPLNPK	40.12	1953.057	18	33.3	18	0.0416	0.58	-4.1	652.0252	3	17.906	P63260|ACTG_MOUSE:E9Q5F4|E9Q5F4_MOUSE:G3			0 0 4 0 0 0 0 0 2 3	VAPEEHPVLLTE/	DB Search	1330	VAPEEHPVLLTE/	3
70	SGPKPFSAPKPQTSPSPKP	40.12	1934.026	19	5.3	19	0.9942	0.57	2.1	645.6856	3	10.3903	Q3TC53|Q3TC53_MOUSE:P40124|CAP1_MOUSE:Q3			0 0 0 0 0 0 1 1 0 (	SGPKPFSAPKPQ	DB Search	1310	SGPKPFSAPKPQ	3
75	MRYVASYLLAALGGNSSPSAKDIKKIL	40.12	2865.579	27	29.6	27	-0.1673	0.35	5.8	717.4078	4	25.0343	A0A5F8MPY2|A0A5F8MPY2_MOUSE:P99027|RLA2_			0 0 0 0 0 5 20 3	MRYVASYLLAAL	DB Search	1280	MRYVASYLLAAL	3
76	GPKPFSAPKPQTSPSPKP	40.12	1846.994	18	11.1	18	0.8943	0.45	3.2	616.6754	3	10.2271	Q3TC53|Q3TC53_MOUSE:P40124|CAP1_MOUSE:Q3			0 0 4 1 0 0 0 0 0 (	GPKPFSAPKPQT	DB Search	1210	GPKPFSAPKPQT	3
77	GYSFTTTAER	39.32	1131.52	10	50	10	0.0585	0.8	1.2	566.7691	2	11.8015	P63260|ACTG_MOUSE:E9Q5F4|E9Q5F4_MOUSE:Q6			0 0 52 52 41 9 3 (	GYSFTTTAER	DB Search	1200	GYSFTTTAER	3
78	AM(+15.99)GIM(+15.99)NSFVNDIFER	40.12	1774.802	15	33.3	15	0.1726	0.68	6.5	888.4161	2	23.2139	B2RTK3|B2RTK3	Oxidation (M);Oxi	M2:Oxidation (M):	0 0 0 0 2 2 2 2 3 1	AM(+15.99)GIM(+	DB Search	1200	AMGIMNSFVNDII	3
79	AVFPSIVGRPR	40.1	1197.698	11	18.2	11	-0.3674	0.7	-2.7	599.8561	2	16.0117	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:A0			0 0 14 3 0 0 1 0 0	AVFPSIVGRPR	DB Search	1160	AVFPSIVGRPR	3
80	QQLSAEELDAQLDAYNAR	40.12	2033.965	18	11.1	18	-0.6548	0.64	1.9	1017.994	2	19.2369	G3X9I4|G3X9I4_MOUSE:Q9JJW6|ALRF2_MOUSE:O			0 0 0 0 0 0 0 0 1 1	QQLSAEELDAQL	DB Search	1150	QQLSAEELDAQL	3
81	NPLNSVFVAPAVTPVKGVL	40.12	1921.104	19	42.1	19	0.3327	0.78	1.6	961.5629	2	26.4632	P70158|ASM3A_MOUSE			0 0 0 2 2 2 4 4 6 (	NPLNSVFVAPAV	DB Search	1140	NPLNSVFVAPAV	3
82	AVFPSIVGR	38.81	944.5443	9	44.4	9	0.1893	0.89	-1.7	473.2798	2	18.4342	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:A0			2 2 39 38 1 1 0 0	AVFPSIVGR	DB Search	1120	AVFPSIVGR	3
83	PKGKKAKGKKVAPAPAVVKKQEAKKVVNPLF	39.71	3283.038	31	3.2	31	-4.7805	NA	2.4	821.7688	4	9.5821	Q5EBG5|Q5EBG5_MOUSE:Q80UT7|Q80UT7_MOUSI			0 0 0 0 0 0 0 0 0 (	PKGKKAKGKKVA	DB Search	1110	PKGKKAKGKKVA	2
85	ISGLIYEETR	36.72	1179.614	10	60	10	-0.6501	0.79	0.9	590.8146	2	15.5164	P62806|H4_MOUSE:B2RTM0|B2RTM0_MOUSE:Q6B			5 54 14 14 74 21	ISGLIYEETR	DB Search	1110	ISGLIYEETR	3
86	VAIFARGPQAHLLHG	40.09	1585.884	15	53.3	15	0.2118	0.08	0.1	529.6366	3	16.0427	F8VQM0|F8VQM0_MOUSE:Q1LZM2|Q1LZM2_MOUS			5 87 66 22 0 0 0 (	VAIFARGPQAHLI	DB Search	1100	VAIFARGPQAHLI	3
87	ELEEQLGPVAEETR	40.12	1598.779	14	42.9	14	-0.4666	0.88	-1.6	800.3972	2	15.6036	G3UZM8|G3UZM8_MOUSE:G3UWN5|G3UWN5_MOU			0 0 0 4 14 34 46 1	ELEEQLGPVAEE	DB Search	1080	ELEEQLGPVAEE	3
88	NVFENYEASKAYSSVDE	40.12	1950.848	17	70.6	17	-0.986	0.62	3.8	976.4374	2	16.9485	Q9D306|MGT4C_MOUSE			0 0 1 3 4 5 5 5 4 6	NVFENYEASKAY	DB Search	1060	NVFENYEASKAY	3
89	HNYEGPETHTSL	40.12	1383.606	12	41.7	12	-0.096	0.59	3.4	692.814	2	9.4937	P14483|HB2A_MOUSE:Q5XQL0|Q5XQL0_MOUSE:Q5			0 0 0 0 2 0 0 1 2 4	HNYEGPETHTSL	DB Search	1050	HNYEGPETHTSL	3
91	IIAPPERK	26.8	922.56	8	62.5	8	0.6661	0.72	-0.5	462.287	2	5.2645	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:Q3			5 13 97 21 3 0 0 (	IIAPPERK	DB Search	1020	IIAPPERK	3
92	GLPDYSAPNPIKVTHR	40.12	1763.932	16	37.5	16	-0.7502	0.36	-1.6	588.985	3	14.5474	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			0 0 18 15 9 3 3 1	GLPDYSAPNPIK\	DB Search	1010	GLPDYSAPNPIK\	3
93	VFLENVIR	33.97	988.5706	8	50	8	0.6352	0.84	-1.1	495.292	2	19.6776	Q61667|Q61667_MOUSE:P62806|H4_MOUSE:B2RTM			5 24 45 18 1 1 0 (	VFLENVIR	DB Search	996	VFLENVIR	3
94	GDLEYQMSTTARAK	40.12	1569.746	14	42.9	14	-0.6525	0.77	3.1	785.8844	2	11.2684	Q02257|PLAK_MOUSE			0 0 4 4 8 8 9 2 1 1	GDLEYQMSTTAF	DB Search	988	GDLEYQMSTTAF	3
95	LPKSAKPVSQMRMATPLLMRPM	40.12	2482.341	22	27.3	22	-0.1789	0.48	-1.9	621.5928	4	18.2567	P04441|HG2A_MOUSE:Q545Y5|Q545Y5_MOUSE:Q3			5 0 0 0 0 2 0 0 0 (	LPKSAKPVSQMR	DB Search	943	LPKSAKPVSQMR	3
96	DVAIFARGPQAHLVHG	38.81	1686.895	16	18.8	16	-0.136	0.24	5.2	844.4594	2	16.5534	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:(			1 0 0 0 0 0 0 0 0 (	DVAIFARGPQAH	DB Search	935	DVAIFARGPQAH	3
97	TFSRTTKAVVVKKIETRDGKLVS	40.11	2562.486	23	0	23	-2.4155	0.35	6.1	641.6341	4	11.4719	P11679|K2C8_MOUSE			0 0 0 0 0 0 1 1 0 (	TFSRTTKAVVVKI	DB Search	928	TFSRTTKAVVVKI	3
99	LGDLYEEEMR	34.5	1253.56	10	70	10	-1.0493	0.63	1.6	627.7882	2	15.3246	P20152|VIME_MOUSE:A4IF59|A4IF59_MOUSE:Q3TF			5 22 22 29 75 12	LGDLYEEEMR	DB Search	868	LGDLYEEEMR	3
101	IGGIGTVPVGR	39.63	1024.603	11	63.6	11	-0.0909	0.73	-1.7	513.3079	2	14.9226	Q58E64|Q58E64_MOUSE:Q3UZQ3|Q3UZQ3_MOUSE			5 13 10 10 17 15	IGGIGTVPVGR	DB Search	852	IGGIGTVPVGR	3
102	YQSKYEEL	38.04	1058.492	8	100	8	-1.2652	0.73	0.4	530.2535	2	11.3806	P04104|K2C1_MOUSE			5 12 6 5 4 13 19 5	YQSKYEEL	DB Search	847	YQSKYEEL	3
104	FVAPAVTPVKG	40.1	1084.628	11	63.6	11	0.3245	0.65	-5.4	543.3196	2	15.4134	P70158|ASM3A_MOUSE			2 2 88 16 9 7 6 0	FVAPAVTPVKG	DB Search	808	FVAPAVTPVKG	3
105	RKRSRKESYSVYVKVLKQVHPD	39.69	2864.577	23	8.7	23	0.5419	0.44	1.3	717.1525	4	15.442	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:(			0 0 0 0 0 0 0 0 0 (	RKRSRKESYSVY	DB Search	801	RKRSRKESYSVY	3
106	VSHDYKGSTSHSLPY	32.51	1676.779	15	13.3	15	0.1291	0.39	1.1	839.3999	2	9.4573	E9Q1Y3|E9Q1Y3_MOUSE:E9Q414|APOB_MOUSE			0 0 0 0 0 0 0 0 0 (	VSHDYKGSTSHS	DB Search	791	VSHDYKGSTSHS	3
107	GIDPYDQPNAIYIER	40.12	1762.853	15	33.3	15	-0.3513	0.33	5.3	882.4403	2	18.3527	Q3U2X9|Q3U2X9_MOUSE:O88307|SORL_MOUSE			0 0 31 0 1 3 7 0 0	GIDPYDQPNAIYI	DB Search	774	GIDPYDQPNAIYI	3
108	ASGPPVSELITK	40.12	1197.661	12	66.7	12	-0.1532	0.58	-0.9	599.8384	2	16.438	P15864|H12_MOUSE:Q149Z9|Q149Z9_MOUSE:P432			5 18 18 98 11 11	ASGPPVSELITK	DB Search	763	ASGPPVSELITK	3
110	KELEEQLGPVAEETR	40.12	1726.874	15	60	15	-0.3873	0.82	-2.7	576.6317	3	13.5227	G3UZM8|G3UZM8_MOUSE:G3UWN5|G3UWN5_MOU			0 0 1 4 5 15 30 72	KELEEQLGPVAE	DB Search	759	KELEEQLGPVAE	3
113	YLNIYVPAHAHEGSN	40.12	1683.801	15	46.7	15	-0.9051	0.7	2.1	842.9113	2	15.1339	Q8BK48|EST2E_MOUSE			0 0 2 14 14 14 2 2	YLNIYVPAHAHE(	DB Search	731	YLNIYVPAHAHE(	3
114	SLDLDSIIAEVK	40.11	1301.708	12	66.7	12	-0.0073	0.55	-0.7	651.8622	2	25.9394	Q0VDR7|Q0VDR7_MOUSE:Q9Z331|K2C6B_MOUSE:			0 0 42 42 47 13 1	SLDLDSIIAEVK	DB Search	720	SLDLDSIIAEVK	3
115	APM(+15.99)YYRGAQAAIVVY	39.65	1687.839	15	33.3	15	-0.2517	0.55	2.8	844.9312	2	18.1742	Q3TCT9|Q3TCT9	Oxidation (M)	M3:Oxidation (M):	0 0 0 0 0 0 0 0 1 1	APM(+15.99)YYR	DB Search	718	APMYYRGAQAAI	3
118	D(+42.01)DDIAALVVDNGSGMCKA	40.12	1834.808	18	72.2	18	-1.6082	0.74	2.7	918.4157	2	24.5805	E9Q5F4|E9Q5F4	Acetylation (N-ter	D1:Acetylation (N	0 0 2 22 50 91 52	D(+42.01)DDIAAL	DB Search	686	DDDIAALVVDNG	3
120	GPKPFSAPKPQTSPSPK	40.12	1749.941	17	29.4	17	0.448	0.54	1.7	584.3234	3	9.0481	Q3TC53|Q3TC53_MOUSE:P40124|CAP1_MOUSE:Q3			0 0 0 5 5 1 1 2 2 (	GPKPFSAPKPQT	DB Search	679	GPKPFSAPKPQT	3
122	AGFAGDDAPR	39.63	975.441	10	80	10	-0.7674	0.77	2.4	488.7289	2	8.3021	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:A0			5 8 9 81 17 17 3 3	AGFAGDDAPR	DB Search	676	AGFAGDDAPR	3
123	EIAQDFKTDLR	40.12	1334.683	11	63.6	11	-0.007	0.64	1.2	668.3511	2	14.0105	A1L0U3|A1L0U3_MOUSE:A1L0V4|A1L0V4_MOUSE:F			3 3 8 8 5 5 4 1 1 (	EIAQDFKTDLR	DB Search	675	EIAQDFKTDLR	3
124	DVAIFARGPQAHLVHGVQ	40.12	1914.022	18	27.8	18	0.5053	0.33	-0.5	639.0159	3	17.218	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:(			0 0 35 35 1 0 1 0	DVAIFARGPQAH	DB Search	672	DVAIFARGPQAH	3
125	NPPSYYTQPVPVPN	39.56	1571.762	14	35.7	14	0.1962	0.6	4.8	786.892	2	18.1479	Q9JLJ0|LITAF_MOUSE:E0CYR5|E0CYR5_MOUSE			0 0 0 0 1 5 2 3 1 1	NPPSYYTQPVPV	DB Search	665	NPPSYYTQPVPV	3
127	NPLNSVFVAPAVTPVKG	40.12	1708.951	17	47.1	17	0.126	0.71	-0.9	855.4841	2	22.2545	P70158|ASM3A_MOUSE			4 1 1 3 4 4 6 6 10	NPLNSVFVAPAV	DB Search	646	NPLNSVFVAPAV	3
128	VRDMRQTVAVGVIKAVDKKAAGAGKVTK	40.12	2895.68	28	21.4	28	-2.9454	0.49	7.3	580.1489	5	14.3495	Q58E64|Q58E64_MOUSE:Q3UZQ3|Q3UZQ3_MOUSE			0 0 0 0 0 0 0 0 0 (	VRDMRQTVAVG\	DB Search	645	VRDMRQTVAVG\	3
129	FQNAILVR	39.26	959.5552	8	75	8	-0.1679	0.86	-1	480.7844	2	16.0009	Q546G4|Q546G4_MOUSE:P07724|ALBU_MOUSE			5 19 25 12 12 2 0	FQNAILVR	DB Search	639	FQNAILVR	3
130	KYTYGKPVPGHVK	40.12	1472.814	13	69.2	13	-1.611	0.75	-1.6	491.9456	3	2.3405	P28665|MUG1_MOUSE			0 0 12 7 2 15 8 8	KYTYGKPVPGHV	DB Search	639	KYTYGKPVPGHV	3
131	DARSYTAAVANRAKGGG	40.12	1663.839	17	29.4	17	0.9972	0.86	2.5	555.623	3	10.5936	Q91XS1|MTMR4_MOUSE:Q6PE02|Q6PE02_MOUSE			5 0 0 0 0 0 3 5 5 3	DARSYTAAVANR	DB Search	630	DARSYTAAVANR	3
133	FVAPAVTPVK	40.09	1027.607	10	50	10	0.5302	0.53	-5.4	514.809	2	15.4336	P70158|ASM3A_MOUSE			0 0 96 12 8 3 3 0	FVAPAVTPVK	DB Search	620	FVAPAVTPVK	3
134	GLPDYSAPNPIKVTH	40.12	1607.831	15	46.7	15	-0.5581	0.53	-2.3	536.9509	3	16.1556	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			0 0 19 18 2 2 3 2	GLPDYSAPNPIK\	DB Search	619	GLPDYSAPNPIK\	3
135	DARSYTAAVANRAK	39.7	1492.775	14	50	14	0.7225	0.82	-0.1	498.5988	3	9.604	Q91XS1|MTMR4_MOUSE:Q6PE02|Q6PE02_MOUSE			0 0 0 0 11 11 58 5	DARSYTAAVANR	DB Search	612	DARSYTAAVANR	3
138	IFARGPQAHLVHG	40.12	1401.763	13	53.8	13	0.311	0.23	-1	468.2622	3	11.0292	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:(			5 42 4 0 0 0 0 4 7	IFARGPQAHLVH(	DB Search	599	IFARGPQAHLVH(	3
139	APMYYRGAQAAIVV	40.1	1508.781	14	42.9	14	-0.0948	0.68	-1.7	755.3983	2	18.6251	Q3TCT9|Q3TCT9_MOUSE:P61021|RAB5B_MOUSE:(			0 0 0 0 0 0 1 1 2 1	APMYYRGAQAAI	DB Search	596	APMYYRGAQAAI	3
141	GPDGRFVMGPTVAPSQ	39.28	1614.782	16	25	16	-0.1713	0.63	3.7	808.4015	2	16.6922	Q05BQ1|TUTLA_MOUSE			0 0 0 0 0 0 0 7 3 (	GPDGRFVMGPT\	DB Search	591	GPDGRFVMGPT\	3
142	TPAYTIPFYTPIPNG	40.12	1650.829	15	53.3	15	0.3729	0.64	3.7	826.4269	2	26.6087	O08573|LEG9_MOUSE:B1AQR8|B1AQR8_MOUSE:G			0 0 0 0 0 19 6 6 3	TPAYTIPFYTPIPN	DB Search	591	TPAYTIPFYTPIPN	3
143	RHNYEGPETHTSL	40.12	1539.707	13	53.8	13	0.5004	0.59	-1.7	514.2432	3	7.8266	P14483|HB2A_MOUSE:Q5XQL0|Q5XQL0_MOUSE:Q5			0 0 6 29 37 37 16	RHNYEGPETHTS	DB Search	578	RHNYEGPETHTS	3
144	KELEEQLGPVAEETRA	39.7	1797.911	16	50	16	-0.5855	0.86	-6.2	600.3072	3	14.2852	G3UZM8|G3UZM8_MOUSE:G3UWN5|G3UWN5_MOU			0 0 0 0 2 2 15 48	KELEEQLGPVAE	DB Search	575	KELEEQLGPVAE	3
146	DTIEFRGPNGLLVYQG	40.12	1777.9	16	75	16	-0.1877	0.76	6.1	889.9647	2	22.809	F2Z456|F2Z456_MOUSE:Q9DCN2|NB5R3_MOUSE:(			0 0 3 3 4 4 4 1 1 5	DTIEFRGPNGLL\	DB Search	574	DTIEFRGPNGLL\	3
148	VGKARGFFKKGDVVIVLTG	39.87	1990.173	19	26.3	19	0.1353	0.15	-3.5	664.3974	3	16.8498	P52480|KPYM_MOUSE			0 0 0 0 0 0 0 0 1 (	VGKARGFFKKGI	DB Search	564	VGKARGFFKKGI	3
149	GYSFVTTAER	39.41	1129.54	10	50	10	-0.1465	0.83	2.9	565.7791	2	13.9408	Q3UJ36|Q3UJ36_MOUSE:A0A494B9T3|A0A494B9T3			0 0 52 52 84 11 5	GYSFVTTAER	DB Search	563	GYSFVTTAER	3
150	KIVYEGPELNHAFG	40.12	1572.794	14	42.9	14	0.4926	0.62	-3.7	525.2711	3	17.1575	A0A0R4J0I9|A0A0R4J0I9_MOUSE:Q91ZX7|LRP1_MC			0 0 0 6 18 25 29 2	KIVYEGPELNHAF	DB Search	560	KIVYEGPELNHAF	3
151	DNIQGITKPAIR	40.12	1324.746	12	41.7	12	-0.6335	0.59	3.4	663.3842	2	12.6771	P62806|H4_MOUSE:B2RTM0|B2RTM0_MOUSE			0 0 0 10 5 5 2 2 1	DNIQGITKPAIR	DB Search	558	DNIQGITKPAIR	3
152	IPFYTPIPNGLYPS	40.12	1577.813	14	35.7	14	0.7809	0.65	6	789.9204	2	27.1438	O08573|LEG9_MOUSE:B1AQR8|B1AQR8_MOUSE:G			0 0 0 0 1 3 16 25 0	IPFYTPIPNGLYPS	DB Search	558	IPFYTPIPNGLYPS	3
153	A(+42.01)SGVAVSDGVIK	40.12	1143.614	12	66.7	12	0.7507	0.55	-0.6	572.8151	2	17.1403	P18760|COF1_M	Acetylation (N-ter	A1:Acetylation (N-	3 3 8 13 43 36 7 3	A(+42.01)SGVAV	DB Search	555	ASGVAVSDGVIK	3
154	LYIAVGISGAIQHLAGMKDSKTIVAINK	40.12	2910.637	28	25	28	-1.7264	0.53	3.6	728.6707	4	24.4378	Q99LC5|ETFA_MOUSE			0 0 26 31 31 13 1	LYIAVGISGAIQH	DB Search	551	LYIAVGISGAIQH	3
155	GGLPDYSAPNPIKVTH	40.12	1664.852	16	12.5	16	-0.4741	0.21	2.2	833.4372	2	16.2337	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			0 0 0 0 0 1 2 2 0 (	GGLPDYSAPNPII	DB Search	551	GGLPDYSAPNPII	3
156	IREFYSASVAEDAT	40.12	1557.731	14	57.1	14	-0.0289	0.58	1.8	779.876	2	15.5619	E9Q7P9|CDHR2_MOUSE			0 0 0 0 6 16 16 26	IREFYSASVAED/	DB Search	548	IREFYSASVAED/	3
157	FPYVTPAPHEPVKT	40.12	1581.819	14	35.7	14	-0.1849	0.74	0.6	791.9192	2	15.0503	Q9D074|MGRN1_MOUSE			5 1 1 3 5 1 1 0 0 1	FPYVTPAPHEPVI	DB Search	529	FPYVTPAPHEPVI	3
159	GSDMFKASLVIPSKDK	40.12	1721.902	16	37.5	16	-0.2047	0.87	-2.3	574.9747	3	16.3961	Q8BK33|Q8BK33_MOUSE:Q8BJD1|ITIH5_MOUSE			0 0 0 0 1 0 0 3 18	GSDMFKASLVIP!	DB Search	487	GSDMFKASLVIP!	3
160	EVSSVEAPSVSPARHQ	39.69	1678.827	16	12.5	16	0.0737	0.89	5.4	840.4255	2	10.4764	Q8BUJ9|LRP12_MOUSE			0 0 0 0 0 2 3 1 0 (	EVSSVEAPSVSP/	DB Search	486	EVSSVEAPSVSP/	3
161	FPKPPSYNVATTLPSYDEA	40.12	2096.01	19	10.5	19	-0.3124	0.85	6	1049.021	2	20.3572	A0A494BAA4|A0A494BAA4_MOUSE:Q8R0W6|NFIP1			0 0 0 0 0 0 0 0 0 1	FPKPPSYNVATTI	DB Search	476	FPKPPSYNVATTI	3
162	ESEPYTFSHPNKGEIG	40.12	1790.811	16	6.2	16	-0.7317	0.46	3.2	896.4178	2	12.8375	Q5U462|CDCP1_MOUSE			0 0 1 0 0 0 0 0 0 (	ESEPYTFSHPNK	DB Search	473	ESEPYTFSHPNK	3
163	AVFVDLEPTVIDEVR	40.12	1700.898	15	60	15	0.2529	0.85	1.6	851.4598	2	24.6385	P68369|TBA1A_MOUSE:P68373|TBA1C_MOUSE:A0/			0 0 7 7 10 14 30 4	AVFVDLEPTVIDE	DB Search	466	AVFVDLEPTVIDE	2
164	DAVTYTEHAK	40.04	1133.535	10	50	10	-1.3016	0.8	0.5	567.7766	2	2.9665	Q61667|Q61667_MOUSE:P62806|H4_MOUSE:B2RTM			0 0 35 52 23 6 6 1	DAVTYTEHAK	DB Search	463	DAVTYTEHAK	3
166	NVQFNYPQASVTDVT	40.12	1681.795	15	53.3	15	0.0432	0.6	5.7	841.9114	2	20.006	G3X977|G3X977_MOUSE:Q8K016|Q8K016_MOUSE:(			0 0 0 0 0 11 11 6	NVQFNYPQASVT	DB Search	454	NVQFNYPQASVT	3
167	RPGSGFTNTMRVVPVP	27.44	1713.898	16	31.2	16	0.6982	0.1	0.9	572.3073	3	18.3754	P52480|KPYM_MOUSE			0 0 0 0 0 0 0 0 0 (	RPGSGFTNTMR\	DB Search	447	RPGSGFTNTMR\	3
168	VAIFARGPQAHLVHGV	40.05	1670.937	16	31.2	16	0.6207	0.32	-2.7	557.986	3	16.1259	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:(			0 0 55 17 7 1 0 0	VAIFARGPQAHL\	DB Search	435	VAIFARGPQAHL\	3
169	EYQDLLNVK	40.01	1120.576	9	77.8	9	0.0492	0.68	-0.2	561.2967	2	16.7514	P03995|GFAP_MOUSE:P20152|VIME_MOUSE:Q5FW			5 9 60 34 31 8 3 (	EYQDLLNVK	DB Search	435	EYQDLLNVK	3
171	SGGTTM(+15.99)YPGLADR	39.71	1340.603	13	38.5	13	-0.6219	0.9	3.2	671.3109	2	11.1442	Q9QZ83|Q9QZ83	Oxidation (M)	M6:Oxidation (M):	1 0 0 0 22 26 58 9	SGGTTM(+15.99)	DB Search	429	SGGTTMYPGLAD	3
172	SGGTTM(+15.99)YPGIADR	39.71	1340.603	13	38.5	13	-0.2763	0.9	3.2	671.3109	2	11.1442	P63260|ACTG_M	Oxidation (M)	M6:Oxidation (M):	1 0 0 0 22 26 58 9	SGGTTM(+15.99)	DB Search	429	SGGTTMYPGIAD	3
175	VELQELNDR	38.01	1114.562	9	55.6	9	-0.5862	0.62	0.1	558.2896	2	12.8772	P20152|VIME_MOUSE:A4IF59|A4IF59_MOUSE:Q5FV			5 37 90 75 11 1 1	VELQELNDR	DB Search	410	VELQELNDR	3
177	LVRYTQKAPQVSTPTL	40.11	1801.01	16	12.5	16	0.3566	0.4	-2	601.3441	3	15.3474	Q546G4|Q546G4_MOUSE:P07724|ALBU_MOUSE			0 0 0 0 0 1 1 2 0 (	LVRYTQKAPQVS	DB Search	406	LVRYTQKAPQVS	3
178	HVPTLQVLRPGLVVVH	40.12	1763.057	16	6.2	16	0.0677	0.14	-6.6	588.6904	3	19.9678	D3Z7S4|D3Z7S4_MOUSE:Q9D3D9|ATPD_MOUSE:Q			0 0 0 0 0 1 1 2 1 (	HVPTLQVLRPGL\	DB Search	401	HVPTLQVLRPGL\	3
180	GMAFRVPTPNVSVVD	40.12	1587.808	15	80	15	1.1026	0.48	6.1	794.9179	2	22.0558	S4R257|S4R257_MOUSE:Q3V2I5|Q3V2I5_MOUSE:S			0 0 0 3 2 11 4 4 5	GMAFRVPTPNVS	DB Search	393	GMAFRVPTPNVS	3
181	HLQLAIRNDEELNK	39.71	1691.896	14	7.1	14	0.0026	0.5	0.8	846.9557	2	12.997	Q8BFU2|H2A3_MOUSE:A0AUV1|A0AUV1_MOUSE:Q			1 1 0 0 0 0 0 0 0 (	HLQLAIRNDEELI	DB Search	388	HLQLAIRNDEELI	3
182	SINPDEAVAYGAAVQAAILSGDK	40.12	2259.138	23	8.7	23	-0.1537	0.58	4.4	1130.584	2	26.6498	Q3KQJ4|Q3KQJ4_MOUSE:Q3U9L2|Q3U9L2_MOUSE			0 0 0 0 0 0 1 1 3 3	SINPDEAVAYGA/	DB Search	386	SINPDEAVAYGA/	2
183	LHTKGALPLDTVTFYKVIPKSKFVLVKF	40.12	3188.873	28	14.3	28	-0.5306	0.62	4.6	798.231	4	23.6837	P57759|ERP29_MOUSE:A8C1V9|A8C1V9_MOUSE			0 0 0 1 0 0 0 1 1 1	LHTKGALPLDTV	DB Search	385	LHTKGALPLDTV	3
184	PKGKKAKGKKVAPAPAVVKKQEAKKVVNPLFEK	39.71	3540.176	33	24.2	33	-6.0556	NA	2.5	591.0381	6	8.6993	Q5EBG5|Q5EBG5_MOUSE:Q80UT7|Q80UT7_MOUSI			0 0 0 0 0 0 0 0 0 (	PKGKKAKGKKVA	DB Search	376	PKGKKAKGKKVA	3
186	ALAAAGYDVEK	40.1	1106.561	11	45.5	11	0.11	0.73	-0.5	554.2887	2	11.8567	P15864|H12_MOUSE:P43274|H14_MOUSE:Q149Z9|(			0 0 42 61 6 6 (	ALAAAGYDVEK	DB Search	376	ALAAAGYDVEK	3
188	RKESYSVYVYKVLKQVHPD	39.97	2337.248	19	26.3	19	1.0918	0.45	-2	585.3195	4	18.0562	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:(			0 0 0 0 0 5 18 19	RKESYSVYVYKV	DB Search	373	RKESYSVYVYKV	3
189	KESYSVYVYK	40.12	1264.634	10	50	10	-0.0856	0.75	0.5	633.3261	2	11.7107	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:(			3 3 2 1 1 1 3 3 1 1	KESYSVYVYK	DB Search	372	KESYSVYVYK	3
190	ITQVQWNDPGAQYSLVNK	40.12	2060.033	18	22.2	18	0.0965	0.82	4.7	1031.031	2	18.8069	Q3TAN0|Q3TAN0_MOUSE:A2AKS7|A2AKS7_MOUSE			0 0 0 1 3 4 2 2 0 (	ITQVQWNDPGA(	DB Search	369	ITQVQWNDPGA(	3
195	VNVDFNTPRPSTVEA	40.12	1644.811	15	53.3	15	0.1289	0.55	2.2	823.4164	2	16.5684	A0A286YD40|A0A286YD40_MOUSE:G3X939|SL9A3_			1 0 2 5 8 12 17 0	VNVDFNTPRPST	DB Search	363	VNVDFNTPRPST	2
199	EDVAIFARGPQAHLVHG	37.38	1815.938	17	17.6	17	-0.0541	0.14	4.2	606.3225	3	16.3585	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:(			0 0 0 70 70 13 0 (	EDVAIFARGPQA	DB Search	356	EDVAIFARGPQA	3
202	YLNIYVPAHAHEGSNL	40.08	1796.885	16	31.2	16	-0.7025	0.7	0.7	899.4523	2	17.2466	Q8BK48|EST2E_MOUSE			0 0 2 4 5 7 0 0 2 (	YLNIYVPAHAHE(	DB Search	354	YLNIYVPAHAHE(	3
204	A(+42.01)EAKAEAKAEAKAEAK	39.87	1656.868	16	56.2	16	1.3809	0.53	6	553.3013	3	10.069	Q7TNL7|Q7TNL7	Acetylation (N-ter	A1:Acetylation (N-	5 27 27 0 0 0 2 2	A(+42.01)EAKAE/	DB Search	350	AEAKAEAKAEAK	3
206	SLHTLFGDK	40.02	1016.529	9	66.7	9	-0.249	0.59	-2.1	509.2719	2	14.0548	K7R066|K7R066_MOUSE:Q546G4|Q546G4_MOUSE:			5 9 69 4 0 5 0 0 5	SLHTLFGDK	DB Search	344	SLHTLFGDK	3
207	DLYANTVLSGGTTM(+15.99)YPGLADR	40.12	2230.058	21	23.8	21	0.0197	0.66	2.9	1116.042	2	20.9041	Q9QZ83|Q9QZ83	Oxidation (M)	M14:Oxidation (M	0 0 0 1 1 1 4 6 5 2	DLYANTVLSGGT	DB Search	341	DLYANTVLSGGT	2
208	DLYANTVLSGGTTM(+15.99)YPGIADR	40.12	2230.058	21	23.8	21	0.4012	0.66	2.9	1116.042	2	20.9041	P63260|ACTG_M	Oxidation (M)	M14:Oxidation (M	0 0 0 1 1 1 4 6 5 2	DLYANTVLSGGT	DB Search	341	DLYANTVLSGGT	2
211	IREFYSASVAEDATL	40.12	1670.815	15	66.7	15	-0.3692	0.4	2.2	836.4186	2	19.3186	E9Q7P9|CDHR2_MOUSE			0 0 0 1 4 8 8 13 1	IREFYSASVAED/	DB Search	332	IREFYSASVAED/	3
216	KNLDYVATSIHEAVTK	40.12	1787.942	16	37.5	16	-0.5537	0.69	0.4	596.9895	3	15.4453	P05201|AATC_MOUSE			0 0 0 2 1 4 2 1 6 6	KNLDYVATSIHE/	DB Search	321	KNLDYVATSIHE/	3
217	KPVSQMRM(+15.99)ATPLLMRPM	40.04	2002.035	17	35.3	17	-0.3809	0.69	-1	501.5167	4	16.3294	P04441|HG2A_M	Oxidation (M)	M8:Oxidation (M):	0 0 0 0 0 0 0 0 4 2	KPVSQMRM(+15	DB Search	319	KPVSQMRMATPL	3
220	VFVAPAVTPVK	40.07	1126.675	11	72.7	11	0.3357	0.55	-1.4	564.3453	2	17.0313	P70158|ASM3A_MOUSE			3 3 43 43 7 7 5 5	VFVAPAVTPVK	DB Search	316	VFVAPAVTPVK	3
221	FTYQQPQPLSVEPR	40.12	1688.852	14	28.6	14	0.1195	0.89	3	845.4379	2	16.8341	B2RXS4|PLXB2_MOUSE			0 0 8 6 6 1 1 1 1 2	FTYQQPQPLSVE	DB Search	315	FTYQQPQPLSVE	3
222	LPDYSAPNPIKVTHR	40.12	1706.91	15	20	15	-0.3515	0.53	-1.3	569.978	3	13.904	Q8CFG0|SULF2_MOUSE:Q6ZPV3|Q6ZPV3_MOUSE			5 55 0 0 0 0 1 1 1	LPDYSAPNPIKVT	DB Search	310	LPDYSAPNPIKVT	3
225	IEKVIPSTANSNNL	40.12	1498.799	14	57.1	14	0.0225	0.75	1	750.4094	2	14.7453	E9Q7P9|CDHR2_MOUSE			0 0 1 6 41 3 3 4 4	IEKVIPSTANSNN	DB Search	302	IEKVIPSTANSNN	3
226	VRFLEQQNK	40.08	1160.63	9	55.6	9	-0.0521	0.67	-2	581.3226	2	9.4698	P03995|GFAP_MOUSE:P20152|VIME_MOUSE:P9786			0 0 1 1 3 5 5 2 2	VRFLEQQNK	DB Search	301	VRFLEQQNK	3
227	NLDLDSIIAEVK	40.08	1328.719	12	58.3	12	-0.0168	0.6	-0.5	665.3679	2	25.8687	Q8VED5|K2C79_MOUSE			1 1 40 40 45 14 1	NLDLDSIIAEVK	DB Search	300	NLDLDSIIAEVK	3
234	GPDGRFVMGPTVAPSQEKL	40.12	1985.004	19	36.8	19	0.3962	0.89	0.5	662.6772	3	17.388	Q05BQ1|TUTLA_MOUSE			0 0 0 0 0 0 0 29 4	GPDGRFVMGPT\	DB Search	281	GPDGRFVMGPT\	3
240	FEDENFILK	38.26	1153.566	9	66.7	9	-0.2357	0.74	0.5	577.7903	2	18.7423	Q3TE63|Q3TE63_MOUSE:Q5SVY2|Q5SVY2_MOUSE			5 38 23 11 4 4 1 (	FEDENFILK	DB Search	267	FEDENFILK	3
241	QPSTSSLAAPTVEAAASAP	39.71	1754.869	19	36.8	19	-0.0182	0.6	8	878.4486	2	18.0378	A0AAQ4VMX1|A0AAQ4VMX1_MOUSE:A0AAQ4VMV3			0 0 0 0 0 1 1 2 5 1	QPSTSSLAAPTVI	DB Search	267	QPSTSSLAAPTVI	3
245	EDVAIFARGPQAHLVHGVQ	40.09	2043.065	19	36.8	19	0.0124	0.39	0.5	682.0309	3	16.9741	P24823|PPBN_MOUSE:Q7TPW4|Q7TPW4_MOUSE:(			0 0 42 40 40 0 0 (	EDVAIFARGPQA	DB Search	261	EDVAIFARGPQA	3
246	VFVAPAVTPVKG	40.12	1183.696	12	50	12	0.2048	0.55	2.5	592.8584	2	16.973	P70158|ASM3A_MOUSE			4 4 51 56 0 0 3 11	VFVAPAVTPVKG	DB Search	256	VFVAPAVTPVKG	3
247	LVIIESDLER	37.18	1185.661	10	70	10	-0.3034	0.65	-0.1	593.8375	2	18.3435	A0A2R2Y2P8|A0A2R2Y2P8_MOUSE:E9Q456|E9Q45(			4 4 88 88 28 6 6 1	LVIIESDLER	DB Search	254	LVIIESDLER	3
249	FPYVTPAPHEPV	40.12	1352.676	12	66.7	12	-0.3259	0.57	2.8	677.349	2	18.0592	Q9D074|MGRN1_MOUSE			5 11 10 10 20 3 3	FPYVTPAPHEPV	DB Search	251	FPYVTPAPHEPV	3
257	GGSKSISIS	26.41	834.4447	9	55.6	9	-1.7766	0.65	-1.2	418.2291	2	7.5452	Q3UV17|K22O_MOUSE			0 0 1 0 2 11 17 9	GGSKSISIS	DB Search	234	GGSKSISIS	3
259	QTVAVGVIK	39.88	913.5596	9	88.9	9	0.5541	0.82	-0.4	457.788	2	13.1126	Q58E64|Q58E64_MOUSE:Q3UZQ3|Q3UZQ3_MOUSE			5 12 62 24 24 3 2	QTVAVGVIK	DB Search	233	QTVAVGVIK	3
260	YVTQFHPPHIEIQMLK	39.71	1980.029	16	31.2	16	0.0579	0.42	3.8	661.0195	3	20.421	Q9D239|Q9D239_MOUSE:P01887|B2MG_MOUSE			5 11 0 1 5 5 2 0 0	YVTQFHPPHIEIQ	DB Search	231	YVTQFHPPHIEIQ	3
261	NAGVEGSLIVEK	39.94	1214.651	12	58.3	12	0.1365	0.59	2.6	608.3356	2	14.3923	P63038|CH60_MOUSE			2 2 5 5 65 3 0 0 0	NAGVEGSLIVEK	DB Search	231	NAGVEGSLIVEK	2
263	ELISNASDALDK	40.09	1274.635	12	50	12	0.557	0.66	-0.4	638.3262	2	14.7535	D3Z1R1|D3Z1R1_MOUSE:Q91V38|Q91V38_MOUSE:			0 0 47 44 27 27 5	ELISNASDALDK	DB Search	229	ELISNASDALDK	3
264	DPIQNTDEETKTE	40.12	1518.669	13	53.8	13	0.059	0.38	1	760.3441	2	8.2288	Q5G866|DFA23_MOUSE:Q64016|DFA17_MOUSE:P5			0 0 3 5 2 2 2 1 1 2	DPIQNTDEETKTE	DB Search	227	DPIQNTDEETKTE	2
266	VSSVEAPSVSPAR	39.53	1284.667	13	53.8	13	0.2524	0.88	0.3	643.3411	2	11.4568	Q8BUJ9|LRP12_MOUSE			5 4 3 3 34 38 1 1	VSSVEAPSVSPA	DB Search	224	VSSVEAPSVSPA	3
269	VENPEYLAPRAGTASQPHP	37.24	2032.997	19	42.1	19	-0.0025	0.24	1.8	678.6756	3	13.3207	P70424|ERBB2_MOUSE:Q8R2X1|Q8R2X1_MOUSE:(			5 18 50 4 4 10 7 7	VENPEYLAPRAG	DB Search	220	VENPEYLAPRAG	3
274	FADLSEAANR	33.86	1092.52	10	70	10	-0.7765	0.71	-2.3	547.2673	2	12.2154	P20152|VIME_MOUSE:Q3TFD9|Q3TFD9_MOUSE:Q5			5 38 51 51 34 9 9	FADLSEAANR	DB Search	218	FADLSEAANR	3
280	AIILLLLLI	39.87	993.7202	9	11.1	9	-7.4489	0	1.6	994.7313	1	20.0418	Q544T2|Q544T2_MOUSE:G3UXE5|G3UXE5_MOUSE			5 0 0 0 0 0 0 0 0	AIILLLLLI	DB Search	210	AIILLLLLI	3
282	ALLLLLLLL	39.87	993.7202	9	11.1	9	-7.1517	0	1.6	994.7313	1	20.0418	G3UXY8|G3UXY8_MOUSE:Q9JJS0|SCUB2_MOUSE:			5 0 0 0 0 0 0 0 0	ALLLLLLLL	DB Search	210	ALLLLLLLL	3
283	ALLLLLLIL	39.87	993.7202	9	11.1	9	-7.0557	0	1.6	994.7313	1	20.0418	D3Z7F6|D3Z7F6_MOUSE:E9PWV0|E9PWV0_MOUSI			5 0 0 0 0 0 0 0 0	ALLLLLLIL	DB Search	210	ALLLLLLIL	3
284	AIILLLLIL	39.87	993.7202	9	11.1	9	-7.1952	0	1.6	994.7313	1	20.0418	A2AFG7|A2AFG7_MOUSE:Q6PGJ3|Q6PGJ3_MOUSE			5 0 0 0 0 0 0 0 0	AIILLLLIL	DB Search	210	AIILLLLIL	3
285	ALLLLLLLI	39.87	993.7202	9	11.1	9	-7.278	0	1.6	994.7313	1	20.0418	A0A2I3BPJ2|A0A2I3BPJ2_MOUSE			5 0 0 0 0 0 0 0 0	ALLLLLLLI	DB Search	210	ALLLLLLLI	2
286	ALLILILLI	39.87	993.7202	9	11.1	9	-7.1148	0	1.6	994.7313	1	20.0418	A0A1W2P7Y9|A0A1W2P7Y9_MOUSE:Q810U4|NRCA			5 0 0 0 0 0 0 0 0	ALLILILLI	DB Search	210	ALLILILLI	3
287	ALLILILLL	39.87	993.7202	9	11.1	9	-7.0177	0	1.6	994.7313	1	20.0418	A0A0R4IZW5|A0A0R4IZW5_MOUSE:P09803|CADH1			5 0 0 0 0 0 0 0 0	ALLILILLL	DB Search	210	ALLILILLL	3
288	TGM(+15.99)AFRVPTPNVSVVD	40.12	1704.851	16	43.8	16	0.3178	0.4	1.6	853.4359	2	20.1105	S4R257|S4R257	Oxidation (M)	M3:Oxidation (M):	0 0 0 0 1 2 7 0 0 1	TGM(+15.99)AFR	DB Search	208	TGMAFRVPTPNV	3
289	DIIFFKFNTPQQPKKK	40.12	1978.104	16	12.5	16	0.5821	0.35	2.5	660.3785	3	18.595	Q9CZ30|OLA1_MOUSE:Q3TW21|Q3TW21_MOUSE:(			0 0 17 1 0 0 0 1 1	DIIFFKFNTPQQP	DB Search	207	DIIFFKFNTPQQP	3
290	ESTLHLVLR	39.38	1066.614	9	100	9	0.2634	0.79	0	534.314	2	15.6042	P0CG50|UBC_MOUSE:E9Q5F6|E9Q5F6_MOUSE:Q3			5 12 13 17 35 3 3	ESTLHLVLR	DB Search	207	ESTLHLVLR	3
291	LHLRFSAPQIENEPE	39.69	1778.895	15	13.3	15	-0.1464	0.3	-2.1	593.9711	3	17.9241	Q61190|I10R2_MOUSE:Q8VHM7|Q8VHM7_MOUSE:(			0 0 0 0 0 3 25 0 0	LHLRFSAPQIENE	DB Search	206	LHLRFSAPQIENE	3
294	DGQVINETSQHHDDLE	39.71	1835.792	16	6.2	16	-0.2578	0.42	0.8	918.9041	2	10.5174	P20152|VIME_MOUSE:Q5FWJ3|Q5FWJ3_MOUSE:Q			0 0 0 1 1 0 1 1 0 (	DGQVINETSQHH	DB Search	203	DGQVINETSQHH	2
295	IQLVEEELDR	36.96	1242.646	10	70	10	-0.3253	0.65	3.4	622.3322	2	17.0903	D3Z6I8|D3Z6I8_MOUSE:Q9D1R6|Q9D1R6_MOUSE:(			4 4 58 38 13 2 2 (	IQLVEEELDR	DB Search	200	IQLVEEELDR	3
296	MRYVASYLLAALGGNSSPSAKDIKK	40.12	2639.41	25	40	25	0.0165	0.25	5.7	660.8652	4	21.285	A0A5F8MPY2|A0A5F8MPY2_MOUSE:P99027|RLA2_			0 0 0 0 0 5 10 16	MRYVASYLLAAL	DB Search	200	MRYVASYLLAAL	3
297	TTPSYVAFTDTER	39.17	1486.694	13	61.5	13	-0.4503	0.28	-0.6	744.3555	2	15.8578	A1E2B8|A1E2B8_MOUSE:B2CSK2|B2CSK2_MOUSE			5 5 4 3 3 7 10 4 1	TTPSYVAFTDTEI	DB Search	196	TTPSYVAFTDTEI	2
298	DNIQGITKPAIRR	39.7	1480.847	13	53.8	13	-0.3763	0.11	3.4	494.6247	3	10.7853	P62806|H4_MOUSE:B2RTM0|B2RTM0_MOUSE			0 0 30 59 4 4 3 3	DNIQGITKPAIRR	DB Search	192	DNIQGITKPAIRR	2
299	PPSYYTQPVPVPNAN	39.86	1642.799	15	13.3	15	-0.4171	0.77	-2.8	822.4064	2	17.8922	Q9JLJ0|LITAF_MOUSE:E0CYR5|E0CYR5_MOUSE			0 0 0 0 0 0 0 4 4 (	PPSYYTQPVPVPI	DB Search	190	PPSYYTQPVPVPI	3
301	GGEDVAIFARGPQAHLVHG	40.05	1929.981	19	31.6	19	-0.1676	0.22	-1.8	644.3346	3	16.5329	F8VPQ6|F8VPQ6_MOUSE:P24822|PPBI_MOUSE:Q0\			0 0 7 20 20 42 39	GGEDVAIFARGP	DB Search	185	GGEDVAIFARGP	3
302	SYELPDGQVITIGNER	40.12	1789.885	16	56.2	16	0.721	0.64	3.1	895.9545	2	20.5045	P63260|ACTG_MOUSE:Q3UJ36|Q3UJ36_MOUSE:Q6			0 0 4 16 2 2 1 2 7	SYELPDGQVITIG	DB Search	181	SYELPDGQVITIG	3
303	SAKPVSQMRMATPLLMRPM	40.12	2144.109	19	15.8	19	-0.5999	0.47	0	715.712	3	19.0014	P04441|HG2A_MOUSE:Q545Y5|Q545Y5_MOUSE:Q3			0 0 20 5 5 1 1 0 0	SAKPVSQMRMA	DB Search	180	SAKPVSQMRMA	3

304	VSDLTQAANK	37.59	1045.54	10	60	10	0.0116	0.66	7.5	523.7814	2	6.1058	Q3V1K9|Q3V1K9_MOUSE:P31001|DESM_MOUSE:Q			5 54 16 16 17 14	VSDLTQAANK	DB Search	176	VSDLTQAANK	2
305	GPTYRGPVPWHTIN	39.52	1593.805	14	21.4	14	-0.2504	0.53	-1.7	532.2748	3	16.3797	Q78P93|Q78P93_MOUSE:Q9WV54|ASAH1_MOUSE:			0 0 0 0 4 0 0 17	GPTYRGPVPWH	DB Search	175	GPTYRGPVPWH	3
308	VITNQYNSPTGLYSSEN	40.12	1885.869	17	47.1	17	-0.3341	0.65	4	943.948	2	16.3701	O70400|PDLI1_MOUSE:S4R1V0|S4R1V0_MOUSE:Q			0 0 0 0 0 25 20 20	VITNQYNSPTGLY	DB Search	172	VITNQYNSPTGLY	3
316	QITVNDLPVGR	39.87	1210.667	11	63.6	11	0.1124	0.74	-1.1	606.3415	2	16.8138	Q61171|PRDX2_MOUSE:Q5M9N9|Q5M9N9_MOUSE			5 5 11 11 13 13 2	QITVNDLPVGR	DB Search	162	QITVNDLPVGR	2
318	APAAAATTAAPAAAAAPAK	40.12	1562.842	19	31.6	19	0.1681	0.65	7.7	782.4359	2	10.3437	Q5M8R8|Q5M8R8_MOUSE:P14869|RLA0_MOUSE:Q			0 0 0 0 2 3 6 5 5 8	APAAAATTAAPA	DB Search	159	APAAAATTAAPA	3
324	NALESYAFNM(+15.99)K	39.65	1302.591	11	63.6	11	-0.641	0.71	-0.2	652.3044	2	15.4058	A1E2B8|A1E2B8	Oxidation (M)	M10:Oxidation (M	0 0 73 75 67 67 9	NALESYAFNM(+1	DB Search	157	NALESYAFNMK	3
326	VGTKRYMAPEVLDETIN	38.96	1934.977	17	17.6	17	-0.8918	0.34	7.7	968.5033	2	17.2061	Q61271|ACV1B_MOUSE:Q3TZF1|Q3TZF1_MOUSE			0 0 0 0 0 0 0 1 0 0	VGTKRYMAPEVL	DB Search	156	VGTKRYMAPEVL	3
327	A(+42.01)SKRALVILAKGAE	37.26	1467.877	14	50	14	0.658	0.72	-1	490.3004	3	16.4279	A2A815|A2A815	Acetylation (N-ter	A1:Acetylation (N	5 0 0 0 0 3 8 20 1	A(+42.01)SKRAL	DB Search	150	ASKRALVILAKGA	3
329	LVQAFQFTDK	39.42	1195.624	10	60	10	-0.0875	0.64	-2.3	598.8178	2	17.8581	B1AXW5|B1AXW5_MOUSE:P35700|PRDX1_MOUSE			5 10 86 86 0 0 3 3	LVQAFQFTDK	DB Search	147	LVQAFQFTDK	2
330	VFLENVIRDAVTYTEHAK	40.12	2104.095	18	50	18	0.5905	0.36	3.8	702.3767	3	25.6057	Q61667|Q61667_MOUSE:P62806|H4_MOUSE:B2RTM			5 25 38 17 0 0 6 1	VFLENVIRDAVTY	DB Search	145	VFLENVIRDAVTY	2
332	GLQFPVGR	36.19	872.4868	8	50	8	-0.5273	0.85	-2.6	437.2495	2	16.463	Q8BFU2|H2A3_MOUSE:A0AUV1|A0AUV1_MOUSE:Q			0 0 70 77 5 2 0 0	GLQFPVGR	DB Search	142	GLQFPVGR	2
335	IIFFKFNTPQQPKKK	39.71	1863.077	15	6.7	15	0.1549	0.37	3.1	622.0349	3	16.356	Q9CZ30|OLA1_MOUSE:Q3TW21|Q3TW21_MOUSE:			0 0 17 0 0 0 1 1 1	IIFFKFNTPQQPK	DB Search	139	IIFFKFNTPQQPK	3
346	GDIIFFKFNTPQQPKKK	39.71	2035.126	17	17.6	17	0.3356	0.41	6.5	679.3868	3	17.7627	Q9CZ30|OLA1_MOUSE:Q3TW21|Q3TW21_MOUSE:			0 0 8 13 0 0 0 0 0	GDIIFFKFNTPQQ	DB Search	125	GDIIFFKFNTPQQ	3
347	ISGLIYEETRGVLK	39.71	1576.882	14	21.4	14	0.2356	0.51	3.4	789.4512	2	18.6306	P62806|H4_MOUSE:B2RTM0|B2RTM0_MOUSE:Q6B			5 3 0 0 1 2 1 1 1	ISGLIYEETRGVL	DB Search	124	ISGLIYEETRGVL	2
350	LFIGGLSFETTDESLR	40.12	1783.899	16	56.2	16	0.2631	0.39	-1.5	892.9576	2	24.9312	P49312|ROA1_MOUSE:Q3TIK8|Q3TIK8_MOUSE:Q5E			3 3 3 1 1 8 6 6 8 3	LFIGGLSFETTDE	DB Search	122	LFIGGLSFETTDE	2
355	VEIIANDQGNR	37.58	1227.621	11	63.6	11	0.4406	0.59	3.6	614.8199	2	10.4995	Q3TKF8|Q3TKF8_MOUSE:Q3U6V3|Q3U6V3_MOUSE			5 5 50 69 48 13 8	VEIIANDQGNR	DB Search	114	VEIIANDQGNR	2
357	KESYSIYVYK	39.71	1278.65	10	40	10	-0.2595	0.78	4.7	640.3351	2	13.1916	Q8CGP0|H2B3B_MOUSE:Q64524|H2B2E_MOUSE:Q			4 4 1 1 1 1 2 2 1 1	KESYSIYVYK	DB Search	111	KESYSIYVYK	3
366	APIIAVTR	36.08	839.5229	8	75	8	0.063	0.84	-6.1	420.7661	2	13.5179	P52480|KPYM_MOUSE			5 39 77 38 9 2 0 0	APIIAVTR	DB Search	103	APIIAVTR	2
369	ANNVLSGGTTM(+15.99)YPGIADR	40.12	1851.879	18	44.4	18	-0.3408	0.64	2.1	926.9506	2	15.9855	Q3UJ36|Q3UJ36	Oxidation (M)	M11:Oxidation (M	0 0 0 7 7 3 3 2 0	ANNVLSGGTTM(	DB Search	99.5	ANNVLSGGTTMY	3
370	TVTAM(+15.99)DVVYALKR	40.12	1481.791	13	69.2	13	-0.2683	0.44	-0.7	741.9041	2	17.569	Q61667|Q61667	Oxidation (M)	M5:Oxidation (M):	4 4 5 5 9 9 9 13 2	TVTAM(+15.99)D	DB Search	99.2	TVTAMDVVYALK	3
372	ESYSVYVYK	40.04	1136.539	9	77.8	9	-0.7956	0.82	1.2	569.2788	2	14.1616	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:Q			5 6 31 53 50 14 8	ESYSVYVYK	DB Search	98.2	ESYSVYVYK	2
381	IEVIEIM(+15.99)TDR	25.68	1233.627	10	70	10	-0.5791	0.66	-0.9	617.8204	2	17.0008	P49312|ROA1_M	Oxidation (M)	M7:Oxidation (M):	5 8 65 74 52 5 5	IEVIEIM(+15.99)T	DB Search	87.5	IEVIEIMTDR	2
389	LAVNM(+15.99)VPFPR	40.02	1158.622	10	60	10	-0.187	0.9	-4.9	580.3168	2	18.2488	Q9CRT0|Q9CRT	Oxidation (M)	M5:Oxidation (M):	5 8 29 13 13 33 1	LAVNM(+15.99)V	DB Search	83.5	LAVNMVPFPR	3
392	EQVANSAFVER	39.88	1248.61	11	63.6	11	-0.2974	0.74	0.1	625.3137	2	11.5282	E9Q0C3|E9Q0C3_MOUSE:Q80YC2|Q80YC2_MOUSE			0 0 33 62 31 20 1	EQVANSAFVER	DB Search	81.3	EQVANSAFVER	2
394	AAYLWVGAGASEAEKT	40.12	1622.794	16	50	16	-0.2111	0.69	2.4	812.4081	2	18.4536	Q3U9Q8|Q3U9Q8_MOUSE:P13020|GELS_MOUSE:Q			0 0 8 19 32 57 16	AAYLWVGAGASI	DB Search	80.5	AAYLWVGAGASI	3
397	DNLIDDLQR	34.49	1100.546	9	55.6	9	1.2432	0.55	-5.9	551.2784	2	19.5509	Q3V1K9|Q3V1K9_MOUSE:P31001|DESM_MOUSE:Q			3 3 27 99 23 1 1	DNLIDDLQR	DB Search	79.4	DNLIDDLQR	3
403	VRYTQKAPQVSTPTL	38.45	1687.926	15	0	15	0.1695	0.42	5.6	844.9769	2	14.1422	Q546G4|Q546G4_MOUSE:P07724|ALBU_MOUSE			0 0 0 0 0 1 0 0 0	VRYTQKAPQVST	DB Search	73.7	VRYTQKAPQVST	3
406	A(+42.01)SNVTNKTDPR	37.29	1243.616	11	27.3	11	3.9355	0.84	-0.4	622.8149	2	6.4322	A0A2I3BQH3|A0A	Acetylation (N-ter	A1:Acetylation (N	0 0 0 2 6 1 0 0 6	A(+42.01)SNVTNI	DB Search	72.2	ASNVTNKTDPR	2
409	TLM(+15.99)ALGSLAVTK	39.35	1219.685	12	41.7	12	-0.2265	0.65	-5.2	610.8478	2	18.2836	P37804|TAGL_M	Oxidation (M)	M3:Oxidation (M):	0 0 88 48 48 21 0	TLM(+15.99)ALG	DB Search	70.2	TLMALGSLAVTK	3
412	TLTLVDTGIGM(+15.99)TK	39.7	1364.722	13	53.8	13	0.1693	0.59	5.8	683.3723	2	18.0196	P11499|HS90B_M	Oxidation (M)	M11:Oxidation (M	0 0 27 27 72 33 1	TLTLVDTGIGM(+	DB Search	66	TLTLVDTGIGMTK	2
413	TLTIVDTGIGM(+15.99)TK	39.7	1364.722	13	53.8	13	0.4732	0.58	5.8	683.3723	2	18.0196	P07901|HS90A_M	Oxidation (M)	M11:Oxidation (M	0 0 27 27 72 33 1	TLTIVDTGIGM(+1	DB Search	66	TLTIVDTGIGMTK	2
417	A(+42.01)AQGEPQVQFK	40.07	1243.62	11	36.4	11	0.0866	0.75	-0.5	622.8183	2	15.12	P62827|RAN_MO	Acetylation (N-ter	A1:Acetylation (N	0 0 1 5 5 0 0 8 3	A(+42.01)AQGEP	DB Search	60.6	AAQGEPQVQFK	2
418	RVPTPNVSVVD	38.78	1181.64	11	45.5	11	0.0247	0.76	-4	591.8251	2	14.9124	S4R257|S4R257_MOUSE:Q3V2I5|Q3V2I5_MOUSE:S			0 0 0 0 0 0 19 19	RVPTPNVSVVD	DB Search	60.1	RVPTPNVSVVD	3
421	NQVAM(+15.99)NPTNTVFDAK	39.71	1664.783	15	40	15	0.0593	0.55	3	833.4012	2	14.1468	Q3U9L2|Q3U9L2	Oxidation (M)	M5:Oxidation (M):	0 0 2 5 5 14 0 0 0	NQVAM(+15.99)N	DB Search	57.6	NQVAMNPTNTVF	2
426	KYDEELEER	35.7	1209.551	9	44.4	9	-0.2716	0.85	-0.3	605.7842	2	7.0309	P37804|TAGL_MOUSE:A0A1L1STN8|A0A1L1STN8_M			5 12 2 2 1 1 0 0 0	KYDEELEER	DB Search	51.4	KYDEELEER	2
428	DPKFEVIDKPQS	40.12	1401.714	12	66.7	12	-0.4767	0.7	1.7	701.8671	2	13.4855	P97450|ATP5J_MOUSE			5 7 4 4 4 4 5 1 2	DPKFEVIDKPQS	DB Search	50.9	DPKFEVIDKPQS	2
445	AMDYWGQGTSVTVSS	40.12	1587.688	15	20	15	-0.4032	0.55	3.1	794.8554	2	19.3786	X5J5A3|X5J5A3_MOUSE:X5J523|X5J523_MOUSE:K7			0 0 0 2 4 0 0 2 0	AMDYWGQGTSV	DB Search	NA	AMDYWGQGTSV	2
447	LGDVYVNDAFGTAHR	39.71	1633.785	15	60	15	-0.0378	0.64	-3.6	545.6003	3	16.3584	S4R2M7|S4R2M7_MOUSE:P09041|PGK2_MOUSE:P			5 0 0 7 8 10 20 0	LGDVYVNDAFGT	DB Search	NA	LGDVYVNDAFGT	1
461	SPPPYAAYATPTPEVYG	39.71	1779.836	17	41.2	17	0.7664	0.64	2.2	890.927	2	20.1549	Q9QZC7|PKHB2_MOUSE:Q3UFC9|Q3UFC9_MOUSE			0 0 0 0 0 1 10 30	SPPPYAAYATPTI	DB Search	NA	SPPPYAAYATPTI	1
467	NLNDRLASYLDKVRA	39.71	1746.938	15	26.7	15	-0.8803	0.48	-0.7	583.3194	3	19.5984	Q9QWL7|K1C17_MOUSE:P19001|K1C19_MOUSE:Q			0 0 0 0 0 0 1 2 3 4	NLNDRLASYLDK	DB Search	NA	NLNDRLASYLDK	1
470	S(+42.01)VQVVSAAAAAKVPEVELKDLSPSE	39.58	2565.354	25	20	25	-0.2566	0.51	8.9	856.1328	3	24.9041	Q9JJF5|Q9JJF5_I	Acetylation (N-ter	S1:Acetylation (N	0 0 0 37 60 26 0 0	S(+42.01)VQVVS/	DB Search	NA	SVQVVSAAAAAK	1
475	SRDKPLKDVIIVDSGKIEVEKPFAIAKE	39.71	3123.754	28	25	28	-1.5357	0.43	-2.1	625.7568	5	18.8285	Q9DCY1|Q9DCY1_MOUSE:P24369|PPIB_MOUSE			0 0 0 1 0 0 2 1 1	SRDKPLKDVIIVD	DB Search	NA	SRDKPLKDVIIVD	1
476	KPLKDVIIVDSGKIEVEKPFAIAKE	39.71	2765.594	25	20	25	-1.309	0.61	-4.2	692.4029	4	19.0812	Q9DCY1|Q9DCY1_MOUSE:P24369|PPIB_MOUSE			5 0 0 0 0 1 2 4 1 1	KPLKDVIIVDSGK	DB Search	NA	KPLKDVIIVDSGK	1
480	GDGNHTLFHNPHVNPLPTGYE	37.16	2315.072	21	14.3	21	-0.2289	0.39	0.7	772.6984	3	16.6728	Q9DCW5|Q9DCW5_MOUSE:Q8R2L0|Q8R2L0_MOU			0 0 0 0 0 0 0 0 0	GDGNHTLFHNPH	DB Search	NA	GDGNHTLFHNPH	2
482	HTLFHNPHVNPLPT	39.04	1622.832	14	28.6	14	-0.0898	0.13	3.6	541.9531	3	14.6427	Q9DCW5|Q9DCW5_MOUSE:Q8R2L0|Q8R2L0_MOU			0 0 0 0 2 4 1 1 1	HTLFHNPHVNPLI	DB Search	NA	HTLFHNPHVNPLI	2
484	NPHVNPLPTGYE	39.66	1336.641	12	58.3	12	-0.0512	0.74	-3.3	669.3256	2	14.8662	Q9DCW5|Q9DCW5_MOUSE:Q8R2L0|Q8R2L0_MOU			0 0 0 0 12 2 4 2 1	NPHVNPLPTGYE	DB Search	NA	NPHVNPLPTGYE	1
489	TTEDLVAKLKEVGRI	39.71	1670.957	15	33.3	15	0.2013	0.58	5.9	557.9961	3	20.4987	Q9DCW4|ETFB_MOUSE			5 0 0 0 0 10 0 0 1	TTEDLVAKLKEV(	DB Search	NA	TTEDLVAKLKEV(	1
495	LTTAAVSTAQPILSKLEPQIATAS	39.63	2410.332	24	12.5	24	-0.3137	0.61	-0.9	1206.172	2	24.4717	Q9DBG5|PLIN3_MOUSE:Q2XSQ4|Q2XSQ4_MOUSE			0 0 0 0 0 0 1 1 1 2	LTTAAVSTAQPIL	DB Search	NA	LTTAAVSTAQPIL	2
498	SEVKEIEESV	33.72	1147.561	10	60	10	0.7148	0.58	-6.3	574.7841	2	14.249	Q9D312|K1C20_MOUSE			0 0 12 0 0 35 55 3	SEVKEIEESV	DB Search	NA	SEVKEIEESV	1
501	ENYEASKAYSSVDE	40.12	1590.669	14	85.7	14	-0.2077	0.5	0.3	796.3437	2	10.8035	Q9D306|MGT4C_MOUSE			0 0 20 20 36 18 1	ENYEASKAYSSV	DB Search	NA	ENYEASKAYSSV	2
512	LVILEGELER	38.83	1169.666	10	70	10	-0.1004	0.67	0.2	585.8402	2	19.3969	Q9D1R6|Q9D1R6_MOUSE:P58774|TPM2_MOUSE:Q			5 19 96 96 49 3 2	LVILEGELER	DB Search	NA	LVILEGELER	2
517	FIASVSTVLTSK	40.05	1251.707	12	75	12	0.3303	0.64	-0.1	626.8624	2	20.0232	Q9CY06|Q9CY06_MOUSE			5 7 59 28 28 9 2 2	FIASVSTVLTSK	DB Search	NA	FIASVSTVLTSK	2
521	AILVDLEPGTM(+15.99)DSVR	39.7	1630.824	15	40	15	0.557	0.76	7.9	816.4255	2	19.7919	Q9CWF2|TBB2B	Oxidation (M)	M11:Oxidation (M	0 0 4 5 8 8 20 4 0	AILVDLEPGTM(+	DB Search	NA	AILVDLEPGTMDS	1
522	AVLVDLEPGTM(+15.99)DSVR	25.23	1616.808	15	26.7	15	0.397	0.72	9.8	809.4191	2	18.5645	Q9CVR0|Q9CVR(	Oxidation (M)	M11:Oxidation (M	0 0 1 3 6 8 20 0 0	AVLVDLEPGTM(+	DB Search	NA	AVLVDLEPGTMD	1
525	GVVDSEDIPLNLSR	40.12	1512.778	14	78.6	14	-0.0189	0.94	2.5	757.4002	2	19.7498	Q9CQN1|TRAP1_MOUSE:Q3UPJ8|Q3UPJ8_MOUSE:			0 0 4 20 17 17 26	GVVDSEDIPLNLS	DB Search	NA	GVVDSEDIPLNLS	2
530	LGEHNIDVL	30.05	1008.524	9	77.8	9	-0.4148	0.77	-1.8	505.2684	2	17.0197	Q9CPN7|Q9CPN7_MOUSE:Q7TT42|Q7TT42_MOUSE			2 2 0 0 3 5 13 27	LGEHNIDVL	DB Search	NA	LGEHNIDVL	2
543	NNTLVFIVDVKANKHQIKQAVKK	39.58	2634.533	23	13	23	-3.2032	0.29	6.8	879.191	3	13.977	Q91YK6|Q91YK6_MOUSE:P62751|RL23A_MOUSE:Q			0 0 0 1 16 16 5 0	NNTLVFIVDVKAN	DB Search	NA	NNTLVFIVDVKAN	2
551	DARSYTAAVANRAKGG	40.05	1606.818	16	25	16	0.8553	0.86	-1.9	536.6133	3	10.5105	Q91XS1|MTMR4_MOUSE:Q6PE02|Q6PE02_MOUSE			0 0 0 0 0 1 5 19 1	DARSYTAAVANR	DB Search	NA	DARSYTAAVANR	2
555	QPDLNFRNPAVQEEIK	38.86	1896.969	16	31.2	16	-0.4522	0.43	2.1	633.3317	3	16.4467	Q91WV7|SLC31_MOUSE			4 4 3 3 0 0 1 1 0 0	QPDLNFRNPAVQ	DB Search	NA	QPDLNFRNPAVQ	2
564	RRFVNVVPTFGKKKGPNANS	37.39	2215.234	20	15	20	1.6578	0.28	1.6	554.8166	4	11.4917	Q91V99|Q91V99_MOUSE:Q3THB2|Q3THB2_MOUSE			0 0 0 0 0 3 9 0 0 0	RRFVNVVPTFGK	DB Search	NA	RRFVNVVPTFGK	2
565	RFVNVVPTFGKKKGPNANS	33.46	2059.133	19	31.6	19	1.6421	0.64	0.2	515.7905	4	12.9608	Q91V99|Q91V99_MOUSE:Q3THB2|Q3THB2_MOUSE			0 0 0 2 43 2 0 0 0	RFVNVVPTFGKK	DB Search	NA	RFVNVVPTFGKK	2
567	FVNVVPTFGKKKGPNANS	39.23	1903.032	18	5.6	18	0.6611	0.28	-2.9	635.3493	3	14.432	Q91V99|Q91V99_MOUSE:Q3THB2|Q3THB2_MOUSE			0 0 0 0 34 0 0 0 0	FVNVVPTFGKKK	DB Search	NA	FVNVVPTFGKKK	2
568	VNVVPTFGKKKGPNANS	33.62	1755.963	17	17.6	17	0.9169	0.06	0.2	586.3284	3	10.9492	Q91V99|Q91V99_MOUSE:Q3THB2|Q3THB2_MOUSE			5 34 0 0 0 0 6 0 0	VNVVPTFGKKKG	DB Search	NA	VNVVPTFGKKKG	2
575	PVVPVHLDGTF	39.59	1179.629	11	63.6	11	0.7768	0.75	-2.1	590.8204	2	21.2659	Q8VHS0|Q8VHS0_MOUSE:Q5GAN2|Q5GAN2_MOUS			5 14 67 11 11 0 0	PVVPVHLDGTF	DB Search	NA	PVVPVHLDGTF	2
576	M(+15.99)SRGSGGG	26.4	723.297	8	12.5	8	0.7743	0.47	10.3	724.3117	1	16.8276	Q8VED5|K2C79_I	Oxidation (M)	M1:Oxidation (M):	0 0 4 0 0 0 0 0	M(+15.99)SRGSG	DB Search	NA	MSRGSGGG	1
577	KPTVTVVSPLPNDSINPQP	39.71	2002.074	19	21.1	19	0.3266	0.76	1.8	1002.046	2	19.1261	Q8VD58|EVI2B_MOUSE			0 0 0 0 0 0 2 5 0 0	KPTVTVVSPLPND	DB Search	NA	KPTVTVVSPLPND	2
579	EEAVYEKKVHIEPWEEPY(+79.97)EELETEPY(+79.	23.48	4269.78	33	3	33	-6.2125	NA	-1	712.6365	6	16.6879	Q8R4N3|Q8R4N3	Phosphorylation (	Y18:Phosphorylat	0 0 0 0 0 0 0 0 0 0	EEAVYEKKVHIEF	DB Search	NA	EEAVYEKKVHIEF	1
580	TFIAIKPDGVQR	33.02	1343.756	12	25	12	-0.1887	0.6	10.3	672.8923	2	14.7618	Q8R4B4|Q8R4B4_MOUSE:Q5NC81|Q5NC81_MOUSI			0 0 0 2 2 12 1 1 0	TFIAIKPDGVQR	DB Search	NA	TFIAIKPDGVQR	1
589	M(+15.99)ELQEIQLK	27.03	1146.596	9	33.3	9	-0.999	0.54	-0.2	574.3049	2	14.6442	Q8K0Z5|Q8K0Z5	Oxidation (M)	M1:Oxidation (M):	0 0 54 22 17 0 0 0	M(+15.99)ELQEI(	DB Search	NA	MELQEIQLK	2
597	YPDENVRYSFSTVNLSPEN	39.71	2230.018	19	0	19	-0.4506	0.74	-0.6	1116.016	2	19.9662	Q8BWN9|Q8BWN9_MOUSE:Q8BWS8|Q8BWS8_MO			0 0 0 0 0 0 0 0 0 0	YPDENVRYSFST	DB Search	NA	YPDENVRYSFST	2
609	SLQAFSNPSAGISVDVK	40.12	1718.884	17	52.9	17	-0.0892	0.73	1.6	860.4526	2	19.2614	Q8BG07|PLD4_MOUSE			0 0 1 6 17 12 12 7	SLQAFSNPSAGIS	DB Search	NA	SLQAFSNPSAGIS	2
633	GEIKVPEVDIKGPK	39.71	1507.861	14	71.4	14	0.1805	0.67	-1.8	503.6267	3	15.026	Q6UL10|Q6UL10_MOUSE:E9Q616|E9Q616_MOUSE:			0 0 64 9 11 38 38	GEIKVPEVDIKGF	DB Search	NA	GEIKVPEVDIKGF	2
638	LM(+15.99)IEM(+15.99)DGTENK	38.21	1311.569	11	54.5	11	-0.1094	0.59	3.2	656.7937	2	9.373	Q6PHC1|Q6PHC1	Oxidation (M);Oxi	M2:Oxidation (M):	5 12 18 4 4 3 1 0	LM(+15.99)IEM(+	DB Search	NA	LMIEMDGTENK	1
639	IGAEVYHNLK	40.1	1142.608	10	100	10	0.1675	0.61	-0.4	572.3126	2	10.8816	Q6PHC1|Q6PHC1_MOUSE:B0QZL1|B0QZL1_MOUSE			5 11 11 17 17 3 2	IGAEVYHNLK	DB Search	NA	IGAEVYHNLK	1
646	VELDPEIQK	35.86	1069.566	9	66.7	9	-0.2532	0.6	-0.8	535.7896	2	13.3343	Q6NXH9|K2C73_MOUSE:Q6IME9|K2C72_MOUSE:Q			5 43 51 51 6 6 0 0	VELDPEIQK	DB Search	NA	VELDPEIQK	1
648	ALEEANADLEVK	39.64	1300.651	12	66.7	12	-0.0423	0.79	1.5	651.3337	2	13.6424	Q6IFX2|K1C42_MOUSE			0 0 96 88 88 47 1	ALEEANADLEVK	DB Search	NA	ALEEANADLEVK	2
655	K(+42.01)KDGKKRKRSRKESYSIYVYKVLKQVHPD	39.64	3605.032	29	20.7	29	-2.7348	0.51	-9.3	722.0069	5	12.181	Q64524|H2B2E_M	Acetylation (N-ter	K1:Acetylation (N	0 0 0 0 0 0 0 0 0	K(+42.01)KDGKK	DB Search	NA	KKDGKKRKRSRI	1
656	VLLPEYGGTK	29.95	1075.591	10	60	10	-0.5821	0.53	-3.2	538.8012	2	15.4186	Q64433|CH10_MOUSE:Q9JI95|Q9JI95_MOUSE:Q4KI			2 2 40 8 4 2 0 0 0	VLLPEYGGTK	DB Search	NA	VLLPEYGGTK	1
678	TVTAM(+15.99)DVVYALK	40.12	1325.69	12	75	12	-0.5455	0.55	2.5	663.8555	2	19.1833	Q61667|Q61667	Oxidation (M)	M5:Oxidation (M):	5 6 48 38 38 11 1	TVTAM(+15.99)D	DB Search	NA	TVTAMDVVYALK	2
688	HVLVTLGEK	39.68	994.5811	9	77.8	9	0.9008	0.58	1	498.2983	2	12.1012	Q60605|MYL6_MOUSE:A0A1W2P6G5|A0A1W2P6G5			5 23 14 14 9 5 2 1	HVLVTLGEK	DB Search	NA	HVLVTLGEK	1
693	GPSSVEDIK	39.27	930.4658	9	77.8	9	0.0233	0.9	-3	466.2388	2	8.3548	Q5SQB5|Q5SQB5_MOUSE:Q9DAY9|Q9DAY9_MOUS			2 2 44 16 11 6 4 0	GPSSVEDIK	DB Search	NA	GPSSVEDIK	1
700	PIYPVVPVHLDGTF	40.12	1552.829	14	35.7	14	0.6528	0.47	2.4	777.4254	2	25.7465	Q5GAN2|Q5GAN2_MOUSE:F6YUX7|F6YUX7_MOUSI			0 0 37 4 4 4 0 0 2	PIYPVVPVHLDGT	DB Search	NA	PIYPVVPVHLDGT	2
713	RFAVRDMRQTVAVGVIKAVDKKAAGAGKVTK	39.71	3269.887	31	9.7	31	-5.8168	NA	2	545.9895	6	15.9904	Q58E64|Q58E64_MOUSE:Q3UZQ3|Q3UZQ3_MOUSE			0 0 0 0 0 0 0 0 0 0	RFAVRDMRQTV/	DB Search	NA	RFAVRDMRQTV/	2
719	EHALLAYTLGVK	40.12	1313.734	12	58.3	12	0.0016	0.66	1.5	657.877	2	18.3824	Q58E64|Q58E64_MOUSE:Q3UZQ3|Q3UZQ3_MOUSE			0 0 17 17 22 6 6 2	EHALLAYTLGVK	DB Search	NA	EHALLAYTLGVK	1
720	STTTGHLIYK	40.08	1119.592	10	80	10	-0.4128	0.73	5	560.8076	2	8.479	Q58E64|Q58E64_MOUSE:Q3UZQ3|Q3UZQ3_MOUSE			1 1 11 11 4 2 2 8	STTTGHLIYK	DB Search	NA	STTTGHLIYK	1
737	EERAAPFTLEYRVFLKNEKGQY	30.06	2687.371	22	9.1	22	-0.7851	0.64	-0.1	672.8499	4	19.436	Q4FK49|Q4FK49_MOUSE			0 0 0 0 0 1 1 4 3 0	EERAAPFTLEYR	DB Search	NA	EERAAPFTLEYR	1
749	ADVDAATLAR	39.67	1001.514	10	60	10	-0.3683	0.86	-1.1	501.765	2	11.1355	Q3V1K9|Q3V1K9_MOUSE:P31001|DESM_MOUSE:Q			5 14 38 57 36 9 0	ADVDAATLAR	DB Search	NA	ADVDAATLAR	1
750	QPPPAYEPPAPAPAPLPPP	39.53	1902.988	19	0	19	0.0098	0.75	7.3	952.5082	2	20.6757	Q3UXS0|Q3UXS0_MOUSE			0 0 0 0 0 0 1 0 0 0	QPPPAYEPPAPA	DB Search	NA	QPPPAYEPPAPA	1
752	AEAEALYQTK	38.12	1122.556	10	50	10	-0.1986	0.56	3.2	562.2869	2	9.8749	Q3UV17|K22O_MOUSE:Q9R0H5|K2C71_MOUSE			0 0 53 53 29 25 3	AEAEALYQTK	DB Search	NA	AEAEALYQTK	2
778	VAPEEHPTLLTEAPLNPK	39.66	1955.036	18	16.7	18	0.0395	0.56	1.2	652.6868	3	17.2968	Q3UJ36|Q3UJ36_MOUSE:A0A494B9T3|A0A494B9T3			0 0 0 0 0 0 0 0 0 1	VAPEEHPTLLTE/	DB Search	NA	VAPEEHPTLLTE/	2
791	TPSAAYLWVGAGASEAEKT	39.69	1907.927	19	15.8	19	-0.9375	0.68	8.6	954.9787	2	20.23	Q3U9Q8|Q3U9Q8_MOUSE:P13020|GELS_MOUSE:Q			0 0 0 0 0 1 2 2 2 0	TPSAAYLWVGA(	DB Search	NA	TPSAAYLWVGA(	1
799	TLVLLM(+15.99)GK	35	889.5306	8	62.5	8	0.2241	0.53	0.4	445.7728	2	16.7709	Q3U7V7|Q3U7V7	Oxidation (M)	M6:Oxidation (M):	4 4 46 23 8 1 0 0	TLVLLM(+15.99)(	DB Search	NA	TLVLLMGK	1
801	VPPPPPIAR	31.11	942.5651	9	55.6	9	0.8168	0.74	-3.1	472.2884	2	12.0919	Q3U6P5|Q3U6P5_MOUSE:Q9Z204|HNRPC_MOUSE			5 43 26 12 2 0 0 0	VPPPPPIAR	DB Search	NA	VPPPPPIAR	2
806	GIDPYDQPNAIYIERH	40.12	1899.912	16	31.2	16	-0.3744	0.62	-5.4	634.3092	3	16.5268	Q3U2X9|Q3U2X9_MOUSE:O88307|SORL_MOUSE			0 0 0 0 0 0 12 0 0	GIDPYDQPNAIYI	DB Search	NA	GIDPYDQPNAIYI	2
810	YGEPGEVFINK	40.12	1251.614	11	54.5	11	-0.5128	0.5	-3.3	626.8134	2	15.5111	Q3TZL2|Q3TZL2_MOUSE:A0A991ENV6|A0A991ENV6			5 0 0 5 2 2 5 1 0 0	YGEPGEVFINK	DB Search	NA	YGEPGEVFINK	1
828	YPSQASIYSPPAAAAAAAA	39.71	1776.868	19	42.1	19	0.3122	0.22	1.4	889.4426	2	19.0481	Q3TQ49|Q3TQ49_MOUSE:P70297|STAM1_MOUSE:Q			0 0 0 0 0 2 2 5 6 0	YPSQASIYSPPA/	DB Search	NA	YPSQASIYSPPA/	2
832	DAGTIAGLNVM(+15.99)R	36.72	1232.618	12	41.7	12	-0.3089	0.74	-2.1	617.3166	2	15.3353	Q3TKF8|Q3TKF8	Oxidation (M)	M11:Oxidation (M	0 0 1 4 45 48 9 3	DAGTIAGLNVM(+	DB Search	NA	DAGTIAGLNVMR	1
833	IINEPTAAAIAYGLDK	39.71	1658.888	16	62.5	16	0.0173	0.71	2.6	830.4534	2	20.4721	Q3TKF8|Q3TKF8_MOUSE:B2CSK2|B2CSK2_MOUSE			0 0 4 13 2 2 9 15	IINEPTAAAIAYGL	DB Search	NA	IINEPTAAAIAYGL	1
848	PPPAYEPPAPAPAPLPPP	30.56	1774.929	18	0	18	0.0061	0.53	8.6	888.4796	2	20.8986	Q3TDM8|Q3TDM8_MOUSE:Q3UXS0|Q3UXS0_MOUS			0 0 0 0 0 0 0 0 0 0	PPPAYEPPAPAP/	DB Search	NA	PPPAYEPPAPAP/	1
849	EPPPAYEPPAPAPAPLPPP	39.71	1903.972	19	21.1	19	-0.4074	0.73	10.9	953.0036	2	20.9358	Q3TDM8|Q3TDM8_MOUSE:B2M0S3|B2M0S3_MOUS			0 0 0 0 0 0 2 0 0 0	EPPPAYEPPAPAI	DB Search	NA	EPPPAYEPPAPAI	1
850	EPPPAYEPPAPAPAPLPP	31.73	1806.919	18	11.1	18	-0.4837	0.54	6.1	904.4724	2	20.4927	Q3TDM8|Q3TDM8_MOUSE:B2M0S3|B2M0S3_MOUS			0 0 0 0 0 0 0 0 0 0	EPPPAYEPPAPAI	DB Search	NA	EPPPAYEPPAPAI	1
854	LAPMYYRGAQAAIVVYD	39.7	1899.955	17	47.1	17	-0.9711	0.35	7	950.9916	2	20.8116	Q3TCT9|Q3TCT9_MOUSE:P61021|RAB5B_MOUSE:Q			0 0 0 0 0 2 2 2 2 1	LAPMYYRGAQA/	DB Search	NA	LAPMYYRGAQA/	2
859	GPKPFSAPKPQTSPS	40.11	1524.794	15	6.7	15	0.162	0.44	-0.1	763.4058	2	9.9831	Q3TC53|Q3TC53_MOUSE:P40124|CAP1_MOUSE:Q3			0 0 4 0 0 0 0 0 0	GPKPFSAPKPQT	DB Search	NA	GPKPFSAPKPQT	2
862	GDTEGRLEVVTDPTTNAGYVK	40.09	2221.086	21	42.9	21	-0.8317	0.67	-0.9	741.3704	3	15.3548	Q3TAN0|Q3TAN0_MOUSE:A2AKS7|A2AKS7_MOUSE			0 0 0 0 0 0 0 2 11	GDTEGRLEVVTD	DB Search	NA	GDTEGRLEVVTD	2
871	TQVQWNDPGAQYSLVN	39.71	1818.854	16	56.2	16	-0.1846	0.54	7.6	910.441	2	20.4949	Q3TAN0|Q3TAN0_MOUSE:A2AKS7|A2AKS7_MOUSE			0 0 0 12 18 39 39	TQVQWNDPGAQ	DB Search	NA	TQVQWNDPGAQ	1
877	TRLEQEIATYR	39.55	1378.721	11	0	11	0.297	0.53	4.8	690.3708	2	13.549	Q3SYP5|Q3SYP5_MOUSE:Q9QWL7|K1C17_MOUSE			0 0 0 0 0 0 0 0 0 0	TRLEQEIATYR	DB Search	NA	TRLEQEIATYR	2
879	M(+15.99)VNHFIAEFK	39.64	1250.612	10	40	10	0.0148	0.64	9.1	626.3189	2	15.1984	Q3KQJ4|Q3KQJ4	Oxidation (M)	M1:Oxidation (M):	0 0 4 4 0 1 3 4 0 0	M(+15.99)VNHFI/	DB Search	NA	MVNHFIAEFK	1
881	NSLESYAFNM(+15.99)K	39.4	1318.586	11	54.5	11	-0.2244	0.59	3.2	660.3026	2	15.0876	Q3KQJ4|Q3KQJ4	Oxidation (M)	M10:Oxidation (M	0 0 29 89 20 20 2	NSLESYAFNM(+1	DB Search	NA	NSLESYAFNMK	1
882	DAGTIAGLNVLR	39.58	1198.667	12	50	12	0.1636	0.89	-2.3	600.3394	2	20.5894	Q3KQJ4|Q3KQJ4_MOUSE:Q3U9L2|Q3U9L2_MOUSE			0 0 6 6 54 66 6 6	DAGTIAGLNVLR	DB Search	NA	DAGTIAGLNVLR	1
883	LLQDFFNGK	37.5	1080.56	9	66.7	9	-0.2701	0.62	2.6	541.2889	2	20.1927	Q3KQJ4|Q3KQJ4_MOUSE:Q3U9L2|Q3U9L2_MOUSE			5 20 55 14 14 6 0	LLQDFFNGK	DB Search	NA	LLQDFFNGK	1
884	APPSGGASSGPTIEEVD	39.66	1569.716	17	41.2	17	-0.4489	0.45	-1.2	785.8642	2	14.3841	Q3KQJ4|Q3KQJ4_MOUSE:Q3U9L2|Q3U9L2_MOUSE			0 0 0 0 0 0 0 6 6 9	APPSGGASSGPT	DB Search	NA	APPSGGASSGPT	1
897	AAVDTSSEITTKDLKEKKEVVE	39.71	2419.269	22	22.7	22	-1.0632	0.21	-3.4	605.8226	4	11.7112	Q0VGU2|Q0VGU2_MOUSE:Q3U6E4|Q3U6E4_MOUS			0 0 77 0 0 37 7 7	AAVDTSSEITTKD	DB Search	NA	AAVDTSSEITTKD	1
899	DEEAEAPTGKRVAED	35.06	1615.733	15	0	15	0.5856	0.64	0.1	808.8736	2	5.1266	Q0VGU2|Q0VGU2_MOUSE:P26350|PTMA_MOUSE:Q			0 0 0 0 0 0 0 0 0 0	DEEAEAPTGKRV	DB Search	NA	DEEAEAPTGKRV	1
900	S(+42.01)DAAVDTSSEITTK	39.71	1465.678	14	64.3	14	-0.0209	0.77	4.6	733.8499	2	13.6699	Q0VGU2|Q0VGU2	Acetylation (N-ter	S1:Acetylation (N	0 0 3 53 52 41 31	S(+42.01)DAAVD	DB Search	NA	SDAAVDTSSEITT	2
924	GDLEYQMSTTARAKR	34.36	1725.847	15	33.3	15	-0.9497	0.04	1.2	576.2902	3	10.0525	Q02257|PLAK_MOUSE			0 0 21 72 37 6 5 0	GDLEYQMSTTAF	DB Search	NA	GDLEYQMSTTAF	2
930	EEKPVPAAPVPSPVAPAPVPSR	40.12	2191.2	22	13.6	22	-0.5788	0.52	0.4	731.4093	3	16.351	P97825|JUPI1_MOUSE			0 0 0 0 0 0 0 0 0 0	EEKPVPAAPVPSI	DB Search	NA	EEKPVPAAPVPSI	1
943	DVNAAIATIK	38.25	1014.571	10	30	10	0.5939	0.61	0.4	508.2929	2	15.5713	P68369|TBA1A_MOUSE:P68373|TBA1C_MOUSE:Q52			0 0 52 52 8 0 0 0	DVNAAIATIK	DB Search	NA	DVNAAIATIK	1
945	VGINYQPPTVVPGGDLAK	39.64	1823.978	18	22.2	18	-0.447	0.86	5	913.0009	2	19.6299	P68369|TBA1A_MOUSE:P68373|TBA1C_MOUSE:P05			0 0 0 0 2 7 4 0 0	VGINYQPPTVVP(	DB Search	NA	VGINYQPPTVVP(	1
948	LSVDYGKK	39.9	908.4967	8	87.5	8	-0.1719	0.75	0	455.2567	2	6.9163	P68369|TBA1A_MOUSE:P68373|TBA1C_MOUSE:A0			5 50 25 20 16 4 0	LSVDYGKK	DB Search	NA	LSVDYGKK	1
955	LLDFGSLSNLQVTQPTVGM(+15.99)NFK	40.09	2424.236	22	4.5	22	-0.057	0.69	0.8	1213.129	2	25.7075	P63276|RS17_M	Oxidation (M)	M19:Oxidation (M	0 0 0 0 0 0 0 0 0 0	LLDFGSLSNLQV	DB Search	NA	LLDFGSLSNLQV	1
957	LDLAGRDLTDYLM(+15.99)K	39.27	1638.829	14	35.7	14	-0.1229	0.07	-3.5	547.2816	3	20.3234	P63260|ACTG_M	Oxidation (M)	M13:Oxidation (M	5 66 42 22 0 0 1 1	LDLAGRDLTDYL	DB Search	NA	LDLAGRDLTDYL	1
959	DLTDYLM(+15.99)K	36.6	1013.474	8	50	8	-0.5423	0.56	1	507.7448	2	17.5011	P63260|ACTG_M	Oxidation (M)	M7:Oxidation (M):	0 0 35 18 7 4 0 0	DLTDYLM(+15.99	DB Search	NA	DLTDYLMK	2
969	VAPEEHPV	30.66	876.4341	8	75	8	-2.2448	0.72	1.8	439.2251	2	6.1777	P63260|ACTG_MOUSE:E9Q5F4|E9Q5F4_MOUSE:G3			5 8 6 6 2 2 0 0	VAPEEHPV	DB Search	NA	VAPEEHPV	2
970	IWHHTFYNELR	39.71	1514.742	11	63.6	11	0.2141	0.74	0.7	505.9216	3	13.9195	P63260|ACTG_MOUSE:A0A1D5RM20|A0A1D5RM20			5 0 0 45 18 18 36	IWHHTFYNELR	DB Search	NA	IWHHTFYNELR	1
975	VGLQVVAVK	39.5	911.5804	9	100	9	0.4716	0.74	-1.3	456.7969	2	15.8345	P63038|CH60_MOUSE			5 18 18 34 11 8 3	VGLQVVAVK	DB Search	NA	VGLQVVAVK	2
977	LSDGVAVLK	34.6	900.528	9	77.8	9	-0.1971	0.76	0.5	451.2715	2	13.9796	P63038|CH60_MOUSE			5 61 24 4 2 2 3 0	LSDGVAVLK	DB Search	NA	LSDGVAVLK	1
993	YKVIPKSKFVLVKF	39.71	1695.049	14	64.3	14	-0.0943	0.17	-7.6	566.0192	3	17.2198	P57759|ERP29_MOUSE:A8C1V9|A8C1V9_MOUSE			0 0 2 3 0 0 3 3 4 4	YKVIPKSKFVLVK	DB Search	NA	YKVIPKSKFVLVK	1
995	AIAELGIYPAVDPLDSTSR	40.12	1987.026	19	36.8	19	0.2486	0.68	3.4	994.5261	2	24.3206	P56480|ATPB_MOUSE			0 0 4 1 9 10 17 20	AIAELGIYPAVDP	DB Search	NA	AIAELGIYPAVDP	1
996	EAVAKADKLAEEHGS	39.42	1553.769	15	53.3	15	-1.3616	0.47	7.6	518.934	3	5.0503	P56480|ATPB_MOUSE			5 0 0 0 0 2 2 5 7 6	EAVAKADKLAEE	DB Search	NA	EAVAKADKLAEE	1
997	LVLEVAQHLGESTVR	39.71	1649.91	15	40	15	0.1152	0.5	7.9	550.9816	3	18.6846	P56480|ATPB_MOUSE			5 7 0 0 6 1 1 12 1	LVLEVAQHLGES	DB Search	NA	LVLEVAQHLGES	1
###	HLGESTVRT	39.33	998.5145	9	33.3	9	-0.1894	0.9	0.8	500.2649	2	2.643	P56480|ATPB_MOUSE			5 51 1 1 2 1 1 0 0	HLGESTVRT	DB Search	NA	HLGESTVRT	1
###	VARYRPRAPIIAVTRNPQ	40.12	2077.202	18	22.2	18	0.1636	0.68	0.1	520.3091	4	11.9755	P52480|KPYM_MOUSE			0 0 0 0 0 0 0 0 0 0	VARYRPRAPIIAV	DB Search	NA	VARYRPRAPIIAV	2
###	T(+42.01)SRKKVLLKVIILGD	40.11	1724.092	15	33.3	15	-0.0925	0.24	1.8	575.7071	3	19.6521	P51150|RAB7A_M	Acetylation (N-ter	T1:Acetylation (N	0 0 0 1 0 0 2 1 1 7	T(+42.01)SRKKVI	DB Search	NA	TSRKKVLLKVIILC	2
###	YEELQVTAGR	39.05	1164.578	10	70	10	-0.4104	0.79	-0.3	583.2958	2	12.3418	P50446|K2C6A_MOUSE:Q9CV72|Q9CV72_MOUSE:A			5 18 74 56 56 51	YEELQVTAGR	DB Search	NA	YEELQVTAGR	2
###	ATGPPVSELITK	39.71	1211.676	12	50	12	0.1303	0.56	-2.4	606.8439	2	16.815	P43276|H15_MOUSE:Q1WWK3|Q1WWK3_MOUSE			0 0 92 90 10 10 5	ATGPPVSELITK	DB Search	NA	ATGPPVSELITK	1
###	AKAKTVKPKAAKPKTSKPKAAKPKKTAAKKK	39.58	3257.091	31	29	31	-0.5349	NA	-0.5	543.8556	6	1.903	P43274|H14_MOUSE			0 0 0 0 0 0 0 23 7	AKAKTVKPKAAK	DB Search	NA	AKAKTVKPKAAK	2
###	DPPFEVRG	26.46	915.445	8	62.5	8	-0.6651	0.83	-2	458.7289	2	14.256	P35487|ODPAT_MOUSE:Q3UFJ3|Q3UFJ3_MOUSE:P			5 9 16 6 4 0 0 0	DPPFEVRG	DB Search	NA	DPPFEVRG	1
###	PM(+15.99)FIVNTNVPR	39.66	1302.675	11	36.4	11	0.3747	0.66	0.8	652.3455	2	16.785	P34884|MIF_MOU	Oxidation (M)	M2:Oxidation (M):	0 0 6 6 9 5 1 0 0	PM(+15.99)FIVNT	DB Search	NA	PMFIVNTNVPR	1
###	IAVHVVPDQ	37.84	976.5341	9	66.7	9	0.8921	0.86	-1	489.2739	2	13.8639	P34884|MIF_MOUSE:Q545F0|Q545F0_MOUSE			5 6 6 0 28 80 0 0	IAVHVVPDQ	DB Search	NA	IAVHVVPDQ	1
###	LQDEIQNM(+15.99)K	39.13	1133.539	9	77.8	9	0.3769	0.6	4.5	567.7792	2	6.7212	P20152|VIME_M	Oxidation (M)	M8:Oxidation (M):	5 12 7 7 13 11 4 0	LQDEIQNM(+15.9	DB Search	NA	LQDEIQNMK	1
###	FADLSEAANRNNDALR	35.74	1775.855	16	31.2	16	-0.8755	0.14	-2.6	592.9588	3	13.6163	P20152|VIME_MOUSE:Q5FWJ3|Q5FWJ3_MOUSE:Q			5 31 13 13 13 0 0	FADLSEAANRNN	DB Search	NA	FADLSEAANRNN	1
###	QVDQLTNDK	33.28	1059.52	9	77.8	9	0.4139	0.76	5.1	530.7698	2	4.9056	P20152|VIME_MOUSE:Q5FWJ3|Q5FWJ3_MOUSE:A			5 10 8 8 13 3 0 0	QVDQLTNDK	DB Search	NA	QVDQLTNDK	1
###	LLEGEESR	32.18	931.4611	8	50	8	-0.7219	0.82	-3.3	466.7363	2	6.6164	P20152|VIME_MOUSE:G3X981|G3X981_MOUSE:G5E			5 26 22 2 1 1 0 0	LLEGEESR	DB Search	NA	LLEGEESR	1
###	GGGS(+79.97)S(+79.97)CGGGYSGGGGSSCGGG	25.31	2546.741	32	3.1	32	-1.0285	NA	-15.8	849.9075	3	15.9863	P18165|LORI_M	Phosphorylation (	S4:Phosphorylatio	0 0 0 0 0 0 0 0 0 0	GGGS(+79.97)S(	DB Search	NA	GGGSSCGGGYS	1
###	DEEESPGQAKDEL	39.7	1445.616	13	53.8	13	-0.4205	0.61	11.4	723.8234	2	10.7337	P14211|CALR_MOUSE:Q62041|Q62041_MOUSE:B2			0 0 7 7 37 14 1 1	DEEESPGQAKDE	DB Search	NA	DEEESPGQAKDE	1
###	EESPGQAKDEL	39.68	1201.546	11	63.6	11	-0.6215	0.73	-1.7	601.7794	2	9.2096	P14211|CALR_MOUSE:Q62041|Q62041_MOUSE:B2			0 0 35 17 9 9 5 0	EESPGQAKDEL	DB Search	NA	EESPGQAKDEL	1
###	GQTLVVQFTVK	38.39	1218.697	11	54.5	11	0.3831	0.79	-3.5	610.3538	2	19.2848	P14211|CALR_MOUSE:Q3UWP8|Q3UWP8_MOUSE:			0 0 41 67 98 39 5	GQTLVVQFTVK	DB Search	NA	GQTLVVQFTVK	1
###	TAPAPEFTAAQPEVA	39.71	1498.73	15	46.7	15	-0.0026	0.56	6.3	750.3772	2	18.0837	P14206|RSSA_MOUSE:B2CY77|B2CY77_MOUSE			0 0 0 1 2 2 4 10 1	TAPAPEFTAAQP	DB Search	NA	TAPAPEFTAAQP	1
###	SEGVQVPSVPIQQ	39.42	1366.709	13	38.5	13	0.9035	0.77	7	684.3667	2	19.0987	P14206|RSSA_MOUSE:B2CY77|B2CY77_MOUSE			0 0 0 5 5 21 0 0 4	SEGVQVPSVPIQ	DB Search	NA	SEGVQVPSVPIQ	1
###	TITLEVEPSDTIENVK	38.91	1786.92	16	43.8	16	0.2298	0.74	3.2	894.4702	2	19.559	P0CG50|UBC_MOUSE:E9Q5F6|E9Q5F6_MOUSE:Q3			0 0 0 8 17 31 66 0	TITLEVEPSDTIEN	DB Search	NA	TITLEVEPSDTIEN	2
###	TEITELRR	26.46	1016.562	8	12.5	8	-0.7865	0.55	3.4	509.2897	2	8.8251	P08730|K1C13_MOUSE:Q6IFX2|K1C42_MOUSE:Q9			1 1 4 0 0 0 0 1	TEITELRR	DB Search	NA	TEITELRR	2
###	GVVDSEDLPLNISR	40.12	1512.778	14	78.6	14	0.0676	0.9	2.5	757.4002	2	19.7498	P07901|HS90A_MOUSE:E9Q3D6|E9Q3D6_MOUSE:Q			0 0 4 20 17 17 26	GVVDSEDLPLNIS	DB Search	NA	GVVDSEDLPLNIS	2
###	VEIDPEIQK	35.86	1069.566	9	66.7	9	0.1692	0.59	-0.8	535.7896	2	13.3343	P07744|K2C4_MOUSE			5 43 51 51 6 6 0 0	VEIDPEIQK	DB Search	NA	VEIDPEIQK	1
###	EQAQEQVQPKPLES	39.71	1609.795	14	57.1	14	0.0072	0.66	0.7	805.9052	2	10.6223	P06728|APOA4_MOUSE:Q9DBN0|Q9DBN0_MOUSE			0 0 9 2 2 6 15 25	EQAQEQVQPKPI	DB Search	NA	EQAQEQVQPKPI	1
###	VLDELTLSK	36.46	1016.575	9	66.7	9	0.13	0.81	2.5	509.2962	2	16.5633	P02535|K1C10_MOUSE:A2A513|A2A513_MOUSE			5 39 15 7 7 3 0 0	VLDELTLSK	DB Search	NA	VLDELTLSK	2
###	VVYPWTQRF	38.36	1194.619	9	33.3	9	0.1664	0.81	-0.4	598.3164	2	20.6649	P02104|HBE_MOUSE			1 1 56 14 5 0 0 0	VVYPWTQRF	DB Search	NA	VVYPWTQRF	1
###	IGGHGAEYGAEALER	40.12	1528.727	15	46.7	15	-0.7471	0.85	0.5	510.5844	3	11.0379	P01942|HBA_MOUSE:Q9QWJ3|Q9QWJ3_MOUSE:Q			0 0 0 0 0 0 14 33	IGGHGAEYGAEA	DB Search	NA	IGGHGAEYGAEA	2
###	PTTKTYFPHF	38.13	1237.613	10	40	10	-0.3455	0.69	-3.8	413.5434	3	17.0063	P01942|HBA_MOUSE:Q9QWJ3|Q9QWJ3_MOUSE:Q			0 0 0 22 12 0 11 3	PTTKTYFPHF	DB Search	NA	PTTKTYFPHF	1
###	FLASVSTVLTSK	40.05	1251.707	12	75	12	0.0127	0.59	-0.1	626.8624	2	20.0232	P01942|HBA_MOUSE:Q91VB8|Q91VB8_MOUSE:A8D			5 7 59 28 28 9 2 2	FLASVSTVLTSK	DB Search	NA	FLASVSTVLTSK	2
###	LPQEKYVTSAPMPEPGAPG	39.71	1967.966	19	10.5	19	0.3219	0.71	7.9	984.9982	2	16.6614	P01872|IGHM_MOUSE			0 0 0 0 0 0 0 2 1 2	LPQEKYVTSAPM	DB Search	NA	LPQEKYVTSAPM	2
###	EKMRKQ(+15.00)MQKEEYWRRREEEERWRMEIF	23.71	4532.165	32	0	32	-4.9713	NA	-17.6	907.4243	5	13.0702	O88532|ZFR_MO	Deamidation follo	Q6:Deamidation f	0 0 0 0 0 0 0 0 0 0	EKMRKQ(+15.00	DB Search	NA	EKMRKQMQKEE	1
###	VAGQDGSVVQFK	39.71	1233.635	12	83.3	12	0.0509	0.77	3.1	617.8268	2	13.0822	H7BWX9|H7BWX9_MOUSE:D3Z794|D3Z794_MOUSI			5 17 2 2 59 10 10	VAGQDGSVVQFI	DB Search	NA	VAGQDGSVVQFI	1
###	KELEEQLGPVAEETRAR	40.12	1954.012	17	35.3	17	-0.5288	0.17	3.3	489.513	4	12.7178	G3UZM8|G3UZM8_MOUSE:G3UWN5|G3UWN5_MOU			0 0 0 2 6 12 0 67	KELEEQLGPVAE	DB Search	NA	KELEEQLGPVAE	1
###	FRVNFVDPAASSSADD	39.71	1696.769	16	50	16	1.0634	0.71	6.9	849.3978	2	19.867	E9QM38|E9QM38_MOUSE:P55012|S12A2_MOUSE			0 0 0 0 2 6 41 0 0	FRVNFVDPAASS	DB Search	NA	FRVNFVDPAASS	2
###	GDLGIEIPAEK	37.43	1140.603	11	45.5	11	0.163	0.75	0.7	571.309	2	17.7067	E9Q509|E9Q509_MOUSE:G3X925|G3X925_MOUSE:			0 0 5 36 36 18 18	GDLGIEIPAEK	DB Search	NA	GDLGIEIPAEK	1
###	ASLVYENASAIMAHES	39.71	1691.783	16	68.8	16	-1.0415	0.58	2.2	846.9003	2	19.2061	E9Q0N2|PTPRH_MOUSE			0 0 0 24 42 42 25	ASLVYENASAIM/	DB Search	NA	ASLVYENASAIM/	2
###	IVVVTAGVR	32.8	912.5756	9	66.7	9	0.4476	0.73	-1.6	457.2944	2	13.7024	D3Z7F0|D3Z7F0_MOUSE:P16125|LDHB_MOUSE:A0			5 14 39 16 5 2 0 0	IVVVTAGVR	DB Search	NA	IVVVTAGVR	1
###	EETGRVLS	26.79	889.4505	8	87.5	8	-1.1459	0.89	-0.1	445.7325	2	6.2364	D3Z6F5|D3Z6F5_MOUSE:Q03265|ATPA_MOUSE:D6			5 10 40 5 0 12 12	EETGRVLS	DB Search	NA	EETGRVLS	1
###	VLSIGDGIAR	33.35	999.5713	10	60	10	-0.1642	0.8	4	500.7949	2	16.1323	D3Z6F5|D3Z6F5_MOUSE:Q03265|ATPA_MOUSE			5 5 25 25 5 5 0 0	VLSIGDGIAR	DB Search	NA	VLSIGDGIAR	1
###	GILAADESTGSIAK	40.1	1331.693	14	42.9	14	0.0222	0.69	-0.2	666.8554	2	14.3977	D3YV98|D3YV98_MOUSE:D3Z510|D3Z510_MOUSE:			0 0 0 84 31 29 16	GILAADESTGSIA	DB Search	NA	GILAADESTGSIA	1
###	GVVPLAGTNGETTTQGLDGLSER	38.77	2271.134	23	0	23	-0.86	0.54	8.3	1136.584	2	19.3692	D3YV98|D3YV98_MOUSE:D3Z510|D3Z510_MOUSE:			0 0 0 0 0 0 1 0 0 0	GVVPLAGTNGET	DB Search	NA	GVVPLAGTNGET	1
###	ADLINNLGTIAK	39.59	1241.698	12	50	12	-0.2123	0.68	0.3	621.8565	2	19.487	B7ZC50|B7ZC50_MOUSE:P07901|HS90A_MOUSE:Q			0 0 2 38 21 14 7 3	ADLINNLGTIAK	DB Search	NA	ADLINNLGTIAK	1
###	KRSRKESYSVYVYKVLKQVHPD	39.71	2708.476	22	22.7	22	0.0014	0.42	3.7	678.1289	4	16.1453	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:Q			0 0 0 0 0 0 0 0 0 0	KRSRKESYSVYV	DB Search	NA	KRSRKESYSVYV	2
###	FVNDIFER	30.77	1038.513	8	75	8	-0.0902	0.85	-5.9	520.2609	2	18.1203	B2RTK3|B2RTK3_MOUSE:Q64525|H2B2B_MOUSE:Q			5 24 13 13 12 4 0	FVNDIFER	DB Search	NA	FVNDIFER	1
###	M(+42.01)EHKKEET(+79.97)RRKTEEERQKKEDEF	24.68	4499.188	33	3	33	-5.9557	NA	-6.6	750.8669	6	11.3458	B2RRE3|B2RRE3	Acetylation (N-ter	M1:Acetylation (N	5 0 0 0 0 0 0 0 0 0	M(+42.01)EHKKE	DB Search	NA	MEHKKEETRRKT	1
###	LHVDPENFR	38.28	1125.557	9	55.6	9	0.1327	0.67	-1.3	563.7849	2	13.0391	B1Q450|B1Q450_MOUSE:A8DV41|A8DV41_MOUSE:			2 2 54 54 0 0 2 0	LHVDPENFR	DB Search	NA	LHVDPENFR	2
###	TIAPALVSK	35.46	898.5488	9	66.7	9	-0.3686	0.56	-8.4	450.2789	2	13.4405	B1ARR7|B1ARR7_MOUSE:Q5FW97|Q5FW97_MOUS			2 2 45 4 4 3 0 0 0	TIAPALVSK	DB Search	NA	TIAPALVSK	1
###	YRPGTVALR	39.11	1031.588	9	55.6	9	0.0262	0.79	-3.9	344.8693	3	9.6315	A1L0U3|A1L0U3_MOUSE:F8WI35|F8WI35_MOUSE:E			0 0 5 6 47 67 23 0	YRPGTVALR	DB Search	NA	YRPGTVALR	2
###	NQVALNPQNTVFDAK	39.63	1657.842	15	60	15	-0.1736	0.58	10.2	829.937	2	17.219	A1E2B8|A1E2B8_MOUSE:Q3TAI8|Q3TAI8_MOUSE:P			0 0 6 24 19 55 2 1	NQVALNPQNTVF	DB Search	NA	NQVALNPQNTVF	1
###	AQIHDLVLVGGSTR	39.76	1464.805	14	42.9	14	0.0152	0.8	-3.1	489.2752	3	15.8627	A1E2B8|A1E2B8_MOUSE:P17879|HS71B_MOUSE:Q			0 0 0 0 4 13 13 35	AQIHDLVLVGGS	DB Search	NA	AQIHDLVLVGGS	1
###	LLQDFFNGR	37.07	1108.567	9	77.8	9	-0.3587	0.84	2.1	555.2917	2	20.4455	A1E2B8|A1E2B8_MOUSE:P17879|HS71B_MOUSE:Q			5 13 81 43 22 5 4	LLQDFFNGR	DB Search	NA	LLQDFFNGR	1
###	GGGGNFGPGPGSNFR	39.71	1376.622	15	40	15	-0.7638	0.89	0.3	689.3185	2	12.6953	A0ABA7IW04|A0ABA7IW04_MOUSE:B7ZP22|B7ZP22			0 0 0 1 13 48 7	GGGGNFGPGPG	DB Search	NA	GGGGNFGPGPG	1
###	GGNFGFGDSR	37.56	1012.436	10	40	10	-0.4493	0.78	0.9	507.2258	2	12.5339	A0ABA7IW04|A0ABA7IW04_MOUSE:B7ZP22|B7ZP22			0 0 6 29 34 11 0 0	GGNFGFGDSR	DB Search	NA	GGNFGFGDSR	1
###	IDTIEIITDR	37.52	1187.64	10	80	10	-1.0951	0.75	-1.3	594.8264	2	19.313	A0ABA7IW04|A0ABA7IW04_MOUSE:B7ZP22|B7ZP22			5 16 19 19 32 26	IDTIEIITDR	DB Search	NA	IDTIEIITDR	1
###	QPSTSSLAAPTVEAAAS	39.71	1586.779	17	47.1	17	-0.7088	0.39	-3.1	794.3942	2	16.1107	A0AAQ4VMX1|A0AAQ4VMX1_MOUSE:A0AAQ4VMV3			0 0 0 0 0 1 6 14	QPSTSSLAAPTVI	DB Search	NA	QPSTSSLAAPTVI	2
###	YVASYLLAALGGNSSPSAK	39.71	1867.968	19	52.6	19	-0.3937	0.79	2.5	934.9936	2	24.8614	A0A5F8MPY2|A0A5F8MPY2_MOUSE:P99027|RLA2_			0 0 0 6 0 22 38 52	YVASYLLAALGG	DB Search	NA	YVASYLLAALGG	1
###	VQFLEQQNK	35.38	1132.588	9	77.8	9	0.1136	0.57	0.5	567.3014	2	12.2762	A0A2R8VHP3|A0A2R8VHP3_MOUSE:Q6IFZ8|Q6IFZ8			4 4 29 26 3 3 2 0	VQFLEQQNK	DB Search	NA	VQFLEQQNK	2
###	M(+15.99)EIQEIQLK	27.03	1146.596	9	33.3	9	-0.226	0.52	-0.2	574.3049	2	14.6442	A0A2R2Y2P8|A0A	Oxidation (M)	M1:Oxidation (M):	0 0 54 22 17 0 0 0	M(+15.99)EIQEIQ	DB Search	NA	MEIQEIQLK	2
###	KSDVEAIFSK	39.68	1122.592	10	70	10	0.0874	0.6	3.1	562.3051	2	13.8021	A0A2I3BQH3|A0A2I3BQH3_MOUSE:A0A2I3BRM6|A0			5 9 0 1 4 0 11 3 3	KSDVEAIFSK	DB Search	NA	KSDVEAIFSK	1
###	A(+42.01)SNVTNKTD	27.94	990.4618	9	44.4	9	1.7902	0.59	-7.6	496.2344	2	4.9728	A0A2I3BQH3|A0A	Acetylation (N-ter	A1:Acetylation (N	1 1 5 14 2 2 0 0 1	A(+42.01)SNVTNI	DB Search	NA	ASNVTNKTD	1
###	A(+42.01)DKPDM(+15.99)GEIASFDK	39.67	1580.703	14	0	14	-0.857	0.63	5.2	791.3628	2	14.2828	A0A0N4SVF0|A0A	Acetylation (N-ter	A1:Acetylation (N	0 0 1 0 0 0 0 0 1 1	A(+42.01)DKPDM	DB Search	NA	ADKPDMGEIASF	1
###	GPPPYHESLAGASQPP	24.81	1603.763	16	12.5	16	1.0704	0.56	4.9	802.8927	2	13.1943	A0A0G2JGP8|A0A0G2JGP8_MOUSE:Q8BU09|Q8BU(			0 0 0 0 0 0 0 0 0 1	GPPPYHESLAGA	DB Search	NA	GPPPYHESLAGA	2
###	SGRDYSFSISNLEPED	39.71	1814.796	16	56.2	16	-0.0514	0.86	7.2	908.4117	2	20.3616	A0A0G2JFZ3|A0A0G2JFZ3_MOUSE:Q921A6|Q921A6			0 0 0 0 1 2 2 7 9 4	SGRDYSFSISNLI	DB Search	NA	SGRDYSFSISNLI	1
###	SGRDYSFSISNLEPE	39.7	1699.769	15	53.3	15	0.0553	0.68	3.9	850.895	2	20.4863	A0A0G2JFZ3|A0A0G2JFZ3_MOUSE:Q921A6|Q921A6			0 0 0 0 0 2 2 6 6 6	SGRDYSFSISNLI	DB Search	NA	SGRDYSFSISNLI	1
###	VPVRPISYTPSIPSDSRNN	39.64	2098.081	19	31.6	19	-0.1737	0.77	-4.6	700.3643	3	15.7202	A0A087WRT4|A0A087WRT4_MOUSE:Q497H5|Q497I			0 0 0 0 0 0 0 1 5 4	VPVRPISYTPSIPS	DB Search	NA	VPVRPISYTPSIPS	2
###	VPVRPISYTPSIPSDSRN	39.71	1984.038	18	33.3	18	-0.3437	0.74	0.2	662.3533	3	15.8152	A0A087WRT4|A0A087WRT4_MOUSE:Q497H5|Q497I			0 0 0 0 0 0 0 3 10	VPVRPISYTPSIPS	DB Search	NA	VPVRPISYTPSIPS	1

Table S2 Information of peptides identified in IEC MHCII immunopeptidome (related to Supplementary Fig. S7e)

Table S3 Information of peptides identified in IEC MHCII immunopeptidome (related to Supplementary Fig. S20e)							
PGNP_pep							
Peptide	Accession	PTM	AScore	Length	Area..1	Area.2	Area.3
AAEDYGVIK	P37804|TAGL_MOUSE	NA	NA	9	119	NA	239
AAKRMALLMAEMSR	Q64727|VINC_MOUSE	NA	NA	14	82.1	NA	47
AALHAAVIAINEAIDRR	Q9JKF1|IQGA1_MOUSE	NA	NA	17	120	90.5	222
AAPAPVEK	P43276|H15_MOUSE:P43277	NA	NA	8	88.2	NA	NA
AAVDTSSEITTK	P26350|PTMA_MOUSE	NA	NA	12	132	NA	NA
AEADVASLNR	P58774|TPM2_MOUSE:P587	NA	NA	10	358	NA	NA
AEAEALYQTK	Q3UV17|K22O_MOUSE:Q9R	NA	NA	10	838	479	306
AEEKTISAKYAEER	Q8VDD5|MYH9_MOUSE	NA	NA	14	260	111	NA
AEIIEKNLKSASSK	Q9CPY7|AMPL_MOUSE	NA	NA	14	130	NA	NA
AETAAPAPVEK	P43276|H15_MOUSE	NA	NA	11	419	NA	NA
AFKINELKAEVANHL	O70628|PDE9A_MOUSE	NA	NA	15	340	83.8	NA
AGFAGDDAPR	P63260|ACTG_MOUSE:P607	NA	NA	10	1880	3950	2790
AGVRLELANIQAELVAKP	E9Q414|APOB_MOUSE	NA	NA	18	68	NA	471
AGVRLELANIQAELVAKPS	E9Q414|APOB_MOUSE	NA	NA	19	929	NA	1100
AKLVEGRTHISISK	A0AAQ4VMX2|CO4A_MOUS	NA	NA	14	451	187	124
AKNKQKPITPETAEK	P60766|CDC42_MOUSE	NA	NA	15	179	NA	NA
ALAAAGYDVEK	P15864|H12_MOUSE:P43274	NA	NA	11	120	1080	1160
ALDVANKIGII	P62751|RL23A_MOUSE	NA	NA	11	1060	NA	1230
ALEEANADLEVK	Q6IFX2|K1C42_MOUSE	NA	NA	12	205	236	286
ALEESNYELEGK	P02535|K1C10_MOUSE	NA	NA	12	349	NA	NA
ALGQNPTNAEVLK	Q60605|MYL6_MOUSE:Q8CI	NA	NA	13	347	NA	NA
ANQIVLLLAELARRDR	Q99PE8|ABCG5_MOUSE	NA	NA	16	3070	739	4170
APIIAVTR	P52480|KPYM_MOUSE	NA	NA	8	140	NA	209
APQVSTPTLVEAAR	P07724|ALBU_MOUSE	NA	NA	14	42	NA	NA
APQVSTPTLVEAARNL	P07724|ALBU_MOUSE	NA	NA	16	179	NA	NA
APQVSTPTLVEAARNLG	P07724|ALBU_MOUSE	NA	NA	17	909	305	NA
AQLRELNITAAKEIE	P62082|RS7_MOUSE	NA	NA	15	76.1	NA	NA
AQYEDIAQK	Q3UV17|K22O_MOUSE	NA	NA	9	1070	168	75.1
AQYETIAAK	P31001|DESM_MOUSE	NA	NA	9	317	329	222
ASFEAQGALANIAVDK	P14439|HA23_MOUSE:P0422	NA	NA	16	5190	2630	3220
ASLENSLEETK	Q9Z2K1|K1C16_MOUSE	NA	NA	11	142	NA	NA
ATDSEALIHCLRAK	Q8QZR3|EST2A_MOUSE	NA	NA	14	79.9	NA	NA
ATHPDEELLRALLSKFK	O08601|MTP_MOUSE	NA	NA	17	116	NA	128
AVDAFRVNVIHAR	P84091|AP2M1_MOUSE	NA	NA	13	88	NA	NA
AVDTSSEITTK	P26350|PTMA_MOUSE	NA	NA	11	1000	NA	NA
AVFPSIVGR	P63260|ACTG_MOUSE:P607	NA	NA	9	2180	NA	2670
AVFPSIVGRPR	P63260|ACTG_MOUSE:P607	NA	NA	11	502	3830	4330
AVNYASRIRAHGGTN	A6X935|ITIH4_MOUSE	NA	NA	15	1430	880	1270
AVSEGTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8C	NA	NA	16	464	157	422
DAVTYTEHAK	P62806|H4_MOUSE	NA	NA	10	208	NA	NA
DAYHSRAIQVVRAR	P21460|CYTC_MOUSE	NA	NA	14	2230	NA	653
DEEESPGQAKDEL	P14211|CALR_MOUSE	NA	NA	13	76.1	NA	87
DEELQEGHVLVVPQN	Glycinin_438	NA	NA	15	189	NA	NA
DESGPSIVHR	P63260|ACTG_MOUSE:P607	NA	NA	10	202	284	450
DFEARYVQAKLSVHDR	O70228|ATP9A_MOUSE	NA	NA	16	208	NA	204
DFEQEMATAASSSSLEK	P63260|ACTG_MOUSE:P607	NA	NA	17	43.8	NA	NA
DGKLVSESSDVVSK	P11679|K2C8_MOUSE	NA	NA	14	240	NA	NA
DIEEVEQHIQTIRSK	Q8K0B2|LMBD1_MOUSE	NA	NA	15	2210	2760	3110
DIEEVEQHIQTIRSKSK	Q8K0B2|LMBD1_MOUSE	NA	NA	17	5750	228	268
DIEQSIKSETSG	P97429|ANXA4_MOUSE	NA	NA	12	109	NA	NA
DIEQSIKSETSGS	P97429|ANXA4_MOUSE	NA	NA	13	103	NA	NA
DIEQSIKSETSGSF	P97429|ANXA4_MOUSE	NA	NA	14	320	242	360
DLREQERGVIPNQSR	Q9QXY1|ZO3_MOUSE	NA	NA	15	216	NA	NA
DMQYQHVIETLIGKK	P80316|TCPE_MOUSE	NA	NA	15	1220	649	1090
DRLIEETISIAMATK	O88630|GOSR1_MOUSE	NA	NA	15	143	NA	NA
DSGKIEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	16	5050	8460	9300
DSYVGDEAQSK	P63260|ACTG_MOUSE:P607	NA	NA	11	2510	5490	3790
DTANRLRISSIQATTAAGSG	P40142|TKT_MOUSE	NA	NA	20	179	NA	NA
DVANKIGII	P62751|RL23A_MOUSE	NA	NA	9	3240	NA	NA
DVASKAKAVGIQGNLSGDL	Q9DB60|PXL2B_MOUSE	NA	NA	19	103	NA	NA
EAALHAAVIAINEAIDR	Q9JKF1|IQGA1_MOUSE	NA	NA	17	34.6	NA	NA
EAALHAAVIAINEAIDRR	Q9JKF1|IQGA1_MOUSE	NA	NA	18	174	NA	154
EAEYQEIRLMVMEIR	P97371|PSME1_MOUSE	NA	NA	15	87.1	NA	NA
EAFQLFDR	Q60605|MYL6_MOUSE	NA	NA	8	111	161	134
EAKDFQKAMIVFQSEFK	Q8R3G9|TSN8_MOUSE	NA	NA	17	513	121	365
EAVAKADKLAEEHGS	P56480|ATPB_MOUSE	NA	NA	15	85.3	NA	336
EDIEEVEQHIQTIRSK	Q8K0B2|LMBD1_MOUSE	NA	NA	16	471	NA	579
EDIEEVEQHIQTIRSKSK	Q8K0B2|LMBD1_MOUSE	NA	NA	18	3590	NA	2580
EDKYEEEIK	P58774|TPM2_MOUSE:Q6IR	NA	NA	9	79.8	173	114
EDSFVTAVLAEETR	O08601|MTP_MOUSE	NA	NA	14	90.7	NA	279
EEETEEKVPVKK	Q61937|NPM_MOUSE	NA	NA	12	82.1	NA	NA
EENKEAVITAQER	P70695|F16P2_MOUSE	NA	NA	13	153	NA	NA
EEVEQHIQTIRSK	Q8K0B2|LMBD1_MOUSE	NA	NA	13	550	NA	NA
EFEFFENTIVSRVAR	Q62179|SEM4B_MOUSE	NA	NA	15	1070	NA	NA
EFFENTIVSRVAR	Q62179|SEM4B_MOUSE	NA	NA	13	63.7	NA	NA
EGTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8C	NA	NA	13	84.6	267	558
EGTVEENQVNVEVMR	O55111|DSG2_MOUSE	NA	NA	15	623	NA	509

EGTVEENQVNVEVMRIK	O55111|DSG2_MOUSE	NA	NA	17	167	NA	598
EIAQDFK	P02301|H3C_MOUSE:P6843	NA	NA	7	381	NA	NA
EIQEESKRIIANVGK	Q8CAS9|PARP9_MOUSE	NA	NA	15	659	NA	590
EIQTAVR	P70696|H2B1A_MOUSE:Q8C	NA	NA	7	662	NA	NA
EISPKEMTIIYVEASGK	Q05117|PPA5_MOUSE	NA	NA	17	502	NA	486
ELEEQLGPVAEETR	P08226|APOE_MOUSE	NA	NA	14	573	217	593
ELEEQLGPVAEETRA	P08226|APOE_MOUSE	NA	NA	15	912	350	1570
ELEEQLGPVAEETRAR	P08226|APOE_MOUSE	NA	NA	16	471	NA	NA
EMLAVAVLAAERGGDE	Q80V26|IMPA3_MOUSE	NA	NA	16	1060	NA	1020
EPATEYILSIFAEKGQQK	Q80YX1|TENA_MOUSE	NA	NA	18	58.5	NA	NA
EPGQEYTVLLIAEKGR	Q80YX1|TENA_MOUSE	NA	NA	16	145	NA	70.6
EPGQEYTVLLIAEKGRHK	Q80YX1|TENA_MOUSE	NA	NA	18	781	789	653
EPGTEYTIYVIALKNNQK	P11276|FINC_MOUSE	NA	NA	18	94	NA	NA
EQAQEQAQEQVQPKPLES	P06728|APOA4_MOUSE	NA	NA	18	49.6	NA	NA
EQAQEQVQPKPLES	P06728|APOA4_MOUSE	NA	NA	14	158	87.7	103
EQTQQIRLQAEIFQAR	P08226|APOE_MOUSE	NA	NA	16	135	NA	761
ESEEFLKRLHPYK	Q8CE08|PPAP_MOUSE	NA	NA	13	117	NA	266
ETAAPAPVEK	P43276|H15_MOUSE	NA	NA	10	338	NA	NA
ETESVYRVQVVATEVGGSS	Q9R100|CAD17_MOUSE	NA	NA	19	392	NA	399
EVATNSELVQSGK	Q9QWL7|K1C17_MOUSE:Q6	NA	NA	13	121	NA	NA
EVEQHIQTIRSK	Q8K0B2|LMBD1_MOUSE	NA	NA	12	153	109	NA
EVEQHIQTIRSKSK	Q8K0B2|LMBD1_MOUSE	NA	NA	14	55.4	NA	NA
EVSTYIK	P10126|EF1A1_MOUSE	NA	NA	7	189	NA	NA
EVVSSIRAEMGSDR	Q8VBZ0|DHRSX_MOUSE	NA	NA	14	352	NA	342
FASFEAQGALANIAVDK	P14439|HA23_MOUSE:P042	NA	NA	17	210	NA	192
FASFEAQGALANIAVDKA	P14439|HA23_MOUSE:P042	NA	NA	18	315	NA	314
FASFEAQGALANIAVDKAN	P14439|HA23_MOUSE:P042	NA	NA	19	228	NA	102
FASFIDK	Q6NXH9|K2C73_MOUSE:P1	NA	NA	7	1980	NA	2630
FDQLLAEEK	Q6URW6|MYH14_MOUSE:Q	NA	NA	9	130	69.3	NA
FEAQGALANIAVDK	P14439|HA23_MOUSE:P042	NA	NA	14	728	205	528
FEFFENTIVSRVAR	Q62179|SEM4B_MOUSE	NA	NA	14	6410	2860	5400
FENKVPEKQK	P48771|CX7A2_MOUSE	NA	NA	10	284	NA	NA
FFHESGLEARVALK	E9Q414|APOB_MOUSE	NA	NA	14	10900	5330	8800
FGPAHALIIAGRSVSG	P14246|GTR2_MOUSE	NA	NA	16	1440	889	936
FGSGFAAPFFIVRHQLLKK	P17665|COX7C_MOUSE	NA	NA	19	88.3	NA	1440
FHESGLEARVALK	E9Q414|APOB_MOUSE	NA	NA	13	224	NA	252
FIEHVVEVARGK	Q61168|LAPM5_MOUSE	NA	NA	12	216	140	211
FLEQQNK	P20152|VIME_MOUSE:P0399	NA	NA	7	908	NA	NA
FLEQQNQVLQTK	Q6NXH9|K2C73_MOUSE:P04	NA	NA	12	1230	NA	NA
FNPRFDESTIVCNTSEGGR	Q9CQW5|LEG2_MOUSE	NA	NA	19	697	733	1190
FPYVEEAIKIAYCEER	P70274|SEPP1_MOUSE	NA	NA	16	327	NA	NA
FQNAILVR	P07724|ALBU_MOUSE	NA	NA	8	888	2540	2450
FTASAGIQVVGDDLTVTNPK	P17182|ENOA_MOUSE	NA	NA	20	509	NA	65.8
FYNPLVPEAQKR	Q9Z0G9|CLD3_MOUSE	NA	NA	12	669	NA	539
GALYRIGDLQAFVGRDAG	P10852|4F2_MOUSE	NA	NA	18	260	270	584
GEKEVNLAVENAK	Q9JLJ2|AL9A1_MOUSE	NA	NA	13	97.5	NA	NA
GFSSGSAVVSGGSR	Q3TTY5|K22E_MOUSE	NA	NA	14	91.6	NA	NA
GHEVAAMLKSELQK	Q8K135|K319L_MOUSE	NA	NA	14	216	157	252
GHFFVEDQIYCEKHARE	O70400|PDLI1_MOUSE	NA	NA	17	204	NA	NA
GKTIENFLVVNKER	Q3UR85|MYRF_MOUSE	NA	NA	14	2230	1990	1900
GMVQAVRLIAEGTAPR	Q8R0Y6|AL1L1_MOUSE	NA	NA	16	1700	552	1050
GNIEIALEAAKALDDK	Q8CIE6|COPA_MOUSE	NA	NA	16	2490	476	2320
GNMEVARIHAENAIR	Q99LU0|CH1B1_MOUSE	NA	NA	15	2670	2120	2740
GNMEVARIHAENAIRQ	Q99LU0|CH1B1_MOUSE	NA	NA	16	624	NA	727
GNTEVARIHAENAIR	Q9CQD4|CH1B2_MOUSE	NA	NA	15	604	276	455
GQEFEFFENTIVSRVAR	Q62179|SEM4B_MOUSE	NA	NA	17	48.9	NA	NA
GQEVVSSIRAEMGSDR	Q8VBZ0|DHRSX_MOUSE	NA	NA	16	1560	1020	1310
GRFAVHRITPEEAK	P62702|RS4X_MOUSE	NA	NA	14	326	NA	NA
GRLQSELK	P07744|K2C4_MOUSE	NA	NA	8	100	417	NA
GTGASGSFK	P43276|H15_MOUSE:P15864	NA	NA	9	266	NA	NA
GTGASGSFKLNKK	P43276|H15_MOUSE:P15864	NA	NA	13	796	NA	150
GTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8C	NA	NA	12	111	NA	NA
GTVEENQVNVEVMR	O55111|DSG2_MOUSE	NA	NA	14	119	NA	341
GVETPAREGAMSAQLGYPV	Q62165|DAG1_MOUSE	NA	NA	20	106	NA	NA
GVETPAREGAMSAQLGYPV	Q62165|DAG1_MOUSE	NA	NA	21	898	NA	NA
GYSFTTTAER	P63260|ACTG_MOUSE:P607	NA	NA	10	410	251	1010
GYSFVTTAER	P68134|ACTS_MOUSE:P680	NA	NA	10	901	567	835
HAVSEGTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8C	NA	NA	17	95.3	9810	8200
HPLVWDFVRSNWKK	P97449|AMPN_MOUSE	NA	NA	14	1760	NA	NA
HSKEQQCVIMAENSK	P20918|PLMN_MOUSE	NA	NA	15	814	NA	161
HVLVTLGEK	Q60605|MYL6_MOUSE	NA	NA	9	152	NA	228
IALENYLAALQSDPPR	Q06335|APLP2_MOUSE	NA	NA	16	424	NA	351
IALENYLAALQSDPPRP	Q06335|APLP2_MOUSE	NA	NA	17	50.2	NA	73.2
IDIAGR	P61164|ACTZ_MOUSE	NA	NA	6	1350	NA	NA
IDQEGNIYVTQALDR	Q9R100|CAD17_MOUSE	NA	NA	15	73.5	NA	154
IEDSFVTAVLAEETR	O08601|MTP_MOUSE	NA	NA	15	8400	655	4640
IEDSFVTAVLAEETRA	O08601|MTP_MOUSE	NA	NA	16	4220	NA	2750
IEETGILAERAR	P02468|LAMC1_MOUSE	NA	NA	12	82.9	NA	NA
IEEVEQHIQTIRSK	Q8K0B2|LMBD1_MOUSE	NA	NA	14	1240	575	NA
IEEVEQHIQTIRSKSK	Q8K0B2|LMBD1_MOUSE	NA	NA	16	2630	197	933
IEKAQQIQALQSNVR	E9PV24|FIBA_MOUSE	NA	NA	15	106	152	306

IERSQVVALLGAQLSPAR	Q9R0A1|CLCN2_MOUSE	NA	NA	18	196	NA	440
IEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	12	112	NA	NA
IGGHGAEYGAEALER	P01942|HBA_MOUSE	NA	NA	15	86.7	3050	1000
IGGIGTVPVGR	P10126|EF1A1_MOUSE:P62	NA	NA	11	207	197	283
IIAPPER	P63260|ACTG_MOUSE:P607	NA	NA	7	7040	NA	NA
IIAPPERK	P63260|ACTG_MOUSE:P607	NA	NA	8	963	NA	NA
IIAPPERKY	P63260|ACTG_MOUSE:P607	NA	NA	9	487	NA	2840
IKNLEISIDALMAK	Q64331|MYO6_MOUSE	NA	NA	14	242	NA	261
IKNLEISIDALMAKIK	Q64331|MYO6_MOUSE	NA	NA	16	198	NA	177
IMPAAHPVAINASSE	Arah1_506	NA	NA	15	349	NA	NA
IPGKQVAGVIKAVDSK	O08601|MTP_MOUSE	NA	NA	16	642	474	417
IPNVENETMIPVLTSKR	Q80XR2|AT2C1_MOUSE	NA	NA	17	512	217	594
IQELESHLEAEEGAR	Q6URW6|MYH14_MOUSE	NA	NA	15	135	NA	116
IQLQEELAAAERAK	Q8VDD5|MYH9_MOUSE	NA	NA	14	988	549	954
IQRVAAGVLCELAQDK	Q02257|PLAK_MOUSE:Q022	NA	NA	16	1280	61.4	996
IRSQVMTHLRVIYER	P12023|A4_MOUSE	NA	NA	15	99	NA	NA
ISDEFSEAIKAFRGQDDK	Q9EQP2|EHD4_MOUSE	NA	NA	18	124	NA	NA
ISLAQYLINARLSSEK	P60335|PCBP1_MOUSE	NA	NA	16	379	99.8	277
ISPKEMTIIYVEASGK	Q05117|PPA5_MOUSE	NA	NA	16	12800	1950	6510
ISQKDIEQSIKSETSG	P97429|ANXA4_MOUSE	NA	NA	16	224	NA	NA
ISQKDIEQSIKSETSGS	P97429|ANXA4_MOUSE	NA	NA	17	361	228	399
ISQKDIEQSIKSETSGSF	P97429|ANXA4_MOUSE	NA	NA	18	10300	3420	5370
IVDSGKIEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	18	479	NA	NA
IVEGLMTTVHAITATQK	P16858|G3P_MOUSE	NA	NA	17	430	92.7	470
IVTEKSTVPVRAAESIR	O70475|UGDH_MOUSE	NA	NA	17	139	NA	NA
IWHHTFYNELR	P63260|ACTG_MOUSE:P607	NA	NA	11	254	NA	NA
IYHTIAYLTPLPQPNR	Q91VS7|MGST1_MOUSE	NA	NA	16	52.6	NA	NA
KDSEGYIYARGSQDMK	Q99JW2|ACY1_MOUSE	NA	NA	16	114	NA	NA
KELEEQLGPVAEETR	P08226|APOE_MOUSE	NA	NA	15	997	723	694
KELEEQLGPVAEETRA	P08226|APOE_MOUSE	NA	NA	16	598	349	353
KELEEQLGPVAEETRAR	P08226|APOE_MOUSE	NA	NA	17	1470	547	965
KGHEVAAMLKSELQK	Q8K135|K319L_MOUSE	NA	NA	15	189	158	556
KGHEVVVIAPEASIHIK	Q63886|UD11_MOUSE	NA	NA	17	197	NA	NA
KGRSQLIVVEEGSEP	Q60604|SCIN_MOUSE	NA	NA	15	923	NA	NA
KGTGASGSFKLNK	P43276|H15_MOUSE:P15864	NA	NA	13	1340	NA	404
KGVIEAFLHAWKGYQK	A2AJ15|MA1B1_MOUSE	NA	NA	16	282	60.8	219
KIEDSFVTAVLAEETR	O08601|MTP_MOUSE	NA	NA	16	5060	1040	4430
KITEVSLVGHLSYDKK	E9Q414|APOB_MOUSE	NA	NA	16	1640	1090	1160
KKITEVSLVGHLSYDK	E9Q414|APOB_MOUSE	NA	NA	16	3210	2070	579
KNPHDASLVSRIGQAYV	Q8C0S4|TT21A_MOUSE	NA	NA	17	12300	NA	14400
KPFQEYLEAQRQK	Q99KU0|VMP1_MOUSE	NA	NA	13	61.4	179	256
KPVTEGYVEVKEGK	P58022|LOXL2_MOUSE	NA	NA	14	45.7	NA	NA
KPVTEGYVEVKEGKA	P58022|LOXL2_MOUSE	NA	NA	15	999	NA	79.3
KQVSEHIAVYRQEEDG	P70274|SEPP1_MOUSE	NA	NA	16	47.9	NA	NA
KTIENFLVVNKER	Q3UR85|MYRF_MOUSE	NA	NA	13	114	101	NA
KVIEKAQQIQALQSN	E9PV24|FIBA_MOUSE	NA	NA	15	176	129	224
KVIEKAQQIQALQSNV	E9PV24|FIBA_MOUSE	NA	NA	16	141	NA	81
KVIEKAQQIQALQSNVR	E9PV24|FIBA_MOUSE	NA	NA	17	3350	2060	2460
KVTVGKDDIQK	O08638|MYH11_MOUSE	NA	NA	11	84.1	NA	101
KYDEELEER	P37804|TAGL_MOUSE	NA	NA	9	264	NA	158
KYEEVAR	P58774|TPM2_MOUSE:Q6IR	NA	NA	7	255	NA	NA
LAADDFR	P02535|K1C10_MOUSE:Q9Q	NA	NA	7	433	NA	NA
LAEEEHKVKAEVAAGDHP	P30416|FKBP4_MOUSE	NA	NA	18	2230	NA	171
LAEEKTISAKYAEER	Q8VDD5|MYH9_MOUSE	NA	NA	15	387	NA	116
LAKNKQKPITPETAEK	P60766|CDC42_MOUSE	NA	NA	16	4280	2320	2760
LALDIEIATYR	P03995|GFAP_MOUSE:Q6NX	NA	NA	11	326	62.4	NA
LALENYITALQAVPPRP	P12023|A4_MOUSE	NA	NA	17	139	NA	120
LAPITSDPTEAAAVGAVEASI	P52480|KPYM_MOUSE	NA	NA	22	81.6	NA	NA
LASYLDK	Q9QWL7|K1C17_MOUSE:P1	NA	NA	7	1070	NA	163
LATALQK	P58774|TPM2_MOUSE:P211	NA	NA	7	757	NA	459
LDIAGR	P61161|ARP2_MOUSE	NA	NA	6	1350	NA	NA
LDLAGR	P63260|ACTG_MOUSE:P607	NA	NA	6	1350	NA	NA
LDVANKIGII	P62751|RL23A_MOUSE	NA	NA	10	64.5	NA	NA
LEESRAQAEQALSEK	Q91ZV0|MIA2_MOUSE	NA	NA	15	257	NA	NA
LENEIQTYR	P02535|K1C10_MOUSE	NA	NA	9	55.7	NA	NA
LEQEIATYR	Q9QWL7|K1C17_MOUSE:P1	NA	NA	9	69.8	NA	62.8
LFIEHVVEVARGK	Q61168|LAPM5_MOUSE	NA	NA	13	436	542	432
LHVDPENFR	P02089|HBB2_MOUSE:P020	NA	NA	9	688	1020	1950
LLAEEKTISAKYAEER	Q8VDD5|MYH9_MOUSE	NA	NA	16	2200	456	1010
LLEGEESR	P20152|VIME_MOUSE:P310	NA	NA	8	422	NA	NA
LLLPGELAK	P70696|H2B1A_MOUSE:Q8C	NA	NA	9	1690	NA	NA
LLVVYPWTQR	P02089|HBB2_MOUSE:P021	NA	NA	10	389	353	144
LPHAGTQVRVTVFPSK	Q61739|ITA6_MOUSE	NA	NA	16	361	NA	NA
LPHAGTQVRVTVFPSKT	Q61739|ITA6_MOUSE	NA	NA	17	1800	NA	NA
LPKSAKPVSQMRMATPLLMI	P04441|HG2A_MOUSE	NA	NA	21	458	415	428
LPKSAKPVSQMRMATPLLMI	P04441|HG2A_MOUSE	NA	NA	22	4650	2520	3840
LPKSAKPVSQMRMATPLLMI	P04441|HG2A_MOUSE	NA	NA	23	186	NA	NA
LPRQDEEKPLHALLHGR	Q07079|IBP5_MOUSE	NA	NA	17	405	284	NA
LPVQLQRAMAAEAEAARE	P54116|STOM_MOUSE	NA	NA	18	664	186	284
LQQELDDLLVDLDHQR	Q8VDD5|MYH9_MOUSE	NA	NA	16	103	NA	NA
LRVDPVNFK	P01942|HBA_MOUSE:P0646	NA	NA	9	180	1280	869

LSGSTAITAYRMKR	Q99N03|M4A10_MOUSE	NA	NA	14	191	154	NA
LVLQVESLTTELSAER	Q6URW6|MYH14_MOUSE	NA	NA	16	347	NA	100
LYDIDVAKVNTLIRPD	P62751|RL23A_MOUSE	NA	NA	16	113	NA	NA
MEEQTQQIRLQAEIFQ	P08226|APOE_MOUSE	NA	NA	16	52.9	NA	39.3
MEEQTQQIRLQAEIFQAR	P08226|APOE_MOUSE	NA	NA	18	392	NA	268
MPAAHPVAINASSE	Arah1_506	NA	NA	14	743	NA	NA
MVQAVRLIAEGTAPR	Q8R0Y6|AL1L1_MOUSE	NA	NA	15	120	NA	NA
NDMQYQHVIETLIGKK	P80316|TCPE_MOUSE	NA	NA	16	405	177	370
NFAVAGKSQSE	Glycinin_448	NA	NA	11	229	NA	NA
NFFHESGLEARVALK	E9Q414|APOB_MOUSE	NA	NA	15	20400	16800	31300
NGMYPHKLVF	P47911|RL6_MOUSE	NA	NA	10	114	NA	NA
NIEIALEAAKALDDK	Q8CIE6|COPA_MOUSE	NA	NA	15	1020	49.7	599
NIKIISKIENHEGVR	P52480|KPYM_MOUSE	NA	NA	15	231	NA	NA
NKKITEVSLVGHLSYDK	E9Q414|APOB_MOUSE	NA	NA	17	704	352	578
NKYEDEINK	Q922U2|K2C5_MOUSE:Q8VE	NA	NA	9	311	204	275
NKYEDEINKR	Q922U2|K2C5_MOUSE:Q8VE	NA	NA	10	191	NA	NA
NLLSVAYK	P68254|1433T_MOUSE:P619	NA	NA	8	67.5	NA	NA
NPLVPEAQKR	Q9Z0G9|CLD3_MOUSE	NA	NA	10	6480	2140	2580
NPRFDESTIVCNTSEGGR	Q9CQW5|LEG2_MOUSE	NA	NA	18	5880	868	2100
NPSDLYAEGCEALVVKK	Q9QY33|TSN3_MOUSE	NA	NA	17	124	27.6	216
NSEYVAEPIQAYIIPS	Q6P1B1|XPP1_MOUSE	NA	NA	16	5020	NA	1220
NTEDIEEVEQHIQTIRSKSK	Q8K0B2|LMBD1_MOUSE	NA	NA	20	140	NA	NA
NTIEETGILAERAR	P02468|LAMC1_MOUSE	NA	NA	14	412	451	NA
NTIEETGILAERARSR	P02468|LAMC1_MOUSE	NA	NA	16	1620	846	1510
PAAHPVAINASSE	Arah1_506	NA	NA	13	5250	NA	NA
PDPAKSAPAP	Q64525|H2B2B_MOUSE	NA	NA	10	266	NA	NA
PDPAKSAPAPK	Q64525|H2B2B_MOUSE	NA	NA	11	562	NA	NA
PEPAKSAPAP	Q6ZWY9|H2B1C_MOUSE:P1	NA	NA	10	1530	NA	NA
PEPAKSAPAPK	Q6ZWY9|H2B1C_MOUSE:P1	NA	NA	11	3220	NA	NA
PEPSKSAPAP	Q64475|H2B1B_MOUSE	NA	NA	10	135	NA	NA
PVVPVHLDGTF	O35291|RNAS2_MOUSE:P97	NA	NA	11	5160	NA	923
PYVEEAIKIAYCEER	P70274|SEPP1_MOUSE	NA	NA	15	506	NA	401
QAQEQVQPKPLES	P06728|APOA4_MOUSE	NA	NA	13	146	NA	NA
QDFEARYVQAKLSVHDR	O70228|ATP9A_MOUSE	NA	NA	17	1790	1170	1680
QELQEYEVVAESEKR	Q9D5V6|SYAP1_MOUSE	NA	NA	15	1330	133	163
QEPKTEDIVAVQKAK	Q61391|NEP_MOUSE	NA	NA	15	108	NA	NA
QGQATVTVANGNNRK	Arah1_234	NA	NA	15	206	NA	NA
QPRPAEQYPLRALLNGR	P47878|IBP3_MOUSE	NA	NA	17	341	NA	236
RELIEAMLKAYQQK	O35114|SCRB2_MOUSE	NA	NA	14	146	NA	197
RFDESTIVCNTSEGGR	Q9CQW5|LEG2_MOUSE	NA	NA	16	102	NA	NA
RGILTLK	P63260|ACTG_MOUSE:P607	NA	NA	7	1350	NA	NA
RHPYFYAPELLYYAEQ	P07724|ALBU_MOUSE	NA	NA	16	170	NA	NA
RIALENYLAALQSD	Q06335|APLP2_MOUSE	NA	NA	14	1290	NA	741
RIALENYLAALQSDPPR	Q06335|APLP2_MOUSE	NA	NA	17	16400	1870	6140
RIALENYLAALQSDPPRP	Q06335|APLP2_MOUSE	NA	NA	18	2920	648	3160
RIALENYLAALQSDPPRPH	Q06335|APLP2_MOUSE	NA	NA	19	121	38.7	243
RLALENYITALQAVPPR	P12023|A4_MOUSE	NA	NA	17	11500	1820	5960
RLALENYITALQAVPPRP	P12023|A4_MOUSE	NA	NA	18	6410	432	5090
RRIALENYLAALQSD	Q06335|APLP2_MOUSE	NA	NA	15	5940	1990	4250
RRIALENYLAALQSDPP	Q06335|APLP2_MOUSE	NA	NA	17	33200	11400	34600
RRIALENYLAALQSDPPR	Q06335|APLP2_MOUSE	NA	NA	18	24800	6340	21700
RRIALENYLAALQSDPPRP	Q06335|APLP2_MOUSE	NA	NA	19	16900	6130	9770
RRIALENYLAALQSDPPRPH	Q06335|APLP2_MOUSE	NA	NA	20	3760	1710	3860
RRLALENYITAL	P12023|A4_MOUSE	NA	NA	12	493	64.5	75.3
RRLALENYITALQAVPP	P12023|A4_MOUSE	NA	NA	17	12800	NA	9930
RRLALENYITALQAVPPR	P12023|A4_MOUSE	NA	NA	18	121000	45000	88400
RRLALENYITALQAVPPRP	P12023|A4_MOUSE	NA	NA	19	162000	56100	153000
RRLALENYITALQAVPPRPH	P12023|A4_MOUSE	NA	NA	20	7350	5000	9300
RSQVVALLGAQLSPAR	Q9R0A1|CLCN2_MOUSE	NA	NA	16	145	NA	NA
SAKPVSQMRMATPLLMRP	P04441|HG2A_MOUSE	NA	NA	18	2840	NA	2150
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	NA	NA	19	9540	5960	4080
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	NA	NA	20	1940	441	1230
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	NA	NA	21	575	117	280
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	NA	NA	22	217	190	NA
SALQAIGVEAHQAIM	Q9D7I5|LHPP_MOUSE	NA	NA	15	202	NA	NA
SARLSAKPAPPKPEPKPK	P09602|HMGN2_MOUSE	NA	NA	18	256	NA	NA
SARLSAKPAPPKPEPKPKK	P09602|HMGN2_MOUSE	NA	NA	19	1410	204	108
SDPQVHTVLVERSTLK	Q9JHU4|DYHC1_MOUSE	NA	NA	16	1520	555	1200
SDPTEAAAVGAVEASFK	P52480|KPYM_MOUSE	NA	NA	17	194	NA	184
SDRLIEETISIAMATK	O88630|GOSR1_MOUSE	NA	NA	16	1450	NA	1100
SFEAQGALANIAVDK	P14439|HA23_MOUSE:P042	NA	NA	15	113	116	179
SGEKEVNLAVENAK	Q9JLJ2|AL9A1_MOUSE	NA	NA	14	161	131	NA
SGKIEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	15	3260	3510	2870
SGSTAITAYRMKR	Q99N03|M4A10_MOUSE	NA	NA	13	68.7	NA	NA
SGVEYTRLAVESARG	Q62178|SEM4A_MOUSE	NA	NA	15	277	218	216
SKMEEQTQQIRLQAEIFQAR	P08226|APOE_MOUSE	NA	NA	20	115	NA	240
SLDLDSIIAEVK	Q922U2|K2C5_MOUSE:P504	NA	NA	12	349	NA	NA
SLHTLFGDK	P07724|ALBU_MOUSE	NA	NA	9	306	737	2160
SLLEGQDAK	P08730|K1C13_MOUSE	NA	NA	9	477	NA	146
SLVSKGTLVQ	P43276|H15_MOUSE:P43274	NA	NA	10	71.2	NA	NA
SLVSKGTLVQT	P43276|H15_MOUSE:P43274	NA	NA	11	4150	NA	162

SLVSKGTLVQTK	P43276|H15_MOUSE:P43274	NA	NA	12	103	NA	77
SPGVTASWIEANLSDDSK	Q80U87|UBP8_MOUSE	NA	NA	18	404	NA	395
SPKEMTIIYVEASGK	Q05117|PPA5_MOUSE	NA	NA	15	767	275	709
SPTVHFTPAEISR	Q9QXH4|ITAX_MOUSE	NA	NA	13	198	67.7	128
SQMLEKEMKAQEQR	Q8BTZ7|GMPPB_MOUSE	NA	NA	14	111	NA	NA
SSTVTEAPIAVVTSRT	Q8K1R7|NEK9_MOUSE	NA	NA	16	253	NA	220
STDREASIDILHSIVK	Q8BG32|PSD11_MOUSE	NA	NA	16	321	NA	131
STELLIR	P02301|H3C_MOUSE:P68433	NA	NA	7	398	NA	NA
STTTGHLIYK	P10126|EF1A1_MOUSE:P626	NA	NA	10	324	295	207
SVSNSVKEIMAEIYK	P10605|CATB_MOUSE	NA	NA	15	135	NA	131
SYELPDGQVITIGNER	P63260|ACTG_MOUSE:P607	NA	NA	16	1020	523	1320
TAAPAPVEK	P43276|H15_MOUSE	NA	NA	9	234	NA	NA
TANQIVLLLAELARR	Q99PE8|ABCG5_MOUSE	NA	NA	15	1770	127	1720
TANQIVLLLAELARRDR	Q99PE8|ABCG5_MOUSE	NA	NA	17	15900	2880	15600
TAPAETAAPAPVEK	P43276|H15_MOUSE	NA	NA	14	1800	NA	NA
TDEAKDFQKAMIVFQSEFK	Q8R3G9|TSN8_MOUSE	NA	NA	19	36.8	NA	NA
TDLDYVHSVVANLEK	Q812G0|MGT4A_MOUSE	NA	NA	15	69.4	NA	NA
TDREASIDILHSIVK	Q8BG32|PSD11_MOUSE	NA	NA	15	425	NA	NA
TEAPLNPK	P63260|ACTG_MOUSE:P607	NA	NA	8	1400	4210	2280
TEEISEVKMDAEFGHDSG	P12023|A4_MOUSE	NA	NA	18	286	235	393
TENEVEPVDARPAADR	P12023|A4_MOUSE	NA	NA	16	888	NA	NA
THPDEELLRALLSK	O08601|MTP_MOUSE	NA	NA	14	2080	2170	3520
THPDEELLRALLSKFK	O08601|MTP_MOUSE	NA	NA	16	1140	390	1870
TIAPALVSK	P17182|ENOA_MOUSE	NA	NA	9	126	NA	389
TIEETGILAERAR	P02468|LAMC1_MOUSE	NA	NA	13	167	NA	NA
TIEETGILAERARSR	P02468|LAMC1_MOUSE	NA	NA	15	261	NA	NA
TLDNDIMLIK	P07146|TRY2_MOUSE	NA	NA	10	71.7	NA	NA
TNAENEFVTIK	P04104|K2C1_MOUSE	NA	NA	11	126	NA	NA
TNAENEFVTIKK	P04104|K2C1_MOUSE	NA	NA	12	58.9	NA	NA
TNFFHESGLEARVALK	E9Q414|APOB_MOUSE	NA	NA	16	3540	2250	6140
TNQELQEINR	P07356|ANXA2_MOUSE	NA	NA	10	87.9	NA	NA
TPVLHQKTLQAMKSHSEK	Q76KF0|SEM6D_MOUSE	NA	NA	18	7410	904	781
TQLLEDYVKAIEGIK	A2AJ15|MA1B1_MOUSE	NA	NA	15	132	NA	146
TRLEEIRLAVEDGAT	Q91YP3|DEOC_MOUSE	NA	NA	15	612	NA	NA
TTGIVMDSGDGVTHTVPIYE(	P63260|ACTG_MOUSE:P607	NA	NA	30	239	NA	NA
TVEENQVNVEVMR	O55111|DSG2_MOUSE	NA	NA	13	329	NA	281
TVEENQVNVEVMRIK	O55111|DSG2_MOUSE	NA	NA	15	177	NA	NA
TVGQLYK	Q6URW6|MYH14_MOUSE:Q	NA	NA	7	139	NA	NA
TYWIIIELKHKER	Q99JW5|EPCAM_MOUSE	NA	NA	13	57.4	NA	NA
VALEESRAQAEQA	Q91ZV0|MIA2_MOUSE	NA	NA	13	23.8	NA	NA
VALEESRAQAEQALS	Q91ZV0|MIA2_MOUSE	NA	NA	15	1900	457	1010
VALEESRAQAEQALSE	Q91ZV0|MIA2_MOUSE	NA	NA	16	2110	549	2240
VALEESRAQAEQALSEK	Q91ZV0|MIA2_MOUSE	NA	NA	17	198	NA	NA
VANKIGII	P62751|RL23A_MOUSE	NA	NA	8	5590	NA	2030
VAPEEHPVLLTEAPLNPK	P63260|ACTG_MOUSE:P607	NA	NA	18	33.9	902	1040
VDFLERPIIAFVR	Q8BTY2|S4A7_MOUSE	NA	NA	13	343	144	601
VDFLSEASIMGQFSHH	Q03145|EPHA2_MOUSE	NA	NA	16	91.7	NA	155
VDFLSEASIMGQFSHHN	Q03145|EPHA2_MOUSE	NA	NA	17	418	NA	175
VDLREMLAVAVLAAER	Q80V26|IMPA3_MOUSE	NA	NA	16	153	NA	712
VDPVNFK	P01942|HBA_MOUSE:P0646	NA	NA	7	192	NA	929
VDSGKIEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	17	1420	NA	2120
VDTSSEITTK	P26350|PTMA_MOUSE	NA	NA	10	1170	130	237
VEHEVNLLVEEIHR	Q4KML4|ABRAL_MOUSE	NA	NA	14	1770	1070	1400
VEIIANDQGNR	P17879|HS71B_MOUSE:P16	NA	NA	11	80.7	NA	125
VELQELNDR	P20152|VIME_MOUSE:P310	NA	NA	9	162	NA	NA
VENETMIPVLTSKR	Q80XR2|AT2C1_MOUSE	NA	NA	14	150	NA	NA
VFLENVIR	P62806|H4_MOUSE	NA	NA	8	657	467	142
VIEKAQQIQALQSN	E9PV24|FIBA_MOUSE	NA	NA	14	69.2	NA	NA
VIEKAQQIQALQSNVR	E9PV24|FIBA_MOUSE	NA	NA	16	1060	331	769
VIIVDSGKIEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	20	614	79.4	NA
VKPYVEEGLHPQIIIR	P80313|TCPH_MOUSE	NA	NA	16	288	293	579
VLDELTLSK	P02535|K1C10_MOUSE	NA	NA	9	151	NA	NA
VLDGEQLSIEALRQEH	Q9D2Z1|CEA20_MOUSE	NA	NA	16	930	242	779
VLDGEQLSIEALRQEHQ	Q9D2Z1|CEA20_MOUSE	NA	NA	17	868	198	910
VLLFIEHVVEVARGK	Q61168|LAPM5_MOUSE	NA	NA	15	166	NA	132
VLRSQHVQVEEGSEP	P13020|GELS_MOUSE	NA	NA	15	109	NA	NA
VNDIFERIASEASR	Q8CGP2|H2B1P_MOUSE:Q8	NA	NA	14	220	55.2	NA
VPDEHMIPIENLMNPR	Q91ZX7|LRP1_MOUSE	NA	NA	16	162	146	238
VPEGHPVR	Q5DTJ9|MYPN_MOUSE	NA	NA	8	254	NA	NA
VPGLTETAVFSCEAHNDK	Q60805|MERTK_MOUSE	NA	NA	18	1250	180	1370
VPQNFAVAGKSQSE	Glycinin_448	NA	NA	14	419	NA	NA
VPSEAIRGLSALQSLR	A2ARI4|LGR4_MOUSE	NA	NA	16	366	NA	448
VPTEEVSLEVLLSNGQK	Q8BVL3|SNX17_MOUSE	NA	NA	17	1850	NA	3630
VRFLEQQNK	P20152|VIME_MOUSE:P0399	NA	NA	9	1200	1320	2590
VSDLTQAANK	P31001|DESM_MOUSE	NA	NA	10	626	2070	1230
VSHLLGINVTDFTR	Q8VDD5|MYH9_MOUSE	NA	NA	14	311	NA	NA
VSNSVKEIMAEIYK	P10605|CATB_MOUSE	NA	NA	14	2280	749	1440
VSPTVHFTPAEISR	Q9QXH4|ITAX_MOUSE	NA	NA	14	418	232	201
VSPTVHFTPAEISRS	Q9QXH4|ITAX_MOUSE	NA	NA	15	156	73.7	NA
VSPTVHFTPAEISRSV	Q9QXH4|ITAX_MOUSE	NA	NA	16	412	195	262
VSQVVHKAVLDVAETGTEAA	Q91WP6|SPA3N_MOUSE:Q5	NA	NA	24	83.2	NA	78.6

VTMQNLNDR	Q8VCW2|K1C25_MOUSE:P0	NA	NA	9	306	NA	NA
VVPQNFAVAGKSQ	Glycinin_448	NA	NA	13	68.7	NA	NA
VVPQNFAVAGKSQSE	Glycinin_448	NA	NA	15	316	NA	NA
VVSTHEQVLR	Q61781|K1C14_MOUSE	NA	NA	10	63.5	126	104
VYFGSGFAAPFFIVRHQLLKI	P17665|COX7C_MOUSE	NA	NA	21	2320	NA	9030
YAAIMGFILAHKAR	Q8BW75|AOFB_MOUSE	NA	NA	14	50.5	76.7	256
YADSIHAIFVETSAK	P35285|RB22A_MOUSE	NA	NA	15	766	351	400
YDALDVANKIGII	P62751|RL23A_MOUSE	NA	NA	13	801	NA	373
YEELQQTAGR	Q922U2|K2C5_MOUSE	NA	NA	10	244	205	213
YEELQVTAGR	P50446|K2C6A_MOUSE:Q8B	NA	NA	10	61.9	145	221
YIDQEELNK	P07901|HS90A_MOUSE:P11	NA	NA	9	180	NA	NA
YIIQEEMVVTEHVRDK	Q91VK4|ITM2C_MOUSE	NA	NA	16	763	NA	698
YKIEDSFVTAVLAEETR	O08601|MTP_MOUSE	NA	NA	17	169	NA	NA
YNPLVPEAQK	Q9Z0G9|CLD3_MOUSE	NA	NA	10	1140	499	858
YNPLVPEAQKR	Q9Z0G9|CLD3_MOUSE	NA	NA	11	5600	1530	7360
YQDFEARYVQAKLSVHDR	O70228|ATP9A_MOUSE	NA	NA	18	1100	551	716
YQTIEENIKIFEED	O89051|ITM2B_MOUSE	NA	NA	14	4740	NA	4310
YQTIEENIKIFEEDA	O89051|ITM2B_MOUSE	NA	NA	15	5290	NA	4060
YRQKVAPLGAELQESAR	Q00623|APOA1_MOUSE	NA	NA	17	1600	416	1120
YSNRVVDLMAYMASKE	P16858|G3P_MOUSE	NA	NA	16	618	NA	256

Peptide	Accession	PTM	AScore	Length	Area..1	Area.2	Area.3
free_pep							
AAIMGFILAHKAR	Q8BW75|AOFB_MOUSE	NA	NA	13	NA	41.9	NA
AALHAAVIAINEAIDRR	Q9JKF1|IQGA1_MOUSE	NA	NA	17	120	90.5	222
ADLINNLGTIAK	P07901|HS90A_MOUSE:P11	NA	NA	12	NA	92.3	NA
AEAEALYQTK	Q3UV17|K22O_MOUSE:Q9R	NA	NA	10	838	479	306
AEEKTISAKYAEER	Q8VDD5|MYH9_MOUSE	NA	NA	14	260	111	NA
AFKINELKAEVANHL	O70628|PDE9A_MOUSE	NA	NA	15	340	83.8	NA
AGDDAPRAVFPSIVGRPR	P63260|ACTG_MOUSE:P607	NA	NA	18	NA	415	NA
AGFAGDDAPR	P63260|ACTG_MOUSE:P607	NA	NA	10	1880	3950	2790
AGFAGDDAPRAVFPSIVGRP	P63260|ACTG_MOUSE:P607	NA	NA	21	NA	3710	3920
AGVAPLQVK	Q8BTM8|FLNA_MOUSE	NA	NA	9	NA	268	166
AKLVEGRTHISISK	A0AAQ4VMX2|CO4A_MOUS	NA	NA	14	451	187	124
ALAAAGYDVEK	P15864|H12_MOUSE:P43274	NA	NA	11	120	1080	1160
ALEEANADLEVK	Q6IFX2|K1C42_MOUSE	NA	NA	12	205	236	286
ALESPERPFLAILGGAK	P09411|PGK1_MOUSE	NA	NA	17	NA	348	481
ALTQTGGPHVK	Q8BTM8|FLNA_MOUSE	NA	NA	11	NA	59.5	NA
ANQIVLLLAELARRDR	Q99PE8|ABCG5_MOUSE	NA	NA	16	3070	739	4170
APQVSTPTLVEAARN	P07724|ALBU_MOUSE	NA	NA	15	NA	314	777
APQVSTPTLVEAARNLG	P07724|ALBU_MOUSE	NA	NA	17	909	305	NA
AQYEDIAQK	Q3UV17|K22O_MOUSE	NA	NA	9	1070	168	75.1
AQYETIAAK	P31001|DESM_MOUSE	NA	NA	9	317	329	222
ASFEAQGALANIAVDK	P14439|HA23_MOUSE:P0422	NA	NA	16	5190	2630	3220
ASGPPVSELITK	P15864|H12_MOUSE:P43277	NA	NA	12	NA	916	NA
AVFPSIVGRPR	P63260|ACTG_MOUSE:P607	NA	NA	11	502	3830	4330
AVNYASRIRAHGGTN	A6X935|ITIH4_MOUSE	NA	NA	15	1430	880	1270
AVSEGTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8C	NA	NA	16	464	157	422
DATNVGDEGGFAPNILENK	P17182|ENOA_MOUSE	NA	NA	19	NA	159	113
DEAGPSIVHR	P68134|ACTS_MOUSE:P680	NA	NA	10	NA	238	325
DESGPSIVHR	P63260|ACTG_MOUSE:P607	NA	NA	10	202	284	450
DFYNPLVPEAQKRE	Q9Z0G9|CLD3_MOUSE	NA	NA	14	NA	108	NA
DGEVVSEATQQQHEV	P31001|DESM_MOUSE	NA	NA	15	NA	119	NA
DIEEVEQHIQTIRSK	Q8K0B2|LMBD1_MOUSE	NA	NA	15	2210	2760	3110
DIEEVEQHIQTIRSKSK	Q8K0B2|LMBD1_MOUSE	NA	NA	17	5750	228	268
DIEQSIKSETSGSF	P97429|ANXA4_MOUSE	NA	NA	14	320	242	360
DIISDTSGDFRK	P07356|ANXA2_MOUSE	NA	NA	12	NA	399	105
DMQYQHVIETLIGKK	P80316|TCPE_MOUSE	NA	NA	15	1220	649	1090
DMRQTVAVGVIKAVDK	P10126|EF1A1_MOUSE	NA	NA	16	NA	159	202
DSGKIEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	16	5050	8460	9300
DSYVGDEAQSK	P63260|ACTG_MOUSE:P607	NA	NA	11	2510	5490	3790
DVNAAIATIK	P68369|TBA1A_MOUSE:P68	NA	NA	10	NA	370	NA
EAETRAEFAER	P58774|TPM2_MOUSE:Q6IR	NA	NA	11	NA	208	76.6
EAFQLFDR	Q60605|MYL6_MOUSE	NA	NA	8	111	161	134
EAKDFQKAMIVFQSEFK	Q8R3G9|TSN8_MOUSE	NA	NA	17	513	121	365
EDKYEEEIK	P58774|TPM2_MOUSE:Q6IR	NA	NA	9	79.8	173	114
EGTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8C	NA	NA	13	84.6	267	558
ELEEQLGPVAEETR	P08226|APOE_MOUSE	NA	NA	14	573	217	593
ELEEQLGPVAEETRA	P08226|APOE_MOUSE	NA	NA	15	912	350	1570
ENADLAGELRVLGQAK	O08638|MYH11_MOUSE	NA	NA	16	NA	103	NA
ENAIDRAEQAEADKK	P58774|TPM2_MOUSE	NA	NA	15	NA	76.8	NA
ENALDRAEQAEADKK	P58771|TPM1_MOUSE	NA	NA	15	NA	76.8	NA
EPGQEYTVLLIAEKGRHK	Q80YX1|TENA_MOUSE	NA	NA	18	781	789	653
EQAQEQVQPKPLES	P06728|APOA4_MOUSE	NA	NA	14	158	87.7	103
EVEQHIQTIRSK	Q8K0B2|LMBD1_MOUSE	NA	NA	12	153	109	NA
FADLSEAANR	P20152|VIME_MOUSE	NA	NA	10	NA	229	170
FADLSEAANRNNDALR	P20152|VIME_MOUSE	NA	NA	16	NA	99.2	NA
FDQLLAEEK	Q6URW6|MYH14_MOUSE:Q	NA	NA	9	130	69.3	NA
FEAQGALANIAVDK	P14439|HA23_MOUSE:P0422	NA	NA	14	728	205	528
FEDENFILK	P17742|PPIA_MOUSE	NA	NA	9	NA	164	303
FEFFENTIVSRVAR	Q62179|SEM4B_MOUSE	NA	NA	14	6410	2860	5400
FFHESGLEARVALK	E9Q414|APOB_MOUSE	NA	NA	14	10900	5330	8800
FGPAHALIIAGRSVSG	P14246|GTR2_MOUSE	NA	NA	16	1440	889	936
FIEHVVEVARGK	Q61168|LAPM5_MOUSE	NA	NA	12	216	140	211
FLASVSTVLTSK	P01942|HBA_MOUSE	NA	NA	12	NA	2060	1870
FNPRFDESTIVCNTSEGGR	Q9CQW5|LEG2_MOUSE	NA	NA	19	697	733	1190
FPLGESFLVAK	O08710|THYG_MOUSE	NA	NA	11	NA	2080	744
FQNAILVR	P07724|ALBU_MOUSE	NA	NA	8	888	2540	2450
GALYRIGDLQAFVGRDAG	P10852|4F2_MOUSE	NA	NA	18	260	270	584
GFSGLDGAK	P11087|CO1A1_MOUSE	NA	NA	9	NA	213	NA
GHEVAAMLKSELQK	Q8K135|K319L_MOUSE	NA	NA	14	216	157	252
GKTIENFLVVNKER	Q3UR85|MYRF_MOUSE	NA	NA	14	2230	1990	1900
GLVGIVVGTIFIIQGLRSGGTS	P23150|HA2J_MOUSE:P1443	NA	NA	28	NA	84.1	NA
GMVQAVRLIAEGTAPR	Q8R0Y6|AL1L1_MOUSE	NA	NA	16	1700	552	1050
GNIEIALEAAKALDDK	Q8CIE6|COPA_MOUSE	NA	NA	16	2490	476	2320
GNMEVARIHAENAIR	Q99LU0|CH1B1_MOUSE	NA	NA	15	2670	2120	2740
GNTEVARIHAENAIR	Q9CQD4|CH1B2_MOUSE	NA	NA	15	604	276	455
GPAGPQGPR	P11087|CO1A1_MOUSE	NA	NA	9	NA	158	NA
GQEVVSSIRAEMGSDR	Q8VBZ0|DHRSX_MOUSE	NA	NA	16	1560	1020	1310
GRLQSELK	P07744|K2C4_MOUSE	NA	NA	8	100	417	NA
GTNESLER	P20152|VIME_MOUSE:P0399	NA	NA	8	NA	227	NA
GYSFTTTAER	P63260|ACTG_MOUSE:P607	NA	NA	10	410	251	1010

GYSFVTTAER	P68134|ACTS_MOUSE:P680	NA	NA	10	901	567	835
HAVSEGTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8C	NA	NA	17	95.3	9810	8200
HLQLAIR	C0HKE3|H2A1D_MOUSE:Q8	NA	NA	7	NA	219	319
IAQLEEQVEQEAR	O08638|MYH11_MOUSE	NA	NA	13	NA	143	85.7
IEDSFVTAVLAEETR	O08601|MTP_MOUSE	NA	NA	15	8400	655	4640
IEEVEQHIQTIRSK	Q8K0B2|LMBD1_MOUSE	NA	NA	14	1240	575	NA
IEEVEQHIQTIRSKSK	Q8K0B2|LMBD1_MOUSE	NA	NA	16	2630	197	933
IEKAQQIQALQSNVR	E9PV24|FIBA_MOUSE	NA	NA	15	106	152	306
IGGHGAEYGAEALER	P01942|HBA_MOUSE	NA	NA	15	86.7	3050	1000
IGGIGTVPVGR	P10126|EF1A1_MOUSE:P62	NA	NA	11	207	197	283
ILLAELEQLK	P20152|VIME_MOUSE	NA	NA	10	NA	671	803
ILTERGYSFVTTAER	P68134|ACTS_MOUSE:P680	NA	NA	15	NA	20.8	NA
IPGKQVAGVIKAVDSK	O08601|MTP_MOUSE	NA	NA	16	642	474	417
IPNVENETMIPVLTSKR	Q80XR2|AT2C1_MOUSE	NA	NA	17	512	217	594
IQLQEELAAAERAK	Q8VDD5|MYH9_MOUSE	NA	NA	14	988	549	954
IQRVAAGVLCELAQDK	Q02257|PLAK_MOUSE:Q022	NA	NA	16	1280	61.4	996
IRYESLTDPSK	P07901|HS90A_MOUSE:P11	NA	NA	11	NA	161	NA
ISLAQYLINARLSSEK	P60335|PCBP1_MOUSE	NA	NA	16	379	99.8	277
ISPKEMTIIYVEASGK	Q05117|PPA5_MOUSE	NA	NA	16	12800	1950	6510
ISQKDIEQSIKSETSGS	P97429|ANXA4_MOUSE	NA	NA	17	361	228	399
ISQKDIEQSIKSETSGSF	P97429|ANXA4_MOUSE	NA	NA	18	10300	3420	5370
IVEGLMTTVHAITATQK	P16858|G3P_MOUSE	NA	NA	17	430	92.7	470
KELEEQLGPVAEETR	P08226|APOE_MOUSE	NA	NA	15	997	723	694
KELEEQLGPVAEETRA	P08226|APOE_MOUSE	NA	NA	16	598	349	353
KELEEQLGPVAEETRAR	P08226|APOE_MOUSE	NA	NA	17	1470	547	965
KGHEVAAMLKSELQK	Q8K135|K319L_MOUSE	NA	NA	15	189	158	556
KGVIEAFLHAWKGYQK	A2AJ15|MA1B1_MOUSE	NA	NA	16	282	60.8	219
KIEDSFVTAVLAEETR	O08601|MTP_MOUSE	NA	NA	16	5060	1040	4430
KITEVSLVGHLSYDK	E9Q414|APOB_MOUSE	NA	NA	15	NA	58.4	NA
KITEVSLVGHLSYDKK	E9Q414|APOB_MOUSE	NA	NA	16	1640	1090	1160
KKELEEQLGPVAEETR	P08226|APOE_MOUSE	NA	NA	16	NA	386	497
KKITEVSLVGHLSYDK	E9Q414|APOB_MOUSE	NA	NA	16	3210	2070	579
KPFQEYLEAQRQK	Q99KU0|VMP1_MOUSE	NA	NA	13	61.4	179	256
KTIENFLVVNKER	Q3UR85|MYRF_MOUSE	NA	NA	13	114	101	NA
KVIEKAQQIQALQSN	E9PV24|FIBA_MOUSE	NA	NA	15	176	129	224
KVIEKAQQIQALQSNVR	E9PV24|FIBA_MOUSE	NA	NA	17	3350	2060	2460
LAKNKQKPITPETAEK	P60766|CDC42_MOUSE	NA	NA	16	4280	2320	2760
LALDIEIATYR	P03995|GFAP_MOUSE:Q6NX	NA	NA	11	326	62.4	NA
LALQFTTNPK	O08710|THYG_MOUSE	NA	NA	10	NA	645	692
LALQFTTNPKR	O08710|THYG_MOUSE	NA	NA	11	NA	66.8	NA
LFIEHVVEVARGK	Q61168|LAPM5_MOUSE	NA	NA	13	436	542	432
LHVDPENFR	P02089|HBB2_MOUSE:P020	NA	NA	9	688	1020	1950
LKPGAPLRPK	Q8BTM8|FLNA_MOUSE	NA	NA	10	NA	203	176
LLAEEKTISAKYAEER	Q8VDD5|MYH9_MOUSE	NA	NA	16	2200	456	1010
LLEGEESRINLPIQT	P31001|DESM_MOUSE	NA	NA	15	NA	109	71.8
LLQDFFNGRDLNK	P17879|HS71B_MOUSE:Q61	NA	NA	13	NA	68.7	NA
LLVVYPWTQR	P02089|HBB2_MOUSE:P021	NA	NA	10	389	353	144
LPKSAKPVSQMRMATPLLMF	P04441|HG2A_MOUSE	NA	NA	21	458	415	428
LPKSAKPVSQMRMATPLLMF	P04441|HG2A_MOUSE	NA	NA	22	4650	2520	3840
LPRQDEEKPLHALLHGR	Q07079|IBP5_MOUSE	NA	NA	17	405	284	NA
LPVQLQRAMAAEAEAARE	P54116|STOM_MOUSE	NA	NA	18	664	186	284
LRVDPVNFK	P01942|HBA_MOUSE:P0646	NA	NA	9	180	1280	869
LSDGVAVLK	P63038|CH60_MOUSE	NA	NA	9	NA	96.5	419
LSGSTAITAYRMKR	Q99N03|M4A10_MOUSE	NA	NA	14	191	154	NA
MEVARIHAENAIR	Q99LU0|CH1B1_MOUSE	NA	NA	13	NA	107	189
NDMQYQHVIETLIGKK	P80316|TCPE_MOUSE	NA	NA	16	405	177	370
NELRVAPEEHPTLLTEAPLNP	P68134|ACTS_MOUSE:P680	NA	NA	22	NA	321	313
NELRVAPEEHPVLLTEAPLNP	P63260|ACTG_MOUSE:P607	NA	NA	22	NA	447	171
NFFHESGLEARVALK	E9Q414|APOB_MOUSE	NA	NA	15	20400	16800	31300
NGKTIENFLVVNKER	Q3UR85|MYRF_MOUSE	NA	NA	15	NA	239	58.2
NIEIALEAAKALDDK	Q8CIE6|COPA_MOUSE	NA	NA	15	1020	49.7	599
NKKITEVSLVGHLSYDK	E9Q414|APOB_MOUSE	NA	NA	17	704	352	578
NKYEDEINK	Q922U2|K2C5_MOUSE:Q8VE	NA	NA	9	311	204	275
NMEVARIHAENAIR	Q99LU0|CH1B1_MOUSE	NA	NA	14	NA	133	265
NPLVPEAQKR	Q9Z0G9|CLD3_MOUSE	NA	NA	10	6480	2140	2580
NPRFDESTIVCNTSEGGR	Q9CQW5|LEG2_MOUSE	NA	NA	18	5880	868	2100
NPSDLYAEGCEALVVKK	Q9QY33|TSN3_MOUSE	NA	NA	17	124	27.6	216
NTIEETGILAERAR	P02468|LAMC1_MOUSE	NA	NA	14	412	451	NA
NTIEETGILAERARSR	P02468|LAMC1_MOUSE	NA	NA	16	1620	846	1510
NTQWVHGIVVYTGHDT	P70704|AT8A1_MOUSE	NA	NA	16	NA	29.3	NA
PLRLPLQDVYK	P10126|EF1A1_MOUSE:P62	NA	NA	11	NA	904	649
QDFEARYVQAKLSVHDR	O70228|ATP9A_MOUSE	NA	NA	17	1790	1170	1680
QELQEYEVVAESEKR	Q9D5V6|SYAP1_MOUSE	NA	NA	15	1330	133	163
QVHPDTGISSK	P70696|H2B1A_MOUSE:Q8C	NA	NA	11	NA	563	1050
REQEVTVLKK	O08638|MYH11_MOUSE	NA	NA	10	NA	113	116
RIALENYLAALQSDPP	Q06335|APLP2_MOUSE	NA	NA	16	NA	760	8330
RIALENYLAALQSDPPR	Q06335|APLP2_MOUSE	NA	NA	17	16400	1870	6140
RIALENYLAALQSDPPRP	Q06335|APLP2_MOUSE	NA	NA	18	2920	648	3160
RIALENYLAALQSDPPRPH	Q06335|APLP2_MOUSE	NA	NA	19	121	38.7	243
RISGLIYEETRGVLK	P62806|H4_MOUSE	NA	NA	15	NA	1140	2030
RLALENYITALQAVPPR	P12023|A4_MOUSE	NA	NA	17	11500	1820	5960

RLALENYITALQAVPPRP	P12023|A4_MOUSE	NA	NA	18	6410	432	5090
RRIALENYLAALQSD	Q06335|APLP2_MOUSE	NA	NA	15	5940	1990	4250
RRIALENYLAALQSDPP	Q06335|APLP2_MOUSE	NA	NA	17	33200	11400	34600
RRIALENYLAALQSDPPR	Q06335|APLP2_MOUSE	NA	NA	18	24800	6340	21700
RRIALENYLAALQSDPPRP	Q06335|APLP2_MOUSE	NA	NA	19	16900	6130	9770
RRIALENYLAALQSDPPRPH	Q06335|APLP2_MOUSE	NA	NA	20	3760	1710	3860
RRLALENYITAL	P12023|A4_MOUSE	NA	NA	12	493	64.5	75.3
RRLALENYITALQAVPPR	P12023|A4_MOUSE	NA	NA	18	121000	45000	88400
RRLALENYITALQAVPPRP	P12023|A4_MOUSE	NA	NA	19	162000	56100	153000
RRLALENYITALQAVPPRPH	P12023|A4_MOUSE	NA	NA	20	7350	5000	9300
RTAAENDFVVLKK	P07744|K2C4_MOUSE	NA	NA	13	NA	468	248
RTAAENEFVTLKK	P50446|K2C6A_MOUSE	NA	NA	13	NA	79.5	NA
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	NA	NA	19	9540	5960	4080
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	NA	NA	20	1940	441	1230
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	NA	NA	21	575	117	280
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	NA	NA	22	217	190	NA
SARLSAKPAPPKPEPKPKK	P09602|HMGN2_MOUSE	NA	NA	19	1410	204	108
SDPQVHTVLVERSTLK	Q9JHU4|DYHC1_MOUSE	NA	NA	16	1520	555	1200
SFEAQGALANIAVDK	P14439|HA23_MOUSE:P042	NA	NA	15	113	116	179
SGEKEVNLAVENAK	Q9JLJ2|AL9A1_MOUSE	NA	NA	14	161	131	NA
SGKIEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	15	3260	3510	2870
SGVEYTRLAVESARG	Q62178|SEM4A_MOUSE	NA	NA	15	277	218	216
SLEAQAEK	P21107|TPM3_MOUSE:P587	NA	NA	8	NA	341	NA
SLHTLFGDK	P07724|ALBU_MOUSE	NA	NA	9	306	737	2160
SPFEVYVDK	Q8BTM8|FLNA_MOUSE	NA	NA	9	NA	144	NA
SPKEMTIIYVEASGK	Q05117|PPA5_MOUSE	NA	NA	15	767	275	709
SPTVHFTPAEISR	Q9QXH4|ITAX_MOUSE	NA	NA	13	198	67.7	128
STTTGHLIYK	P10126|EF1A1_MOUSE:P626	NA	NA	10	324	295	207
SYELPDGQVITIGNER	P63260|ACTG_MOUSE:P607	NA	NA	16	1020	523	1320
TANQIVLLLAELARR	Q99PE8|ABCG5_MOUSE	NA	NA	15	1770	127	1720
TANQIVLLLAELARRDR	Q99PE8|ABCG5_MOUSE	NA	NA	17	15900	2880	15600
TATPQQAQEVHEK	P17751|TPIS_MOUSE	NA	NA	13	NA	142	160
TEAPLNPK	P63260|ACTG_MOUSE:P607	NA	NA	8	1400	4210	2280
TEEISEVKMDAEFGHDSG	P12023|A4_MOUSE	NA	NA	18	286	235	393
THPDEELLRALLSK	O08601|MTP_MOUSE	NA	NA	14	2080	2170	3520
THPDEELLRALLSKFK	O08601|MTP_MOUSE	NA	NA	16	1140	390	1870
TITLEVEPSDTIENVK	P0CG50|UBC_MOUSE:P6298	NA	NA	16	NA	498	738
TKYEEEINK	P07744|K2C4_MOUSE	NA	NA	9	NA	193	134
TNFFHESGLEARVALK	E9Q414|APOB_MOUSE	NA	NA	16	3540	2250	6140
TPAQYDASELK	P07356|ANXA2_MOUSE	NA	NA	11	NA	89.3	NA
TPVLHQKTLQAMKSHSEK	Q76KF0|SEM6D_MOUSE	NA	NA	18	7410	904	781
TSGGAGGLGSLR	P31001|DESM_MOUSE	NA	NA	12	NA	392	233
VALEESRAQAEQALS	Q91ZV0|MIA2_MOUSE	NA	NA	15	1900	457	1010
VALEESRAQAEQALSE	Q91ZV0|MIA2_MOUSE	NA	NA	16	2110	549	2240
VAPEEHPT	P68134|ACTS_MOUSE:P680	NA	NA	8	NA	507	632
VAPEEHPTLLTEAPLNPK	P68134|ACTS_MOUSE:P680	NA	NA	18	NA	603	500
VAPEEHPVLLTEAPLNPK	P63260|ACTG_MOUSE:P607	NA	NA	18	33.9	902	1040
VDFLERPIIAFVR	Q8BTY2|S4A7_MOUSE	NA	NA	13	343	144	601
VDTSSEITTK	P26350|PTMA_MOUSE	NA	NA	10	1170	130	237
VDVGKDQEFTVK	Q8BTM8|FLNA_MOUSE	NA	NA	12	NA	50.3	NA
VEGTARGIVVYTGDR	Q8VDN2|AT1A1_MOUSE	NA	NA	15	NA	482	321
VEHEVNLLVEEIHR	Q4KML4|ABRAL_MOUSE	NA	NA	14	1770	1070	1400
VELQELNDRFANYIEK	P31001|DESM_MOUSE	NA	NA	16	NA	561	1050
VETHMARVEAMLNDRR	P12023|A4_MOUSE	NA	NA	16	NA	228	243
VFLENVIR	P62806|H4_MOUSE	NA	NA	8	657	467	142
VFLENVIRDAVT	P62806|H4_MOUSE	NA	NA	12	NA	196	222
VGENADSQIK	P10922|H10_MOUSE	NA	NA	10	NA	118	NA
VGINYQPPTVVPGGDLAK	P68369|TBA1A_MOUSE:P68	NA	NA	18	NA	232	295
VGLQVVAVK	P63038|CH60_MOUSE	NA	NA	9	NA	170	764
VGVNGFGR	P16858|G3P_MOUSE	NA	NA	8	NA	169	118
VIEKAQQIQALQSNVR	E9PV24|FIBA_MOUSE	NA	NA	16	1060	331	769
VIIVDSGKIEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	20	614	79.4	NA
VIQYLAVVASSHK	O08638|MYH11_MOUSE	NA	NA	13	NA	301	445
VKPYVEEGLHPQIIIR	P80313|TCPH_MOUSE	NA	NA	16	288	293	579
VLDGEQLSIEALRQEH	Q9D2Z1|CEA20_MOUSE	NA	NA	16	930	242	779
VLDGEQLSIEALRQEHQ	Q9D2Z1|CEA20_MOUSE	NA	NA	17	868	198	910
VLDGEQLSIEALRQEHQG	Q9D2Z1|CEA20_MOUSE	NA	NA	18	NA	75.2	285
VNDIFERIASEASR	Q8CGP2|H2B1P_MOUSE:Q8	NA	NA	14	220	55.2	NA
VPDEHMIPIENLMNPR	Q91ZX7|LRP1_MOUSE	NA	NA	16	162	146	238
VPGLTETAVFSCEAHNDK	Q60805|MERTK_MOUSE	NA	NA	18	1250	180	1370
VPVHDVTDASK	Q8BTM8|FLNA_MOUSE	NA	NA	11	NA	32.3	NA
VRALEAANADLEVK	P08730|K1C13_MOUSE	NA	NA	14	NA	210	NA
VRALEEANADLEVK	Q6IFX2|K1C42_MOUSE	NA	NA	14	NA	1750	985
VRALEEANTELEVK	Q9QWL7|K1C17_MOUSE:Q6	NA	NA	14	NA	61.4	NA
VRFLEQQNAALAAEVNRLK	P31001|DESM_MOUSE	NA	NA	19	NA	454	704
VRFLEQQNK	P20152|VIME_MOUSE:P0399	NA	NA	9	1200	1320	2590
VSDLTQAANK	P31001|DESM_MOUSE	NA	NA	10	626	2070	1230
VSFELFADK	P17742|PPIA_MOUSE	NA	NA	9	NA	121	234
VSHVSTGGGASLELLEGK	P09041|PGK2_MOUSE:P094	NA	NA	18	NA	105	105
VSNSVKEIMAEIYK	P10605|CATB_MOUSE	NA	NA	14	2280	749	1440
VSPTVHFTPAEISR	Q9QXH4|ITAX_MOUSE	NA	NA	14	418	232	201

VSPTVHFTPAEISRS	Q9QXH4|ITAX_MOUSE	NA	NA	15	156	73.7	NA
VSPTVHFTPAEISRSV	Q9QXH4|ITAX_MOUSE	NA	NA	16	412	195	262
VSPTVHFTPAEISRSVF	Q9QXH4|ITAX_MOUSE	NA	NA	17	NA	911	1270
VTAQGPGLEPSGNIANK	Q8BTM8|FLNA_MOUSE	NA	NA	17	NA	183	NA
VTIAQGGVLPNIQAV	C0HKE3|H2A1D_MOUSE:Q8	NA	NA	15	NA	122	NA
VVDLLAPYAK	P56480|ATPB_MOUSE	NA	NA	10	NA	83.8	595
VVSTHEQVLR	Q61781|K1C14_MOUSE	NA	NA	10	63.5	126	104
YAAIMGFILAHKAR	Q8BW75|AOFB_MOUSE	NA	NA	14	50.5	76.7	256
YAAIMGFILAHKARK	Q8BW75|AOFB_MOUSE	NA	NA	15	NA	35	NA
YADSIHAIFVETSAK	P35285|RB22A_MOUSE	NA	NA	15	766	351	400
YEELQQTAGR	Q922U2|K2C5_MOUSE	NA	NA	10	244	205	213
YEELQVTAGR	P50446|K2C6A_MOUSE:Q8B	NA	NA	10	61.9	145	221
YNPLVPEAQK	Q9Z0G9|CLD3_MOUSE	NA	NA	10	1140	499	858
YNPLVPEAQKR	Q9Z0G9|CLD3_MOUSE	NA	NA	11	5600	1530	7360
YPIEHGIITNWDDMEK	P68134|ACTS_MOUSE:P680	NA	NA	16	NA	24.3	NA
YQDFEARYVQAKLSVHDR	O70228|ATP9A_MOUSE	NA	NA	18	1100	551	716
YRQKVAPLGAELQESAR	Q00623|APOA1_MOUSE	NA	NA	17	1600	416	1120

Peptide	Accession	PTM	AScore	Length	Area..1	Area.2	Area.3
intact_PN							
AAEDYGVIK	P37804|TAGL_MOUSE	NA	NA	9	119	NA	239
AAKRMALLMAEMSR	Q64727|VINC_MOUSE	NA	NA	14	82.1	NA	47
AALHAAVIAINEAIDRR	Q9JKF1|IQGA1_MOUSE	NA	NA	17	120	90.5	222
ADDGRPFPQVIK	P05064|ALDOA_MOUSE	NA	NA	12	NA	NA	91.4
ADVDAATLAR	P31001|DESM_MOUSE	NA	NA	10	NA	NA	127
AEAEALYQTK	Q3UV17|K22O_MOUSE:Q9R(	NA	NA	10	838	479	306
AGFAGDDAPR	P63260|ACTG_MOUSE:P607	NA	NA	10	1880	3950	2790
AGFAGDDAPRAVFPSIVGRP	P63260|ACTG_MOUSE:P607	NA	NA	21	NA	3710	3920
AGLQFPVGR	C0HKE3|H2A1D_MOUSE:Q8I	NA	NA	9	NA	NA	1790
AGVAPLQVK	Q8BTM8|FLNA_MOUSE	NA	NA	9	NA	268	166
AGVRLELANIQAELVAK	E9Q414|APOB_MOUSE	NA	NA	17	NA	NA	172
AGVRLELANIQAELVAKP	E9Q414|APOB_MOUSE	NA	NA	18	68	NA	471
AGVRLELANIQAELVAKPS	E9Q414|APOB_MOUSE	NA	NA	19	929	NA	1100
AHGGYSVFAGVGER	P56480|ATPB_MOUSE	NA	NA	14	NA	NA	279
AIAELGIYPAVDPLDSTSR	P56480|ATPB_MOUSE	NA	NA	19	NA	NA	679
AKLVEGRTHISISK	A0AAQ4VMX2|CO4A_MOUSE	NA	NA	14	451	187	124
ALAAAGYDVEK	P15864|H12_MOUSE:P43274	NA	NA	11	120	1080	1160
ALDVANKIGII	P62751|RL23A_MOUSE	NA	NA	11	1060	NA	1230
ALEEANADLEVK	Q6IFX2|K1C42_MOUSE	NA	NA	12	205	236	286
ALESPERPFLAILGGAK	P09411|PGK1_MOUSE	NA	NA	17	NA	348	481
ALKEASMVITESPA	P54116|STOM_MOUSE	NA	NA	14	NA	NA	64.7
ANQIVLLLAELARRDR	Q99PE8|ABCG5_MOUSE	NA	NA	16	3070	739	4170
APALVSKKVNVVEQEK	P17182|ENOA_MOUSE	NA	NA	16	NA	NA	228
APGFGDNRK	P63038|CH60_MOUSE	NA	NA	9	NA	NA	43.9
APIIAVTR	P52480|KPYM_MOUSE	NA	NA	8	140	NA	209
APQVSTPTLVEAARN	P07724|ALBU_MOUSE	NA	NA	15	NA	314	777
AQYEDIAQK	Q3UV17|K22O_MOUSE	NA	NA	9	1070	168	75.1
AQYETIAAK	P31001|DESM_MOUSE	NA	NA	9	317	329	222
ASFEAQGALANIAVDK	P14439|HA23_MOUSE:P0422	NA	NA	16	5190	2630	3220
ATHPDEELLRALLSK	O08601|MTP_MOUSE	NA	NA	15	NA	NA	320
ATHPDEELLRALLSKFK	O08601|MTP_MOUSE	NA	NA	17	116	NA	128
ATIAGGGVIPHIHK	Q3THW5|H2AV_MOUSE:P0C	NA	NA	14	NA	NA	74.5
ATSFGSLR	O08710|THYG_MOUSE	NA	NA	8	NA	NA	337
AVDSLVPIGR	Q03265|ATPA_MOUSE	NA	NA	10	NA	NA	839
AVFPSIVGR	P63260|ACTG_MOUSE:P607	NA	NA	9	2180	NA	2670
AVFPSIVGRPR	P63260|ACTG_MOUSE:P607	NA	NA	11	502	3830	4330
AVNYASRIRAHGGTN	A6X935|ITIH4_MOUSE	NA	NA	15	1430	880	1270
AVSEGTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8C	NA	NA	16	464	157	422
DALDVANKIGII	P62751|RL23A_MOUSE	NA	NA	12	NA	NA	1800
DATNVGDEGGFAPNILENK	P17182|ENOA_MOUSE	NA	NA	19	NA	159	113
DAYHSRAIQVVRAR	P21460|CYTC_MOUSE	NA	NA	14	2230	NA	653
DEAGPSIVHR	P68134|ACTS_MOUSE:P6803	NA	NA	10	NA	238	325
DEAKDFQKAMIVFQSEFK	Q8R3G9|TSN8_MOUSE	NA	NA	18	NA	NA	71.3
DEEESPGQAKDEL	P14211|CALR_MOUSE	NA	NA	13	76.1	NA	87
DESGPSIVHR	P63260|ACTG_MOUSE:P607	NA	NA	10	202	284	450
DFAALLHAGLSVKR	Q78IQ7|S39A4_MOUSE	NA	NA	14	NA	NA	103
DFEARYVQAKLSVHDR	O70228|ATP9A_MOUSE	NA	NA	16	208	NA	204
DGYAQILR	Q99KI0|ACON_MOUSE	NA	NA	8	NA	NA	45.1
DIEEVEQHIQTIRSK	Q8K0B2|LMBD1_MOUSE	NA	NA	15	2210	2760	3110
DIEEVEQHIQTIRSKSK	Q8K0B2|LMBD1_MOUSE	NA	NA	17	5750	228	268
DIEQSIKSETSGSF	P97429|ANXA4_MOUSE	NA	NA	14	320	242	360
DIISDTSGDFRK	P07356|ANXA2_MOUSE	NA	NA	12	NA	399	105
DKGEYTLVVK	Q8BTM8|FLNA_MOUSE	NA	NA	10	NA	NA	101
DKTEFSIIHYAGK	O08638|MYH11_MOUSE	NA	NA	13	NA	NA	78.2
DLDYVHSVVANLEK	Q812G0|MGT4A_MOUSE	NA	NA	14	NA	NA	85.1
DMQYQHVIETLIGKK	P80316|TCPE_MOUSE	NA	NA	15	1220	649	1090
DMRQTVAVGVIKAVDK	P10126|EF1A1_MOUSE	NA	NA	16	NA	159	202
DNIQGITKPAIR	P62806|H4_MOUSE	NA	NA	12	NA	NA	90.1
DNLIDDLQR	P31001|DESM_MOUSE	NA	NA	9	NA	NA	99.9
DQGTYEDYVEGLRVFDK	Q60605|MYL6_MOUSE	NA	NA	17	NA	NA	123
DRVTDALNATR	P63038|CH60_MOUSE	NA	NA	11	NA	NA	356
DSGKIEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	16	5050	8460	9300
DSYVGDEAQSK	P63260|ACTG_MOUSE:P607	NA	NA	11	2510	5490	3790
EAALHAAVIAINEAIDRR	Q9JKF1|IQGA1_MOUSE	NA	NA	18	174	NA	154
EAETRAEFAER	P58774|TPM2_MOUSE:Q6IRU	NA	NA	11	NA	208	76.6
EAFQLFDR	Q60605|MYL6_MOUSE	NA	NA	8	111	161	134
EAFQLFDRTGDGK	Q60605|MYL6_MOUSE	NA	NA	13	NA	NA	98.3
EAKDFQKAMIVFQSEFK	Q8R3G9|TSN8_MOUSE	NA	NA	17	513	121	365
EAVAKADKLAEEHGS	P56480|ATPB_MOUSE	NA	NA	15	85.3	NA	336
EAYPGDVFYLHSR	Q03265|ATPA_MOUSE	NA	NA	13	NA	NA	393
EDIEEVEQHIQTIRSK	Q8K0B2|LMBD1_MOUSE	NA	NA	16	471	NA	579
EDIEEVEQHIQTIRSKSK	Q8K0B2|LMBD1_MOUSE	NA	NA	18	3590	NA	2580
EDKYEEEIK	P58774|TPM2_MOUSE:Q6IRU	NA	NA	9	79.8	173	114
EDSFVTAVLAEETR	O08601|MTP_MOUSE	NA	NA	14	90.7	NA	279
EEQTQQIRLQAEIFQAR	P08226|APOE_MOUSE	NA	NA	17	NA	NA	560
EGTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8C	NA	NA	13	84.6	267	558
EGTSLQEESLR	Q64016|DFA17_MOUSE:P50	NA	NA	11	NA	NA	109

EGTVEENQVNVEVMR	O55111|DSG2_MOUSE	NA	NA	15	623	NA	509
EGTVEENQVNVEVMRIK	O55111|DSG2_MOUSE	NA	NA	17	167	NA	598
EIQEESKRIIANVGK	Q8CAS9|PARP9_MOUSE	NA	NA	15	659	NA	590
EISPKEMTIIYVEASGK	Q05117|PPA5_MOUSE	NA	NA	17	502	NA	486
ELEEQLGPVAEETR	P08226|APOE_MOUSE	NA	NA	14	573	217	593
ELEEQLGPVAEETRA	P08226|APOE_MOUSE	NA	NA	15	912	350	1570
EMLAVAVLAAERGGDE	Q80V26|IMPA3_MOUSE	NA	NA	16	1060	NA	1020
EPGQEYTVLLIAEKGR	Q80YX1|TENA_MOUSE	NA	NA	16	145	NA	70.6
EPGQEYTVLLIAEKGRHK	Q80YX1|TENA_MOUSE	NA	NA	18	781	789	653
EQAQEQVQPKPLES	P06728|APOA4_MOUSE	NA	NA	14	158	87.7	103
EQTQQIRLQAEIFQAR	P08226|APOE_MOUSE	NA	NA	16	135	NA	761
ESEEFLKRLHPYK	Q8CE08|PPAP_MOUSE	NA	NA	13	117	NA	266
ESYSVYVYK	Q64525|H2B2B_MOUSE:Q8C	NA	NA	9	NA	NA	402
ETDLDYVHSVVANLEK	Q812G0|MGT4A_MOUSE	NA	NA	16	NA	NA	86
ETESVYRVQVVATEVGGSS	Q9R100|CAD17_MOUSE	NA	NA	19	392	NA	399
EVVSSIRAEMGSDR	Q8VBZ0|DHRSX_MOUSE	NA	NA	14	352	NA	342
FADLSEAANR	P20152|VIME_MOUSE	NA	NA	10	NA	229	170
FASFEAQGALANIAVDK	P14439|HA23_MOUSE:P0422	NA	NA	17	210	NA	192
FASFEAQGALANIAVDKA	P14439|HA23_MOUSE:P0422	NA	NA	18	315	NA	314
FASFEAQGALANIAVDKAN	P14439|HA23_MOUSE:P0422	NA	NA	19	228	NA	102
FASFIDK	Q6NXH9|K2C73_MOUSE:P11	NA	NA	7	1980	NA	2630
FEAQGALANIAVDK	P14439|HA23_MOUSE:P0422	NA	NA	14	728	205	528
FEDENFILK	P17742|PPIA_MOUSE	NA	NA	9	NA	164	303
FEFFENTIVSRVAR	Q62179|SEM4B_MOUSE	NA	NA	14	6410	2860	5400
FFHESGLEARVALK	E9Q414|APOB_MOUSE	NA	NA	14	10900	5330	8800
FGERAFK	P07724|ALBU_MOUSE	NA	NA	7	NA	NA	312
FGPAHALIIAGRSV	P14246|GTR2_MOUSE	NA	NA	14	NA	NA	60.7
FGPAHALIIAGRSVSG	P14246|GTR2_MOUSE	NA	NA	16	1440	889	936
FGSGFAAPFFIVRHQLLKK	P17665|COX7C_MOUSE	NA	NA	19	88.3	NA	1440
FHESGLEARVALK	E9Q414|APOB_MOUSE	NA	NA	13	224	NA	252
FIEHVVEVARGK	Q61168|LAPM5_MOUSE	NA	NA	12	216	140	211
FLASVSTVLTSK	P01942|HBA_MOUSE	NA	NA	12	NA	2060	1870
FLFVDK	P60521|GBRL2_MOUSE:O08	NA	NA	6	NA	NA	164
FNPRFDESTIVCNTSEGGR	Q9CQW5|LEG2_MOUSE	NA	NA	19	697	733	1190
FPLGESFLVAK	O08710|THYG_MOUSE	NA	NA	11	NA	2080	744
FQNAILVR	P07724|ALBU_MOUSE	NA	NA	8	888	2540	2450
FTASAGIQVVGDDLTVTNPK	P17182|ENOA_MOUSE	NA	NA	20	509	NA	65.8
FTQAGSEVSALLGR	P56480|ATPB_MOUSE	NA	NA	14	NA	NA	264
FVTVQTISGTGALR	P05202|AATM_MOUSE	NA	NA	14	NA	NA	101
FYNPLVPEAQKR	Q9Z0G9|CLD3_MOUSE	NA	NA	12	669	NA	539
GALYRIGDLQAFVGRDAG	P10852|4F2_MOUSE	NA	NA	18	260	270	584
GANPVEIRR	P63038|CH60_MOUSE	NA	NA	9	NA	NA	99.8
GHEVAAMLKSELQK	Q8K135|K319L_MOUSE	NA	NA	14	216	157	252
GHYTEGAELVDSVLDVVRK	Q9CWF2|TBB2B_MOUSE:P9	NA	NA	19	NA	NA	69.1
GILAADESTGSIAK	P05064|ALDOA_MOUSE	NA	NA	14	NA	NA	71.4
GIRPAINVGLSVSR	Q03265|ATPA_MOUSE	NA	NA	14	NA	NA	534
GITHIGYTDLPSR	Q61941|NNTM_MOUSE	NA	NA	13	NA	NA	42.8
GKTIENFLVVNKER	Q3UR85|MYRF_MOUSE	NA	NA	14	2230	1990	1900
GMVQAVRLIAEGTAPR	Q8R0Y6|AL1L1_MOUSE	NA	NA	16	1700	552	1050
GNIEIALEAAKALDDK	Q8CIE6|COPA_MOUSE	NA	NA	16	2490	476	2320
GNMEVARIHAENAIR	Q99LU0|CH1B1_MOUSE	NA	NA	15	2670	2120	2740
GNMEVARIHAENAIRQ	Q99LU0|CH1B1_MOUSE	NA	NA	16	624	NA	727
GNTEVARIHAENAIR	Q9CQD4|CH1B2_MOUSE	NA	NA	15	604	276	455
GNTEVARIHAENAIRQ	Q9CQD4|CH1B2_MOUSE	NA	NA	16	NA	NA	78.9
GPGLERGEAGIPAEFSIWTR	Q80X90|FLNB_MOUSE	NA	NA	20	NA	NA	147
GQEVVSSIRAEMGSDR	Q8VBZ0|DHRSX_MOUSE	NA	NA	16	1560	1020	1310
GSLGEYLFERLTLKHD	P29391|FRIL1_MOUSE	NA	NA	16	NA	NA	39.8
GTGASGSFKLNKK	P43276|H15_MOUSE:P15864	NA	NA	13	796	NA	150
GTVEENQVNVEVMR	O55111|DSG2_MOUSE	NA	NA	14	119	NA	341
GVDEATIIDILTK	P10107|ANXA1_MOUSE	NA	NA	13	NA	NA	77.6
GVIEAFLHAWKGYQK	A2AJ15|MA1B1_MOUSE	NA	NA	15	NA	NA	254
GYISPYFINTSK	P63038|CH60_MOUSE	NA	NA	12	NA	NA	77.7
GYLGPEQLPDCLKG	P08249|MDHM_MOUSE	NA	NA	14	NA	NA	39.2
GYSFTTTAER	P63260|ACTG_MOUSE:P607	NA	NA	10	410	251	1010
GYSFVTTAER	P68134|ACTS_MOUSE:P680	NA	NA	10	901	567	835
GYSNRVVDLMAYMASKE	P16858|G3P_MOUSE	NA	NA	17	NA	NA	83.8
HALIIYDDLSK	Q03265|ATPA_MOUSE	NA	NA	11	NA	NA	213
HAVSEGTKAVTKYTSS	P70696|H2B1A_MOUSE:Q8C	NA	NA	16	NA	NA	44.8
HAVSEGTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8C	NA	NA	17	95.3	9810	8200
HLQLAIR	C0HKE3|H2A1D_MOUSE:Q8	NA	NA	7	NA	219	319
HLQLAIRNDEELNK	C0HKE3|H2A1D_MOUSE:Q8	NA	NA	14	NA	NA	364
HPDEELLRALLSK	O08601|MTP_MOUSE	NA	NA	13	NA	NA	105
HSKEQQCVIMAENSK	P20918|PLMN_MOUSE	NA	NA	15	814	NA	161
HVLVTLGEK	Q60605|MYL6_MOUSE	NA	NA	9	152	NA	228
HVVFGK	P30412|PPIC_MOUSE:P2436	NA	NA	6	NA	NA	223
IALENYLAALQSDPPR	Q06335|APLP2_MOUSE	NA	NA	16	424	NA	351
IALENYLAALQSDPPRP	Q06335|APLP2_MOUSE	NA	NA	17	50.2	NA	73.2
IAQLEEQVEQEAR	O08638|MYH11_MOUSE	NA	NA	13	NA	143	85.7
IDLEKERHVSIQEAES	P35282|RAB21_MOUSE	NA	NA	16	NA	NA	208

IDQEGNIYVTQALDR	Q9R100|CAD17_MOUSE	NA	NA	15	73.5	NA	154
IEANEALVK	Q9D3D9|ATPD_MOUSE	NA	NA	9	NA	NA	85.3
IEDSFVTAVLAEETR	O08601|MTP_MOUSE	NA	NA	15	8400	655	4640
IEDSFVTAVLAEETRA	O08601|MTP_MOUSE	NA	NA	16	4220	NA	2750
IEDSFVTAVLAEETRAF	O08601|MTP_MOUSE	NA	NA	17	NA	NA	271
IEEVEQHIQTIRSKSK	Q8K0B2|LMBD1_MOUSE	NA	NA	16	2630	197	933
IEKAQQIQALQSNVR	E9PV24|FIBA_MOUSE	NA	NA	15	106	152	306
IERSQVVALLGAQLSPAR	Q9R0A1|CLCN2_MOUSE	NA	NA	18	196	NA	440
IFGVTTLDIVR	P08249|MDHM_MOUSE	NA	NA	11	NA	NA	242
IGGHGAEYGAEALER	P01942|HBA_MOUSE	NA	NA	15	86.7	3050	1000
IGGIGTVPVGR	P10126|EF1A1_MOUSE:P626	NA	NA	11	207	197	283
IGLFGGAGVGK	P56480|ATPB_MOUSE	NA	NA	11	NA	NA	1090
IIAPPERKY	P63260|ACTG_MOUSE:P607	NA	NA	9	487	NA	2840
IIQEEMVVTEHVRDK	Q91VK4|ITM2C_MOUSE	NA	NA	15	NA	NA	102
IKIIAPPERK	P63260|ACTG_MOUSE:P607	NA	NA	10	NA	NA	340
IKNLEISIDALMAK	Q64331|MYO6_MOUSE	NA	NA	14	242	NA	261
IKNLEISIDALMAKIK	Q64331|MYO6_MOUSE	NA	NA	16	198	NA	177
ILGADTSVDLEETGR	Q03265|ATPA_MOUSE	NA	NA	15	NA	NA	461
ILLAELEQLK	P20152|VIME_MOUSE	NA	NA	10	NA	671	803
IPGKQVAGVIKAVDSK	O08601|MTP_MOUSE	NA	NA	16	642	474	417
IPNVENETMIPVLTSKR	Q80XR2|AT2C1_MOUSE	NA	NA	17	512	217	594
IPVGPETLGR	P56480|ATPB_MOUSE	NA	NA	10	NA	NA	613
IQEESKRIIANVGK	Q8CAS9|PARP9_MOUSE	NA	NA	14	NA	NA	862
IQELESHLEAEEGAR	Q6URW6|MYH14_MOUSE	NA	NA	15	135	NA	116
IQLQEELAAAERAK	Q8VDD5|MYH9_MOUSE	NA	NA	14	988	549	954
IQLQEELAAAERAKR	Q8VDD5|MYH9_MOUSE	NA	NA	15	NA	NA	285
IQRVAAGVLCELAQDK	Q02257|PLAK_MOUSE:Q022	NA	NA	16	1280	61.4	996
ISLAQYLINARLSSEK	P60335|PCBP1_MOUSE	NA	NA	16	379	99.8	277
ISPKEMTIIYVEASGK	Q05117|PPA5_MOUSE	NA	NA	16	12800	1950	6510
ISQKDIEQSIKSETSGS	P97429|ANXA4_MOUSE	NA	NA	17	361	228	399
ISQKDIEQSIKSETSGSF	P97429|ANXA4_MOUSE	NA	NA	18	10300	3420	5370
ITLPVDFVTADKFDENAK	P09411|PGK1_MOUSE	NA	NA	18	NA	NA	105
IVEGLMTTVHAITATQK	P16858|G3P_MOUSE	NA	NA	17	430	92.7	470
IYVDDGLISLQVK	P52480|KPYM_MOUSE	NA	NA	13	NA	NA	85.3
KELEEQLGPVAEETR	P08226|APOE_MOUSE	NA	NA	15	997	723	694
KELEEQLGPVAEETRA	P08226|APOE_MOUSE	NA	NA	16	598	349	353
KELEEQLGPVAEETRAR	P08226|APOE_MOUSE	NA	NA	17	1470	547	965
KGEDFVK	P08249|MDHM_MOUSE	NA	NA	7	NA	NA	126
KGHEVAAMLKSELQK	Q8K135|K319L_MOUSE	NA	NA	15	189	158	556
KGNFNYVEFTRILK	Q9CQ19|MYL9_MOUSE	NA	NA	14	NA	NA	238
KGNMEVARIHAENAIR	Q99LU0|CH1B1_MOUSE	NA	NA	16	NA	NA	129
KGTGASGSFKLNK	P43276|H15_MOUSE:P15864	NA	NA	13	1340	NA	404
KGVIEAFLHAWKGYQK	A2AJ15|MA1B1_MOUSE	NA	NA	16	282	60.8	219
KIEDSFVTAVLAEETR	O08601|MTP_MOUSE	NA	NA	16	5060	1040	4430
KIEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	13	NA	NA	81.9
KITEVSLVGHLSYDKK	E9Q414|APOB_MOUSE	NA	NA	16	1640	1090	1160
KKELEEQLGPVAEETR	P08226|APOE_MOUSE	NA	NA	16	NA	386	497
KKITEVSLVGHLSYDK	E9Q414|APOB_MOUSE	NA	NA	16	3210	2070	579
KNPHDASLVSRIGQAYV	Q8C0S4|TT21A_MOUSE	NA	NA	17	12300	NA	14400
KPDGTYAAIMGFILAHKAR	Q8BW75|AOFB_MOUSE	NA	NA	19	NA	NA	91.2
KPFQEYLEAQRQK	Q99KU0|VMP1_MOUSE	NA	NA	13	61.4	179	256
KPVTEGYVEVKEGKA	P58022|LOXL2_MOUSE	NA	NA	15	999	NA	79.3
KVIEKAQQIQALQS	E9PV24|FIBA_MOUSE	NA	NA	14	NA	NA	77.3
KVIEKAQQIQALQSN	E9PV24|FIBA_MOUSE	NA	NA	15	176	129	224
KVIEKAQQIQALQSNV	E9PV24|FIBA_MOUSE	NA	NA	16	141	NA	81
KVIEKAQQIQALQSNVR	E9PV24|FIBA_MOUSE	NA	NA	17	3350	2060	2460
KVIQYLAVVASSHK	O08638|MYH11_MOUSE	NA	NA	14	NA	NA	130
KVTVGKDDIQK	O08638|MYH11_MOUSE	NA	NA	11	84.1	NA	101
KYDEELEER	P37804|TAGL_MOUSE	NA	NA	9	264	NA	158
LAEEEHKVKAEVAAGDHP	P30416|FKBP4_MOUSE	NA	NA	18	2230	NA	171
LAEEKTISAKYAEER	Q8VDD5|MYH9_MOUSE	NA	NA	15	387	NA	116
LAKNKQKPITPETAEK	P60766|CDC42_MOUSE	NA	NA	16	4280	2320	2760
LALDVEIATYRK	P50446|K2C6A_MOUSE:Q92	NA	NA	12	NA	NA	1470
LALENYITALQAVPPR	P12023|A4_MOUSE	NA	NA	16	NA	NA	3490
LALENYITALQAVPPRP	P12023|A4_MOUSE	NA	NA	17	139	NA	120
LALQFTTNPK	O08710|THYG_MOUSE	NA	NA	10	NA	645	692
LASYLDK	Q9QWL7|K1C17_MOUSE:P1	NA	NA	7	1070	NA	163
LATALQK	P58774|TPM2_MOUSE:P211	NA	NA	7	757	NA	459
LDFEQEMATAASSSSLEK	P63260|ACTG_MOUSE:P607	NA	NA	18	NA	NA	33.3
LELAQYR	Q03265|ATPA_MOUSE	NA	NA	7	NA	NA	354
LEQEIATYR	Q9QWL7|K1C17_MOUSE:P1	NA	NA	9	69.8	NA	62.8
LFIEHVVEVARGK	Q61168|LAPM5_MOUSE	NA	NA	13	436	542	432
LGDVYVNDAFGTAHR	P09041|PGK2_MOUSE:P094	NA	NA	15	NA	NA	74.1
LHVDPENFR	P02089|HBB2_MOUSE:P0208	NA	NA	9	688	1020	1950
LKPGAPLRPK	Q8BTM8|FLNA_MOUSE	NA	NA	10	NA	203	176
LLADPTGAFGK	P99029|PRDX5_MOUSE	NA	NA	11	NA	NA	157
LLAEEKTISAKYAEER	Q8VDD5|MYH9_MOUSE	NA	NA	16	2200	456	1010
LLEGEESRINLPIQT	P31001|DESM_MOUSE	NA	NA	15	NA	109	71.8
LLLQVQHASK	P48962|ADT1_MOUSE:P5188	NA	NA	10	NA	NA	305

LLVVYPWTQR	P02089|HBB2_MOUSE:P0210	NA	NA	10	389	353	144
LNEHFLNTTDFLDTIK	P54071|IDHP_MOUSE	NA	NA	16	NA	NA	124
LNKALEEALSIQASPSSPP	Q9WUU8|TNIP1_MOUSE	NA	NA	19	NA	NA	566
LPKSAKPVSQMRMATPLLMR	P04441|HG2A_MOUSE	NA	NA	21	458	415	428
LPKSAKPVSQMRMATPLLMR	P04441|HG2A_MOUSE	NA	NA	22	4650	2520	3840
LPVQLQRAMAAEAEAARE	P54116|STOM_MOUSE	NA	NA	18	664	186	284
LQWVQRNIAAFGGNPK	Q03311|CHLE_MOUSE	NA	NA	16	NA	NA	59
LRVDPVNFK	P01942|HBA_MOUSE:P06467	NA	NA	9	180	1280	869
LSDGVAVLK	P63038|CH60_MOUSE	NA	NA	9	NA	96.5	419
LTFDSSFSPNTGKK	Q60932|VDAC1_MOUSE	NA	NA	14	NA	NA	45.4
LTIQGLK	Q99KI0|ACON_MOUSE	NA	NA	7	NA	NA	165
LTLSALIDGK	Q60931|VDAC3_MOUSE	NA	NA	10	NA	NA	483
LTLSALLDGK	Q60932|VDAC1_MOUSE	NA	NA	10	NA	NA	483
LVIIESDLERAEERAELSEGK	P58771|TPM1_MOUSE	NA	NA	21	NA	NA	627
LVLEVAQHLGESTVR	P56480|ATPB_MOUSE	NA	NA	15	NA	NA	2150
LVLQVESLTTELSAER	Q6URW6|MYH14_MOUSE	NA	NA	16	347	NA	100
LVNEERTLEVEIEPG	Q99KV1|DJB11_MOUSE	NA	NA	15	NA	NA	1070
MEEQTQQIRLQAEIFQ	P08226|APOE_MOUSE	NA	NA	16	52.9	NA	39.3
MEEQTQQIRLQAEIFQAR	P08226|APOE_MOUSE	NA	NA	18	392	NA	268
MEVARIHAENAIR	Q99LU0|CH1B1_MOUSE	NA	NA	13	NA	107	189
MQQYTEHFMVAGYTA	Q03145|EPHA2_MOUSE	NA	NA	15	NA	NA	55.3
MTANQIVLLLAELARRDR	Q99PE8|ABCG5_MOUSE	NA	NA	18	NA	NA	775
MTVYFGSGFAAPFFIVRHQLL	P17665|COX7C_MOUSE	NA	NA	23	NA	NA	386
NAGVEGSLIVEK	P63038|CH60_MOUSE	NA	NA	12	NA	NA	88
NAVTQEFGPVPDTAR	Q99KI0|ACON_MOUSE	NA	NA	15	NA	NA	111
NDMQYQHVIETLIGKK	P80316|TCPE_MOUSE	NA	NA	16	405	177	370
NELRVAPEEHPTLLTEAPLNP	P68134|ACTS_MOUSE:P6803	NA	NA	22	NA	321	313
NELRVAPEEHPVLLTEAPLNP	P63260|ACTG_MOUSE:P607	NA	NA	22	NA	447	171
NFFHESGLEARVALK	E9Q414|APOB_MOUSE	NA	NA	15	20400	16800	31300
NGKTIENFLVVNKER	Q3UR85|MYRF_MOUSE	NA	NA	15	NA	239	58.2
NIEIALEAAKALDDK	Q8CIE6|COPA_MOUSE	NA	NA	15	1020	49.7	599
NKKITEVSLVGHLSYDK	E9Q414|APOB_MOUSE	NA	NA	17	704	352	578
NKYEDEINK	Q922U2|K2C5_MOUSE:Q8VE	NA	NA	9	311	204	275
NMEVARIHAENAIR	Q99LU0|CH1B1_MOUSE	NA	NA	14	NA	133	265
NPLVPEAQKR	Q9Z0G9|CLD3_MOUSE	NA	NA	10	6480	2140	2580
NPRFDESTIVCNTSEGGR	Q9CQW5|LEG2_MOUSE	NA	NA	18	5880	868	2100
NPSDLYAEGCEALVVKK	Q9QY33|TSN3_MOUSE	NA	NA	17	124	27.6	216
NQIVLLLAELARRDR	Q99PE8|ABCG5_MOUSE	NA	NA	15	NA	NA	99.8
NSDRLIEETISIAMATK	O88630|GOSR1_MOUSE	NA	NA	17	NA	NA	53.5
NSEYVAEPIQAYIIPS	Q6P1B1|XPP1_MOUSE	NA	NA	16	5020	NA	1220
NSPLVSR	P08249|MDHM_MOUSE	NA	NA	7	NA	NA	201
NSVKEIMAEIYK	P10605|CATB_MOUSE	NA	NA	12	NA	NA	85.4
NTDKELVSEPVTVSLSPA	B2RTN2|IGS23_MOUSE	NA	NA	18	NA	NA	48.3
NTIEETGILAERARSR	P02468|LAMC1_MOUSE	NA	NA	16	1620	846	1510
PLRLPLQDVYK	P10126|EF1A1_MOUSE:P626	NA	NA	11	NA	904	649
PVVPVHLDGTF	O35291|RNAS2_MOUSE:P97	NA	NA	11	5160	NA	923
PVYRMVD	Q922Q1|MARC2_MOUSE	NA	NA	7	NA	NA	137
PYVEEAIKIAYCEER	P70274|SEPP1_MOUSE	NA	NA	15	506	NA	401
QAASSLQQASLK	P38647|HSPA9_MOUSE	NA	NA	12	NA	NA	104
QASEGPLK	P16858|G3P_MOUSE	NA	NA	8	NA	NA	103
QDFEARYVQAKLSVHDR	O70228|ATP9A_MOUSE	NA	NA	17	1790	1170	1680
QEFEFFENTIVSRVAR	Q62179|SEM4B_MOUSE	NA	NA	16	NA	NA	80.1
QELQEYEVVAESEKR	Q9D5V6|SYAP1_MOUSE	NA	NA	15	1330	133	163
QEYDESGPSIVHR	P63260|ACTG_MOUSE:P607	NA	NA	13	NA	NA	191
QPRPAEQYPLRALLNGR	P47878|IBP3_MOUSE	NA	NA	17	341	NA	236
QVHPDTGISSK	P70696|H2B1A_MOUSE:Q8C	NA	NA	11	NA	563	1050
RELIEAMLKAYQQK	O35114|SCRB2_MOUSE	NA	NA	14	146	NA	197
REQEVTVLKK	O08638|MYH11_MOUSE	NA	NA	10	NA	113	116
RIALENYLAALQSD	Q06335|APLP2_MOUSE	NA	NA	14	1290	NA	741
RIALENYLAALQSDPP	Q06335|APLP2_MOUSE	NA	NA	16	NA	760	8330
RIALENYLAALQSDPPR	Q06335|APLP2_MOUSE	NA	NA	17	16400	1870	6140
RIALENYLAALQSDPPRP	Q06335|APLP2_MOUSE	NA	NA	18	2920	648	3160
RIALENYLAALQSDPPRPH	Q06335|APLP2_MOUSE	NA	NA	19	121	38.7	243
RISGLIYEETRGVLK	P62806|H4_MOUSE	NA	NA	15	NA	1140	2030
RLALENYITALQAVPPR	P12023|A4_MOUSE	NA	NA	17	11500	1820	5960
RLALENYITALQAVPPRP	P12023|A4_MOUSE	NA	NA	18	6410	432	5090
RLNRPLTLSEK	Q99KI0|ACON_MOUSE	NA	NA	11	NA	NA	131
RRIALENYLAALQSD	Q06335|APLP2_MOUSE	NA	NA	15	5940	1990	4250
RRIALENYLAALQSDPP	Q06335|APLP2_MOUSE	NA	NA	17	33200	11400	34600
RRIALENYLAALQSDPPR	Q06335|APLP2_MOUSE	NA	NA	18	24800	6340	21700
RRIALENYLAALQSDPPRP	Q06335|APLP2_MOUSE	NA	NA	19	16900	6130	9770
RRIALENYLAALQSDPPRPH	Q06335|APLP2_MOUSE	NA	NA	20	3760	1710	3860
RRLALENYITAL	P12023|A4_MOUSE	NA	NA	12	493	64.5	75.3
RRLALENYITALQAVPP	P12023|A4_MOUSE	NA	NA	17	12800	NA	9930
RRLALENYITALQAVPPR	P12023|A4_MOUSE	NA	NA	18	121000	45000	88400
RRLALENYITALQAVPPRP	P12023|A4_MOUSE	NA	NA	19	162000	56100	153000
RRLALENYITALQAVPPRPH	P12023|A4_MOUSE	NA	NA	20	7350	5000	9300
RTAAENDFVVLKK	P07744|K2C4_MOUSE	NA	NA	13	NA	468	248
RTGAIVDVPVGEELLGR	Q03265|ATPA_MOUSE	NA	NA	17	NA	NA	881

SAKPVSQMRMATPLLMRP	P04441|HG2A_MOUSE	NA	NA	18	2840	NA	2150
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	NA	NA	19	9540	5960	4080
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	NA	NA	20	1940	441	1230
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	NA	NA	21	575	117	280
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	NA	NA	25	NA	NA	47.3
SARLSAKPAPPKPEPKPKK	P09602|HMGN2_MOUSE	NA	NA	19	1410	204	108
SDEFSEAIKAFRGQDDK	Q9EQP2|EHD4_MOUSE	NA	NA	17	NA	NA	111
SDPQVHTVLVERSTLK	Q9JHU4|DYHC1_MOUSE	NA	NA	16	1520	555	1200
SDPTEAAAVGAVEASFK	P52480|KPYM_MOUSE	NA	NA	17	194	NA	184
SDRLIEETISIAMATK	O88630|GOSR1_MOUSE	NA	NA	16	1450	NA	1100
SFEAQGALANIAVDK	P14439|HA23_MOUSE:P0422	NA	NA	15	113	116	179
SGKIEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	15	3260	3510	2870
SGVEYTRLAVESARG	Q62178|SEM4A_MOUSE	NA	NA	15	277	218	216
SKMEEQTQQIRLQAEIFQAR	P08226|APOE_MOUSE	NA	NA	20	115	NA	240
SLHTLFGDK	P07724|ALBU_MOUSE	NA	NA	9	306	737	2160
SLLEGQDAK	P08730|K1C13_MOUSE	NA	NA	9	477	NA	146
SLVSKGTLVQT	P43276|H15_MOUSE:P43274	NA	NA	11	4150	NA	162
SLVSKGTLVQTK	P43276|H15_MOUSE:P43274	NA	NA	12	103	NA	77
SPGVTASWIEANLSDDSK	Q80U87|UBP8_MOUSE	NA	NA	18	404	NA	395
SPKEMTIIYVEASGK	Q05117|PPA5_MOUSE	NA	NA	15	767	275	709
SPNKLYTLVTYVPVTTFK	P62900|RL31_MOUSE	NA	NA	18	NA	NA	166
SPTVHFTPAEISR	Q9QXH4|ITAX_MOUSE	NA	NA	13	198	67.7	128
SSTVTEAPIAVVTSRT	Q8K1R7|NEK9_MOUSE	NA	NA	16	253	NA	220
STDREASIDILHSIVK	Q8BG32|PSD11_MOUSE	NA	NA	16	321	NA	131
STTTGHLIYK	P10126|EF1A1_MOUSE:P626	NA	NA	10	324	295	207
STVAQLVK	Q03265|ATPA_MOUSE	NA	NA	8	NA	NA	119
SVSNSVKEIMAEIYK	P10605|CATB_MOUSE	NA	NA	15	135	NA	131
SVYVYK	Q8CGP2|H2B1P_MOUSE:Q6	NA	NA	6	NA	NA	296
SYELPDGQVITIGNER	P63260|ACTG_MOUSE:P607	NA	NA	16	1020	523	1320
TANQIVLLLAELARR	Q99PE8|ABCG5_MOUSE	NA	NA	15	1770	127	1720
TANQIVLLLAELARRDR	Q99PE8|ABCG5_MOUSE	NA	NA	17	15900	2880	15600
TATPQQAQEVHEK	P17751|TPIS_MOUSE	NA	NA	13	NA	142	160
TDRQIKTIRPNSAVR	Q04592|PCSK5_MOUSE	NA	NA	15	NA	NA	127
TEAPLNPK	P63260|ACTG_MOUSE:P607	NA	NA	8	1400	4210	2280
TEAPLNPKANREK	P63260|ACTG_MOUSE:P607	NA	NA	13	NA	NA	126
TEEISEVKMDAEFGHDSG	P12023|A4_MOUSE	NA	NA	18	286	235	393
TEITELRR	P08730|K1C13_MOUSE:Q6IF	NA	NA	8	NA	NA	231
THINIVVIGHVDSGK	P10126|EF1A1_MOUSE:P626	NA	NA	15	NA	NA	116
THPDEELLRALLSK	O08601|MTP_MOUSE	NA	NA	14	2080	2170	3520
THPDEELLRALLSKFK	O08601|MTP_MOUSE	NA	NA	16	1140	390	1870
TIAPALVSK	P17182|ENOA_MOUSE	NA	NA	9	126	NA	389
TIEAEAAHGTVTR	P54071|IDHP_MOUSE	NA	NA	13	NA	NA	60.5
TIGGGDDSFNTFFSETGAGK	P68369|TBA1A_MOUSE:P683	NA	NA	20	NA	NA	51.9
TITLEVEPSDTIENVK	P0CG50|UBC_MOUSE:P6298	NA	NA	16	NA	498	738
TKYEEEINK	P07744|K2C4_MOUSE	NA	NA	9	NA	193	134
TNFAVLMSFK	Q8BM96|AGRG7_MOUSE	NA	NA	10	NA	NA	63.4
TNFFHESGLEARVALK	E9Q414|APOB_MOUSE	NA	NA	16	3540	2250	6140
TPVLHQKTLQAMKSHSEK	Q76KF0|SEM6D_MOUSE	NA	NA	18	7410	904	781
TQLEELEDELQATEDAK	Q61879|MYH10_MOUSE:Q8V	NA	NA	17	NA	NA	37.2
TQLLEDYVKAIEGIK	A2AJ15|MA1B1_MOUSE	NA	NA	15	132	NA	146
TRLEQEIATYRSLLEGQDAK	P08730|K1C13_MOUSE	NA	NA	20	NA	NA	489
TSGGAGGLGSLR	P31001|DESM_MOUSE	NA	NA	12	NA	392	233
TSIAIDTIINQK	Q03265|ATPA_MOUSE	NA	NA	12	NA	NA	254
TTLTAAITK	Q8BFR5|EFTU_MOUSE	NA	NA	9	NA	NA	86.6
TVEENQVNVEVMR	O55111|DSG2_MOUSE	NA	NA	13	329	NA	281
VAGILTVK	Q99KI0|ACON_MOUSE	NA	NA	8	NA	NA	120
VALEESRAQAEQALS	Q91ZV0|MIA2_MOUSE	NA	NA	15	1900	457	1010
VALEESRAQAEQALSE	Q91ZV0|MIA2_MOUSE	NA	NA	16	2110	549	2240
VANKIGII	P62751|RL23A_MOUSE	NA	NA	8	5590	NA	2030
VAPEEHPT	P68134|ACTS_MOUSE:P6803	NA	NA	8	NA	507	632
VAPEEHPTLLTEAPLNPK	P68134|ACTS_MOUSE:P6803	NA	NA	18	NA	603	500
VAPEEHPV	P63260|ACTG_MOUSE:P607	NA	NA	8	NA	NA	1020
VAPEEHPVLLTEAPLNPK	P63260|ACTG_MOUSE:P607	NA	NA	18	33.9	902	1040
VAVLGASGGIGQPLSLLLK	P08249|MDHM_MOUSE	NA	NA	19	NA	NA	317
VDFLERPIIAFVR	Q8BTY2|S4A7_MOUSE	NA	NA	13	343	144	601
VDFLSEASIMGQFSHH	Q03145|EPHA2_MOUSE	NA	NA	16	91.7	NA	155
VDFLSEASIMGQFSHHN	Q03145|EPHA2_MOUSE	NA	NA	17	418	NA	175
VDFPQDQLATLTGR	P08249|MDHM_MOUSE	NA	NA	14	NA	NA	125
VDIINAKQ	P17751|TPIS_MOUSE	NA	NA	8	NA	NA	56.3
VDLREMLAVAVLAAER	Q80V26|IMPA3_MOUSE	NA	NA	16	153	NA	712
VDPVNFK	P01942|HBA_MOUSE:P06467	NA	NA	7	192	NA	929
VDSGKIEVEKPFAIAKE	P24369|PPIB_MOUSE	NA	NA	17	1420	NA	2120
VDTSSEITTK	P26350|PTMA_MOUSE	NA	NA	10	1170	130	237
VEGTARGIVVYTGDR	Q8VDN2|AT1A1_MOUSE	NA	NA	15	NA	482	321
VEHEVNLLVEEIHR	Q4KML4|ABRAL_MOUSE	NA	NA	14	1770	1070	1400
VEIIANDQGNR	P17879|HS71B_MOUSE:P166	NA	NA	11	80.7	NA	125
VELQELNDRFANYIDK	P20152|VIME_MOUSE	NA	NA	16	NA	NA	610
VELQELNDRFANYIEK	P31001|DESM_MOUSE	NA	NA	16	NA	561	1050
VETHMARVEAMLNDRR	P12023|A4_MOUSE	NA	NA	16	NA	228	243

VFLENVIR	P62806|H4_MOUSE	NA	NA	8	657	467	142
VFLENVIRDAVT	P62806|H4_MOUSE	NA	NA	12	NA	196	222
VGEVIVTK	P63038|CH60_MOUSE	NA	NA	8	NA	NA	140
VGGTSDVEVNEK	P63038|CH60_MOUSE	NA	NA	12	NA	NA	302
VGINYQPPTVVPGGDLAK	P68369|TBA1A_MOUSE:P683	NA	NA	18	NA	232	295
VGLQVVAVK	P63038|CH60_MOUSE	NA	NA	9	NA	170	764
VGVNGFGR	P16858|G3P_MOUSE	NA	NA	8	NA	169	118
VIEKAQQIQALQSNVR	E9PV24|FIBA_MOUSE	NA	NA	16	1060	331	769
VINEPTAAALAYGLDK	P38647|HSPA9_MOUSE	NA	NA	16	NA	NA	89
VIQYLAVVASSHK	O08638|MYH11_MOUSE	NA	NA	13	NA	301	445
VKPYVEEGLHPQIIIR	P80313|TCPH_MOUSE	NA	NA	16	288	293	579
VLAAVYK	P05063|ALDOC_MOUSE:P05	NA	NA	7	NA	NA	157
VLDGEQLSIEALRQEH	Q9D2Z1|CEA20_MOUSE	NA	NA	16	930	242	779
VLDGEQLSIEALRQEHQ	Q9D2Z1|CEA20_MOUSE	NA	NA	17	868	198	910
VLDGEQLSIEALRQEHQG	Q9D2Z1|CEA20_MOUSE	NA	NA	18	NA	75.2	285
VLDSGAPIK	P56480|ATPB_MOUSE	NA	NA	9	NA	NA	277
VLDSGAPIKIPVGPETLGR	P56480|ATPB_MOUSE	NA	NA	19	NA	NA	37.2
VLENAEGAR	P38647|HSPA9_MOUSE	NA	NA	9	NA	NA	104
VLKQVHPD	P70696|H2B1A_MOUSE:Q8C	NA	NA	8	NA	NA	77.2
VLLFIEHVVEVARGK	Q61168|LAPM5_MOUSE	NA	NA	15	166	NA	132
VLQVESLTTELSAER	Q6URW6|MYH14_MOUSE	NA	NA	15	NA	NA	29.7
VLSIGDGIAR	Q03265|ATPA_MOUSE	NA	NA	10	NA	NA	463
VLTPELYAELRAK	Q04447|KCRB_MOUSE	NA	NA	13	NA	NA	139
VLTVINQTQKENLR	Q6ZWV7|RL35_MOUSE	NA	NA	14	NA	NA	78.3
VNLAELFK	P99029|PRDX5_MOUSE	NA	NA	8	NA	NA	198
VNNSSLIGVGYTQTLRPGVK	Q60930|VDAC2_MOUSE	NA	NA	20	NA	NA	27.2
VNVPVIGGHAGK	P08249|MDHM_MOUSE	NA	NA	12	NA	NA	151
VPDEHMIPIENLMNPR	Q91ZX7|LRP1_MOUSE	NA	NA	16	162	146	238
VPGLTETAVFSCEAHNDK	Q60805|MERTK_MOUSE	NA	NA	18	1250	180	1370
VPSEAIRGLSALQSLR	A2ARI4|LGR4_MOUSE	NA	NA	16	366	NA	448
VPSNQVACLTVLKER	Q5U462|CDCP1_MOUSE	NA	NA	15	NA	NA	38.5
VPTEEVSLEVLLSNGQK	Q8BVL3|SNX17_MOUSE	NA	NA	17	1850	NA	3630
VQQTVQDLFGR	P38647|HSPA9_MOUSE	NA	NA	11	NA	NA	58
VRALEEANADLEVK	Q6IFX2|K1C42_MOUSE	NA	NA	14	NA	1750	985
VRFLEQQNAALAAEVNRLK	P31001|DESM_MOUSE	NA	NA	19	NA	454	704
VRFLEQQNK	P20152|VIME_MOUSE:P0399	NA	NA	9	1200	1320	2590
VRLAPDYDALDVANKIGII	P62751|RL23A_MOUSE	NA	NA	19	NA	NA	76.7
VSDLTQAANK	P31001|DESM_MOUSE	NA	NA	10	626	2070	1230
VSFELFADK	P17742|PPIA_MOUSE	NA	NA	9	NA	121	234
VSHVSTGGGASLELLEGK	P09041|PGK2_MOUSE:P094	NA	NA	18	NA	105	105
VSNSVKEIMAEIYK	P10605|CATB_MOUSE	NA	NA	14	2280	749	1440
VSPTVHFTPAEISR	Q9QXH4|ITAX_MOUSE	NA	NA	14	418	232	201
VSPTVHFTPAEISRSV	Q9QXH4|ITAX_MOUSE	NA	NA	16	412	195	262
VSPTVHFTPAEISRSVF	Q9QXH4|ITAX_MOUSE	NA	NA	17	NA	911	1270
VSQVVHKAVLDVAETGTEAA	Q91WP6|SPA3N_MOUSE:Q5	NA	NA	24	83.2	NA	78.6
VTIAQGGVLPNIQAVLLPK	C0HKE3|H2A1D_MOUSE:Q8I	NA	NA	19	NA	NA	773
VTYVPVTTFK	P62900|RL31_MOUSE	NA	NA	10	NA	NA	926
VTYVPVTTFKNLQTVNVDEN	P62900|RL31_MOUSE	NA	NA	20	NA	NA	1870
VVDLLAPYAK	P56480|ATPB_MOUSE	NA	NA	10	NA	83.8	595
VVFEQTK	P17751|TPIS_MOUSE	NA	NA	7	NA	NA	128
VVSSVLQLGNIVFKK	O08638|MYH11_MOUSE	NA	NA	15	NA	NA	485
VVSTHEQVLR	Q61781|K1C14_MOUSE	NA	NA	10	63.5	126	104
VYFGSGFAAPFFIVRHQLLKK	P17665|COX7C_MOUSE	NA	NA	21	2320	NA	9030
VYQVSR	P31001|DESM_MOUSE	NA	NA	6	NA	NA	95.2
YAAIMGFILAHKAR	Q8BW75|AOFB_MOUSE	NA	NA	14	50.5	76.7	256
YADSIHAIFVETSAK	P35285|RB22A_MOUSE	NA	NA	15	766	351	400
YDALDVANKIGII	P62751|RL23A_MOUSE	NA	NA	13	801	NA	373
YEELQQTAGR	Q922U2|K2C5_MOUSE	NA	NA	10	244	205	213
YEELQVTAGR	P50446|K2C6A_MOUSE:Q8B	NA	NA	10	61.9	145	221
YENELALR	Q64291|K1C12_MOUSE	NA	NA	8	NA	NA	109
YGDYTVRVRAELADEHS	Q61190|I10R2_MOUSE	NA	NA	17	NA	NA	450
YIIQEEMVVTEHVR	Q91VK4|ITM2C_MOUSE	NA	NA	14	NA	NA	216
YIIQEEMVVTEHVRDK	Q91VK4|ITM2C_MOUSE	NA	NA	16	763	NA	698
YNPLVPEAQK	Q9Z0G9|CLD3_MOUSE	NA	NA	10	1140	499	858
YNPLVPEAQKR	Q9Z0G9|CLD3_MOUSE	NA	NA	11	5600	1530	7360
YQDFEARYVQAKLSVHDR	O70228|ATP9A_MOUSE	NA	NA	18	1100	551	716
YQTIEENIKIFEED	O89051|ITM2B_MOUSE	NA	NA	14	4740	NA	4310
YQTIEENIKIFEEDA	O89051|ITM2B_MOUSE	NA	NA	15	5290	NA	4060
YRPGTVALR	P02301|H3C_MOUSE:P68433	NA	NA	9	NA	NA	487
YRQKVAPLGAELQESAR	Q00623|APOA1_MOUSE	NA	NA	17	1600	416	1120
YSNRVVDLMAYMASKE	P16858|G3P_MOUSE	NA	NA	16	618	NA	256
YVRPGGGFVPNFQLFEK	P46412|GPX3_MOUSE	NA	NA	17	NA	NA	317

Table S3 Information of peptides identified in IEC MHCII immunopeptidome (related to Supplementary Fig. S20e)

Table S4.Luminal peptides indentified in C57BL/6 and BALB/c mice.

PN-derived peptides identified in intestinal lumen of BALB/c mice

Master Protein	No.	Peptide	H-2-IAd			H-2-IEd		
			Core	Score	Rank	Core	Score	Rank
AAA60336.1	1	REEGGRWGPAEPRERE REE	WGPAEPRER	0.017666	61.9	WGPAEPRER	0.011613	19.2
AAA60336.1	2	EEGGRWGPAEPRERE REE	WGPAEPRER	0.024489	54.29	WGPAEPRER	0.019053	12.39
AAA60336.1	3	EGGRWGPAEPRERE REE	WGPAEPRER	0.038489	43.18	WGPAEPRER	0.028152	8.41
AAA60336.1	4	RWGPAEPRERE REE	WGPAEPRER	0.008799	76.24	WGPAEPRER	0.002968	46.36
AAA60336.1	5	EQEWGTPGSEVR	EWGTPGSEV	0.010682	72.6	WGTPGSEVR	0.000189	92.41
AAA60336.1	6	GSEEEDITNPINLR	EEDITNPIN	0.07543	27.67	EEDITNPIN	0.002476	50.57
AAA60336.1	7	EQEWEEEEEDEEEEGSNR	EEEDEEEEG	0.006328	81.81	WEEEEEDEE	0.000444	82.84
AAA60336.1	8	LLEENAGGEQEERG	EENAGGEQE	0.02266	56.16	LEENAGGEQ	0.000369	85.23
AAA60336.1	9	AGGEQEERGQRRRSTRS	EERGQRRRS	0.007342	79.37	EERGQRRRS	0.001995	55.4
AAA60336.1	10	EQEWEEEEEDEEEEGS	EEEEEDEEE	0.010263	73.37	WEEEEEDEE	0.001252	65.28
AAA60336.1	11	NPINLRDGEPDLSNN	LRDGEPDLS	0.115503	19.11	LRDGEPDLS	0.009457	22.61
AAA60336.1	12	NPINLRDGEPDLSN	LRDGEPDLS	0.085835	24.91	LRDGEPDLS	0.004411	37.81
AAA60336.1	13	LEENAGGEQEERGQ	AGGEQEERG	0.021206	57.73	LEENAGGEQ	0.000166	93.42
AAA60336.1	14	LRDGEPDLSNNFGRLFEVKPDKKNPQ	LFEVKPDKK	0.008227	77.47	FEVKPDKKN	0.023018	10.31
AAA60336.1	15	QFQNLQNHRIVQIE	FQNLQNHRI	0.029115	49.96	FQNLQNHRI	0.016426	14.19
AAA60336.1	16	EEEEEDEEEEGSNREVRRYTARLK	EEEEGSNRE	0.009166	75.45	EEGSNREVR	0.002211	53.19
AAA60336.1	17	EEEEEDEEEEGSNRE	EEDEEEEGS	0.027023	51.91	EEEDEEEEG	0.000182	92.72
AAA60336.1	18	DEEEEGSNREVRRYTARLK	NREVRRYTA	0.004554	86.46	VRRYTARLK	0.00284	47.36
AAA60336.1	19	EEEEEDEEEEG	EEEDEEEEG	0.000368	95	EEEDEEEEG	0.000009	95
AAA60336.1	20	INAENNHRIFLAGDK	ENNHRIFLA	0.15336	14.32	ENNHRIFLA	0.003823	40.89
AAA60336.1	21	LAGDKDNVIDQIEKQAK	NVIDQIEKQ	0.029208	49.88	NVIDQIEKQ	0.006373	30.09
AAA60336.1	22	LAGDKDNVIDQIEK	DKDNVIDQI	0.011731	70.67	KDNVIDQIE	0.000734	75.03
AAA60336.1	23	FLAGDKDNVIDQIEK	DKDNVIDQI	0.012664	69.12	LAGDKDNVI	0.002061	54.67
AAA60336.1	24	IFLAGDKDNVIDQIEK	LAGDKDNVI	0.011525	71.05	LAGDKDNVI	0.00414	39.15
AAK96887.1	25	QSDRLQGRQQEQQFKR	LQGRQQEQQ	0.013771	67.4	LQGRQQEQQ	0.004456	37.59
AAK96887.1	26	QSDRLQGRQQEQQFKRELR	LQGRQQEQQ	0.003096	90.79	LQGRQQEQQ	0.001013	69.4

PN-derived peptides identified in intestinal lumen of C57BL/6 mice

Master Protein	No.	Peptide
AAA60336.1	1	AGDKDNVIDQIEK
AAA60336.1	2	SSDNEGVIVKVSKEHVQELTKHAKSVS
AAA60336.1	3	SSDNEGVIVKVSKEHVQELTKHAKSV
AAA60336.1	4	EGGRWGPAEPRERE REE
AAA60336.1	5	GGRWGPAEPRERE REE
AAA60336.1	6	REEGGRWGPAEPR
AAA60336.1	7	RQPGDYDDDRRQP
AAA60336.1	8	REQEWEEEEEDEEEEGSNREV
AAA60336.1	9	REQEWEEEEEDEEEEGSNRE
AAA60336.1	10	MLPHFNSKAMVIVVVNKGTGN
AAA60336.1	11	GRQPGDYDDDRRQPR
AAA60336.1	12	FEVKPDKKNPQLQD
AAA60336.1	13	FEVKPDKKNPQLQ
AAA60336.1	14	EQEWEEEEEDEEEEGSNRE
AAA60336.1	15	EEEEEDEEEEGSNRE
AAA60336.1	16	EQEWEEEEEDEEEEGSNREV
AAA60336.1	17	LLEENAGGEQEERGQ
AAA60336.1	18	LEENAGGEQEERGQ
AAA60336.1	19	LAGDKDNVIDQIEKQ
AAA60336.1	20	LAGDKDNVIDQIEKQAKDLAFPGSGEQV
AAA60336.1	21	LAGDKDNVIDQIEK
AAA60336.1	22	KVSKEHVQELTKHAKSVSKKGSEEED
AAA60336.1	23	LAGDKDNVIDQIEKQA

Table S4.Luminal peptides indentified in C57BL/6 and BALB/c mice.

Table S5 Information of peptides identified in IEC MHCII immunopeptidome (Independent replicate experiment for Fig. 2d)

5-WT_CAD						
Peptide	Accession	X.10LgP	Length	Area.1	Area.3	Area.5
A(+42.01)AAAPAAAASPEA	P58069|RASA2_MOUSE	28.4	13	69.5	NA	NA
A(+42.01)AKPKTSKPKAAKPKK	P43274|H14_MOUSE	45.04	16	595	NA	NA
A(+42.01)ATPKKAKKPKVVKVKPVK	P10922|H10_MOUSE	49.95	19	6310	4450	3690
A(+42.01)AVKTLNPKAEVAR	P80317|TCPZ_MOUSE	30.66	14	162	NA	283
A(+42.01)EERS(+79.97)RILVPSLDSMLD	Q8R420|ABCA3_MOUSE	26.19	18	3250	NA	NA
A(+42.01)ESSAATQSPSVSSSSSGAEP	Q9ES97|RTN3_MOUSE	30.02	21	247	NA	791
A(+42.01)ESSAATQSPSVSSSSSGAEPS	Q9ES97|RTN3_MOUSE	29.91	22	238	NA	829
A(+42.01)GYEYVSPEQLSG	Q80TA1|EPT1_MOUSE	30.88	13	303	NA	436
A(+42.01)GYEYVSPEQLSGFD	Q80TA1|EPT1_MOUSE	47.17	15	457	NA	533
A(+42.01)GYEYVSPEQLSGFDK	Q80TA1|EPT1_MOUSE	49.49	16	20800	247	23400
A(+42.01)GYEYVSPEQLSGFDKY	Q80TA1|EPT1_MOUSE	49.92	17	545	NA	415
A(+42.01)KKTVKKTPKKAKKPAA	P43276|H15_MOUSE	37.96	17	422	NA	NA
A(+42.01)QAPTVIVTQPG	Q9JI48|PLAC8_MOUSE	30.92	12	2880	NA	NA
A(+42.01)SKRALVILAKGAE	Q99LX0|PARK7_MOUSE	29.71	14	536	94	1390
AAAAAAVAAAAAAAAAA	Q3TSG4|ALKB5_MOUSE	29.52	17	131	NA	NA
AAAGAKKAKSP	P43274|H14_MOUSE	35.21	11	2190	2920	3580
AAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.74	16	190	NA	NA
AAAKKTVKTPKKPKKPAVSKK	P43275|H11_MOUSE	49.95	21	764	301	509
AAASAYYNPGNPHNVYM(+15.99)PT	P97765|WBP2_MOUSE	48.51	19	254	NA	151
AAATTAAPAAAAAPA	P14869|RLA0_MOUSE	32.69	15	187	NA	NA
AAAVTKKVAKS	P15864|H12_MOUSE	25.66	11	80.3	NA	NA
AAEEFKVPAATSAII	P61961|UFM1_MOUSE	47.57	15	153	NA	52.1
AAEEFKVPAATSAIIT	P61961|UFM1_MOUSE	49.64	16	2400	NA	1250
AAEEFKVPAATSAIITN	P61961|UFM1_MOUSE	49.91	17	2010	NA	NA
AAEEFKVPAATSAIITNDG	P61961|UFM1_MOUSE	49.86	19	330	NA	247
AAGVFSNPAVRTAAA	O35609|SCAM3_MOUSE	39.57	15	538	NA	664
AAGVFSNPAVRTAAAN	O35609|SCAM3_MOUSE	45.87	16	686	NA	640
AAGVKKVAKSPKKAKAAAKPKKAAKSP/	P43276|H15_MOUSE	49.95	31	315	376	1400
AAIPGTNM(+15.99)YNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	47.67	22	398	NA	190
AAIPGTNMYNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	39.51	22	122	NA	235
AAKKTKKPA	P43275|H11_MOUSE	26.57	9	185	NA	NA
AAKKTKKPAKAAAPRK	P43275|H11_MOUSE	48.26	16	1760	NA	NA
AAKKTKKPAKAAAPRKKP	P43275|H11_MOUSE	26.13	18	348	NA	NA
AAKKTPKKAKKPA	P15864|H12_MOUSE	46.81	13	377	NA	NA
AAKPKKAAKSPAKAKAPKAK	P43277|H13_MOUSE	42.23	20	2570	NA	NA
AAKPKKAAKSPAKAKAPKAKASKPKA	P43277|H13_MOUSE	49.95	26	221	NA	NA
AAKPKKAAKSPAKPKA	P43276|H15_MOUSE	25.36	16	316	NA	NA
AAKPKTSKPKAAKPK	P43274|H14_MOUSE	36.04	15	365	NA	NA
AAKPKVAKAKKVAAKK	P15864|H12_MOUSE	49.94	16	2600	408	NA
AAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	17	20900	861	3560
AAKSPAKAKAPKAKASKPKA	P43277|H13_MOUSE	42.6	20	87.4	NA	NA
AALYSFKAARALLDHR	Q9WTN3|SRBP1_MOUSE	48.1	16	387	NA	316
AALYSFKAARALLDHRK	Q9WTN3|SRBP1_MOUSE	49.81	17	4360	NA	3300
AAPAAAATTAAPAAAAAPAKAE	P14869|RLA0_MOUSE	49.94	22	127	NA	545
AAPAAAATTAAPAAAAAPAKAEAKEE	P14869|RLA0_MOUSE	49.95	26	910	NA	172
AAPFFIVRHQLLKK	P17665|COX7C_MOUSE	35.69	14	329	NA	NA
AAPQAQAGPTTSPAYSSY	Q99LI8|HGS_MOUSE	49.76	18	705	NA	298
AAPQQAAAPEPTSAFNPR	E9Q555|RN213_MOUSE	49.35	18	788	NA	1050
AARDNMFSGSKINYTENR	P06745|G6PI_MOUSE	48.86	18	73.5	NA	440
AASAYYNPGNPHNVYM(+15.99)PT	P97765|WBP2_MOUSE	49.89	18	3450	NA	1650
AASAYYNPGNPHNVYMPT	P97765|WBP2_MOUSE	49.94	18	506	NA	1750
AASTIYGPHTLSAY	Q9JHE3|ASAH2_MOUSE	35.82	14	70.6	NA	NA
AASTIYGPHTLSAYI	Q9JHE3|ASAH2_MOUSE	46.3	15	91.9	NA	NA
AASTIYGPHTLSAYIQ	Q9JHE3|ASAH2_MOUSE	48.79	16	3460	NA	1640
AATPKKAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	41.17	27	316	NA	4110
ADASFVAAIPSTQVV	Q62178|SEM4A_MOUSE	27.43	15	2980	NA	1070
ADFHYAASKALRVPA	Q80TA9|EPG5_MOUSE	49.9	15	5790	NA	9540
ADFSYRGPAGSIEQGP	Q99LI2|CLCC1_MOUSE	48.14	16	590	NA	372
ADFSYRGPAGSIEQGPY	Q99LI2|CLCC1_MOUSE	49.63	17	802	NA	752
ADGREVSSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	32.18	18	152	NA	62.5
ADKEFHAPLIIDE	Q91YN5|UAP1_MOUSE	41.83	13	722	NA	111
ADKEFHAPLIIDEN	Q91YN5|UAP1_MOUSE	46.95	14	2100	NA	616
ADKEFHAPLIIDENG	Q91YN5|UAP1_MOUSE	48.49	15	12000	NA	6000
ADPPASVVVGPVVVPR	P29699|FETUA_MOUSE	49.89	16	149	NA	NA
ADPSAFAAAAPAAAAT	P14869|RLA0_MOUSE	38.46	16	258	NA	683
ADPSAFAAAAPAAAATT	P14869|RLA0_MOUSE	48.62	17	6470	620	5020
ADPSAFAAAAPAAAATTA	P14869|RLA0_MOUSE	47.31	18	172	NA	245
ADPSAFAAAAPAAAATTAAPAAAA	P14869|RLA0_MOUSE	36.68	24	58.9	NA	NA
ADTTYELPSVSALVS	O89020|AFAM_MOUSE	25.55	15	110	NA	NA
AEAAAAPAPAAGPGQ(+15.00)MSFTFA	Q9D3D9|ATPD_MOUSE	29.82	21	1200	NA	NA
AEAAAAPAPAAGPGQM(+15.99)SFTFA	Q9D3D9|ATPD_MOUSE	27.18	21	283	NA	NA
AEEFKVPAATSAIIT	P61961|UFM1_MOUSE	49.29	15	725	NA	207
AEEFKVPAATSAIITN	P61961|UFM1_MOUSE	49.67	16	1580	NA	1220
AEEFKVPAATSAIITNDG	P61961|UFM1_MOUSE	37.89	18	1220	NA	634

AEELVKDSELSPPTSAPSLVS	Q9WUU8|TNIP1_MOUSE	40.85	21	332	NA	250
AEEYLGMPVANAVIS	Q8BM72|HSP13_MOUSE	39.16	15	92.3	NA	107
AEKGFEVDAPLANALAIQ	Q6PDE7|GGT6_MOUSE	49.1	18	157	NA	75.4
AEPLALIVSHDYKGSTSHSLPYE	E9Q414|APOB_MOUSE	48.93	23	171	NA	512
AEPSYRGSEPEPEY	Q60598|SRC8_MOUSE	29.73	14	151	NA	351
AEPSYRGSEPEPEYS	Q60598|SRC8_MOUSE	44.04	15	1040	NA	NA
AEQEVLAPQVVLSLG	O09159|MA2B1_MOUSE	41.03	15	344	NA	NA
AEQEVLAPQVVLSLGG	O09159|MA2B1_MOUSE	45.07	16	965	NA	NA
AERLKPYVAAQVDVLPD	A2A8L5|PTPRF_MOUSE	49.49	17	245	NA	575
AERLKPYVAAQVDVLPDT	A2A8L5|PTPRF_MOUSE	49.94	18	505	NA	1670
AFKKTKKEVKKVATPKKAAKPKK	P10922|H10_MOUSE	49.56	23	66.4	732	NA
AFPTVFHSSLVQHEVVA	Q8C165|P20D1_MOUSE	49.15	17	228	NA	NA
AFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	45.04	12	154	NA	NA
AFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	48.33	13	13500	87.4	11200
AFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.49	14	171	NA	NA
AFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MC	46.95	15	418	NA	NA
AGAKKTVKKTPKKAKKPA	P43276|H15_MOUSE	40.78	18	320	NA	NA
AGATPKKPKKTAGAKKTVKKTPKKAKKP	P43276|H15_MOUSE	49.95	29	621	NA	NA
AGEQSWIQALPSVAKEE	Q8BH86|GLUCM_MOUSE	49.73	17	64.4	NA	NA
AGEQSWIQALPSVAKEEK	Q8BH86|GLUCM_MOUSE	48.91	18	508	NA	370
AGGGDPEAPAPAPAAERPP	Q68FL4|SAHH3_MOUSE	49.53	19	487	NA	106
AGGGDPEAPAPAPAAERPPA	Q68FL4|SAHH3_MOUSE	49.79	20	60.8	NA	NA
AGGSYLSPAPGDTSS	Q05BQ1|TUTLA_MOUSE	45.2	15	168	NA	NA
AGKLQDQGPDVLLAKVS	A6X935|ITIH4_MOUSE	49.87	17	727	NA	1290
AGKLQDQGPDVLLAKVSG	A6X935|ITIH4_MOUSE	49.58	18	1060	NA	1410
AGKLQDQGPDVLLAKVSGQ	A6X935|ITIH4_MOUSE	44.23	19	59.4	NA	NA
AGNDLSFIHPKALSGLKE	A2ARI4|LGR4_MOUSE	44.92	18	601	NA	594
AGNFYVPAEPKLAFVI	P14148|RL7_MOUSE	42.99	16	351	NA	376
AGPNFEYAEAPSRLSPDD	P11152|LIPL_MOUSE	48.72	18	260	NA	NA
AGPNFEYAEAPSRLSPDDA	P11152|LIPL_MOUSE	49.65	19	169	NA	180
AGPNVLQPYAAYAPPG	Q7M758|NALDL_MOUSE	28.32	16	1120	NA	330
AGPNVLQPYAAYAPPGTPK	Q7M758|NALDL_MOUSE	36.5	19	384	NA	NA
AGPQWADPQISESNFSPK	Q8BVU5|NUDT9_MOUSE	47.26	18	130	NA	56
AGTRYSAPANLYVR	Q64487|PTPRD_MOUSE:A2A8L5|PTPRF	41.56	14	1090	NA	1050
AGTRYSAPANLYVRVR	A2A8L5|PTPRF_MOUSE	45.64	16	261	NA	285
AGVFSNPAVRTAAAN	O35609|SCAM3_MOUSE	43.73	15	127	NA	NA
AGVKKVAKSPKKAK	P43276|H15_MOUSE	36.84	14	80.8	NA	NA
AHELRYQVPGAVPAK	Q9Z280|PLD1_MOUSE	49.87	15	13300	NA	8350
AHELRYQVPGAVPAKVQ	Q9Z280|PLD1_MOUSE	48.68	17	79.1	NA	224
AHELRYQVPGAVPAKVQL	Q9Z280|PLD1_MOUSE	49.57	18	47.7	NA	53.5
AIDIFSTPSSSNSTSK	Q7M6Y3|PICAL_MOUSE	34.87	16	615	NA	600
AIFARGPQAHLVH	P24823|PPBN_MOUSE:P24822|PPBI_MC	48.18	13	2390	NA	1270
AIFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_MC	48.85	14	14300	NA	8530
AIFARGPQAHLVHGVQ	P24823|PPBN_MOUSE:P24822|PPBI_MC	49.62	16	982	NA	488
AIFFQVSPRDNSALDPI	Q05909|PTPRG_MOUSE	49.11	17	1640	NA	645
AIFFQVSPRDNSALDPII	Q05909|PTPRG_MOUSE	47.84	18	114	NA	NA
AIIKFPLTTE	P62751|RL23A_MOUSE	44.86	10	89.5	NA	NA
AIKNNSFYGPEVKIEKG	Q00519|XDH_MOUSE	46.46	17	88.2	NA	94.8
AILVRYTQKAPQVSTP	P07724|ALBU_MOUSE	49.72	16	139	NA	168
AILVRYTQKAPQVSTPT	P07724|ALBU_MOUSE	48.6	17	194	NA	445
AILVRYTQKAPQVSTPTL	P07724|ALBU_MOUSE	49.94	18	339	NA	658
AILVRYTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.82	19	1490	NA	1870
AILVRYTQKAPQVSTPTLVE	P07724|ALBU_MOUSE	49.94	20	506	NA	871
AINDYKGAVIVVSHD	Q6P542|ABCF1_MOUSE	47.91	15	259	NA	237
AINDYKGAVIVVSHDAR	Q6P542|ABCF1_MOUSE	48.68	17	540	NA	293
AIPGTNM(+15.99)YNTDRANPVLD	E9Q7P9|CDHR2_MOUSE	32.81	18	623	NA	NA
AIPGTNM(+15.99)YNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	49.78	20	2200	NA	2160
AIPGTNM(+15.99)YNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	49.94	21	3420	NA	2990
AIPGTNMYNTDRANPVLD	E9Q7P9|CDHR2_MOUSE	49.92	18	272	NA	1030
AIPGTNMYNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	29.87	20	874	NA	2380
AIPGTNMYNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	49.93	21	1300	NA	2410
AIT(+79.97)NC(+57.02)ALSYKGAFWYKN	Q80YX1|TENA_MOUSE	30.9	28	525	NA	NA
AITSYSIPESIKSLE	Q91Y74|SIA4C_MOUSE	31.38	15	1240	NA	908
AIYYHASRAIPFG	Q9ET30|TM9S3_MOUSE	46.9	13	459	NA	355
AKAKAVKPKASKAKVTKPKTPAKPKKAA	P43275|H11_MOUSE	32.2	32	532	NA	NA
AKAKKVAAK	P15864|H12_MOUSE	38.42	9	65.9	NA	NA
AKAKTVKPKAAKPKTSKPKAAKPKKT	P43274|H14_MOUSE	49.95	26	3250	NA	1450
AKAKTVKPKAAKPKTSKPKAAKPKKTAA	P43274|H14_MOUSE	49.95	31	34000	NA	13000
AKASKPKASKPKATKAKKAAPRKK	P43277|H13_MOUSE	49.95	24	2760	NA	NA
AKAVKPKASKAKVTKPKTPAKPKKAAPK	P43275|H11_MOUSE	49.95	30	741	NA	NA
AKGLFRAAVPSGAS	P17183|ENOG_MOUSE:P17182|ENOA_M	44.63	14	477	NA	427
AKGLFRAAVPSGAST	P17183|ENOG_MOUSE:P17182|ENOA_M	48.43	15	5860	NA	6230
AKGLFRAAVPSGASTG	P17183|ENOG_MOUSE:P17182|ENOA_M	47.46	16	1380	NA	1060
AKKAAPRK	P43277|H13_MOUSE	29.46	8	1120	NA	697
AKKAAPRKK	P43277|H13_MOUSE	38.79	9	2090	1950	NA
AKKAVSKKK	P43276|H15_MOUSE	30.96	9	428	NA	NA
AKKPAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.95	20	1600	1550	1120

AKKPKKTAGAAAKKTV	P43275|H11_MOUSE	29.19	16	970	NA	NA
AKKRKKKSYTTPKKN	P62983|RS27A_MOUSE	49.83	15	530	NA	NA
AKKRKKKSYTTPKKNKHKRKK	P62983|RS27A_MOUSE	49.95	21	4190	68400	4020
AKKRKKKSYTTPKKNKHKRKKVK	P62983|RS27A_MOUSE	49.95	23	8090	NA	NA
AKKRKKKSYTTPKKNKHKRKKVKLAVL	P62983|RS27A_MOUSE	49.95	27	4690	4190	8760
AKKRKKKSYTTPKKNKHKRKKVKLAVLK	P62983|RS27A_MOUSE	49.95	28	8370	24200	18100
AKKRKKKSYTTPKKNKHKRKKVKLAVLK	P62983|RS27A_MOUSE	49.95	29	10600	3020	18400
AKKRKKKSYTTPKKNKHKRKKVKLAVLK	P62983|RS27A_MOUSE	49.95	30	1920	6610	1150
AKKRKKKSYTTPKKNKHKRKKVKLAVLK	P62983|RS27A_MOUSE	49.95	31	4430	10600	8230
AKKRKKKSYTTPKKNKHKRKKVKLAVLK	P62983|RS27A_MOUSE	49.94	33	757	NA	282
AKKTVKTPKKPKKPAVSKK	P43275|H11_MOUSE	49.94	19	456	401	NA
AKKVAAKKK	P15864|H12_MOUSE	42.65	9	5880	543	673
AKPKAAKAKKAVSKKK	P43276|H15_MOUSE	49.9	16	782	NA	NA
AKPKAVKSKASKPKVTKPKTAKPKAAKA	P43276|H15_MOUSE	44.58	30	1840	NA	NA
AKPKKAAKSPAKPK	P43276|H15_MOUSE	25.16	14	770	NA	621
AKPKKAAPK	P43275|H11_MOUSE	37.64	9	3120	603	NA
AKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	16	3040	NA	334
AKPSGYNPPISILGIL	Q61739|ITA6_MOUSE	36.77	16	468	NA	669
AKPVSQM(+15.99)RMATPLLM(+15.99)R	P04441|HG2A_MOUSE	36.34	18	397	NA	14300
AKPVSQM(+15.99)RMATPLLMRPM(+15	P04441|HG2A_MOUSE	49.55	18	17300	NA	14800
AKPVSQMRM(+15.99)ATPLLM(+15.99)R	P04441|HG2A_MOUSE	29.43	17	2180	NA	NA
AKPVSQMRM(+15.99)ATPLLM(+15.99)R	P04441|HG2A_MOUSE	48.79	18	16700	NA	NA
AKPVSQMRM(+15.99)ATPLLMRP	P04441|HG2A_MOUSE	36.94	17	1130	NA	679
AKPVSQMRM(+15.99)ATPLLMRPM	P04441|HG2A_MOUSE	42.97	18	3490	NA	288
AKPVSQMRM(+15.99)ATPLLMRPM(+15	P04441|HG2A_MOUSE	49.63	18	17700	NA	NA
AKPVSQMRMATPLLM(+15.99)RP	P04441|HG2A_MOUSE	29.53	17	1070	NA	NA
AKPVSQMRMATPLLM(+15.99)RPM(+15	P04441|HG2A_MOUSE	45.33	18	12400	NA	11800
AKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	49.41	18	301	NA	11400
AKPVSQMRMATPLLMRPM(+15.99)	P04441|HG2A_MOUSE	49.8	18	6530	NA	21900
AKSPKKAK	P15864|H12_MOUSE:P43276|H15_MOU	38.45	8	269	85.9	NA
AKSPKKAKATKAKKAPKSPAKAKTVKPK	P43274|H14_MOUSE	49.94	28	3100	NA	NA
AKTHDLYIQSHISENREE	Q9R111|GUAD_MOUSE	49.86	18	277	NA	216
AKTVKPKAAKPKTSKPKAAKPKKTAAKK	P43274|H14_MOUSE	49.95	29	1140	NA	304
AKTVKPKAKSSAKR	P10922|H10_MOUSE	49.8	14	539	484	1230
AKTVKPKAKSSAKRASKK	P10922|H10_MOUSE	46.93	18	3160	NA	1200
AKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.94	19	9210	NA	NA
AKVELVPPTPAEIPT	Q9CPQ8|ATP5L_MOUSE	28.48	15	397	NA	284
AKVTKPKKVKSASKAVKPKAAKPK	P15864|H12_MOUSE	49.22	24	6890	NA	2590
AKVTKPKTPAKPKKAAPKKK	P43275|H11_MOUSE	49.94	20	4470	NA	NA
ALAVAGAPIALSAVG	Q8VC49|IF27B_MOUSE	48.26	15	3170	NA	2880
ALAVAGAPVALSAVG	Q8VC49|IF27B_MOUSE	46.3	15	1200	NA	953
ALDGVETPSVTEAVKK	Q61194|P3C2A_MOUSE	42.88	16	285	NA	NA
ALIQYFSPYVSADM(+15.99)H	Q99LD4|CSN1_MOUSE	39.98	15	281	NA	87.8
ALIQYFSPYVSADM(+15.99)HK	Q99LD4|CSN1_MOUSE	41.58	16	113	NA	NA
ALIYGTPRAATVKA	Q9DBC7|KAP0_MOUSE:P12849|KAP1_M	45.16	14	400	NA	275
ALKAKKAVLKGVHSHKKKKIRTSPTFRR	P62751|RL23A_MOUSE	48.95	33	272	3610	1930
ALKPEYVAPLVL	P51660|DHB4_MOUSE	30.78	12	268	NA	622
ALLSPYSYSTTAVVSNPQ	P07309|TTHY_MOUSE	49.47	18	237	NA	414
ALRNYEYYASHVPESVK	Q9Z0S1|BPNT1_MOUSE	49.62	17	223	NA	NA
ALRNYEYYASHVPESVKN	Q9Z0S1|BPNT1_MOUSE	49.18	18	690	NA	262
ALYSFKAARALLDH	Q9WTN3|SRBP1_MOUSE	49.58	14	181	NA	104
ALYSFKAARALLDHR	Q9WTN3|SRBP1_MOUSE	49.45	15	3770	NA	2820
ALYSFKAARALLDHRK	Q9WTN3|SRBP1_MOUSE	49.89	16	10700	NA	5770
AM(+15.99)LQVLGPKPALPEG	P13020|GELS_MOUSE	49.41	15	3260	NA	1970
AMLQVLGPKPALPEG	P13020|GELS_MOUSE	48.78	15	1240	NA	1810
AN(+15.00)DLFLQEQKTLGADDTM(+15.9	P18826|KPB1_MOUSE	32.67	19	377	NA	NA
ANNTTYGLAAGLFTKDLD	P24549|AL1A1_MOUSE	36.52	18	23.2	NA	NA
ANPVVIPEPPNPIPSYSEVV	Q99N10|M4A8_MOUSE	49.94	20	157	NA	NA
ANVVWDYFTQLSNNAKE	P06728|APOA4_MOUSE	49.87	17	310	NA	139
ANVVWDYFTQLSNNAKEA	P06728|APOA4_MOUSE	49.84	18	188	NA	352
APAAAATTAAPAAAAAPA	P14869|RLA0_MOUSE	43.33	18	879	NA	NA
APAAAATTAAPAAAAAPAK	P14869|RLA0_MOUSE	49.89	19	7290	135	NA
APAAAATTAAPAAAAAPAKAE	P14869|RLA0_MOUSE	49.9	21	1020	NA	1310
APAAAATTAAPAAAAAPAKAEAKEE	P14869|RLA0_MOUSE	49.95	25	1420	NA	83
APAAAATTAAPAAAAAPAKAEAKEES	P14869|RLA0_MOUSE	49.94	26	327	NA	NA
APAAAEAPAAAEAPA	Q80TM9|NISCH_MOUSE	27.76	15	1060	NA	NA
APAEAQAAM(+15.99)EEPVVQPSVVD	Q9DBG5|PLIN3_MOUSE	44.65	20	482	NA	338
APAEAQAAM(+15.99)EEPVVQPSVVDR	Q9DBG5|PLIN3_MOUSE	49.93	21	1050	NA	748
APAEAQAAMEEPVVQPSVVDR	Q9DBG5|PLIN3_MOUSE	49.95	21	241	NA	734
APAIDIFSTPSSSNSTS	Q7M6Y3|PICAL_MOUSE	48.95	17	291	NA	354
APAIDIFSTPSSSNSTSK	Q7M6Y3|PICAL_MOUSE	48.63	18	6410	67.7	7340
APAIDIFSTPSSSNSTSKLPN	Q7M6Y3|PICAL_MOUSE	48.93	21	756	NA	1280
APAPAPAAAPAPAPAAQA	Q9Z1W9|STK39_MOUSE	48.96	18	137	NA	NA
APAQM(+15.99)AYPTAYPSFPG	Q7TN29|SMAP2_MOUSE	46.68	16	1720	NA	1220
APAQMAYPTAYPSFPG	Q7TN29|SMAP2_MOUSE	31.9	16	495	NA	1040
APATPAAEAKAAEAAASAYYNPG	P97765|WBP2_MOUSE	48.92	23	519	NA	269
APAVTPVK	P70158|ASM3A_MOUSE	30.12	8	1960	NA	3650

APAVTPVKG	P70158|ASM3A_MOUSE	29.78	9	155	NA	1170
APDAWDYSQGFVNEEM(+15.99)IR	Q9DCN2|NB5R3_MOUSE	49.94	18	703	NA	236
APDAWDYSQGFVNEEMIR	Q9DCN2|NB5R3_MOUSE	49.89	18	132	NA	154
APDFVFYAPRLRINK	P26043|RADI_MOUSE:P26040|EZRI_MC	36.66	15	419	NA	387
APDRTEEIKTPEPLEEGPA	Q6EDY6|CARL1_MOUSE	48.91	19	2600	NA	3140
APDTRFVAPGAL	Q3U2C5|RN149_MOUSE	29.47	12	613	80.2	466
APDTRFVAPGALG	Q3U2C5|RN149_MOUSE	41.65	13	16000	2460	9780
APDTRFVAPGALGN	Q3U2C5|RN149_MOUSE	45.5	14	2300	801	1830
APDTRFVAPGALGNAP	Q3U2C5|RN149_MOUSE	49.44	16	10600	224	10600
APDTRFVAPGALGNAPW	Q3U2C5|RN149_MOUSE	49.57	17	4780	151	4320
APDYAKATVSASHIIR	P21447|MDR1A_MOUSE	49.92	16	553	NA	150
APETRSQVTPSVPSEALD	Q7TQH7|LRP10_MOUSE	49.9	18	560	NA	314
APETRSQVTPSVPSEALDD	Q7TQH7|LRP10_MOUSE	49.94	19	5440	NA	4120
APETRSQVTPSVPSEALDDS	Q7TQH7|LRP10_MOUSE	49.93	20	12000	213	9320
APETRSQVTPSVPSEALDDST	Q7TQH7|LRP10_MOUSE	49.94	21	3310	NA	2310
APETRSQVTPSVPSEALDDSTG	Q7TQH7|LRP10_MOUSE	49.93	22	225	NA	197
APFDWEGAQASQAL	Q91W98|S15A4_MOUSE	45.55	14	561	NA	368
APFDWEGAQASQALL	Q91W98|S15A4_MOUSE	38.58	15	190	NA	141
APFFIVRHQLLKK	P17665|COX7C_MOUSE	43.42	13	219	NA	NA
APFFTPNAAPAE	Q80TA9|EPG5_MOUSE	38.82	12	591	NA	532
APGGYVAPKAVWL	Q9DBG3|AP2B1_MOUSE	46.44	13	192	NA	189
APGGYVAPKAVWLP	Q9DBG3|AP2B1_MOUSE	44.63	14	475	NA	389
APGGYVAPKAVWLPA	Q9DBG3|AP2B1_MOUSE	49.84	15	9520	NA	9060
APGHYTYSSPHSGSIH	O09114|PTGDS_MOUSE	49.88	16	1010	NA	413
APGKKVIYSQPSTRSEGEF	O88792|JAM1_MOUSE	49.6	19	6480	NA	4320
APGLAFTTPVVASAAPV	Q80VC9|CAMP3_MOUSE	42.06	17	553	NA	676
APGM(+15.99)HTYSQPYSSRSRL	Q9ET43|CLD12_MOUSE	30.66	17	246	NA	334
APGMHTYSQPYSSRSR	Q9ET43|CLD12_MOUSE	48.19	16	4370	NA	4290
APGMHTYSQPYSSRSRLS	Q9ET43|CLD12_MOUSE	48.21	18	739	NA	891
APGPSHTVAAPQAAAAAA	Q80U93|NU214_MOUSE	46.08	18	261	NA	NA
APGPSHTVAAPQAAAAAAL	Q80U93|NU214_MOUSE	49.31	19	4130	74.1	4350
APGPSQPAVLQPSVEPAQ	Q9ERN0|SCAM2_MOUSE	48.84	18	574	NA	1130
APGPSQPAVLQPSVEPAQP	Q9ERN0|SCAM2_MOUSE	49.83	19	3970	NA	4370
APGPSQPAVLQPSVEPAQPT	Q9ERN0|SCAM2_MOUSE	49.89	20	4430	NA	4120
APGPSQPAVLQPSVEPAQPTP	Q9ERN0|SCAM2_MOUSE	49.94	21	3390	NA	4450
APGPSQPAVLQPSVEPAQPTPQ	Q9ERN0|SCAM2_MOUSE	49.94	22	6130	NA	7890
APGPYQAAAGPSVVPTAPPT	Q9JLJ0|LITAF_MOUSE	49.4	20	231	NA	177
APGRDLHYQNPHSNAVGNP	Q01279|EGFR_MOUSE	35.94	19	3080	NA	2620
APINAFIGGLAAQEVM(+15.99)	Q02053|UBA1_MOUSE	49.56	16	316	NA	252
APINAFIGGLAAQEVM(+15.99)K	Q02053|UBA1_MOUSE	47.69	17	518	NA	175
APISSHTAPRPNPTP	Q6PB44|PTN23_MOUSE	45.73	15	461	NA	8920
APISSHTAPRPNPTPA	Q6PB44|PTN23_MOUSE	45.55	16	20800	NA	17000
APISSHTAPRPNPTPAL	Q6PB44|PTN23_MOUSE	27.1	17	329	NA	NA
APISSHTAPRPNPTPALP	Q6PB44|PTN23_MOUSE	49.67	18	4970	NA	1360
APISSHTAPRPNPTPALPQ	Q6PB44|PTN23_MOUSE	49.9	19	2000	NA	1860
APKAKASKPKA	P43277|H13_MOUSE	40.1	11	601	NA	369
APKAKASKPKASKPKATKAKKAAPRKK	P43277|H13_MOUSE	43.18	27	411	887	NA
APKDIM(+15.99)GPQVTPVLS	O54782|MA2B2_MOUSE	41.68	15	971	NA	539
APKETTIWVSPSPILE	P29533|VCAM1_MOUSE	41.15	16	228	NA	NA
APKETTIWVSPSPILEEG	P29533|VCAM1_MOUSE	36.13	18	217	NA	93.1
APKETTIWVSPSPILEEGSPV	P29533|VCAM1_MOUSE	29.44	21	50.6	NA	NA
APLDELVGAYPNYNEE	Q8VCW4|UN93B_MOUSE	48.34	16	508	NA	NA
APLNVQFSSPLPGEAVK	Q80X90|FLNB_MOUSE	49.92	17	2410	NA	3010
APLNVQFSSPLPGEAVKD	Q80X90|FLNB_MOUSE	49.94	18	11600	554	12600
APLNVQFSSPLPGEAVKDL	Q80X90|FLNB_MOUSE	49.93	19	382	NA	283
APM(+15.99)DAFSGSRAVLSGPA	Q8K010|OPLA_MOUSE	49.33	17	816	NA	256
APM(+15.99)YYRGAQAA	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	41.71	11	1230	NA	1150
APM(+15.99)YYRGAQAAIV	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	45.29	13	4700	57.2	2450
APM(+15.99)YYRGAQAAIVV	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	37.79	14	22400	2590	17500
APM(+15.99)YYRGAQAAIVVY	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	49.55	15	79700	13700	62300
APM(+15.99)YYRGAQAAIVVYD	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	49.61	16	118000	12500	81100
APMDAFSGSRAVLSGPA	Q8K010|OPLA_MOUSE	49.89	17	420	NA	588
APMYYRGAQAA	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	45.76	11	1100	NA	1670
APMYYRGAQAAIV	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	43.7	13	2430	NA	3670
APMYYRGAQAAIVV	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	45.67	14	8860	NA	15900
APMYYRGAQAAIVVY	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	47.63	15	28000	NA	57100
APMYYRGAQAAIVVYD	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	49.47	16	39800	NA	79400
APNLHFHNPNPEIPA	P19096|FAS_MOUSE	37.01	15	337	NA	827
APPAGSLYSSPVNSSAP	Q99LI8|HGS_MOUSE	48.45	17	4650	NA	3740
APPAGSLYSSPVNSSAPL	Q99LI8|HGS_MOUSE	39.72	18	1060	NA	NA
APPAGSLYSSPVNSSAPLA	Q99LI8|HGS_MOUSE	48.89	19	544	NA	1200
APPLPIKTPIPTPS	Q7TQH7|LRP10_MOUSE	49.91	14	1660	NA	1340
APPLPIKTPIPTPST	Q7TQH7|LRP10_MOUSE	49.89	15	11900	169	12500
APPLPIKTPIPTPSTL	Q7TQH7|LRP10_MOUSE	49.86	16	1740	NA	1290
APPLPIKTPIPTPSTLP	Q7TQH7|LRP10_MOUSE	49.88	17	8360	142	11300
APPLPIKTPIPTPSTLPA	Q7TQH7|LRP10_MOUSE	49.94	18	8210	NA	6980
APQAQAGPTTSPAYSS	Q99LI8|HGS_MOUSE	37.86	16	197	NA	NA

APQAQAGPTTSPAYSSY	Q99LI8|HGS_MOUSE	49.15	17	291	NA	155
APQQAAAPEPTSAFNPR	E9Q555|RN213_MOUSE	49.22	17	5010	NA	4170
APQVSTPTLVEAAR	P07724|ALBU_MOUSE	46.37	14	103	NA	96.6
APQVSTPTLVEAARNLG	P07724|ALBU_MOUSE	49.84	17	161	NA	104
APRAGTASQPHPSPAFSPA	P70424|ERBB2_MOUSE	36.66	19	258	NA	NA
APRKKPAGPSVSELIVQAVSSSKER	P43275|H11_MOUSE	49.94	25	256	NA	NA
APRPFGSVSSPKVTSIPSPS	Q8CI51|PDLI5_MOUSE	44.78	20	191	NA	425
APSAGGSYLSPAPGDTS	Q05BQ1|TUTLA_MOUSE	46.34	17	553	NA	232
APSAGGSYLSPAPGDTSS	Q05BQ1|TUTLA_MOUSE	48.68	18	1820	NA	1160
APSNTFVAPQPVVASPA	Q61191|HCFC1_MOUSE	38.78	17	96.2	NA	NA
APSNYLNNPYVRKAL	P16675|PPGB_MOUSE	49.53	15	876	NA	564
APSNYLNNPYVRKALHIP	P16675|PPGB_MOUSE	27.17	18	2060	NA	NA
APSNYLNNPYVRKALHIPE	P16675|PPGB_MOUSE	47.55	19	51800	NA	22400
APSTRVITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.95	22	1320	NA	2300
APSTRVITNQYNSPTGLYSSENIS	O70400|PDLI1_MOUSE	49.94	24	67.7	NA	321
APSWHASVPTRAGPD	O88839|ADA15_MOUSE	36.12	15	1630	NA	2160
APSYSYATPTPQASSQ	Q8K135|K319L_MOUSE	49.09	16	70.3	NA	NA
APTAAIPGTNM(+15.99)YNTDRANPVLD	E9Q7P9|CDHR2_MOUSE	49.7	25	367	NA	164
APTSALGPKASPAP	Q8K0V4|CNOT3_MOUSE	41.73	14	748	NA	357
APTSALGPKASPAPS	Q8K0V4|CNOT3_MOUSE	43.76	15	2350	NA	1590
APVFYTPQAYAAIPS	Q5YD48|A1CF_MOUSE	48.83	15	873	NA	996
APVPSPVAPAPVPSR	P97825|JUPI1_MOUSE	49.36	15	163	NA	124
APVPSPVAPAPVPSRRNPPG	P97825|JUPI1_MOUSE	35.94	20	96.7	NA	301
APVVFSTPQATQM(+15.99)NTPS	Q6NZJ6|IF4G1_MOUSE	49.8	17	712	NA	764
APWQWSGPASHNSLPA	G3X9J0|SI1L3_MOUSE	46.07	16	321	NA	600
APYGARYVGSM(+15.99)VADIH	Q9QXD6|F16P1_MOUSE	48.08	16	809	NA	470
APYGARYVGSM(+15.99)VADIHR	Q9QXD6|F16P1_MOUSE	49.9	17	4960	NA	5950
APYGARYVGSM(+15.99)VADIHRT	Q9QXD6|F16P1_MOUSE	49.93	18	2420	NA	2450
APYGARYVGSMVADIHR	Q9QXD6|F16P1_MOUSE	49.92	17	3920	NA	7950
APYGARYVGSMVADIHRT	Q9QXD6|F16P1_MOUSE	49.88	18	2340	NA	3870
APYQGPDAAPGALD	P57780|ACTN4_MOUSE	36.29	14	1000	NA	643
AQAAM(+15.99)EEPVVQPSVVD	Q9DBG5|PLIN3_MOUSE	46.99	16	1260	NA	737
AQAAM(+15.99)EEPVVQPSVVDR	Q9DBG5|PLIN3_MOUSE	49.72	17	542	NA	365
AQAAMEEPVVQPSVVD	Q9DBG5|PLIN3_MOUSE	48.21	16	199	NA	561
AQAQAQAPAPAPAPAPAP	Q9Z1R2|BAG6_MOUSE	49.72	18	192	NA	188
AQEQAQEQVQPKPLES	P06728|APOA4_MOUSE	49.81	16	1930	NA	NA
AQEQVQPKPLES	P06728|APOA4_MOUSE	44.7	12	111	NA	NA
AQKKDGKKRKRSRKESYSVYVYKVLKQ	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	49.95	31	23600	251000	24000
AQPATAPQAAAAQEPG	Q3UHJ0|AAK1_MOUSE	48.78	16	1260	NA	NA
AQPPEYTFPSGSGAH	Q2TBE6|P4K2A_MOUSE	49.59	15	931	NA	892
AQPPEYTFPSGSGAHFP	Q2TBE6|P4K2A_MOUSE	47.51	17	5350	NA	4950
AQPPEYTFPSGSGAHFPQ	Q2TBE6|P4K2A_MOUSE	49.88	18	10700	NA	10800
AQRAGYKAAIVHNVDS	O54965|RNF13_MOUSE	47.02	16	377	NA	252
AQSPYINPIIPFTGPI	O08573|LEG9_MOUSE	47.73	16	482	NA	462
AQWIAPSVQLTGYR	P11276|FINC_MOUSE	29.32	14	125	NA	NA
AQYVLTSPEASSRFG	O70362|PHLD_MOUSE	27.85	15	252	NA	132
ARDNM(+15.99)FSGSKINYTENR	P06745|G6PI_MOUSE	49.26	17	133	NA	NA
ARDNMFSGSKINYTENR	P06745|G6PI_MOUSE	49.15	17	931	NA	967
ARM(+15.99)APYQGPDAAPGALD	P57780|ACTN4_MOUSE	42.14	17	680	NA	536
ARM(+15.99)PYTNAVIHEVQ	P24456|CP2DA_MOUSE:P24457|CP2DB	39.71	14	1440	NA	409
ARM(+15.99)PYTNAVIHEVQR	P24456|CP2DA_MOUSE:P24457|CP2DB	47.49	15	3990	NA	1970
ARMAPYQGPDAAPGALD	P57780|ACTN4_MOUSE	39.97	17	224	NA	581
ARMPYTNAVIHEVQ	P24456|CP2DA_MOUSE:P24457|CP2DB	43.42	14	1840	NA	533
ARMPYTNAVIHEVQR	P24456|CP2DA_MOUSE:P24457|CP2DB	46.83	15	4840	NA	4500
ARPDDEVGPAVAPGHP	B2RXV4|FLVC1_MOUSE	44.94	16	427	NA	NA
ARPDDEVGPAVAPGHPL	B2RXV4|FLVC1_MOUSE	48.03	17	90.7	NA	NA
ARQQVRSPVTNIAR	P84091|AP2M1_MOUSE	48.69	14	11000	NA	11400
ARQQVRSPVTNIARTS	P84091|AP2M1_MOUSE	45.75	16	4610	NA	4370
ARVLEM(+15.99)VEPLVTRTRDR	Q61268|APOC4_MOUSE	36.29	17	294	NA	NA
ARYIYGKPVQGVAYT	P01029|CO4B_MOUSE	47.97	15	233	NA	107
ARYIYGKPVQGVAYTR	P01029|CO4B_MOUSE	49.82	16	782	NA	1300
ARYIYGKPVQGVAYTRF	P01029|CO4B_MOUSE	49.27	17	95.7	NA	NA
ARYRPRAPIIAVTRNP	P52480|KPYM_MOUSE	36.4	16	543	NA	NA
ARYRPRAPIIAVTRNPQ	P52480|KPYM_MOUSE	46.28	17	249	NA	680
ASAGLLGAHAAAITAY	P01029|CO4B_MOUSE	40.97	16	118	NA	NA
ASAYYNPGNPHNVY	P97765|WBP2_MOUSE	46.05	14	214	NA	227
ASAYYNPGNPHNVYM(+15.99)PT	P97765|WBP2_MOUSE	49.85	17	9780	55.7	4990
ASAYYNPGNPHNVYMPT	P97765|WBP2_MOUSE	49.86	17	4120	NA	7510
ASDPKYATPQVIQAPGPR	O54967|ACK1_MOUSE	49.81	18	685	NA	1480
ASERYVPTYSVPALQ	Q9D956|MALD3_MOUSE	28.49	15	488	NA	390
ASGVVSGPAAAPAAQ	P46938|YAP1_MOUSE	26.18	15	150	NA	NA
ASGVVSGPAAAPAAQH	P46938|YAP1_MOUSE	31.22	16	542	NA	NA
ASGVVSGPAAAPAAQHL	P46938|YAP1_MOUSE	37.13	17	177	NA	NA
ASIYQSVVINTSKE	P97872|FMO5_MOUSE	47.95	14	879	NA	679
ASIYSPPAAAAAAA	P70297|STAM1_MOUSE	46.37	14	1280	NA	997
ASIYSPPAAAAAAAA	P70297|STAM1_MOUSE	39.66	15	177	NA	66.1
ASKAKVTKPKTPAKPKKAAPKK	P43275|H11_MOUSE	49.95	22	431	NA	NA

ASKAKVTKPKTPAKPKKAAPKKK	P43275|H11_MOUSE	49.95	23	480	NA	NA
ASKPKASKPKATKAKKAAPRKK	P43277|H13_MOUSE	49.95	22	745	NA	1910
ASKPKATKAKKAAPR	P43277|H13_MOUSE	48.93	15	333	1000	4030
ASKPKATKAKKAAPRK	P43277|H13_MOUSE	49.94	16	292	NA	866
ASKPKATKAKKAAPRKK	P43277|H13_MOUSE	49.94	17	8790	NA	14100
ASKPKKAKTVKPKAKSSAKRASKK	P10922|H10_MOUSE	49.95	24	1050	NA	905
ASKPKKAKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.95	25	4010	2260	NA
ASKPKVTKPKTAKPKAAKAKKAVSKKK	P43276|H15_MOUSE	49.95	27	8160	8190	3110
ASLVYENASAIM(+15.99)AHE	E9Q0N2|PTPRH_MOUSE	48.34	15	1170	53.1	855
ASLVYENASAIM(+15.99)AHES	E9Q0N2|PTPRH_MOUSE	49.55	16	535	NA	641
ASLVYENASAIM(+15.99)AHESE	E9Q0N2|PTPRH_MOUSE	49.24	17	517	NA	NA
ASLVYENASAIMAHE	E9Q0N2|PTPRH_MOUSE	48.66	15	926	NA	1260
ASLVYENASAIMAHES	E9Q0N2|PTPRH_MOUSE	48.53	16	961	NA	1910
ASLVYENASAIMAHESE	E9Q0N2|PTPRH_MOUSE	49.74	17	940	NA	1380
ASPAPSTRVITNQYNSPTGLYSSENISNF	O70400|PDLI1_MOUSE	49.88	32	76.8	NA	284
ASPELTSPLANQSL	Q8CHY3|DYM_MOUSE	36.39	14	406	NA	263
ASPPPYAAYATPTPEVYG	Q9QZC7|PKHB2_MOUSE	48.16	18	227	NA	NA
ASPPPYAAYATPTPEVYGYG	Q9QZC7|PKHB2_MOUSE	49.88	20	558	NA	1080
ASRQYIPPGFPGPPGPPG	A6X935|ITIH4_MOUSE	48.23	18	104	NA	NA
ASVATNPIITPVAQENQ	P08226|APOE_MOUSE	49.68	17	944	NA	738
ASYEFVQRL	Q9JHU4|DYHC1_MOUSE	36.33	9	315	NA	115
ASYLLAALGGNSSPSAKDIKK	P99027|RLA2_MOUSE	49.72	21	58.1	NA	NA
ATDDVFSPSHAIPI	Q91ZH7|ABHD3_MOUSE	43.94	14	114	NA	NA
ATDDVFSPSHAIPIE	Q91ZH7|ABHD3_MOUSE	47.57	15	374	NA	217
ATDDVFSPSHAIPIET	Q91ZH7|ABHD3_MOUSE	49.25	16	3120	NA	2160
ATDDVFSPSHAIPIETA	Q91ZH7|ABHD3_MOUSE	49.15	17	536	NA	369
ATDDVFSPSHAIPIETAK	Q91ZH7|ABHD3_MOUSE	49.52	18	17.9	NA	NA
ATKAKKAAPR	P43277|H13_MOUSE	43.09	10	685	2220	3420
ATKAKKAAPRKK	P43277|H13_MOUSE	46.15	12	1910	NA	NA
ATKAKKAPKSPAKAK	P43274|H14_MOUSE	47.61	15	928	NA	1990
ATLEIKGPQADLID	Q8CAS9|PARP9_MOUSE	30.54	14	378	NA	326
ATLEIKGPQADLIDA	Q8CAS9|PARP9_MOUSE	36.61	15	940	NA	579
ATLEIKGPQADLIDAV	Q8CAS9|PARP9_MOUSE	31.27	16	1250	NA	NA
ATNPIITPVAQEN	P08226|APOE_MOUSE	41.36	13	435	NA	232
ATNPIITPVAQENQ	P08226|APOE_MOUSE	45.99	14	17500	548	12300
ATPAPSAPAAASATSPSPAPS	Q9JKV1|ADRM1_MOUSE	38.96	21	188	NA	195
ATPKKAAKPKKAASKAPSKKPKA	P10922|H10_MOUSE	36.55	23	796	NA	NA
ATPKKAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.94	26	258	NA	430
ATPKKAKKPKVVKVKPVKASKPKKAKTV	P10922|H10_MOUSE	49.95	33	1790	NA	NA
ATPKKTAKKTPKKAKKPA	P43277|H13_MOUSE	49.94	18	2240	3320	5610
ATPSTNPFVAATGPSAASSTNPFQ	Q8K2K6|AGFG1_MOUSE	49.94	24	140	NA	491
ATRYLAPTILTDVDPN	P47740|AL3A2_MOUSE	49.75	16	300	NA	NA
ATSSHASPTPVAAATPL	Q8CI51|PDLI5_MOUSE	47.3	17	504	NA	515
ATVSWRAPTAQVES	Q80YX1|TENA_MOUSE	47.89	14	1650	NA	998
ATVSWRAPTAQVESFR	Q80YX1|TENA_MOUSE	49.92	16	3790	NA	2370
ATYKLSAPWVEQEGP	P14432|HA1T_MOUSE	49.21	15	954	NA	1040
ATYKLSAPWVEQEGPE	P14432|HA1T_MOUSE	49.9	16	8980	87.9	8400
AVDALASSHPLSSPA	P97449|AMPN_MOUSE	46.09	15	1660	NA	336
AVDALASSHPLSSPAD	P97449|AMPN_MOUSE	48.26	16	606	NA	105
AVDALASSHPLSSPADE	P97449|AMPN_MOUSE	49.62	17	277	NA	NA
AVDVFFPPEAQND	Q68FD5|CLH1_MOUSE	41.28	13	2260	NA	1120
AVDVFFPPEAQNDF	Q68FD5|CLH1_MOUSE	36.93	14	1140	NA	515
AVDVFFPPEAQNDFP	Q68FD5|CLH1_MOUSE	45.27	15	1550	NA	1280
AVDVFFPPEAQNDFPV	Q68FD5|CLH1_MOUSE	48.1	16	3140	NA	3990
AVEQPSTSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	47.53	23	244	NA	405
AVGKVIPELNGKLTGM(+15.99)AFRVPTI	P16858|G3P_MOUSE	49.8	26	174	NA	NA
AVGKVIPELNGKLTGM(+15.99)AFRVPTI	P16858|G3P_MOUSE	49.86	29	3670	NA	11200
AVGKVIPELNGKLTGMAFRVPTPNVSVV	P16858|G3P_MOUSE	49.95	29	2590	NA	13800
AVIFNFPGTRNEVIPM(+15.99)	Q9D304|RN128_MOUSE	48.18	16	1560	NA	NA
AVKPKAAKPKVAKAKKVAAKK	P15864|H12_MOUSE	35.81	21	1300	NA	NA
AVKPKAAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	22	214	NA	NA
AVKSKYKASIAALEAK	Q8VDD5|MYH9_MOUSE	49.91	16	2720	NA	1780
AVKSKYKASIAALEAKI	Q8VDD5|MYH9_MOUSE	49.49	17	2370	NA	4900
AVKTTYKDSLSHTAFPS	Q2EMV9|PAR14_MOUSE	47.98	17	1070	NA	439
AVKVSWRSPVPNKQHG	Q64487|PTPRD_MOUSE	44.17	16	1090	NA	1530
AVSEGTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8CGP0|H2B3E	49.68	16	113	393	NA
AVTM(+15.99)LSAPEALTEEE	Q62393|TPD52_MOUSE	37.55	15	101	NA	NA
AVTM(+15.99)LSAPEALTEEEQ	Q62393|TPD52_MOUSE	41.91	16	377	NA	NA
AVVNYETGKVIATKY	Q9D309|FAM3B_MOUSE	47.81	15	146	NA	105
AVYEHPSVLSPNPL	Q8CIF4|BTD_MOUSE	48.44	14	334	NA	118
AVYEHPSVLSPNPLE	Q8CIF4|BTD_MOUSE	48.56	15	90.4	NA	NA
AVYETPTAHNGAKNPR	Q9QZ06|TOLIP_MOUSE	42.84	16	463	NA	NA
AVYHTSSM(+15.99)LPAPP	P70665|SIAE_MOUSE	27.35	13	980	NA	361
AVYHTSSMLPAPP	P70665|SIAE_MOUSE	37.01	13	327	NA	NA
AYPAGSPGYNPPQM(+15.99)NTLP	Q8K419|LEG4_MOUSE	44.08	18	292	NA	NA
AYPNTPYISPVASYSGQPQ	Q3UPL0|SC31A_MOUSE	49.8	19	376	NA	3690
AYTIPFYTPIPNG	O08573|LEG9_MOUSE	43.21	13	641	NA	712

AYVVALGSLVPSSR	P97499|TEP1_MOUSE	25.77	14	109	NA	NA
C(+57.02)(+42.01)QASQLSQKVC(+57.02	A2ARP1|VIP1_MOUSE	25.86	23	201	NA	NA
C(+57.02)(+42.01)RHNY(+79.97)EGPETH	P14483|HB2A_MOUSE	40.18	15	13300	NA	12400
C(+57.02)RHN(+15.00)YEGPETHTSLR	P14483|HB2A_MOUSE	49.34	15	2180	NA	3160
D(+42.01)AFYDRIETILLN(+15.00)GTDRK	Q91ZX7|LRP1_MOUSE	43.06	29	1000	NA	NA
D(+42.01)LSQ(+15.00)HATPLPTPAVLPG	O88746|TOM1_MOUSE	37.03	17	15500	NA	NA
D(+42.01)LSQ(+15.00)HATPLPTPAVLPG	O88746|TOM1_MOUSE	36.72	21	35	NA	NA
DAADKAAVVKFHPIQGHRVEVKKAVPKE	Q9CX86|ROA0_MOUSE	49.95	28	260	NA	NA
DADFSYRGPAGSIEQGPY	Q99LI2|CLCC1_MOUSE	49.88	18	266	NA	165
DAEYWNSQPEILER	P14483|HB2A_MOUSE:P01921|HB2D_M	49.78	14	405	NA	NA
DAFVLKTPSAAYL	P13020|GELS_MOUSE	48.19	13	128	NA	NA
DAGNAFKKADPQEAIN	Q9DB05|SNAA_MOUSE	41.95	16	596	NA	260
DAIKNNSFYGPEVKIEKGDL	Q00519|XDH_MOUSE	49.89	20	333	NA	NA
DAPAEAQAAM(+15.99)EEPVVQPSVVDI	Q9DBG5|PLIN3_MOUSE	49.95	22	378	NA	294
DAPAEAQAAMEEPVVQPSVVDR	Q9DBG5|PLIN3_MOUSE	49.95	22	66.3	NA	85
DARSYAAAVANRAK	Q8K296|MTMR3_MOUSE	48.21	14	4760	NA	3890
DARSYAAAVANRAKG	Q8K296|MTMR3_MOUSE	44.6	15	764	NA	1290
DARSYAAAVANRAKGG	Q8K296|MTMR3_MOUSE	45.34	16	1370	NA	1350
DARSYAAAVANRAKGGG	Q8K296|MTMR3_MOUSE	47.77	17	9720	NA	6500
DARSYTAAVANRA	Q91XS1|MTMR4_MOUSE	48.06	13	6590	NA	4360
DARSYTAAVANRAK	Q91XS1|MTMR4_MOUSE	47.02	14	25400	896	19800
DARSYTAAVANRAKG	Q91XS1|MTMR4_MOUSE	46.53	15	10400	155	5790
DARSYTAAVANRAKGG	Q91XS1|MTMR4_MOUSE	48.38	16	17600	420	13400
DARSYTAAVANRAKGGG	Q91XS1|MTMR4_MOUSE	49.93	17	86000	2710	49900
DASTPPSPKVTYKAPVPTGEVYFA	P35564|CALX_MOUSE	46.39	24	153	NA	NA
DATLYVPSAPLSGP	Q60928|GGT1_MOUSE	40.12	14	1220	NA	720
DATLYVPSAPLSGPV	Q60928|GGT1_MOUSE	43.86	15	668	NA	476
DAVSKKTFPTVNPTTGEVIGHVA	Q9CZS1|AL1B1_MOUSE	49.2	23	199	NA	NA
DDAPRAVFPSIVG	P63260|ACTG_MOUSE:P60710|ACTB_M	28.93	13	917	NA	160
DDAPRAVFPSIVGRPRHQ	P63260|ACTG_MOUSE:P60710|ACTB_M	49.63	18	98.1	NA	NA
DDDVYRAPPIDRSILPT	Q8BGD9|IF4B_MOUSE	48.64	17	752	NA	130
DDFEPYLSPQARPNN	Q91YT7|YTHD2_MOUSE	49.04	15	712	NA	398
DDFEPYLSPQARPNNA	Q91YT7|YTHD2_MOUSE	49.44	16	109	NA	NA
DDGHGGYKPFQNPVPNQSPS	P16382|IL4RA_MOUSE	48.76	20	951	NA	3800
DDGHGGYKPFQNPVPNQSPSS	P16382|IL4RA_MOUSE	49.38	21	600	NA	1300
DDHKLSLDELHRKYG	Q8VDN2|AT1A1_MOUSE	46.07	15	228	NA	173
DDIEADHVG	P14434|HA2B_MOUSE:P01910|HA2K_M	30.37	9	976	NA	379
DDKDKKKKYEPPVPTRVGKK	P62192|PRS4_MOUSE	49.67	20	468	NA	NA
DDLKYKKPTALPAP	Q8VE04|MOB3B_MOUSE	48.68	14	1270	NA	NA
DDLKYKKPTALPAPQ	Q8VE04|MOB3B_MOUSE	49.82	15	1610	NA	416
DDRIAEGTFPGKI	P56391|CX6B1_MOUSE	32.29	13	1710	NA	NA
DDTYQSYSSPSPRVSRFK	Q60997|DMBT1_MOUSE	45.4	18	173	NA	1050
DDVFSPSHAIPIE	Q91ZH7|ABHD3_MOUSE	42.46	13	52.4	NA	NA
DDVFSPSHAIPIET	Q91ZH7|ABHD3_MOUSE	48.76	14	813	NA	NA
DDVFSPSHAIPIETA	Q91ZH7|ABHD3_MOUSE	48.23	15	173	NA	NA
DEAKERASFITPVPGGVG	Q922D8|C1TC_MOUSE	44.62	18	538	NA	1340
DEATRYLAPTIL	P47740|AL3A2_MOUSE	40.22	12	538	NA	218
DEATRYLAPTILT	P47740|AL3A2_MOUSE	35.65	13	650	NA	216
DEATRYLAPTILTDVD	P47740|AL3A2_MOUSE	48.73	16	739	NA	NA
DEATRYLAPTILTDVDPN	P47740|AL3A2_MOUSE	49.55	18	28900	NA	8640
DEELIYHKVTAAELQ	Q4PZA2|ECE1_MOUSE	40.2	15	81.9	NA	NA
DEGERYIAPTVL	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	39.01	12	1790	NA	1650
DEGERYIAPTVLVD	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	40.51	14	1590	NA	NA
DEGERYIAPTVLVDVQE	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	49.7	17	5880	NA	4310
DEGKLLEAKGPVTDVAYSHDG	O88342|WDR1_MOUSE	42.34	21	467	NA	NA
DEIDAALPNKAP	Q64464|CP3AD_MOUSE	42.01	12	1900	NA	1150
DEIDAALPNKAPA	Q64464|CP3AD_MOUSE	45.45	13	1070	NA	1000
DEIDAALPNKAPAT	Q64464|CP3AD_MOUSE	46.73	14	1050	NA	702
DEIQRYQKPVVAAIQG	Q9DBM2|ECHP_MOUSE	49.74	16	3490	NA	6140
DEKKGPLIVSGPDGAPAKGDG	Q8VBW1|SC6A8_MOUSE	49.89	21	4890	NA	7850
DESGFPKPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	49.94	22	5220	NA	1410
DESGFPKPPSYNVATTLPSYDEA	Q8R0W6|NFIP1_MOUSE	49.95	23	5290	NA	2940
DFHYAASKALRVPA	Q80TA9|EPG5_MOUSE	49.75	14	143	NA	620
DFIYHEAVPALDTL	Q6PB44|PTN23_MOUSE	44.65	14	68.4	NA	NA
DFKPSYGTPAPGFSS	P23249|MOV10_MOUSE	44.12	15	350	NA	407
DFKPSYGTPAPGFSSM(+15.99)	P23249|MOV10_MOUSE	48.28	16	498	NA	610
DFLKKWETPSQNTAQ	P05132|KAPCA_MOUSE	25.84	15	82	NA	NA
DFNTPRPSTVEA	G3X939|SL9A3_MOUSE	42.9	12	335	NA	NA
DFPSVVVVGLGKRS	Q9CPY7|AMPL_MOUSE	47.93	14	350	91.6	351
DFPSVVVVGLGKRSAG	Q9CPY7|AMPL_MOUSE	48.37	16	696	520	1390
DFYGSPIPSVSLK	Q9Z0M6|AGRE5_MOUSE	49.54	13	39.9	NA	NA
DGDM(+15.99)RLVNGASANEGRVE	Q07797|LG3BP_MOUSE	46.11	18	656	NA	NA
DGDMRLVNGASANEGRVE	Q07797|LG3BP_MOUSE	47.14	18	614	NA	NA
DGDSVVFAGPAGNSVET	Q8R146|ACPH_MOUSE	44.71	17	1150	NA	201
DGDSVVFAGPAGNSVETR	Q8R146|ACPH_MOUSE	49.37	18	3990	NA	2920
DGDSYRSPWSNKYD	P47757|CAPZB_MOUSE	49.7	14	782	NA	362
DGDSYRSPWSNKYDPP	P47757|CAPZB_MOUSE	49.88	16	44700	310	38500

DGDSYRSPWSNKYDPPL	P47757|CAPZB_MOUSE	49.16	17	50900	551	46300
DGEEAGAYDGPRTADGIV	P27773|PDIA3_MOUSE	49.64	18	351	NA	NA
DGEEAGAYDGPRTADGIVS	P27773|PDIA3_MOUSE	49.93	19	2580	NA	492
DGELTYENVQVSPVPGGPP	P21855|CD72_MOUSE	48.99	19	800	NA	NA
DGELTYENVQVSPVPGGPPG	P21855|CD72_MOUSE	49.53	20	1840	208	785
DGEQAPPLPIKTPIPTPST	Q7TQH7|LRP10_MOUSE	49.93	19	650	NA	592
DGKGM(+15.99)NPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.87	21	121	NA	167
DGKKRKRSRKESYSVYVYKVLKQ	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.92	23	138	NA	NA
DGKKRKRSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.95	27	23700	38500	3300
DGLLSYTAPVGQTM(+15.99)Q	Q03146|DDR1_MOUSE	46.11	15	820	NA	361
DGLLSYTAPVGQTM(+15.99)QL	Q03146|DDR1_MOUSE	47.41	16	3690	NA	2380
DGLLSYTAPVGQTMQL	Q03146|DDR1_MOUSE	49.58	16	299	NA	322
DGNHTLFH	P43023|CX6A2_MOUSE:P43024|CX6A1_	43.1	8	987	312	737
DGNHTLFHNPHVN	P43023|CX6A2_MOUSE:P43024|CX6A1_	47.19	13	118	NA	723
DGNHTLFHNPHVNPL	P43023|CX6A2_MOUSE:P43024|CX6A1_	47.14	15	347	NA	815
DGNHTLFHNPHVNPLP	P43023|CX6A2_MOUSE:P43024|CX6A1_	47.86	16	818	NA	NA
DGNHTLFHNPHVNPLPT	P43023|CX6A2_MOUSE:P43024|CX6A1_	49.33	17	6930	NA	7530
DGNHTLFHNPHVNPLPTG	P43023|CX6A2_MOUSE:P43024|CX6A1_	49.31	18	2420	NA	4170
DGNHTLFHNPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	49.22	20	2540	769	3350
DGPSTSSAHLAPVASSSVSYDPRKP	Q8CB77|ELOA1_MOUSE	49.65	25	185	NA	1140
DGPSTSSAHLAPVASSSVSYDPRKPA	Q8CB77|ELOA1_MOUSE	48.17	26	372	NA	559
DGQINYQAASPDEGAL	Q148W0|AT8B1_MOUSE	43.54	16	476	NA	251
DGREVSSVEAPSVSPA	Q8BUJ9|LRP12_MOUSE	36	16	163	NA	NA
DGREVSSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	47.51	17	964	NA	894
DGREVSSVEAPSVSPARHQ	Q8BUJ9|LRP12_MOUSE	49.82	19	480	NA	327
DGRFVM(+15.99)GPTVAPSQEK	Q05BQ1|TUTLA_MOUSE	47.49	16	297	NA	238
DGRFVMGPTVAPSQ	Q05BQ1|TUTLA_MOUSE	43.37	14	85.4	NA	143
DGTVPFWAHAGNAIPSADQ	Q9D0F3|LMAN1_MOUSE	25.93	19	595	NA	264
DHLTYGISGPNASY	E9Q7P9|CDHR2_MOUSE	45.87	14	119	NA	NA
DHLTYGISGPNASYF	E9Q7P9|CDHR2_MOUSE	49.66	15	516	NA	211
DHLTYGISGPNASYFS	E9Q7P9|CDHR2_MOUSE	47.8	16	2630	NA	NA
DHNFPYKDPVAALYED	P16301|LCAT_MOUSE	48.71	16	4920	NA	1450
DHNFPYKDPVAALYEDG	P16301|LCAT_MOUSE	49.84	17	4500	NA	1860
DHNPLYPGSPPPGGYGQPSVLPGGYPA	Q8BJZ3|LFG3_MOUSE	49.95	27	4280	NA	1270
DHVDFSQPEPHTVL	Q9QUR8|SEM7A_MOUSE	49.82	14	1420	NA	694
DHVDFSQPEPHTVLF	Q9QUR8|SEM7A_MOUSE	49.76	15	10100	NA	6740
DHVDFSQPEPHTVLFH	Q9QUR8|SEM7A_MOUSE	49.89	16	2080	NA	374
DIDTAAKFIGAG	P56383|AT5G2_MOUSE:Q9CR84|AT5G1	42.39	12	37.6	NA	NA
DIELFAGKLKEVQARNSHKKTKLGRKKK	Q91WL0|ES8L3_MOUSE	49.95	31	630	NA	NA
DIEVAPPKAHEVR	P00329|ADH1_MOUSE	42.38	13	2980	NA	2160
DIEVAPPKAHEVRIK	P00329|ADH1_MOUSE	46.75	15	1300	NA	1030
DIEVAPPKAHEVRIKM(+15.99)	P00329|ADH1_MOUSE	36.47	16	122	NA	NA
DIFIGPKAEEH	P61164|ACTZ_MOUSE	27.57	11	134	NA	NA
DIFIGPKAEEHR	P61164|ACTZ_MOUSE	37.23	12	2250	NA	1250
DIFIGPKAEEHRG	P61164|ACTZ_MOUSE	39.87	13	4490	NA	2810
DIHIVYIRKKKPKPP	Q8C436|MT21D_MOUSE	48.27	15	577	NA	NA
DIKSFITSIANKN	Q8CHR6|DPYD_MOUSE	47.94	13	169	NA	230
DIPGVRFKVVKVANVSLLALYKGKKERP	P62267|RS23_MOUSE	49.95	29	1300	NA	3600
DIPGVRFKVVKVANVSLLALYKGKKERP	P62267|RS23_MOUSE	49.81	30	3540	NA	3040
DIQTVFNGPFAHKEGPN	Q62181|SEM3C_MOUSE	46.67	17	1070	NA	574
DIYQAPSADSADH	P26361|CFTR_MOUSE	32.26	13	1430	NA	435
DIYQAPSADSADHL	P26361|CFTR_MOUSE	37.08	14	676	NA	567
DKDFLVGPHISLADL	Q64471|GSTT1_MOUSE	49.25	15	198	NA	NA
DKDKKKKYEPPVPTRVGKK	P62192|PRS4_MOUSE	49.94	19	779	NA	952
DKEFHAPLIIDE	Q91YN5|UAP1_MOUSE	39.43	12	67.1	NA	NA
DKEFHAPLIIDEN	Q91YN5|UAP1_MOUSE	44.49	13	450	NA	NA
DKEFHAPLIIDENG	Q91YN5|UAP1_MOUSE	47.1	14	1360	NA	287
DKEKVIVDFSSPNIAKE	Q9D0I9|SYRC_MOUSE	29.83	17	177	NA	NA
DKIIYQAASPDEGAL	P70704|AT8A1_MOUSE	41.48	15	144	NA	NA
DKIYFAFPLANHRK	Q3UUQ7|PGAP1_MOUSE	44.84	14	312	NA	115
DKKKKYEPPVPTRVGKK	P62192|PRS4_MOUSE	49.66	17	2510	NA	2430
DKNGNPLNSVFVAPAVTPVKGVL	P70158|ASM3A_MOUSE	26.84	23	184	NA	NA
DKNIVFSPLSISA	Q03734|SPA3M_MOUSE:Q91WP6|SPA3	44.86	13	98.3	NA	NA
DKNIVFSPLSISAA	Q03734|SPA3M_MOUSE:Q91WP6|SPA3	44.75	14	2090	NA	198
DKNIVFSPLSISAAL	Q03734|SPA3M_MOUSE:Q91WP6|SPA3	48.75	15	400	NA	NA
DKNIVFSPLSISAALA	Q03734|SPA3M_MOUSE:Q91WP6|SPA3	46.33	16	3530	NA	NA
DKYEPAAVSEHGDK	Q8VDN2|AT1A1_MOUSE	47.76	14	1430	NA	459
DLEYQMSTTARAKR	Q02257|PLAK_MOUSE	31	14	188	NA	419
DLFIGPKAEEH	Q8R5C5|ACTY_MOUSE	27.57	11	134	NA	NA
DLFIGPKAEEHR	Q8R5C5|ACTY_MOUSE	37.23	12	2250	NA	1250
DLFIGPKAEEHRG	Q8R5C5|ACTY_MOUSE	39.87	13	4490	NA	2810
DLLTQYSTPEGSSVPI	E9Q414|APOB_MOUSE	36.91	16	124	NA	421
DLLYSFPVVIKNK	P14152|MDHC_MOUSE	48.48	13	3320	NA	1630
DLLYSFPVVIKNKT	P14152|MDHC_MOUSE	49.87	14	3880	NA	2830
DLNFFNQKKKKKKTKK	Q99L45|IF2B_MOUSE	45.45	16	306	NA	304
DLNFRNPAVQEE	Q91WV7|SLC31_MOUSE	42.37	12	247	NA	NA
DLNFRNPAVQEEIK	Q91WV7|SLC31_MOUSE	46	14	3360	NA	942

DLPTTFQGATASTSYG	Q9JJZ4|UB2J1_MOUSE	32.28	16	131	NA	272
DLQHGSLFLKTPKIVSSKD	P06151|LDHA_MOUSE	49.93	19	551	NA	439
DLQHGSLFLKTPKIVSSKDY	P06151|LDHA_MOUSE	49.89	20	565	NA	588
DLRHAFSPVASVESA	P29699|FETUA_MOUSE	49.4	15	644	NA	654
DLRHAFSPVASVESAS	P29699|FETUA_MOUSE	49.84	16	1100	NA	638
DLRHAFSPVASVESASG	P29699|FETUA_MOUSE	49.88	17	2840	NA	1100
DLRHAFSPVASVESASGET	P29699|FETUA_MOUSE	49.94	19	1490	NA	NA
DLSEGFSSPSSLM(+15.99)SPSTPS	Q9D2V7|CORO7_MOUSE	45.64	19	289	NA	NA
DLSFIHPKALSGLK	A2ARI4|LGR4_MOUSE	42.16	14	110	NA	NA
DLSFIHPKALSGLKE	A2ARI4|LGR4_MOUSE	45.99	15	496	NA	NA
DLSQHATPLPTPAV	O88746|TOM1_MOUSE	46.27	14	330	NA	196
DLSQHATPLPTPAVL	O88746|TOM1_MOUSE	49.39	15	104	NA	NA
DLSQHATPLPTPAVLP	O88746|TOM1_MOUSE	47.37	16	87.9	NA	NA
DLSQHATPLPTPAVLPG	O88746|TOM1_MOUSE	49.82	17	5450	NA	2560
DLTGGYRYPRALEEEV	Q8K3K8|OPTN_MOUSE	25.39	16	11400	NA	22700
DLTGGYRYPRALEEEVE	Q8K3K8|OPTN_MOUSE	29.22	17	21200	NA	NA
DLTGGYRYPRALEEEVEK	Q8K3K8|OPTN_MOUSE	35.83	18	4690	NA	NA
DLVEVNPHLATS	O08691|ARGI2_MOUSE	29.8	12	283	NA	NA
DLVEVNPHLATSE	O08691|ARGI2_MOUSE	36.37	13	188	NA	NA
DM(+15.99)FKASLVIPSKD	Q8BJD1|ITIH5_MOUSE	38.05	13	495	NA	159
DM(+15.99)RQTVAVGVIKAVDKKAAGAG	P10126|EF1A1_MOUSE	49.95	23	1490	965	2150
DM(+15.99)RQTVAVGVIKAVDKKAAGAG	P10126|EF1A1_MOUSE	49.76	25	939	NA	NA
DMFKASLVIPSKD	Q8BJD1|ITIH5_MOUSE	43.28	13	205	NA	170
DMRQTVAVGVIKAVDKKAAGAGK	P10126|EF1A1_MOUSE	49.94	23	808	NA	2570
DNDFIYHEAVPALDTL	Q6PB44|PTN23_MOUSE	47.38	16	187	NA	NA
DNDHLTYGISGPNASYFS	E9Q7P9|CDHR2_MOUSE	49.88	18	177	NA	NA
DNDNIFLSPLSIST	P32261|ANT3_MOUSE	41.43	14	147	NA	69.8
DNDNIFLSPLSISTA	P32261|ANT3_MOUSE	48.5	15	2110	278	1180
DNDNIFLSPLSISTAF	P32261|ANT3_MOUSE	48.34	16	370	NA	NA
DNIFLSPLSISTA	P32261|ANT3_MOUSE	47.47	13	1390	NA	114
DNNTLVFIVDVKANKHQIKQAVKK	P62751|RL23A_MOUSE	49.73	24	728	NA	NA
DNPNYLGPAPLEDIA	Q9CQG1|CHAC2_MOUSE	45.3	15	348	NA	NA
DNQSESSVSTPSASFEPD	Q8VCH8|UBXN4_MOUSE	44.45	18	253	NA	NA
DNVYLVPTPSKTQQGLYQAPGPNPQFQ	Q61140|BCAR1_MOUSE	48.52	27	97	NA	NA
DNYRFAHTNIESLV	P27773|PDIA3_MOUSE	48.19	14	140	NA	90.9
DPAGGQYLTVSAAKAPGGK	Q91V88|NPNT_MOUSE	49.78	19	508	NA	337
DPAGPNFEYAEAPSRLSPDD	P11152|LIPL_MOUSE	49.4	20	2270	NA	NA
DPAGPNFEYAEAPSRLSPDDA	P11152|LIPL_MOUSE	49.67	21	1760	NA	225
DPETGVFTAPLAGRYL	Q99K41|EMIL1_MOUSE	49.1	16	1150	NA	578
DPEVFSQPKVLPSA	Q91YD3|DCP1A_MOUSE	49.73	14	533	NA	308
DPEVFSQPKVLPSAIP	Q91YD3|DCP1A_MOUSE	49.86	16	1960	NA	NA
DPEVFSQPKVLPSAIPI	Q91YD3|DCP1A_MOUSE	49.92	17	304	NA	208
DPGESKSYSYSEVLPTEGPP	Q8BHT7|RGP1_MOUSE	48.27	20	190	NA	NA
DPGESKSYSYSEVLPTEGPPS	Q8BHT7|RGP1_MOUSE	46.69	21	788	NA	427
DPGFGAPAASQVASA	Q6IRU5|CLCB_MOUSE	40.76	15	274	NA	263
DPGFGAPAASQVASAQPG	Q6IRU5|CLCB_MOUSE	47.89	18	848	NA	966
DPGFRSPSTQVANNS	Q6A037|N4BP1_MOUSE	44.87	15	322	NA	NA
DPGFRSPSTQVANNSHQPPP	Q6A037|N4BP1_MOUSE	47.55	20	3840	NA	6620
DPHNVPRILS(+79.97)PGYEATERPR	P10493|NID1_MOUSE	42.08	20	1090	NA	NA
DPIQKYLTPQM(+15.99)ATS	Q6P9J9|ANO6_MOUSE	48.66	14	2240	NA	712
DPIQKYLTPQM(+15.99)ATSIT	Q6P9J9|ANO6_MOUSE	49.85	16	73800	2180	31700
DPIQKYLTPQMATS	Q6P9J9|ANO6_MOUSE	47.6	14	510	NA	644
DPIQKYLTPQMATSIT	Q6P9J9|ANO6_MOUSE	49.84	16	39300	106	30500
DPIQKYLTPQMATSITA	Q6P9J9|ANO6_MOUSE	48.69	17	415	NA	NA
DPKLTYHGFTLEDAASPK	Q62312|TGFR2_MOUSE	47.44	18	2230	NA	1580
DPKTQEFILNSPTVTSIK	Q9R0H0|ACOX1_MOUSE	49.87	18	240	NA	490
DPKYATPQVIQAPG	O54967|ACK1_MOUSE	45.51	14	991	NA	921
DPKYATPQVIQAPGP	O54967|ACK1_MOUSE	49.75	15	608	NA	540
DPKYATPQVIQAPGPR	O54967|ACK1_MOUSE	49.6	16	1420	NA	1430
DPLHYSIVSAPAAQKVR	Q8BH86|GLUCM_MOUSE	49.93	17	133	NA	NA
DPLHYSIVSAPAAQKVRE	Q8BH86|GLUCM_MOUSE	49.92	18	351	NA	133
DPLHYSIVSAPAAQKVREL	Q8BH86|GLUCM_MOUSE	49.94	19	1210	NA	886
DPLTPYLPAHPSS	Q7M758|NALDL_MOUSE	25.72	13	202	NA	NA
DPNTAYASYPSASVEN	O55101|SNG2_MOUSE	48.53	16	109	NA	106
DPNTAYASYPSASVENYQQPP	O55101|SNG2_MOUSE	49.94	21	201	NA	588
DPPALNRVPKKKKM(+15.99)PENFMPPV	Q3UPL0|SC31A_MOUSE	49.84	33	3340	NA	NA
DPPALNRVPKKKKMPENFM(+15.99)PPV	Q3UPL0|SC31A_MOUSE	46	33	3140	NA	NA
DPPALNRVPKKKKMPENFMPPVPITSPII	Q3UPL0|SC31A_MOUSE	44.39	33	462	NA	NA
DPPASVVVGPVVVPR	P29699|FETUA_MOUSE	49.52	15	1170	NA	615
DPPASVVVGPVVVPRGL	P29699|FETUA_MOUSE	49.89	17	1600	NA	1560
DPRTPQDSPM(+15.99)YPVVPVHLDGTP	P97426|ECP1_MOUSE	36.46	22	116	NA	NA
DPSAFAAAAPAAAAT	P14869|RLA0_MOUSE	46.7	15	2730	NA	2550
DPSAFAAAAPAAAATT	P14869|RLA0_MOUSE	49.72	16	2180	73.1	1340
DPSGKVSHTYGDPHVNLVIG	Q80T32|AGRD1_MOUSE	49.94	20	2330	NA	696
DPSGKVSHTYGDPHVNLVIGSE	Q80T32|AGRD1_MOUSE	29.23	22	416	NA	NA
DPSLGIYNSPYIIPGS	P18894|OXDA_MOUSE	49.57	16	505	NA	626
DPSLGIYNSPYIIPGSK	P18894|OXDA_MOUSE	49.83	17	7430	48.4	9780

DPSLGIYNSPYIIPGSKT	P18894|OXDA_MOUSE	49.77	18	6420	NA	7180
DPSM(+15.99)VSAYM(+15.99)YPTGAPG	Q99LI8|HGS_MOUSE	48.07	19	507	NA	162
DPSVTQLTNAPQSGLAE	Q9ERN0|SCAM2_MOUSE	49.3	17	330	NA	NA
DPTFHTPLDLYAY	Q07797|LG3BP_MOUSE	41.5	13	1260	NA	533
DPTFHTPLDLYAYA	Q07797|LG3BP_MOUSE	40.9	14	924	NA	401
DPTFHTPLDLYAYAR	Q07797|LG3BP_MOUSE	46.85	15	27300	275	13400
DPTIRIEPPKSLPSSDK	O88343|S4A4_MOUSE	26.26	17	2060	NA	NA
DPTIRIEPPKSLPSSDKR	O88343|S4A4_MOUSE	48.36	18	2390	NA	NA
DPTPDPNTAYASYPSASVE	O55101|SNG2_MOUSE	49.62	19	2690	NA	2270
DPTPDPNTAYASYPSASVEN	O55101|SNG2_MOUSE	49.93	20	14900	126	13300
DPTPDPNTAYASYPSASVENY	O55101|SNG2_MOUSE	49.94	21	9160	NA	9260
DPTPDPNTAYASYPSASVENYQ	O55101|SNG2_MOUSE	49.95	22	6320	NA	5260
DPTPDPNTAYASYPSASVENYQQPP	O55101|SNG2_MOUSE	49.95	25	2190	NA	3650
DPTTAFQAPDVGQAL	A2ASQ1|AGRIN_MOUSE	48.6	15	6170	247	3110
DPTTAFQAPDVGQALL	A2ASQ1|AGRIN_MOUSE	49.77	16	1440	NA	1070
DPTTAFQAPDVGQALLQ	A2ASQ1|AGRIN_MOUSE	49.82	17	1530	NA	471
DPYDQPNAIYIE	O88307|SORL_MOUSE	26.7	12	136	NA	NA
DPYDQPNAIYIER	O88307|SORL_MOUSE	48.69	13	4520	217	3060
DPYDQPNAIYIERH	O88307|SORL_MOUSE	49.77	14	741	NA	612
DPYQRYHTPTPRDE	Q91XT4|SC16B_MOUSE	35.35	14	710	NA	585
DPYQRYHTPTPRDEYA	Q91XT4|SC16B_MOUSE	48.3	16	7150	NA	8610
DPYQRYHTPTPRDEYAY	Q91XT4|SC16B_MOUSE	41.37	17	357	NA	NA
DPYQRYHTPTPRDEYAYG	Q91XT4|SC16B_MOUSE	46.21	18	262	NA	NA
DQARM(+15.99)PYTNAVIHEVQ	P24456|CP2DA_MOUSE:P24457|CP2DB	48.31	16	691	NA	NA
DQARMPYTNAVIHEVQ	P24456|CP2DA_MOUSE:P24457|CP2DB	49.43	16	682	NA	1090
DQARMPYTNAVIHEVQR	P24456|CP2DA_MOUSE:P24457|CP2DB	49.6	17	692	NA	903
DQFSPYAAPSPQGSYQPS	O55201|SPT5H_MOUSE	35.79	18	122	NA	NA
DQFSPYAAPSPQGSYQPSP	O55201|SPT5H_MOUSE	28.46	19	104	NA	NA
DQGIPQLRIVLLGKTGAGKSS	Q99JY3|GIMA4_MOUSE	47.28	21	212	NA	NA
DQLFSGPLPGRLP	Q60805|MERTK_MOUSE	46.92	13	1410	NA	742
DQLFSGPLPGRLPVNHRPFS	Q60805|MERTK_MOUSE	49.02	20	1210	NA	168
DQNLRPYQGGKANILGYN	Q6XQH0|G3ST2_MOUSE	44.83	18	132	NA	180
DQRDLISNHEQLPILG	P04441|HG2A_MOUSE	40.02	16	109	NA	391
DQTVVEPNIAIQSVTR	Q8BM96|AGRG7_MOUSE	47.97	16	61.4	NA	60
DRDSLVHSSPHVALSH	Q9WV91|FPRP_MOUSE	49.79	16	99	NA	NA
DRDSLVHSSPHVALSHVD	Q9WV91|FPRP_MOUSE	49.94	18	2410	NA	2120
DRDSLVHSSPHVALSHVDT	Q9WV91|FPRP_MOUSE	49.78	19	310	NA	620
DRKIVYEGPELNH	Q91ZX7|LRP1_MOUSE	44.71	13	277	NA	78.6
DRKIVYEGPELNHA	Q91ZX7|LRP1_MOUSE	47.81	14	4870	NA	3790
DRKIVYEGPELNHAF	Q91ZX7|LRP1_MOUSE	49.92	15	4070	NA	2670
DRKIVYEGPELNHAFG	Q91ZX7|LRP1_MOUSE	49.94	16	323000	12800	342000
DRPELTGAKVVVSGGRGLKSGENFK	Q99LC5|ETFA_MOUSE	49.94	25	262	NA	NA
DRPHTYFGPETSAS	P70277|SIA7B_MOUSE	49.39	14	203	NA	NA
DRPHTYFGPETSASK	P70277|SIA7B_MOUSE	48.47	15	9900	177	7540
DRPHTYFGPETSASKF	P70277|SIA7B_MOUSE	49.89	16	11600	NA	11300
DRPHTYFGPETSASKFK	P70277|SIA7B_MOUSE	49.93	17	21100	NA	13500
DRQVWSGSKAAGAPP	Q8K2C7|OS9_MOUSE	43.54	15	2870	NA	789
DRQVWSGSKAAGAPPK	Q8K2C7|OS9_MOUSE	48.79	16	745	NA	759
DRYVASLAARNK	Q00560|IL6RB_MOUSE	36.31	12	174	NA	101
DRYYTPTISRERA	Q9R1P3|PSB2_MOUSE	46.2	13	822	NA	750
DRYYTPTISRERAV	Q9R1P3|PSB2_MOUSE	25.85	14	442	NA	NA
DSDNDHLTYGISGPNASYFS	E9Q7P9|CDHR2_MOUSE	49.82	20	599	NA	NA
DSGGFYISPRSTFSSLQ	P08103|HCK_MOUSE	45.52	17	400	NA	116
DSGNFRPANPNWG	E9PV24|FIBA_MOUSE	47.95	13	479	NA	416
DSGNFRPANPNWGVF	E9PV24|FIBA_MOUSE	49.31	15	373	NA	472
DSGNFRPANPNWGVFS	E9PV24|FIBA_MOUSE	49.49	16	695	NA	632
DSIVLPSGPVAHLALHG	Q8K0B3|LRC66_MOUSE	28.35	17	184	NA	135
DSKSKSDASTPPSPKVTYKAPVPTGEVY	P35564|CALX_MOUSE	49.48	30	198	NA	NA
DSLVHSSPHVALSH	Q9WV91|FPRP_MOUSE	47.36	14	272	NA	896
DSLVHSSPHVALSHVD	Q9WV91|FPRP_MOUSE	49.86	16	7980	50.4	6710
DSLVHSSPHVALSHVDT	Q9WV91|FPRP_MOUSE	49.89	17	800	NA	1070
DSNFGAPSASVAA	O35643|AP1B1_MOUSE	38.13	13	109	NA	NA
DSNFGAPSASVAAAP	O35643|AP1B1_MOUSE	44.89	15	758	NA	511
DSNFGAPSASVAAAPA	O35643|AP1B1_MOUSE	42.82	16	1300	NA	1150
DSNFGAPSASVAAAPAP	O35643|AP1B1_MOUSE	42.35	17	3050	NA	3040
DSNFGAPSASVAAAPAPA	O35643|AP1B1_MOUSE	49.82	18	713	NA	2930
DSNFGAPSASVAAAPAPAR	O35643|AP1B1_MOUSE	49.89	19	1950	NA	1220
DSNFGAPSASVAAAPAPARLG	O35643|AP1B1_MOUSE	49.94	21	1130	NA	327
DSNFGAPSASVAAAPAPARLGAPI	O35643|AP1B1_MOUSE	49.95	24	30.1	NA	NA
DSNFGAPSASVAAAPAPARLGAPIS	O35643|AP1B1_MOUSE	49.94	25	72.5	NA	114
DSNFGAPSASVAAAPAPARLGAPISSGL	O35643|AP1B1_MOUSE	49.94	29	132	NA	NA
DSNPTSGSAANSSFG	Q8R317|UBQL1_MOUSE	44.74	15	180	NA	NA
DSPDVVYSPETIEAR	Q9JHU9|INO1_MOUSE	44.41	15	819	NA	469
DSPDVVYSPETIEARY	Q9JHU9|INO1_MOUSE	49.26	16	200	NA	NA
DSPDVVYSPETIEARYE	Q9JHU9|INO1_MOUSE	49.88	17	2550	NA	1640
DSPNKLYTLVTYVPVTT	P62900|RL31_MOUSE	28.96	17	142	NA	NA
DSQFEFKGPQAAQEQD	Q6RHR9|MAGI1_MOUSE	49.75	16	1410	NA	NA

DSQFEFKGPQAAQEQDF	Q6RHR9|MAGI1_MOUSE	49.92	17	340	NA	NA
DSRTNTAYVGSAILSEET	Q9QZC7|PKHB2_MOUSE	47.93	18	172	NA	267
DSSSPATRKEYHTGKAVTSKGDKELLIG	E9PV24|FIBA_MOUSE	49.95	31	670	NA	90.2
DSVTTDHISPAGNIA	P28271|ACOHC_MOUSE	45.98	15	304	NA	112
DSVTTDHISPAGNIAR	P28271|ACOHC_MOUSE	47.04	16	339	NA	NA
DSVTTDHISPAGNIARN	P28271|ACOHC_MOUSE	49.63	17	198	NA	NA
DSVTTDHISPAGNIARNSP	P28271|ACOHC_MOUSE	49.78	19	240	NA	55.9
DSVTTDHISPAGNIARNSPA	P28271|ACOHC_MOUSE	49.89	20	6390	NA	4610
DSVVFAGPAGNSVE	Q8R146|ACPH_MOUSE	41.56	14	993	NA	589
DSVVFAGPAGNSVET	Q8R146|ACPH_MOUSE	45.38	15	4490	NA	3670
DSVVFAGPAGNSVETR	Q8R146|ACPH_MOUSE	41	16	773	NA	400
DSYRSPWSNKYDPP	P47757|CAPZB_MOUSE	49.79	14	3960	NA	3660
DSYRSPWSNKYDPPL	P47757|CAPZB_MOUSE	49.69	15	294	NA	627
DTEGRLEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	49.89	20	9600	47.9	9180
DTEGRLEVVTDPTTNAGYVKIK	Q9R100|CAD17_MOUSE	49.93	22	934	NA	1190
DTEGRLEVVTDPTTNAGYVKIKKP	Q9R100|CAD17_MOUSE	48.93	24	342	NA	505
DTEGRLEVVTDPTTNAGYVKIKKPLD	Q9R100|CAD17_MOUSE	49.95	26	172	NA	NA
DTGAKKKKKQKK	O70310|NMT1_MOUSE	48.76	13	1810	NA	NA
DTGENPIYKSAVTTVVNPK	P09055|ITB1_MOUSE	49.3	19	94.1	NA	679
DTIEFRGPNGLLV	Q9DCN2|NB5R3_MOUSE	44.54	13	613	NA	243
DTIEFRGPNGLLVY	Q9DCN2|NB5R3_MOUSE	47.52	14	766	NA	529
DTIEFRGPNGLLVYQ	Q9DCN2|NB5R3_MOUSE	46.07	15	17100	NA	10200
DTIEFRGPNGLLVYQG	Q9DCN2|NB5R3_MOUSE	49.28	16	49200	711	28100
DTIEFRGPNGLLVYQGK	Q9DCN2|NB5R3_MOUSE	49.93	17	7210	NA	5960
DTKVVFLSPAVPEEP	B2RXS4|PLXB2_MOUSE	49.26	15	302	NA	81.5
DTKVVFLSPAVPEEPE	B2RXS4|PLXB2_MOUSE	49.9	16	6020	NA	2490
DTKVVFLSPAVPEEPEA	B2RXS4|PLXB2_MOUSE	49.85	17	115	NA	74.3
DTSSKVIQSVANYAKGDL	Q99KY4|GAK_MOUSE	47.54	18	1240	NA	1130
DTSYKPPAGRTAAPE	Q69ZQ1|MYORG_MOUSE	44.25	15	843	NA	468
DTVPLEEPKVISAFSGK	Q4U2R1|HERC2_MOUSE	49.13	17	515	NA	220
DTVTFYKVIPKSKFVLVKF	P57759|ERP29_MOUSE	49.41	19	278	NA	119
DVAIFARGPQAHLVH	P24823|PPBN_MOUSE:P24822|PPBI_M	49	15	12200	313	11600
DVAIFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_M	49.62	16	22200	711	18600
DVAIFARGPQAHLVHGV	P24823|PPBN_MOUSE:P24822|PPBI_M	41.57	17	194	NA	110
DVAIFARGPQAHLVHGVQ	P24823|PPBN_MOUSE:P24822|PPBI_M	49.57	18	21200	NA	19700
DVAIFARGPQAHLVHGVQE	P24823|PPBN_MOUSE:P24822|PPBI_M	49.8	19	50.6	NA	NA
DVDFDFAGPAIHGSAV	Q60930|VDAC2_MOUSE	49.85	16	102	NA	NA
DVGGAYVGPTQNRIL	Q64133|AOFA_MOUSE	35.68	15	265	NA	158
DVLTPVPTGSQE	Q921M4|GOGA2_MOUSE	39.22	12	75.5	NA	NA
DVRRAFLGPFAHKEGP	Q62177|SEM3B_MOUSE	47.46	16	364	NA	6440
DVRRAFLGPFAHKEGPT	Q62177|SEM3B_MOUSE	48.69	17	12200	NA	9620
DVVKAAKKFVS	Q9DB77|QCR2_MOUSE	44.7	11	266	NA	496
DVWGIEGPIDAAFTR	P29788|VTNC_MOUSE	42.92	15	1470	425	NA
DVYVFLGPEPKSVVQ	P70699|LYAG_MOUSE	36.4	15	244	NA	128
DWLRYSPAYAHLVAPG	O09012|PEX5_MOUSE	46.73	16	683	NA	349
DWPTFLNPNVDKAGPA	Q61508|ECM1_MOUSE	47.06	16	375	NA	379
DWQGGVYASPSIAGSRPG	Q8R0X7|SGPL1_MOUSE	49.79	18	452	NA	364
DYFTQLSNNAKE	P06728|APOA4_MOUSE	47.75	12	156	NA	NA
DYKDESGFPKPPSYNVATTLPSYDEA	Q8R0W6|NFIP1_MOUSE	49.32	26	435	NA	NA
DYKDESGFPKPPSYNVATTLPSYDEAE	Q8R0W6|NFIP1_MOUSE	49.95	27	241	NA	NA
DYKGSTSHSLPYE	E9Q414|APOB_MOUSE	45.45	13	489	NA	NA
DYLAVFDGPSTNSR	Q9JLB4|CUBN_MOUSE	48.07	14	1950	NA	1110
DYLAVFDGPSTNSRL	Q9JLB4|CUBN_MOUSE	45.7	15	952	NA	522
DYLAVFDGPSTNSRLI	Q9JLB4|CUBN_MOUSE	47.91	16	382	NA	256
DYNSPEAGNIF	B2RXV4|FLVC1_MOUSE	38.64	11	589	NA	NA
DYPFKPPKVAFTTR	P61079|UB2D3_MOUSE:P62838|UB2D2_	47.99	14	63.1	NA	229
DYSAPNPIKVTHR	Q8CFG0|SULF2_MOUSE	46.79	13	407	NA	966
E(+42.01)LC(+57.02)FAYNQSAGNPN	Q62470|ITA3_MOUSE	31.3	14	756	NA	NA
EAAASAYYNPGNPHNVYM(+15.99)PT	P97765|WBP2_MOUSE	49.92	20	350	NA	398
EAASTIYGPHTLSAYIQ	Q9JHE3|ASAH2_MOUSE	49.32	17	768	NA	378
EAGAYDGPRTADGIV	P27773|PDIA3_MOUSE	40.17	15	429	NA	246
EAGAYDGPRTADGIVS	P27773|PDIA3_MOUSE	42.99	16	211	NA	NA
EALVGPEANVGPYG	O09159|MA2B1_MOUSE	44.52	14	254	NA	NA
EAQAAM(+15.99)EEPVVQPSVVDR	Q9DBG5|PLIN3_MOUSE	49.75	18	351	NA	190
EATRYLAPTILTDVD	P47740|AL3A2_MOUSE	47.98	15	116	NA	NA
EATRYLAPTILTDVDPN	P47740|AL3A2_MOUSE	49.88	17	6520	46.4	2810
EATSQELVRAPTAALSPEPQ	D3YXK2|SAFB1_MOUSE:Q80YR5|SAFB	48.9	20	170	NA	167
EATSQELVRAPTAALSPEPQDSKEDVKK	D3YXK2|SAFB1_MOUSE:Q80YR5|SAFB	49.95	28	1670	NA	1040
EDDIEADHVG	P14434|HA2B_MOUSE:P01910|HA2K_M	35.74	10	3190	NA	1820
EDDIEADHVGTY	P14434|HA2B_MOUSE	36.2	12	214	NA	NA
EDEDELFQSIMEHNVSY(+79.97)PKSLSI	P20444|KPCA_MOUSE	25.38	24	1950	NA	NA
EDFYGSPIPSVSLK	Q9Z0M6|AGRE5_MOUSE	48.36	14	330	NA	NA
EDGELTYENVQVSPVPGGPPG	P21855|CD72_MOUSE	49.85	21	113	NA	NA
EDGGGWWYNR	Q8K0E8|FIBB_MOUSE	42.94	10	9100	2480	371
EDIEVAPPKAHEVR	P00329|ADH1_MOUSE	48.37	14	21300	237	9970
EDIEVAPPKAHEVRI	P00329|ADH1_MOUSE	45.77	15	453	NA	165
EDIEVAPPKAHEVRIK	P00329|ADH1_MOUSE	49.9	16	6870	NA	4540

EDLSYQSSLASWNYN	Q8R0I0|ACE2_MOUSE	49.28	15	1100	NA	559
EDNVFEAPTLVKVF	Q61490|CD166_MOUSE	49.63	14	908	NA	277
EDRRYNPPIIHQGFQ	P27784|CCL6_MOUSE	44.03	15	18900	NA	21000
EDVAIFARGPQAHLVH	P24823|PPBN_MOUSE:P24822|PPBI_M	48.56	16	4270	NA	4150
EDVAIFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_M	46.36	17	12600	232	11700
EDVAIFARGPQAHLVHGVQ	P24823|PPBN_MOUSE:P24822|PPBI_M	49.45	19	11100	NA	7170
EDWPTFLNPNVDKAGP	Q61508|ECM1_MOUSE	49.91	16	73.1	NA	NA
EDWPTFLNPNVDKAGPA	Q61508|ECM1_MOUSE	49.93	17	1100	NA	915
EDYVELPPSVSQAAKSPP	P26955|IL3RB_MOUSE	34.96	18	2340	209	388
EDYVELPPSVSQAAKSPPG	P26955|IL3RB_MOUSE	42.01	19	2130	190	1280
EEAAAEITRKLEKQEKKRLKKEKKR	Q9D6Z1|NOP56_MOUSE	44.06	25	394	NA	345
EEAGAYDGPRTADGIVS	P27773|PDIA3_MOUSE	48.82	17	615	NA	171
EEEYSAPLPTPAPS	P97467|AMD_MOUSE	48.78	14	338	NA	182
EEEYYAEPGVTEAEP	Q6P6J9|TXD15_MOUSE	48.18	15	248	NA	NA
EEEYYAEPGVTEAEPV	Q6P6J9|TXD15_MOUSE	49.7	16	1670	NA	586
EEFKVPAATSAIIT	P61961|UFM1_MOUSE	35.91	14	74.3	NA	NA
EEFKVPAATSAIITN	P61961|UFM1_MOUSE	44.05	15	190	NA	168
EEFKVPAATSAIITNDG	P61961|UFM1_MOUSE	49.77	17	110	NA	NA
EEIEVAPPKAHEVR	P28474|ADHX_MOUSE	45.2	14	2500	NA	1440
EEIEVAPPKAHEVRIK	P28474|ADHX_MOUSE	48.7	16	526	NA	391
EEKPVPAAPVPSPVAPA	P97825|JUPI1_MOUSE	49.53	17	636	NA	482
EEKPVPAAPVPSPVAPAP	P97825|JUPI1_MOUSE	49.84	18	1140	NA	1000
EEKPVPAAPVPSPVAPAPV	P97825|JUPI1_MOUSE	49.94	19	3210	NA	2400
EEKPVPAAPVPSPVAPAPVP	P97825|JUPI1_MOUSE	49.94	20	20000	457	17600
EEKPVPAAPVPSPVAPAPVPS	P97825|JUPI1_MOUSE	49.94	21	6170	30.2	4210
EEKPVPAAPVPSPVAPAPVPSR	P97825|JUPI1_MOUSE	49.94	22	1600	NA	609
EEKPVPAAPVPSPVAPAPVPSRRNPP	P97825|JUPI1_MOUSE	49.95	26	1490	NA	2400
EEKPVPAAPVPSPVAPAPVPSRRNPPG	P97825|JUPI1_MOUSE	49.93	27	2960	NA	4800
EEKPVPAAPVPSPVAPAPVPSRRNPPG	P97825|JUPI1_MOUSE	49.95	29	1180	NA	197
EEKPVPAAPVPSPVAPAPVPSRRNPPG	P97825|JUPI1_MOUSE	49.94	30	2880	NA	NA
EELKGHLTPRANEL	P06728|APOA4_MOUSE	36.14	14	207	NA	300
EELKGHLTPRANELK	P06728|APOA4_MOUSE	49.46	15	8470	NA	5340
EELKGHLTPRANELKA	P06728|APOA4_MOUSE	40.42	16	1070	NA	154
EELVITPLPSGDVA	Q8BXQ2|PIGT_MOUSE	29.72	14	322	NA	67.4
EELVKDSELSPPTSAPSLVS	Q9WUU8|TNIP1_MOUSE	47.63	20	291	NA	NA
EENFRS(+79.97)NLREVAQM(+15.99)LK	E9Q0S6|TENS1_MOUSE	25.66	17	7860	NA	NA
EEPKKQLVRPDQLPIYTAPPLHSK	Q78IK4|MIC27_MOUSE	49.94	24	233	NA	NA
EEPPVFSRPTVSASYPPY	Q61187|TS101_MOUSE	45.49	18	3080	NA	8940
EEPPVFSRPTVSASYPPYT	Q61187|TS101_MOUSE	32.19	19	723	NA	787
EEQYQDFEARYVQAK	O70228|ATP9A_MOUSE	47.23	15	115	NA	NA
EETAFQTPKPSQTPSVPP	Q8VCB1|NDC1_MOUSE	38.07	18	3770	NA	2920
EETELDQLFSGPLPGRLPVN	Q60805|MERTK_MOUSE	49.95	20	271	NA	NA
EEYEFVSPSSVAIAE	Q99MZ6|MYO7B_MOUSE	37.8	15	635	NA	NA
EEYSAPLPTPAPS	P97467|AMD_MOUSE	48.19	13	1490	NA	1470
EFILNSPTVTSIK	Q9R0H0|ACOX1_MOUSE	32.35	13	183	NA	325
EFQAWKSPGASLL	Q8VC30|TKFC_MOUSE	48.25	13	130	NA	128
EFQAWKSPGASLLPV	Q8VC30|TKFC_MOUSE	49.3	15	7550	NA	8650
EFTFERSNTNPSVT	P22892|AP1G1_MOUSE	29.25	14	47.2	NA	NA
EFVVIAPAAHSDA	Q80UJ7|RB3GP_MOUSE	29.67	13	650	NA	351
EGDIFIGPKAEEHR	P61164|ACTZ_MOUSE	36.57	14	1460	NA	1580
EGDIFIGPKAEEHRG	P61164|ACTZ_MOUSE	47.98	15	4010	NA	2630
EGDLFIGPKAEEHR	Q8R5C5|ACTY_MOUSE	36.57	14	1460	NA	1580
EGDLFIGPKAEEHRG	Q8R5C5|ACTY_MOUSE	47.98	15	4010	NA	2630
EGERYIAPTVL	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	29.68	11	690	NA	562
EGERYIAPTVLVD	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	36.71	13	1450	NA	461
EGERYIAPTVLVDVQ	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	46.83	15	3370	NA	2750
EGERYIAPTVLVDVQE	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	48.37	16	2460	44.7	638
EGFGHLSPTGTTEFWLGNEK	Q8VCM7|FIBG_MOUSE	49.93	20	7100	1540	733
EGHKYVTVVANFGET	P01027|CO3_MOUSE	49.59	15	74	NA	NA
EGKEVRYPVILNAREK	Q6ZQB6|VIP2_MOUSE	40.49	16	753	NA	667
EGPYYVKPVATTAVEG	Q8BJY1|PSMD5_MOUSE	29.25	16	121	NA	NA
EGRLEVVTDPTTNAG	Q9R100|CAD17_MOUSE	47.29	15	345	NA	214
EGRLEVVTDPTTNAGYV	Q9R100|CAD17_MOUSE	49.88	17	422	NA	496
EGRLEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	49.84	18	4730	NA	6150
EGRLEVVTDPTTNAGYVKIK	Q9R100|CAD17_MOUSE	49.93	20	107	NA	714
EHFQDDVFNER	Q99KQ4|NAMPT_MOUSE	37.03	11	300	NA	NA
EHPQTYYYAVAVVKKG	Q921I1|TRFE_MOUSE	49.92	16	437	NA	NA
EIEVAPPKAHEVR	P28474|ADHX_MOUSE	44.82	13	28.8	NA	NA
EIKVYWDAPSPAPDHIR	Q8K385|FRRS1_MOUSE	49.23	17	24.3	NA	NA
EIPENYNSAM(+15.99)PFKILY	Q64487|PTPRD_MOUSE	49.69	16	931	NA	NA
EIPENYNSAM(+15.99)PFKILYD	Q64487|PTPRD_MOUSE	49.93	17	552	NA	NA
EIPENYNSAMPFKILY	Q64487|PTPRD_MOUSE	42.84	16	660	NA	NA
EIPENYNSAMPFKILYD	Q64487|PTPRD_MOUSE	49.64	17	324	NA	NA
EIQDWSASSPHSAAYV	Q80SY4|MIB1_MOUSE	49.87	16	632	NA	358
EIQPFHRAAAIQAIS	Q9QUR8|SEM7A_MOUSE	38.41	15	112	NA	NA
EIQRYQKPVVAAIQG	Q9DBM2|ECHP_MOUSE	48.95	15	330	NA	711
EISHLIEPLASAARAE	P26039|TLN1_MOUSE	46.83	16	127	NA	308

EISYTGSRPASN	P28666|MUG2_MOUSE:P28665|MUG1_M	46.06	12	1330	NA	313
EISYTGSRPASNM(+15.99)	P28666|MUG2_MOUSE:P28665|MUG1_M	46.48	13	290	NA	NA
EISYTGSRPASNM(+15.99)V	P28666|MUG2_MOUSE:P28665|MUG1_M	47.74	14	3220	NA	NA
EISYTGSRPASNM(+15.99)VI	P28666|MUG2_MOUSE:P28665|MUG1_M	49.19	15	203	NA	NA
EISYTGSRPASNMV	P28666|MUG2_MOUSE:P28665|MUG1_M	49.32	14	1580	NA	1180
EIWETPEVEKVNS(+79.97)E	Q99MS7|EH1L1_MOUSE	32.47	14	44.8	NA	NA
EKDPYALDVPNTAFG	Q91ZV0|MIA2_MOUSE	26.19	15	52.5	NA	NA
EKFGFQAPNVTFLHG	Q91WU5|AS3MT_MOUSE	47.58	15	244	NA	157
EKFQVVSPYDSEVLR	Q61190|I10R2_MOUSE	40.64	15	64.4	NA	NA
EKGFEVDAPLANALAIQ	Q6PDE7|GGT6_MOUSE	48.57	17	232	NA	NA
EKPVPAAPVPSPVAP	P97825|JUPI1_MOUSE	48.7	15	134	NA	NA
EKPVPAAPVPSPVAPA	P97825|JUPI1_MOUSE	47.91	16	2090	NA	1780
EKPVPAAPVPSPVAPAP	P97825|JUPI1_MOUSE	48.19	17	2440	NA	2790
EKPVPAAPVPSPVAPAPV	P97825|JUPI1_MOUSE	49.83	18	3960	NA	3880
EKPVPAAPVPSPVAPAPVP	P97825|JUPI1_MOUSE	49.94	19	11900	184	12100
EKPVPAAPVPSPVAPAPVPS	P97825|JUPI1_MOUSE	49.94	20	3590	NA	4190
EKPVPAAPVPSPVAPAPVPSRRNPP	P97825|JUPI1_MOUSE	49.94	25	1330	NA	1960
EKPVPAAPVPSPVAPAPVPSRRNPPG	P97825|JUPI1_MOUSE	49.93	26	1580	NA	1280
EKTHEQLTPLVRSAGTS	P09813|APOA2_MOUSE	49.67	17	1670	NA	964
EKVIVDFSSPNIAKE	Q9D0I9|SYRC_MOUSE	26.34	15	79.1	NA	NA
EKYVTSAPM(+15.99)PEPGAPG	P01872|IGHM_MOUSE	47.53	16	2010	NA	NA
EKYVTSAPMPEPGAPG	P01872|IGHM_MOUSE	49.81	16	1440	NA	1260
ELDQLFSGPLPGRLP	Q60805|MERTK_MOUSE	45	15	1290	NA	549
ELDQLFSGPLPGRLPV	Q60805|MERTK_MOUSE	46.5	16	1200	NA	633
ELDQLFSGPLPGRLPVN	Q60805|MERTK_MOUSE	48.87	17	1220	NA	238
ELEEQLGPVAEETR	P08226|APOE_MOUSE	47.71	14	28300	3310	13700
ELEEQLGPVAEETRA	P08226|APOE_MOUSE	48.55	15	52900	7230	26300
ELEEQLGPVAEETRAR	P08226|APOE_MOUSE	40.78	16	12800	NA	390
ELHRSVAPHAAASPA	Q8C7G5|APOA5_MOUSE	38.07	15	199	NA	NA
ELKGHLTPRANEL	P06728|APOA4_MOUSE	46.94	13	241	NA	292
ELKGHLTPRANELK	P06728|APOA4_MOUSE	47.69	14	2780	NA	1990
ELKGHLTPRANELKA	P06728|APOA4_MOUSE	29.49	15	2240	NA	1460
ELQRQASPNIVIALA	P35278|RAB5C_MOUSE	48.34	15	296	NA	206
ELRYQVPGAVPAK	Q9Z280|PLD1_MOUSE	39.66	13	976	NA	845
ELVAPRANTLK	O54782|MA2B2_MOUSE	26.16	11	264	NA	280
ELVAPRANTLKF	O54782|MA2B2_MOUSE	30.81	12	89.2	NA	38.5
ELVKDSELSPPTSAPSLVS	Q9WUU8|TNIP1_MOUSE	43.38	19	3730	NA	NA
ELVKDSELSPPTSAPSLVSF	Q9WUU8|TNIP1_MOUSE	35.28	20	71.9	NA	NA
EM(+15.99)ESYDEAIANLQR	Q9WUD1|CHIP_MOUSE	46.25	14	595	NA	304
EM(+15.99)NLM(+15.99)HAPQVADAIL	Q68FD5|CLH1_MOUSE	42.47	15	93	NA	NA
EM(+15.99)NLM(+15.99)HAPQVADAILG	Q68FD5|CLH1_MOUSE	42.13	16	407	NA	NA
EM(+15.99)NLMHAPQVADAIL	Q68FD5|CLH1_MOUSE	44.56	15	97.7	NA	154
ENDPGFGAPAASQVASAQPG	Q6IRU5|CLCB_MOUSE	49.94	20	65.7	NA	477
ENIWKAPEPVEI	Q9R100|CAD17_MOUSE	46.06	12	36.3	NA	NA
ENIWKAPEPVEIR	Q9R100|CAD17_MOUSE	48.58	13	6340	NA	4240
ENIWKAPEPVEIRE	Q9R100|CAD17_MOUSE	48.23	14	38100	200	9150
ENIWKAPEPVEIREN(+15.00)ST	Q9R100|CAD17_MOUSE	49.33	17	49500	127	12000
ENKKNWFGPSPYVEVT	Q8C863|ITCH_MOUSE	49.64	16	1260	NA	NA
ENLYPYLGPSTLRDRPQ	P97390|VPS45_MOUSE	28.7	17	893	NA	1080
ENM(+15.99)DLYLSPVAQSQEF	Q91XS1|MTMR4_MOUSE	49.7	16	566	NA	334
ENPEYLAPRAGTAS	P70424|ERBB2_MOUSE	40.03	14	544	NA	619
ENPEYLAPRAGTASQP	P70424|ERBB2_MOUSE	47.82	16	1790	NA	1400
ENPEYLAPRAGTASQPH	P70424|ERBB2_MOUSE	49.86	17	21600	52.9	4970
ENPEYLAPRAGTASQPHP	P70424|ERBB2_MOUSE	49.76	18	31300	NA	29500
ENPIYKSAVTTVVN	P09055|ITB1_MOUSE	49.07	14	385	NA	503
ENPIYKSAVTTVVNPK	P09055|ITB1_MOUSE	49.91	16	11800	209	12500
ENYEASKAYSSVD	Q9D306|MGT4C_MOUSE	47.65	13	873	NA	NA
ENYEASKAYSSVDE	Q9D306|MGT4C_MOUSE	45.27	14	1330	NA	NA
EPAGPAGRAASAPEAAQAEED	Q9JJX7|TYDP2_MOUSE	49.94	21	3330	NA	NA
EPAGPAGRAASAPEAAQAEEDR	Q9JJX7|TYDP2_MOUSE	49.84	22	1470	NA	1030
EPEAM(+15.99)LQVLGPKPALPEG	P13020|GELS_MOUSE	49.92	18	5050	NA	3390
EPEAM(+15.99)LQVLGPKPALPEGTE	P13020|GELS_MOUSE	49.94	20	354	NA	NA
EPEAMLQVLGPKPALPEG	P13020|GELS_MOUSE	49.9	18	2600	NA	3850
EPENPEYNTGYAVVAYR	Q64282|IFIT1_MOUSE	49.94	17	3630	117	3230
EPENPEYNTGYAVVAYRQ	Q64282|IFIT1_MOUSE	49.95	18	1600	NA	990
EPEVDYRTVTVNTEQ	Q6PDN3|MYLK_MOUSE	48.99	15	587	NA	314
EPEVDYRTVTVNTEQK	Q6PDN3|MYLK_MOUSE	45.12	16	2190	NA	1940
EPFFYSKYSAPRLPAAL	P97432|NBR1_MOUSE	49.94	17	309	NA	68.5
EPFFYSKYSAPRLPAALE	P97432|NBR1_MOUSE	49.94	18	6230	NA	5280
EPFFYSKYSAPRLPAALEQ	P97432|NBR1_MOUSE	49.93	19	9390	NA	7370
EPGNFIAATSLYSPER	Q80XN0|BDH_MOUSE	43.21	16	211	NA	158
EPIKSFEAPATINSASL	Q9Z1Z2|STRAP_MOUSE	47.22	17	553	NA	NA
EPLSTVTAPDSPEAAEQ	P15261|INGR1_MOUSE	49.46	17	1070	NA	NA
EPLTPSGAVPNQAQ	P70424|ERBB2_MOUSE	40.86	14	81.6	NA	NA
EPPPAYEPPAPAPA	O35609|SCAM3_MOUSE	42.31	14	8350	NA	3190
EPPPAYEPPAPAPAP	O35609|SCAM3_MOUSE	46.08	15	1630	NA	2760
EPPPAYEPPAPAPAPL	O35609|SCAM3_MOUSE	49.28	16	717	NA	NA

EPPPAYEPPAPAPAPLP	O35609|SCAM3_MOUSE	49.88	17	160	NA	106
EPPPAYEPPAPAPAPLPP	O35609|SCAM3_MOUSE	49.94	18	96400	1840	184000
EPPPAYEPPAPAPAPLPPP	O35609|SCAM3_MOUSE	49.93	19	1610000	19500	1530000
EPPPAYEPPAPAPAPLPPPS	O35609|SCAM3_MOUSE	49.9	20	14700	NA	22300
EPPPYQEPRPRGTPP	Q03146|DDR1_MOUSE	30.93	15	4440	NA	9410
EPPSDLDFFSPRPVPA	Q8BMI3|GGA3_MOUSE	49.91	16	1850	NA	1450
EPPSDLDFFSPRPVPAAS	Q8BMI3|GGA3_MOUSE	49.94	18	19400	NA	18500
EPPVFSRPTVSASYPPY	Q61187|TS101_MOUSE	30.77	17	2180	NA	2220
EPQPAGSQPLLANSPL	Q8R1U2|CGRE1_MOUSE	42.93	16	119	NA	NA
EPRRPRYRVPDVLVADPP	Q8BHN3|GANAB_MOUSE	35.87	18	3270	NA	NA
EPRRPRYRVPDVLVADPPT	Q8BHN3|GANAB_MOUSE	38.45	19	2390	NA	NA
EPSKLKRSYSSPDITQALQ	Q80U87|UBP8_MOUSE	44.02	19	3680	NA	796
EPSKLKRSYSSPDITQALQE	Q80U87|UBP8_MOUSE	48.53	20	3360	NA	5740
EPSKLKRSYSSPDITQALQEE	Q80U87|UBP8_MOUSE	47.35	21	328	NA	163
EPSKYYYEVSLPSGLEE	P21855|CD72_MOUSE	45.19	17	333	NA	NA
EPSVFNGPEVTM(+15.99)LKD	Q8BHN3|GANAB_MOUSE	38.29	15	1870	NA	293
EPSVFNGPEVTMLKD	Q8BHN3|GANAB_MOUSE	49.88	15	198	NA	255
EPYGARYVGSM(+15.99)VADVH	P70695|F16P2_MOUSE	49.79	16	2510	NA	3710
EPYGARYVGSM(+15.99)VADVHR	P70695|F16P2_MOUSE	49.89	17	24300	NA	23100
EPYGARYVGSM(+15.99)VADVHRT	P70695|F16P2_MOUSE	49.91	18	11300	NA	9350
EPYGARYVGSMVADVH	P70695|F16P2_MOUSE	48.11	16	1640	NA	2760
EPYGARYVGSMVADVHR	P70695|F16P2_MOUSE	49.93	17	21500	885	31800
EPYGARYVGSMVADVHRT	P70695|F16P2_MOUSE	49.78	18	10500	343	14100
EPYM(+15.99)YLSPLQQAVSD	O88668|CREG1_MOUSE	36.68	15	481	NA	NA
EPYTFSHPNK	Q5U462|CDCP1_MOUSE	46.36	10	132	NA	NA
EPYTFSHPNKG	Q5U462|CDCP1_MOUSE	45.79	11	890	NA	930
EPYTFSHPNKGE	Q5U462|CDCP1_MOUSE	48.96	12	220	NA	NA
EPYTFSHPNKGEIG	Q5U462|CDCP1_MOUSE	49.69	14	4500	NA	3700
EQ(+15.00)PSTSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	43.82	21	199	NA	NA
EQAQEQAQEQVQPKPLES	P06728|APOA4_MOUSE	49.93	18	2750	NA	2290
EQAQEQVQPKPLES	P06728|APOA4_MOUSE	47.94	14	3270	NA	NA
EQIYYAGPVNNPGLD	O88188|LY86_MOUSE	45.64	15	7300	360	999
EQIYYAGPVNNPGLDVP	O88188|LY86_MOUSE	47.8	17	7420	520	1400
EQIYYAGPVNNPGLDVPQ	O88188|LY86_MOUSE	49.9	18	2730	168	1590
EQPDLNFRNPAVQEE	Q91WV7|SLC31_MOUSE	44.81	15	735	NA	509
EQPDLNFRNPAVQEEIKE	Q91WV7|SLC31_MOUSE	48.94	18	2410	NA	2410
EQPSTSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	49.9	21	6430	NA	13800
EQTYVISAPKILRVGS	P06684|CO5_MOUSE	48.75	16	24.9	NA	401
EQTYVISAPKILRVGSS	P06684|CO5_MOUSE	49.33	17	362	NA	1700
ERASFITPVPGG	Q922D8|C1TC_MOUSE	29.88	12	784	NA	643
ERASFITPVPGGVG	Q922D8|C1TC_MOUSE	46.2	14	8260	185	8330
ERASFITPVPGGVGP	Q922D8|C1TC_MOUSE	48.42	15	3090	NA	2750
ERASFITPVPGGVGPM	Q922D8|C1TC_MOUSE	49.74	16	536	NA	1620
ERASFITPVPGGVGPM(+15.99)	Q922D8|C1TC_MOUSE	49.73	16	4480	NA	3510
ERDSKIVVPPLPGKAL	O70493|SNX12_MOUSE	28.04	16	106	NA	NA
ERELYIPSVDLLTAQD	P97432|NBR1_MOUSE	44.28	16	31.3	NA	NA
ERESKVVVPPLPGKAF	O70492|SNX3_MOUSE	39.98	16	116	NA	184
ERLKPYVAAQVDVLPDT	A2A8L5|PTPRF_MOUSE	49.72	17	148	NA	NA
ESEEEYSAPLPTPAP	P97467|AMD_MOUSE	48.81	15	101	NA	142
ESEEEYSAPLPTPAPS	P97467|AMD_MOUSE	49.9	16	1790	NA	1300
ESEPYTFSHPNK	Q5U462|CDCP1_MOUSE	48.28	12	1130	NA	582
ESEPYTFSHPNKG	Q5U462|CDCP1_MOUSE	47.86	13	4520	NA	1610
ESEPYTFSHPNKGE	Q5U462|CDCP1_MOUSE	49.4	14	2430	NA	241
ESEPYTFSHPNKGEI	Q5U462|CDCP1_MOUSE	49.87	15	1160	NA	1240
ESEPYTFSHPNKGEIG	Q5U462|CDCP1_MOUSE	49.86	16	54100	1090	43200
ESGFPKPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	37.05	21	132	NA	NA
ESGFPKPPSYNVATTLPSYDEA	Q8R0W6|NFIP1_MOUSE	38.55	22	323	NA	NA
ESKEAFQEALAAAGDK	P10639|THIO_MOUSE	49.87	16	5340	56.9	4870
ESKEAFQEALAAAGDKL	P10639|THIO_MOUSE	49.79	17	590	NA	309
ESLHLRFSAPQIENEPE	Q61190|I10R2_MOUSE	40.46	17	209	NA	203
ESLPPALQEPQPAGSQPL	Q8R1U2|CGRE1_MOUSE	45.82	18	294	NA	NA
ESPAEYAGPEGSYFG	P43406|ITAV_MOUSE	29.8	15	97.7	NA	NA
ESPEQIRAPSGIITSPG	Q8BUJ9|LRP12_MOUSE	48.01	17	351	NA	334
ESVAPYGGPSSSPAEEG	P10493|NID1_MOUSE	48.72	17	567	NA	261
ETATYKLSAPWVEQEGPE	P14432|HA1T_MOUSE	49.82	18	393	NA	382
ETDSVVSSVTTKAKGVA	Q9JJX6|P2RX4_MOUSE	45.76	17	1270	NA	751
ETDYNGFPVLVSRDS	Q61418|CLCN4_MOUSE	49.73	15	243	NA	NA
ETDYNGFPVLVSRDSE	Q61418|CLCN4_MOUSE	49.51	16	308	NA	NA
ETELDQLFSGPLPGRLP	Q60805|MERTK_MOUSE	49.89	17	145	NA	NA
ETELDQLFSGPLPGRLPVN	Q60805|MERTK_MOUSE	49.9	19	102	NA	117
ETFHASQPSLTVDG	Q62432|SMAD2_MOUSE	39.66	14	2010	NA	1710
ETHGGEDVAIFARGPQAHLVHGVQ	P24822|PPBI_MOUSE	49.61	24	225	NA	NA
ETNEAQPPGPAPSDDAPL	Q3U9N9|MOT10_MOUSE	29.41	18	1170	NA	514
EVDQIYHLASPASPP	Q91XL3|UXS1_MOUSE	41.99	15	1140	NA	1340
EVDRYDAPGIAFYPG	Q9D771|PACC1_MOUSE	49.15	15	7520	NA	4320
EVKAFFESHPAPSAER	Q11011|PSA_MOUSE	49.77	16	874	NA	456
EVLDYSTPTTNGTPE	Q9DBG7|SRPRA_MOUSE	32.68	15	4350	NA	2390

EVLDYSTPTTNGTPEA	Q9DBG7|SRPRA_MOUSE	37.86	16	555	NA	362
EVPDSYKSAVPFKIL	A2A8L5|PTPRF_MOUSE	45.43	15	322	NA	172
EVPDSYKSAVPFKILY	A2A8L5|PTPRF_MOUSE	49.93	16	1930	NA	1910
EVPDSYKSAVPFKILYN	A2A8L5|PTPRF_MOUSE	49.91	17	1720	NA	1220
EVPDSYKSAVPFKILYNG	A2A8L5|PTPRF_MOUSE	49.84	18	112	NA	NA
EVSSPITLQALVQ	E9Q414|APOB_MOUSE	42.33	13	487	NA	162
EVSSVEAPSVSPA	Q8BUJ9|LRP12_MOUSE	42.19	13	10200	42.6	7820
EVSSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	48.43	14	106000	3030	72800
EVSSVEAPSVSPARH	Q8BUJ9|LRP12_MOUSE	48.69	15	13800	NA	2180
EVSSVEAPSVSPARHQ	Q8BUJ9|LRP12_MOUSE	49.86	16	63800	NA	10400
EVSSVEAPSVSPARHQL	Q8BUJ9|LRP12_MOUSE	49.9	17	3870	NA	3430
EVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	36.26	14	482	NA	NA
EVYTFPVPERH	P09803|CADH1_MOUSE	42.63	11	212	NA	NA
EVYTFPVPERHLE	P09803|CADH1_MOUSE	42.79	13	285	NA	236
EWKDYKAGFGNLER	P12804|FGL2_MOUSE	28.58	14	334	NA	NA
EWKDYKAGFGNLEREF	P12804|FGL2_MOUSE	26.13	16	45.1	NA	NA
EYSGSVANEAN	E9Q414|APOB_MOUSE	39.43	11	1430	NA	1410
EYSGSVANEANVY	E9Q414|APOB_MOUSE	46.37	13	663	NA	1210
EYVAPEVILNKG	Q61410|KGP2_MOUSE	30.85	12	92.3	NA	126
FAAEEFKVPAATSAIIT	P61961|UFM1_MOUSE	43.19	17	221	NA	NA
FAAEEFKVPAATSAIITN	P61961|UFM1_MOUSE	49.78	18	1390	NA	1450
FAAEEFKVPAATSAIITNDG	P61961|UFM1_MOUSE	49.92	20	656	NA	542
FAAGVFSNPAVRTAAAN	O35609|SCAM3_MOUSE	49.38	17	414	NA	488
FAAPFFIVRHQLLKK	P17665|COX7C_MOUSE	36.01	15	1600	NA	907
FDALLINPRASDSPID	Q9R111|GUAD_MOUSE	42.4	16	394	NA	64.8
FDFAGPAIHGSAV	Q60930|VDAC2_MOUSE	37.71	13	357	NA	217
FDGYRSPLPTNESQP	Q8CCN5|BCAS3_MOUSE	48.41	15	2220	NA	2070
FDGYRSPLPTNESQPL	Q8CCN5|BCAS3_MOUSE	49.1	16	790	NA	648
FDHYYHEAALGEAL	O89001|CBPD_MOUSE	29.85	14	93.1	NA	NA
FDPGFRSPSTQVAN	Q6A037|N4BP1_MOUSE	49.28	14	515	NA	389
FDPGFRSPSTQVANNS	Q6A037|N4BP1_MOUSE	47.63	16	1390	NA	1080
FDPGFRSPSTQVANNSHQPPP	Q6A037|N4BP1_MOUSE	49.72	21	10200	NA	11500
FDPTTAFQAPDVGQAL	A2ASQ1|AGRIN_MOUSE	47.13	16	622	NA	287
FDPTTAFQAPDVGQALLQ	A2ASQ1|AGRIN_MOUSE	49.82	18	169	NA	259
FDSNYVNSRAHLIK	Q80TF3|PCD19_MOUSE	38.3	14	418	NA	NA
FEKTHEQLTPLVRSAG	P09813|APOA2_MOUSE	49.52	16	687	NA	670
FEKTHEQLTPLVRSAGTS	P09813|APOA2_MOUSE	49.53	18	4910	NA	4430
FEKTHEQLTPLVRSAGTSL	P09813|APOA2_MOUSE	49.83	19	990	NA	486
FENYEASKAYSSVD	Q9D306|MGT4C_MOUSE	47.99	14	147	NA	NA
FENYEASKAYSSVDE	Q9D306|MGT4C_MOUSE	49.39	15	179	NA	NA
FGGTGGGSVRIGSGGVFRAPSIHGGSG	P19001|K1C19_MOUSE	38.58	30	939	NA	582
FGNIYSTPLALQ	O88968|TCO2_MOUSE	33	12	96.7	NA	NA
FGNIYSTPLALQM	O88968|TCO2_MOUSE	46.27	13	65.2	NA	212
FGNIYSTPLALQM(+15.99)	O88968|TCO2_MOUSE	48.52	13	1030	NA	542
FGNIYSTPLALQM(+15.99)L	O88968|TCO2_MOUSE	48.2	14	919	NA	474
FGNIYSTPLALQM(+15.99)LM(+15.99)	O88968|TCO2_MOUSE	49.69	15	5640	NA	4220
FGNIYSTPLALQM(+15.99)LM(+15.99)T	O88968|TCO2_MOUSE	36.86	16	121	NA	NA
FGNIYSTPLALQMLM(+15.99)	O88968|TCO2_MOUSE	49.63	15	685	NA	791
FGNSEFDPPGPNVATTT	Q9Z1D1|EIF3G_MOUSE	49.88	17	1070	NA	863
FGPYYTEPVIAGLD	Q9R1P1|PSB3_MOUSE	45.5	14	252	NA	138
FGPYYTEPVIAGLDP	Q9R1P1|PSB3_MOUSE	42.93	15	209	NA	NA
FGPYYTEPVIAGLDPK	Q9R1P1|PSB3_MOUSE	49.92	16	17700	362	11500
FHFPYDYPNLQTAQ	Q3TCT4|ENTP7_MOUSE	49.64	14	153	NA	NA
FHFPYDYPNLQTAQL	Q3TCT4|ENTP7_MOUSE	49.31	15	742	NA	401
FIEKVIPSTANSN	E9Q7P9|CDHR2_MOUSE	47.34	13	1410	NA	654
FIEKVIPSTANSNN	E9Q7P9|CDHR2_MOUSE	48.31	14	1440	NA	632
FIEKVIPSTANSNNL	E9Q7P9|CDHR2_MOUSE	48.89	15	5770	NA	3500
FIEKVIPSTANSNNLF	E9Q7P9|CDHR2_MOUSE	47.94	16	537	NA	299
FISPDSLLGVEK	Q9D871|CEA18_MOUSE	36.11	12	260	NA	NA
FIVNTNVPRASVPE	P34884|MIF_MOUSE	48.9	14	301	NA	270
FIYVAPGIANTYL	Q9WVK5|B4GT6_MOUSE	47.7	13	205	NA	NA
FKIVTDPKTNEGIL	P55292|DSC2_MOUSE	41.4	14	57.2	NA	NA
FKPSYGTPAPGFSSM(+15.99)	P23249|MOV10_MOUSE	49.76	15	107	NA	NA
FLLYQEPVLGPVRGPFPI	P02666	32.77	18	201	NA	NA
FLPAQADIVATK	P10852|4F2_MOUSE	38.88	12	1170	NA	682
FNNQAYHSPATALAIVD	Q8R420|ABCA3_MOUSE	48.82	17	4930	NA	6370
FNNQAYHSPATALAIVDN	Q8R420|ABCA3_MOUSE	49.29	18	2230	NA	2150
FPGSVIDPPAVNLAAQN	O88738|BIRC6_MOUSE	45.25	17	282	NA	309
FPIKWTAPEAALYG	P39688|FYN_MOUSE:Q04736|YES_MOU	43.69	14	372	NA	309
FPKPPSYNVA	Q8R0W6|NFIP1_MOUSE	32.42	10	259	NA	NA
FPKPPSYNVATTLP	Q8R0W6|NFIP1_MOUSE	39	14	578	NA	NA
FPKPPSYNVATTLPSY	Q8R0W6|NFIP1_MOUSE	46.13	16	2250	NA	1550
FPKPPSYNVATTLPSYD	Q8R0W6|NFIP1_MOUSE	49.91	17	16100	636	21300
FPKPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	49.92	18	474000	18000	304000
FPKPPSYNVATTLPSYDEA	Q8R0W6|NFIP1_MOUSE	49.9	19	247000	NA	213000
FPKPPSYNVATTLPSYDEAE	Q8R0W6|NFIP1_MOUSE	49.94	20	8290	NA	5400
FPKPQIITQPETTM(+15.99)AVVG	P70193|LRIG1_MOUSE	39.06	18	281	NA	NA

FPKPQITVQPETQSAIKG	Q6P1C6|LRIG3_MOUSE	37.45	18	593	NA	NA
FPKPYNSSRAILDE	E9Q555|RN213_MOUSE	25.88	14	105	NA	NA
FPNIHPPQIPATPP	Q9CX00|IST1_MOUSE	37.89	14	536	NA	NA
FPPFPEGHPAVLPGEDPPP	Q3TWL2|PP4P1_MOUSE	49.17	19	2320	NA	NA
FPSVVVVGLGKRSAG	Q9CPY7|AMPL_MOUSE	42.19	15	329	NA	NA
FPTDYPFKPPKVAFTTR	P61079|UB2D3_MOUSE:P62838|UB2D2_	49.93	17	6610	NA	7150
FPTLKFFPASADRTVID	P09103|PDIA1_MOUSE	48.6	17	2790	NA	1370
FPTLKFFPASADRTVIDY	P09103|PDIA1_MOUSE	47.86	18	287	NA	163
FPYEGPAPLEAIA	Q8R4G6|MGT5A_MOUSE:Q765H6|MGT5	47.34	13	2590	NA	1730
FPYEGPAPLEAIAN	Q8R4G6|MGT5A_MOUSE:Q765H6|MGT5	46.07	14	2950	NA	1510
FPYEGPAPLEAIANG	Q8R4G6|MGT5A_MOUSE:Q765H6|MGT5	37.9	15	1610	NA	1140
FPYVTPAPH	Q9D074|MGRN1_MOUSE	39.58	9	580	NA	845
FPYVTPAPHEP	Q9D074|MGRN1_MOUSE	46.72	11	10200	NA	10600
FPYVTPAPHEPV	Q9D074|MGRN1_MOUSE	48.15	12	21000	778	22300
FPYVTPAPHEPVK	Q9D074|MGRN1_MOUSE	48.13	13	142000	6760	167000
FPYVTPAPHEPVKT	Q9D074|MGRN1_MOUSE	49.65	14	29100	639	31200
FPYVTPAPHEPVKTL	Q9D074|MGRN1_MOUSE	49.53	15	785	NA	2590
FPYVTPAPHEPVKTLR	Q9D074|MGRN1_MOUSE	49.91	16	1270	NA	801
FRALLQ(+15.00)IRAV	Q9D074|MGRN1_MOUSE	26.12	10	34.6	NA	NA
FRDQGRQVYLS(+79.97)RPPAC(+57.02)	Q03146|DDR1_MOUSE	27.94	30	4730	NA	NA
FRPAHQAPM(+15.99)AQTTIH	O08573|LEG9_MOUSE	48.4	15	8610	NA	7170
FRPAHQAPM(+15.99)AQTTIHM(+15.99)	O08573|LEG9_MOUSE	29.48	16	236	NA	NA
FRPAHQAPMAQTTIH	O08573|LEG9_MOUSE	48.81	15	10600	NA	12200
FRPAHQAPMAQTTIHM(+15.99)	O08573|LEG9_MOUSE	44.45	16	123	NA	NA
FRVNFVDPAASSSA	P55012|S12A2_MOUSE	49.67	14	224	NA	209
FRVNFVDPAASSSAD	P55012|S12A2_MOUSE	49.06	15	4420	NA	4900
FRVNFVDPAASSSADD	P55012|S12A2_MOUSE	49.92	16	23600	644	23800
FRVNFVDPAASSSADDS	P55012|S12A2_MOUSE	49.87	17	3830	NA	3250
FRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MO	47.84	12	5120	NA	4390
FRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MO	45.26	14	553	NA	161
FSDAFFNSAVQKATPG	O54734|OST48_MOUSE	46.17	16	220	NA	NA
FSEYRYPVATFQPS	Q8CGK5|INLR1_MOUSE	36.14	14	273	NA	214
FSGPLPGRLPVNHRPFS	Q60805|MERTK_MOUSE	49.63	17	1330	NA	NA
FSSEVYTFPVPERH	P09803|CADH1_MOUSE	49.08	14	382	NA	517
FSSEVYTFPVPERHLE	P09803|CADH1_MOUSE	49.87	16	506	NA	952
FSSEVYTFPVPERHLER	P09803|CADH1_MOUSE	47.09	17	547	NA	574
FSSRSFTSGPGARISSSSF	P11679|K2C8_MOUSE	48.37	19	938	NA	1080
FSYVDPVITSISPR	P16056|MET_MOUSE	49.55	14	278	NA	149
FTAQWIAPSVQLTGYR	P11276|FINC_MOUSE	48.5	16	4380	43.9	4260
FTVHWVAPRAPITG	P11276|FINC_MOUSE	48.86	14	913	NA	1130
FTVHWVAPRAPITGY	P11276|FINC_MOUSE	48.34	15	331	NA	473
FTYQNAAAQPETGPG	Q9QZM4|TR10B_MOUSE	32.48	15	252	NA	NA
FTYQQPQPLSVEP	B2RXS4|PLXB2_MOUSE	47.74	13	400	NA	269
FTYQQPQPLSVEPR	B2RXS4|PLXB2_MOUSE	48.82	14	32900	670	21200
FVAPAVTPVK	P70158|ASM3A_MOUSE	42.39	10	22300	472	30400
FVAPAVTPVKG	P70158|ASM3A_MOUSE	45.22	11	14100	NA	14500
FVAPAVTPVKGVL	P70158|ASM3A_MOUSE	49.51	13	5200	NA	4280
FVGGRFQSPGTQSSRPI	Q571I9|A16A1_MOUSE	46.14	17	585	NA	635
FVGPTPAPAPAPRTLPA	Q501J7|PHAR4_MOUSE	49.79	17	83.6	NA	NA
FVYVAPGIVNTY	Q9JMK0|B4GT5_MOUSE	29.64	12	31.6	NA	NA
FYSKYSAPRLPAAL	P97432|NBR1_MOUSE	49.84	14	5520	NA	5430
FYSKYSAPRLPAALE	P97432|NBR1_MOUSE	49.88	15	7180	12.9	6590
FYSKYSAPRLPAALEQ	P97432|NBR1_MOUSE	49.93	16	5370	NA	4840
FYTPIPNGLYPS	O08573|LEG9_MOUSE	45.41	12	897	NA	765
G(+42.01)ELPFLSPEGARGPH	Q99PE8|ABCG5_MOUSE	25.7	15	795	NA	NA
G(+42.01)FPKPPSYN(+15.00)VATTLPSY	Q8R0W6|NFIP1_MOUSE	43.65	19	1090	NA	NA
G(+42.01)FPKPPSYN(+15.00)VATTLPSY	Q8R0W6|NFIP1_MOUSE	29.55	20	344	NA	NA
G(+42.01)FPKPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	29.08	19	2630	NA	1780
G(+42.01)N(+15.00)PLNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	49	17	824	NA	755
G(+42.01)N(+15.00)PLNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	49.58	18	872	NA	1120
G(+42.01)NPLNSVFVAPAVTPVKG	P70158|ASM3A_MOUSE	25.17	18	888	NA	NA
G(+42.01)PPGAIALAAFLQAL	Q8BH86|GLUCM_MOUSE	27.25	15	1930	NA	NA
GAAAKKTVKTPKKPKKPAVSKK	P43275|H11_MOUSE	49.95	22	859	549	500
GAEM(+15.99)VNLPLVHAAIR	Q64442|DHSO_MOUSE	42.99	15	109	NA	NA
GAGKEAAGKSSGPTSLFAVTVAPPGAR	Q8VEK3|HNRPU_MOUSE	49.79	29	205	NA	NA
GAIVDGPVPITIEVKD	Q9R100|CAD17_MOUSE	49.82	16	196	NA	NA
GAKKTVKKTPKKA	P43276|H15_MOUSE	47.7	13	2410	NA	NA
GAKKTVKKTPKKAKKP	P43276|H15_MOUSE	49.94	16	36900	NA	7610
GAKKTVKKTPKKAKKPA	P43276|H15_MOUSE	49.95	17	3010	NA	7160
GAKKTVKKTPKKAKKPAAAGVKKVAKSI	P43276|H15_MOUSE	49.95	32	158	2400	2940
GALAVAGAPIALSAVG	Q8VC49|IF27B_MOUSE	45.65	16	209	NA	462
GALLLNAPVVSITQGR	O09046|OXLA_MOUSE	41.19	16	497	NA	219
GAPAAAPTPASVPQ	P22892|AP1G1_MOUSE	29.53	14	129	NA	NA
GAPKDIM(+15.99)GPQVTPVLSVDT	O54782|MA2B2_MOUSE	47.7	19	823	NA	NA
GAPKDIM(+15.99)GPQVTPVLSVDTRPV	O54782|MA2B2_MOUSE	49.93	22	114	NA	NA
GAPVFYTPQAYAAIPS	Q5YD48|A1CF_MOUSE	48.98	16	1070	NA	591
GAQEM(+15.99)VSSSVSSAKETV	Q9DBG5|PLIN3_MOUSE	49.04	17	102	NA	NA

GAQEMVSSSVSSAKETV	Q9DBG5|PLIN3_MOUSE	42.56	17	197	NA	288
GARYVGSMVADVHR	P70695|F16P2_MOUSE	42.14	14	178	NA	153
GATPKKPKKTAGAKKTVKKTPKKAKKPA	P43276|H15_MOUSE	49.95	28	1090	NA	NA
GAVIFNFPGTRNEVIP	Q9D304|RN128_MOUSE	45.03	16	1300	NA	431
GAVIFNFPGTRNEVIPM	Q9D304|RN128_MOUSE	49.7	17	5730	NA	7450
GAVIFNFPGTRNEVIPM(+15.99)	Q9D304|RN128_MOUSE	49.89	17	34900	NA	13400
GDATLYVPSAPLSGP	Q60928|GGT1_MOUSE	41.75	15	1960	NA	315
GDATLYVPSAPLSGPV	Q60928|GGT1_MOUSE	40.43	16	861	NA	671
GDEKKGPLIVSGPDGAPAKGDG	Q8VBW1|SC6A8_MOUSE	49.92	22	7670	NA	5410
GDGNHTLFH	P43023|CX6A2_MOUSE:P43024|CX6A1_	39.23	9	576	256	334
GDGNHTLFHNPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	47.29	21	1330	664	2170
GDIFIGPKAEEHRG	P61164|ACTZ_MOUSE	36.78	14	1210	NA	822
GDLEYQM(+15.99)STTARAK	Q02257|PLAK_MOUSE	41.35	14	396	NA	143
GDLEYQM(+15.99)STTARAKR	Q02257|PLAK_MOUSE	35.15	15	2090	NA	1030
GDLEYQM(+15.99)STTARAKRV	Q02257|PLAK_MOUSE	31.04	16	82.8	NA	NA
GDLEYQM(+15.99)STTARAKRVR	Q02257|PLAK_MOUSE	45.66	17	351	NA	NA
GDLEYQMSTTARAK	Q02257|PLAK_MOUSE	48.09	14	9900	NA	1220
GDLEYQMSTTARAKR	Q02257|PLAK_MOUSE	44.19	15	6180	NA	6540
GDLEYQMSTTARAKRV	Q02257|PLAK_MOUSE	37.1	16	253	NA	438
GDLEYQMSTTARAKRVR	Q02257|PLAK_MOUSE	43.42	17	952	NA	1230
GDLFIGPKAEEHRG	Q8R5C5|ACTY_MOUSE	36.78	14	1210	NA	822
GDLSQHATPLPTPAV	O88746|TOM1_MOUSE	43.45	15	1610	NA	1400
GDLSQHATPLPTPAVL	O88746|TOM1_MOUSE	47.1	16	671	NA	507
GDLSQHATPLPTPAVLP	O88746|TOM1_MOUSE	46.8	17	1000	NA	804
GDLSQHATPLPTPAVLPG	O88746|TOM1_MOUSE	49.39	18	33100	833	13800
GDQTVVEPNIAIQSVT	Q8BM96|AGRG7_MOUSE	36.57	16	312	NA	NA
GDQTVVEPNIAIQSVTR	Q8BM96|AGRG7_MOUSE	44.7	17	1380	NA	1260
GDQTVVEPNIAIQSVTRDDN	Q8BM96|AGRG7_MOUSE	44.7	20	85.7	NA	NA
GDRPHTYFGPETSASK	P70277|SIA7B_MOUSE	43.54	16	619	NA	NA
GDRPHTYFGPETSASKF	P70277|SIA7B_MOUSE	49.72	17	151	NA	372
GDRPHTYFGPETSASKFK	P70277|SIA7B_MOUSE	49.94	18	1230	NA	1930
GDSNFGAPSASVAA	O35643|AP1B1_MOUSE	36.51	14	399	NA	446
GDSNFGAPSASVAAAP	O35643|AP1B1_MOUSE	44.21	16	8740	NA	8330
GDSNFGAPSASVAAAPA	O35643|AP1B1_MOUSE	46.93	17	3880	NA	2970
GDSNFGAPSASVAAAPAP	O35643|AP1B1_MOUSE	46.27	18	5440	NA	3420
GDSVTTDHISPAGNIARNSPA	P28271|ACOHC_MOUSE	49.37	21	285	NA	NA
GDSVVFAGPAGNSVETR	Q8R146|ACPH_MOUSE	48.01	17	108	NA	89.4
GDSYRSPWSNKYDPP	P47757|CAPZB_MOUSE	48.43	15	5500	NA	4520
GDSYRSPWSNKYDPPL	P47757|CAPZB_MOUSE	46.96	16	6760	NA	6070
GDTEGRLEVVTDPTTNAG	Q9R100|CAD17_MOUSE	49.61	18	1630	NA	1300
GDTEGRLEVVTDPTTNAGY	Q9R100|CAD17_MOUSE	49.91	19	204	NA	NA
GDTEGRLEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	49.94	21	23700	1070	23400
GDTEGRLEVVTDPTTNAGYVKIK	Q9R100|CAD17_MOUSE	49.94	23	220	NA	1050
GDTIEFRGPNGLLVYQ	Q9DCN2|NB5R3_MOUSE	48.61	16	1620	NA	882
GDTIEFRGPNGLLVYQG	Q9DCN2|NB5R3_MOUSE	49.54	17	9470	NA	6890
GDTIEFRGPNGLLVYQGK	Q9DCN2|NB5R3_MOUSE	49.83	18	8450	NA	9260
GDTIEFRGPNGLLVYQGKG	Q9DCN2|NB5R3_MOUSE	49.7	19	750	NA	NA
GDVAFGVPSVIVSRGHR	Q91WU0|EST1F_MOUSE	29.79	17	156	NA	NA
GDVLTPVPTGSQE	Q921M4|GOGA2_MOUSE	34.24	13	358	NA	529
GEANQWKQSLVQATEEN	A6X935|ITIH4_MOUSE	49.47	17	111	NA	124
GEDVAIFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_M	48.78	18	4470	NA	3600
GEDVAIFARGPQAHLVHGVQ	P24823|PPBN_MOUSE:P24822|PPBI_M	49.52	20	6220	NA	4180
GEDVAIFARGPQAHLVHGVQE	P24823|PPBN_MOUSE:P24822|PPBI_M	48.95	21	191	NA	NA
GELLGIKLESGEQSD	O08784|TCOF_MOUSE	30.76	15	234	NA	NA
GELTYENVQVSPVPGGPP	P21855|CD72_MOUSE	48.32	18	179	NA	NA
GELVYEAPETIAAEPPP	O88738|BIRC6_MOUSE	47.52	17	431	NA	496
GELYTFNTPSGTAGVE	Q9QYY0|GAB1_MOUSE	40.29	16	80	NA	28.5
GENPIYKSAVTTVVN	P09055|ITB1_MOUSE	48.64	15	284	NA	471
GENPIYKSAVTTVVNPK	P09055|ITB1_MOUSE	49.83	17	7600	120	9660
GEPEAM(+15.99)LQVLGPKPALPEG	P13020|GELS_MOUSE	49.94	19	1010	NA	651
GEQKLFISPGLLPEAPT	Q91WD0|GP108_MOUSE	42.87	17	400	NA	118
GERFEAPEALFQ	P61161|ARP2_MOUSE	38.42	12	210	NA	NA
GERFEAPEALFQP	P61161|ARP2_MOUSE	47.82	13	624	NA	154
GERFEAPEALFQPH	P61161|ARP2_MOUSE	48.81	14	8370	NA	3920
GERYIAPTVL	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	26.26	10	131	NA	196
GERYIAPTVLVDVQ	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	38.44	14	321	NA	NA
GETATYKLSAPWVEQEGPE	P14432|HA1T_MOUSE	49.71	19	220	NA	NA
GEVKAFFESHPAPSAER	Q11011|PSA_MOUSE	49.82	17	401	NA	356
GFAAPFFIVRHQLLKK	P17665|COX7C_MOUSE	31.32	16	75.8	NA	141
GFGDLKTPAGLQVLN	O70251|EF1B_MOUSE	31.19	15	63.3	NA	NA
GFHFPYDYPNLQTAQ	Q3TCT4|ENTP7_MOUSE	48.39	15	274	NA	185
GFHFPYDYPNLQTAQL	Q3TCT4|ENTP7_MOUSE	49.58	16	2040	NA	NA
GFPKPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	49.85	19	8650	NA	4570
GFPKPPSYNVATTLPSYDEA	Q8R0W6|NFIP1_MOUSE	49.87	20	4500	NA	2750
GFPKPPSYNVATTLPSYDEAE	Q8R0W6|NFIP1_MOUSE	26.19	21	44.4	NA	NA
GFPYEGPAPLEAIA	Q8R4G6|MGT5A_MOUSE:Q765H6|MGT5	45.44	14	2170	NA	1470
GFPYEGPAPLEAIAN	Q8R4G6|MGT5A_MOUSE:Q765H6|MGT5	47.31	15	1040	NA	546

GFPYEGPAPLEAIANG	Q8R4G6|MGT5A_MOUSE:Q765H6|MGT5	47.6	16	461	NA	308
GFTNTM(+15.99)RVVPVP	P52480|KPYM_MOUSE	26.46	12	1000	NA	746
GFTNTMRVVPVP	P52480|KPYM_MOUSE	37	12	617	NA	1150
GGASALLIEKL	Q8QZT1|THIL_MOUSE	27.88	11	468	NA	460
GGDPEAPAPAPAAERPP	Q68FL4|SAHH3_MOUSE	49.16	17	517	NA	NA
GGDPEAPAPAPAAERPPAPGPG	Q68FL4|SAHH3_MOUSE	49.93	22	288	NA	224
GGEDVAIFARGPQAHLVH	P24822|PPBI_MOUSE	47.48	18	3770	NA	3510
GGEDVAIFARGPQAHLVHG	P24822|PPBI_MOUSE	48.84	19	6710	137	7420
GGEDVAIFARGPQAHLVHGVQ	P24822|PPBI_MOUSE	49.47	21	8230	NA	6720
GGEDVAIFARGPQAHLVHGVQE	P24822|PPBI_MOUSE	49.3	22	149	NA	69.3
GGEPEAMLQVLGPKPALPEG	P13020|GELS_MOUSE	49.14	20	116	NA	414
GGERFEAPEALFQPH	P61161|ARP2_MOUSE	47.24	15	519	NA	396
GGFLYSGPLALRLYS	Q9Z222|B3GN2_MOUSE	44.79	15	65.5	NA	NA
GGGASALLIEKL	Q8QZT1|THIL_MOUSE	29.53	12	157	NA	235
GGGDPEAPAPAPAAERPP	Q68FL4|SAHH3_MOUSE	48.78	18	912	NA	1980
GGGSVRIGSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	49.34	26	2840	NA	7660
GGLDSLIGDSNFGAPSASVAAAPAPA	O35643|AP1B1_MOUSE	38.38	26	144	NA	403
GGLDSLIGDSNFGAPSASVAAAPAPAR	O35643|AP1B1_MOUSE	49.94	27	108	NA	NA
GGLPDYSAPNPIK	Q8CFG0|SULF2_MOUSE	48.02	13	4790	181	4790
GGLPDYSAPNPIKV	Q8CFG0|SULF2_MOUSE	48.14	14	285	NA	326
GGLPDYSAPNPIKVT	Q8CFG0|SULF2_MOUSE	49.89	15	6100	290	7490
GGLPDYSAPNPIKVTH	Q8CFG0|SULF2_MOUSE	49.47	16	80800	3880	96600
GGLPDYSAPNPIKVTHR	Q8CFG0|SULF2_MOUSE	49.9	17	108000	6930	162000
GGPRIRGNVYIHPTAKVAPS	Q922H4|GMPPA_MOUSE	49.78	20	135	NA	NA
GGSPYIAAKINEAKDL	Q9CQV7|TIM14_MOUSE	47.19	16	160	NA	103
GGTSRHPGPL	P23150|HA2J_MOUSE:P14434|HA2B_M	38.47	10	1650	NA	782
GGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	27.71	17	154	NA	NA
GGVYASPSIAGSRP	Q8R0X7|SGPL1_MOUSE	44.84	14	363	NA	154
GGVYASPSIAGSRPG	Q8R0X7|SGPL1_MOUSE	46.01	15	5900	NA	2770
GGYKFSAPVVPSS	Q9EPL8|IPO7_MOUSE	25.77	13	111	NA	NA
GGYKFSAPVVPSSFN	Q9EPL8|IPO7_MOUSE	47.71	15	714	NA	1080
GGYKPFQNPVPNQSPS	P16382|IL4RA_MOUSE	49.82	16	1130	NA	3090
GGYKPFQNPVPNQSPSS	P16382|IL4RA_MOUSE	49.76	17	497	NA	771
GGYRYPRALEEE	Q8K3K8|OPTN_MOUSE	29.51	12	1760	NA	NA
GGYRYPRALEEEV	Q8K3K8|OPTN_MOUSE	29.14	13	12200	NA	5720
GGYRYPRALEEEVE	Q8K3K8|OPTN_MOUSE	36.86	14	7040	NA	NA
GHEVVVIAPEASIHIK	Q63886|UD11_MOUSE	48.97	16	2070	NA	929
GIDPYDQPNAIYIE	O88307|SORL_MOUSE	42.53	14	4110	NA	2140
GIDPYDQPNAIYIER	O88307|SORL_MOUSE	49.38	15	66300	3900	52900
GIDPYDQPNAIYIERH	O88307|SORL_MOUSE	49.67	16	40800	992	33800
GIDPYDQPNAIYIERHE	O88307|SORL_MOUSE	49.93	17	1080	NA	731
GIDPYDQPNAIYIERHEP	O88307|SORL_MOUSE	49.69	18	4330	NA	3400
GIFKGPTAENAEY	Q01279|EGFR_MOUSE	36	13	193	NA	NA
GIKLESGEQSD	O08784|TCOF_MOUSE	41.77	11	233	158	438
GIKTPEIVAPESAHAAFD	Q8R0X7|SGPL1_MOUSE	43.06	18	165	NA	NA
GIKTPEIVAPESAHAAFDK	Q8R0X7|SGPL1_MOUSE	49.93	19	325	NA	131
GINYQPPTVVPGGDL	P68369|TBA1A_MOUSE:P68373|TBA1C	46.96	15	351	NA	114
GIPFAAPTALASRDG	Q91VX2|UBAP2_MOUSE	39.27	15	296	NA	250
GIPVYRFVLPANA	Q08857|CD36_MOUSE	30.09	13	1130	NA	278
GIPVYRFVLPANAF	Q08857|CD36_MOUSE	29.62	14	368	NA	114
GIPVYRFVLPANAFA	Q08857|CD36_MOUSE	39.76	15	9570	122	3800
GIPVYRFVLPANAFASP	Q08857|CD36_MOUSE	36.33	17	963	NA	NA
GIPVYRFVLPANAFASPL	Q08857|CD36_MOUSE	45.51	18	647	NA	368
GIVNLKSPKTTSATK	Q99LJ1|FUCO_MOUSE	33.42	15	131	NA	NA
GKEFQFLNPNPVPEDL	Q8R0K2|TRI31_MOUSE	49.75	16	1040	NA	1030
GKEFQFLNPNPVPEDLE	Q8R0K2|TRI31_MOUSE	49.86	17	1620	NA	NA
GKFM(+15.99)KPGKVVLVLAGRYSGRKA	P61358|RL27_MOUSE	49.94	22	993	NA	NA
GKFM(+15.99)KPGKVVLVLAGRYSGRKA	P61358|RL27_MOUSE	49.92	29	26900	NA	9180
GKFMKPGKVVLVLAGRYSGRKAVIVKNI	P61358|RL27_MOUSE	49.95	29	12600	NA	NA
GKFNFHTMTIQIEK	Q2HJ10|ZNT2_MOUSE	31.56	14	313	NA	NA
GKFNFHTMTIQIEKY	Q2HJ10|ZNT2_MOUSE	31.24	15	126	NA	NA
GKFNFHTMTIQIEKYS	Q2HJ10|ZNT2_MOUSE	48.17	16	107	NA	NA
GKGM(+15.99)NPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.88	20	344	NA	155
GKGM(+15.99)NPPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	49.94	21	431	NA	220
GKITTDYNSPEAGNIF	B2RXV4|FLVC1_MOUSE	49.86	16	365	NA	213
GKKAKGKKVAPAPAVVKKQEAKKVVNP	P12970|RL7A_MOUSE	49.95	33	1690	NA	2230
GKKFTAPHILIAT	P47791|GSHR_MOUSE	41.85	13	74.6	NA	NA
GKKFTAPHILIATG	P47791|GSHR_MOUSE	44.54	14	191	NA	NA
GKKFTAPHILIATGG	P47791|GSHR_MOUSE	48.49	15	4570	NA	2440
GKKFTAPHILIATGGVP	P47791|GSHR_MOUSE	25.6	17	918	NA	NA
GKKFTAPHILIATGGVPT	P47791|GSHR_MOUSE	28.84	18	183	NA	87.2
GKKRKRSRKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2	47.74	18	7380	94000	4270
GKKRKRSRKESYSVYVYKVLKQ	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2	49.94	22	84.6	NA	348
GKKRKRSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2	49.44	26	10200	117000	29300
GKKRKRSRKESYSVYVYKVLKQVHPDT	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2	45.71	32	1620	NA	126
GKLLEAKGPVTDVAYSHD	O88342|WDR1_MOUSE	49.28	18	109	NA	NA
GKLLEAKGPVTDVAYSHDG	O88342|WDR1_MOUSE	47.76	19	269	NA	NA

GKLQDQGPDVLLAKVS	A6X935|ITIH4_MOUSE	45.79	16	184	NA	355
GKLTGM(+15.99)AFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	48.9	19	11300	374	14900
GKLTGM(+15.99)AFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MC	42.84	21	800	NA	513
GKLTGMAFRVPTPNVS	P16858|G3P_MOUSE:Q64467|G3PT_MC	48.77	16	244	NA	620
GKLTGMAFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.94	19	7490	NA	17800
GKMQHLEQTLN(+15.00)KELIS(+79.97)K	Q00898|A1AT5_MOUSE:P22599|A1AT2_	25.87	17	847	NA	NA
GKNKRLTKGGKKGAKKK	P97351|RS3A_MOUSE	41.69	17	2360	NA	NA
GKNKRLTKGGKKGAKKKVVDPFSKKDW	P97351|RS3A_MOUSE	48.95	33	250	NA	11100
GKTAWVGSLASGVGL	Q7TM99|MOT9_MOUSE	41.55	15	283	NA	250
GKVFIYHGSPTGIITKP	Q61739|ITA6_MOUSE	49.59	17	352	NA	141
GKYTYGKPVPGHVK	P28665|MUG1_MOUSE	49.88	14	6920	NA	1790
GKYTYGKPVPGHVKI	P28665|MUG1_MOUSE	49.94	15	52600	80.2	18800
GKYTYGKPVPGHVKIN	P28665|MUG1_MOUSE	49.92	16	3420	NA	762
GLELEEPPLVLAAANV	O35522|PSB9_MUSMB:P28076|PSB9_M	43.05	16	101	NA	NA
GLGKGHKFHHTIGGSRRAAWRRRNTLQ	Q9CZM2|RL15_MOUSE	49.11	32	1080	NA	NA
GLGKKS(+79.97)LEERIQEET(+79.97)HH	O54749|CP2J5_MOUSE	25.54	19	1280	NA	NA
GLPDYSAPNPIK	Q8CFG0|SULF2_MOUSE	47.58	12	10700	739	12300
GLPDYSAPNPIKV	Q8CFG0|SULF2_MOUSE	46.2	13	605	NA	662
GLPDYSAPNPIKVT	Q8CFG0|SULF2_MOUSE	49.87	14	12100	NA	14100
GLPDYSAPNPIKVTH	Q8CFG0|SULF2_MOUSE	49.53	15	92000	3850	83700
GLPDYSAPNPIKVTHR	Q8CFG0|SULF2_MOUSE	49.91	16	50300	3540	61600
GLVPIVEPEVLPDG	Q91Y97|ALDOB_MOUSE	44.76	14	801	NA	207
GLVPIVEPEVLPDGDH	Q91Y97|ALDOB_MOUSE	48.76	16	3860	NA	1330
GLVPIVEPEVLPDGDHD	Q91Y97|ALDOB_MOUSE	49.72	17	789	NA	NA
GLYEYLQPLGTPSQES	Q571I9|A16A1_MOUSE	38.76	16	364	NA	161
GM(+15.99)AFRVPTPNVS	P16858|G3P_MOUSE:Q64467|G3PT_MC	38.83	12	746	NA	92.6
GM(+15.99)AFRVPTPNVSV	P16858|G3P_MOUSE:Q64467|G3PT_MC	46.17	13	2060	NA	1330
GM(+15.99)AFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	48.51	14	7420	NA	8010
GM(+15.99)AFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	48.97	15	173000	NA	94500
GM(+15.99)AFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.31	16	1630	NA	979
GM(+15.99)AFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.07	17	1490	NA	566
GM(+15.99)NPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.56	18	2920	NA	1890
GM(+15.99)NPPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	49.81	19	2570	NA	1670
GMAFRVPTPNVS	P16858|G3P_MOUSE:Q64467|G3PT_MC	43.13	12	333	NA	325
GMAFRVPTPNVSV	P16858|G3P_MOUSE:Q64467|G3PT_MC	47.4	13	990	NA	1380
GMAFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.6	14	3070	NA	4350
GMAFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.38	15	76600	NA	85700
GMAFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.83	16	579	NA	785
GMAFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.44	17	467	NA	NA
GMN(+15.00)GSTLWSSPLPEEAQD	Q8BYI8|F234B_MOUSE	44.22	18	2870	NA	1400
GMNPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.84	18	341	NA	807
GMNPPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	48.68	19	470	NA	817
GN(+15.00)PLN(+15.00)SVFVAPAVTPVK	P70158|ASM3A_MOUSE	44.09	17	1010	NA	1070
GN(+15.00)PLN(+15.00)SVFVAPAVTPVK	P70158|ASM3A_MOUSE	36.12	18	641	NA	810
GNDLSFIHPKALSGLKE	A2ARI4|LGR4_MOUSE	40.38	17	1240	NA	1240
GNENGNFKIVTDPKTNEGIL	P55292|DSC2_MOUSE	40.8	20	359	NA	399
GNFKIVTDPKTNEG	P55292|DSC2_MOUSE	31.28	14	65.9	NA	NA
GNFKIVTDPKTNEGIL	P55292|DSC2_MOUSE	48.74	16	4570	NA	3130
GNHTLFHNPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	37.74	19	565	NA	NA
GNHYFYSPYPTKTQT	Q91YQ5|RPN1_MOUSE	32.77	15	135	NA	NA
GNIYIYNGPVLGGTR	P50284|TNR3_MOUSE	44.33	15	4620	53.7	5830
GNIYIYNGPVLGGTRG	P50284|TNR3_MOUSE	40.96	16	331	NA	382
GNIYIYNGPVLGGTRGPG	P50284|TNR3_MOUSE	49.57	18	2010	NA	2780
GNIYIYNGPVLGGTRGPGDPP	P50284|TNR3_MOUSE	37.11	21	211	NA	NA
GNKGFFVQPTVFSNVT	O35945|AL1A7_MOUSE:P24549|AL1A1_	48.96	16	3520	NA	1520
GNKGFFVQPTVFSNVTD	O35945|AL1A7_MOUSE:P24549|AL1A1_	49.04	17	492	NA	NA
GNKGFFVQPTVFSNVTDE	O35945|AL1A7_MOUSE:P24549|AL1A1_	49.61	18	1150	NA	275
GNLDPVESPEGYVAFSKPT	Q62351|TFR1_MOUSE	48.04	19	37.4	NA	NA
GNPLNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	49.83	17	6810	NA	7380
GNPLNSVFVAPAVTPVKG	P70158|ASM3A_MOUSE	49.88	18	4540	NA	5290
GNPLNSVFVAPAVTPVKGV	P70158|ASM3A_MOUSE	49.9	19	146	NA	350
GNPLNSVFVAPAVTPVKGVL	P70158|ASM3A_MOUSE	49.92	20	2550	NA	4580
GNSEFDPPGPNVAT	Q9Z1D1|EIF3G_MOUSE	44.06	14	339	NA	NA
GNSEFDPPGPNVATTT	Q9Z1D1|EIF3G_MOUSE	45.36	16	1920	NA	1310
GNVYIHPTAKVAPS	Q922H4|GMPPA_MOUSE	47.2	14	10500	NA	175
GNVYIHPTAKVAPSA	Q922H4|GMPPA_MOUSE	47.3	15	823	NA	489
GPAGPGAVEGPNPASSPD	Q99MS7|EH1L1_MOUSE	49.43	18	806	NA	NA
GPAGPGAVEGPNPASSPDA	Q99MS7|EH1L1_MOUSE	49.2	19	1070	NA	619
GPAGPGAVEGPNPASSPDANP	Q99MS7|EH1L1_MOUSE	47.42	21	135	NA	NA
GPDGKGM(+15.99)NPPSYYTQPVPVPN	Q9JLJ0|LITAF_MOUSE	49.9	21	1370	NA	1210
GPDGKGM(+15.99)NPPSYYTQPVPVPN	Q9JLJ0|LITAF_MOUSE	49.94	22	554	NA	737
GPDGKGM(+15.99)NPPSYYTQPVPVPN	Q9JLJ0|LITAF_MOUSE	49.94	23	16800	404	16700
GPDGKGM(+15.99)NPPSYYTQPVPVPN	Q9JLJ0|LITAF_MOUSE	49.94	24	8360	24.9	9710
GPDGKGMNPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.94	23	2210	NA	10600
GPDGKGMNPPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	49.94	24	1630	NA	5100
GPDGRFVM(+15.99)GPTVAPSQ	Q05BQ1|TUTLA_MOUSE	44.67	16	31200	1070	21100
GPDGRFVM(+15.99)GPTVAPSQE	Q05BQ1|TUTLA_MOUSE	44.48	17	8610	80	5570

GPDGRFVM(+15.99)GPTVAPSQEK	Q05BQ1|TUTLA_MOUSE	49.44	18	105000	2280	98700
GPDGRFVM(+15.99)GPTVAPSQEKL	Q05BQ1|TUTLA_MOUSE	49.88	19	57600	1550	20700
GPDGRFVMGPTVAPS	Q05BQ1|TUTLA_MOUSE	41.23	15	108	NA	261
GPDGRFVMGPTVAPSQ	Q05BQ1|TUTLA_MOUSE	48.47	16	14200	NA	20200
GPDGRFVMGPTVAPSQE	Q05BQ1|TUTLA_MOUSE	49.11	17	4000	NA	6170
GPDGRFVMGPTVAPSQEK	Q05BQ1|TUTLA_MOUSE	49.66	18	51300	NA	89100
GPDGRFVMGPTVAPSQEKL	Q05BQ1|TUTLA_MOUSE	49.94	19	22200	NA	42500
GPDYAHAEARKSPAL	A2ARP1|VIP1_MOUSE:Q6ZQB6|VIP2_M	49.59	15	149	NA	113
GPEAPLDELVGAYPNYNEE	Q8VCW4|UN93B_MOUSE	36.36	19	71	NA	NA
GPEPGPYAQPSVNTPLPN	Q64010|CRK_MOUSE	48.25	18	503	NA	NA
GPETHTSLRRLEQPNVVISLSR	P14483|HB2A_MOUSE	49.43	22	516	NA	NA
GPETHTSLRRLEQPNVVISLSRT	P14483|HB2A_MOUSE	49.71	23	59.7	NA	NA
GPGLGYLSSHIANVE	P13020|GELS_MOUSE	49.33	15	209	NA	305
GPGLGYLSSHIANVER	P13020|GELS_MOUSE	49.69	16	1120	NA	1690
GPGLGYLSSHIANVERVP	P13020|GELS_MOUSE	49.53	18	386	NA	509
GPGLYYVDSEGNRISG	O55234|PSB5_MOUSE	41.4	16	964	NA	716
GPGQGTTGQLFFPEVNKN	P11911|CD79A_MOUSE	39.55	18	149	NA	NA
GPHSMRYFETAVSRPGLEEP	P01899|HA11_MOUSE	47.29	20	276	NA	NA
GPIYKYPDAQNE	Q61526|ERBB3_MOUSE	46.67	12	1060	NA	909
GPKPFSAPKPQTSP	P40124|CAP1_MOUSE	48.51	14	2570	NA	1260
GPKPFSAPKPQTSPS	P40124|CAP1_MOUSE	49.85	15	43500	1420	8390
GPKPFSAPKPQTSPS(+79.97)PK	P40124|CAP1_MOUSE	49.83	17	198	NA	NA
GPKPFSAPKPQTSPS(+79.97)PKP	P40124|CAP1_MOUSE	35.76	18	288	NA	NA
GPKPFSAPKPQTSPSP	P40124|CAP1_MOUSE	49.8	16	128000	7880	94000
GPKPFSAPKPQTSPSPK	P40124|CAP1_MOUSE	49.93	17	65300	3810	54000
GPKPFSAPKPQTSPSPKP	P40124|CAP1_MOUSE	49.91	18	111000	6820	77500
GPKPFSAPKPQTSPSPKPA	P40124|CAP1_MOUSE	49.93	19	2570	NA	1760
GPLIVSGPDGAPAK	Q8VBW1|SC6A8_MOUSE	41.34	14	701	NA	670
GPLIVSGPDGAPAKG	Q8VBW1|SC6A8_MOUSE	47.42	15	1750	NA	1750
GPLIVSGPDGAPAKGDG	Q8VBW1|SC6A8_MOUSE	47.74	17	15300	194	15200
GPLIVSGPDGAPAKGDGP	Q8VBW1|SC6A8_MOUSE	49.03	18	623	NA	1210
GPM(+15.99)AKFIQSTPSKS	Q9D309|FAM3B_MOUSE	36.64	14	174	NA	NA
GPM(+15.99)AKFIQSTPSKSL	Q9D309|FAM3B_MOUSE	49.48	15	1590	NA	1540
GPM(+15.99)AKFIQSTPSKSLL	Q9D309|FAM3B_MOUSE	49.76	16	3580	NA	3940
GPM(+15.99)AKFIQSTPSKSLLF	Q9D309|FAM3B_MOUSE	49.52	17	2580	NA	2370
GPMAKFIQSTPSKS	Q9D309|FAM3B_MOUSE	49.13	14	121	NA	387
GPMAKFIQSTPSKSL	Q9D309|FAM3B_MOUSE	49.72	15	1550	NA	2330
GPMAKFIQSTPSKSLL	Q9D309|FAM3B_MOUSE	49.57	16	1640	NA	3500
GPMAKFIQSTPSKSLLF	Q9D309|FAM3B_MOUSE	49.81	17	1010	NA	2500
GPNASYFSVNANTGEVK	E9Q7P9|CDHR2_MOUSE	49.29	17	4130	NA	2560
GPNFEYAEAPSRLSPDD	P11152|LIPL_MOUSE	45.7	17	1750	NA	246
GPPIFNPVANEVY	Q07113|MPRI_MOUSE	47.64	13	286	NA	241
GPPIFNPVANEVYL	Q07113|MPRI_MOUSE	44.99	14	230	NA	NA
GPPIFNPVANEVYLN	Q07113|MPRI_MOUSE	49.32	15	1880	NA	1660
GPPNTSYM(+15.99)PGM(+15.99)PSGIS	Q61187|TS101_MOUSE	29.31	17	193	NA	NA
GPPPGWEGPHPQRG	Q91WT8|RBM47_MOUSE	47.06	14	47.1	NA	NA
GPPPYHESLAGASQPP	Q9D7I0|SHSA5_MOUSE	48.04	16	41900	NA	44400
GPPPYHESLAGASQPPY	Q9D7I0|SHSA5_MOUSE	48.92	17	5470	NA	4210
GPQVILAKEPKAQVAVHERK	Q99MZ6|MYO7B_MOUSE	49.94	20	568	NA	NA
GPRGPPPAGLLQ	P06345|HB2S_MOUSE:P06346|HB2F_M	27.81	12	3460	NA	1890
GPRIRGNVYIHPTAKVAPS	Q922H4|GMPPA_MOUSE	49.42	19	1150	NA	1160
GPSAPATPAAEAKAAEAAASAYY	P97765|WBP2_MOUSE	49.85	23	865	NA	NA
GPSAPATPAAEAKAAEAAASAYYNP	P97765|WBP2_MOUSE	35.92	25	206	NA	NA
GPSAPATPAAEAKAAEAAASAYYNPG	P97765|WBP2_MOUSE	49.8	26	1470	NA	723
GPSQPAVLQPSVEPAQ	Q9ERN0|SCAM2_MOUSE	47.78	16	158	NA	NA
GPSQPAVLQPSVEPAQP	Q9ERN0|SCAM2_MOUSE	49.31	17	1070	NA	1480
GPSQPAVLQPSVEPAQPT	Q9ERN0|SCAM2_MOUSE	49.16	18	969	NA	NA
GPSQPAVLQPSVEPAQPTP	Q9ERN0|SCAM2_MOUSE	49.86	19	3250	NA	4460
GPSQPAVLQPSVEPAQPTPQ	Q9ERN0|SCAM2_MOUSE	49.76	20	984	NA	1530
GPSQPRQYNNPIGLYSAE	Q9JKS4|LDB3_MOUSE	29.39	18	72.8	NA	NA
GPSQPRQYNNPIGLYSAET	Q9JKS4|LDB3_MOUSE	47.66	19	841	NA	917
GPSRGQYYGGSLPNVNQ	Q68ED7|CRTC1_MOUSE	29.62	17	48.7	NA	42.7
GPTYRGPVPWHT	Q9WV54|ASAH1_MOUSE	34.63	12	380	NA	868
GPTYRGPVPWHTIN	Q9WV54|ASAH1_MOUSE	44.64	14	13100	114	17100
GPVHNTLMSPQVSSSQG	Q3U2P1|SC24A_MOUSE	45.26	17	728	NA	2210
GPVPEFSGATVERVSE	Q99KP3|CRYL1_MOUSE	37.26	16	148	NA	NA
GPVPEFSGATVERVSEDM(+15.99)	Q99KP3|CRYL1_MOUSE	25.63	18	262	NA	NA
GPVTPLSPSVLPSLPQ	Q6NS82|RETR2_MOUSE	44.83	16	739	NA	434
GPYQAAAGPSVVPTAPP	Q9JLJ0|LITAF_MOUSE	48.95	17	288	NA	314
GPYSNPYSTSYSGPYPAAAPPVPA	Q9WVH9|FBLN5_MOUSE	46.65	24	64.6	NA	NA
GPYYTEPVIAGLDPK	Q9R1P1|PSB3_MOUSE	49.65	15	643	NA	330
GQDHVDFSQPEPHTVLFH	Q9QUR8|SEM7A_MOUSE	49.42	18	1380	NA	NA
GQDHVDFSQPEPHTVLFHEPG	Q9QUR8|SEM7A_MOUSE	31.16	21	31	NA	NA
GQLPDYTSPVVLPYSR	P32233|DRG1_MOUSE	48.74	16	289	NA	300
GQNAWFLPAQADIVATK	P10852|4F2_MOUSE	48.81	17	4290	NA	5220
GRDKYEPAAVSEHGDK	Q8VDN2|AT1A1_MOUSE	49.32	16	2040	NA	1340
GRDKYEPAAVSEHGDKKGKKAKKER	Q8VDN2|AT1A1_MOUSE	49.95	25	1600	NA	NA

GREVSSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	36.64	16	114	NA	260
GREVSSVEAPSVSPARHQ	Q8BUJ9|LRP12_MOUSE	48.91	18	321	NA	390
GRFTYQNAAAQPETGPG	Q9QZM4|TR10B_MOUSE	48.32	17	22300	200	14000
GRFVM(+15.99)GPTVAPSQ	Q05BQ1|TUTLA_MOUSE	39.68	13	2210	NA	1190
GRFVM(+15.99)GPTVAPSQE	Q05BQ1|TUTLA_MOUSE	27.83	14	477	NA	NA
GRFVM(+15.99)GPTVAPSQEK	Q05BQ1|TUTLA_MOUSE	46.74	15	8810	NA	3260
GRFVM(+15.99)GPTVAPSQEKL	Q05BQ1|TUTLA_MOUSE	44.91	16	906	NA	246
GRFVMGPTVAPSQ	Q05BQ1|TUTLA_MOUSE	36.08	13	1230	NA	1230
GRFVMGPTVAPSQE	Q05BQ1|TUTLA_MOUSE	45.23	14	257	NA	336
GRFVMGPTVAPSQEK	Q05BQ1|TUTLA_MOUSE	48.49	15	4750	NA	4970
GRFVMGPTVAPSQEKL	Q05BQ1|TUTLA_MOUSE	45.26	16	164	NA	438
GRIEHLYKNPQAHIEGNM	Q8K0C9|GMDS_MOUSE	32.61	18	117	NA	379
GRIEHLYKNPQAHIEGNM(+15.99)	Q8K0C9|GMDS_MOUSE	49.93	18	505	NA	387
GRKFVYAGSNSGVVQAPL	O09126|SEM4D_MOUSE	28.35	18	204	153	289
GRLEVVTDPTTNAG	Q9R100|CAD17_MOUSE	48.44	14	2180	NA	1400
GRLEVVTDPTTNAGY	Q9R100|CAD17_MOUSE	49.65	15	1350	NA	844
GRLEVVTDPTTNAGYV	Q9R100|CAD17_MOUSE	49.9	16	3750	38.3	3240
GRLEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	49.93	17	31900	415	34800
GRLEVVTDPTTNAGYVKI	Q9R100|CAD17_MOUSE	49.77	18	251	NA	NA
GRLEVVTDPTTNAGYVKIK	Q9R100|CAD17_MOUSE	49.93	19	267	NA	354
GRLSYLPATTEPALPIPG	Q9JIA7|SPHK2_MOUSE	39.85	18	883	NA	741
GRPDAEYWNSQPEIL	P14483|HB2A_MOUSE:P01921|HB2D_M	40.76	15	172	NA	NA
GRPDAEYWNSQPEILE	P14483|HB2A_MOUSE:P01921|HB2D_M	48.15	16	917	NA	333
GRPDAEYWNSQPEILER	P14483|HB2A_MOUSE:P01921|HB2D_M	49.31	17	2160	NA	1740
GRRASHTAPQVLFSHREPP	Q9CVB6|ARPC2_MOUSE	43.86	19	2130	NA	2200
GRYEKLAEPTVSYSSYR	Q04592|PCSK5_MOUSE	29.55	17	153	NA	NA
GSDIFAAPAPQSTAT	Q8K2K6|AGFG1_MOUSE	45.42	15	1230	NA	1670
GSDM(+15.99)FKASLVIPSK	Q8BJD1|ITIH5_MOUSE	31.3	14	82.3	NA	85.2
GSDM(+15.99)FKASLVIPSKD	Q8BJD1|ITIH5_MOUSE	48.49	15	11700	2210	5020
GSDM(+15.99)FKASLVIPSKDK	Q8BJD1|ITIH5_MOUSE	46.93	16	9800	1590	4880
GSDM(+15.99)FKASLVIPSKDKA	Q8BJD1|ITIH5_MOUSE	36.87	17	2350	NA	874
GSDMFKASLVIPSK	Q8BJD1|ITIH5_MOUSE	44.23	14	182	NA	233
GSDMFKASLVIPSKD	Q8BJD1|ITIH5_MOUSE	48.44	15	5480	108	4270
GSDMFKASLVIPSKDK	Q8BJD1|ITIH5_MOUSE	49.2	16	6190	NA	6600
GSDMFKASLVIPSKDKA	Q8BJD1|ITIH5_MOUSE	48.86	17	1360	NA	1460
GSFVYKGGKIYKVPS	P50396|GDIA_MOUSE:Q61598|GDIB_M(	48.44	15	144	NA	103
GSGFAAPFFIVRHQLLKK	P17665|COX7C_MOUSE	48.82	18	386	NA	298
GSGGVFRAPSIHGGSG	P19001|K1C19_MOUSE	45.91	16	2100	118	7250
GSGGVFRAPSIHGGSGGR	P19001|K1C19_MOUSE	49.68	18	4070	278	10200
GSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	49.67	19	3650	222	6610
GSGIFVSPKGVLEN	Q9QXW9|LAT2_MOUSE	29.63	14	434	NA	NA
GSGIFVSPKGVLENA	Q9QXW9|LAT2_MOUSE	46.79	15	133	NA	NA
GSILWSQPLPSLPGGPP	Q8C0Z1|F234A_MOUSE	49.56	17	6940	NA	8200
GSILWSQPLPSLPGGPPS	Q8C0Z1|F234A_MOUSE	49.76	18	1790	NA	1020
GSLFLKTPKIVSSKD	P06151|LDHA_MOUSE	49.91	15	15000	130	10900
GSLFLKTPKIVSSKDY	P06151|LDHA_MOUSE	49.85	16	12200	116	9930
GSLSTYLPSQPAPG	P47878|IBP3_MOUSE	38.5	14	1330	NA	1340
GSLSTYLPSQPAPGNIS	P47878|IBP3_MOUSE	48.52	17	1440	NA	NA
GSPGYNPPQM(+15.99)NTLP	Q8K419|LEG4_MOUSE	38.24	14	540	NA	252
GSPGYNPPQM(+15.99)NTLPV	Q8K419|LEG4_MOUSE	45.95	15	3880	NA	1400
GSPGYNPPQMNTLPV	Q8K419|LEG4_MOUSE	44.49	15	1630	NA	2420
GSPNYAAPEVISGRL	Q5EG47|AAPK1_MOUSE:Q8BRK8|AAPK	43.44	15	986	NA	1190
GSTLWSSPLPEEA	Q8BYI8|F234B_MOUSE	41.69	13	153	NA	84.1
GSTLWSSPLPEEAQ	Q8BYI8|F234B_MOUSE	45.81	14	48.6	NA	NA
GSTLWSSPLPEEAQD	Q8BYI8|F234B_MOUSE	49.28	15	5410	NA	3210
GSTLWSSPLPEEAQDV	Q8BYI8|F234B_MOUSE	46.59	16	142	NA	56.7
GSTLWSSPLPEEAQDVT	Q8BYI8|F234B_MOUSE	29.5	17	99.5	NA	NA
GSVLWERPVAQDVA	Q8C0Z1|F234A_MOUSE	46.93	14	761	NA	798
GSVLWERPVAQDVAL	Q8C0Z1|F234A_MOUSE	49.73	15	2050	NA	1770
GSVLWERPVAQDVALV	Q8C0Z1|F234A_MOUSE	49.94	16	236	NA	215
GSVRIGSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	46.53	24	337	NA	1010
GSVTYIAPPGNYD	P50516|VATA_MOUSE	27.88	13	206	NA	174
GSVTYIAPPGNYDAS	P50516|VATA_MOUSE	29.67	15	711	NA	693
GTAKVLQPSAARNK	Q9EQK5|MVP_MOUSE	27.83	14	272	NA	294
GTAKVLQPSAARNKT	Q9EQK5|MVP_MOUSE	37.05	15	263	NA	NA
GTATAKKSTKKTPKKAKKPA	P43274|H14_MOUSE	49.95	20	8900	NA	4020
GTDRKIVYEGPELNHAFG	Q91ZX7|LRP1_MOUSE	49.83	18	4760	NA	65000
GTGAAGSFKLNKKAESKAITTKVSVKAK	P43275|H11_MOUSE	49.78	28	92.9	NA	NA
GTGGGSVRIGSGGVFRAPSIHGGSGGR	P19001|K1C19_MOUSE	49.94	28	15200	NA	18000
GTGGLPDYSAPNPIKVTHR	Q8CFG0|SULF2_MOUSE	49.77	19	1330	NA	2300
GTIRYM(+15.99)APEVLEG	O35607|BMPR2_MOUSE	33.37	13	114	NA	NA
GTIRYM(+15.99)APEVLEGAV	O35607|BMPR2_MOUSE	47.94	15	829	NA	368
GTIRYM(+15.99)APEVLEGAVN	O35607|BMPR2_MOUSE	46.04	16	1550	NA	708
GTIRYMAPEVLEGAV	O35607|BMPR2_MOUSE	45.18	15	266	NA	354
GTIRYMAPEVLEGAVN	O35607|BMPR2_MOUSE	47.11	16	302	NA	433
GTKRYM(+15.99)APEVLDETIN	Q61271|ACV1B_MOUSE	49.08	16	3680	NA	2530
GTKRYMAPEVLDESL	P36895|BMR1A_MOUSE	35.84	15	332	NA	NA

GTKRYMAPEVLDET	Q61271|ACV1B_MOUSE:P37172|ACVR1	27.9	14	147	NA	NA
GTKRYMAPEVLDETI	Q61271|ACV1B_MOUSE:P37172|ACVR1	27.08	15	42.5	NA	NA
GTKRYMAPEVLDETIN	Q61271|ACV1B_MOUSE	47.76	16	5140	NA	5090
GTLVQTKGTGAAGSFKLNK	P43275|H11_MOUSE	49.88	19	89.6	NA	NA
GTLVQTKGTGAAGSFKLNKKAESK	P43275|H11_MOUSE	49.93	24	153	NA	144
GTNM(+15.99)YNTDRANPVLD	E9Q7P9|CDHR2_MOUSE	49.04	15	2770	NA	2370
GTNM(+15.99)YNTDRANPVLDL	E9Q7P9|CDHR2_MOUSE	39.12	16	260	NA	214
GTNM(+15.99)YNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	49.84	17	8090	253	7800
GTNM(+15.99)YNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	49.92	18	1040	NA	944
GTNMYNTDRANPVLD	E9Q7P9|CDHR2_MOUSE	48.59	15	1480	NA	2640
GTNMYNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	49.01	17	4050	NA	9330
GTNMYNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	49.78	18	269	NA	927
GTPDYIAPEIIAYQP	P63318|KPCG_MOUSE:P20444|KPCA_M	35.78	15	69.1	NA	96.3
GTPDYIAPEIIAYQPY	P63318|KPCG_MOUSE:P20444|KPCA_M	46.51	16	991	NA	1220
GTPDYIAPEILQG	P28867|KPCD_MOUSE	32.16	13	899	NA	416
GTPDYIAPEILQGLK	P28867|KPCD_MOUSE	45.34	15	733	NA	570
GTPEFVAPEVINYE	Q6PDN3|MYLK_MOUSE	41.69	14	268	NA	NA
GTPEFVAPEVINYEPI	Q6PDN3|MYLK_MOUSE	47.28	16	1930	NA	1190
GTPEYLAPEIILS	P68181|KAPCB_MOUSE:P05132|KAPCA	38.87	13	630	NA	465
GTPEYLAPEIILSK	P68181|KAPCB_MOUSE:P05132|KAPCA	48.76	14	12000	189	11100
GTPEYLAPEIILSKG	P68181|KAPCB_MOUSE:P05132|KAPCA	49.35	15	57800	2170	50000
GTPEYLAPEIILSKGY	P68181|KAPCB_MOUSE:P05132|KAPCA	49.52	16	69.1	NA	95.4
GTPEYLAPEIILSKGYN	P68181|KAPCB_MOUSE:P05132|KAPCA	46.36	17	6070	NA	5720
GTPEYLAPEVIQSKG	Q922R0|PRKX_MOUSE	40.07	15	110	NA	208
GTPEYVAPEVILN	Q61410|KGP2_MOUSE	47.49	13	158	NA	NA
GTPEYVAPEVILNK	Q61410|KGP2_MOUSE	48.86	14	12800	NA	NA
GTPEYVAPEVILNKG	Q61410|KGP2_MOUSE	48.3	15	14300	255	11200
GTPEYVAPEVILNKGHD	Q61410|KGP2_MOUSE	48.84	17	1150	NA	1070
GTRELVAPRANTLK	O54782|MA2B2_MOUSE	38.87	14	610	NA	368
GTRELVAPRANTLKF	O54782|MA2B2_MOUSE	29.08	15	814	NA	290
GTRRYM(+15.99)APEVLEGAI	P27038|AVR2A_MOUSE:P27040|AVR2B	26.3	15	722	NA	NA
GTRRYM(+15.99)APEVLEGAIN	P27038|AVR2A_MOUSE:P27040|AVR2B	25.66	16	6510	NA	2310
GTRRYMAPEVLEGAI	P27038|AVR2A_MOUSE:P27040|AVR2B	28.2	15	204	NA	640
GTRRYMAPEVLEGAIN	P27038|AVR2A_MOUSE:P27040|AVR2B	25.59	16	4750	NA	5130
GTSRHPGPL	P23150|HA2J_MOUSE:P14434|HA2B_M	41.86	9	10700	644	6880
GTSYQSPHGIPID	Q9WTM5|RUVB2_MOUSE	29.94	13	207	NA	71.5
GVAYEAPSLATGYG	P99026|PSB4_MOUSE	48.37	14	186	NA	178
GVELYRAPFPLYA	Q9WUQ2|PREB_MOUSE	42.7	13	119	NA	NA
GVELYRAPFPLYALR	Q9WUQ2|PREB_MOUSE	48.39	15	1250	NA	659
GVFRAPSIHGGSG	P19001|K1C19_MOUSE	32.58	13	142	NA	1300
GVFRAPSIHGGSGGR	P19001|K1C19_MOUSE	30.59	15	361	NA	674
GVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	42.81	16	1080	NA	440
GVFSNPAVRTAAAN	O35609|SCAM3_MOUSE	44.9	14	370	NA	263
GVKKVAKSPKKAK	P43276|H15_MOUSE	49.56	13	2150	NA	NA
GVLPNIQAVLLPKKTESHHKAK	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	49.94	22	2900	10300	6150
GVPDDLLYSFPVVIKNK	P14152|MDHC_MOUSE	49.9	17	789	NA	1120
GVPTVPLLPPQVNQSLA	Q99JX3|GORS2_MOUSE	42.86	17	558	NA	585
GVPTVPLLPPQVNQSLASM(+15.99)PP	Q99JX3|GORS2_MOUSE	48.1	21	254	NA	566
GVPVQAPQVPEAIEK	Q8VDP3|MICA1_MOUSE	48.11	15	391	NA	1170
GVPVQAPQVPEAIEKGD	Q8VDP3|MICA1_MOUSE	49.73	17	890	NA	209
GVSSEFYSQPGALPPPP	Q91XT4|SC16B_MOUSE	48.64	17	180	NA	165
GVSSQETAGIGASAHLVNFK	Q99KQ4|NAMPT_MOUSE	49.55	20	2540	1850	2510
GVYASPSIAGSRP	Q8R0X7|SGPL1_MOUSE	33.38	13	195	NA	NA
GVYASPSIAGSRPG	Q8R0X7|SGPL1_MOUSE	46.29	14	3880	NA	1970
GVYTYGKPVPGLV	Q61838|PZP_MOUSE	44.33	13	64	NA	129
GVYTYGKPVPGLVT	Q61838|PZP_MOUSE	49.38	14	8490	318	9740
GVYTYGKPVPGLVTL	Q61838|PZP_MOUSE	49.68	15	4600	NA	5510
GVYTYGKPVPGLVTLR	Q61838|PZP_MOUSE	49.91	16	1330	NA	1020
GYAVYETPTAH	Q9QZ06|TOLIP_MOUSE	38.11	11	299	NA	348
GYAVYETPTAHN	Q9QZ06|TOLIP_MOUSE	39.39	12	666	NA	441
GYAVYETPTAHNG	Q9QZ06|TOLIP_MOUSE	39.3	13	1080	NA	764
GYAVYETPTAHNGA	Q9QZ06|TOLIP_MOUSE	44.95	14	328	NA	254
GYAVYETPTAHNGAK	Q9QZ06|TOLIP_MOUSE	45.75	15	1880	NA	525
GYAVYETPTAHNGAKN	Q9QZ06|TOLIP_MOUSE	48.73	16	1010	NA	NA
GYAVYETPTAHNGAKNP	Q9QZ06|TOLIP_MOUSE	49.86	17	13700	NA	6850
GYAVYETPTAHNGAKNPR	Q9QZ06|TOLIP_MOUSE	49.92	18	24800	408	22800
GYGPYSGAYPAGTQVV	Q9QZC7|PKHB2_MOUSE	48.92	16	685	NA	NA
GYKFSAPVVPSSFN	Q9EPL8|IPO7_MOUSE	48.26	14	65.1	NA	NA
GYKPFQNPVPNQSPS	P16382|IL4RA_MOUSE	49.59	15	20200	890	33200
GYKPFQNPVPNQSPSS	P16382|IL4RA_MOUSE	49.49	16	1700	NA	1300
GYPTAYPAAAPAYNPS	Q8BGZ2|F168A_MOUSE	46.91	16	3930	56.1	3340
GYRYPRALEEEVE	Q8K3K8|OPTN_MOUSE	42.23	13	489	NA	NA
HAAHFAQAFPNAEWQPS	Q9DCS2|MTL26_MOUSE	43.46	17	616	NA	531
HARQQVRSPVTNIA	P84091|AP2M1_MOUSE	26.27	14	455	NA	436
HARQQVRSPVTNIAR	P84091|AP2M1_MOUSE	47.15	15	3810	NA	4240
HARQQVRSPVTNIART	P84091|AP2M1_MOUSE	32.62	16	672	NA	NA
HDLRHAFSPVASVESA	P29699|FETUA_MOUSE	49.68	16	9210	NA	12800

HDLRHAFSPVASVESAS	P29699|FETUA_MOUSE	49.89	17	13200	NA	10300
HDLRHAFSPVASVESASG	P29699|FETUA_MOUSE	49.93	18	2670	NA	1830
HDLRHAFSPVASVESASGET	P29699|FETUA_MOUSE	49.59	20	2590	NA	1230
HDLRHAFSPVASVESASGETLHSPK	P29699|FETUA_MOUSE	49.95	25	533	NA	128
HDTSYKPPAGRTAAP	Q69ZQ1|MYORG_MOUSE	38.41	15	1270	NA	842
HDTSYKPPAGRTAAPE	Q69ZQ1|MYORG_MOUSE	49.6	16	5840	NA	5570
HDYKGSTSHSLPY	E9Q414|APOB_MOUSE	46.91	13	1680	NA	898
HDYKGSTSHSLPYE	E9Q414|APOB_MOUSE	37.38	14	1180	NA	857
HELRYQVPGAVPAK	Q9Z280|PLD1_MOUSE	49.69	14	3470	NA	2960
HELRYQVPGAVPAKVQ	Q9Z280|PLD1_MOUSE	48.17	16	243	NA	239
HEVVVIAPEASIH	Q63886|UD11_MOUSE	44.97	13	161	NA	NA
HEVVVIAPEASIHIK	Q63886|UD11_MOUSE	49.42	15	7140	84.6	2430
HGAIVDGPVPITIEV	Q9R100|CAD17_MOUSE	47.17	15	636	NA	508
HGDKKGKKAKKER	Q8VDN2|AT1A1_MOUSE	49.85	13	21300	NA	NA
HGFYVSPSVLSALVPS	Q8BXQ2|PIGT_MOUSE	40.76	16	139	NA	NA
HGGEDVAIFARGPQAHLVHG	P24822|PPBI_MOUSE	37.16	20	180	NA	NA
HGGEDVAIFARGPQAHLVHGVQ	P24822|PPBI_MOUSE	49.92	22	446	NA	NA
HGGYKFSAPVVPSSFN	Q9EPL8|IPO7_MOUSE	48.59	16	1880	NA	1890
HGGYKFSAPVVPSSFNF	Q9EPL8|IPO7_MOUSE	26.57	17	154	NA	NA
HGLELEEPPLVLAAANV	O35522|PSB9_MUSMB:P28076|PSB9_M	45.14	17	974	NA	344
HGSLFLKTPKIVSSKD	P06151|LDHA_MOUSE	49.91	16	2950	NA	2230
HGSLFLKTPKIVSSKDY	P06151|LDHA_MOUSE	49.94	17	2380	NA	2110
HGTDDGVVWM(+15.99)NWK	Q8K0E8|FIBB_MOUSE	47.78	13	656	145	NA
HGTDDGVVWMNWK	Q8K0E8|FIBB_MOUSE	48.39	13	2850	NA	NA
HHPADFTPAVHASLDK	P01942|HBA_MOUSE	49.93	16	1050	NA	1410
HIFNKVVGPNGLLSGKT	Q8VI47|MRP2_MOUSE	49.89	17	196	NA	NA
HINIVVIGH	P62631|EF1A2_MOUSE:P10126|EF1A1_	43.13	9	109	324	470
HLKIVYRRFRHGFREGTTPKPKR	Q9D823|RL37_MOUSE	48.89	23	8700	12200	5560
HLKIVYRRFRHGFREGTTPKPKRA	Q9D823|RL37_MOUSE	49.56	24	9660	4100	685
HLQLAIRN	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	37.48	8	386	1000	194
HLQLAIRND	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	42.59	9	1760	1920	302
HLRFNYPEVQKVM(+15.99)PR	Q6XQH0|G3ST2_MOUSE	49.88	15	7780	NA	3150
HLRFNYPEVQKVMPR	Q6XQH0|G3ST2_MOUSE	49.77	15	4970	NA	4590
HLRFSAPQIENEP	Q61190|I10R2_MOUSE	42.27	13	466	NA	324
HLRFSAPQIENEPE	Q61190|I10R2_MOUSE	49.18	14	10700	NA	8060
HLRFSAPQIENEPET	Q61190|I10R2_MOUSE	48.83	15	393	NA	380
HNFPYKDPVAALYED	P16301|LCAT_MOUSE	48.01	15	1400	NA	NA
HNFPYKDPVAALYEDG	P16301|LCAT_MOUSE	46.94	16	1480	NA	NA
HNYEGPETHTSL	P14483|HB2A_MOUSE	48.17	12	9200	2730	4350
HNYEGPETHTSLR	P14483|HB2A_MOUSE	49.57	13	22500	3730	14600
HPADFTPAVHASLDK	P01942|HBA_MOUSE	48.78	15	438	NA	74.9
HPAPGRDLHYQNPHSNAVGNP	Q01279|EGFR_MOUSE	45.39	21	3750	NA	3320
HPDRFAYPIPHTTRPP	O70589|CSKP_MOUSE	49.77	16	9910	NA	7140
HPIQWNAPEPSHITK	P11276|FINC_MOUSE	49.45	15	4220	NA	5800
HPQTYYYAVAVVKKG	Q921I1|TRFE_MOUSE	49.27	15	325	NA	681
HPQTYYYAVAVVKKGTD	Q921I1|TRFE_MOUSE	49.82	17	104	NA	179
HPQTYYYAVAVVKKGTDF	Q921I1|TRFE_MOUSE	49.88	18	188	NA	192
HPQTYYYAVAVVKKGTDFQ	Q921I1|TRFE_MOUSE	49.91	19	334	NA	325
HPSFGVDFPNSQFSKDR	P32507|NECT2_MOUSE	49.46	17	159	NA	NA
HPSSHVFM(+15.99)PPSPSTTPP	Q571K4|TAB3_MOUSE	33.46	17	1060	NA	NA
HPSSHVFM(+15.99)PPSPSTTPPH	Q571K4|TAB3_MOUSE	41.4	18	4590	NA	3060
HPSSHVFMPPSPSTTPP	Q571K4|TAB3_MOUSE	48.42	17	206	NA	747
HPSSHVFMPPSPSTTPPH	Q571K4|TAB3_MOUSE	48.12	18	623	NA	1040
HQ(+15.00)VARYRPRAPIIAVTRNP	P52480|KPYM_MOUSE	40.67	19	1440	NA	NA
HRDPYATSVGHLIE	Q923U0|TM1L1_MOUSE	47.72	14	99.3	NA	NA
HRDPYATSVGHLIEK	Q923U0|TM1L1_MOUSE	49.42	15	322	NA	151
HRPFSAPHSSRDQLPPP	Q60805|MERTK_MOUSE	40.19	17	6420	NA	4450
HRSPVATPTPTM(+15.99)SLPE	Q61805|LBP_MOUSE	45.72	16	537	NA	NA
HRSPVATPTPTMSLPE	Q61805|LBP_MOUSE	36.71	16	527	NA	822
HSEPEYATPIVERHLL	Q9D4J3|DCBD1_MOUSE	49.63	16	30.4	NA	NA
HSVIVNSPVITAAINK	Q80TS3|AGRL3_MOUSE	47.77	16	692	NA	137
HSVLTGDGYILSIHRIPRGRK	Q9Z0M5|LICH_MOUSE	49.63	21	165	NA	NA
HTIAYLTPLPQPN	Q91VS7|MGST1_MOUSE	46.67	13	396	NA	118
HTIAYLTPLPQPNR	Q91VS7|MGST1_MOUSE	45.72	14	3410	NA	1260
HTIAYLTPLPQPNRG	Q91VS7|MGST1_MOUSE	47.62	15	3070	NA	1590
HTKGALPLDTVTFYKVIPKSKFVLVKF	P57759|ERP29_MOUSE	47.37	27	5180	NA	200
HTLFHNPHVNPL	P43023|CX6A2_MOUSE:P43024|CX6A1_	42.03	12	335	NA	155
HTLFHNPHVNPLP	P43023|CX6A2_MOUSE:P43024|CX6A1_	48.51	13	1780	160	2210
HTLFHNPHVNPLPT	P43023|CX6A2_MOUSE:P43024|CX6A1_	49.64	14	8410	662	7000
HTLFHNPHVNPLPTG	P43023|CX6A2_MOUSE:P43024|CX6A1_	48.26	15	510	NA	700
HTLFHNPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	47.07	17	324	NA	654
HTYGDPHVNLVIG	Q80T32|AGRD1_MOUSE	39.64	13	193	NA	64.6
HVPTLQVLRPGLVVVH	Q9D3D9|ATPD_MOUSE	46.92	16	968	NA	3900
HVPTLQVLRPGLVVVHTE	Q9D3D9|ATPD_MOUSE	26.53	18	1030	NA	NA
HYQSFQYPTTAGTFR	Q3V3F6|MPZL3_MOUSE	47.51	15	127	NA	104
I(+42.01)PGTN(+15.00)MYNTDRANPVLI	E9Q7P9|CDHR2_MOUSE	37.29	17	281	NA	492
I(+42.01)TN(+15.00)QYNSPTGLYSSEN	O70400|PDLI1_MOUSE	45.03	16	403	NA	NA

IAEDYFMAKAIADRG	O88693|CEGT_MOUSE	49.71	15	225	NA	298
IAFLSPKVDPS	Q9CQU3|RER1_MOUSE	26.3	11	555	NA	336
IAFLSPKVDPSL	Q9CQU3|RER1_MOUSE	36.75	12	287	NA	195
IAIYYHASRAIPF	Q9ET30|TM9S3_MOUSE	47.8	13	268	NA	283
IAIYYHASRAIPFG	Q9ET30|TM9S3_MOUSE	49.34	14	917	NA	1640
IAPSVQLTGYR	P11276|FINC_MOUSE	44.95	11	300	NA	200
IARQNFTEPTAIQAQG	Q61656|DDX5_MOUSE	41.55	16	178	NA	238
IASFKDPKISTSLPV	Q61233|PLSL_MOUSE	49.02	15	601	NA	NA
IAVVNYETGKVIATKYF	Q9D309|FAM3B_MOUSE	46.61	17	42.6	NA	NA
IAYLTPLPQPNR	Q91VS7|MGST1_MOUSE	35.82	12	235	NA	NA
IAYLTPLPQPNRG	Q91VS7|MGST1_MOUSE	38.09	13	83.7	NA	NA
IDAVYEAPQEEKA	P33434|MMP2_MOUSE	41.96	13	116	NA	NA
IDAVYEAPQEEKAVF	P33434|MMP2_MOUSE	47.11	15	418	NA	209
IDAVYEAPQEEKAVFF	P33434|MMP2_MOUSE	48.8	16	936	NA	530
IDDM(+15.99)YTPAYGDFNFD	Q69ZQ1|MYORG_MOUSE	36.84	15	105	NA	NA
IDDQNLRPYQGGKANILGYN	Q6XQH0|G3ST2_MOUSE	49.68	20	133	NA	NA
IDIFARPTAGFITG	P57787|MOT4_MOUSE	41.14	14	179	NA	198
IDIFSTPSSSNSTSK	Q7M6Y3|PICAL_MOUSE	35.12	15	804	NA	824
IDPYDQPNAIYIE	O88307|SORL_MOUSE	35.71	13	425	NA	NA
IDPYDQPNAIYIER	O88307|SORL_MOUSE	49.37	14	10100	372	6190
IDPYDQPNAIYIERH	O88307|SORL_MOUSE	49.67	15	3110	NA	2490
IDPYDQPNAIYIERHEP	O88307|SORL_MOUSE	40.2	17	160	NA	174
IDTTIAYPKAEPID	Q91YX5|LGAT1_MOUSE	44.45	14	2940	NA	2130
IDTTIAYPKAEPIDIQ	Q91YX5|LGAT1_MOUSE	49.19	16	195	NA	NA
IDWTYRPPSSSRTES	Q3V3F6|MPZL3_MOUSE	25.39	15	714	NA	1220
IEDIEVAPPKAHEVR	P00329|ADH1_MOUSE	47.48	15	17800	188	16200
IEDIEVAPPKAHEVRIK	P00329|ADH1_MOUSE	49.93	17	7350	NA	5670
IEDNYIQPGAGEM(+15.99)E	Q9CQM1|CA210_MOUSE	27.18	14	832	NA	122
IEEIEVAPPKAHEVR	P28474|ADHX_MOUSE	43.14	15	2750	NA	2700
IEEIEVAPPKAHEVRIK	P28474|ADHX_MOUSE	49.09	17	367	NA	537
IEFRGPNGLLVYQ	Q9DCN2|NB5R3_MOUSE	35.95	13	268	NA	146
IEFRGPNGLLVYQG	Q9DCN2|NB5R3_MOUSE	44.63	14	3730	NA	2600
IEFRGPNGLLVYQGK	Q9DCN2|NB5R3_MOUSE	49.01	15	1550	NA	1130
IEFTFERSNTNPSVT	P22892|AP1G1_MOUSE	49.07	15	363	NA	NA
IEHLYKNPQAHIE	Q8K0C9|GMDS_MOUSE	40.34	13	101	NA	NA
IEHLYKNPQAHIEG	Q8K0C9|GMDS_MOUSE	49.63	14	5350	NA	4420
IEHLYKNPQAHIEGN	Q8K0C9|GMDS_MOUSE	49.83	15	1370	NA	1180
IEHLYKNPQAHIEGNM	Q8K0C9|GMDS_MOUSE	49.94	16	2530	NA	4550
IEHLYKNPQAHIEGNM(+15.99)	Q8K0C9|GMDS_MOUSE	49.91	16	6660	NA	2880
IEKVIPSTANSN	E9Q7P9|CDHR2_MOUSE	37.67	12	5560	NA	3020
IEKVIPSTANSNN	E9Q7P9|CDHR2_MOUSE	41.06	13	3540	NA	1760
IEKVIPSTANSNNL	E9Q7P9|CDHR2_MOUSE	44.74	14	15300	239	8440
IEKVIPSTANSNNLF	E9Q7P9|CDHR2_MOUSE	44.31	15	2670	NA	1770
IEKVIPSTANSNNLFR	E9Q7P9|CDHR2_MOUSE	35	16	53.9	NA	NA
IENDPGFGAPAASQVASAQPG	Q6IRU5|CLCB_MOUSE	49.11	21	464	NA	1020
IESKEAFQEALAAAGDK	P10639|THIO_MOUSE	49.86	17	3020	NA	3000
IESKEAFQEALAAAGDKL	P10639|THIO_MOUSE	49.92	18	397	NA	286
IEVAPPKAHEVR	P28474|ADHX_MOUSE:P00329|ADH1_M	38.42	12	2780	NA	1630
IEVAPPKAHEVRIK	P28474|ADHX_MOUSE:P00329|ADH1_M	37.3	14	2000	NA	1680
IEVDQIYHLASPASPP	Q91XL3|UXS1_MOUSE	30.75	16	132	NA	NA
IEVSSPITLQAL	E9Q414|APOB_MOUSE	44.18	12	12900	NA	4990
IEVSSPITLQALV	E9Q414|APOB_MOUSE	48.35	13	184	NA	85.5
IEVSSPITLQALVQ	E9Q414|APOB_MOUSE	48.6	14	3460	NA	1100
IFARGPQAHLVH	P24823|PPBN_MOUSE:P24822|PPBI_M	44.42	12	6120	NA	4310
IFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_M	48.05	13	45900	1060	29000
IFARGPQAHLVHGVQ	P24823|PPBN_MOUSE:P24822|PPBI_M	48.76	15	3320	NA	2120
IFDQVIGPEGVLAGKT	B2RX12|MRP3_MOUSE	28.94	16	231	NA	301
IFFQVSPRDNSALDPI	Q05909|PTPRG_MOUSE	47.65	16	194	NA	NA
IFGIHHNPSVWPDPEV	Q9EP75|CP4FE_MOUSE	26.12	16	184	NA	NA
IFIYNASKPQNLE	Q921R7|S35A5_MOUSE	37	13	138	NA	202
IFNKVVGPNGLLSGKT	Q8VI47|MRP2_MOUSE	49.62	16	716	NA	NA
IGDSNFGAPSASVAAAP	O35643|AP1B1_MOUSE	35.17	17	942	NA	188
IGDSNFGAPSASVAAAPA	O35643|AP1B1_MOUSE	49.69	18	4660	46.9	4110
IGDSNFGAPSASVAAAPAP	O35643|AP1B1_MOUSE	49.64	19	14600	377	15400
IGDSNFGAPSASVAAAPAPA	O35643|AP1B1_MOUSE	46.73	20	1300	NA	1580
IGDTIEFRGPNGLLVYQG	Q9DCN2|NB5R3_MOUSE	49.89	18	5150	NA	5430
IGDTIEFRGPNGLLVYQGK	Q9DCN2|NB5R3_MOUSE	49.88	19	5880	NA	10400
IGGDPFAAPQVVPAFAS	Q80WC7|AGFG2_MOUSE	47.94	17	341	NA	360
IGM(+15.99)LGILVKTGKYKAA	Q3UGR5|HDHD2_MOUSE	32.32	16	180	NA	NA
IGMLGILVKTGKYKA	Q3UGR5|HDHD2_MOUSE	48.12	15	39.8	NA	113
IGMLGILVKTGKYKAA	Q3UGR5|HDHD2_MOUSE	45.89	16	250	NA	NA
IGSGGVFRAPSIHGGSG	P19001|K1C19_MOUSE	48.87	17	467	NA	7630
IGSGGVFRAPSIHGGSGGR	P19001|K1C19_MOUSE	49.8	19	6220	475	14800
IGSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	49.94	20	12100	608	12000
IGSGIFVSPKGVLE	Q9QXW9|LAT2_MOUSE	40.22	14	2280	NA	1770
IGSGIFVSPKGVLEN	Q9QXW9|LAT2_MOUSE	47.66	15	2500	NA	1780
IGSGIFVSPKGVLENA	Q9QXW9|LAT2_MOUSE	48.32	16	3080	NA	2830

IGSGIFVSPKGVLENAG	Q9QXW9|LAT2_MOUSE	48.67	17	4020	NA	2710
IIDTTIAYPKAEPID	Q91YX5|LGAT1_MOUSE	48.6	15	1630	NA	1020
IIGSGIFVSPKGVLE	Q9QXW9|LAT2_MOUSE	39.32	15	211	NA	NA
IIYTWQGANATRDE	Q60604|SCIN_MOUSE	29.8	14	143	NA	NA
IKATIAGGGVIPHIHKSLIGKKGQQK	Q3THW5|H2AV_MOUSE:P0C0S6|H2AZ_	49.82	26	393	NA	NA
IKETDYNGFPVLVSRDS	Q61418|CLCN4_MOUSE	49.91	17	1400	NA	1450
IKETDYNGFPVLVSRDSE	Q61418|CLCN4_MOUSE	49.94	18	2060	NA	1410
IKIAWESPQGQVS	P11276|FINC_MOUSE	47.26	13	260	NA	NA
IKIAWESPQGQVSR	P11276|FINC_MOUSE	48.45	14	3340	NA	1430
IKIAWESPQGQVSRY	P11276|FINC_MOUSE	49.84	15	389	NA	230
IKIAWESPQGQVSRYR	P11276|FINC_MOUSE	42.5	16	1310	NA	NA
IKNNSFYGPEVKIEK	Q00519|XDH_MOUSE	47.58	15	139	NA	331
IKNNSFYGPEVKIEKG	Q00519|XDH_MOUSE	49.79	16	3260	NA	4790
IKNNSFYGPEVKIEKGDL	Q00519|XDH_MOUSE	49.85	18	1930	NA	1650
IKTPEIVAPESAHAAFD	Q8R0X7|SGPL1_MOUSE	46.17	17	328	NA	NA
IKTPEIVAPESAHAAFDK	Q8R0X7|SGPL1_MOUSE	49.78	18	220	NA	121
IKVYWDAPSPAPD	Q8K385|FRRS1_MOUSE	48.73	13	1620	NA	873
IKVYWDAPSPAPDH	Q8K385|FRRS1_MOUSE	49.9	14	2590	NA	2490
ILDARSYTAAVANRAK	Q91XS1|MTMR4_MOUSE	47.79	16	79.6	NA	192
ILDARSYTAAVANRAKGGG	Q91XS1|MTMR4_MOUSE	49.69	19	1250	NA	892
ILDRYYTPTISRE	Q9R1P3|PSB2_MOUSE	28.36	13	88.8	NA	NA
ILDRYYTPTISRER	Q9R1P3|PSB2_MOUSE	49.28	14	2880	NA	2750
ILDRYYTPTISRERA	Q9R1P3|PSB2_MOUSE	47.9	15	8910	NA	6230
ILDRYYTPTISRERAV	Q9R1P3|PSB2_MOUSE	25.75	16	1180	NA	NA
ILPEETPTASASADTPH	E9Q7D5|ARHG5_MOUSE	38.02	17	155	NA	50
ILVRYTQKAPQVSTP	P07724|ALBU_MOUSE	49.91	15	824	NA	644
ILVRYTQKAPQVSTPT	P07724|ALBU_MOUSE	49.9	16	4580	NA	6170
ILVRYTQKAPQVSTPTL	P07724|ALBU_MOUSE	49.94	17	11400	250	14800
ILVRYTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.94	18	19300	NA	22000
ILVRYTQKAPQVSTPTLVE	P07724|ALBU_MOUSE	49.36	19	6020	94.9	7850
ILVRYTQKAPQVSTPTLVEA	P07724|ALBU_MOUSE	49.93	20	411	NA	438
INDIIRAPTIEQM(+15.99)KD	P63085|MK01_MOUSE	33.02	15	677	NA	NA
INDIIRAPTIEQMKD	P63085|MK01_MOUSE	44.29	15	26.9	NA	NA
INDYKGAVIVVSHDAR	Q6P542|ABCF1_MOUSE	49.48	16	90.6	NA	282
INETSYNGFPVIM(+15.99)SKE	P51791|CLCN3_MOUSE	49.9	16	1690	NA	1110
INETSYNGFPVIM(+15.99)SKES	P51791|CLCN3_MOUSE	49.66	17	900	NA	567
INETSYNGFPVIM(+15.99)SKESQ	P51791|CLCN3_MOUSE	49.93	18	1800	NA	1330
INETSYNGFPVIMSKE	P51791|CLCN3_MOUSE	49.87	16	740	NA	1240
INETSYNGFPVIMSKES	P51791|CLCN3_MOUSE	49.89	17	482	NA	940
INETSYNGFPVIMSKESQ	P51791|CLCN3_MOUSE	49.6	18	904	NA	1330
INFDFPKL	P54823|DDX6_MOUSE	27.84	8	234	NA	66.4
INFYMYQGPAPRIRTR	Q6DYE8|ENPP3_MOUSE	44.56	16	118	NA	383
INM(+15.99)KQYASPM(+15.99)PTQTDV	Q69ZW3|EHBP1_MOUSE	48.36	16	91.5	NA	NA
INPDNVATPIAASFG	Q8BYR8|S41A2_MOUSE	47.61	15	1480	NA	400
INPDNVATPIAASFGD	Q8BYR8|S41A2_MOUSE	47.61	16	472	NA	286
INPDNVATPIAASFGDL	Q8BYR8|S41A2_MOUSE	48.12	17	978	NA	465
INYQPPTVVPGGDL	P68369|TBA1A_MOUSE:P68373|TBA1C_	43.97	14	3820	NA	2620
IPAWTGPEIPESGPS	Q8K4G1|LTBP4_MOUSE	48.99	15	139	NA	NA
IPAYPAGSPGYNPPQM(+15.99)NTL	Q8K419|LEG4_MOUSE	49.91	19	434	NA	468
IPAYPAGSPGYNPPQM(+15.99)NTLP	Q8K419|LEG4_MOUSE	49.89	20	2950	NA	3010
IPAYPAGSPGYNPPQM(+15.99)NTLPV	Q8K419|LEG4_MOUSE	49.94	21	3630	NA	3450
IPAYPAGSPGYNPPQM(+15.99)NTLPVM	Q8K419|LEG4_MOUSE	49.95	22	465	NA	372
IPAYPAGSPGYNPPQMNTL	Q8K419|LEG4_MOUSE	48.82	19	322	NA	900
IPAYPAGSPGYNPPQMNTLP	Q8K419|LEG4_MOUSE	48.8	20	357	NA	NA
IPAYPAGSPGYNPPQMNTLPV	Q8K419|LEG4_MOUSE	49.93	21	516	NA	1230
IPAYPAGSPGYNPPQMNTLPVM(+15.99)	Q8K419|LEG4_MOUSE	49.49	22	104	NA	288
IPEAQWQSSLARTSSAE	P19096|FAS_MOUSE	47.84	17	227	NA	318
IPELNGKLTGM(+15.99)AFRVPTPNVSV\	P16858|G3P_MOUSE	48.66	24	788	NA	NA
IPENYNSAM(+15.99)PFKILY	Q64487|PTPRD_MOUSE	48.92	15	617	NA	174
IPENYNSAMPFKILY	Q64487|PTPRD_MOUSE	48.68	15	293	NA	510
IPEPAHAYAQPQTTTPLPT	P47941|CRKL_MOUSE	49.77	19	237	NA	279
IPEQSFYTKPLPGIIM(+15.99)	P58021|TM9S2_MOUSE	49.8	16	678	NA	570
IPEQSFYTKPLPGIIM(+15.99)G	P58021|TM9S2_MOUSE	49.93	17	2860	NA	2090
IPEQSFYTKPLPGIIM(+15.99)GG	P58021|TM9S2_MOUSE	49.94	18	582	NA	321
IPEQSFYTKPLPGIIMG	P58021|TM9S2_MOUSE	49.86	17	209	NA	922
IPFAAPTALASRDG	Q91VX2|UBAP2_MOUSE	37.91	14	313	NA	378
IPFYTPIPN(+15.00)GL	O08573|LEG9_MOUSE	25.33	11	23.8	NA	NA
IPFYTPIPNG	O08573|LEG9_MOUSE	34.95	10	23600	682	21700
IPFYTPIPNGL	O08573|LEG9_MOUSE	38.89	11	9750	NA	7680
IPFYTPIPNGLY	O08573|LEG9_MOUSE	47.9	12	1450	NA	855
IPFYTPIPNGLYP	O08573|LEG9_MOUSE	46.71	13	20400	913	26600
IPFYTPIPNGLYPS	O08573|LEG9_MOUSE	47.45	14	89400	3720	56700
IPFYTPIPNGLYPSK	O08573|LEG9_MOUSE	49.01	15	898	NA	631
IPGMTGPIIAKSLTPD	Q8BN82|S17A5_MOUSE	49.11	16	269	NA	180
IPGTNM(+15.99)YNTDRANPV	E9Q7P9|CDHR2_MOUSE	48.82	15	6510	NA	3200
IPGTNM(+15.99)YNTDRANPVL	E9Q7P9|CDHR2_MOUSE	49.67	16	10600	NA	6580
IPGTNM(+15.99)YNTDRANPVLD	E9Q7P9|CDHR2_MOUSE	49.85	17	142000	5480	93800

IPGTNM(+15.99)YNTDRANPVLDL	E9Q7P9|CDHR2_MOUSE	47.66	18	14900	NA	9740
IPGTNM(+15.99)YNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	49.91	19	356000	10900	224000
IPGTNM(+15.99)YNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	49.87	20	65100	1940	44500
IPGTNMYNTDRANPV	E9Q7P9|CDHR2_MOUSE	49.88	15	2760	NA	2010
IPGTNMYNTDRANPVL	E9Q7P9|CDHR2_MOUSE	49.78	16	7240	NA	8530
IPGTNMYNTDRANPVLD	E9Q7P9|CDHR2_MOUSE	49.94	17	67800	NA	87500
IPGTNMYNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	49.92	19	146000	NA	182000
IPGTNMYNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	49.92	20	23500	NA	37300
IPIRWTAPEAIAH	Q60750|EPHA1_MOUSE	47.68	13	1440	NA	1770
IPIRWTAPEAIAHRI	Q60750|EPHA1_MOUSE	47.84	15	1420	NA	2060
IPIRWTAPEAIQYR	P54763|EPHB2_MOUSE	40.98	14	74	NA	97.3
IPIRWTAPEAIQYRK	P54763|EPHB2_MOUSE	49	15	149	NA	199
IPIRWTAPEAISY	Q03145|EPHA2_MOUSE	37.22	13	822	NA	1060
IPIRWTAPEAISYR	Q03145|EPHA2_MOUSE	47.98	14	2150	NA	2670
IPIRWTAPEAISYRK	Q03145|EPHA2_MOUSE	48.01	15	7200	64.8	9010
IPKVVKSPSSLPAKP	Q8BHK6|SLAF7_MOUSE	49.86	15	1040	NA	NA
IPKVVKSPSSLPAKPLVP	Q8BHK6|SLAF7_MOUSE	49.88	18	376	NA	NA
IPM(+15.99)DFAQPIAFKNADI	Q60675|LAMA2_MOUSE	42.13	16	39300	NA	30500
IPM(+15.99)YDAAQALKTNPE	Q6EDY6|CARL1_MOUSE	47.95	15	220	NA	149
IPM(+15.99)YSIITPNVLRLE	P01027|CO3_MOUSE	41.83	15	586	NA	433
IPM(+15.99)YSIITPNVLRLES	P01027|CO3_MOUSE	49.47	16	3300	NA	3520
IPM(+15.99)YSIITPNVLRLESE	P01027|CO3_MOUSE	47.77	17	2630	NA	1680
IPMYSIITPNVLRLE	P01027|CO3_MOUSE	47.53	15	208	NA	349
IPMYSIITPNVLRLES	P01027|CO3_MOUSE	46.92	16	1050	NA	2110
IPMYSIITPNVLRLESE	P01027|CO3_MOUSE	44.91	17	927	NA	1120
IPPTHYAASRAASVAE	P70202|LXN_MOUSE	49.24	16	21600	NA	NA
IPPTHYAASRAASVAEN	P70202|LXN_MOUSE	49.47	17	5480	NA	NA
IPQAERYQEALPTVAN	P30999|CTND1_MOUSE	46.38	16	2720	NA	2610
IPQAERYQEALPTVANS	P30999|CTND1_MOUSE	47.33	17	416	NA	991
IPQAERYQEALPTVANST	P30999|CTND1_MOUSE	48.85	18	3600	NA	4770
IPQAERYQEALPTVANSTGPH	P30999|CTND1_MOUSE	47.96	21	1120	NA	1550
IPRARAFFPPIPAPTPPRPPP	Q99MZ3|MLXPL_MOUSE	49.93	21	65.8	NA	NA
IPSPSSAFTPAHAATSSH	Q8CI51|PDLI5_MOUSE	49.86	18	1860	NA	1070
IPSPSSAFTPAHAATSSHA	Q8CI51|PDLI5_MOUSE	49.94	19	16700	NA	13200
IPSRYSSPTTIAT	Q9DBM2|ECHP_MOUSE	35.94	13	199	NA	369
IPSRYSSPTTIATVM	Q9DBM2|ECHP_MOUSE	41.88	15	910	NA	3570
IPSRYSSPTTIATVM(+15.99)	Q9DBM2|ECHP_MOUSE	45.3	15	4700	134	5630
IPSSVPATFAPSPTPAVVS	Q9DBG3|AP2B1_MOUSE	49.77	19	369	NA	NA
IPSSVPATFAPSPTPAVVSSG	Q9DBG3|AP2B1_MOUSE	49.93	21	165	NA	911
IPTSASKTEAPAAAKSLTSPL	Q9QY76|VAPB_MOUSE	49.71	21	1260	NA	2550
IPVKTLKYSIDPSVVNISDEM(+15.99)	Q8BTY2|S4A7_MOUSE	49.95	21	545	NA	283
IPVYRFVLPANAFA	Q08857|CD36_MOUSE	44.07	14	250	NA	NA
IPYQGPSSDYVVVK	O88307|SORL_MOUSE	48.98	14	356	NA	303
IQASVATNPIITPVAQEN	P08226|APOE_MOUSE	49.47	18	168	NA	110
IQEPYTFPAILKS	Q8BFR4|GNS_MOUSE	48.09	13	4900	36.6	3280
IQEPYTFPAILKSV	Q8BFR4|GNS_MOUSE	49.68	14	956	NA	666
IQEPYTFPAILKSVC(+57.02)	Q8BFR4|GNS_MOUSE	42.55	15	276	NA	NA
IQLSFSQPKAHEAS	Q5PT54|NTCP5_MOUSE	42.49	14	713	NA	426
IQLSFSQPKAHEASV	Q5PT54|NTCP5_MOUSE	37.49	15	456	NA	396
IQLSFSQPKAHEASVA	Q5PT54|NTCP5_MOUSE	49.13	16	3030	NA	2130
IQYKEGFGHLSPTG	Q8VCM7|FIBG_MOUSE	46.46	14	145	NA	165
IREFYSASVAEDA	E9Q7P9|CDHR2_MOUSE	47.87	13	2940	36	2600
IREFYSASVAEDAT	E9Q7P9|CDHR2_MOUSE	48.39	14	5320	67.7	5790
IREFYSASVAEDATL	E9Q7P9|CDHR2_MOUSE	49.38	15	25900	NA	36200
IREFYSASVAEDATLG	E9Q7P9|CDHR2_MOUSE	49.15	16	28700	900	24900
IRENIWKAPEPVE	Q9R100|CAD17_MOUSE	43.41	13	276	NA	237
IRENIWKAPEPVEIR	Q9R100|CAD17_MOUSE	49.88	15	2780	NA	2930
IRENIWKAPEPVEIRE	Q9R100|CAD17_MOUSE	49.87	16	6590	NA	12500
IRENIWKAPEPVEIREN(+15.00)ST	Q9R100|CAD17_MOUSE	49.91	19	20200	NA	16100
IRGNVYIHPTAKVAPS	Q922H4|GMPPA_MOUSE	49.75	16	10700	121	11800
IRGNVYIHPTAKVAPSA	Q922H4|GMPPA_MOUSE	49.11	17	1100	NA	948
IRLPYTASSGLM(+15.99)AP	Q9R1Q9|VAS1_MOUSE	49.43	14	354	NA	138
IRLPYTASSGLM(+15.99)APR	Q9R1Q9|VAS1_MOUSE	48.55	15	5010	NA	3900
IRLPYTASSGLM(+15.99)APRE	Q9R1Q9|VAS1_MOUSE	49.69	16	4100	NA	2920
IRLPYTASSGLMAPR	Q9R1Q9|VAS1_MOUSE	48.88	15	657	NA	3610
IRLPYTASSGLMAPRE	Q9R1Q9|VAS1_MOUSE	49.8	16	494	NA	1590
IRPFFPQQ	Q8K0E8|FIBB_MOUSE	39.65	8	1460	156	NA
IRPSVYQPVPASSYSPS	Q9JKS4|LDB3_MOUSE	49.93	17	143	NA	164
IRPSVYQPVPASSYSPSP	Q9JKS4|LDB3_MOUSE	49.65	18	249	NA	285
IRPSVYQPVPASSYSPSPG	Q9JKS4|LDB3_MOUSE	49.93	19	1010	NA	484
IRYM(+15.99)APEVLEGAVN	O35607|BMPR2_MOUSE	39.91	14	501	NA	167
ISALFVTPKTAGAQVV	P16330|CN37_MOUSE	36.51	16	231	NA	NA
ISARWKNPITSVDAA	Q91X72|HEMO_MOUSE	47.51	15	512	NA	468
ISKQEYDESGPSIVH	P63260|ACTG_MOUSE:P60710|ACTB_M	45.94	15	448	NA	521
ISKQEYDESGPSIVHR	P63260|ACTG_MOUSE:P60710|ACTB_M	49.88	16	914	NA	697
ISKQEYDESGPSIVHRK	P63260|ACTG_MOUSE:P60710|ACTB_M	48.66	17	510	NA	474
ISLNTYTPTKILPTPP	Q6ZQB6|VIP2_MOUSE	40.82	16	231	NA	276

ISLQEVEPVISRAVM(+15.99)D	Q8R1J9|TOR2A_MOUSE	37.62	16	202	NA	NA
ISQIFSQAM(+15.99)AARSIN	P34914|HYES_MOUSE	48.04	15	697	NA	904
ISQIFSQAM(+15.99)AARSINRP	P34914|HYES_MOUSE	28.66	17	5770	NA	6490
ISQIFSQAMAARSIN	P34914|HYES_MOUSE	46.79	15	1140	NA	1610
ISQIFSQAMAARSINR	P34914|HYES_MOUSE	36.69	16	4420	NA	5500
ISQIFSQAMAARSINRP	P34914|HYES_MOUSE	49.56	17	23000	NA	35600
ISQIFSQAMAARSINRPM(+15.99)	P34914|HYES_MOUSE	35.98	18	410	NA	273
ISSDENAPSVIKSVED	Q62469|ITA2_MOUSE	48.23	16	1680	NA	1110
ISYTGSRPASN	P28666|MUG2_MOUSE:P28665|MUG1_M	44.61	11	1050	NA	388
ISYTGSRPASNM(+15.99)V	P28666|MUG2_MOUSE:P28665|MUG1_M	46.71	13	1820	NA	NA
ISYTGSRPASNMV	P28666|MUG2_MOUSE:P28665|MUG1_M	48.47	13	478	NA	387
ITDENWLSPRPASGPS	P97305|NFAC3_MOUSE	28.87	16	260	NA	385
ITNNQDFRGSAGAPSVENV	P49443|PPM1A_MOUSE	48.46	19	108	NA	222
ITNQYNSPTGLYS	O70400|PDLI1_MOUSE	46.48	13	2940	NA	2600
ITNQYNSPTGLYSS	O70400|PDLI1_MOUSE	49.22	14	2690	NA	1900
ITNQYNSPTGLYSSE	O70400|PDLI1_MOUSE	49.64	15	4200	NA	4460
ITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.66	16	86900	4640	82400
ITNQYNSPTGLYSSENI	O70400|PDLI1_MOUSE	49.9	17	2350	NA	2560
ITNQYNSPTGLYSSENIS	O70400|PDLI1_MOUSE	49.86	18	515	NA	438
ITPDIIINPHAIPSR	Q8CFI7|RPB2_MOUSE	29.45	15	47.1	NA	NA
ITPSYVAFTPEGER	P20029|BIP_MOUSE	47.93	14	2180	NA	2080
ITPSYVAFTPEGERL	P20029|BIP_MOUSE	47.22	15	6820	161	6540
ITPSYVAFTPEGERLI	P20029|BIP_MOUSE	46.62	16	4170	NA	2660
ITQ(+15.00)VQ(+15.00)WNDPGAQYSLV	Q9R100|CAD17_MOUSE	26.54	18	111	NA	NA
ITQVQWNDPGAQYS	Q9R100|CAD17_MOUSE	49.81	14	156	NA	159
ITQVQWNDPGAQYSLV	Q9R100|CAD17_MOUSE	49.49	16	267	NA	667
ITQVQWNDPGAQYSLVN	Q9R100|CAD17_MOUSE	49.94	17	21900	NA	30000
ITQVQWNDPGAQYSLVNK	Q9R100|CAD17_MOUSE	49.94	18	9350	315	11100
ITQVQWNDPGAQYSLVNKE	Q9R100|CAD17_MOUSE	49.94	19	1170	NA	1590
ITQVQWNDPGAQYSLVNKEK	Q9R100|CAD17_MOUSE	49.44	20	229	NA	161
ITTDYNSPEAGNIF	B2RXV4|FLVC1_MOUSE	47.91	14	27800	160	11700
ITTDYNSPEAGNIFL	B2RXV4|FLVC1_MOUSE	48.65	15	1330	NA	676
ITYSYAGARAPM(+15.99)GQG	Q7TQH7|LRP10_MOUSE	48.16	15	1310	NA	551
ITYSYAGARAPMGQG	Q7TQH7|LRP10_MOUSE	48.75	15	617	NA	1110
IVLGYNGSLPNGDRG	Q8C669|PELI1_MOUSE	48.39	15	394	NA	421
IVLKLKGPRAANSFNPN	E9Q555|RN213_MOUSE	49.94	17	6900	NA	13400
IVSHDYKGSTSHSLP	E9Q414|APOB_MOUSE	40.44	15	9760	NA	9550
IVSHDYKGSTSHSLPY	E9Q414|APOB_MOUSE	49.73	16	36900	NA	31200
IVSHDYKGSTSHSLPYE	E9Q414|APOB_MOUSE	49.81	17	15900	NA	13500
IVTERVYAPTSTLVDQ	O55111|DSG2_MOUSE	49.83	16	558	NA	1160
IVTERVYAPTSTLVDQH	O55111|DSG2_MOUSE	49.89	17	1230	NA	1060
IVTERVYAPTSTLVDQHY	O55111|DSG2_MOUSE	49.93	18	670	NA	348
IVVYTPVINGIGGN	Q8BYR8|S41A2_MOUSE	47.57	14	83.8	NA	NA
IVYEGPELNHAFG	Q91ZX7|LRP1_MOUSE	47.68	13	5780	NA	3370
IWRDYVPPTANLDQKD	Q78PY7|SND1_MOUSE	38.47	16	107	NA	52.8
IYIYNGPVLGGTR	P50284|TNR3_MOUSE	40.31	13	648	NA	898
K(+42.01)HVPRAVMVDLEPTVVD	Q9JJZ2|TBA8_MOUSE	30.86	17	9700	NA	NA
K(+42.01)KDGKKRKRSRKESYSIYVYKV	Q64524|H2B2E_MOUSE	49.43	29	819	NA	NA
K(+42.01)KRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.36	20	885	2770	NA
K(+42.01)KTKKEVKKVATPKKAAKPKK	P10922|H10_MOUSE	46.67	21	658	1600	NA
K(+42.01)KTKKPAKAAAPRK	P43275|H11_MOUSE	34.28	14	467	NA	798
K(+42.01)KTKKPAKAAAPRKKPA	P43275|H11_MOUSE	36.78	17	149	NA	NA
K(+42.01)PKKAAKSPAKAKAPKA	P43277|H13_MOUSE	37.26	17	188	NA	NA
K(+42.01)PKVVKVKPVKASKPKKAKTVK	P10922|H10_MOUSE	49.71	26	2820	4260	2230
K(+42.01)PVKASKPKKAKTVKPKAKSSA	P10922|H10_MOUSE	49.86	24	46.7	NA	NA
KAAAKPKKAA	P43276|H15_MOUSE	31.02	10	298	NA	NA
KAAKPKKAAKSPAKAKAPKAKASKPKA	P43277|H13_MOUSE	49.95	27	733	NA	NA
KAAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	18	2230	NA	233
KADPLQPPQALTAASK	Q61001|LAMA5_MOUSE	46.33	16	576	NA	NA
KAKAAAKPKKAAK	P43276|H15_MOUSE	49.29	13	290	233	NA
KAKAPKAKASKPKA	P43277|H13_MOUSE	46.36	14	818	NA	393
KAKASKPKASKPKATKAKKAAPRK	P43277|H13_MOUSE	49.64	24	776	NA	NA
KAKATKAKKAPKSPAKAKTVK	P43274|H14_MOUSE	49.43	21	2780	3830	4710
KAKKAPKSPAKAKTVKPKAAKP	P43274|H14_MOUSE	49.08	22	18500	NA	7010
KAKKKPAATPKKAK	P10922|H10_MOUSE	36.93	14	5580	NA	NA
KAKKKPAATPKKAKK	P10922|H10_MOUSE	32.15	15	382	NA	566
KAKKKPAATPKKAKKPKVVKVKPVKASK	P10922|H10_MOUSE	49.95	33	1730	1470	1200
KAKKPAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.95	21	2440	1910	2140
KAKKPKVVKVKPVK	P10922|H10_MOUSE	49.74	14	213	NA	NA
KAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	22	2180	2210	6890
KAKKVAAKKK	P15864|H12_MOUSE	41.88	10	127	NA	NA
KAKT(+79.97)VKPKAKSSAKRA	P10922|H10_MOUSE	45.93	16	338	NA	NA
KAKTVKPKA	P43274|H14_MOUSE:P10922|H10_MOU	41.72	9	186	359	1310
KAKTVKPKAAKPKTSKPK	P43274|H14_MOUSE	29.79	18	7910	NA	NA
KAKTVKPKAK	P10922|H10_MOUSE	42.68	10	290	NA	633
KAKTVKPKAKSSAK	P10922|H10_MOUSE	48.59	14	477	519	947
KAKTVKPKAKSSAKR	P10922|H10_MOUSE	48.93	15	324	NA	3800

KAKTVKPKAKSSAKRASKK	P10922|H10_MOUSE	49.94	19	5680	NA	1780
KAKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.95	20	10500	NA	3320
KAKVTKPKKVKSAS(+79.97)KAVKPKAA	P15864|H12_MOUSE	49.9	31	59.4	NA	NA
KAKVTKPKKVKSASKAVKPKAAKP	P15864|H12_MOUSE	48.39	24	6890	NA	NA
KAKVTKPKTPAKPKKA	P43275|H11_MOUSE	31.06	16	3380	NA	1010
KAPEPVEIR	Q9R100|CAD17_MOUSE	38.44	9	777	NA	491
KAPEPVEIRE	Q9R100|CAD17_MOUSE	37.51	10	7270	106	4430
KAPEPVEIREN(+15.00)ST	Q9R100|CAD17_MOUSE	40.26	13	2680	NA	NA
KAPQVSTPTLVEAA	P07724|ALBU_MOUSE	35.89	14	105	NA	NA
KAPSKKPKATPVKK	P10922|H10_MOUSE	38.33	14	1590	NA	NA
KAQKKDGKKRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	48.95	32	1850	68300	4550
KASKPKKAK	P10922|H10_MOUSE	41.9	9	5370	3520	NA
KASKPKKAKTVKPKAK	P10922|H10_MOUSE	49.94	16	510	183	976
KASKPKKAKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.91	26	1500	NA	NA
KASKPKVTKPKTAKPKAAKAK	P43276|H15_MOUSE	47.42	21	869	NA	NA
KAVDVFFPPEAQND	Q68FD5|CLH1_MOUSE	45.1	14	51.2	NA	NA
KAVDVFFPPEAQNDF	Q68FD5|CLH1_MOUSE	34.93	15	139	NA	151
KAVDVFFPPEAQNDFP	Q68FD5|CLH1_MOUSE	49.84	16	744	NA	995
KAVDYPPVANAGPN	Q8K135|K319L_MOUSE	46.78	14	781	NA	831
KAVDYPPVANAGPNQ	Q8K135|K319L_MOUSE	48.7	15	3250	NA	3410
KAVGKVIPELNGKLTGM(+15.99)AFRVPT	P16858|G3P_MOUSE	49.9	30	1550	NA	2760
KAVGKVIPELNGKLTGMAFRVPTPNVSV	P16858|G3P_MOUSE	48.95	30	1640	NA	19600
KAVKPKAAKPKVAKAKKVAAK	P15864|H12_MOUSE	35.48	21	1300	NA	NA
KAVKPKASKAKVTKPKTPAKP	P43275|H11_MOUSE	27.7	21	71.2	NA	NA
KAVKSKASKPKVTKPKTAKPKAAKAKKA	P43276|H15_MOUSE	49.95	33	690	NA	NA
KAVTTAVPAT(+79.97)TQ	P54728|RD23B_MOUSE	25.39	12	4570	NA	NA
KDESGFPKPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	46.07	23	2040	NA	894
KDESGFPKPPSYNVATTLPSYDEA	Q8R0W6|NFIP1_MOUSE	49.63	24	3070	NA	2310
KDESGFPKPPSYNVATTLPSYDEAE	Q8R0W6|NFIP1_MOUSE	49.94	25	497	NA	177
KDGKKRKRSRKESYSVYVYKVLKQVHP	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	43.25	28	4700	10800	1780
KDSELSPPTSAPSLVS	Q9WUU8|TNIP1_MOUSE	43.58	16	319	NA	171
KEAFQEALAAAGDK	P10639|THIO_MOUSE	49.46	14	535	NA	367
KEFQFLNPNPVPED	Q8R0K2|TRI31_MOUSE	48.84	14	169	NA	NA
KEFQFLNPNPVPEDL	Q8R0K2|TRI31_MOUSE	49.82	15	2280	NA	1440
KEFQFLNPNPVPEDLE	Q8R0K2|TRI31_MOUSE	49.75	16	442	NA	NA
KEIFEQPESVVN	P47856|GFPT1_MOUSE	29.68	12	182	NA	NA
KEIFEQPESVVNTM(+15.99)	P47856|GFPT1_MOUSE	29.69	14	121	NA	NA
KELEEQLGPVAEETR	P08226|APOE_MOUSE	48.95	15	53600	2230	37800
KELEEQLGPVAEETRA	P08226|APOE_MOUSE	49.63	16	37300	2070	29400
KELEEQLGPVAEETRAR	P08226|APOE_MOUSE	48.68	17	30800	NA	26700
KERASFITPVPGGVG	Q922D8|C1TC_MOUSE	39.86	15	583	NA	706
KERASFITPVPGGVGP	Q922D8|C1TC_MOUSE	45.82	16	719	NA	1180
KERASFITPVPGGVGPM(+15.99)	Q922D8|C1TC_MOUSE	49.36	17	310	NA	385
KEVDRYDAPGIAFYPG	Q9D771|PACC1_MOUSE	36.93	16	944	NA	1530
KEVLDYSTPTTNGTPEA	Q9DBG7|SRPRA_MOUSE	27.23	17	38.7	NA	NA
KFLPNAPKALIVEPS	Q91VR5|DDX1_MOUSE	38.84	15	2440	NA	NA
KFYKGKKYKPLDLRPK	Q6ZWV7|RL35_MOUSE	49.89	16	732	146	634
KFYKGKKYKPLDLRPKK	Q6ZWV7|RL35_MOUSE	49.94	17	272	NA	388
KFYKGKKYKPLDLRPKKT	Q6ZWV7|RL35_MOUSE	49.94	18	1220	1850	2460
KFYKGKKYKPLDLRPKKTR	Q6ZWV7|RL35_MOUSE	49.95	19	1500	7630	5510
KFYKGKKYKPLDLRPKKTRAMRR	Q6ZWV7|RL35_MOUSE	49.95	23	631	6760	5610
KGFEVDAPLANAL	Q6PDE7|GGT6_MOUSE	39.83	13	442	NA	224
KGFEVDAPLANALA	Q6PDE7|GGT6_MOUSE	49.43	14	562	NA	434
KGFEVDAPLANALAI	Q6PDE7|GGT6_MOUSE	48.69	15	1630	NA	1400
KGFEVDAPLANALAIQ	Q6PDE7|GGT6_MOUSE	47.35	16	186	NA	104
KGFFEGSIASKGKGG	Q8CIE6|COPA_MOUSE	32.62	15	65.2	NA	NA
KGFPTIYFSPANKKLTPKKY	P27773|PDIA3_MOUSE	26.31	20	92.8	NA	NA
KGHEVVVIAPEASIHIK	Q63886|UD11_MOUSE	29.18	17	63.3	NA	NA
KGIPVYRFVLPANAFA	Q08857|CD36_MOUSE	49.75	16	1080	NA	253
KGKTKKKEEKPNGKIPEHDLDPNVTIILK	Q99PL5|RRBP1_MOUSE	49.95	33	284	NA	NA
KGLFRAAVPSGAST	P17183|ENOG_MOUSE:P17182|ENOA_M	48.12	14	1380	NA	1600
KGM(+15.99)NPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.02	19	162	NA	297
KGPKLKRLAFIAHPKLGKR	P47915|RL29_MOUSE	49.95	19	215	NA	NA
KGPKLKRLAFIAHPKLGKRIR	P47915|RL29_MOUSE	49.95	21	1140	NA	NA
KGPLIVSGPDGAPAK	Q8VBW1|SC6A8_MOUSE	47.62	15	64.6	NA	NA
KGPLIVSGPDGAPAKG	Q8VBW1|SC6A8_MOUSE	49.17	16	494	NA	654
KGPLIVSGPDGAPAKGDG	Q8VBW1|SC6A8_MOUSE	49.86	18	13300	NA	13200
KGQDHVDFSQPEPHTVLFH	Q9QUR8|SEM7A_MOUSE	49.29	19	99.6	NA	NA
KGVKYEAPQTTDGLA	O88746|TOM1_MOUSE	47.52	15	469	NA	NA
KHKRKKVKLAVLKYY	P62983|RS27A_MOUSE	49.95	15	187	NA	NA
KHPDRFAYPIPHTTRPP	O70589|CSKP_MOUSE	49.33	17	8080	NA	7180
KHPDRFAYPIPHTTRPPK	O70589|CSKP_MOUSE	49.91	18	424	NA	280
KIQASVATNPIITPVAQENQ	P08226|APOE_MOUSE	49.87	20	118	NA	105
KIQEPYTFPAILKS	Q8BFR4|GNS_MOUSE	49.32	14	385	NA	442
KITTDYNSPEAGNIF	B2RXV4|FLVC1_MOUSE	47.5	15	516	NA	467
KIVYEGPELNHA	Q91ZX7|LRP1_MOUSE	48.02	12	630	NA	629
KIVYEGPELNHAF	Q91ZX7|LRP1_MOUSE	49.66	13	460	NA	625

KIVYEGPELNHAFG	Q91ZX7|LRP1_MOUSE	49.77	14	106000	2980	110000
KKAKATKAKKAPKSPAK	P43274|H14_MOUSE	49.94	17	251	26.3	295
KKAKATKAKKAPKSPAKAK	P43274|H14_MOUSE	49.95	19	4410	2030	1870
KKAKATKAKKAPKSPAKAKTVKPKAAKP	P43274|H14_MOUSE	49.95	31	256	NA	NA
KKAKATKAKKAPKSPAKAKTVKPKAAKP	P43274|H14_MOUSE	42.93	33	970	NA	NA
KKAKKPAAAAGAKKAKSPKKAK	P43274|H14_MOUSE	47.68	22	92.8	NA	NA
KKAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	23	7790	3290	6130
KKAKKPTLVA	P57776|EF1D_MOUSE	31.03	10	127	NA	NA
KKAKTVKPKAKSSAKRASKK	P10922|H10_MOUSE	49.8	20	9040	NA	NA
KKAKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.95	21	1100	1200	NA
KKDGKKRKRSRKESYSVYVYKVLKQVH	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.95	29	6630	40200	6410
KKEKPM(+15.99)KKFY(+79.97)SESEEEI	Q9Z1T1|AP3B1_MOUSE	41.38	32	221	NA	NA
KKEKPMKKFY(+79.97)S(+79.97)ESEEE	Q9Z1T1|AP3B1_MOUSE	35.83	16	468	NA	NA
KKELEEQLGPVAEETR	P08226|APOE_MOUSE	49.9	16	14200	178	20300
KKELEEQLGPVAEETRA	P08226|APOE_MOUSE	49.81	17	5110	NA	5330
KKELEEQLGPVAEETRAR	P08226|APOE_MOUSE	49.04	18	12500	221	11500
KKGPLIVSGPDGAPAKGDG	Q8VBW1|SC6A8_MOUSE	49.86	19	80.7	NA	131
KKGSKKAVTKAQKKDGKKRKRSRKESY	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	49.04	33	842	74400	14300
KKKKKKKKPFM(+15.99)	Q99L45|IF2B_MOUSE	49.94	11	367	NA	NA
KKKKYEPPVPTRVGKK	P62192|PRS4_MOUSE	47.95	16	1550	NA	1040
KKLQDEIDAALPNKAP	Q64464|CP3AD_MOUSE	36.68	16	475	NA	404
KKLQDEIDAALPNKAPA	Q64464|CP3AD_MOUSE	49.9	17	481	NA	NA
KKLQDEIDAALPNKAPAT	Q64464|CP3AD_MOUSE	49.28	18	714	NA	874
KKPAATPKKAKKPKVVKVKPVKAS(+79.9	P10922|H10_MOUSE	41.14	27	67.2	266	NA
KKPAGAAKKPKKATGAATPKKAAKK	P15864|H12_MOUSE	35.75	25	1080	NA	NA
KKPAVSKKTSKSPKKPKVVKAKKVAKS(	P43275|H11_MOUSE	44.79	31	1120	NA	NA
KKPFVYTQGQAVLNR	Q8VCT3|AMPB_MOUSE	49.42	15	907	NA	1070
KKPFVYTQGQAVLNRA	Q8VCT3|AMPB_MOUSE	49.08	16	483	NA	483
KKPGPPVL	Q99P88|NU155_MOUSE	25.69	8	442	NA	NA
KKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	20	3790	NA	NA
KKPPPRLP	Q5I012|S38AA_MOUSE	33.31	8	747	NA	NA
KKPSKIKSLFKK	P83093|STIM2_MOUSE	38.32	12	264	NA	NA
KKSPVYKNPTPGSSEL	Q99PG0|AAAD_MOUSE	42.57	16	1230	NA	1570
KKSPVYKNPTPGSSELA	Q99PG0|AAAD_MOUSE	40.79	17	788	NA	536
KKSTKKTPKKAKKP	P43274|H14_MOUSE	49.78	14	3160	NA	NA
KKSTKKTPKKAKKPA	P43274|H14_MOUSE	49.93	15	2060	2280	NA
KKTKKEVKKVATPKKAAKPKK	P10922|H10_MOUSE	49.94	21	301	NA	NA
KKTPKKAKKPAA	P15864|H12_MOUSE:P43276|H15_MOU	48.89	12	845	624	1130
KKTVKKTPKKAKKPA	P43276|H15_MOUSE	46.56	15	171	NA	NA
KKVAAKKK	P15864|H12_MOUSE	34.34	8	566	NA	91.2
KKVAKSPAKAKAVKPK	P43275|H11_MOUSE	40.75	16	452	401	208
KKVAKSPAKAKAVKPKASKAK	P43275|H11_MOUSE	27.1	21	343	NA	NA
KKVAKSPKKAKVTKPKKVKS	P15864|H12_MOUSE	49.94	20	380	NA	935
KKVAKSPKKAKVTKPKKVKSASKAVKPK	P15864|H12_MOUSE	49.95	29	539	542	1390
KKVATPKKAAKPK	P10922|H10_MOUSE	25.39	13	1640	NA	NA
KKVATPKKAAKPKK	P10922|H10_MOUSE	33.01	14	437	NA	NA
KKVTFSSGYVNLSPEN	P06684|CO5_MOUSE	49.49	16	544	NA	220
KLLEAKGPVTDVAYSHD	O88342|WDR1_MOUSE	49.88	17	3720	NA	1890
KLPSPLIM(+15.99)SPGPIYAVDGD	Q8VHF2|CDHR5_MOUSE	49.91	19	347	NA	210
KLPSPLIM(+15.99)SPGPIYAVDGDQ	Q8VHF2|CDHR5_MOUSE	49.95	20	197	NA	114
KLQDEIDAALPNKAP	Q64464|CP3AD_MOUSE	43.75	15	2430	NA	2020
KLQDEIDAALPNKAPA	Q64464|CP3AD_MOUSE	49.36	16	3840	NA	2780
KLQDEIDAALPNKAPAT	Q64464|CP3AD_MOUSE	49.76	17	4010	NA	3770
KLQDEIDAALPNKAPATYD	Q64464|CP3AD_MOUSE	49.81	19	48.4	NA	NA
KLQDEIDEALPNKAPP	Q64459|CP3AB_MOUSE	48.4	16	1050	NA	NA
KLTGM(+15.99)AFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MO	49.91	18	12700	93.4	9300
KLTGMAFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MO	49.92	18	3860	NA	9710
KLVAYTSDQAHSSVER	O88533|DDC_MOUSE	49.35	16	237	NA	NA
KNIVFSPLSISAA	Q03734|SPA3M_MOUSE:Q6P4P1|SPA3A	43.49	13	265	NA	NA
KNLDYVATSIHEA	P05201|AATC_MOUSE	45.14	13	250	NA	118
KNLDYVATSIHEAV	P05201|AATC_MOUSE	49.51	14	106	NA	116
KNLDYVATSIHEAVT	P05201|AATC_MOUSE	49.61	15	15700	414	11300
KNLDYVATSIHEAVTK	P05201|AATC_MOUSE	49.86	16	18500	514	13500
KNNSFYGPEVKIEK	Q00519|XDH_MOUSE	48.47	14	1130	NA	1110
KNNSFYGPEVKIEKG	Q00519|XDH_MOUSE	49.39	15	19900	162	12600
KNNSFYGPEVKIEKGDL	Q00519|XDH_MOUSE	49.21	17	2100	NA	1230
KNSEEFAAAMSRYELK	E9Q414|APOB_MOUSE	48	16	238	NA	430
KNWIQYKEGFGHLSPTG	Q8VCM7|FIBG_MOUSE	48.47	17	232	NA	358
KNYLYLSPSGNTSPPG	Q62393|TPD52_MOUSE	44.39	16	659	NA	617
KPAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.94	18	5370	4520	5380
KPAGATPKKPKKTAGAKKTVKKTPKKAK	P43276|H15_MOUSE	49.95	31	266	NA	NA
KPAQTPVLTSPAPADSTPG	P54728|RD23B_MOUSE	49.91	19	366	NA	815
KPASQQKAEASSPVPYLSPET	P39447|ZO1_MOUSE	41.58	21	172	NA	624
KPAVSKKTSKSPKKPKVVKAKKVAK	P43275|H11_MOUSE	49.95	25	1520	NA	456
KPEGTETTAPTTNGSLGDPS	Q8VEE1|LMCD1_MOUSE	26.91	20	259	NA	NA
KPFQNPVPNQSP	P16382|IL4RA_MOUSE	33.46	12	288	NA	769
KPFQNPVPNQSPS	P16382|IL4RA_MOUSE	48.1	13	9190	NA	8170

KPFTIEDIEVAPPKAHEVR	P00329|ADH1_MOUSE	49.94	19	658	NA	460
KPFTIEDIEVAPPKAHEVRIK	P00329|ADH1_MOUSE	49.94	21	504	NA	266
KPGSDTIKPDVNKSKEY	P35700|PRDX1_MOUSE	48.64	17	695	NA	NA
KPGSDTIKPDVNKSKEYF	P35700|PRDX1_MOUSE	28.35	18	3890	NA	NA
KPGTTVEYLAPWANQ	Q8VEE0|RPE_MOUSE	30.67	15	183	NA	NA
KPGTTVEYLAPWANQID	Q8VEE0|RPE_MOUSE	49.47	17	1930	NA	1620
KPGTTVEYLAPWANQIDM(+15.99)	Q8VEE0|RPE_MOUSE	48.75	18	305	NA	57.2
KPIDYYTETKILQER	Q9R1J0|NSDHL_MOUSE	49.74	15	464	NA	410
KPIDYYTETKILQERA	Q9R1J0|NSDHL_MOUSE	49.84	16	1380	NA	1120
KPIDYYTETKILQERAV	Q9R1J0|NSDHL_MOUSE	49.91	17	558	NA	374
KPIEVQM(+15.99)TPQPSREEVD	Q80W94|MOGT2_MOUSE	46.08	17	497	NA	NA
KPKAAKPK	P15864|H12_MOUSE:P43274|H14_MOU	41.71	8	727	186	NA
KPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.89	15	7130	NA	NA
KPKAAKPKTSKPKAAKP	P43274|H14_MOUSE	33.22	17	305	NA	NA
KPKAAKPKTSKPKAAKPKKTAAKK	P43274|H14_MOUSE	48.93	24	2590	818	1390
KPKAKKTGAAKAKKPA	P43276|H15_MOUSE	43.15	16	1170	NA	1080
KPKAKQLKIKAEPPPKKRKK	A0A338P6K9|QSER1_MOUSE	33.03	20	266	NA	NA
KPKAKSSAKR	P10922|H10_MOUSE	33.34	10	131	NA	NA
KPKAKSSAKRASK	P10922|H10_MOUSE	33.97	13	1870	1110	NA
KPKAKSSAKRASKK	P10922|H10_MOUSE	25.53	14	1510	NA	NA
KPKAKSSAKRASKKK	P10922|H10_MOUSE	26.15	15	2790	NA	NA
KPKASKPKA	P43277|H13_MOUSE	29.3	9	1910	NA	475
KPKATKAKKAAPR	P43277|H13_MOUSE	46.85	13	2850	NA	NA
KPKATKAKKAAPRKK	P43277|H13_MOUSE	49.94	15	1260	1150	NA
KPKATPVKKAKKKPA	P10922|H10_MOUSE	48.49	15	1110	NA	NA
KPKFQEHIIQAPKPVEAIKRPSP	Q9D1P4|CHRD1_MOUSE	49.89	23	129	NA	189
KPKFQEHIIQAPKPVEAIKRPSPD	Q9D1P4|CHRD1_MOUSE	40.82	24	62.6	NA	NA
KPKGQLPDYTSPVVLPYSR	P32233|DRG1_MOUSE	49.58	19	121	NA	270
KPKKAAKSPAKAKAPK	P43277|H13_MOUSE	40.05	16	1340	NA	NA
KPKKAAPK	P43275|H11_MOUSE	25.66	8	852	NA	3940
KPKKAKPH	P47911|RL6_MOUSE	40.93	8	395	NA	341
KPKKAKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.95	23	1300	1910	NA
KPKKRRPPRAEKKKA	Q62018|CTR9_MOUSE	26.21	15	282	NA	NA
KPKKTAAKKK	P43274|H14_MOUSE	41.64	10	258	NA	NA
KPKKTAGAKKTVKKTPKKAKKPA	P43276|H15_MOUSE	49.95	23	1060	NA	NA
KPKKVVKVKPRPPL	D3Z3C6|ZFAN4_MOUSE	41.38	14	9200	NA	NA
KPKQDSQFEFKGPQAAQEQD	Q6RHR9|MAGI1_MOUSE	49.92	20	1580	NA	1320
KPKQDSQFEFKGPQAAQEQDF	Q6RHR9|MAGI1_MOUSE	49.19	21	461	NA	558
KPKTSKPKAAKPK	P43274|H14_MOUSE	42.61	13	596	1370	NA
KPKVVKAKKVAKSPAK	P43275|H11_MOUSE	40.71	16	402	NA	NA
KPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.91	19	193	834	602
KPLSVFKGPLLHISPA	Q9CWP6|MSPD2_MOUSE	29.59	16	956	NA	1230
KPLYQDFTAISNEAYRQ	P09470|ACE_MOUSE	49.56	17	115	NA	NA
KPPLGSLRFAPPQPAEPWS	Q8VCT4|EST1D_MOUSE:Q91WU0|EST1	49.79	19	2000	NA	3760
KPPSPWSSYQSPSPTPSSS	Q7TN98|CPEB4_MOUSE	49.3	19	855	NA	658
KPPSYNVATTLPSYD	Q8R0W6|NFIP1_MOUSE	43.91	15	2680	54.8	3050
KPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	49.04	16	24400	922	25000
KPPSYNVATTLPSYDEA	Q8R0W6|NFIP1_MOUSE	49.3	17	3730	27.3	5630
KPRGEFHTPVTVAGPH	Q8JZQ5|AOC1_MOUSE	49.79	16	28900	706	21900
KPRGEFHTPVTVAGPHV	Q8JZQ5|AOC1_MOUSE	49.59	17	22900	264	18300
KPRGEFHTPVTVAGPHVV	Q8JZQ5|AOC1_MOUSE	48.77	18	150	NA	NA
KPSGYNPPISILGIL	Q61739|ITA6_MOUSE	36.81	15	1700	NA	1590
KPSGYNPPISILGILE	Q61739|ITA6_MOUSE	41.28	16	860	NA	290
KPSPIYISSYSSPAR	Q68FH0|PKP4_MOUSE	45.91	15	628	NA	121
KPSPIYISSYSSPARE	Q68FH0|PKP4_MOUSE	45.16	16	615	NA	56.2
KPSPIYISSYSSPAREQ	Q68FH0|PKP4_MOUSE	49.61	17	4120	NA	3220
KPSPIYISSYSSPAREQN	Q68FH0|PKP4_MOUSE	47.58	18	1370	NA	1050
KPSTFAYPAPLEVP	Q3TXS7|PSMD1_MOUSE	43.47	14	655	NA	312
KPSTFAYPAPLEVPK	Q3TXS7|PSMD1_MOUSE	49.78	15	3110	NA	2320
KPSTFAYPAPLEVPKE	Q3TXS7|PSMD1_MOUSE	49.93	16	678	NA	440
KPTVTVVSPLPNDS	Q8VD58|EVI2B_MOUSE	41.65	14	284	NA	118
KPTVTVVSPLPNDSIN	Q8VD58|EVI2B_MOUSE	49.21	16	480	96.6	165
KPTVTVVSPLPNDSINPQ	Q8VD58|EVI2B_MOUSE	49.94	18	2890	905	1680
KPTVTVVSPLPNDSINPQP	Q8VD58|EVI2B_MOUSE	49.94	19	6290	1700	3750
KPVKASKPKKAKTVKPKA	P10922|H10_MOUSE	49.22	18	979	1420	NA
KPVKASKPKKAKTVKPKAKSSAKRASKK	P10922|H10_MOUSE	49.25	28	510	NA	2420
KPVPAAPVPSPVAPAPV	P97825|JUPI1_MOUSE	49.28	17	411	NA	465
KPVPAAPVPSPVAPAPVP	P97825|JUPI1_MOUSE	48.9	18	3290	NA	4070
KPVPAAPVPSPVAPAPVPS	P97825|JUPI1_MOUSE	49.77	19	171	NA	305
KPVPAAPVPSPVAPAPVPSRRNPP	P97825|JUPI1_MOUSE	48.9	24	406	NA	NA
KPVPAAPVPSPVAPAPVPSRRNPPG	P97825|JUPI1_MOUSE	49.94	25	807	NA	423
KPVPITSPAVSKVTST	Q8CI51|PDLI5_MOUSE	48.42	16	149	NA	436
KPVSQM(+15.99)RM(+15.99)ATPLLMRP	P04441|HG2A_MOUSE	47.62	17	29300	NA	232000
KPVSQM(+15.99)RMATPLLM(+15.99)RP	P04441|HG2A_MOUSE	39.73	16	751	NA	NA
KPVSQM(+15.99)RMATPLLM(+15.99)RP	P04441|HG2A_MOUSE	42.79	17	14700	NA	226000
KPVSQM(+15.99)RMATPLLMRPM	P04441|HG2A_MOUSE	49.16	17	20500	NA	179000
KPVSQM(+15.99)RMATPLLMRPM(+15.9	P04441|HG2A_MOUSE	48.6	17	540000	NA	90100

KPVSQMRM(+15.99)ATPLLM(+15.99)RP	P04441|HG2A_MOUSE	46.1	16	2080	NA	NA
KPVSQMRM(+15.99)ATPLLM(+15.99)RP	P04441|HG2A_MOUSE	46.8	17	223000	NA	263000
KPVSQMRM(+15.99)ATPLLMRPM	P04441|HG2A_MOUSE	48.9	17	42800	NA	193000
KPVSQMRM(+15.99)ATPLLMRPM(+15.9	P04441|HG2A_MOUSE	47.76	17	380000	NA	386000
KPVSQMRMATPLLM(+15.99)R	P04441|HG2A_MOUSE	31.06	15	1040	NA	NA
KPVSQMRMATPLLM(+15.99)RP	P04441|HG2A_MOUSE	41.4	16	275	NA	11600
KPVSQMRMATPLLM(+15.99)RPM	P04441|HG2A_MOUSE	48.48	17	76900	NA	268000
KPVSQMRMATPLLM(+15.99)RPM(+15.9	P04441|HG2A_MOUSE	47.11	17	194000	NA	239000
KPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	49.04	17	17600	NA	236000
KPVSQMRMATPLLMRPM(+15.99)	P04441|HG2A_MOUSE	49.42	17	115000	NA	301000
KPWNQYRLPKTLIPDS	P97449|AMPN_MOUSE	42.31	16	253	NA	NA
KQPYFGAVVGRVANR	Q8K157|GALM_MOUSE	30.97	15	837	NA	NA
KRKKKSYTTPKKNKHKRKK	P62983|RS27A_MOUSE	49.95	19	2460	175000	60600
KRKKKSYTTPKKNKHKRKKVKLAVLKYY	P62983|RS27A_MOUSE	49.95	28	550	4430	6280
KRKRSRKESYSVYVYKVLKQ	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.95	20	196	NA	NA
KRKRSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.95	24	3080	3870	NA
KRQEFLASVARGVAPA	Q6ZPS6|AKIB1_MOUSE	46.49	16	287	NA	NA
KRQQLYIASRSAVAQ	Q62177|SEM3B_MOUSE	38.33	15	1090	NA	1090
KRQQLYIASRSAVAQIA	Q62177|SEM3B_MOUSE	30.23	17	527	NA	NA
KRRYDRKQS(+79.97)GY(+79.97)GGQTI	P83882|RL36A_MOUSE	31	32	286	NA	NA
KRSRKESYSVYVYKVLKQ	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.76	18	784	NA	NA
KRSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.95	22	6810	8360	1960
KRYM(+15.99)APEVLDETIN	Q61271|ACV1B_MOUSE	41.75	14	547	NA	NA
KRYMAPEVLDETIN	Q61271|ACV1B_MOUSE	47.99	14	357	NA	205
KSFVGPTPAPAPA	Q501J7|PHAR4_MOUSE	36.3	13	118	NA	224
KSFVGPTPAPAPAP	Q501J7|PHAR4_MOUSE	33.34	14	97.7	NA	NA
KSFVQNYPVVSIED	P17182|ENOA_MOUSE	49.5	14	470	NA	242
KSFVQNYPVVSIEDP	P17182|ENOA_MOUSE	49.13	15	98.5	NA	451
KSFVQNYPVVSIEDPF	P17182|ENOA_MOUSE	49.94	16	19600	411	18700
KSFVQNYPVVSIEDPFD	P17182|ENOA_MOUSE	49.92	17	5750	NA	3830
KSKASKPKVTKPKTAKPKAAKAKKAVSK	P43276|H15_MOUSE	49.95	30	7090	NA	NA
KSKTVYEGPFASRSLS	Q60680|IKKA_MOUSE	44.07	16	1180	NA	761
KSPAKAKAPK	P43277|H13_MOUSE	25.56	10	2900	NA	NA
KSPKKAKVTKPKK	P15864|H12_MOUSE	49.93	13	13200	2230	1390
KSPKKAKVTKPKKVK	P15864|H12_MOUSE	49.95	15	1540	NA	NA
KSPKKVKAAKPKKAA	P43277|H13_MOUSE	49.73	15	404	NA	NA
KSPKKVKAAKPKKAAKS(+79.97)PAKAK	P43277|H13_MOUSE	35.87	25	2690	NA	NA
KSPVYKNPTPGSSE	Q99PG0|AAAD_MOUSE	49.88	14	652	NA	NA
KSPVYKNPTPGSSEL	Q99PG0|AAAD_MOUSE	49.58	15	6600	NA	761
KSPVYKNPTPGSSELA	Q99PG0|AAAD_MOUSE	49.72	16	1430	NA	NA
KSTKKTPKKAKKPA	P43274|H14_MOUSE	49.94	14	6320	2030	2300
KSTKKTPKKAKKPAA	P43274|H14_MOUSE	49.87	15	420	1330	2010
KTAGAKKTVKKTPKKAKKPA	P43276|H15_MOUSE	49.95	20	800	NA	356
KTASYYSPSGQREFTA	O88310|ITL1A_MOUSE	29.99	16	264	NA	NA
KTHDLYIQSHISENR	Q9R111|GUAD_MOUSE	49.88	15	551	NA	408
KTHDLYIQSHISENRE	Q9R111|GUAD_MOUSE	49.94	16	1570	NA	1190
KTHDLYIQSHISENREE	Q9R111|GUAD_MOUSE	49.88	17	3350	NA	2330
KTHDLYIQSHISENREEI	Q9R111|GUAD_MOUSE	25.14	18	167	NA	NA
KTHEQLTPLVRSAGT	P09813|APOA2_MOUSE	37.54	15	230	NA	NA
KTHEQLTPLVRSAGTS	P09813|APOA2_MOUSE	44.4	16	431	NA	NA
KTITYESSQVDPGADL	Q9WV92|E41L3_MOUSE	48.78	16	5320	210	4760
KTITYESSQVDPGADLEPG	Q9WV92|E41L3_MOUSE	49.94	19	530	NA	NA
KTPEIVAPESAHAAF	Q8R0X7|SGPL1_MOUSE	49.75	15	635	NA	226
KTPEIVAPESAHAAFD	Q8R0X7|SGPL1_MOUSE	46.03	16	397	NA	237
KTPEIVAPESAHAAFDK	Q8R0X7|SGPL1_MOUSE	49.48	17	339	NA	329
KTPESFLGPNAALVD	Q80VP1|EPN1_MOUSE	48.13	15	229	NA	267
KTPESFLGPNAALVDL	Q80VP1|EPN1_MOUSE	45.09	16	454	NA	419
KTPESFLGPNAALVDLD	Q80VP1|EPN1_MOUSE	49.58	17	11200	NA	9480
KTPESFLGPNAALVDLDS	Q80VP1|EPN1_MOUSE	49.69	18	1780	NA	1950
KTPIETTAPTAAIPGTN	E9Q7P9|CDHR2_MOUSE	48.79	17	208	NA	213
KTPKKAKKPA	P15864|H12_MOUSE:P43276|H15_MOU	49.09	10	1920	NA	1010
KTQYISPNLNPN	P97499|TEP1_MOUSE	46.7	12	4790	NA	5130
KTQYISPNLNPND	P97499|TEP1_MOUSE	48.31	13	2910	111	8450
KTQYISPNLNPNDV	P97499|TEP1_MOUSE	48.87	14	1700	NA	1280
KTQYISPNLNPNDVT	P97499|TEP1_MOUSE	49.78	15	2240	NA	1610
KTRLSRTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	43.25	26	354	1850	NA
KTSKPKAAKPKKTAAKK	P43274|H14_MOUSE	46.32	17	696	NA	NA
KTSKSPKKPKVVKAKKVAK	P43275|H11_MOUSE	49.95	19	3840	3710	2830
KTVKKTPKKAKKPA	P43276|H15_MOUSE	49.95	14	6350	2180	2660
KTVKKTPKKAKKPAA	P43276|H15_MOUSE	36.87	15	1360	NA	NA
KTVKKTPKKAKKPAAAGVKK	P43276|H15_MOUSE	49	20	660	533	277
KTVKKTPKKAKKPAAAGVKKVAKSPKKA	P43276|H15_MOUSE	49.95	29	1680	696	1660
KTVKPKAAKP	P43274|H14_MOUSE	30.88	10	2650	NA	NA
KTVKPKAAKPKTSKPKAAKP	P43274|H14_MOUSE	29.82	20	12200	NA	NA
KTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.94	18	1520	NA	NA
KTVKTPKKPKKPAVSK	P43275|H11_MOUSE	37.01	16	823	NA	NA
KTVKTPKKPKKPAVSKK	P43275|H11_MOUSE	49.49	17	489	401	NA

KTVKTPKKPKKPAVSKKTS	P43275|H11_MOUSE	30.85	19	133	NA	NA
KTVTYEDPQAVGGLA	Q5SRX1|TM1L2_MOUSE	46.33	15	1410	NA	2750
KVAKSPAKAK	P43275|H11_MOUSE	31.15	10	2830	922	NA
KVAKSPAKAKAVKPKA	P43275|H11_MOUSE	49.77	16	1380	NA	3320
KVAKSPKKAK	P15864|H12_MOUSE:P43276|H15_MOU	42.43	10	846	243	471
KVAKSPKKAKAAAKPKKAAK	P43276|H15_MOUSE	49.94	20	1690	1300	1060
KVEYHFLSPYVSPR	Q62351|TFR1_MOUSE	41.35	14	408	NA	497
KVEYHFLSPYVSPRE	Q62351|TFR1_MOUSE	46.16	15	356	NA	241
KVEYHFLSPYVSPRESP	Q62351|TFR1_MOUSE	49.49	17	478	NA	257
KVFIYHGSPTGIITKP	Q61739|ITA6_MOUSE	48.92	16	1340	NA	NA
KVFIYHGSPTGIITKPT	Q61739|ITA6_MOUSE	49.33	17	127	NA	NA
KVIPELNGKLTGM(+15.99)AFRVPTPNV	P16858|G3P_MOUSE	49.93	26	783	NA	2560
KVIPELNGKLTGMAFRVPTPNVSVVD	P16858|G3P_MOUSE	48.94	26	2260	NA	5230
KVIPKSKFVLVKF	P57759|ERP29_MOUSE	49.82	13	576	NA	125
KVKAAKPKKAAKSPAKAKAPKAKASKPK	P43277|H13_MOUSE	49.93	29	203	1140	NA
KVKAAVKK	Q8BH86|GLUCM_MOUSE	25.86	8	116	NA	NA
KVKPVKASKPKKAK	P10922|H10_MOUSE	49.94	14	369	495	1060
KVLPTYDASKVTASGPG	Q80X90|FLNB_MOUSE	49.51	17	2980	NA	2360
KVTFNSALAQKE	O89051|ITM2B_MOUSE	45.01	12	982	NA	780
KVTFNSALAQKEA	O89051|ITM2B_MOUSE	46.58	13	802	NA	350
KVTFNSALAQKEAK	O89051|ITM2B_MOUSE	49.59	14	3630	NA	3020
KVTFNSALAQKEAKK	O89051|ITM2B_MOUSE	49.81	15	26000	513	20700
KVTFNSALAQKEAKKD	O89051|ITM2B_MOUSE	49.72	16	2840	NA	1770
KVVFLSPAVPEEPE	B2RXS4|PLXB2_MOUSE	48.75	14	197	NA	NA
KVYIYHSSSGGLL	Q62470|ITA3_MOUSE	49.12	13	314	NA	345
KVYIYHSSSGGLLR	Q62470|ITA3_MOUSE	48.17	14	1060	NA	1470
KVYIYHSSSGGLLRQPQ	Q62470|ITA3_MOUSE	49.89	17	119	NA	NA
KVYWDAPSPAPD	Q8K385|FRRS1_MOUSE	42.91	12	121	NA	173
KWKALYTDPKSSETAA	Q920A5|RISC_MOUSE	48.58	16	306	NA	NA
KYHFVTPLTSM(+15.99)VVTKP	Q61704|ITIH3_MOUSE	29.57	16	215	NA	NA
KYLLSQSSPAPLTAAEEE	Q91YR1|TWF1_MOUSE	49.93	18	73.8	NA	NA
KYNFVTPLTHM(+15.99)VVTKP	A6X935|ITIH4_MOUSE	49.62	16	4020	NA	3160
KYNFVTPLTHMVVT	A6X935|ITIH4_MOUSE	48.86	14	25.8	NA	99.3
KYNFVTPLTHMVVTKP	A6X935|ITIH4_MOUSE	49.94	16	2520	NA	5220
KYSIDPSVVNISDE	Q8BTY2|S4A7_MOUSE	43.37	14	83.3	NA	NA
KYSIDPSVVNISDEM(+15.99)	Q8BTY2|S4A7_MOUSE	49.29	15	706	NA	399
KYTYGKPVPGHVK	P28665|MUG1_MOUSE	48.79	13	45400	1290	26400
KYTYGKPVPGHVKI	P28665|MUG1_MOUSE	49.85	14	9230	NA	5060
KYTYGKPVPGHVKIN	P28665|MUG1_MOUSE	48.71	15	386	NA	NA
LALIYGTPRAATVK	Q9DBC7|KAP0_MOUSE:P12849|KAP1_M	31.25	14	1460	NA	988
LALIYGTPRAATVKA	Q9DBC7|KAP0_MOUSE:P12849|KAP1_M	48.7	15	22300	NA	20800
LALIYGTPRAATVKAK	Q9DBC7|KAP0_MOUSE:P12849|KAP1_M	49.67	16	5160	NA	4430
LALIYGTPRAATVKAKT	Q9DBC7|KAP0_MOUSE:P12849|KAP1_M	33.2	17	559	NA	168
LALM(+15.99)YNTPRAATIIA	P12367|KAP2_MOUSE	49.11	15	1180	NA	664
LALMYNTPRAATIIA	P12367|KAP2_MOUSE	48.79	15	232	NA	464
LANM(+15.99)ISEPRISYGNDA	P12023|A4_MOUSE	48.13	16	152	NA	NA
LANMISEPRISYGND	P12023|A4_MOUSE	42.31	15	46.2	NA	NA
LAPFFTPNAAPAE	Q80TA9|EPG5_MOUSE	46.57	13	276	NA	160
LAPM(+15.99)YYRGAQAAIVV	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	41.61	15	447	NA	370
LAPM(+15.99)YYRGAQAAIVVY	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	38.88	16	161	NA	259
LAPM(+15.99)YYRGAQAAIVVYD	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	46.89	17	3720	172	3730
LAPMYYRGAQAAIVV	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	41.21	15	150	NA	183
LAPMYYRGAQAAIVVYD	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	45.94	17	326	NA	3210
LAQVYGAPQLQVEK	P27808|MGAT1_MOUSE	48.79	14	319	NA	196
LAQVYGAPQLQVEKV	P27808|MGAT1_MOUSE	49.78	15	465	NA	245
LARTYLPSQVSRVVK	O55029|COPB2_MOUSE	49.69	15	1480	NA	1690
LAVAGAPIALSAVG	Q8VC49|IF27B_MOUSE	47.99	14	1240	NA	954
LAVAGAPVALSAVG	Q8VC49|IF27B_MOUSE	37.95	14	307	NA	200
LAVFDGPSTNSR	Q9JLB4|CUBN_MOUSE	36.88	12	121	NA	NA
LDARSYTAAVANRAK	Q91XS1|MTMR4_MOUSE	46.46	15	503	NA	912
LDARSYTAAVANRAKGGG	Q91XS1|MTMR4_MOUSE	49.45	18	6650	NA	5590
LDEFYSDPHAVAGAL	Q3UIA2|RHG17_MOUSE	38.03	15	89.5	NA	144
LDHYIYEAEEANLGPG	P02469|LAMB1_MOUSE	49.26	16	2460	NA	1040
LDIDSEPVAARSTS	P53657|KPYR_MOUSE	45.34	14	814	NA	704
LDIDSEPVAARSTSI	P53657|KPYR_MOUSE	47.63	15	629	NA	611
LDIDSEPVAARSTSII	P53657|KPYR_MOUSE	49.29	16	823	NA	815
LDIKSFITSIANKN	Q8CHR6|DPYD_MOUSE	49.38	14	347	NA	200
LDIKSFITSIANKNYYG	Q8CHR6|DPYD_MOUSE	49.87	17	91.6	NA	379
LDKFLASVSTVLTSKYR	P01942|HBA_MOUSE	49.68	17	36.2	NA	NA
LDLLDLAPEPRYAHIPV	Q09200|B4GN1_MOUSE	29.92	17	498	NA	257
LDLYKGSVALRDIH	Q6P4T0|ATG2A_MOUSE	47.3	14	109	NA	NA
LDNYDAPDIANIA	Q68FD5|CLH1_MOUSE	46.81	13	146	NA	NA
LDQLFSGPLPGRLP	Q60805|MERTK_MOUSE	47.53	14	5790	NA	3390
LDQLFSGPLPGRLPV	Q60805|MERTK_MOUSE	48.82	15	21500	NA	12900
LDQLFSGPLPGRLPVN	Q60805|MERTK_MOUSE	49.51	16	120	NA	NA
LDRDSLVHSSPHVALSHVD	Q9WV91|FPRP_MOUSE	49.89	19	527	NA	993
LDRDSLVHSSPHVALSHVDT	Q9WV91|FPRP_MOUSE	48.85	20	592	NA	128

LDRYYTPTISRER	Q9R1P3|PSB2_MOUSE	49.19	13	1860	NA	2050
LDRYYTPTISRERA	Q9R1P3|PSB2_MOUSE	39.44	14	5080	NA	6390
LDRYYTPTISRERAV	Q9R1P3|PSB2_MOUSE	31.24	15	1830	NA	1970
LDTELNYPM(+15.99)ISAGSYG	Q3UWA6|GUC2C_MOUSE	26.12	16	159	NA	NA
LDYHFVTPLTSLT	Q61702|ITIH1_MOUSE	39.33	13	317	NA	257
LDYLAVFDGPSTNSR	Q9JLB4|CUBN_MOUSE	43.8	15	150	NA	NA
LEALVGPEANVGP	O09159|MA2B1_MOUSE	38.98	13	183	NA	NA
LEALVGPEANVGPY	O09159|MA2B1_MOUSE	46.88	14	113	NA	NA
LEALVGPEANVGPYG	O09159|MA2B1_MOUSE	48.46	15	710	NA	NA
LEAYYSSPQDLPYPDPA	Q61316|HSP74_MOUSE	49.49	17	663	NA	393
LEDFYGSPIPSVS	Q9Z0M6|AGRE5_MOUSE	40.04	13	568	NA	NA
LEDFYGSPIPSVSLK	Q9Z0M6|AGRE5_MOUSE	49.82	15	2680	547	1200
LEDFYGSPIPSVSLKL	Q9Z0M6|AGRE5_MOUSE	49.64	16	1210	NA	384
LEEQLGPVAEETR	P08226|APOE_MOUSE	42.59	13	3480	102	1690
LEEQLGPVAEETRA	P08226|APOE_MOUSE	44.96	14	2720	120	2540
LEEQLGPVAEETRAR	P08226|APOE_MOUSE	48.42	15	2980	NA	1230
LEISYTGSRPA	P28666|MUG2_MOUSE:P28665|MUG1_M	31.44	11	54.7	NA	NA
LEISYTGSRPASN	P28666|MUG2_MOUSE:P28665|MUG1_M	40.68	13	4770	NA	1720
LEISYTGSRPASNM(+15.99)	P28666|MUG2_MOUSE:P28665|MUG1_M	45.71	14	1210	NA	219
LEISYTGSRPASNM(+15.99)V	P28666|MUG2_MOUSE:P28665|MUG1_M	48.69	15	11200	NA	2060
LEISYTGSRPASNM(+15.99)VI	P28666|MUG2_MOUSE:P28665|MUG1_M	49.6	16	1060	NA	NA
LEISYTGSRPASNMV	P28666|MUG2_MOUSE:P28665|MUG1_M	49.38	15	3300	NA	2860
LEISYTGSRPASNMVI	P28666|MUG2_MOUSE:P28665|MUG1_M	49.57	16	212	NA	108
LEKKQ(+15.00)RKEKEKLLLQKREIE	Q9WTY1|PDCD7_MOUSE	36.81	20	2840	NA	NA
LERESKVVVPPLPGKAF	O70492|SNX3_MOUSE	42.09	17	227	NA	126
LERFYDPM(+15.99)AGSVF	P06795|MDR1B_MOUSE:P21447|MDR1A	49.62	13	484	NA	NA
LERFYDPM(+15.99)AGSVFL	P06795|MDR1B_MOUSE:P21447|MDR1A	49.19	14	587	NA	130
LEVVTDPTTNAG	Q9R100|CAD17_MOUSE	42.88	12	520	NA	340
LEVVTDPTTNAGY	Q9R100|CAD17_MOUSE	46.64	13	145	NA	92.1
LEVVTDPTTNAGYV	Q9R100|CAD17_MOUSE	49.3	14	1390	NA	980
LEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	45.42	15	9360	142	7570
LFPQYTAPSILPSDIT	Q3UHA3|SPTCS_MOUSE	25.59	16	255	NA	NA
LFTQYFQSM(+15.99)TDYGKD	P09813|APOA2_MOUSE	48.52	15	861	NA	361
LFTQYFQSM(+15.99)TDYGKDL	P09813|APOA2_MOUSE	49.57	16	808	NA	182
LFTQYFQSMTDYGKD	P09813|APOA2_MOUSE	49.31	15	725	NA	506
LFTQYFQSMTDYGKDL	P09813|APOA2_MOUSE	48.86	16	300	NA	NA
LGDATLYVPSAPLSGP	Q60928|GGT1_MOUSE	38.28	16	62	NA	143
LGFPYEGPAPLEAIA	Q8R4G6|MGT5A_MOUSE	49.5	15	1720	NA	1820
LGFPYEGPAPLEAIANG	Q8R4G6|MGT5A_MOUSE	49.66	17	1440	NA	695
LGVAYEAPSLATGYG	P99026|PSB4_MOUSE	47.32	15	810	NA	807
LGYAVYETPTAHNGAKNPR	Q9QZ06|TOLIP_MOUSE	49.88	19	1700	NA	2500
LHLRFSAPQIENE	Q61190|I10R2_MOUSE	43.95	13	24.4	NA	NA
LHLRFSAPQIENEP	Q61190|I10R2_MOUSE	49.63	14	25400	386	20600
LHLRFSAPQIENEPE	Q61190|I10R2_MOUSE	49.86	15	115000	3110	93000
LHLRFSAPQIENEPET	Q61190|I10R2_MOUSE	49.86	16	27600	86.3	18200
LHTKGALPLDTVTFYKVIPKSKFVLVKF	P57759|ERP29_MOUSE	49.95	28	494	NA	NA
LIERYVAAM(+15.99)VLSAAG	P54923|ADPRH_MOUSE	30.88	15	91.8	NA	NA
LIEVSSPITLQALVQ	E9Q414|APOB_MOUSE	49.89	15	144	NA	212
LIGDSNFGAPSASVAAAPAPA	O35643|AP1B1_MOUSE	48.49	21	417	NA	841
LIIQWNGPESNRM(+15.99)E	Q62468|VILI_MOUSE	49.09	14	457	NA	115
LIRLPYTASSGLM(+15.99)APRE	Q9R1Q9|VAS1_MOUSE	49.45	17	426	NA	338
LIRLPYTASSGLMAPRE	Q9R1Q9|VAS1_MOUSE	49.91	17	57.6	NA	255
LIVSHDYKGSTSHSLPY	E9Q414|APOB_MOUSE	49.86	17	715	NA	858
LIVSHDYKGSTSHSLPYE	E9Q414|APOB_MOUSE	44.72	18	676	NA	822
LIYGTPRAATVK	Q9DBC7|KAP0_MOUSE:P12849|KAP1_M	26.88	12	377	NA	NA
LIYGTPRAATVKA	Q9DBC7|KAP0_MOUSE:P12849|KAP1_M	47.26	13	4360	NA	3640
LKRSYSSPDITQALQ	Q80U87|UBP8_MOUSE	49.73	15	3690	NA	6540
LKRSYSSPDITQALQE	Q80U87|UBP8_MOUSE	49.77	16	4360	NA	3890
LKYNFVTPLTHM(+15.99)VVT	A6X935|ITIH4_MOUSE	49.87	15	1410	NA	719
LKYNFVTPLTHM(+15.99)VVTKP	A6X935|ITIH4_MOUSE	49.93	17	13700	NA	8600
LKYNFVTPLTHMVVT	A6X935|ITIH4_MOUSE	49.81	15	307	NA	803
LKYNFVTPLTHMVVTKP	A6X935|ITIH4_MOUSE	49.93	17	6720	NA	12900
LKYSIDPSVVNISDEM(+15.99)	Q8BTY2|S4A7_MOUSE	49.05	16	464	NA	175
LLERFYDPM(+15.99)AGSVFL	P06795|MDR1B_MOUSE:P21447|MDR1A	49.01	15	618	NA	94.5
LLKDFRTPLSHAAN	Q08ED0|B2L15_MOUSE	26.09	14	109	NA	NA
LLKDFRTPLSHAANR	Q08ED0|B2L15_MOUSE	49.64	15	1470	NA	1460
LLLPGELAKHAVSEGTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8CGP0|H2B3B	42.42	26	711	NA	3240
LLPPYDDATAVPSTAKEPPPP	Q91XQ6|LAP4B_MOUSE	49.94	21	5140	NA	7510
LLPQEKYVTSAPM(+15.99)PEPGAPG	P01872|IGHM_MOUSE	45.54	20	141	NA	NA
LLPSVSQPKAQATPS	Q3UHJ0|AAK1_MOUSE	49.4	15	31	NA	NA
LLQ(+15.00)KTQ(+15.00)YISPNLNPND	P97499|TEP1_MOUSE	37.43	16	7900	NA	NA
LLQPPPPPPPLLF	Q69ZA1|CDK13_MOUSE	32.36	13	302	NA	NA
LLREYYGAGVNGDPV	Q8VCS0|PGRP2_MOUSE	26.32	15	260	NA	NA
LLTQYSTPEGSSVPI	E9Q414|APOB_MOUSE	48.47	15	1160	NA	10400
LLTQYSTPEGSSVPIF	E9Q414|APOB_MOUSE	47.06	16	203	NA	255
LLVHNLPLALGAFA	P31809|CEAM1_MOUSE	31.15	14	143	NA	NA
LLVQWKNPQNFRSR	O09030|I13R1_MOUSE	25.3	14	1020	NA	1080

LLVSWQAPRARITG	P11276|FINC_MOUSE	41.85	14	340	NA	NA
LLVSWQAPRARITGYI	P11276|FINC_MOUSE	27.55	16	45.9	NA	NA
LLVVNHPDSSSTVE	P52430|PON1_MOUSE	46.36	14	109	NA	504
LLYNVPAVAEEIQ	P12023|A4_MOUSE	45.18	13	245	NA	NA
LLYNVPAVAEEIQD	P12023|A4_MOUSE	29.06	14	111	NA	NA
LLYNVPAVAEEIQDE	P12023|A4_MOUSE	48.11	15	331	NA	NA
LM(+15.99)PFRQPITTIVGKP	Q80W94|MOGT2_MOUSE	32.79	15	180	NA	97.8
LM(+15.99)YNTPRAATIIA	P12367|KAP2_MOUSE	31.13	13	293	NA	NA
LNFRNPAVQEEIK	Q91WV7|SLC31_MOUSE	46.01	13	5040	NA	4640
LNFRNPAVQEEIKE	Q91WV7|SLC31_MOUSE	42.14	14	457	NA	136
LNIYTPAHAHEG	Q91WG0|EST2C_MOUSE	39.97	12	578	NA	NA
LNIYTPAHAHEGSN	Q91WG0|EST2C_MOUSE	44.66	14	1710	NA	NA
LNIYTPAHAHEGSNL	Q91WG0|EST2C_MOUSE	47.21	15	2660	NA	513
LNIYTPAHAHEGSNLP	Q91WG0|EST2C_MOUSE	44.07	16	422	NA	NA
LNIYTPAHAHEGSNLPV	Q91WG0|EST2C_MOUSE	49.01	17	5760	NA	3710
LNIYVPAHAHEG	Q8BK48|EST2E_MOUSE	39.17	12	4000	NA	2100
LNIYVPAHAHEGS	Q8BK48|EST2E_MOUSE	36.2	13	412	NA	312
LNIYVPAHAHEGSN	Q8BK48|EST2E_MOUSE	45.01	14	15700	194	12000
LNIYVPAHAHEGSNL	Q8BK48|EST2E_MOUSE	46.84	15	13600	41.2	6770
LNIYVPAHAHEGSNLP	Q8BK48|EST2E_MOUSE	48.06	16	5460	NA	2710
LNIYVPAHAHEGSNLPV	Q8BK48|EST2E_MOUSE	49.79	17	13500	76.9	10200
LNLAYIGAVPHSGIE	P48441|IDUA_MOUSE	37.82	15	442	NA	286
LNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	48.92	14	872	NA	1180
LNSVFVAPAVTPVKG	P70158|ASM3A_MOUSE	49.13	15	562	NA	629
LNVLRIINEPTAAAIAYG	P17879|HS71B_MOUSE:P16627|HS71L_	49.91	18	469	NA	427
LNVQFSSPLPGEAVK	Q80X90|FLNB_MOUSE	49.22	15	190	NA	206
LPAAAQAPDALPAGWE	Q9DBH0|WWP2_MOUSE	38.06	16	1530	NA	536
LPADIPSYLSSQGTLADRQ	Q6P1C6|LRIG3_MOUSE	26.17	19	215	NA	NA
LPADPPASVVVGPVVVPR	P29699|FETUA_MOUSE	49.81	18	252	NA	NA
LPADPPASVVVGPVVVPRGLS	P29699|FETUA_MOUSE	49.88	21	105	NA	197
LPADPPASVVVGPVVVPRGLSD	P29699|FETUA_MOUSE	36.69	22	84.2	NA	NA
LPANAFASPLQNPDN	Q08857|CD36_MOUSE	42.64	15	2650	NA	NA
LPDDINVYATTAANPKE	O89017|LGMN_MOUSE	44.51	17	766	NA	231
LPDDINVYATTAANPKES	O89017|LGMN_MOUSE	49.94	18	763	NA	568
LPDDINVYATTAANPKESS	O89017|LGMN_MOUSE	49.94	19	5130	179	3320
LPDDINVYATTAANPKESSY	O89017|LGMN_MOUSE	49.94	20	285	NA	170
LPDDINVYATTAANPKESSYA	O89017|LGMN_MOUSE	49.92	21	439	NA	NA
LPDIYGWPVASDN	Q61391|NEP_MOUSE	44.95	13	877	NA	260
LPDIYGWPVASDNWD	Q61391|NEP_MOUSE	49.89	15	658	NA	202
LPDIYGWPVASDNWDQ	Q61391|NEP_MOUSE	49.8	16	3380	NA	1140
LPDLTNIHFPSPLPTPLDPE	Q68ED7|CRTC1_MOUSE	47.11	20	126	NA	NA
LPDYSAPNPIK	Q8CFG0|SULF2_MOUSE	42.07	11	1400	NA	1600
LPDYSAPNPIKVT	Q8CFG0|SULF2_MOUSE	49.69	13	2090	NA	2600
LPDYSAPNPIKVTH	Q8CFG0|SULF2_MOUSE	49.82	14	22700	849	30000
LPDYSAPNPIKVTHR	Q8CFG0|SULF2_MOUSE	49.87	15	23700	1080	32500
LPEEVGEYRQPSGGSVPVSPG	P08101|FCGR2_MOUSE	35.28	21	154	NA	NA
LPEEYFTPAPSPGDQ	O08983|HPS1_MOUSE	41.46	15	202	NA	NA
LPESTFEPVPIQAKTSPV	P11859|ANGT_MOUSE	38.05	18	110	NA	NA
LPFGAYTNPFATPAQ	Q80WC7|AGFG2_MOUSE	47.5	15	1070	NA	998
LPFGAYTNPFATPAQAQ	Q80WC7|AGFG2_MOUSE	47.88	17	2350	NA	3080
LPGELAKHAVSEGTKAVTKYTSSK	P70696|H2B1A_MOUSE:Q8CGP0|H2B3E	47.23	24	2150	NA	NA
LPGPSQPRQYNNPIGLYSAE	Q9JKS4|LDB3_MOUSE	49.87	20	838	NA	680
LPGPSQPRQYNNPIGLYSAET	Q9JKS4|LDB3_MOUSE	49.94	21	13700	NA	12000
LPGPSQPRQYNNPIGLYSAETL	Q9JKS4|LDB3_MOUSE	49.53	22	507	NA	474
LPIPERYLSPDATVSTE	Q640N1|AEBP1_MOUSE	49.81	17	2960	NA	1590
LPIPERYLSPDATVSTEV	Q640N1|AEBP1_MOUSE	49.88	18	8620	NA	4350
LPKSAKPVSQM(+15.99)RMATPLLMRPM	P04441|HG2A_MOUSE	46.72	22	57.2	NA	4100
LPKSAKPVSQM(+15.99)RMATPLLMRPM	P04441|HG2A_MOUSE	46.87	22	2620	NA	4040
LPKSAKPVSQMRM(+15.99)ATPLLM(+15	P04441|HG2A_MOUSE	35.63	21	272	NA	NA
LPKSAKPVSQMRM(+15.99)ATPLLMRPM	P04441|HG2A_MOUSE	49.11	22	2620	NA	3960
LPKSAKPVSQMRMATPLLM(+15.99)RPM	P04441|HG2A_MOUSE	49.85	22	1200	NA	5270
LPKSAKPVSQMRMATPLLM(+15.99)RPM	P04441|HG2A_MOUSE	45.05	22	1350	NA	4970
LPKSAKPVSQMRMATPLLMRPM(+15.99	P04441|HG2A_MOUSE	49.94	22	1200	NA	5270
LPLPEQAQEQAQEQAQEQVQPKPLES	P06728|APOA4_MOUSE	49.95	26	306	NA	80.8
LPLPYEVSAPGPGYAPLR	Q8VCE9|PKHH3_MOUSE	45.02	18	80.2	NA	130
LPLRSQFKGPAPRETKD	Q9JM76|ARPC3_MOUSE	37.43	17	1600	NA	3000
LPLRSQFKGPAPRETKDT	Q9JM76|ARPC3_MOUSE	43.99	18	1970	NA	5190
LPNKPTVTVVSPLPNDSINPQP	Q8VD58|EVI2B_MOUSE	49.95	22	704	NA	360
LPPALQEPQPAGSQP	Q8R1U2|CGRE1_MOUSE	48.37	15	1030	NA	NA
LPPALQEPQPAGSQPL	Q8R1U2|CGRE1_MOUSE	49.65	16	4880	NA	1840
LPPASLPESTPVPSSSPP	Q6PB44|PTN23_MOUSE	49.74	18	1440	NA	4640
LPPASLPESTPVPSSSPPP	Q6PB44|PTN23_MOUSE	49.91	19	16800	NA	23600
LPPHVYSTPQPSLPP	Q3UPH1|PRRC1_MOUSE	49.78	15	175000	2250	172000
LPPHVYSTPQPSLPPV	Q3UPH1|PRRC1_MOUSE	49.56	16	125000	2330	133000
LPPHVYSTPQPSLPPVQ	Q3UPH1|PRRC1_MOUSE	49.78	17	53500	703	59200
LPPHVYSTPQPSLPPVQP	Q3UPH1|PRRC1_MOUSE	49.71	18	13500	NA	16900
LPPHVYSTPQPSLPPVQPS	Q3UPH1|PRRC1_MOUSE	49.93	19	34700	NA	42300

LPPHVYSTPQPSLPPVQPSAPPP	Q3UPH1|PRRC1_MOUSE	49.95	23	18800	NA	25700
LPPVSPPKAALSVDE	Q6NZJ6|IF4G1_MOUSE	49.84	15	3660	NA	2230
LPPYDDATAVPSTA	Q91XQ6|LAP4B_MOUSE	27.81	14	2330	NA	1300
LPPYDDATAVPSTAK	Q91XQ6|LAP4B_MOUSE	42.34	15	731	NA	940
LPPYDDATAVPSTAKEP	Q91XQ6|LAP4B_MOUSE	47.31	17	633	NA	976
LPPYDDATAVPSTAKEPP	Q91XQ6|LAP4B_MOUSE	49.91	18	50300	NA	52800
LPPYDDATAVPSTAKEPPP	Q91XQ6|LAP4B_MOUSE	49.93	19	179000	2600	185000
LPPYDDATAVPSTAKEPPPP	Q91XQ6|LAP4B_MOUSE	49.93	20	951000	19800	927000
LPPYDDATAVPSTAKEPPPPY	Q91XQ6|LAP4B_MOUSE	49.84	21	349	NA	81.6
LPQDPTFHTPLDLYA	Q07797|LG3BP_MOUSE	49.71	15	1160	NA	570
LPQDPTFHTPLDLYAY	Q07797|LG3BP_MOUSE	49.68	16	4880	NA	2740
LPQDPTFHTPLDLYAYA	Q07797|LG3BP_MOUSE	49.25	17	3850	NA	1780
LPQDPTFHTPLDLYAYAR	Q07797|LG3BP_MOUSE	49.93	18	96600	439	47800
LPQDPTFHTPLDLYAYARA	Q07797|LG3BP_MOUSE	49.66	19	369	NA	NA
LPQEKYVTSAPM(+15.99)PEP	P01872|IGHM_MOUSE	48.68	15	151	NA	NA
LPQEKYVTSAPM(+15.99)PEPG	P01872|IGHM_MOUSE	49.86	16	17900	201	8160
LPQEKYVTSAPM(+15.99)PEPGAPG	P01872|IGHM_MOUSE	49.94	19	27100	641	13300
LPQEKYVTSAPMPEPG	P01872|IGHM_MOUSE	49.52	16	4720	NA	6720
LPQEKYVTSAPMPEPGAPG	P01872|IGHM_MOUSE	49.92	19	6830	NA	12100
LPQLIEVSSPITLQAL	E9Q414|APOB_MOUSE	49.56	16	364	NA	279
LPQLPPTVLPVE	Q99LJ1|FUCO_MOUSE	36.19	12	389	NA	NA
LPSNSVYAGTVPSRVPA	Q8VCF0|MAVS_MOUSE	46.24	17	728	NA	1060
LPSPLIM(+15.99)SPGPIYAVD	Q8VHF2|CDHR5_MOUSE	49.77	16	383	NA	NA
LPSPLIM(+15.99)SPGPIYAVDG	Q8VHF2|CDHR5_MOUSE	49.93	17	9110	63.4	7480
LPSPLIM(+15.99)SPGPIYAVDGD	Q8VHF2|CDHR5_MOUSE	49.94	18	12700	NA	8810
LPSPLIM(+15.99)SPGPIYAVDGDQ	Q8VHF2|CDHR5_MOUSE	49.94	19	7620	NA	4930
LPSPLIM(+15.99)SPGPIYAVDGDQA	Q8VHF2|CDHR5_MOUSE	49.91	20	132	NA	NA
LPSPLIMSPGPIYAVD	Q8VHF2|CDHR5_MOUSE	49.93	16	174	NA	488
LPSPLIMSPGPIYAVDG	Q8VHF2|CDHR5_MOUSE	49.76	17	2480	NA	4120
LPSPLIMSPGPIYAVDGD	Q8VHF2|CDHR5_MOUSE	49.94	18	5730	NA	10100
LPSPLIMSPGPIYAVDGDQ	Q8VHF2|CDHR5_MOUSE	49.94	19	2930	NA	4740
LPSQVPFETRGPHINNSVH	Q8K296|MTMR3_MOUSE	49.59	19	750	NA	1130
LPSQVPFETRGPHINNSVHM(+15.99)	Q8K296|MTMR3_MOUSE	35.93	20	342	NA	291
LPSTWSDPSVNISLDN	Q99KN9|EPN4_MOUSE	49	16	1380	NA	NA
LPTTFQGATASTSYG	Q9JJZ4|UB2J1_MOUSE	41.35	15	1130	NA	524
LPTYDASKVTASGPG	Q80X90|FLNB_MOUSE	49.34	15	6580	259	5790
LPVKWTAPEAIRT	Q922K9|FRK_MOUSE	49.2	13	416	NA	737
LPVKWTAPEAIRTN	Q922K9|FRK_MOUSE	49.09	14	1370	NA	1350
LPVKWTAPEAIRTNK	Q922K9|FRK_MOUSE	49.5	15	3390	NA	2280
LPVKWTAPEAIRTNKF	Q922K9|FRK_MOUSE	49.74	16	819	NA	756
LPVNHRPFSAPHSSRDQLPPP	Q60805|MERTK_MOUSE	47.61	21	593	NA	1070
LPVNHRPFSAPHSSRDQLPPPQ	Q60805|MERTK_MOUSE	26.82	22	160	NA	NA
LPYKPSTVVIPR	Q9Z0S5|CLD15_MOUSE	37.07	12	131	NA	28.5
LPYKSPGINVD	Q9JHJ8|ICOSL_MOUSE	36.52	11	364	NA	442
LPYKSPGINVDS	Q9JHJ8|ICOSL_MOUSE	47.8	12	881	NA	273
LPYKSPGINVDSS	Q9JHJ8|ICOSL_MOUSE	49.19	13	1960	NA	1390
LPYKSPGINVDSSY	Q9JHJ8|ICOSL_MOUSE	49.65	14	1080	NA	833
LPYSFLTFPYVEEAIK	P70274|SEPP1_MOUSE	41.46	16	743	NA	715
LPYTASSGLM(+15.99)APR	Q9R1Q9|VAS1_MOUSE	38.8	13	96.1	NA	NA
LPYTASSGLM(+15.99)APRE	Q9R1Q9|VAS1_MOUSE	41.45	14	439	NA	NA
LPYVQYFGGVSALSKQQ	P15535|B4GT1_MOUSE	44.11	17	420	NA	216
LPYVSWQEKQPEASISQ	E9PYK3|PARP4_MOUSE	49.93	17	567	NA	426
LPYVSWQEKQPEASISQT	E9PYK3|PARP4_MOUSE	49.15	18	450	NA	535
LPYVSWQEKQPEASISQTE	E9PYK3|PARP4_MOUSE	49.94	19	2240	NA	2250
LQDEIDAALPNKAP	Q64464|CP3AD_MOUSE	48.9	14	10400	79.4	6980
LQDEIDAALPNKAPA	Q64464|CP3AD_MOUSE	48.31	15	12900	171	8150
LQDEIDAALPNKAPAT	Q64464|CP3AD_MOUSE	49.32	16	11400	191	7590
LQDEIDEALPNKAPP	Q64459|CP3AB_MOUSE	48.47	15	700	NA	318
LQEPQPAGSQPLLANSPL	Q8R1U2|CGRE1_MOUSE	49.84	18	333	NA	1170
LQKQPYFGAVVGRVA	Q8K157|GALM_MOUSE	49.28	15	1410	NA	1300
LQKQPYFGAVVGRVAN	Q8K157|GALM_MOUSE	49.63	16	264	NA	166
LQKQPYFGAVVGRVANR	Q8K157|GALM_MOUSE	49.86	17	2330	NA	2070
LQKTQYISPNLNPN	P97499|TEP1_MOUSE	49.62	14	2530	NA	1660
LQKTQYISPNLNPND	P97499|TEP1_MOUSE	49.55	15	4910	NA	3710
LQKTQYISPNLNPNDVT	P97499|TEP1_MOUSE	49.91	17	1260	NA	1450
LQSINFLGGQPAAAPYPG	Q8K419|LEG4_MOUSE	46.69	18	684	NA	1070
LQSTDYGNFLANEASPL	P51863|VA0D1_MOUSE	49.82	17	418	NA	848
LRDMYSKSSAAM(+15.99)STY	Q05020|APOC2_MOUSE	27.24	15	326	NA	547
LRDMYSKSSAAM(+15.99)STYA	Q05020|APOC2_MOUSE	37.82	16	275	NA	NA
LRDMYSKSSAAMSTYA	Q05020|APOC2_MOUSE	28.49	16	386	NA	548
LRDNYRFAHTNIESLV	P27773|PDIA3_MOUSE	32.12	16	1540	NA	1230
LREFVVIAPAAHSDA	Q80UJ7|RB3GP_MOUSE	29.79	15	157	NA	NA
LRFNYPEVQKVM(+15.99)PR	Q6XQH0|G3ST2_MOUSE	49.37	14	106	NA	NA
LRFNYPEVQKVMPR	Q6XQH0|G3ST2_MOUSE	48.94	14	146	NA	NA
LRFSAPQIENEPE	Q61190|I10R2_MOUSE	48.21	13	2040	NA	1610
LRHAFSPVASVESAS	P29699|FETUA_MOUSE	48.56	15	75	NA	142
LRKFYKGKKYKPLDLRPKKTR	Q6ZWV7|RL35_MOUSE	49.95	21	199	225	365

LRLQVESPQVHWEPT	Q9D8T2|GSDMD_MOUSE	41.57	15	218	NA	177
LRNVQFNYPQASVTDVT	Q61703|ITIH2_MOUSE	49.61	17	35	NA	158
LRNYEYYASHVPESVK	Q9Z0S1|BPNT1_MOUSE	49.72	16	3500	NA	3800
LRNYEYYASHVPESVKN	Q9Z0S1|BPNT1_MOUSE	49.8	17	2490	NA	1400
LRPVTIFGPIADVAREK	P39447|ZO1_MOUSE	49.91	17	130	NA	141
LRPYQGGKANILGYN	Q6XQH0|G3ST2_MOUSE	47.57	15	95.2	NA	NA
LRRQPKYPRKSAPRRNKLDHYAIIKF	P62751|RL23A_MOUSE	49.95	26	8320	629	3370
LRRQPKYPRKSAPRRNKLDHYAIIKFPLT	P62751|RL23A_MOUSE	49.76	31	2040	NA	NA
LSDIYQAPSADSADH	P26361|CFTR_MOUSE	46.83	15	2360	NA	2150
LSDIYQAPSADSADHL	P26361|CFTR_MOUSE	47.07	16	1280	NA	2390
LSEGFSSPSSLM(+15.99)SPS	Q9D2V7|CORO7_MOUSE	33.57	15	691	NA	497
LSLAEAKPQVLSSQEE	Q91X58|ZFN2B_MOUSE	44.24	16	166	NA	68.1
LSLLYKVPYVAQEIQ	Q06335|APLP2_MOUSE	49.93	15	2860	NA	3490
LSLLYKVPYVAQEIQE	Q06335|APLP2_MOUSE	49.93	16	927	NA	519
LSLLYNVPAVAEE	P12023|A4_MOUSE	44.81	13	132	NA	NA
LSLLYNVPAVAEEIQ	P12023|A4_MOUSE	48.78	15	10300	213	4910
LSLLYNVPAVAEEIQD	P12023|A4_MOUSE	49.55	16	6990	160	5470
LSLLYNVPAVAEEIQDE	P12023|A4_MOUSE	49.93	17	4090	NA	1400
LSPYSYSTTAVVSNPQ	P07309|TTHY_MOUSE	43.14	16	409	NA	NA
LSQEYSGSVANEAN	E9Q414|APOB_MOUSE	46.18	14	1760	NA	NA
LSQEYSGSVANEANVY	E9Q414|APOB_MOUSE	48.87	16	206	NA	6910
LSQHATPLPTPAVLPG	O88746|TOM1_MOUSE	49.03	16	624	NA	660
LSRDLEAPEVQESYRQ	Q9Z1R2|BAG6_MOUSE	48.94	16	330	NA	NA
LSRFTSGVPSFVLD	Q9R097|SPIT1_MOUSE	38.23	14	3910	NA	3010
LSRFTSGVPSFVLDT	Q9R097|SPIT1_MOUSE	40.66	15	3900	NA	2580
LSRFTSGVPSFVLDTE	Q9R097|SPIT1_MOUSE	47.08	16	926	NA	909
LSRTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	49.95	23	1090	NA	2910
LSVTWSIPVSQQSR	Q03145|EPHA2_MOUSE	37.02	14	134	NA	186
LSYIGPSVNKA	O35604|NPC1_MOUSE	25.53	11	103	NA	NA
LSYIQTPLPSRAIV	O89093|CCL20_MOUSE	49	14	134	NA	215
LSYIQTPLPSRAIVG	O89093|CCL20_MOUSE	48.57	15	6550	1050	5030
LTEAYQVPDASVSSM(+15.99)H	P58242|ASM3B_MOUSE	45.37	16	742	NA	295
LTFTDVAPRGVESGQ	Q8JZQ5|AOC1_MOUSE	47.14	15	66.4	NA	NA
LTFTDVAPRGVESGQR	Q8JZQ5|AOC1_MOUSE	40.78	16	310	NA	NA
LTGGYRYPRALEEE	Q8K3K8|OPTN_MOUSE	26.18	14	18100	NA	NA
LTGGYRYPRALEEEV	Q8K3K8|OPTN_MOUSE	29.39	15	32300	1770	85700
LTGM(+15.99)AFRVPTPNVS	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.48	14	3440	NA	2260
LTGM(+15.99)AFRVPTPNVSV	P16858|G3P_MOUSE:Q64467|G3PT_MC	36.4	15	84.8	NA	93.9
LTGM(+15.99)AFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	48.99	16	632	NA	335
LTGM(+15.99)AFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.85	17	50800	3740	51700
LTGM(+15.99)AFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.9	18	9310	NA	9500
LTGM(+15.99)AFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.9	19	15900	NA	7150
LTGMAFRVPTPNVS	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.65	14	7420	NA	4580
LTGMAFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.8	16	272	NA	459
LTGMAFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.86	17	25000	NA	43000
LTGMAFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.9	18	2290	NA	5370
LTGMAFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.93	19	2870	NA	5690
LTNDRYVASLAARNK	Q00560|IL6RB_MOUSE	46.89	15	405	NA	696
LTNDRYVASLAARNKVG	Q00560|IL6RB_MOUSE	47.76	17	530	NA	724
LTPFHSPSPLQSTA	B2RY04|DOCK5_MOUSE	41.93	14	63.3	NA	75.9
LTQYSTPEGSSVPI	E9Q414|APOB_MOUSE	44.1	14	274	NA	989
LTTSSYSNPTIGYENR	Q07797|LG3BP_MOUSE	49.76	16	292	NA	166
LTVNKAVDYPPVANAGP	Q8K135|K319L_MOUSE	46.9	17	137	NA	165
LTVNKAVDYPPVANAGPN	Q8K135|K319L_MOUSE	46.34	18	58.4	NA	NA
LTVNKAVDYPPVANAGPNQ	Q8K135|K319L_MOUSE	49.94	19	1700	NA	1880
LTVNKAVDYPPVANAGPNQVIT	Q8K135|K319L_MOUSE	49.95	22	90.2	NA	125
LTYISPSAAIFQ	Q9WVL3|S12A7_MOUSE	37.43	12	1420	NA	1280
LTYISPSAAIFQA	Q9WVL3|S12A7_MOUSE	39.83	13	337	NA	264
LTYQYGIPTSLRNTG	Q9JLT2|TREA_MOUSE	41.34	15	280	NA	119
LVAYYTLIGASGQR	P01027|CO3_MOUSE	46.28	14	558	399	NA
LVDFINPSIIRE	Q3TTY0|PLB1_MOUSE	30.07	12	221	NA	NA
LVFDVTAPNTFKT	P51150|RAB7A_MOUSE	47.55	13	213	NA	256
LVFDVTAPNTFKTLD	P51150|RAB7A_MOUSE	47.14	15	2090	NA	1500
LVFDVTAPNTFKTLDS	P51150|RAB7A_MOUSE	43.78	16	290	NA	262
LVNPFVGPLTNRIG	Q8R090|VMAT1_MOUSE	40.45	14	2540	NA	1110
LVNPFVGPLTNRIGYH	Q8R090|VMAT1_MOUSE	44.1	16	742	NA	240
LVPIVEPEVLPDG	Q91Y97|ALDOB_MOUSE	49.34	13	377	NA	219
LVPIVEPEVLPDGDH	Q91Y97|ALDOB_MOUSE	49.47	15	5770	63	2940
LVPIVEPEVLPDGDHD	Q91Y97|ALDOB_MOUSE	49.76	16	274	NA	NA
LVPRQPRIPKPQHK	Q8VCW4|UN93B_MOUSE	31.41	14	100	NA	NA
LVQANSPASLVGLRF	O08992|SDCB1_MOUSE	48.96	15	107	NA	NA
LVQANSPASLVGLRFG	O08992|SDCB1_MOUSE	49.56	16	333	NA	NA
LVRYTQKAPQVSTP	P07724|ALBU_MOUSE	48.47	14	2120	NA	2080
LVRYTQKAPQVSTPT	P07724|ALBU_MOUSE	49.82	15	23100	541	17000
LVRYTQKAPQVSTPTL	P07724|ALBU_MOUSE	49.89	16	59000	3760	72100
LVRYTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.92	17	54100	2330	59400
LVRYTQKAPQVSTPTLVE	P07724|ALBU_MOUSE	49.89	18	10800	87.3	12800

LVTQVANPAAAPEAPE	Q80Y55|BSDC1_MOUSE	48.39	16	486	NA	471
LVYENASAIMAHE	E9Q0N2|PTPRH_MOUSE	46.58	13	61.3	NA	200
LWAYLTIQELLAK	Q61702|ITIH1_MOUSE	43.39	13	95.3	NA	NA
LYPENFAPSFPHGSPG	Q3UDK1|TRAD1_MOUSE	44.95	16	239	NA	78.9
LYSFKAARALLDHR	Q9WTN3|SRBP1_MOUSE	36.97	14	72.7	NA	NA
LYSFKAARALLDHRK	Q9WTN3|SRBP1_MOUSE	48.25	15	133	NA	NA
LYTAKGLFRAAVPSGASTG	P17183|ENOG_MOUSE:P17182|ENOA_M	49.93	19	343	NA	428
M(+15.99)AFRVPTPNVSV	P16858|G3P_MOUSE:Q64467|G3PT_MO	44.88	12	445	NA	320
M(+15.99)AFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MO	46.22	13	917	NA	538
M(+15.99)AFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MO	49.4	14	38900	1090	22300
M(+15.99)AFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MO	47.73	15	348	NA	146
M(+15.99)AFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MO	49.65	16	205	NA	NA
M(+15.99)APYQGPDAAPGAL	P57780|ACTN4_MOUSE	33.19	14	661	NA	415
M(+15.99)APYQGPDAAPGALD	P57780|ACTN4_MOUSE	40.44	15	1350	NA	809
M(+15.99)EELKGHLTPRANELK	P06728|APOA4_MOUSE	48.3	16	261	NA	NA
M(+15.99)ENQIKSPTAVPDAPPD	P58196|PLS4_MOUSE	42.48	17	582	NA	NA
M(+15.99)GPTELLIEM(+15.99)EDWKGD	Q8K0E8|FIBB_MOUSE	48.49	17	76.7	NA	NA
M(+15.99)GPTELLIEMEDWK	Q8K0E8|FIBB_MOUSE	41.17	14	265	NA	NA
M(+15.99)IPAHDSPLAALAFDAS	Q80W47|WIPI2_MOUSE	29.5	17	818	NA	NA
M(+15.99)KISFIEPAILLNA	Q9DC26|S46A3_MOUSE	47.13	14	332	NA	NA
M(+15.99)LQVLGPKPALPEG	P13020|GELS_MOUSE	46.24	14	248	NA	77.5
M(+15.99)NPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	47.59	17	417	NA	543
M(+15.99)PIPM(+15.99)YDAAQALKTNPE	Q6EDY6|CARL1_MOUSE	47.53	17	5190	NA	4140
M(+15.99)PIPMYDAAQALKTNPE	Q6EDY6|CARL1_MOUSE	49.71	17	2970	NA	3800
M(+15.99)PIYPSNQPQVHVISG	Q99N10|M4A8_MOUSE	46.23	16	871	NA	497
M(+15.99)PPVPITSPIM(+15.99)NPSG	Q3UPL0|SC31A_MOUSE	46.05	15	103	NA	NA
M(+15.99)QKEITALA	P63260|ACTG_MOUSE:P60710|ACTB_M	25.59	9	146	469	NA
M(+15.99)RYVASYLLAALGGNSSPSAKD	P99027|RLA2_MOUSE	49.95	25	19900	NA	3760
M(+15.99)SLDYHFVTPLTSL	Q61702|ITIH1_MOUSE	38.08	14	339	NA	NA
M(+15.99)SLDYHFVTPLTSLT	Q61702|ITIH1_MOUSE	41.84	15	1440	NA	991
M(+15.99)SPEEVAPSPRASPA	Q8CH72|TRI32_MOUSE	43.47	15	1330	NA	263
M(+15.99)YSTYKTPVPETNIPG	Q60855|RIPK1_MOUSE	28.93	16	1250	NA	855
M(+42.01)(+15.99)DETSPLVSPER	Q2TBE6|P4K2A_MOUSE	38.86	12	2240	NA	1250
M(+42.01)(+15.99)DETSPLVSPERAQPP	Q2TBE6|P4K2A_MOUSE	48.54	16	15000	NA	14900
M(+42.01)(+15.99)DETSPLVSPERAQPP	Q2TBE6|P4K2A_MOUSE	43.6	17	1340	NA	1440
M(+42.01)(+15.99)DLFHTPAGALDK	Q8VI93|OAS3_MOUSE	29.21	13	102	NA	NA
M(+42.01)(+15.99)N(+15.00)PPSYYTQPV	Q9JLJ0|LITAF_MOUSE	45.56	17	2920	NA	NA
M(+42.01)DETSPLVSPER	Q2TBE6|P4K2A_MOUSE	45.58	12	156	NA	737
M(+42.01)DETSPLVSPERAQPP	Q2TBE6|P4K2A_MOUSE	49.22	16	2080	NA	4250
MAFRVPTPNVSV	P16858|G3P_MOUSE:Q64467|G3PT_MO	45.3	12	374	NA	253
MAFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MO	49.51	13	598	NA	658
MAFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MO	48.89	14	30600	368	30700
MAFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MO	49.44	15	535	NA	NA
MAPYQGPDAAPGAL	P57780|ACTN4_MOUSE	35.95	14	79.7	NA	304
MAPYQGPDAAPGALD	P57780|ACTN4_MOUSE	41.48	15	538	NA	783
MEELKGHLTPRANELK	P06728|APOA4_MOUSE	48.43	16	176	NA	152
MENQIKSPTAVPDAPPD	P58196|PLS4_MOUSE	33.03	17	113	NA	NA
MGPTELLIEMEDWK	Q8K0E8|FIBB_MOUSE	41.01	14	966	NA	NA
MGPTELLIEMEDWKGDK	Q8K0E8|FIBB_MOUSE	49.72	17	422	NA	NA
MIPAHDSPLAALAFDAS	Q80W47|WIPI2_MOUSE	37.08	17	346	NA	355
MKISFIEPAILLNA	Q9DC26|S46A3_MOUSE	41.41	14	89	NA	NA
MKLPKSAKPVSQMRM(+15.99)ATPLLM(	P04441|HG2A_MOUSE	47.86	24	445	NA	938
MKLPKSAKPVSQMRMATPLLM(+15.99)I	P04441|HG2A_MOUSE	46.92	24	215	NA	849
MLQVLGPKPALPEG	P13020|GELS_MOUSE	46.94	14	134	NA	270
MLRQILGQAKKH	Q62425|NDUA4_MOUSE	43.26	12	126	NA	168
MNPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.23	17	121	NA	559
MNPPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	48.19	18	140	NA	401
MPFRQPITTIVGKPI	Q80W94|MOGT2_MOUSE	47.07	15	41.8	NA	NA
MPIPM(+15.99)YDAAQALKTNPE	Q6EDY6|CARL1_MOUSE	49.04	17	2050	NA	5800
MPIPMYDAAQALKTNPE	Q6EDY6|CARL1_MOUSE	49.82	17	2980	NA	5590
MQKEITALA	P63260|ACTG_MOUSE:P60710|ACTB_M	29.18	9	261	113	319
MRYVASYLLAALGGNSSPSAKDIKK	P99027|RLA2_MOUSE	49.95	25	14500	NA	4780
MSLDYHFVTPLTSL	Q61702|ITIH1_MOUSE	32.82	14	87.3	NA	NA
MSLDYHFVTPLTSLT	Q61702|ITIH1_MOUSE	42.45	15	446	NA	593
MSPEEVAPSPRASPA	Q8CH72|TRI32_MOUSE	41.3	15	876	NA	1230
MSPEEVAPSPRASPAK	Q8CH72|TRI32_MOUSE	46.88	16	330	NA	NA
MVRAKFRSNLPAKAIGHR	O55142|RL35A_MOUSE	48.85	18	127	NA	174
MYSTYKTPVPETNIPG	Q60855|RIPK1_MOUSE	37.28	16	410	NA	NA
N(+15.00)VLRVINEPTAAALAYG	P38647|GRP75_MOUSE	41.54	17	410	NA	NA
N(+42.01)(+15.00)ENGNFKIVTDPKTNEG	P55292|DSC2_MOUSE	32.79	19	162	NA	NA
N(+42.01)(+15.00)IYIYNGPVLGGTRGPG	P50284|TNR3_MOUSE	37.04	17	2010	NA	NA
N(+42.01)(+15.00)IYIYNGPVLGGTRGPG	P50284|TNR3_MOUSE	43.5	20	211	NA	NA
N(+42.01)(+15.00)KGFFVQPTVFSNVTDI	O35945|AL1A7_MOUSE:P24549|AL1A1_	43.05	18	144	NA	NA
N(+42.01)(+15.00)PLNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	48.38	16	6810	71.3	NA
N(+42.01)(+15.00)PPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	40.67	16	2580	NA	2810
N(+42.01)(+15.00)PPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	43.46	17	119	NA	42.9
N(+42.01)(+15.00)VYIHPTAKVAPS	Q922H4|GMPPA_MOUSE	36.2	13	5730	NA	NA

N(+42.01)APVFNPST(+79.97)YQGQVPE	P09803|CADH1_MOUSE	27.82	18	15400	NA	NA
N(+42.01)ENGN(+15.00)FKIVTDPKTNEG	P55292|DSC2_MOUSE	42.1	19	359	NA	NA
NATDDVFSPSHAIPIET	Q91ZH7|ABHD3_MOUSE	49.84	17	495	NA	372
NATDDVFSPSHAIPIETA	Q91ZH7|ABHD3_MOUSE	49.64	18	452	NA	165
NDDDVYRAPPIDRSILPT	Q8BGD9|IF4B_MOUSE	49.93	18	517	NA	330
NDHLTYGISGPNASYFS	E9Q7P9|CDHR2_MOUSE	49.92	17	244	NA	NA
NDLQYAAPGGLIG	Q9Z0N2|IF2H_MOUSE:Q9Z0N1|IF2G_M	38.78	13	47.8	NA	NA
NDLQYAAPGGLIGVG	Q9Z0N2|IF2H_MOUSE:Q9Z0N1|IF2G_M	46.97	15	825	NA	622
NDLQYAAPGGLIGVGTK	Q9Z0N2|IF2H_MOUSE:Q9Z0N1|IF2G_M	44.84	17	423	NA	NA
NDLSFIHPKALSG	A2ARI4|LGR4_MOUSE	45.6	13	63	NA	NA
NDLSFIHPKALSGLK	A2ARI4|LGR4_MOUSE	49.63	15	5020	NA	3660
NDLSFIHPKALSGLKE	A2ARI4|LGR4_MOUSE	49.76	16	1620	NA	836
NDNDNIFLSPLSISTA	P32261|ANT3_MOUSE	47.09	16	137	NA	242
NDPGAQYSLVN	Q9R100|CAD17_MOUSE	38.39	11	271	NA	381
NDPGAQYSLVNK	Q9R100|CAD17_MOUSE	46.08	12	620	NA	399
NDPGAQYSLVNKE	Q9R100|CAD17_MOUSE	47.76	13	164	NA	NA
NDPGFGAPAASQVAS	Q6IRU5|CLCB_MOUSE	46.97	15	813	NA	874
NDPGFGAPAASQVASA	Q6IRU5|CLCB_MOUSE	48.69	16	1330	NA	1170
NDRYVASLAARNK	Q00560|IL6RB_MOUSE	36.26	13	78.8	NA	NA
NEPSVFNGPEVTM(+15.99)LKD	Q8BHN3|GANAB_MOUSE	49.88	16	829	NA	536
NEPSVFNGPEVTMLKD	Q8BHN3|GANAB_MOUSE	49.84	16	297	NA	NA
NFDGYRSPLPTNESQP	Q8CCN5|BCAS3_MOUSE	46.49	16	701	NA	681
NFDGYRSPLPTNESQPL	Q8CCN5|BCAS3_MOUSE	49.7	17	192	NA	208
NFKIVTDPKTNEGIL	P55292|DSC2_MOUSE	49.57	15	3490	NA	2480
NFRPAHQAPM(+15.99)AQTTIH	O08573|LEG9_MOUSE	49.21	16	2540	NA	2050
NFRPAHQAPMAQTTIH	O08573|LEG9_MOUSE	49.91	16	2260	NA	2890
NFRPAHQAPMAQTTIHM(+15.99)	O08573|LEG9_MOUSE	48.49	17	114	NA	352
NGLVPIVEPEVLPDG	Q91Y97|ALDOB_MOUSE	49.46	15	777	NA	234
NGLVPIVEPEVLPDGDH	Q91Y97|ALDOB_MOUSE	48.28	17	1210	NA	439
NGLVPIVEPEVLPDGDHD	Q91Y97|ALDOB_MOUSE	49.52	18	1330	NA	NA
NGLVPIVEPEVLPDGDHDL	Q91Y97|ALDOB_MOUSE	49.65	19	59.1	NA	NA
NGNPLNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	49.94	18	872	NA	1120
NGNPLNSVFVAPAVTPVKGVL	P70158|ASM3A_MOUSE	49.95	21	171	NA	860
NGSDMFKASLVIPSKDK	Q8BJD1|ITIH5_MOUSE	44.13	17	183	NA	NA
NHGYTIPVVNIEVSPF	E9Q414|APOB_MOUSE	49.03	16	93.7	NA	NA
NHLRFNYPEVQKV	Q6XQH0|G3ST2_MOUSE	38	13	394	NA	171
NHLRFNYPEVQKVM(+15.99)PR	Q6XQH0|G3ST2_MOUSE	49.84	16	27500	NA	15900
NHLRFNYPEVQKVMPR	Q6XQH0|G3ST2_MOUSE	49.92	16	17800	NA	17700
NHTLFHNPHVNPLP	P43023|CX6A2_MOUSE:P43024|CX6A1_	47.66	14	706	NA	320
NHTLFHNPHVNPLPT	P43023|CX6A2_MOUSE:P43024|CX6A1_	48.58	15	1690	NA	1670
NHTLFHNPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	49.75	18	2600	1540	5410
NILFVITKPDVYKSPA	P70670|NACAM_MOUSE:Q60817|NACA_	45.23	16	33.8	NA	NA
NIWKAPEPVEIRE	Q9R100|CAD17_MOUSE	47.93	13	147	NA	NA
NIWKAPEPVEIREN(+15.00)ST	Q9R100|CAD17_MOUSE	36.31	16	199	NA	NA
NIYDLVAPFPSAPN	P09470|ACE_MOUSE	45.77	14	969	NA	117
NIYDLVAPFPSAPNID	P09470|ACE_MOUSE	48.07	16	1730	NA	1620
NIYIYNGPVLGGTR	P50284|TNR3_MOUSE	45.59	14	3040	NA	2730
NIYIYNGPVLGGTRGPG	P50284|TNR3_MOUSE	47.05	17	290	NA	250
NIYSTPLALQM(+15.99)L	O88968|TCO2_MOUSE	47.49	12	230	NA	NA
NIYSTPLALQM(+15.99)LM(+15.99)	O88968|TCO2_MOUSE	49.14	13	181	NA	NA
NIYTPAHAHEGSNL	Q91WG0|EST2C_MOUSE	46.41	14	2330	NA	NA
NIYTPAHAHEGSNLP	Q91WG0|EST2C_MOUSE	47.74	15	502	NA	NA
NIYTPAHAHEGSNLPV	Q91WG0|EST2C_MOUSE	49.66	16	3870	NA	911
NIYVPAHAHEG	Q8BK48|EST2E_MOUSE	38.06	11	2800	NA	1440
NIYVPAHAHEGS	Q8BK48|EST2E_MOUSE	35.98	12	680	NA	NA
NIYVPAHAHEGSN	Q8BK48|EST2E_MOUSE	42.66	13	4460	171	564
NIYVPAHAHEGSNL	Q8BK48|EST2E_MOUSE	46.18	14	35100	629	22100
NIYVPAHAHEGSNLP	Q8BK48|EST2E_MOUSE	45.73	15	8700	NA	8770
NIYVPAHAHEGSNLPV	Q8BK48|EST2E_MOUSE	49.66	16	35800	423	29900
NKGFFVQPTVFSNVT	O35945|AL1A7_MOUSE:P24549|AL1A1_	49.52	15	1480	NA	519
NKKMIFVPSYINIS	Q8VCR2|DHB13_MOUSE	25.12	14	62.9	NA	NA
NKTRLSRTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	48.94	27	296	1110	2230
NLAVGSPSAAEAPG	Q03157|APLP1_MOUSE	44.02	14	2350	NA	2620
NLAVGSPSAAEAPGS	Q03157|APLP1_MOUSE	48.46	15	380	NA	590
NLAVGSPSAAEAPGSA	Q03157|APLP1_MOUSE	38.66	16	440	NA	465
NLAVGSPSAAEAPGSAQ	Q03157|APLP1_MOUSE	46.73	17	566	NA	435
NLDYVATSIHEAVTK	P05201|AATC_MOUSE	49.69	15	407	NA	305
NLRDNYRFAHTNIESLV	P27773|PDIA3_MOUSE	43.81	17	2440	NA	NA
NLRKMGAPEAGM(+15.99)AEYL	P09528|FRIH_MOUSE	44.61	16	389	NA	NA
NLRKMGAPEAGMAEYL	P09528|FRIH_MOUSE	46.97	16	196	NA	472
NM(+15.99)DLYLSPVAQSQEF	Q91XS1|MTMR4_MOUSE	48.81	15	614	NA	350
NM(+15.99)LQYQLPSSLSSLA	P41233|ABCA1_MOUSE	35.92	15	205	NA	NA
NM(+15.99)LQYQLPSSLSSLAR	P41233|ABCA1_MOUSE	41.41	16	43.7	NA	NA
NMDLYLSPVAQSQEF	Q91XS1|MTMR4_MOUSE	48.52	15	174	NA	138
NNFEIKAPIVC(+57.02)PNQA	Q3TTY0|PLB1_MOUSE	42.83	15	68.1	NA	NA
NNIPYFETSAKEAIN	P51150|RAB7A_MOUSE	26.87	15	170	NA	282
NNQAYHSPATALA	Q8R420|ABCA3_MOUSE	47.48	13	420	NA	NA

NNQAYHSPATALAIV	Q8R420|ABCA3_MOUSE	45.14	15	3650	NA	4780
NNQAYHSPATALAIVD	Q8R420|ABCA3_MOUSE	47.8	16	31000	1820	32400
NNQAYHSPATALAIVDN	Q8R420|ABCA3_MOUSE	49.1	17	1200	NA	1430
NNQDFRGSAGAPSVEN	P49443|PPM1A_MOUSE	43.79	16	493	NA	NA
NNQDFRGSAGAPSVENV	P49443|PPM1A_MOUSE	48.38	17	638	NA	722
NNSFYGPEVKIEK	Q00519|XDH_MOUSE	48.18	13	814	NA	527
NNSFYGPEVKIEKG	Q00519|XDH_MOUSE	48.53	14	5180	NA	3550
NNSFYGPEVKIEKGD	Q00519|XDH_MOUSE	48.98	15	71.6	NA	NA
NNSFYGPEVKIEKGDL	Q00519|XDH_MOUSE	49.93	16	1840	NA	701
NNSIM(+15.99)SNPVAGLVIG	Q9DBP0|NPT2B_MOUSE	45.94	15	1810	NA	797
NNSIMSNPVAGLVIG	Q9DBP0|NPT2B_MOUSE	49.14	15	546	NA	433
NNTLVFIVDVKANKHQIKQAVKK	P62751|RL23A_MOUSE	45.6	23	2000	NA	NA
NNYALFLSPRAQQASWQ	E9Q414|APOB_MOUSE	47.68	17	262	NA	647
NPDKNIVFSPLSISAA	Q03734|SPA3M_MOUSE:Q91WP6|SPA3	46.52	16	413	NA	536
NPEAM(+15.99)VAPSVLSNIQ	Q3UQN2|FCHO2_MOUSE	48.36	15	604	NA	NA
NPEAMVAPSVLSNIQ	Q3UQN2|FCHO2_MOUSE	48.63	15	198	NA	366
NPEGAVFTWEPSTGKDAVQKK	P01878|IGHA_MOUSE	49.69	21	185	NA	509
NPEITTNRFYGSQVNNISHT	Q91YD9|WASL_MOUSE	40.01	20	144	NA	NA
NPEYLAPRAGTAS	P70424|ERBB2_MOUSE	36.95	13	147	NA	73.6
NPEYLAPRAGTASQP	P70424|ERBB2_MOUSE	39.02	15	467	NA	322
NPEYLAPRAGTASQPH	P70424|ERBB2_MOUSE	49.19	16	4890	NA	582
NPEYLAPRAGTASQPHP	P70424|ERBB2_MOUSE	49.91	17	34100	460	12100
NPEYLAPRAGTASQPHPS	P70424|ERBB2_MOUSE	47.3	18	142	NA	NA
NPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	45.33	12	159	268	668
NPIITPVAQENQ	P08226|APOE_MOUSE	46.21	12	603	NA	234
NPIYKSAVTTVVNPK	P09055|ITB1_MOUSE	49.13	15	84.5	NA	133
NPLLKQYQGPTGDSSAT	P51912|AAAT_MOUSE	41.26	17	4830	NA	4120
NPLNSVFVAPAVT	P70158|ASM3A_MOUSE	42.92	13	73.7	NA	99.7
NPLNSVFVAPAVTP	P70158|ASM3A_MOUSE	48.57	14	1240	NA	1910
NPLNSVFVAPAVTPV	P70158|ASM3A_MOUSE	49.61	15	10300	542	5970
NPLNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	49.93	16	381000	26400	413000
NPLNSVFVAPAVTPVKG	P70158|ASM3A_MOUSE	49.94	17	355000	22400	313000
NPLNSVFVAPAVTPVKGV	P70158|ASM3A_MOUSE	49.94	18	41200	NA	44400
NPLNSVFVAPAVTPVKGVL	P70158|ASM3A_MOUSE	49.95	19	75100	2560	77700
NPLNSVFVAPAVTPVKGVLQ	P70158|ASM3A_MOUSE	49.94	20	97.4	NA	NA
NPPSYYTQPVPV	Q9JLJ0|LITAF_MOUSE	48.89	12	244	NA	274
NPPSYYTQPVPVP	Q9JLJ0|LITAF_MOUSE	39.31	13	450	NA	702
NPPSYYTQPVPVPN	Q9JLJ0|LITAF_MOUSE	49.22	14	49100	2750	49800
NPPSYYTQPVPVPNA	Q9JLJ0|LITAF_MOUSE	49.48	15	28100	1310	29600
NPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.7	16	231000	17200	241000
NPPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	49.82	17	30200	1160	27300
NPPSYYTQPVPVPNANAI	Q9JLJ0|LITAF_MOUSE	49.72	18	134	NA	120
NPRPQASAYSPAAAASPAPS	Q9JKS4|LDB3_MOUSE	49.41	20	246	NA	365
NPRTPQDSPM(+15.99)YPVVPVHLDGTF	P97425|ECP2_MOUSE	49.94	22	230	102	336
NPSIFVHSPHALM(+15.99)LQD	Q9ESE1|LRBA_MOUSE	47.8	16	151	NA	NA
NPSWVAEPIPHSAVQS	Q8K0B3|LRC66_MOUSE	48.26	16	186	NA	178
NPTDAYLDAM(+15.99)M(+15.99)NEAPG	Q3THE2|ML12B_MOUSE	49.63	18	903	NA	699
NPTDAYLDAM(+15.99)M(+15.99)NEAPG	Q3THE2|ML12B_MOUSE	49.4	19	147	NA	NA
NPTDAYLDAM(+15.99)MNEAPGPI	Q3THE2|ML12B_MOUSE	49.78	18	206	NA	NA
NPTDAYLDAMM(+15.99)NEAPGPI	Q3THE2|ML12B_MOUSE	49.57	18	206	NA	227
NPTDEYLEGM(+15.99)M(+15.99)NEAPG	Q9CQ19|MYL9_MOUSE	48.51	18	160	NA	NA
NPTLPYKRPIPG	O54891|LEG6_MOUSE:Q8K419|LEG4_M	48.11	12	407	NA	556
NPTLPYKRPIPGG	O54891|LEG6_MOUSE:Q8K419|LEG4_M	46.25	13	2300	NA	2220
NPTLPYKRPIPGGL	O54891|LEG6_MOUSE:Q8K419|LEG4_M	48.07	14	1390	NA	348
NPTLPYKRPIPGGLS	O54891|LEG6_MOUSE:Q8K419|LEG4_M	48.81	15	6680	NA	3870
NPTLPYKRPIPGGLSV	O54891|LEG6_MOUSE:Q8K419|LEG4_M	47.76	16	1620	NA	1250
NPVQGAM(+15.99)YSFPQIQLPLK	Q8QZR5|ALAT1_MOUSE	49.93	18	74.1	NA	NA
NPVVIPEPPNPIPSY	Q99N10|M4A8_MOUSE	48.86	15	257	NA	NA
NPVVIPEPPNPIPSYSE	Q99N10|M4A8_MOUSE	49.88	17	3740	NA	NA
NPVVIPEPPNPIPSYSEVV	Q99N10|M4A8_MOUSE	49.94	19	784	NA	158
NPVVIPEPPNPIPSYSEVVQ	Q99N10|M4A8_MOUSE	49.72	20	416	NA	NA
NPYSTSYSGPYPAAAPP	Q9WVH9|FBLN5_MOUSE	49.72	17	15100	248	10000
NPYSTSYSGPYPAAAPPV	Q9WVH9|FBLN5_MOUSE	49.83	18	780	NA	512
NPYSTSYSGPYPAAAPPVP	Q9WVH9|FBLN5_MOUSE	49.88	19	10400	NA	10200
NPYSTSYSGPYPAAAPPVPA	Q9WVH9|FBLN5_MOUSE	49.93	20	10300	251	7810
NPYTTVTPQIINSK	P57780|ACTN4_MOUSE	49.84	14	447	NA	654
NPYTTVTPQIINSKWE	P57780|ACTN4_MOUSE	49.87	16	184	NA	187
NQAYHSPATALAIV	Q8R420|ABCA3_MOUSE	46.86	14	1270	NA	1680
NQAYHSPATALAIVD	Q8R420|ABCA3_MOUSE	45.76	15	9630	NA	10400
NQAYHSPATALAIVDN	Q8R420|ABCA3_MOUSE	41.76	16	724	NA	644
NQDFRGSAGAPSVEN	P49443|PPM1A_MOUSE	40.2	15	193	NA	NA
NQDFRGSAGAPSVENV	P49443|PPM1A_MOUSE	36.11	16	218	NA	NA
NQHKSKVIKRQ(+15.00)TVITTM(+15.99)	Q3V3N7|BBS1_MOUSE	27.52	22	46400	NA	NA
NQLEALVGPEANVGP	O09159|MA2B1_MOUSE	37.87	15	94.4	NA	NA
NQLEALVGPEANVGPY	O09159|MA2B1_MOUSE	49.57	16	331	NA	NA
NQLEALVGPEANVGPYG	O09159|MA2B1_MOUSE	49.61	17	1080	NA	643
NQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	48.94	14	500	NA	242

NRDGDSYRSPWSNKYDPPL	P47757|CAPZB_MOUSE	32.41	19	1880	NA	NA
NRLDNYDAPDIANIA	Q68FD5|CLH1_MOUSE	48.28	15	2380	NA	1190
NRLDNYDAPDIANIAIS	Q68FD5|CLH1_MOUSE	49.64	17	379	NA	439
NRPAFMPSEGRM(+15.99)VSDIN	P57780|ACTN4_MOUSE:Q7TPR4|ACTN1	26.8	17	109	NA	184
NSEEFAAAM(+15.99)SRYELK	E9Q414|APOB_MOUSE	49.52	15	379	NA	433
NSEEFAAAMSRYELK	E9Q414|APOB_MOUSE	49.73	15	1230	NA	1620
NSEFDPPGPNVAT	Q9Z1D1|EIF3G_MOUSE	45.44	13	233	NA	NA
NSEFDPPGPNVATTT	Q9Z1D1|EIF3G_MOUSE	49.47	15	991	NA	742
NSIM(+15.99)SNPVAGLVIG	Q9DBP0|NPT2B_MOUSE	47.47	14	1610	NA	1130
NSIMSNPVAGLVIG	Q9DBP0|NPT2B_MOUSE	46.42	14	536	NA	624
NSNSYGIPEPAHAYA	P47941|CRKL_MOUSE	48.41	15	285	NA	783
NSNSYGIPEPAHAYAQP	P47941|CRKL_MOUSE	47.94	17	224	NA	179
NSNSYGIPEPAHAYAQPQ	P47941|CRKL_MOUSE	49.7	18	944	NA	1590
NSQPEILER	P14483|HB2A_MOUSE:P01921|HB2D_M	30.65	9	675	NA	360
NSVFVAPAVTPVK	P70158|ASM3A_MOUSE	47.66	13	7410	262	7870
NSVFVAPAVTPVKG	P70158|ASM3A_MOUSE	47.86	14	2370	45.8	2420
NSVYVVAPPNSYPVVPG	Q99N10|M4A8_MOUSE	44	17	1150	NA	NA
NTLVFIVDVKANKHQIKQAVKK	P62751|RL23A_MOUSE	40	22	302	NA	NA
NTPIKVDGKDVM(+15.99)PEV	P06745|G6PI_MOUSE	27.97	15	385	NA	NA
NVDFNTPRPST	G3X939|SL9A3_MOUSE	41.75	11	187	NA	372
NVDFNTPRPSTVE	G3X939|SL9A3_MOUSE	44.94	13	165	NA	257
NVDFNTPRPSTVEA	G3X939|SL9A3_MOUSE	48.86	14	4010	37.6	6690
NVDFNTPRPSTVEAS	G3X939|SL9A3_MOUSE	36.72	15	299	NA	411
NVDVFYSSGIPATARP	Q91VN0|LRP5_MOUSE	46.35	16	106	NA	NA
NVFENYEASKAYSSVD	Q9D306|MGT4C_MOUSE	49.91	16	2860	NA	1770
NVFENYEASKAYSSVDE	Q9D306|MGT4C_MOUSE	49.93	17	6560	NA	3000
NVFENYEASKAYSSVDEY	Q9D306|MGT4C_MOUSE	49.87	18	261	NA	NA
NVIGEPIDERGPIKTKQFAP	P56480|ATPB_MOUSE	27.24	20	356	NA	NA
NVKQFIAPETSEGVS	Q9EPS3|GLCE_MOUSE	43.66	15	753	NA	743
NVKQFIAPETSEGVSL	Q9EPS3|GLCE_MOUSE	35.78	16	248	NA	NA
NVLRIINEPTAAAIA	P17879|HS71B_MOUSE:P16627|HS71L_	48.23	15	460	NA	288
NVLRIINEPTAAAIAY	P17879|HS71B_MOUSE:P16627|HS71L_	48.82	16	117	NA	85.5
NVLRIINEPTAAAIAYG	P17879|HS71B_MOUSE:P16627|HS71L_	49.93	17	5460	NA	4410
NVM(+15.99)RIINEPTAAAIAYG	P20029|BIP_MOUSE	49.41	17	302	NA	267
NVNIFKFIIPNIVK	P06151|LDHA_MOUSE	49.53	14	1410	NA	NA
NVQFNYPQASVT	Q61703|ITIH2_MOUSE	36.46	12	111	NA	57.3
NVQFNYPQASVTD	Q61703|ITIH2_MOUSE	48.24	13	9280	340	7920
NVQFNYPQASVTDV	Q61703|ITIH2_MOUSE	48.4	14	1210	NA	927
NVQFNYPQASVTDVT	Q61703|ITIH2_MOUSE	49.62	15	65800	3480	14600
NVQFNYPQASVTDVTQ	Q61703|ITIH2_MOUSE	49.74	16	737	NA	521
NVQFSSPLPGEAVK	Q80X90|FLNB_MOUSE	43.04	14	375	NA	457
NVQFSSPLPGEAVKD	Q80X90|FLNB_MOUSE	48.73	15	583	NA	417
NVQPYSGSPANFAVYT	P50431|GLYC_MOUSE	48.71	16	633	NA	137
NVTELNEPLSNEER	P61982|1433G_MOUSE	38.97	14	248	NA	NA
NVTELNEPLSNEERNL	P61982|1433G_MOUSE	47.81	16	299	NA	269
NVVWDYFTQLSNNAK	P06728|APOA4_MOUSE	49.78	15	144	NA	147
NVVWDYFTQLSNNAKE	P06728|APOA4_MOUSE	49.91	16	2600	NA	1690
NVVWDYFTQLSNNAKEA	P06728|APOA4_MOUSE	49.94	17	1250	NA	1150
NWIQYKEGFGHLSPT	Q8VCM7|FIBG_MOUSE	49.16	15	279	NA	522
NWIQYKEGFGHLSPTG	Q8VCM7|FIBG_MOUSE	49.78	16	741	NA	1030
NYALFLSPRAQQAS	E9Q414|APOB_MOUSE	38.87	14	37.8	NA	130
NYALFLSPRAQQASWQ	E9Q414|APOB_MOUSE	48.09	16	311	NA	643
NYEGPETHTSL	P14483|HB2A_MOUSE	37.32	11	2320	368	2210
NYEGPETHTSLR	P14483|HB2A_MOUSE	43.09	12	3170	429	1140
NYEGPETHTSLRR	P14483|HB2A_MOUSE	28.37	13	2840	NA	1790
NYEYYASHVPES	Q9Z0S1|BPNT1_MOUSE	45.6	12	103	NA	NA
NYEYYASHVPESV	Q9Z0S1|BPNT1_MOUSE	44.21	13	164	NA	NA
NYEYYASHVPESVK	Q9Z0S1|BPNT1_MOUSE	49.43	14	9230	117	5770
NYEYYASHVPESVKN	Q9Z0S1|BPNT1_MOUSE	49.93	15	2620	NA	1620
P(+42.01)KASKPKATKAKKAAPRKK	P43277|H13_MOUSE	48.12	19	1180	NA	NA
PAAAGVKKVAKSPKK	P43276|H15_MOUSE	47.64	15	755	NA	681
PAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.94	17	22200	21600	21100
PAAAGVKKVAKSPKKAKA	P43276|H15_MOUSE	49.94	18	4660	3740	4460
PAAAGVKKVAKSPKKAKAA	P43276|H15_MOUSE	49.93	19	1300	2230	2900
PAAAGVKKVAKSPKKAKAAAKPKKAA	P43276|H15_MOUSE	49.7	26	109	NA	NA
PAAAGVKKVAKSPKKAKAAAKPKKAAK	P43276|H15_MOUSE	49.95	27	1900	NA	854
PAATPKKAKKPKVVKVKPVKASKPKKA	P10922|H10_MOUSE	48.94	27	272	410	373
PAATPKKAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	28	3610	2560	4120
PAEGC(+57.02)APDT(+79.97)RFVAPG	Q3U2C5|RN149_MOUSE	28.03	15	29900	NA	NA
PAGAAKKPKKATGAATPKKTAKKTPKKA	P43277|H13_MOUSE	49.95	32	1610	NA	2450
PAGATPKKPKKTAGAKKTVKKTPKKAKK	P43276|H15_MOUSE	49.95	30	704	NA	NA
PAGGGDPEAPAPAPAAERPP	Q68FL4|SAHH3_MOUSE	49.25	20	556	NA	566
PAHAHEGSN	Q91WG0|EST2C_MOUSE:Q8BK48|EST2	31.26	9	213	NA	NA
PAKAKAPKAKASKPKA	P43277|H13_MOUSE	49.92	16	9900	6200	4320
PAKAKAPKAKASKPKASKPKATKAKKAA	P43277|H13_MOUSE	49.95	32	903	NA	NA
PAKAKTVKPKAAKPKTSKPKAAKPKKTA	P43274|H14_MOUSE	49.94	32	678	NA	NA
PAKPKKAAPK	P43275|H11_MOUSE	47.5	10	888	512	864

PAKPKKAAPKK	P43275|H11_MOUSE	49.3	11	699	927	571
PAPAPPAPIPPP	Q5I1X5|IASPP_MOUSE	38.6	12	5460	NA	12100
PAPKKGSKKAVTKAQKKDGKKR	Q8CGP2|H2B1P_MOUSE:Q8CGP0|H2B3	49.71	22	1380	NA	NA
PAPKKGSKKAVTKAQKKDGKKRKRSR	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	49.95	26	1700	8460	11400
PAPSTRVITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.95	23	754	NA	980
PAVSKKTSKSPKKPKVVKAKKVAK	P43275|H11_MOUSE	49.95	24	12500	4070	3600
PAVTPVKG	P70158|ASM3A_MOUSE	32.21	8	785	NA	2160
PAYTIPFYTPIPNG	O08573|LEG9_MOUSE	49.21	14	863	NA	480
PAYTIPFYTPIPNGLYP	O08573|LEG9_MOUSE	49.82	17	132	NA	NA
PAYTIPFYTPIPNGLYPS	O08573|LEG9_MOUSE	49.94	18	566	NA	424
PC(+57.02)LQVYAPEVS(+79.97)PESIM(	Q9ESY9|GILT_MOUSE	46.1	16	435	NA	137
PC(+57.02)LQVYAPEVSPES(+79.97)IM(	Q9ESY9|GILT_MOUSE	39.46	16	435	NA	NA
PELNHAFG	Q91ZX7|LRP1_MOUSE	32.78	8	61.6	NA	437
PFYTPIPNG	O08573|LEG9_MOUSE	28.58	9	4080	NA	2250
PFYTPIPNGL	O08573|LEG9_MOUSE	29.9	10	91.6	NA	540
PGPSQPRQYNNPIGLYSAET	Q9JKS4|LDB3_MOUSE	41.19	20	401	NA	NA
PHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	41.51	11	52.1	NA	179
PIQKYLTPQM(+15.99)ATSIT	Q6P9J9|ANO6_MOUSE	29.99	15	1440	NA	950
PIQKYLTPQMATSIT	Q6P9J9|ANO6_MOUSE	48.82	15	204	NA	243
PKAAKAKKAVSKKK	P43276|H15_MOUSE	49.94	14	6710	1350	NA
PKAAKPKKT	P43274|H14_MOUSE	36.35	9	5980	NA	NA
PKAAKPKKTAAKK	P43274|H14_MOUSE	43.16	13	377	NA	NA
PKAAKPKKTAAKKK	P43274|H14_MOUSE	49.66	14	17300	8850	4000
PKAAKPKTS	P43274|H14_MOUSE	29.73	9	290	NA	NA
PKAAKPKTSKPKAAKPKK	P43274|H14_MOUSE	49.94	18	869	61.1	NA
PKAAKPKTSKPKAAKPKKT	P43274|H14_MOUSE	49.94	19	804	1560	3100
PKAAKPKTSKPKAAKPKKTAAKK	P43274|H14_MOUSE	49.95	23	255	NA	NA
PKAAKPKTSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.95	24	2590	NA	NA
PKAAKPKVAKAKKVAAK	P15864|H12_MOUSE	49.95	17	723	NA	611
PKAAKPKVAKAKKVAAKK	P15864|H12_MOUSE	49.94	18	9290	1350	3100
PKAAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	19	41200	6630	5690
PKAKASKPKA	P43277|H13_MOUSE	41.21	10	124	2330	1040
PKAKASKPKASKPKATKAKKAAPRKK	P43277|H13_MOUSE	49.95	26	147	NA	NA
PKAKSSAKR	P10922|H10_MOUSE	42.93	9	1940	2080	3110
PKAKSSAKRASKKK	P10922|H10_MOUSE	46.46	14	27900	2950	8100
PKASKAIY(+79.97)DYANKYH	E9Q414|APOB_MOUSE	27.87	15	488	NA	NA
PKASKAKVTKPKTPAKPKKAAPKK	P43275|H11_MOUSE	49.95	24	140	NA	NA
PKASKAKVTKPKTPAKPKKAAPKKK	P43275|H11_MOUSE	49.95	25	1800	NA	536
PKASKPKATKAKKA	P43277|H13_MOUSE	43.24	14	608	588	3260
PKASKPKATKAKKAAPR	P43277|H13_MOUSE	49.77	17	2920	3630	6580
PKASKPKATKAKKAAPRK	P43277|H13_MOUSE	49.94	18	3010	1100	2670
PKASKPKATKAKKAAPRKK	P43277|H13_MOUSE	49.95	19	9430	7170	4220
PKATKAKKA	P43277|H13_MOUSE	30.23	9	428	NA	717
PKATKAKKAAPRK	P43277|H13_MOUSE	48.02	13	1640	5030	6390
PKATKAKKAAPRKK	P43277|H13_MOUSE	49.94	14	27500	27600	17100
PKGKKAKGKKVAPAPAVVKKQEAKKVV	P12970|RL7A_MOUSE	45.45	31	298	NA	NA
PKGKKAKGKKVAPAPAVVKKQEAKKVV	P12970|RL7A_MOUSE	49.92	32	1420	157	NA
PKGKKAKGKKVAPAPAVVKKQEAKKVV	P12970|RL7A_MOUSE	49.95	33	245	NA	NA
PKKAAKKTPKKAKKPAAA	P15864|H12_MOUSE	40.18	18	1180	NA	NA
PKKAAKSPAKAKAPKAKASKPKA	P43277|H13_MOUSE	49.94	23	676	NA	NA
PKKAAKSPAKPKA	P43276|H15_MOUSE	49.02	13	2340	6100	5560
PKKAAKSPAKPKAVKSKASKPKVT	P43276|H15_MOUSE	31.37	24	1080	NA	NA
PKKAAPKKK	P43275|H11_MOUSE	42.75	9	5630	606	NA
PKKAKAAAKPKKAAK	P43276|H15_MOUSE	49.93	15	131	NA	NA
PKKAKAKPKEVRK	Q8VIK3|H18_MOUSE	28.25	13	747	NA	NA
PKKAKATKAKKAPK	P43274|H14_MOUSE	41.92	14	6160	NA	NA
PKKAKKPA	P15864|H12_MOUSE:P43276|H15_MOU	40.95	8	5530	5630	NA
PKKAKKPAAAGVKK	P43276|H15_MOUSE	48.64	14	301	203	176
PKKAKKPAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.95	23	271	NA	258
PKKAKKPKVVKVKPVKAS(+79.97)K	P10922|H10_MOUSE	31.28	19	928	NA	NA
PKKAKKPKVVKVKPVKAS(+79.97)KPKK	P10922|H10_MOUSE	26.13	29	1200	NA	NA
PKKAKTVKPKAKSSAKR	P10922|H10_MOUSE	49.94	17	203	460	372
PKKAKTVKPKAKSSAKRASKK	P10922|H10_MOUSE	49.95	21	5660	405	2440
PKKAKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.95	22	11700	NA	3200
PKKPKKPAVSKKTSKSPKKPKVVKAKK\	P43275|H11_MOUSE	49.95	30	640	NA	NA
PKKPKKTAGAKKTVKKTPKKAKKPA	P43276|H15_MOUSE	49.95	25	302	NA	NA
PKKPKVVKAKKVAK	P43275|H11_MOUSE	49.95	14	8250	2680	2840
PKKTAAKK	P43274|H14_MOUSE	29.21	8	442	NA	NA
PKKTAGAKKTVKKTPKKAKKPA	P43276|H15_MOUSE	49.95	22	2050	NA	546
PKKTAKKTPKKAKKPA	P43277|H13_MOUSE	49.95	16	688	NA	554
PKKVKAAKPKKAAKSPA	P43277|H13_MOUSE	45.3	17	2950	NA	NA
PKKVKSASKAVKPKAAKPKVAKAKKVAA	P15864|H12_MOUSE	49.95	31	607	NA	NA
PKTAKPKAAKAKKAVSKK	P43276|H15_MOUSE	49.94	18	718	105	NA
PKTAKPKAAKAKKAVSKKK	P43276|H15_MOUSE	49.95	19	1960	137	NA
PKTPAKPKKA	P43275|H11_MOUSE	36.88	10	494	528	NA
PKTPAKPKKAAP	P43275|H11_MOUSE	41.92	12	181	NA	1260
PKTPAKPKKAAPK	P43275|H11_MOUSE	45.06	13	141	NA	NA

PKTPAKPKKAAPKK	P43275|H11_MOUSE	45.36	14	2180	NA	2160
PKTPAKPKKAAPKKK	P43275|H11_MOUSE	48.83	15	9220	1050	4150
PKTSKPKAAKPKKT	P43274|H14_MOUSE	47.32	14	1310	646	1890
PKTSKPKAAKPKKTAAK	P43274|H14_MOUSE	48.67	17	121	NA	187
PKTSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.95	19	8780	5000	4610
PKVAKAKKVAAKKK	P15864|H12_MOUSE	49.94	14	22100	4050	6120
PKVTKPKTAKPKAAKAKKAVSKKK	P43276|H15_MOUSE	49.88	24	590	NA	NA
PKVVKAKK	P43275|H11_MOUSE	25.53	8	277	NA	NA
PKVVKAKKV	P43275|H11_MOUSE	37.1	9	246	NA	NA
PKVVKAKKVAKSPAK	P43275|H11_MOUSE	49.93	15	2740	1640	2200
PKVVKAKKVAKSPAKAK	P43275|H11_MOUSE	49.86	17	973	1590	843
PKVVKVKPVKASKPKKA	P10922|H10_MOUSE	49.95	17	1720	1270	NA
PKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.94	18	7680	6720	9460
PLNSVFVAPAVTPV	P70158|ASM3A_MOUSE	46.73	14	71.6	NA	162
PLNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	49.85	15	4810	NA	4840
PLNSVFVAPAVTPVKG	P70158|ASM3A_MOUSE	49.85	16	4180	71.9	3910
PLNSVFVAPAVTPVKGVL	P70158|ASM3A_MOUSE	49.9	18	724	NA	562
PLQHYLEQPVERVQ(+15.00)	A2AAJ9|OBSCN_MOUSE	25.69	14	612	NA	NA
PM(+15.99)FIVNTNVPRASVPE	P34884|MIF_MOUSE	49.85	16	536	NA	NA
PM(+15.99)YPVVPVHLDGTF	O35291|RNAS2_MOUSE:P97425|ECP2_	48.83	14	125	NA	NA
PMFIVNTNVPRASVPE	P34884|MIF_MOUSE	49.56	16	253	NA	358
PPALQEPQPAGSQPLLANSPL	Q8R1U2|CGRE1_MOUSE	49.91	21	212	NA	201
PPAPAPAPLPPP	O35609|SCAM3_MOUSE	39.5	12	5460	NA	12100
PPASLPESTPVPSSSPPP	Q6PB44|PTN23_MOUSE	27.13	18	421	NA	NA
PPAYEPPAPAPAPLPP	O35609|SCAM3_MOUSE	30.84	16	57.1	NA	NA
PPAYEPPAPAPAPLPPP	O35609|SCAM3_MOUSE	49.87	17	31900	NA	12900
PPHVQFTYQQPQPLS	B2RXS4|PLXB2_MOUSE	28.87	15	70.3	NA	NA
PPHVQFTYQQPQPLSVEPR	B2RXS4|PLXB2_MOUSE	49.94	19	15800	77.6	9070
PPPAYEPPAPAPA	O35609|SCAM3_MOUSE	30.64	13	443	NA	NA
PPPAYEPPAPAPAPLPP	O35609|SCAM3_MOUSE	49.91	17	22500	NA	NA
PPPAYEPPAPAPAPLPPP	O35609|SCAM3_MOUSE	49.93	18	96300	244	34000
PPPLQHYLEQ(+15.00)PVERVQ(+15.00)	A2AAJ9|OBSCN_MOUSE	28.43	16	2150	NA	NA
PPPYAAYATPTPEVYG	Q9QZC7|PKHB2_MOUSE	44.24	16	1490	NA	NA
PPPYPPAAFQGPSDHAAYPI	Q9JJ00|PLS1_MOUSE	49.29	20	777	NA	NA
PPPYPPAAFQGPSDHAAYPIPQ	Q9JJ00|PLS1_MOUSE	37.69	22	328	NA	NA
PPSPKVTYKAPVPTGEVY	P35564|CALX_MOUSE	29.99	18	681	NA	NA
PPSYYTQPVPVPN	Q9JLJ0|LITAF_MOUSE	43.18	13	3460	48	2800
PPSYYTQPVPVPNA	Q9JLJ0|LITAF_MOUSE	48.35	14	1790	NA	1820
PPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	48.39	15	26400	1030	24300
PPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	49.43	16	2890	NA	2410
PPYDDATAVPSTAKEPPPP	Q91XQ6|LAP4B_MOUSE	49.88	19	9680	NA	2840
PQLIEVSSPITLQAL	E9Q414|APOB_MOUSE	49.65	15	308	NA	241
PRGPPPAGLLQ	P06345|HB2S_MOUSE:P06346|HB2F_M	29.51	11	2860	NA	1530
PRTPQDSPM(+15.99)YPVVPVHLDGTF	P97425|ECP2_MOUSE:P97426|ECP1_M	49.94	21	192	NA	221
PSTSSLAAPTVEAAAS	Q91ZP6|NFIP2_MOUSE	46.7	16	389	NA	107
PSTSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	49.02	19	629	NA	518
PSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	47.88	14	210	NA	175
PTFHTPLDLYAYAR	Q07797|LG3BP_MOUSE	46.39	14	692	NA	361
PTFLNPNVDKAGPA	Q61508|ECM1_MOUSE	42.71	14	127	NA	NA
PTPAYTIPFYTPIPN	O08573|LEG9_MOUSE	49.29	15	133	NA	NA
PTPAYTIPFYTPIPNG	O08573|LEG9_MOUSE	47.2	16	5110	NA	1970
PTPAYTIPFYTPIPNGL	O08573|LEG9_MOUSE	46.1	17	431	NA	NA
PTPAYTIPFYTPIPNGLYP	O08573|LEG9_MOUSE	49.68	19	483	NA	318
PTPAYTIPFYTPIPNGLYPS	O08573|LEG9_MOUSE	49.86	20	2710	NA	1130
PTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	31.01	11	633	NA	3920
PVKASKPKK	P10922|H10_MOUSE	36.1	9	182	NA	NA
PVKASKPKKA	P10922|H10_MOUSE	40.68	10	400	NA	NA
PVKASKPKKAKTVKP	P10922|H10_MOUSE	48.85	15	964	196	3850
PVKASKPKKAKTVKPK	P10922|H10_MOUSE	48.92	16	145	NA	653
PVKASKPKKAKTVKPKA	P10922|H10_MOUSE	49.95	17	1390	227	1740
PVKASKPKKAKTVKPKAK	P10922|H10_MOUSE	49.94	18	861	4280	3110
PVKASKPKKAKTVKPKAKSSAKR	P10922|H10_MOUSE	49.95	23	710	417	3920
PVKASKPKKAKTVKPKAKSSAKRASKK	P10922|H10_MOUSE	49.95	27	1500	NA	3580
PVKASKPKKAKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.95	28	8110	NA	2420
PVQFPYVTPAPHEPV	Q9D074|MGRN1_MOUSE	49.94	15	93.9	NA	NA
PVQFPYVTPAPHEPVK	Q9D074|MGRN1_MOUSE	48.63	16	162	NA	54.9
PVSQM(+15.99)RMATPLLM(+15.99)RPM	P04441|HG2A_MOUSE	44.92	16	256	NA	879
PVSQM(+15.99)RMATPLLMRPM(+15.99	P04441|HG2A_MOUSE	31.31	16	181	NA	643
PVSQM(+15.99)RMATPLLMRPM(+15.99	P04441|HG2A_MOUSE	30.97	17	728	NA	NA
PVSQMRMATPLLM(+15.99)RPM(+15.99	P04441|HG2A_MOUSE	44.57	16	1040	NA	1160
PVSQMRMATPLLM(+15.99)RPMS	P04441|HG2A_MOUSE	27.74	17	42.2	NA	NA
PVSQMRMATPLLMRPM(+15.99)S	P04441|HG2A_MOUSE	44.27	17	372	NA	307
PVVLSYLGPDVN	Q6T3U4|NPCL1_MOUSE	45.57	12	136	NA	80.8
PVVLSYLGPDVNQA	Q6T3U4|NPCL1_MOUSE	43.98	14	193	NA	110
PVVLSYLGPDVNQAL	Q6T3U4|NPCL1_MOUSE	48.16	15	201	NA	NA
PVVPVHLDGTF	O35291|RNAS2_MOUSE:P97425|ECP2_	47.39	11	2190	NA	1940
PVVVPPFLQPEVM(+15.99)G	P02666	48.15	14	228	NA	NA

PVVVPPFLQPEVM(+15.99)GVSK	P02666	49.89	17	9190	NA	NA
PVVVPPFLQPEVMGVSK	P02666	49.67	17	1630	NA	NA
PYDQPNAIYIER	O88307|SORL_MOUSE	44.12	12	131	NA	212
Q(+42.01)(+15.00)DGEQAPPLPIKTPIPTI	Q7TQH7|LRP10_MOUSE	44.84	20	284	NA	400
Q(+42.01)(+15.00)PPTGYSTPTAPQAYS(	Q61545|EWS_MOUSE	42.41	20	1010	NA	5180
QAQEQVQPKPLES	P06728|APOA4_MOUSE	43.16	13	2360	NA	NA
QASAPVGPQANGVLDEK	Q80XK6|ATG2B_MOUSE	25.84	17	135	NA	NA
QASIYSPPAAAAAAA	P70297|STAM1_MOUSE	48.73	15	12500	NA	11400
QASIYSPPAAAAAAAA	P70297|STAM1_MOUSE	49.02	16	3910	NA	3580
QAYHSPATALAIVD	Q8R420|ABCA3_MOUSE	42.47	14	308	NA	228
QDEIDAALPNKAP	Q64464|CP3AD_MOUSE	44.87	13	591	NA	286
QDEIDAALPNKAPA	Q64464|CP3AD_MOUSE	46.03	14	656	NA	409
QDGSVDFGR	Q8K0E8|FIBB_MOUSE	42.32	9	279	72.8	NA
QDHVDFSQPEPHTVLF	Q9QUR8|SEM7A_MOUSE	48.89	16	78.8	NA	NA
QDHVDFSQPEPHTVLFH	Q9QUR8|SEM7A_MOUSE	49.84	17	367	NA	NA
QDPEVFSQPKVLPSA	Q91YD3|DCP1A_MOUSE	49.84	15	270	NA	193
QDPEVFSQPKVLPSAIP	Q91YD3|DCP1A_MOUSE	49.89	17	1730	NA	1630
QDPEVFSQPKVLPSAIPI	Q91YD3|DCP1A_MOUSE	49.94	18	1230	NA	1270
QDPTFHTPLDLYAYAR	Q07797|LG3BP_MOUSE	49.85	16	1270	NA	384
QDQAYKAPVVVEGKV	P56974|NRG2_MOUSE	49.23	15	385	NA	141
QEFILNSPTVTSIK	Q9R0H0|ACOX1_MOUSE	41.69	14	361	NA	654
QEPQPAGSQPLLANSPL	Q8R1U2|CGRE1_MOUSE	49.85	17	204	NA	NA
QEQAQEQVQPKPLES	P06728|APOA4_MOUSE	49.43	15	466	NA	NA
QEYSGSVANEAN	E9Q414|APOB_MOUSE	43.41	12	701	NA	1060
QEYSGSVANEANVY	E9Q414|APOB_MOUSE	48.49	14	745	NA	108
QFNYPQASVTDVT	Q61703|ITIH2_MOUSE	48.17	13	157	NA	305
QGGVYASPSIAGSRP	Q8R0X7|SGPL1_MOUSE	45.45	15	540	NA	321
QGGVYASPSIAGSRPG	Q8R0X7|SGPL1_MOUSE	47.02	16	10100	NA	6540
QIFISPDSLLGVEK	Q9D871|CEA18_MOUSE	44.61	14	152	NA	NA
QINWTVLYRRKHKK	Q8BP67|RL24_MOUSE	29.74	14	109	NA	NA
QIPKVVKSPSSLPAKP	Q8BHK6|SLAF7_MOUSE	48.56	16	331	NA	NA
QKAEASSPVPYLSPET	P39447|ZO1_MOUSE	49.43	16	3460	NA	3070
QKKDGKKRKRSRKESYSVYVYKVLKQV	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.95	30	20700	99700	1240
QKQPYFGAVVGRVA	Q8K157|GALM_MOUSE	46.6	14	478	NA	208
QKQPYFGAVVGRVAN	Q8K157|GALM_MOUSE	25.14	15	156	NA	NA
QKQPYFGAVVGRVANR	Q8K157|GALM_MOUSE	33.81	16	1320	NA	998
QKTQYISPNLNPN	P97499|TEP1_MOUSE	46.92	13	2560	NA	1870
QKTQYISPNLNPND	P97499|TEP1_MOUSE	48.04	14	3050	NA	2750
QKTQYISPNLNPNDV	P97499|TEP1_MOUSE	47.74	15	1810	NA	803
QKTQYISPNLNPNDVT	P97499|TEP1_MOUSE	49.83	16	773	NA	432
QLDEYSSSVANFL	Q91VE0|S27A4_MOUSE	42.93	13	303	NA	NA
QLDEYSSSVANFLQA	Q91VE0|S27A4_MOUSE	47.47	15	1570	NA	877
QLDEYSSSVANFLQAR	Q91VE0|S27A4_MOUSE	49.9	16	380	NA	227
QLEALVGPEANVGP	O09159|MA2B1_MOUSE	42	14	612	NA	168
QLEALVGPEANVGPY	O09159|MA2B1_MOUSE	48.88	15	1000	NA	263
QLEALVGPEANVGPYG	O09159|MA2B1_MOUSE	49.85	16	2990	NA	1300
QLNAFVLPEAEPGET	Q8K135|K319L_MOUSE	47.5	15	101	NA	NA
QLPYSEPKGNPTPA	Q148V8|FA83H_MOUSE	25.88	14	161	NA	NA
QNAWFLPAQADIVATK	P10852|4F2_MOUSE	49.76	16	2370	NA	1820
QNHGYTIPVVNIEVSPF	E9Q414|APOB_MOUSE	49.73	17	943	NA	1490
QPDLNFRNPAVQEE	Q91WV7|SLC31_MOUSE	48.98	14	8900	NA	5670
QPDLNFRNPAVQEEIK	Q91WV7|SLC31_MOUSE	49.94	16	132000	NA	89800
QPDLNFRNPAVQEEIKE	Q91WV7|SLC31_MOUSE	49.66	17	50900	NA	40100
QPPEYTFPSGSGAH	Q2TBE6|P4K2A_MOUSE	42.91	14	196	NA	NA
QPPEYTFPSGSGAHFP	Q2TBE6|P4K2A_MOUSE	49.87	16	7160	NA	6660
QPPEYTFPSGSGAHFPQ	Q2TBE6|P4K2A_MOUSE	38.68	17	2380	NA	2120
QPPTGYSTPTAPQAYSQPV	Q61545|EWS_MOUSE	47.53	19	190	NA	1200
QPPTGYSTPTAPQAYSQPVQ	Q61545|EWS_MOUSE	48.95	20	157	NA	2130
QPRQYNNPIGLYSAET	Q9JKS4|LDB3_MOUSE	47.96	16	130	NA	NA
QPSTSSLAAPTVEAA	Q91ZP6|NFIP2_MOUSE	41.87	15	2810	NA	2110
QPSTSSLAAPTVEAAA	Q91ZP6|NFIP2_MOUSE	45.93	16	7240	93.2	4790
QPSTSSLAAPTVEAAAS	Q91ZP6|NFIP2_MOUSE	48.58	17	72000	3110	61100
QPSTSSLAAPTVEAAASA	Q91ZP6|NFIP2_MOUSE	49.39	18	82000	4570	61400
QPSTSSLAAPTVEAAASAP	Q91ZP6|NFIP2_MOUSE	49.72	19	78200	2610	89900
QPSTSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	49.77	20	231000	8860	248000
QPTGPPPYHESLAGASQPP	Q9D7I0|SHSA5_MOUSE	48.26	19	48700	NA	48300
QPTGPPPYHESLAGASQPPY	Q9D7I0|SHSA5_MOUSE	49.26	20	14800	NA	15600
QPTGPPPYHESLAGASQPPYN	Q9D7I0|SHSA5_MOUSE	49.58	21	724	NA	637
QPTGPPPYHESLAGASQPPYNP	Q9D7I0|SHSA5_MOUSE	48.33	22	202	NA	NA
QPTGPPPYHESLAGASQPPYNPT	Q9D7I0|SHSA5_MOUSE	36.92	23	250	NA	NA
QPVLQYGNPYSAQETR	Q3UKC1|TAXB1_MOUSE	49.72	16	578	NA	639
QPVLQYGNPYSAQETRD	Q3UKC1|TAXB1_MOUSE	49.55	17	118	NA	154
QPVLQYGNPYSAQETRDG	Q3UKC1|TAXB1_MOUSE	49.94	18	396	NA	363
QQKAEASSPVPYLSPET	P39447|ZO1_MOUSE	48.59	17	322	NA	NA
QQLAFKQPSSAYA	P01027|CO3_MOUSE	44.89	13	228	NA	NA
QQLAFKQPSSAYAA	P01027|CO3_MOUSE	49.11	14	1560	NA	873
QQLAFKQPSSAYAAF	P01027|CO3_MOUSE	49.78	15	6320	164	7560

QQLAFKQPSSAYAAFN	P01027|CO3_MOUSE	49.91	16	11500	658	17700
QQLAFKQPSSAYAAFNN	P01027|CO3_MOUSE	49.94	17	167	NA	126
QQVRSPVTNIAR	P84091|AP2M1_MOUSE	45.48	12	457	NA	456
QRAGYKAAIVHNVD	O54965|RNF13_MOUSE	42.75	14	147	NA	79.5
QRAGYKAAIVHNVDS	O54965|RNF13_MOUSE	49.19	15	355	NA	NA
QRFLYQSSSASTDHDPL	Q9DBH0|WWP2_MOUSE	49.65	17	723	NA	1100
QSINFLGGQPAAAPYP	Q8K419|LEG4_MOUSE	41.8	16	377	NA	378
QSPYINPIIPFTGP	O08573|LEG9_MOUSE	36.62	14	4940	NA	NA
QSTDYGNFLANEASP	P51863|VA0D1_MOUSE	46.42	15	292	NA	236
QSTDYGNFLANEASPL	P51863|VA0D1_MOUSE	49.7	16	2850	NA	2510
QTKFLPNAPKALIVEPS	Q91VR5|DDX1_MOUSE	49.02	17	2670	NA	3170
QVPFETRGPHINNSVH	Q8K296|MTMR3_MOUSE	45.71	16	159	NA	NA
QVQWNDPGAQYSLVN	Q9R100|CAD17_MOUSE	49.86	15	5830	NA	2670
QVQWNDPGAQYSLVNK	Q9R100|CAD17_MOUSE	49.91	16	2460	NA	1900
QVQWNDPGAQYSLVNKE	Q9R100|CAD17_MOUSE	49.94	17	512	NA	552
QWNDPGAQYSLVNK	Q9R100|CAD17_MOUSE	49.38	14	127	NA	123
QWNDPGAQYSLVNKE	Q9R100|CAD17_MOUSE	49.75	15	231	NA	129
QYNSPTGLYSSEN	O70400|PDLI1_MOUSE	37.98	13	260	NA	NA
QYPNFAGPQAALANKS	Q8BJW6|EIF2A_MOUSE	48.9	16	860	NA	562
R(+42.01)IVYFILSRV	Q6P9J9|ANO6_MOUSE	25.61	10	127	NA	NA
R(+42.01)KRGRKESYSIYVYKVLKQVHP	Q8CGP0|H2B3B_MOUSE:Q9D2U9|H2B3	49.39	23	723	5430	NA
R(+42.01)PVQ(+15.00)FPYVTPAPHEPVI	Q9D074|MGRN1_MOUSE	48.73	17	579	NA	1310
R(+42.01)RAKFRKKQRSLQKEQLQ(+15.	Q91ZK4|DMBX1_MOUSE	25.6	21	18000	NA	NA
R(+42.01)YYTRTIYQFQ(+15.00)FQEAL	Q8R0I0|ACE2_MOUSE	28.51	16	516	NA	NA
RAGYKAAIVHNVD	O54965|RNF13_MOUSE	47.75	13	238	NA	NA
RAGYKAAIVHNVDS	O54965|RNF13_MOUSE	48	14	693	NA	334
RASIYQSVVINTSK	P97872|FMO5_MOUSE	46.45	14	495	NA	198
RASIYQSVVINTSKE	P97872|FMO5_MOUSE	48.97	15	4950	NA	4120
RASIYQSVVINTSKEM(+15.99)	P97872|FMO5_MOUSE	44.6	16	211	NA	NA
RATPAPSAPAAASATSPSPAPSSGNG	Q9JKV1|ADRM1_MOUSE	36.02	26	132	NA	NA
RAYAFSPPRGLLSKSL	Q91WC9|DGLB_MOUSE	26.15	16	77.7	NA	NA
RDAGYAGSRINSYPD	Q32NZ6|TMC5_MOUSE	29.14	15	159	NA	NA
RDGDSYRSPWSNKYDPPL	P47757|CAPZB_MOUSE	41.34	18	3660	NA	4870
RDNMFSGSKINYTENR	P06745|G6PI_MOUSE	49.51	16	775	NA	966
RDNYRFAHTNIESLV	P27773|PDIA3_MOUSE	35.84	15	987	NA	NA
RDPYATSVGHLIEK	Q923U0|TM1L1_MOUSE	45.89	14	168	NA	129
RDSLVHSSPHVALSHVD	Q9WV91|FPRP_MOUSE	49.93	17	139	NA	592
REELVITPLPSGDVA	Q8BXQ2|PIGT_MOUSE	25.59	15	83.7	NA	NA
REFYSASVAEDA	E9Q7P9|CDHR2_MOUSE	39.54	12	594	NA	747
REGSYEAAKILLDHFA	O35516|NOTC2_MOUSE	40.16	16	41.3	NA	NA
RELRAM(+15.99)LAIEEWQ(+15.00)KTVA	Q99MS7|EH1L1_MOUSE	44.11	22	3290	NA	NA
RENIWKAPEPVE	Q9R100|CAD17_MOUSE	37.08	12	473	NA	159
RENIWKAPEPVEIR	Q9R100|CAD17_MOUSE	49.68	14	13600	NA	11000
RENIWKAPEPVEIRE	Q9R100|CAD17_MOUSE	49.61	15	70200	653	50300
RENIWKAPEPVEIREN(+15.00)ST	Q9R100|CAD17_MOUSE	49.91	18	53900	593	23400
REPPPAYEPPAPAPAPLPPP	O35609|SCAM3_MOUSE	49.95	20	2380	NA	5520
REPPPAYEPPAPAPAPLPPPS	O35609|SCAM3_MOUSE	49.94	21	2610	NA	5550
RESKVVVPPLPGKAF	O70492|SNX3_MOUSE	43.89	15	123	NA	NA
REVSSVEAPSVSPA	Q8BUJ9|LRP12_MOUSE	38.08	14	470	NA	645
REVSSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	39.74	15	1390	NA	1930
REVSSVEAPSVSPARH	Q8BUJ9|LRP12_MOUSE	48.04	16	186	NA	323
REVSSVEAPSVSPARHQ	Q8BUJ9|LRP12_MOUSE	49.75	17	1500	NA	1610
RFGSLSKGIKDTFKIKSKKNK	Q8K3X6|ANS4B_MOUSE	49.94	21	1010	NA	694
RFTYQNAAAQPETGPG	Q9QZM4|TR10B_MOUSE	48.73	16	10600	197	9630
RGILYAAPQLHSIQSGPS	P25918|CD19_MOUSE	42.27	18	165	NA	55.8
RGNVYIHPTAKVAPS	Q922H4|GMPPA_MOUSE	48.68	15	6480	NA	4900
RGYTYTASAIKHVIT	Q9QXH4|ITAX_MOUSE	49.37	15	105	NA	NA
RHKYIYKSPELPR	Q99LR1|ABD12_MOUSE	48.85	13	294	NA	NA
RHKYIYKSPELPRIL	Q99LR1|ABD12_MOUSE	49.91	15	4900	NA	2240
RHNYEGPETHTSL	P14483|HB2A_MOUSE	47.89	13	20800	3910	13500
RHNYEGPETHTSLR	P14483|HB2A_MOUSE	49.05	14	53400	3850	53100
RHNYEGPETHTSLRR	P14483|HB2A_MOUSE	49.81	15	3850	NA	2510
RIEHLYKNPQAHIEG	Q8K0C9|GMDS_MOUSE	49.79	15	776	NA	823
RIEHLYKNPQAHIEGN	Q8K0C9|GMDS_MOUSE	26.27	16	318	NA	216
RIEHLYKNPQAHIEGNM	Q8K0C9|GMDS_MOUSE	49.93	17	206	NA	3820
RIEHLYKNPQAHIEGNM(+15.99)	Q8K0C9|GMDS_MOUSE	49.77	17	2520	NA	2540
RIGSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	48.19	21	836	NA	2820
RIINEPTAAAIAYG	P17879|HS71B_MOUSE:P16627|HS71L_	46.02	14	351	NA	NA
RIKRFLAKKQKQNRPIPQ	Q9CQD0|RL39L_MOUSE:P62892|RL39_	49.94	18	285	121	NA
RIKRFLAKKQKQNRPIPQWIRM(+15.99)K	P62892|RL39_MOUSE	43.67	23	739	NA	1580
RINAWNSPTLPIYEPG	O70475|UGDH_MOUSE	36.81	16	96.9	NA	90.5
RIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	49.94	16	282	1090	218
RKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	49.95	19	1440	NA	NA
RKFEPKGPLINSEF	P23780|BGAL_MOUSE	37.01	14	223	NA	171
RKFEPKGPLINSEFY	P23780|BGAL_MOUSE	29.49	15	382	NA	NA
RKFEPKGPLINSEFYT	P23780|BGAL_MOUSE	32.16	16	142	NA	NA
RKIVYEGPELNH	Q91ZX7|LRP1_MOUSE	43.47	12	175	NA	164

RKIVYEGPELNHA	Q91ZX7|LRP1_MOUSE	49.25	13	3620	NA	2800
RKIVYEGPELNHAF	Q91ZX7|LRP1_MOUSE	49.49	14	3880	NA	3980
RKIVYEGPELNHAFG	Q91ZX7|LRP1_MOUSE	49.91	15	407000	17700	350000
RKIVYEGPELNHAFGLC(+57.02)H	Q91ZX7|LRP1_MOUSE	37.29	18	690	NA	NA
RKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.94	18	212	NA	NA
RKRSRKESYSVYVYKVLKQ	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.94	19	861	NA	NA
RKRSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.95	23	8610	NA	282
RLDNYDAPDIANIA	Q68FD5|CLH1_MOUSE	48.78	14	833	NA	583
RLDNYDAPDIANIAI	Q68FD5|CLH1_MOUSE	49.79	15	141	NA	45.5
RLDNYDAPDIANIAIS	Q68FD5|CLH1_MOUSE	47.58	16	135	NA	NA
RLEVVTDPTTNAGYV	Q9R100|CAD17_MOUSE	49.88	15	751	NA	691
RLEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	49.45	16	3220	NA	2120
RLKEYRSKLILFPRKPSAPKK	P47963|RL13_MOUSE	49.94	21	486	NA	NA
RLKEYRSKLILFPRKPSAPKKG	P47963|RL13_MOUSE	48.75	22	275	NA	NA
RLPYTASSGLM(+15.99)APR	Q9R1Q9|VAS1_MOUSE	40.54	14	904	NA	999
RLPYTASSGLM(+15.99)APRE	Q9R1Q9|VAS1_MOUSE	48.89	15	3350	NA	2860
RLPYTASSGLMAPR	Q9R1Q9|VAS1_MOUSE	45.5	14	332	NA	352
RLPYTASSGLMAPRE	Q9R1Q9|VAS1_MOUSE	47.44	15	353	NA	196
RM(+15.99)APYQGPDAAPGAL	P57780|ACTN4_MOUSE	42.25	15	649	NA	532
RMAPYQGPDAAPG	P57780|ACTN4_MOUSE	49.01	13	383	NA	322
RMAPYQGPDAAPGAL	P57780|ACTN4_MOUSE	47.54	15	188	NA	383
RMAPYQGPDAAPGALD	P57780|ACTN4_MOUSE	49.39	16	701	NA	1080
RMPYTNAVIHEVQR	P24456|CP2DA_MOUSE:P24457|CP2DB	47.14	14	76.7	NA	181
RNM(+15.99)EELKGHLTPRANELK	P06728|APOA4_MOUSE	48.89	18	388	NA	239
RNMEELKGHLTPRANELK	P06728|APOA4_MOUSE	49.93	18	497	NA	982
RNPRQINWTVLYRRKHKKGQSEEIQKK	Q8BP67|RL24_MOUSE	48.55	27	537	NA	18400
RNPRQINWTVLYRRKHKKGQSEEIQKKI	Q8BP67|RL24_MOUSE	48.81	28	1070	NA	4480
RNVQFNYPQASVTD	Q61703|ITIH2_MOUSE	49.72	14	3200	NA	2650
RNVQFNYPQASVTDV	Q61703|ITIH2_MOUSE	49.57	15	338	NA	501
RNVQFNYPQASVTDVT	Q61703|ITIH2_MOUSE	49.85	16	26500	1230	31000
RNVQFNYPQASVTDVTQ	Q61703|ITIH2_MOUSE	49.92	17	118	NA	115
RNYEYYASHVPESV	Q9Z0S1|BPNT1_MOUSE	29.7	14	145	NA	NA
RNYEYYASHVPESVK	Q9Z0S1|BPNT1_MOUSE	49.79	15	12400	NA	11700
RNYEYYASHVPESVKN	Q9Z0S1|BPNT1_MOUSE	49.08	16	4610	NA	3060
RPDAEYWNSQPEIL	P14483|HB2A_MOUSE:P01921|HB2D_M	47.92	14	3370	214	2370
RPDAEYWNSQPEILE	P14483|HB2A_MOUSE:P01921|HB2D_M	48.91	15	14100	485	6790
RPDAEYWNSQPEILER	P14483|HB2A_MOUSE:P01921|HB2D_M	49.76	16	44800	2110	30900
RPDAEYWNSQPEILERT	P14483|HB2A_MOUSE:P01921|HB2D_M	49.07	17	2350	NA	1020
RPEPWGPSWDAAPTPGPAPWG	Q9D956|MALD3_MOUSE	42.17	21	632	NA	763
RPGPREPPPYQEPRPRGTPPH	Q03146|DDR1_MOUSE	48.04	21	1010	NA	1450
RPGRHEYALPLTHSEPE	Q9D4J3|DCBD1_MOUSE	46.55	17	829	NA	10800
RPHTYFGPETSASKF	P70277|SIA7B_MOUSE	48.53	15	558	NA	479
RPHTYFGPETSASKFK	P70277|SIA7B_MOUSE	49.91	16	198	NA	NA
RPKQESYKHADIKVAPP	Q6Q473|CLA4A_MOUSE	46.84	17	342	NA	178
RPPGPPPAPQPPSPAPSPPP	Q9D1F4|AKTS1_MOUSE	35.68	20	3740	NA	NA
RPPLPDNYPE	P09470|ACE_MOUSE	29.47	10	353	NA	NA
RPSFFKDFRPPYVKADHG	Q8BK48|EST2E_MOUSE	49.94	18	375	NA	393
RPSFFKDFRPPYVKADHGDE	Q8BK48|EST2E_MOUSE	49.91	20	809	NA	NA
RPVQFPYVTPAPH	Q9D074|MGRN1_MOUSE	48.87	13	5020	NA	7520
RPVQFPYVTPAPHEP	Q9D074|MGRN1_MOUSE	49.75	15	18300	222	38200
RPVQFPYVTPAPHEPV	Q9D074|MGRN1_MOUSE	49.53	16	47700	1210	65200
RPVQFPYVTPAPHEPVK	Q9D074|MGRN1_MOUSE	49.92	17	208000	9070	191000
RPVQFPYVTPAPHEPVKT	Q9D074|MGRN1_MOUSE	49.92	18	20600	92.1	28400
RPVQFPYVTPAPHEPVKTL	Q9D074|MGRN1_MOUSE	49.93	19	264	NA	844
RPVQFPYVTPAPHEPVKTLR	Q9D074|MGRN1_MOUSE	49.95	20	900	NA	633
RPVTIFGPIADVAREK	P39447|ZO1_MOUSE	49.37	16	1510	NA	1740
RPVTIFGPIADVAREKL	P39447|ZO1_MOUSE	49.91	17	54.9	NA	NA
RQFEYEDPIVRGGKQ	Q4U2R1|HERC2_MOUSE	48.84	15	214	NA	380
RQLDEYSSSVANFL	Q91VE0|S27A4_MOUSE	49.2	14	386	NA	184
RQLDEYSSSVANFLQ	Q91VE0|S27A4_MOUSE	48.65	15	199	NA	173
RQLDEYSSSVANFLQAR	Q91VE0|S27A4_MOUSE	49.92	17	298	NA	237
RQPKYPRKSAPRRNKLDHYAIIKF	P62751|RL23A_MOUSE	49.93	24	2890	NA	1390
RQPKYPRKSAPRRNKLDHYAIIKFPLTTE	P62751|RL23A_MOUSE	29.43	29	411	NA	NA
RQQLYIASRSAVAQ	Q62177|SEM3B_MOUSE	42.19	14	1450	NA	1090
RQQLYIASRSAVAQIA	Q62177|SEM3B_MOUSE	36.47	16	779	NA	828
RRASHTAPQVLFSHREPP	Q9CVB6|ARPC2_MOUSE	40.56	18	1980	NA	1450
RRQPKYPRKSAPRRNKLDHYAIIKF	P62751|RL23A_MOUSE	49.85	25	5900	247	4230
RRQPKYPRKSAPRRNKLDHYAIIKFPLTT	P62751|RL23A_MOUSE	48.93	30	2420	NA	1320
RSAHQVARYRPRAPIIAVTRNPQ	P52480|KPYM_MOUSE	49.49	23	64.6	NA	238
RSDVIHAPLPSPVD	Q3URD3|SLMAP_MOUSE	47.38	14	121	NA	NA
RSESYHAGLPM(+15.99)EPDYPG	Q32NZ6|TMC5_MOUSE	43.57	17	1220	NA	287
RSESYHAGLPMEPDYPG	Q32NZ6|TMC5_MOUSE	40.32	17	177	NA	262
RSFFWNVAPGAESAVAS	P57716|NICA_MOUSE	41.05	17	536	NA	1280
RSKPSFHAPEPKPHYDPA	P97820|M4K4_MOUSE	41.34	18	157	NA	286
RSNEFDYPSVGQLA	P11835|ITB2_MOUSE	37.01	14	135	NA	NA
RSPHPYQLPQALAPHVD	O89023|TPP1_MOUSE	49.93	17	395	NA	429
RSQVTPSVPSEALDD	Q7TQH7|LRP10_MOUSE	48.57	15	562	NA	282

RSQVTPSVPSEALDDS	Q7TQH7|LRP10_MOUSE	49.2	16	457	NA	281
RSQVTPSVPSEALDDST	Q7TQH7|LRP10_MOUSE	49.8	17	273	NA	98.2
RSRKESYSVYVYKVLKQ	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.68	17	190	NA	NA
RSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.95	21	997	NA	466
RSYSSPDITQALQ	Q80U87|UBP8_MOUSE	45.84	13	1060	NA	949
RSYSSPDITQALQE	Q80U87|UBP8_MOUSE	45.03	14	2800	NA	2310
RSYSSPDITQALQEE	Q80U87|UBP8_MOUSE	46.43	15	819	NA	518
RSYSSPDITQALQEEE	Q80U87|UBP8_MOUSE	49.59	16	82.1	NA	NA
RSYTAAVANRA	Q91XS1|MTMR4_MOUSE	36.52	11	301	NA	308
RSYTAAVANRAKGGG	Q91XS1|MTMR4_MOUSE	47.23	15	2530	NA	2300
RTEEIKTPEPLEEGPA	Q6EDY6|CARL1_MOUSE	31.01	16	340	NA	NA
RTPGNRIVYLYTKKVGKAP	Q9D1R9|RL34_MOUSE	49.94	19	402	2030	3390
RTPGNRIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	49.95	20	700	6680	2800
RTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	49.95	21	1910	2640	1080
RTTTWQRPTAEYVR	Q9DBH0|WWP2_MOUSE	31.03	14	445	NA	539
RTTTWQRPTAEYVRNY	Q9DBH0|WWP2_MOUSE	49.31	16	332	NA	426
RVEAQSSPVPAYAWY	Q9D2Z1|CEA20_MOUSE	48.14	15	503	NA	1120
RVEAQSSPVPAYAWYLP	Q9D2Z1|CEA20_MOUSE	47.56	17	171	NA	636
RVITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.93	18	3560	NA	4950
RVITNQYNSPTGLYSSENIS	O70400|PDLI1_MOUSE	49.94	20	1470	NA	2070
RVITNQYNSPTGLYSSENISN	O70400|PDLI1_MOUSE	49.95	21	223	NA	409
RVNFVDPAASSSADD	P55012|S12A2_MOUSE	47.9	15	277	NA	NA
RVPKKKKM(+15.99)PENFMPPVPITSPIM	Q3UPL0|SC31A_MOUSE	49.94	27	1330	NA	NA
RVPKKKKMPENFM(+15.99)PPVPITSPIM	Q3UPL0|SC31A_MOUSE	49.95	27	2830	NA	106
RVPKKKKMPENFMPPVPITSPIM(+15.99	Q3UPL0|SC31A_MOUSE	49.87	27	83.3	NA	NA
RVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MO	38.55	11	3970	NA	6250
RVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MO	49.56	13	128	NA	131
RVQIYHNPTAN	P70460|VASP_MOUSE	41.29	11	53	NA	NA
RVQIYHNPTANSFR	P70460|VASP_MOUSE	46.65	14	2570	NA	3170
RVTIMPKDIQLARRIRGERA	P02301|H3C_MOUSE:P68433|H31_MOU	32.46	20	109	NA	NA
RYIAPTVLVDVQ	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	38.48	12	105	NA	232
RYIAPTVLVDVQE	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	43.03	13	363	NA	703
RYLAPTILTDVDPN	P47740|AL3A2_MOUSE	49.72	14	212	NA	NA
RYM(+15.99)APEVLDESLN	P36895|BMR1A_MOUSE	44.92	13	485	NA	211
RYM(+15.99)APEVLDET	Q61271|ACV1B_MOUSE:P37172|ACVR1	29.89	11	162	NA	NA
RYM(+15.99)APEVLDETIN	Q61271|ACV1B_MOUSE	48.68	13	5310	18.6	3170
RYM(+15.99)APEVLDETIQ	P37172|ACVR1_MOUSE	36.94	13	733	NA	375
RYM(+15.99)APEVLEGAIN	P27038|AVR2A_MOUSE:P27040|AVR2B	37.71	13	1470	NA	989
RYMAPEVLDESLN	P36895|BMR1A_MOUSE	40.22	13	133	NA	NA
RYMAPEVLDET	Q61271|ACV1B_MOUSE:P37172|ACVR1	37.09	11	78.3	NA	63.6
RYMAPEVLDETIN	Q61271|ACV1B_MOUSE	48.1	13	1880	NA	2590
RYMAPEVLDETIQ	P37172|ACVR1_MOUSE	43.41	13	182	NA	352
RYMAPEVLEGAIN	P27038|AVR2A_MOUSE:P27040|AVR2B	41.94	13	481	NA	1640
RYRPRAPIIAVTRNPQ	P52480|KPYM_MOUSE	46.53	16	1250	NA	4710
RYTQKAPQVSTPT	P07724|ALBU_MOUSE	47.89	13	299	NA	NA
RYTQKAPQVSTPTL	P07724|ALBU_MOUSE	49.29	14	2110	NA	3500
RYTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.93	15	4780	NA	7310
RYTQKAPQVSTPTLVE	P07724|ALBU_MOUSE	49.93	16	2050	NA	8120
RYTQKAPQVSTPTLVEA	P07724|ALBU_MOUSE	49.88	17	2450	NA	1610
RYVASYLLAALGGNSSPSAKDIKK	P99027|RLA2_MOUSE	49.94	24	5150	NA	NA
S(+42.01)(+79.97)KAVKPKAAKPKVAKAI	P15864|H12_MOUSE	25.68	18	393	NA	NA
S(+42.01)AEREAAEAATVAAATEA	Q62465|VAT1_MOUSE	37.36	18	740	NA	455
S(+42.01)AEREAAEAATVAAATEAG	Q62465|VAT1_MOUSE	40.23	19	1040	NA	946
S(+42.01)APGPYQAAAGPSVVPTAPPT	Q9JLJ0|LITAF_MOUSE	47.03	21	315	NA	NA
S(+42.01)ETAPVAQAASTA	P43275|H11_MOUSE	32.69	13	2210	NA	1510
S(+42.01)ETAPVAQAASTAT	P43275|H11_MOUSE	31.22	14	134	NA	NA
S(+42.01)ETAPVAQAASTATE	P43275|H11_MOUSE	43.95	15	850	NA	1100
S(+42.01)ETAPVAQAASTATEKP	P43275|H11_MOUSE	48.91	17	1000	NA	2050
S(+42.01)ETAPVAQAASTATEKPA	P43275|H11_MOUSE	49.91	18	3010	NA	5870
S(+42.01)ETAPVAQAASTATEKPAA	P43275|H11_MOUSE	49.89	19	3410	NA	1660
S(+42.01)ETAPVAQAASTATEKPAAA	P43275|H11_MOUSE	49.9	20	108	NA	NA
S(+42.01)ETAPVAQAASTATEKPAAAK	P43275|H11_MOUSE	49.94	21	696	NA	1270
S(+42.01)ETAPVAQAASTATEKPAAAKK	P43275|H11_MOUSE	48.77	22	1420	NA	310
S(+42.01)ETAPVAQAASTATEKPAAAKK	P43275|H11_MOUSE	43.76	26	557	NA	660
S(+42.01)ETAPVAQAASTATEKPAAAKK	P43275|H11_MOUSE	28.5	27	947	NA	NA
S(+42.01)ETAPVAQAASTATEKPAAAKK	P43275|H11_MOUSE	49.94	28	171	NA	NA
S(+42.01)GRGKQGGKARAKAKTRSSRA	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	49.94	29	3790	50400	3350
S(+42.01)GRGKQGGKARAKAKTRSSRA	C0HKE3|H2A1D_MOUSE:C0HKE7|H2A1	49.94	31	2830	3660	NA
S(+42.01)GRGKQGGKARAKAKTRSSRA	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	43.24	32	2530	19000	2330
S(+42.01)ILYVSPHPDAFPS	Q9Z1Q9|SYVC_MOUSE	42.27	14	292	NA	382
S(+42.01)IRVTQKSYKM(+15.99)STSGPI	P11679|K2C8_MOUSE	48.16	23	280	NA	NA
S(+42.01)IRVTQKSYKM(+15.99)STSGPI	P11679|K2C8_MOUSE	48.95	25	390	NA	3540
S(+42.01)IRVTQKSYKMSTSGPRAFSSR	P11679|K2C8_MOUSE	48.94	22	168	NA	464
S(+42.01)IRVTQKSYKMSTSGPRAFSSR	P11679|K2C8_MOUSE	49.72	23	688	NA	860
S(+42.01)IRVTQKSYKMSTSGPRAFSSR	P11679|K2C8_MOUSE	49.84	25	644	NA	11300
S(+42.01)IRVTQKSYKMSTSGPRAFSSR	P11679|K2C8_MOUSE	49.94	26	1550	NA	707
S(+42.01)IRVTQKSYKMSTSGPRAFSSR	P11679|K2C8_MOUSE	38.1	29	7120	NA	2820

S(+42.01)KAVKPKAAKPKVAKAKKVAAK	P15864|H12_MOUSE	47.41	23	645	NA	NA
S(+42.01)KKAVTKVQKKDGKKRK	Q64525|H2B2B_MOUSE	45.59	17	548	NA	NA
S(+42.01)KPPPKPVKPGQVKVFRALYTF	Q62422|OSTF1_MOUSE	49.91	22	611	NA	355
S(+42.01)KSPKKPKVVKAKKVAKSPAK	P43275|H11_MOUSE	49.94	21	2290	221	1560
S(+42.01)PKKVKAAKPKKAAKSPAK	P43277|H13_MOUSE	49.9	19	3910	NA	3100
S(+42.01)PPHVQ(+15.00)FTYQQPQPLS	B2RXS4|PLXB2_MOUSE	48.75	20	836	NA	851
S(+42.01)Q(+15.00)PLLANSPLQSETQQ	Q8R1U2|CGRE1_MOUSE	46.32	19	68.3	NA	NA
S(+42.01)RLPKARPSKVKAEPPPKKRK	E9PYL2|PRR12_MOUSE	27.6	21	6770	NA	NA
S(+42.01)SKKAKTKTTKKRPQRATSNVF	Q3THE2|ML12B_MOUSE	48.39	25	913	NA	683
S(+42.01)SNGTDAPAEAQAAM(+15.99)E	Q9DBG5|PLIN3_MOUSE	49.94	27	475	NA	214
S(+42.01)VQVVSAAAAAKVPE	Q68FL4|SAHH3_MOUSE	46.93	15	253	NA	NA
S(+42.01)VQVVSAAAAAKVPEV	Q68FL4|SAHH3_MOUSE	48.4	16	1190	118	1820
S(+42.01)VQVVSAAAAAKVPEVE	Q68FL4|SAHH3_MOUSE	49.84	17	2690	137	3370
S(+42.01)VQVVSAAAAAKVPEVEL	Q68FL4|SAHH3_MOUSE	48.47	18	142	NA	NA
S(+42.01)VQVVSAAAAAKVPEVELKDLS	Q68FL4|SAHH3_MOUSE	49.61	25	779	NA	NA
S(+42.01)YGPLDM(+15.99)YRNPGPSGP	Q9ER00|STX12_MOUSE	36.88	19	905	NA	5420
S(+42.01)YGPLDMYRNPGPSGPQPR	Q9ER00|STX12_MOUSE	48.77	19	94.9	NA	372
S(+42.01)YKPIAPAPSSTPG	Q9CPY4|CDKA2_MOUSE	28.8	14	207	NA	136
S(+42.01)YTPGQPVTAVVQR	Q9DBG9|TX1B3_MOUSE	44.6	14	519	NA	460
SAFQYLQSTPARSPAT	Q66K08|CILP1_MOUSE	41.49	16	160	NA	NA
SAFSYVDPVITSISPR	P16056|MET_MOUSE	49.7	16	18100	220	13200
SAGTRYSAPANLYVR	Q64487|PTPRD_MOUSE:A2A8L5|PTPRF	48.91	15	197	NA	227
SAKPVSQM(+15.99)RM(+15.99)ATPLLM	P04441|HG2A_MOUSE	29.64	20	234	NA	NA
SAKPVSQM(+15.99)RMATPLLM(+15.99)	P04441|HG2A_MOUSE	37.61	19	2610	NA	15000
SAKPVSQM(+15.99)RMATPLLMRPM(+1	P04441|HG2A_MOUSE	46.92	19	8950	NA	9210
SAKPVSQM(+15.99)RMATPLLMRPMS	P04441|HG2A_MOUSE	29.76	20	606	NA	1670
SAKPVSQMRM(+15.99)ATPLLMRPM	P04441|HG2A_MOUSE	42.29	19	1460	NA	4680
SAKPVSQMRM(+15.99)ATPLLMRPM(+1	P04441|HG2A_MOUSE	32.36	19	8950	NA	NA
SAKPVSQMRM(+15.99)ATPLLMRPM(+1	P04441|HG2A_MOUSE	49.79	20	698	NA	NA
SAKPVSQMRMATPLLM(+15.99)RPM	P04441|HG2A_MOUSE	48.55	19	1740	NA	12100
SAKPVSQMRMATPLLM(+15.99)RPM(+1	P04441|HG2A_MOUSE	49.75	19	7660	NA	11000
SAKPVSQMRMATPLLM(+15.99)RPM(+1	P04441|HG2A_MOUSE	25.69	20	1750	NA	NA
SAKPVSQMRMATPLLMRPM(+15.99)	P04441|HG2A_MOUSE	49.86	19	2600	NA	10500
SAKPVSQMRMATPLLMRPM(+15.99)S	P04441|HG2A_MOUSE	46.29	20	933	NA	NA
SALEYGM(+15.99)PVTLIGEA	Q9DCD0|6PGD_MOUSE	46.23	15	161	NA	NA
SALEYGM(+15.99)PVTLIGEAV	Q9DCD0|6PGD_MOUSE	42.6	16	219	NA	NA
SAPAPKKGSKKAISKAQKKDGKKR	Q64475|H2B1B_MOUSE	37.69	24	6210	NA	NA
SAPAPKKGSKKAISKAQKKDGKKRKR	Q64475|H2B1B_MOUSE	49.95	26	8450	21000	NA
SAPAPKKGSKKAVTKAQKKDGKKR	Q8CGP0|H2B3B_MOUSE:Q6ZWY9|H2B1	49.95	24	11100	1810	NA
SAPAPKKGSKKAVTKAQKKDGKKRK	Q8CGP0|H2B3B_MOUSE:Q6ZWY9|H2B1	49.95	25	4980	NA	NA
SAPAPKKGSKKAVTKAQKKDGKKRKR	Q8CGP0|H2B3B_MOUSE:Q6ZWY9|H2B1	49.95	26	9760	2820	32900
SAPAPKKGSKKAVTKAQKKDGKKRKRS	Q6ZWY9|H2B1C_MOUSE:Q64524|H2B2	49.95	28	7740	NA	15300
SAQSPYINPIIPFTGPI	O08573|LEG9_MOUSE	49.83	17	408	NA	409
SARTVITPDPNLSIDQ	P08775|RPB1_MOUSE	45.36	16	137	NA	NA
SASFLRPPSTAPSAGG	Q05BQ1|TUTLA_MOUSE	43.34	16	1650	NA	998
SASGLNAALAHYSPT	B1AVD1|XPP2_MOUSE	49.67	15	92.8	NA	NA
SASGLNAALAHYSPTK	B1AVD1|XPP2_MOUSE	49.37	16	691	NA	159
SASKAVKPKAAKPKVAKAKKVAAKK	P15864|H12_MOUSE	49.94	25	298	NA	NA
SASKAVKPKAAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	26	11500	2420	723
SASKTEAPAAAKSLTSPL	Q9QY76|VAPB_MOUSE	48.85	18	1930	NA	1850
SAYYNPGNPHNVYM(+15.99)PT	P97765|WBP2_MOUSE	49.71	16	33.8	NA	NA
SDGTVPFWAHAGNAIPSADQ	Q9D0F3|LMAN1_MOUSE	45.68	20	610	NA	NA
SDHTYQSALLSGSDE	Q8VCZ2|TM45B_MOUSE	29.21	15	190	NA	NA
SDIYQAPSADSADH	P26361|CFTR_MOUSE	41.52	14	1010	NA	217
SDIYQAPSADSADHL	P26361|CFTR_MOUSE	44.4	15	712	NA	657
SDKNGNPLNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	49.94	21	70.6	NA	NA
SDKNGNPLNSVFVAPAVTPVKGVL	P70158|ASM3A_MOUSE	49.94	24	381	NA	396
SDM(+15.99)FKASLVIPSKD	Q8BJD1|ITIH5_MOUSE	38.56	14	1220	NA	332
SDMFKASLVIPSKD	Q8BJD1|ITIH5_MOUSE	47.43	14	528	NA	345
SDNDHLTYGISGPNASYFS	E9Q7P9|CDHR2_MOUSE	49.24	19	168	NA	NA
SDNLFIAPVGISTAM(+15.99)	P49182|HEP2_MOUSE	35.89	15	336	NA	NA
SDPKYATPQVIQAPG	O54967|ACK1_MOUSE	49.55	15	1490	NA	2620
SDPKYATPQVIQAPGP	O54967|ACK1_MOUSE	48.51	16	1860	NA	1790
SDPKYATPQVIQAPGPR	O54967|ACK1_MOUSE	49.82	17	12600	NA	15500
SDSGNFRPANPNWG	E9PV24|FIBA_MOUSE	48.16	14	464	NA	561
SDSGNFRPANPNWGVF	E9PV24|FIBA_MOUSE	48.28	16	433	NA	632
SDSGNFRPANPNWGVFS	E9PV24|FIBA_MOUSE	49.89	17	886	NA	1090
SDSGNFRPANPNWGVFSE	E9PV24|FIBA_MOUSE	49.94	18	144	NA	111
SDTIKPDVN	P35700|PRDX1_MOUSE	41.53	9	224	164	261
SDTSGFQPGFPSLSVLPK	Q62190|RON_MOUSE	46.69	18	137	NA	NA
SDVIHAPLPSPVD	Q3URD3|SLMAP_MOUSE	46.6	13	780	NA	502
SDVIHAPLPSPVDK	Q3URD3|SLMAP_MOUSE	47.33	14	143	NA	NA
SEEEYSAPLPTPA	P97467|AMD_MOUSE	43.23	13	149	NA	88.4
SEEEYSAPLPTPAP	P97467|AMD_MOUSE	49.34	14	1070	NA	1070
SEEEYSAPLPTPAPS	P97467|AMD_MOUSE	49.9	15	8700	60.2	6230
SEKLEVKDPHPQESSG	Q9DBR4|APBB2_MOUSE	42.07	16	361	NA	329
SEPEYATPIVERH	Q9D4J3|DCBD1_MOUSE	42.77	13	1250	NA	1240

SEPEYATPIVERHL	Q9D4J3|DCBD1_MOUSE	49.06	14	1280	NA	1170
SEPFFYSKYSAPRLPAALEQ	P97432|NBR1_MOUSE	48.92	20	102	NA	349
SEPYTFSHPNK	Q5U462|CDCP1_MOUSE	41.57	11	425	NA	437
SEPYTFSHPNKG	Q5U462|CDCP1_MOUSE	48.22	12	1060	NA	790
SEPYTFSHPNKGE	Q5U462|CDCP1_MOUSE	47.79	13	432	NA	NA
SEPYTFSHPNKGEIG	Q5U462|CDCP1_MOUSE	49.76	15	7410	NA	1840
SERELYIPSVDLLTAQD	P97432|NBR1_MOUSE	49.62	17	655	NA	199
SERTHSAPLPNISKADD	Q3UMF0|COBL1_MOUSE	25.55	17	122	NA	NA
SESEPYTFSHPNKGEIG	Q5U462|CDCP1_MOUSE	49.58	17	640	NA	532
SESSFNSPQGVAIADN	Q8BZW8|NHLC2_MOUSE	41.28	16	241	NA	174
SESSVSTPSASFEPD	Q8VCH8|UBXN4_MOUSE	42.59	15	286	NA	NA
SESSVSTPSASFEPDV	Q8VCH8|UBXN4_MOUSE	36.33	16	399	NA	358
SESYHAGLPM(+15.99)EPDYPG	Q32NZ6|TMC5_MOUSE	49.85	16	136	NA	NA
SEVLYERPQPVPSFS	A2AEV7|CC120_MOUSE	48.72	15	167	NA	70.6
SEVYTFPVPERH	P09803|CADH1_MOUSE	46.45	12	508	NA	93
SEVYTFPVPERHLE	P09803|CADH1_MOUSE	47.01	14	537	NA	NA
SFFWNVAPGAESAVA	P57716|NICA_MOUSE	36.2	15	1210	NA	1070
SFFWNVAPGAESAVAS	P57716|NICA_MOUSE	37.89	16	2040	NA	1840
SFPKFKGSLALRTLD	Q8BMT4|LRC33_MOUSE	44.65	15	388	NA	NA
SFVQNYPVVSIEDPF	P17182|ENOA_MOUSE	49.84	15	585	NA	650
SGAQEMVSSSVSSAKE	Q9DBG5|PLIN3_MOUSE	48.61	16	60.3	NA	NA
SGAQEMVSSSVSSAKETV	Q9DBG5|PLIN3_MOUSE	49.86	18	554	NA	NA
SGAQEMVSSSVSSAKETVA	Q9DBG5|PLIN3_MOUSE	49.9	19	78.9	NA	114
SGAVIFNFPGTRNEVIPM	Q9D304|RN128_MOUSE	49.92	18	980	NA	2050
SGAVIFNFPGTRNEVIPM(+15.99)	Q9D304|RN128_MOUSE	49.94	18	7180	NA	1910
SGDEKKGPLIVSGPDGAPAKGDG	Q8VBW1|SC6A8_MOUSE	48.31	23	1940	NA	866
SGDGVTHTVPIYEG	P63260|ACTG_MOUSE:P60710|ACTB_M	32.82	14	479	109	NA
SGFAAPFFIVRHQL	P17665|COX7C_MOUSE	35.52	14	169	NA	96.9
SGFAAPFFIVRHQLLKK	P17665|COX7C_MOUSE	43.52	17	3850	NA	2460
SGFPKPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	49.92	20	569	NA	NA
SGFTNTM(+15.99)RVVPVP	P52480|KPYM_MOUSE	43.73	13	21600	14100	15400
SGFTNTMRVVPVP	P52480|KPYM_MOUSE	47.62	13	16800	NA	24700
SGGTSRHPGPL	P23150|HA2J_MOUSE:P14434|HA2B_M	36.29	11	1100	NA	648
SGGVFRAPSIHGGSG	P19001|K1C19_MOUSE	46.94	15	2840	NA	2160
SGGVFRAPSIHGGSGGR	P19001|K1C19_MOUSE	45.7	17	960	NA	1230
SGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	45.15	18	1140	NA	874
SGIFVSPKGVLE	Q9QXW9|LAT2_MOUSE	29.37	12	77.7	NA	NA
SGIFVSPKGVLEN	Q9QXW9|LAT2_MOUSE	44.64	13	48.9	NA	NA
SGIFVSPKGVLENAG	Q9QXW9|LAT2_MOUSE	40.34	15	309	NA	180
SGIYKAAFPLHD	Q6P9J9|ANO6_MOUSE	46.53	12	101	NA	NA
SGKDKKKKTKKIKEKY	P11499|HS90B_MOUSE	49.91	16	3960	757	1490
SGKDKKKKTKKIKEKYIDQ	P11499|HS90B_MOUSE	49.56	19	161	1080	795
SGKSLFKTSLPRRPRP	Q05117|PPA5_MOUSE	49.7	16	3530	NA	4130
SGNFRPANPNWG	E9PV24|FIBA_MOUSE	40.33	12	575	NA	1700
SGNFRPANPNWGV	E9PV24|FIBA_MOUSE	37.22	13	313	NA	482
SGNFRPANPNWGVF	E9PV24|FIBA_MOUSE	49.32	14	1730	NA	2440
SGNFRPANPNWGVFS	E9PV24|FIBA_MOUSE	49.02	15	7300	39.7	6670
SGNFRPANPNWGVFSE	E9PV24|FIBA_MOUSE	49.73	16	771	NA	549
SGPKPFSAPKPQT(+79.97)SPSPKP	P40124|CAP1_MOUSE	32.87	19	786	NA	NA
SGPKPFSAPKPQTSPS	P40124|CAP1_MOUSE	48.57	16	3230	NA	NA
SGPKPFSAPKPQTSPSP	P40124|CAP1_MOUSE	45.96	17	7240	189	13300
SGPKPFSAPKPQTSPSPK	P40124|CAP1_MOUSE	49.86	18	12300	690	16300
SGPKPFSAPKPQTSPSPKP	P40124|CAP1_MOUSE	49.91	19	140000	5420	88700
SGPKPFSAPKPQTSPSPKPA	P40124|CAP1_MOUSE	49.94	20	12300	244	6210
SGPKPFSAPKPQTSPSPKPAT	P40124|CAP1_MOUSE	49.93	21	193	NA	NA
SGPNASYFSVNANTGEVK	E9Q7P9|CDHR2_MOUSE	49.88	18	863	NA	914
SGPVTPLSPSVLPSLPQ	Q6NS82|RETR2_MOUSE	43.72	17	526	NA	315
SGQIFISPDSLLGVEK	Q9D871|CEA18_MOUSE	44.81	16	2880	NA	1080
SGQIFISPDSLLGVEKY	Q9D871|CEA18_MOUSE	45.05	17	510	NA	NA
SGRFTYQNAAAQPETGPG	Q9QZM4|TR10B_MOUSE	48.94	18	10500	266	589
SGRHKFRPSFPASSP	O89023|TPP1_MOUSE	29.45	15	668	NA	252
SGRHKFRPSFPASSPYV	O89023|TPP1_MOUSE	42.77	17	2670	NA	1490
SGRHKFRPSFPASSPYVT	O89023|TPP1_MOUSE	38.43	18	348	NA	96.7
SGTSVASPVVAGAVT	Q9WTZ2|MBTP1_MOUSE	42.84	15	1220	NA	1020
SGVSLAALKKSLAAAGYDVEKNNSRIKL	P43275|H11_MOUSE	49.95	31	650	NA	NA
SHDYKGSTSHSLPY	E9Q414|APOB_MOUSE	36.91	14	314	NA	NA
SHDYKGSTSHSLPYE	E9Q414|APOB_MOUSE	32.47	15	1160	NA	910
SHRAVYVGVHVPFSKE	Q8BTY2|S4A7_MOUSE	49.68	16	60	NA	156
SHRDPYATSVGHLIE	Q923U0|TM1L1_MOUSE	49.27	15	1150	NA	899
SHRDPYATSVGHLIEK	Q923U0|TM1L1_MOUSE	49.76	16	1340	NA	1010
SHRDPYATSVGHLIEKA	Q923U0|TM1L1_MOUSE	49.84	17	421	NA	295
SIASFKDPKISTSLP	Q61233|PLSL_MOUSE	47.26	15	1040	NA	580
SIASFKDPKISTSLPV	Q61233|PLSL_MOUSE	49.85	16	23900	2600	16300
SILDRYYTPTISRE	Q9R1P3|PSB2_MOUSE	36.93	14	433	NA	355
SILDRYYTPTISRER	Q9R1P3|PSB2_MOUSE	45.21	15	7440	NA	7850
SILDRYYTPTISRERA	Q9R1P3|PSB2_MOUSE	46.69	16	21300	NA	NA
SILDRYYTPTISRERAV	Q9R1P3|PSB2_MOUSE	47.18	17	626	NA	179

SILWSQPLPSLPGGPP	Q8C0Z1|F234A_MOUSE	49.66	16	3530	NA	2530
SINFLGGQPAAAPY	Q8K419|LEG4_MOUSE	45.57	14	180	NA	98.8
SINFLGGQPAAAPYP	Q8K419|LEG4_MOUSE	49.41	15	1340	NA	1030
SINFLGGQPAAAPYPG	Q8K419|LEG4_MOUSE	49.26	16	10700	NA	7350
SIPAWTGPEIPESGPS	Q8K4G1|LTBP4_MOUSE	48.71	16	850	NA	232
SIRPSVYQPVPASSYSPSPG	Q9JKS4|LDB3_MOUSE	49.94	20	297	NA	587
SITVEAPTTSDTDVY	Q91ZP6|NFIP2_MOUSE	42.5	15	503	NA	258
SKAKVTKPKTPAKPKKAAPKK	P43275|H11_MOUSE	49.95	21	69.2	222	211
SKAKVTKPKTPAKPKKAAPKKK	P43275|H11_MOUSE	49.95	22	7630	1850	443
SKAPSKKPKATPVKKAKK	P10922|H10_MOUSE	36.86	18	404	NA	NA
SKASKPKVTKPKTAKPKAAKAKKAVSKK	P43276|H15_MOUSE	49.95	28	1260	NA	1750
SKASKPKVTKPKTAKPKAAKAKKAVSKK	P43276|H15_MOUSE	49.95	29	45900	12400	1620
SKAVKPKAAKPKVAKAKKVAAKK	P15864|H12_MOUSE	49.95	23	461	NA	336
SKAVKPKAAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	24	5860	340	1400
SKDTKYQSVYVLSAEKD	Q61483|DLL1_MOUSE	49.94	17	503	NA	492
SKDTKYQSVYVLSAEKDE	Q61483|DLL1_MOUSE	49.36	18	184	NA	NA
SKEAFQEALAAAGDK	P10639|THIO_MOUSE	49.64	15	2680	NA	1750
SKEIERLQKQIERHKKKIQQLKNNH	O35143|ATIF1_MOUSE	49.75	25	810	NA	NA
SKGKKKKEKKK	Q05D44|IF2P_MOUSE	40.35	11	816	NA	NA
SKKKKKFRTPSFLKKNKKK	Q9QYB5|ADDG_MOUSE	49.95	19	1240	4710	2560
SKKKKKKKKP	Q99L45|IF2B_MOUSE	43.23	10	16100	12700	15400
SKKKKKKKKPFM(+15.99)	Q99L45|IF2B_MOUSE	49.94	12	3370	2990	NA
SKKTSKSPKKPKVVKAKKVAK	P43275|H11_MOUSE	48.41	21	365	NA	NA
SKLLYKTSVVKKAAAR	Q9JJY3|NSMA2_MOUSE	49.91	16	384	NA	338
SKLVNNSPLPQSVVF	Q61703|ITIH2_MOUSE	46.03	15	101	NA	151
SKLVNNSPLPQSVVFD	Q61703|ITIH2_MOUSE	49.9	16	241	NA	NA
SKNVFLSPM(+15.99)SISS	Q60854|SPB6_MOUSE	28.18	13	389	NA	128
SKNVFLSPM(+15.99)SISSA	Q60854|SPB6_MOUSE	43.03	14	426	NA	232
SKNVFLSPM(+15.99)SISSAL	Q60854|SPB6_MOUSE	48.01	15	907	NA	369
SKNVFLSPMSISS	Q60854|SPB6_MOUSE	43.43	13	198	NA	367
SKNVFLSPMSISSA	Q60854|SPB6_MOUSE	47.24	14	357	NA	319
SKNVFLSPMSISSAL	Q60854|SPB6_MOUSE	38.4	15	230	NA	638
SKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.95	16	2920	2240	NA
SKPKATKAKKAAPR	P43277|H13_MOUSE	49.9	14	2620	NA	3680
SKPKATKAKKAAPRK	P43277|H13_MOUSE	49.91	15	30000	9690	3560
SKPKATKAKKAAPRKK	P43277|H13_MOUSE	49.95	16	82800	45900	27600
SKPKKAKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.95	24	13200	NA	NA
SKPKVTKPKTAKPKAAKAKKAVSKKK	P43276|H15_MOUSE	49.95	26	2010	NA	551
SKTVYEGPFASRSLS	Q60680|IKKA_MOUSE	42.67	15	863	NA	814
SKTVYEGPFASRSLSD	Q60680|IKKA_MOUSE	46.06	16	447	NA	NA
SKWSYLYPLATNIPN	Q9DBX3|SUSD2_MOUSE	49.71	15	6870	NA	7410
SLAAHTGAHPNRSPF	Q80UF9|OTOP3_MOUSE	37.7	15	83	NA	NA
SLDLYKGSVALRD	Q6P4T0|ATG2A_MOUSE	36.83	13	234	NA	NA
SLDLYKGSVALRDIH	Q6P4T0|ATG2A_MOUSE	49.02	15	195	NA	113
SLDYHFVTPLTSLT	Q61702|ITIH1_MOUSE	37.99	14	109	NA	NA
SLESFLGPRANTEDLP	Q8BSF4|PISD_MOUSE	36.14	16	1850	NA	647
SLESFLGPRANTEDLPF	Q8BSF4|PISD_MOUSE	38.86	17	692	NA	NA
SLFLKTPKIVSSKD	P06151|LDHA_MOUSE	49.89	14	680	NA	331
SLFLKTPKIVSSKDY	P06151|LDHA_MOUSE	48.34	15	282	NA	275
SLFTQYFQSM(+15.99)TDYGKD	P09813|APOA2_MOUSE	49.82	16	216	NA	NA
SLFTQYFQSM(+15.99)TDYGKDL	P09813|APOA2_MOUSE	49.85	17	106	NA	NA
SLFTQYFQSM(+15.99)TDYGKDLM(+15.9	P09813|APOA2_MOUSE	49.84	18	242	NA	NA
SLHLRFSAPQIENEP	Q61190|I10R2_MOUSE	47.84	15	1280	NA	760
SLHLRFSAPQIENEPE	Q61190|I10R2_MOUSE	49.94	16	6040	93.7	5890
SLHLRFSAPQIENEPET	Q61190|I10R2_MOUSE	49.88	17	2280	NA	2210
SLKYNFVTPLTHM(+15.99)VVT	A6X935|ITIH4_MOUSE	49.86	16	1520	NA	1730
SLKYNFVTPLTHM(+15.99)VVTKP	A6X935|ITIH4_MOUSE	49.94	18	23500	481	21700
SLKYNFVTPLTHM(+15.99)VVTKPE	A6X935|ITIH4_MOUSE	49.94	19	705	NA	570
SLKYNFVTPLTHMVVT	A6X935|ITIH4_MOUSE	49.93	16	401	NA	1580
SLKYNFVTPLTHMVVTKP	A6X935|ITIH4_MOUSE	49.94	18	11600	NA	26900
SLKYNFVTPLTHMVVTKPE	A6X935|ITIH4_MOUSE	49.94	19	324	NA	699
SLLKDFRTPLSHAANRN	Q08ED0|B2L15_MOUSE	48.85	17	250	NA	NA
SLLYKVPYVAQEIQ	Q06335|APLP2_MOUSE	49.72	14	100	NA	NA
SLLYNVPAVAEEIQ	P12023|A4_MOUSE	48.97	14	1710	NA	924
SLLYNVPAVAEEIQD	P12023|A4_MOUSE	47.62	15	929	NA	NA
SLLYNVPAVAEEIQDE	P12023|A4_MOUSE	49.19	16	50.7	NA	NA
SLPESTPVPSSSPP	Q6PB44|PTN23_MOUSE	29.16	14	446	NA	278
SLPESTPVPSSSPPP	Q6PB44|PTN23_MOUSE	48.72	15	1120	NA	400
SLPPHVYSTPQPSLPPVQPS	Q3UPH1|PRRC1_MOUSE	49.9	20	157	NA	NA
SLPPHVYSTPQPSLPPVQPSAPPP	Q3UPH1|PRRC1_MOUSE	49.94	24	1230	NA	3830
SLPQLPPTVLPVE	Q99LJ1|FUCO_MOUSE	29.59	13	3670	NA	1530
SLQAFSNPSAGISVDVK	Q8BG07|PLD4_MOUSE	49.26	17	1600	114	NA
SLRDLESPNVDSSPSPP	Q8K0B3|LRC66_MOUSE	49.9	17	773	NA	727
SLRFAPPQPAEPWS	Q8VCT4|EST1D_MOUSE:Q91WU0|EST1	49.65	14	239	NA	208
SLSLLYNVPAVAEEIQDE	P12023|A4_MOUSE	49.94	18	185	NA	NA
SLVHSSPHVALSHVD	Q9WV91|FPRP_MOUSE	49.31	15	294	NA	445
SLVNKGTLVQTKGTGAAGSFKLNKKAES	P43275|H11_MOUSE	49.95	29	1330	NA	1490

SLVSKGTLVQ	P43276|H15_MOUSE:P43274|H14_MOU	28.66	10	72.8	NA	165
SLVSKGTLVQT	P43276|H15_MOUSE:P43274|H14_MOU	34.31	11	338	NA	478
SLVSKGTLVQTK	P43276|H15_MOUSE:P43274|H14_MOU	48.4	12	617	83.3	739
SLVSKGTLVQTKG	P43276|H15_MOUSE:P43274|H14_MOU	48.53	13	1050	137	1550
SLVSKGTLVQTKGTG	P43276|H15_MOUSE:P43274|H14_MOU	49.54	15	779	NA	NA
SLVSKGTLVQTKGTGA	P43276|H15_MOUSE:P43274|H14_MOU	49.71	16	192	NA	NA
SLVSKGTLVQTKGTGASG	P43276|H15_MOUSE:P43274|H14_MOU	49.77	18	1290	NA	508
SLVSKGTLVQTKGTGASGSFK	P43276|H15_MOUSE:P43274|H14_MOU	49.94	21	772	NA	2050
SLVSKGTLVQTKGTGASGSFKLNK	P43276|H15_MOUSE:P43274|H14_MOU	49.95	24	1400	NA	1420
SLVSKGTLVQTKGTGASGSFKLNKK	P43276|H15_MOUSE:P43274|H14_MOU	49.95	25	5780	413	15700
SLVSKGTLVQTKGTGASGSFKLNKKA	P43276|H15_MOUSE:P43274|H14_MOU	49.95	26	308	NA	312
SLVSKGTLVQTKGTGASGSFKLNKKAAS	P43276|H15_MOUSE:P43274|H14_MOU	49.92	28	974	NA	2880
SLVSKGTLVQTKGTGASGSFKLNKKAAS	P43276|H15_MOUSE:P43274|H14_MOU	48.01	29	412	NA	998
SLVSKGTLVQTKGTGASGSFKLNKKAAS	P43276|H15_MOUSE:P43274|H14_MOU	26.11	30	165	NA	NA
SNDDDVYRAPPIDRSILPT	Q8BGD9|IF4B_MOUSE	49.84	19	341	NA	NA
SNDTTVLLPPYDDATAVPSTAKEPPPP	Q91XQ6|LAP4B_MOUSE	49.88	27	492	NA	680
SNHEQLPILG	P04441|HG2A_MOUSE	28.48	10	711	NA	319
SNIKIYNTPSASYLEV	P13595|NCAM1_MOUSE	45.52	16	177	NA	254
SNIYDLVAPFPSAPN	P09470|ACE_MOUSE	48.49	15	806	NA	39.1
SNIYDLVAPFPSAPNID	P09470|ACE_MOUSE	49.61	17	667	NA	2020
SNLLLQSPGVLTAARE	P20934|EVI2A_MOUSE	43.09	16	513	NA	NA
SNM(+15.99)TYEKL	Q3UPW2|ELF3_MOUSE	25.4	8	119	NA	NA
SNNSIM(+15.99)SNPVAGLVIG	Q9DBP0|NPT2B_MOUSE	48.65	16	1750	NA	698
SNNSIMSNPVAGLVIG	Q9DBP0|NPT2B_MOUSE	47.94	16	282	NA	684
SNPTSGSAANSSFG	Q8R317|UBQL1_MOUSE	43.28	14	437	NA	NA
SNPYTTVTPQIINSK	P57780|ACTN4_MOUSE	49.88	15	675	NA	737
SNSYGIPEPAHAYA	P47941|CRKL_MOUSE	43.18	14	879	NA	296
SNSYGIPEPAHAYAQPQ	P47941|CRKL_MOUSE	47.47	17	1480	NA	841
SPAEVFTLSVPNISLPAPS	Q3TYD6|LMTK2_MOUSE	48.87	19	446	NA	NA
SPAEYAGPEGSYFG	P43406|ITAV_MOUSE	41.82	14	313	NA	291
SPAKAKAPKAKASKPKA	P43277|H13_MOUSE	48.59	17	17300	NA	2890
SPAKAKAVKPKASKAKVTKPKTPAKPKK	P43275|H11_MOUSE	44.2	33	530	NA	NA
SPAKAKTVKPKAAKPKTSKPKAAKPKKT	P43274|H14_MOUSE	49.95	33	7770	NA	599
SPAPDSNPTSGSAANSSFG	Q8R317|UBQL1_MOUSE	49.45	19	1960	NA	292
SPAPSTRVITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.95	24	4860	60.4	8050
SPAPSTRVITNQYNSPTGLYSSENI	O70400|PDLI1_MOUSE	49.78	25	155	NA	464
SPAPSTRVITNQYNSPTGLYSSENIS	O70400|PDLI1_MOUSE	49.95	26	1040	NA	2500
SPAPSTRVITNQYNSPTGLYSSENISN	O70400|PDLI1_MOUSE	48.95	27	149	NA	923
SPARSHLYHPSSPWPIG	P97798|NEO1_MOUSE	25.18	17	162	NA	NA
SPATRKEYHTGKAVTSKG	E9PV24|FIBA_MOUSE	49.94	18	508	NA	633
SPATRKEYHTGKAVTSKGDK	E9PV24|FIBA_MOUSE	49.94	20	1510	NA	2520
SPATRKEYHTGKAVTSKGDKELLIGKEK	E9PV24|FIBA_MOUSE	49.55	28	149	NA	NA
SPAVAAAQAPAPTPALPP	P54728|RD23B_MOUSE	49.88	18	10300	NA	11700
SPAVAAAQAPAPTPALPPT	P54728|RD23B_MOUSE	49.88	19	11300	NA	11800
SPAVAAAQAPAPTPALPPTS	P54728|RD23B_MOUSE	38.46	20	1200	NA	1010
SPDDPSRYITPDQLADL	P17182|ENOA_MOUSE	49.22	17	581	NA	NA
SPDVDVISPTTQPSPT	Q9D8N1|CK024_MOUSE	43.08	16	781	NA	363
SPDVDVISPTTQPSPTLP	Q9D8N1|CK024_MOUSE	26.74	18	2330	NA	NA
SPDVDVISPTTQPSPTLPT	Q9D8N1|CK024_MOUSE	46.41	19	1030	NA	823
SPDVVYSPETIEAR	Q9JHU9|INO1_MOUSE	41.51	14	500	NA	381
SPDVVYSPETIEARYE	Q9JHU9|INO1_MOUSE	43.08	16	2150	NA	1860
SPDVVYSPETIEARYEY	Q9JHU9|INO1_MOUSE	48.75	17	73.6	NA	NA
SPEEVAPSPRASPA	Q8CH72|TRI32_MOUSE	38.37	14	3480	NA	1530
SPEEVAPSPRASPAK	Q8CH72|TRI32_MOUSE	41.61	15	342	NA	NA
SPEKVSDYISPLLSFAAE	Q9DBT4|ENTP4_MOUSE	42.54	18	262	NA	NA
SPGFSSEVYTFPVPERH	P09803|CADH1_MOUSE	49.9	17	636	NA	1490
SPGFSSEVYTFPVPERHLE	P09803|CADH1_MOUSE	48.94	19	743	NA	1720
SPGFSSEVYTFPVPERHLER	P09803|CADH1_MOUSE	40.07	20	2580	NA	4480
SPGFSSEVYTFPVPERHLERG	P09803|CADH1_MOUSE	49.94	21	63.7	NA	NA
SPGLKPASQQKAEASSPVPYLSPETTPA	P39447|ZO1_MOUSE	43.45	28	65.8	NA	545
SPGSSRTEVLVTPAGVASKR	P57016|LAD1_MOUSE	47.18	20	143	NA	NA
SPGYNPPQM(+15.99)NTLP	Q8K419|LEG4_MOUSE	44.01	13	1200	NA	703
SPGYNPPQM(+15.99)NTLPV	Q8K419|LEG4_MOUSE	43.14	14	2460	NA	2040
SPGYNPPQMNTLP	Q8K419|LEG4_MOUSE	36.25	13	288	NA	726
SPGYNPPQMNTLPV	Q8K419|LEG4_MOUSE	48.43	14	736	NA	1290
SPHPYQLPQALAPH	O89023|TPP1_MOUSE	49.64	14	624	NA	767
SPHPYQLPQALAPHVD	O89023|TPP1_MOUSE	49.41	16	5100	NA	4470
SPHPYQLPQALAPHVDF	O89023|TPP1_MOUSE	47.72	17	354	NA	NA
SPIKLPFFYSEPVNVLN	E9Q414|APOB_MOUSE	49.94	17	635	NA	307
SPIKLPFFYSEPVNVLNG	E9Q414|APOB_MOUSE	49.94	18	127	NA	262
SPITVEWRA	P06345|HB2S_MOUSE:P06346|HB2F_M	30.46	9	170	NA	239
SPKDRKKKEKKVAKVEPAVSSIVN	Q99PL5|RRBP1_MOUSE	29.83	24	112	NA	NA
SPKKAKAAAKPKKAAK	P43276|H15_MOUSE	49.82	16	12300	7490	3530
SPKKAKATKAKKAPK	P43274|H14_MOUSE	49.92	15	8380	1300	5720
SPKKAKATKAKKAPKSPAK	P43274|H14_MOUSE	49.94	19	788	NA	251
SPKKAKATKAKKAPKSPAKAK	P43274|H14_MOUSE	49.95	21	1130	8700	3400
SPKKPKVVKAKKVA	P43275|H11_MOUSE	49.64	14	573	NA	NA

SPKKPKVVKAKKVAK	P43275|H11_MOUSE	49.95	15	19100	6790	6130
SPKKPKVVKAKKVAKSPAK	P43275|H11_MOUSE	49.95	19	559	NA	619
SPKKVKAAKPKKAAKSPAKAKAPKAKAS	P43277|H13_MOUSE	44.05	32	822	NA	NA
SPKPLLQSPKPSPSARPS	Q6EDY6|CARL1_MOUSE	49.84	18	1400	NA	831
SPKVLPGPSQPRQYNNPIGLYSAET	Q9JKS4|LDB3_MOUSE	49.38	25	111	NA	NA
SPLIM(+15.99)SPGPIYAVDGD	Q8VHF2|CDHR5_MOUSE	49.78	16	46	NA	NA
SPLSISAALAIVSLGAK	P29621|SPA3C_MOUSE	48.13	17	181	NA	177
SPLSISAALALVSLGAK	Q03734|SPA3M_MOUSE:P07759|SPA3K	48.13	17	181	NA	177
SPM(+15.99)YPVVPVHLDGTF	P97425|ECP2_MOUSE:P97426|ECP1_M	46.83	15	281	135	258
SPNYAAPEVISGRL	Q5EG47|AAPK1_MOUSE:Q8BRK8|AAPK	45.9	14	1480	NA	1220
SPPESESEPYTFSHPNK	Q5U462|CDCP1_MOUSE	49.73	17	225	NA	345
SPPESESEPYTFSHPNKG	Q5U462|CDCP1_MOUSE	49.93	18	731	NA	NA
SPPESESEPYTFSHPNKGEIG	Q5U462|CDCP1_MOUSE	48.83	21	1510	NA	5950
SPPHVQFTYQQPQPL	B2RXS4|PLXB2_MOUSE	47.2	15	285	NA	1090
SPPHVQFTYQQPQPLS	B2RXS4|PLXB2_MOUSE	49.9	16	2940	NA	3120
SPPHVQFTYQQPQPLSVE	B2RXS4|PLXB2_MOUSE	49.86	18	982	NA	1500
SPPHVQFTYQQPQPLSVEP	B2RXS4|PLXB2_MOUSE	49.92	19	4100	NA	3980
SPPHVQFTYQQPQPLSVEPR	B2RXS4|PLXB2_MOUSE	49.95	20	292000	10900	299000
SPPPGGYGQPSVLPGG	Q8BJZ3|LFG3_MOUSE	25.69	16	468	NA	NA
SPPPGGYGQPSVLPGGYP	Q8BJZ3|LFG3_MOUSE	43.34	18	39300	NA	1480
SPPPGGYGQPSVLPGGYPA	Q8BJZ3|LFG3_MOUSE	44.27	19	12500	NA	NA
SPPPYAAYATPTPE	Q9QZC7|PKHB2_MOUSE	40.84	14	2380	NA	2650
SPPPYAAYATPTPEV	Q9QZC7|PKHB2_MOUSE	44.93	15	692	NA	535
SPPPYAAYATPTPEVY	Q9QZC7|PKHB2_MOUSE	49.51	16	5320	NA	6070
SPPPYAAYATPTPEVYG	Q9QZC7|PKHB2_MOUSE	49.57	17	79400	1110	15700
SPPPYAAYATPTPEVYGY	Q9QZC7|PKHB2_MOUSE	49.89	18	33800	428	45100
SPPPYAAYATPTPEVYGYG	Q9QZC7|PKHB2_MOUSE	49.89	19	40400	458	45200
SPPPYSSITVEAPTTSDTDV	Q91ZP6|NFIP2_MOUSE	49.83	20	231	NA	262
SPPPYSSITVEAPTTSDTDVY	Q91ZP6|NFIP2_MOUSE	49.37	21	1090	NA	1550
SPPQFQETPPLVLEVKE	Q05BQ1|TUTLA_MOUSE	49.91	17	2370	NA	2210
SPPQFQETPPLVLEVKEL	Q05BQ1|TUTLA_MOUSE	49.93	18	3460	NA	3290
SPPQFQETPPLVLEVKELE	Q05BQ1|TUTLA_MOUSE	49.94	19	211	NA	117
SPPSTPDSASAPSTTPASPA	Q99NB8|UBQL4_MOUSE	49.45	20	1300	NA	NA
SPPVSPAFSAPEPTGSRN	Q0MW30|NEU1B_MOUSE	49.59	18	791	NA	1350
SPPVTRVSPVPSPSQP	Q8VDP3|MICA1_MOUSE	43.29	16	55.7	NA	105
SPRKSVFFYPPYPDEIHG	P50428|ARSA_MOUSE	30.97	18	387	NA	247
SPRPGSDSGNFRPANPNWGVF	E9PV24|FIBA_MOUSE	48.99	21	197	NA	551
SPRPGSDSGNFRPANPNWGVFS	E9PV24|FIBA_MOUSE	48.1	22	271	NA	1280
SPRPGSDSGNFRPANPNWGVFSE	E9PV24|FIBA_MOUSE	48.3	23	616	NA	979
SPRTATLEIKGPQADLIDAV	Q8CAS9|PARP9_MOUSE	25.88	20	94	NA	117
SPRYPPFSPPEPQLSSPA	Q5SSZ5|TENS3_MOUSE	44.61	18	210	NA	NA
SPSSAFTPAHAATSSHA	Q8CI51|PDLI5_MOUSE	48.82	17	90.2	NA	NA
SPTSSATYQPSFAAAVRS	Q8BKX6|SMG1_MOUSE	45.11	18	74.1	NA	NA
SPTVHFTPAEISRSVF	Q9QXH4|ITAX_MOUSE	44.46	16	66.9	NA	NA
SPTVHFTPAEISRSVFE	Q9QXH4|ITAX_MOUSE	44.26	17	931	35.1	299
SPVPYLSPETTPAS	P39447|ZO1_MOUSE	46.56	14	970	NA	1140
SPVPYLSPETTPASSA	P39447|ZO1_MOUSE	48.86	16	5020	NA	7320
SPVYKNPTPGSSE	Q99PG0|AAAD_MOUSE	48.66	13	1760	NA	573
SPVYKNPTPGSSEL	Q99PG0|AAAD_MOUSE	48.58	14	499	NA	440
SPYINPIIPFTGP	O08573|LEG9_MOUSE	37.84	13	1380	NA	2250
SPYINPIIPFTGPI	O08573|LEG9_MOUSE	47.48	14	6780	NA	1720
SPYINPIIPFTGPIQ	O08573|LEG9_MOUSE	45.94	15	75.9	NA	NA
SPYSSGFNSPSSTPVRPP	Q8CI08|SLAI2_MOUSE	49.04	18	1740	NA	1920
SPYSYSTTAVVSNPQ	P07309|TTHY_MOUSE	30.66	15	107	NA	NA
SQASIYSPPAAAAAAAA	P70297|STAM1_MOUSE	49.37	17	448	NA	340
SQELVRAPTAALSPEPQ	D3YXK2|SAFB1_MOUSE:Q80YR5|SAFB	45.52	17	382	NA	488
SQFEFKGPQAAQEQD	Q6RHR9|MAGI1_MOUSE	49.87	15	2650	NA	1970
SQFEFKGPQAAQEQDF	Q6RHR9|MAGI1_MOUSE	49.88	16	982	NA	787
SQIFSQAMAARSINRP	P34914|HYES_MOUSE	40.27	16	619	NA	NA
SQPAAYVAQPATAAAYASQPA	Q8C2Q3|RBM14_MOUSE	41.02	21	56.4	NA	736
SQPLPSLPGGPP	Q8C0Z1|F234A_MOUSE	38.31	12	349	NA	290
SRIEYEPGTGALAVFPS	Q9EPL2|CSTN1_MOUSE	25.9	17	482	NA	354
SRPVQFPYVTPAPHEPVK	Q9D074|MGRN1_MOUSE	49.64	18	131	NA	227
SRTEVLVTPAGVASKR	P57016|LAD1_MOUSE	30.68	16	103	NA	NA
SRTPGNRIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	49.85	21	134	634	1630
SRTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	49.66	22	741	691	2150
SRVQIYHNPTAN	P70460|VASP_MOUSE	41.41	12	126	NA	NA
SRVQIYHNPTANSF	P70460|VASP_MOUSE	48.23	14	143	NA	375
SRVQIYHNPTANSFR	P70460|VASP_MOUSE	45.21	15	5730	NA	7280
SRVQIYHNPTANSFRV	P70460|VASP_MOUSE	49.93	16	8940	NA	8390
SRVQIYHNPTANSFRVV	P70460|VASP_MOUSE	49.2	17	394	NA	NA
SSEFYSQPGALPPPP	Q91XT4|SC16B_MOUSE	49.66	15	2930	NA	1750
SSEFYSQPGALPPPPT	Q91XT4|SC16B_MOUSE	49.5	16	710	NA	363
SSENYISPRTLTSQS	Q9WV66|MARH7_MOUSE	35.81	15	719	NA	1010
SSEVYTFPVPERH	P09803|CADH1_MOUSE	48.29	13	4540	NA	5790
SSEVYTFPVPERHLE	P09803|CADH1_MOUSE	49.8	15	22100	451	25100
SSEVYTFPVPERHLER	P09803|CADH1_MOUSE	45.7	16	1430	NA	1330

SSGIYKAAFPLHD	Q6P9J9|ANO6_MOUSE	48.33	13	277	NA	83.2
SSIASFKDPKISTSLPV	Q61233|PLSL_MOUSE	49.88	17	5370	567	4610
SSITVEAPTTSDTDV	Q91ZP6|NFIP2_MOUSE	42.02	15	86.2	NA	NA
SSKNVFLSPM(+15.99)SISS	Q60854|SPB6_MOUSE	37.15	14	343	NA	NA
SSKNVFLSPM(+15.99)SISSA	Q60854|SPB6_MOUSE	45.9	15	307	NA	389
SSKNVFLSPM(+15.99)SISSAL	Q60854|SPB6_MOUSE	48.08	16	708	NA	290
SSKNVFLSPMSISS	Q60854|SPB6_MOUSE	45.6	14	109	NA	372
SSKNVFLSPMSISSA	Q60854|SPB6_MOUSE	42.68	15	225	NA	1210
SSKNVFLSPMSISSAL	Q60854|SPB6_MOUSE	48.44	16	235	NA	665
SSLAAPTVEAAAS	Q91ZP6|NFIP2_MOUSE	38.07	13	169	NA	297
SSM(+15.99)NYTGPRTNLG	Q32NZ6|TMC5_MOUSE	45.9	13	430	NA	NA
SSM(+15.99)NYTGPRTNLGYL	Q32NZ6|TMC5_MOUSE	49.43	15	24600	1000	14000
SSM(+15.99)NYTGPRTNLGYLG	Q32NZ6|TMC5_MOUSE	49.89	16	6640	128	4390
SSMNYTGPRTNLG	Q32NZ6|TMC5_MOUSE	44.03	13	239	NA	376
SSMNYTGPRTNLGYL	Q32NZ6|TMC5_MOUSE	48.63	15	5210	NA	10200
SSMNYTGPRTNLGYLG	Q32NZ6|TMC5_MOUSE	49.87	16	2370	NA	3440
SSPAVAAAQAPAPTPALPPTS	P54728|RD23B_MOUSE	48.51	21	371	NA	705
SSPLPEEAQDVT	Q8BYI8|F234B_MOUSE	28.39	12	95.8	NA	NA
SSQFFPRSPSANEN	Q3USJ8|FCSD2_MOUSE	29.65	14	106	NA	NA
SSRIEYEPGTGALAVFPS	Q9EPL2|CSTN1_MOUSE	29.44	18	181	NA	NA
SSRSFTSGPGARISSSSF	P11679|K2C8_MOUSE	43.6	18	719	NA	1070
SSSNYHSFVPSSASVD	Q811P8|RHG32_MOUSE	45.01	16	417	NA	525
SSSSFSAAIPTRTST	Q80XQ2|TBCD5_MOUSE	41.66	15	314	NA	375
SSSSFSAAIPTRTSTE	Q80XQ2|TBCD5_MOUSE	29.76	16	368	NA	399
SSVAFIKPGVNKAEVT	Q18PI6|SLAF5_MOUSE	28.53	16	178	NA	NA
SSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	36.46	12	808	NA	707
SSYKYDSL	Q6T3U4|NPCL1_MOUSE	29.04	8	347	NA	100
SSYSNPTIGYENR	Q07797|LG3BP_MOUSE	48.9	13	208	NA	NA
STDYGNFLANEASP	P51863|VA0D1_MOUSE	49.69	14	860	NA	568
STDYGNFLANEASPL	P51863|VA0D1_MOUSE	49.28	15	4600	NA	1830
STKKTPKKAKKP	P43274|H14_MOUSE	48.49	12	1410	NA	729
STKKTPKKAKKPA	P43274|H14_MOUSE	49.9	13	2760	2920	8380
STKKTPKKAKKPAAAAGAKKAK	P43274|H14_MOUSE	49.95	22	1050	952	2460
STKKTPKKAKKPAAAAGAKKAKS(+79.9	P43274|H14_MOUSE	38.92	28	109	NA	NA
STLIWAAPRLQSEVA	Q9CX00|IST1_MOUSE	36.19	15	1190	NA	1320
STLWSSPLPEEAQD	Q8BYI8|F234B_MOUSE	47.02	14	192	NA	NA
STPFQFRAASPVEE	Q3UKC1|TAXB1_MOUSE	47.79	14	1020	NA	1130
STPFQFRAASPVEEL	Q3UKC1|TAXB1_MOUSE	47.14	15	915	NA	1240
STPFQFRAASPVEELL	Q3UKC1|TAXB1_MOUSE	49.7	16	797	NA	1870
STPFQFRAASPVEELLT	Q3UKC1|TAXB1_MOUSE	48.49	17	302	NA	514
STRVITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.94	20	1710	NA	2540
STRVITNQYNSPTGLYSSENI	O70400|PDLI1_MOUSE	49.54	21	41	NA	147
STRVITNQYNSPTGLYSSENIS	O70400|PDLI1_MOUSE	49.95	22	451	NA	1060
STSSLAAPTVEAAAS	Q91ZP6|NFIP2_MOUSE	41.21	15	1340	NA	1240
STSSLAAPTVEAAASA	Q91ZP6|NFIP2_MOUSE	41.07	16	924	NA	538
STSSLAAPTVEAAASAP	Q91ZP6|NFIP2_MOUSE	40.14	17	1310	NA	1650
STSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	49.07	18	1440	NA	1010
STSYSGPYPAAAPP	Q9WVH9|FBLN5_MOUSE	40.73	14	584	NA	185
STSYSGPYPAAAPPVP	Q9WVH9|FBLN5_MOUSE	39.49	16	312	NA	145
SVAPYGGPSSSPAEEG	P10493|NID1_MOUSE	44.05	16	1220	NA	NA
SVAPYGGPSSSPAEEGK	P10493|NID1_MOUSE	49.52	17	640	NA	NA
SVASQAPQSLPAISQPP	Q99LI8|HGS_MOUSE	32.16	17	715	NA	603
SVATNPIITPVAQENQ	P08226|APOE_MOUSE	49.48	16	3000	NA	2650
SVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	36.87	11	6500	NA	3210
SVEAPSVSPARH	Q8BUJ9|LRP12_MOUSE	28.05	12	183	NA	NA
SVEFIAPTLEGTYT	P97432|NBR1_MOUSE	31.26	14	56.1	NA	NA
SVFVAPAVTPV	P70158|ASM3A_MOUSE	40.88	11	1360	NA	982
SVFVAPAVTPVK	P70158|ASM3A_MOUSE	46.67	12	265000	25300	229000
SVFVAPAVTPVKG	P70158|ASM3A_MOUSE	48.63	13	144000	17400	131000
SVFVAPAVTPVKGV	P70158|ASM3A_MOUSE	48.84	14	12300	448	11200
SVFVAPAVTPVKGVL	P70158|ASM3A_MOUSE	49.66	15	15500	NA	11400
SVGSIGPLPNLDLEE	O55111|DSG2_MOUSE	47	15	1010	NA	240
SVHAVFSAPAIPSGTG	Q8BMS2|SPON2_MOUSE	47.06	16	71.6	NA	33.9
SVHTYVGGLPEVSVIS	Q61592|GAS6_MOUSE	27.83	16	160	NA	167
SVILPEETPTASASADTPH	E9Q7D5|ARHG5_MOUSE	49.35	19	773	NA	819
SVLYLASPLASYVSG	Q9WV68|DECR2_MOUSE	49.42	15	415	NA	239
SVPATFAPSPTPAVV	Q9DBG3|AP2B1_MOUSE	25.57	15	41	NA	NA
SVPATFAPSPTPAVVS	Q9DBG3|AP2B1_MOUSE	49.11	16	2450	NA	264
SVPNVHGALAPLAIPSAAAA	P17225|PTBP1_MOUSE	29.06	20	196	NA	NA
SVPNVHGALAPLAIPSAAAAA	P17225|PTBP1_MOUSE	42.26	21	515	NA	671
SVPPSVSPSPATAFSG	Q3UPH1|PRRC1_MOUSE	49.65	16	1400	NA	1410
SVPPSVSPSPATAFSGPP	Q3UPH1|PRRC1_MOUSE	49.76	18	5140	NA	NA
SVRIGSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	49.85	23	377	NA	1090
SVTTDHISPAGNIARNSPA	P28271|ACOHC_MOUSE	49.72	19	451	NA	205
SVTYYGPSGQKTIYS	Q61490|CD166_MOUSE	34.72	15	74.7	NA	NA
SVYVVAPPNSYPVVPG	Q99N10|M4A8_MOUSE	49.68	16	1430	NA	NA
SVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.84	14	1550	9630	1160

SYLGPDVNQAL	Q6T3U4|NPCL1_MOUSE	44.89	11	265	NA	190
SYLGPDVNQALVL	Q6T3U4|NPCL1_MOUSE	45.5	13	122	NA	NA
SYLLAALGGNSSPSAKDIKK	P99027|RLA2_MOUSE	48.92	20	72	NA	NA
SYLYPLATNIPN	Q9DBX3|SUSD2_MOUSE	48.32	12	315	NA	221
SYPSQASIYSPPAAAAAAAA	P70297|STAM1_MOUSE	49.76	20	672	NA	1210
SYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.42	16	156	572	234
T(+42.01)EWEAATPAVAETPDIK	P97461|RS5_MOUSE	49.86	17	379	NA	1800
T(+42.01)GMAFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.92	16	414	NA	NA
T(+42.01)SRKKVLLKVIILG	P51150|RAB7A_MOUSE	48.98	14	73.2	NA	1730
T(+42.01)SYSYRQTSAM(+15.99)SSFG	P19001|K1C19_MOUSE	48.9	15	640	NA	605
T(+42.01)VKPKAAKPKTSKPKAAKPKKT/	P43274|H14_MOUSE	49.95	27	2200	9550	7980
TAGAKKTVKKTPKKAK	P43276|H15_MOUSE	49.89	16	447	NA	NA
TAGAKKTVKKTPKKAKKP	P43276|H15_MOUSE	49.93	18	886	NA	NA
TAGAKKTVKKTPKKAKKPA	P43276|H15_MOUSE	49.95	19	153	NA	NA
TAKGLFRAAVPSGA	P17183|ENOG_MOUSE:P17182|ENOA_M	40.37	14	178	NA	319
TAKGLFRAAVPSGAS	P17183|ENOG_MOUSE:P17182|ENOA_M	49.2	15	2120	NA	2540
TAKGLFRAAVPSGAST	P17183|ENOG_MOUSE:P17182|ENOA_M	49.77	16	30600	762	32900
TAKGLFRAAVPSGASTG	P17183|ENOG_MOUSE:P17182|ENOA_M	49.8	17	16500	149	17100
TAKGLFRAAVPSGASTGIY	P17183|ENOG_MOUSE:P17182|ENOA_M	49.57	19	124	NA	NA
TAKKSTKKTPKKAKKP	P43274|H14_MOUSE	49.95	16	3310	NA	2310
TAKKSTKKTPKKAKKPA	P43274|H14_MOUSE	49.95	17	14400	4180	16400
TAKKSTKKTPKKAKKPAA	P43274|H14_MOUSE	48.95	18	2140	956	3730
TAKPKAAKAKKAVSKKK	P43276|H15_MOUSE	49.94	17	7330	6910	256
TAKPSGYNPPISILGILE	Q61739|ITA6_MOUSE	36.34	18	81	NA	NA
TASNVEEAFINTAKE	P53994|RAB2A_MOUSE	48.67	15	459	NA	404
TASNVEEAFINTAKEIYE	P53994|RAB2A_MOUSE	49.86	18	155	NA	NA
TASVM(+15.99)SAPAALAVAKL	Q9ERH8|S28A3_MOUSE	49.61	16	207	NA	NA
TATAKKSTKKTPKKAKKPA	P43274|H14_MOUSE	49.95	19	7140	NA	3760
TATAKKSTKKTPKKAKKPAA	P43274|H14_MOUSE	49.94	20	1330	NA	NA
TATYKLSAPWVEQEGP	P14432|HA1T_MOUSE	48.68	16	342	NA	375
TATYKLSAPWVEQEGPE	P14432|HA1T_MOUSE	49.9	17	3000	NA	4060
TDANYRQPILVAL	P14246|GTR2_MOUSE	36.95	13	365	NA	264
TDDVFSPSHAIPI	Q91ZH7|ABHD3_MOUSE	42.63	13	67.3	NA	NA
TDDVFSPSHAIPIE	Q91ZH7|ABHD3_MOUSE	43.02	14	419	NA	163
TDDVFSPSHAIPIET	Q91ZH7|ABHD3_MOUSE	48.76	15	3330	NA	1740
TDKQYHDGLPHFVVT	P97927|LAMA4_MOUSE	29.14	15	227	NA	NA
TDPIQKYLTPQM(+15.99)ATS	Q6P9J9|ANO6_MOUSE	30.09	15	234	NA	NA
TDPIQKYLTPQM(+15.99)ATSIT	Q6P9J9|ANO6_MOUSE	48.97	17	4390	NA	2280
TDPIQKYLTPQM(+15.99)ATSITA	Q6P9J9|ANO6_MOUSE	31.22	18	445	NA	NA
TDPIQKYLTPQMATSIT	Q6P9J9|ANO6_MOUSE	49.87	17	2310	NA	2740
TDPIQKYLTPQMATSITA	Q6P9J9|ANO6_MOUSE	47.24	18	168	NA	NA
TDRKIVYEGPELNHAFG	Q91ZX7|LRP1_MOUSE	49.91	17	10500	NA	13700
TDRQVWSGSKAAGAPPK	Q8K2C7|OS9_MOUSE	48.72	17	85.8	NA	279
TDSDNDHLTYGISGPNASYFS	E9Q7P9|CDHR2_MOUSE	36.37	21	177	NA	NA
TDSGFTFSSPNFATIP	Q8BMS2|SPON2_MOUSE	25.6	16	328	NA	NA
TDSGFTFSSPNFATIPQ	Q8BMS2|SPON2_MOUSE	49.02	17	1070	NA	NA
TDSVVSSVTTKAKGVA	Q9JJX6|P2RX4_MOUSE	47.86	16	153	NA	86.6
TDYNSPEAGNIF	B2RXV4|FLVC1_MOUSE	43.66	12	494	NA	NA
TEDDYNEPTVHFAEDT	Q80U72|SCRIB_MOUSE	40.44	16	1380	NA	NA
TEDNVFEAPTLVKVF	Q61490|CD166_MOUSE	49.17	15	74.6	NA	105
TEEIKTPEPLEEGPA	Q6EDY6|CARL1_MOUSE	44.25	15	72.3	NA	NA
TEEQYQDFEARYVQAK	O70228|ATP9A_MOUSE	45.24	16	174	NA	206
TEGRLEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	49.84	19	581	NA	804
TELDQLFSGPLPGRLP	Q60805|MERTK_MOUSE	48.85	16	225	NA	56.1
TELDQLFSGPLPGRLPVN	Q60805|MERTK_MOUSE	49.88	18	191	NA	201
TFPQYETSSATTSPF	Q9QZS3|NUMB_MOUSE	25.58	15	855	NA	NA
TFPQYETSSATTSPFF	Q9QZS3|NUMB_MOUSE	28.56	16	474	NA	NA
TFSRTTKAVVVKKIETRDGKLVSE	P11679|K2C8_MOUSE	36.05	24	366	NA	NA
TFSRTTKAVVVKKIETRDGKLVSESS	P11679|K2C8_MOUSE	28.39	26	180	NA	NA
TFTDVAPRGVESGQR	Q8JZQ5|AOC1_MOUSE	38.41	15	691	NA	391
TFYKVIPKSKFVLV	P57759|ERP29_MOUSE	49.54	14	148	NA	NA
TFYKVIPKSKFVLVKF	P57759|ERP29_MOUSE	49.94	16	1800	NA	1240
TGGGSVRIGSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	49.94	27	1680	NA	2700
TGGLPDYSAPNPIKVTHR	Q8CFG0|SULF2_MOUSE	49.33	18	527	NA	1390
TGGYRYPRALEEEV	Q8K3K8|OPTN_MOUSE	40.34	14	23400	NA	23300
TGGYRYPRALEEEVE	Q8K3K8|OPTN_MOUSE	32.13	15	7190	NA	NA
TGLDFHSPRIA	Q9JLB4|CUBN_MOUSE	40.11	11	563	NA	623
TGLDFHSPRIAQ	Q9JLB4|CUBN_MOUSE	47.59	12	2550	NA	917
TGLDFHSPRIAQL	Q9JLB4|CUBN_MOUSE	45.92	13	586	NA	911
TGM(+15.99)AFRVPTPNVS	P16858|G3P_MOUSE:Q64467|G3PT_MC	47.58	13	10700	152	6960
TGM(+15.99)AFRVPTPNVSV	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.74	14	9070	409	8710
TGM(+15.99)AFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.84	15	44100	605	35100
TGM(+15.99)AFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.9	16	793000	507	490000
TGM(+15.99)AFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.92	17	19400	463	13900
TGM(+15.99)AFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.85	18	5300	NA	2900
TGMAFRVPTPNVS	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.02	13	5710	NA	7240
TGMAFRVPTPNVSV	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.68	14	5350	NA	9860

TGMAFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.87	15	12600	NA	32200
TGMAFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.84	16	362000	6200	478000
TGMAFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.88	17	8670	NA	10000
TGMAFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MC	48.96	18	408000	NA	358000
TGPDGKGM(+15.99)NPPSYYTQPVPVP	Q9JLJ0|LITAF_MOUSE	49.95	24	715	NA	1050
TGPDGKGM(+15.99)NPPSYYTQPVPVP	Q9JLJ0|LITAF_MOUSE	49.35	25	1410	NA	1790
TGPPPYHESLAGASQPP	Q9D7I0|SHSA5_MOUSE	37.69	17	2410	NA	7340
TGQEYKPGNPSAAAVQ	Q8CGC7|SYEP_MOUSE	49.72	16	1070	NA	NA
TGVPTVPLLPPQVNQSL	Q99JX3|GORS2_MOUSE	42.21	17	150	NA	NA
TGVPTVPLLPPQVNQSLA	Q99JX3|GORS2_MOUSE	45.28	18	499	NA	433
TGYPTAYPAAAPAYNPS	Q8BGZ2|F168A_MOUSE	49.3	17	3410	NA	2050
THDLYIQSHISENR	Q9R111|GUAD_MOUSE	49.8	14	2740	NA	1300
THDLYIQSHISENRE	Q9R111|GUAD_MOUSE	49.82	15	11800	254	6490
THDLYIQSHISENREE	Q9R111|GUAD_MOUSE	49.84	16	12900	NA	6820
THDLYIQSHISENREEI	Q9R111|GUAD_MOUSE	49.84	17	177	NA	NA
THDLYIQSHISENREEIE	Q9R111|GUAD_MOUSE	48.09	18	280	NA	NA
THGGEDVAIFARGPQAHLVHGVQ	P24822|PPBI_MOUSE	49.94	23	421	NA	471
TIAGGGVIPHIHKSLIGKKGQQK	Q3THW5|H2AV_MOUSE:P0C0S6|H2AZ_	29.51	23	149	NA	NA
TIAYLTPLPQPNR	Q91VS7|MGST1_MOUSE	41.62	13	118	NA	NA
TIAYLTPLPQPNRG	Q91VS7|MGST1_MOUSE	46.57	14	153	NA	89.3
TIEDIEVAPPKAHEVR	P00329|ADH1_MOUSE	49.21	16	1480	NA	1320
TIEDIEVAPPKAHEVRIK	P00329|ADH1_MOUSE	49.82	18	640	NA	513
TIEFRGPNGLLVYQ	Q9DCN2|NB5R3_MOUSE	40.1	14	1760	NA	1300
TIEFRGPNGLLVYQG	Q9DCN2|NB5R3_MOUSE	47.34	15	3190	NA	2560
TIEFRGPNGLLVYQGK	Q9DCN2|NB5R3_MOUSE	49.73	16	1290	NA	1200
TIPFYTPIPN	O08573|LEG9_MOUSE	27.84	10	944	NA	685
TIPFYTPIPNG	O08573|LEG9_MOUSE	40.06	11	30800	NA	31000
TIPFYTPIPNGL	O08573|LEG9_MOUSE	29.57	12	977	NA	473
TIPFYTPIPNGLY	O08573|LEG9_MOUSE	44.88	13	681	NA	361
TIPFYTPIPNGLYP	O08573|LEG9_MOUSE	48.38	14	12800	477	16900
TIPFYTPIPNGLYPS	O08573|LEG9_MOUSE	47.16	15	20300	521	11300
TIPFYTPIPNGLYPSK	O08573|LEG9_MOUSE	47.7	16	216	NA	164
TIRYM(+15.99)APEVLEGAV	O35607|BMPR2_MOUSE	35.92	14	405	NA	259
TIRYM(+15.99)APEVLEGAVN	O35607|BMPR2_MOUSE	48.85	15	1870	NA	606
TIRYMAPEVLEGAV	O35607|BMPR2_MOUSE	43.62	14	115	NA	184
TIRYMAPEVLEGAVN	O35607|BMPR2_MOUSE	46.7	15	324	NA	337
TITSWYSPDAKFQK	Q9QZI9|SERC3_MOUSE	41.63	14	244	NA	254
TITYESSQVDPGADL	Q9WV92|E41L3_MOUSE	47.12	15	375	NA	327
TKAQKKDGKKRKRSRKESYSVYVYKVL	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	49.95	33	4140	13000	1910
TKFLPNAPKALIVEPS	Q91VR5|DDX1_MOUSE	49.86	16	1630	NA	NA
TKKFRFEEPVVLPDLS	Q01705|NOTC1_MOUSE	27.13	16	623	NA	792
TKKFRFEEPVVLPDLSD	Q01705|NOTC1_MOUSE	43.87	17	741	NA	411
TKKVAKSPKKAKVTK	P15864|H12_MOUSE	36.91	15	222	NA	NA
TKKVAKSPKKAKVTKPKKVK	P15864|H12_MOUSE	49.95	20	1410	NA	NA
TKKVAKSPKKAKVTKPKKVKSASKAVKP	P15864|H12_MOUSE	49.95	30	3330	NA	NA
TKNLDYVATSIHEAVT	P05201|AATC_MOUSE	49.25	16	85.7	NA	160
TKNLDYVATSIHEAVTK	P05201|AATC_MOUSE	49.88	17	1180	NA	1110
TKPKKVKSASKAVKPKAAKPKVAKAKKV	P15864|H12_MOUSE	49.95	33	623	NA	NA
TKPKTPAKPKKAAPKK	P43275|H11_MOUSE	45.16	16	41.9	NA	NA
TKQTARKSTGGKAPRK	P02301|H3C_MOUSE:P68433|H31_MOU	26.14	16	1890	NA	NA
TKRYM(+15.99)APEVLDETIN	Q61271|ACV1B_MOUSE	49.1	15	3670	NA	1110
TKRYM(+15.99)APEVLDETIQ	P37172|ACVR1_MOUSE	46.15	15	246	NA	NA
TKRYMAPEVLDETIN	Q61271|ACV1B_MOUSE	49.5	15	5200	NA	1670
TKRYMAPEVLDETIQ	P37172|ACVR1_MOUSE	42.46	15	109	NA	236
TLFHNPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	48.01	16	720	300	1580
TLPPVSPPKAALSVDE	Q6NZJ6|IF4G1_MOUSE	49.93	16	1720	NA	1490
TLQVLRPGLVVVH	Q9D3D9|ATPD_MOUSE	48.12	13	461	380	1990
TLRLRRQPKYPRKSAPRRNKLDHYAIIKP	P62751|RL23A_MOUSE	29.33	29	873	NA	NA
TM(+15.99)SKKKKKKKKP	Q99L45|IF2B_MOUSE	49.28	12	4090	27800	32000
TMTIHNGMFFSTYDR	Q8K0E8|FIBB_MOUSE	47.14	15	1720	NA	NA
TMTIHNGMFFSTYDRDNDGWVTTDPR	Q8K0E8|FIBB_MOUSE	49.94	26	437	NA	NA
TNDRYVASLAARNK	Q00560|IL6RB_MOUSE	43.92	14	5000	457	4220
TNDRYVASLAARNKV	Q00560|IL6RB_MOUSE	44.09	15	3870	682	4080
TNDRYVASLAARNKVG	Q00560|IL6RB_MOUSE	48.55	16	5300	991	4290
TNLHYSAPLPASLDT	Q91X84|CRTC3_MOUSE	43.36	15	244	NA	195
TNM(+15.99)YNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	49.64	16	1100	NA	516
TNNQDFRGSAGAPSVEN	P49443|PPM1A_MOUSE	36.96	17	69.4	NA	NA
TNNQDFRGSAGAPSVENV	P49443|PPM1A_MOUSE	49.84	18	728	NA	818
TNPIITPVAQENQ	P08226|APOE_MOUSE	46.63	13	4150	110	2360
TNQYNSPTGLYSS	O70400|PDLI1_MOUSE	48.61	13	458	NA	363
TNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.48	15	1380	NA	827
TNTAYVGSAILSEE	Q9QZC7|PKHB2_MOUSE	44.12	14	816	NA	1320
TNTAYVGSAILSEET	Q9QZC7|PKHB2_MOUSE	47.43	15	4510	546	5360
TNVKQFIAPETSEGVS	Q9EPS3|GLCE_MOUSE	41.85	16	205	NA	325
TPAAEAKAAEAAASAY	P97765|WBP2_MOUSE	49.71	16	103	NA	NA
TPAAPTSALGPKASPAP	Q8K0V4|CNOT3_MOUSE	38.51	17	167	NA	151
TPAAPTSALGPKASPAPS	Q8K0V4|CNOT3_MOUSE	48.79	18	2060	NA	1830

TPAAPTSALGPKASPAPSH	Q8K0V4|CNOT3_MOUSE	49.58	19	1710	NA	1040
TPAHAATSSHASPTPVAAATPL	Q8CI51|PDLI5_MOUSE	49.94	22	268	NA	NA
TPAKPKKAAPKKK	P43275|H11_MOUSE	49.84	13	1370	NA	376
TPAPSAPAAASATSPSPAPSSGNG	Q9JKV1|ADRM1_MOUSE	48.76	24	289	NA	532
TPAPTPAATPAASPAPVS	Q9DCH4|EIF3F_MOUSE	47.24	18	227	NA	NA
TPARAPETRSQVTPSVPSEALDD	Q7TQH7|LRP10_MOUSE	49.94	23	78	NA	NA
TPARAPETRSQVTPSVPSEALDDST	Q7TQH7|LRP10_MOUSE	48.82	25	434	NA	306
TPATNEAPQATVFP	P14434|HA2B_MOUSE:P01910|HA2K_M	43.79	14	72.8	NA	NA
TPATNEAPQATVFPK	P14434|HA2B_MOUSE:P01910|HA2K_M	49.01	15	694	NA	528
TPATNEAPQATVFPKSPV	P14434|HA2B_MOUSE:P01910|HA2K_M	49.76	18	231	NA	NA
TPAYTIPFYTPIPN	O08573|LEG9_MOUSE	47.78	14	3250	NA	1880
TPAYTIPFYTPIPNG	O08573|LEG9_MOUSE	48.4	15	49900	1510	36800
TPAYTIPFYTPIPNGL	O08573|LEG9_MOUSE	49.61	16	2300	NA	711
TPAYTIPFYTPIPNGLY	O08573|LEG9_MOUSE	49.44	17	606	NA	344
TPAYTIPFYTPIPNGLYP	O08573|LEG9_MOUSE	49.81	18	20000	NA	26800
TPAYTIPFYTPIPNGLYPS	O08573|LEG9_MOUSE	49.9	19	30700	315	43400
TPAYTIPFYTPIPNGLYPSK	O08573|LEG9_MOUSE	44.97	20	174	NA	NA
TPDPNTAYASYPSASVE	O55101|SNG2_MOUSE	49.43	17	1780	NA	2120
TPDPNTAYASYPSASVEN	O55101|SNG2_MOUSE	49.78	18	4510	NA	5020
TPDPNTAYASYPSASVENY	O55101|SNG2_MOUSE	49.81	19	668	NA	1010
TPDPNTAYASYPSASVENYQ	O55101|SNG2_MOUSE	49.93	20	183	NA	221
TPDPNTAYASYPSASVENYQQPP	O55101|SNG2_MOUSE	49.9	23	190	NA	366
TPDYIAPEIIAYQP	P63318|KPCG_MOUSE:P20444|KPCA_M	42.65	14	122	NA	171
TPDYIAPEIIAYQPY	P63318|KPCG_MOUSE:P20444|KPCA_M	49.76	15	1200	NA	582
TPDYIAPEILQG	P28867|KPCD_MOUSE	38.31	12	655	NA	378
TPDYIAPEILQGLK	P28867|KPCD_MOUSE	43.09	14	877	NA	717
TPDYISPEILQAM(+15.99)E	Q80UW5|MRCKG_MOUSE:Q7TT50|MRC	44.97	14	128	NA	NA
TPDYISPEILQAM(+15.99)ED	Q7TT50|MRCKB_MOUSE:Q3UU96|MRC	45.38	15	217	NA	NA
TPEFVAPEVINYE	Q6PDN3|MYLK_MOUSE	43.91	13	221	NA	NA
TPEFVAPEVINYEPI	Q6PDN3|MYLK_MOUSE	49.24	15	1640	NA	905
TPESFLGPNAALVD	Q80VP1|EPN1_MOUSE	45.89	14	2430	NA	1600
TPESFLGPNAALVDL	Q80VP1|EPN1_MOUSE	46.91	15	4940	NA	3260
TPESFLGPNAALVDLD	Q80VP1|EPN1_MOUSE	49.01	16	15600	545	8510
TPESFLGPNAALVDLDS	Q80VP1|EPN1_MOUSE	49.53	17	156	NA	NA
TPESFLGPNAALVNLD	Q8CHU3|EPN2_MOUSE	49.7	16	128	NA	52.4
TPEYLAPEIILSK	P68181|KAPCB_MOUSE:P05132|KAPCA	47.55	13	4350	NA	3450
TPEYLAPEIILSKG	P68181|KAPCB_MOUSE:P05132|KAPCA	49.61	14	19000	243	15500
TPEYLAPEIILSKGYN	P68181|KAPCB_MOUSE:P05132|KAPCA	48.33	16	745	NA	509
TPEYVAPEVILN	Q61410|KGP2_MOUSE	43.31	12	442	NA	NA
TPEYVAPEVILNK	Q61410|KGP2_MOUSE	48.3	13	2970	NA	2030
TPEYVAPEVILNKG	Q61410|KGP2_MOUSE	47.36	14	12800	NA	10700
TPEYVAPEVILNKGHD	Q61410|KGP2_MOUSE	48	16	622	NA	537
TPFM(+15.99)PPDPDVSPM(+15.99)	P34914|HYES_MOUSE	36.11	13	175	NA	NA
TPFQFRAASPVE	Q3UKC1|TAXB1_MOUSE	43.25	12	182	NA	291
TPFQFRAASPVEE	Q3UKC1|TAXB1_MOUSE	47.8	13	9120	276	11200
TPFQFRAASPVEEL	Q3UKC1|TAXB1_MOUSE	48.36	14	8210	188	10400
TPFQFRAASPVEELL	Q3UKC1|TAXB1_MOUSE	49.8	15	9830	NA	9110
TPFQFRAASPVEELLT	Q3UKC1|TAXB1_MOUSE	42.84	16	478	NA	195
TPFYKPSHAGELS	Q6DYE8|ENPP3_MOUSE	44.84	13	112	NA	NA
TPFYKPSHAGELSTPA	Q6DYE8|ENPP3_MOUSE	42.59	16	1010	NA	189
TPGGPRIRGNVYIHPTAKVAPS	Q922H4|GMPPA_MOUSE	49.89	22	12600	460	19800
TPGGPRIRGNVYIHPTAKVAPSA	Q922H4|GMPPA_MOUSE	49.87	23	3710	NA	4170
TPGQM(+15.99)FSTPGIPPVVY	O08573|LEG9_MOUSE	44.51	16	217	NA	NA
TPIETTAPTAAIPGTN	E9Q7P9|CDHR2_MOUSE	48.78	16	1810	NA	703
TPIPNGLYPS	O08573|LEG9_MOUSE	28.51	10	531	NA	3030
TPKKAAKKTPKKAKKP	P15864|H12_MOUSE	49.94	16	1440	NA	208
TPKKAAKKTPKKAKKPA	P15864|H12_MOUSE	49.95	17	3710	350	1410
TPKKAAKKTPKKAKKPAA	P15864|H12_MOUSE	49.95	18	2730	968	3340
TPKKAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	25	3860	2290	789
TPKKPKKPAVSKKTSKSPKKPKVVKAKK	P43275|H11_MOUSE	49.95	31	2070	NA	NA
TPKKTAKKTPKKA	P43277|H13_MOUSE	45.43	13	438	NA	NA
TPKKTAKKTPKKAKKP	P43277|H13_MOUSE	49.94	16	2950	NA	NA
TPKKTAKKTPKKAKKPA	P43277|H13_MOUSE	49.95	17	12600	6380	8900
TPLPTYEEAKQYLSYET	Q9D6X6|PRS23_MOUSE	35.6	17	237	NA	99.5
TPPETEEQPPQPSVVTPYP	Q8R105|VP37C_MOUSE	49.93	19	668	NA	843
TPPLQTTGPAARIHFH	Q9JLB4|CUBN_MOUSE	28.39	16	200	NA	NA
TPPLQTTGPAARIHFHS	Q9JLB4|CUBN_MOUSE	26.25	17	215	NA	224
TPPPAAAPIPAPSTEE	O54774|AP3D1_MOUSE	45.86	16	1520	NA	1120
TPPPAAAPIPAPSTEEL	O54774|AP3D1_MOUSE	47.16	17	599	NA	488
TPPPAAAPIPAPSTEELA	O54774|AP3D1_MOUSE	48.34	18	702	NA	92.5
TPPSPKVTYKAPVPTG	P35564|CALX_MOUSE	47.67	16	1590	NA	2400
TPPSPKVTYKAPVPTGEV	P35564|CALX_MOUSE	47.62	18	735	NA	2040
TPPSPKVTYKAPVPTGEVY	P35564|CALX_MOUSE	49.6	19	25700	518	38500
TPPSPKVTYKAPVPTGEVYF	P35564|CALX_MOUSE	46.78	20	490	NA	1150
TPPSPKVTYKAPVPTGEVYFA	P35564|CALX_MOUSE	26.17	21	191	NA	NA
TPQDILFVYRDSPVNPN	P12246|SAMP_MOUSE	38.1	17	52.7	NA	332
TPQSPTYTPSSPSYSPS	P08775|RPB1_MOUSE	43.03	17	125	NA	128

TPRDYFFALAHTVRD	Q8CI94|PYGB_MOUSE	42.08	15	226	NA	NA
TPRDYFFALAHTVRDH	Q8CI94|PYGB_MOUSE	44.5	16	1130	NA	722
TPRVLSQAPSPLYSVEF	P70699|LYAG_MOUSE	49.52	17	556	NA	330
TPRVLSQAPSPLYSVEFS	P70699|LYAG_MOUSE	48.11	18	88.2	NA	NA
TPSAAYLWVGAGASEAEKT	P13020|GELS_MOUSE	47.3	19	2360	NA	1800
TPSPAPTYSPSPAPAYTPS	Q9JKS4|LDB3_MOUSE	49.87	19	828	NA	695
TPSPAPTYSPSPAPAYTPSP	Q9JKS4|LDB3_MOUSE	49.89	20	4350	NA	4230
TPSPAPTYSPSPAPAYTPSPA	Q9JKS4|LDB3_MOUSE	49.87	21	669	NA	620
TPSPTAVSSSPAVAAAQAPAP	P54728|RD23B_MOUSE	49.75	21	566	NA	758
TPTPEVYGYGPYSGAYPAGTQ	Q9QZC7|PKHB2_MOUSE	49.73	21	260	NA	150
TPTPEVYGYGPYSGAYPAGTQV	Q9QZC7|PKHB2_MOUSE	49.9	22	164	NA	144
TPTPEVYGYGPYSGAYPAGTQVV	Q9QZC7|PKHB2_MOUSE	49.92	23	691	NA	447
TPTPTPPTRKTPESFLGPNAALVDLDS	Q80VP1|EPN1_MOUSE	25.17	27	419	NA	NA
TPTSFTAQWIAPSVQLTGYR	P11276|FINC_MOUSE	49.6	20	309	NA	569
TPTVSSYTPPQPSYSQPP	Q8VDM6|HNRL1_MOUSE	33.87	18	478	NA	779
TPTVSSYTPPQPSYSQPPY	Q8VDM6|HNRL1_MOUSE	40.43	19	295	NA	398
TPVFVHAGPFANIA	Q922D8|C1TC_MOUSE:Q3V3R1|C1TM_	49.49	14	102	NA	139
TPVFVHAGPFANIAH	Q922D8|C1TC_MOUSE:Q3V3R1|C1TM_	45.61	15	500	NA	562
TPVFVHAGPFANIAHG	Q922D8|C1TC_MOUSE:Q3V3R1|C1TM_	49.8	16	5310	NA	5210
TPVFVHAGPFANIAHGN	Q922D8|C1TC_MOUSE:Q3V3R1|C1TM_	49.89	17	9490	NA	7750
TPVFVHAGPFANIAHGNS	Q922D8|C1TC_MOUSE:Q3V3R1|C1TM_	49.93	18	29400	91.8	28500
TPVPLYSVPATHLAVT	Q91XT4|SC16B_MOUSE	42	16	28.2	NA	139
TPVPLYSVPATHLAVTS	Q91XT4|SC16B_MOUSE	49.92	17	610	NA	614
TPVPLYSVPATHLAVTSG	Q91XT4|SC16B_MOUSE	49.88	18	345	NA	455
TPVVVPPFLQPEV	P02666	46.72	13	554	NA	NA
TPVVVPPFLQPEVM(+15.99)G	P02666	49.6	15	191	NA	NA
TPVVVPPFLQPEVM(+15.99)GVS	P02666	49.92	17	102	NA	NA
TPVVVPPFLQPEVM(+15.99)GVSK	P02666	46.57	18	9480	NA	NA
TPVVVPPFLQPEVMGVSK	P02666	46.77	18	1760	NA	NA
TPYISPVASYSGQP	Q3UPL0|SC31A_MOUSE	42.82	14	96.4	NA	NA
TPYSTPQM(+15.99)SPATTPA	Q6PAR5|GAPD1_MOUSE	30.95	15	202	NA	NA
TPYSTPQMSPATTPA	Q6PAR5|GAPD1_MOUSE	28.53	15	156	NA	156
TPYYVAPEVLGPE	Q3UMW7|MAPK3_MOUSE:P49138|MAP	48.17	13	600	NA	603
TPYYVAPEVLGPEK	Q3UMW7|MAPK3_MOUSE:P49138|MAP	45.89	14	2060	NA	1330
TPYYYARPQTLPLNY	P58854|GCP3_MOUSE	36.57	15	80.1	NA	NA
TQFHPPHIEIQ	P01887|B2MG_MOUSE	36.23	11	133	NA	NA
TQQLAFKQPSSAYAAFN	P01027|CO3_MOUSE	49.92	17	1770	44.8	3240
TQQLAFKQPSSAYAAFNN	P01027|CO3_MOUSE	46.67	18	213	NA	NA
TQSLVYPFPGPIPNS	P02666	40.59	15	115	NA	NA
TQVQWNDPGAQYSL	Q9R100|CAD17_MOUSE	49.1	14	354	NA	228
TQVQWNDPGAQYSLV	Q9R100|CAD17_MOUSE	49.85	15	16000	NA	6830
TQVQWNDPGAQYSLVN	Q9R100|CAD17_MOUSE	49.93	16	32600	801	29000
TQVQWNDPGAQYSLVNK	Q9R100|CAD17_MOUSE	49.93	17	2480	NA	1690
TQVQWNDPGAQYSLVNKE	Q9R100|CAD17_MOUSE	49.93	18	626	NA	NA
TRAILNYIATKYDLYGKDM(+15.99)KERA	P13745|GSTA1_MOUSE:P10648|GSTA2	42.87	23	828	NA	NA
TRAILNYIATKYDLYGKDMKERA	P13745|GSTA1_MOUSE:P10648|GSTA2	49.42	23	256	NA	NA
TREELPVN(+15.00)TSKARPKQEKAC(+5	Q80WJ7|LYRIC_MOUSE	28.75	22	1030	NA	NA
TRPHWLEPTIYSSEE	Q80XK6|ATG2B_MOUSE	46.54	15	1510	NA	NA
TRPHWLEPTIYSSEED	Q80XK6|ATG2B_MOUSE	49.64	16	978	NA	435
TRSQVTPSVPSEALDD	Q7TQH7|LRP10_MOUSE	49.66	16	189	NA	291
TRSQVTPSVPSEALDDS	Q7TQH7|LRP10_MOUSE	49.66	17	808	NA	544
TSDIFGSPVTATAPL	Q6PGH2|JUPI2_MOUSE	48.82	15	271	NA	575
TSDIFGSPVTATAPLA	Q6PGH2|JUPI2_MOUSE	48.82	16	265	NA	301
TSDNLFIAPVGISTAM(+15.99)	P49182|HEP2_MOUSE	45.8	16	389	NA	199
TSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.94	17	4940	5990	5590
TSKSPKKPKVVKAKKVAK	P43275|H11_MOUSE	49.94	18	2740	NA	2080
TSKWSYLYPLATNIPN	Q9DBX3|SUSD2_MOUSE	49.82	16	4660	NA	7580
TSKWSYLYPLATNIPNT	Q9DBX3|SUSD2_MOUSE	49.76	17	131	NA	232
TSLSSGPLPTFPLEQLVNKS	Q62468|VILI_MOUSE	49.93	20	457	NA	145
TSLSSGPLPTFPLEQLVNKSVE	Q62468|VILI_MOUSE	49.94	22	298	NA	316
TSNIFFSPVSIAT	Q00897|A1AT4_MOUSE:P07758|A1AT1_	47.4	13	264	NA	NA
TSRHPGPL	P23150|HA2J_MOUSE:P14434|HA2B_M	32.26	8	9510	NA	7130
TSSLAAPTVEAAA	Q91ZP6|NFIP2_MOUSE	30.45	13	280	NA	365
TSSLAAPTVEAAAS	Q91ZP6|NFIP2_MOUSE	45.77	14	4480	NA	5430
TSSLAAPTVEAAASA	Q91ZP6|NFIP2_MOUSE	48.67	15	1970	NA	1740
TSSLAAPTVEAAASAP	Q91ZP6|NFIP2_MOUSE	47.95	16	2140	NA	971
TSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	48.97	17	1420	NA	481
TSSYSNPTIGYEN	Q07797|LG3BP_MOUSE	47.97	13	5250	234	1260
TSSYSNPTIGYENR	Q07797|LG3BP_MOUSE	49.16	14	17800	483	7790
TSSYSNPTIGYENRV	Q07797|LG3BP_MOUSE	49.7	15	3060	85.9	1980
TSSYYRGAHGIIVVY	P62821|RAB1A_MOUSE:Q9D1G1|RAB1I	26.54	15	413	NA	302
TSWTYNPAAVSKVAPA	Q80SY4|MIB1_MOUSE	49.79	16	903	NA	907
TT(+79.97)PPPAAAPIPAPSTEELA	O54774|AP3D1_MOUSE	33.37	19	555	NA	NA
TTDYNSPEAGNIF	B2RXV4|FLVC1_MOUSE	47.36	13	9160	34.3	4500
TTGAWKNPHVQQAAQ	Q9JKD3|SCAM5_MOUSE	25.72	15	816	NA	1090
TTGQLFFPEVNKN	P11911|CD79A_MOUSE	42.18	13	846	NA	348
TTGQLFFPEVNKNH	P11911|CD79A_MOUSE	47.37	14	968	NA	185

TTGQLFFPEVNKNHR	P11911|CD79A_MOUSE	49.59	15	469	NA	NA
TTHSFGNPSISVSTQQPP	Q8BFW7|LPP_MOUSE	48.89	18	4070	NA	5470
TTHSFGNPSISVSTQQPPK	Q8BFW7|LPP_MOUSE	36.73	19	74.2	NA	189
TTSSYSNPTIGYEN	Q07797|LG3BP_MOUSE	48.67	14	2140	85.5	583
TTSSYSNPTIGYENR	Q07797|LG3BP_MOUSE	49.31	15	11300	364	2710
TTSSYSNPTIGYENRV	Q07797|LG3BP_MOUSE	49.84	16	2310	NA	1320
TTTNLEQPQVIPSQG	Q9DBG3|AP2B1_MOUSE	47.26	15	423	NA	386
TTTNLEQPQVIPSQGDL	Q9DBG3|AP2B1_MOUSE	43.65	17	1240	NA	NA
TTTTNLEQPQVIPSQGDL	Q9DBG3|AP2B1_MOUSE	42.21	18	197	NA	119
TTVSLSAPDALKIIT	O88307|SORL_MOUSE	48	15	389	NA	NA
TTVSLSAPDALKIITEN	O88307|SORL_MOUSE	29.47	17	439	NA	NA
TVATYLGGIPDISFSA	Q08761|PROS_MOUSE	37.27	16	416	NA	436
TVDVVLTPLVAEALDR	A2AAE1|BLTP1_MOUSE	25.74	16	678	NA	644
TVHWVAPRAPITG	P11276|FINC_MOUSE	43.78	13	231	NA	199
TVIHFNNPKVQASL	Q9CQH7|BT3L4_MOUSE:Q64152|BTF3_	49.76	14	564	NA	430
TVIHFNNPKVQASLA	Q64152|BTF3_MOUSE	49.9	15	11400	136	13300
TVIHFNNPKVQASLAA	Q64152|BTF3_MOUSE	49.9	16	7580	NA	1630
TVIHFNNPKVQASLS	Q9CQH7|BT3L4_MOUSE	49.88	15	1930	NA	2340
TVIHFNNPKVQASLSA	Q9CQH7|BT3L4_MOUSE	29.8	16	85.2	NA	NA
TVINQTQKENLRKFYKGKKYKPLDLRPK	Q6ZWV7|RL35_MOUSE	49.94	31	1660	NA	3140
TVKKTPKKAKKPA	P43276|H15_MOUSE	49.92	13	1930	315	NA
TVKPKAAKPKTSKPKAAKPKK	P43274|H14_MOUSE	49.95	21	1920	NA	3340
TVKPKAAKPKTSKPKAAKPKKT	P43274|H14_MOUSE	49.95	22	877	NA	1550
TVKPKAAKPKTSKPKAAKPKKTAAKK	P43274|H14_MOUSE	49.94	26	247	NA	NA
TVKPKAAKPKTSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.95	27	4600	NA	2220
TVKPKAKSSAKRASKK	P10922|H10_MOUSE	49.85	16	6470	NA	2040
TVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.94	17	19600	3220	5040
TVKSFVGPTPAPAPAP	Q501J7|PHAR4_MOUSE	47.89	16	500	NA	548
TVKSFVGPTPAPAPAPR	Q501J7|PHAR4_MOUSE	49.6	17	1780	NA	2710
TVLVEPTVSLIKGPD	Q9JLB9|NECT3_MOUSE	26.54	15	855	NA	234
TVNKAVDYPPVANAGP	Q8K135|K319L_MOUSE	39	16	128	NA	NA
TVNKAVDYPPVANAGPNQ	Q8K135|K319L_MOUSE	49.91	18	3260	NA	3280
TVNKAVDYPPVANAGPNQVIT	Q8K135|K319L_MOUSE	49.94	21	799	NA	780
TVPFWAHAGNAIPSADQ	Q9D0F3|LMAN1_MOUSE	32.82	17	1910	NA	NA
TVSWRAPTAQVESFR	Q80YX1|TENA_MOUSE	49.32	15	42.1	NA	NA
TVTVLVEPTVSLIKGPD	Q9JLB9|NECT3_MOUSE	36.86	17	47.4	NA	81.6
TYHDLRHAFSPVASVESASG	P29699|FETUA_MOUSE	49.2	20	256	NA	NA
TYHDLRHAFSPVASVESASGET	P29699|FETUA_MOUSE	49.7	22	820	NA	277
TYHDLRHAFSPVASVESASGETLH	P29699|FETUA_MOUSE	48.96	24	141	NA	NA
TYKLSAPWVEQEGPE	P14432|HA1T_MOUSE	49.82	15	309	NA	NA
TYPYYTPTGEPVFGG	Q91ZJ9|HYAL1_MOUSE	35.38	15	489	NA	479
TYQSYSSPSPRVSRFK	Q60997|DMBT1_MOUSE	44.71	16	2790	NA	5320
TYVISAPKILRVG	P06684|CO5_MOUSE	49.7	13	602	NA	554
TYVISAPKILRVGS	P06684|CO5_MOUSE	49.86	14	511	NA	459
TYVISAPKILRVGSS	P06684|CO5_MOUSE	49.18	15	293	NA	447
V(+42.01)AIFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_M	29.27	15	36.2	NA	NA
V(+42.01)SAVRSYM(+15.99)EHHAKTPT	B1AVD1|XPP2_MOUSE	25.14	16	3030	NA	NA
VAAVYEHPSVLSPN	Q8CIF4|BTD_MOUSE	46.76	14	222	NA	NA
VAAVYEHPSVLSPNP	Q8CIF4|BTD_MOUSE	46.66	15	262	NA	NA
VAAVYEHPSVLSPNPL	Q8CIF4|BTD_MOUSE	49.58	16	6380	NA	3000
VADFHYAASKALRVPA	Q80TA9|EPG5_MOUSE	49.89	16	1450	NA	2490
VADKEFHAPLIIDEN	Q91YN5|UAP1_MOUSE	48.62	15	2280	NA	930
VADKEFHAPLIIDENG	Q91YN5|UAP1_MOUSE	49.59	16	13100	46.9	9600
VADKEFHAPLIIDENGVH	Q91YN5|UAP1_MOUSE	36.06	18	61.8	NA	NA
VAIFARGPQAHLV	P24823|PPBN_MOUSE:P24822|PPBI_M	42.98	13	106	NA	NA
VAIFARGPQAHLVH	P24823|PPBN_MOUSE:P24822|PPBI_M	47.36	14	185000	8330	143000
VAIFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_M	48.65	15	576000	30700	346000
VAIFARGPQAHLVHGV	P24823|PPBN_MOUSE:P24822|PPBI_M	49.7	16	35500	338	25500
VAIFARGPQAHLVHGVQ	P24823|PPBN_MOUSE:P24822|PPBI_M	49.92	17	263000	10100	214000
VAIFARGPQAHLVHGVQ(+15.00)	P24823|PPBN_MOUSE:P24822|PPBI_M	32.74	17	131	NA	NA
VAKSPKKAKAAAKPKKAAK	P43276|H15_MOUSE	49.12	19	407	NA	NA
VAKSPKKAKAAAKPKKAAKSPAK	P43276|H15_MOUSE	49.29	23	2760	NA	976
VAKSPKKAKAAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	49.95	26	1280	2440	3340
VAKVTGGAASKLSKIRVVRKSIAR	Q6ZWV7|RL35_MOUSE	49.94	24	1560	10000	4300
VAPAVTPVK	P70158|ASM3A_MOUSE	31.34	9	469	NA	1220
VAPYGGPSSSPAEEG	P10493|NID1_MOUSE	48.93	15	233	NA	NA
VARYRPRAPIIAVTR	P52480|KPYM_MOUSE	36.6	15	3090	NA	5530
VARYRPRAPIIAVTRNP	P52480|KPYM_MOUSE	45.56	17	21200	NA	12500
VARYRPRAPIIAVTRNPQ	P52480|KPYM_MOUSE	49.93	18	70900	924	58800
VARYRPRAPIIAVTRNPQT	P52480|KPYM_MOUSE	49.59	19	1600	NA	1180
VASIYRGPFADEN	Q9D868|PPIH_MOUSE	37	13	253	NA	NA
VASYLLAALGGNSSPSAKDIKK	P99027|RLA2_MOUSE	48.65	22	656	NA	171
VATNPIITPVAQEN	P08226|APOE_MOUSE	43.88	14	183	NA	146
VATNPIITPVAQENQ	P08226|APOE_MOUSE	48.17	15	11100	747	9570
VAVNWYAPLVAPISK	Q80VA0|GALT7_MOUSE	49.77	15	178	NA	316
VAVNWYAPLVAPISKD	Q80VA0|GALT7_MOUSE	49.71	16	354	NA	559
VAYEAPSLATGYG	P99026|PSB4_MOUSE	42.44	13	54	NA	NA

VDDEVFYSPRSLVFPE	P11725|OTC_MOUSE	49.62	16	163	NA	NA
VDEIQRYQKPVVAAIQG	Q9DBM2|ECHP_MOUSE	46.67	17	1670	NA	4210
VDFDFAGPAIHGSA	Q60930|VDAC2_MOUSE	46.11	14	530	NA	312
VDFDFAGPAIHGSAV	Q60930|VDAC2_MOUSE	48.84	15	3350	NA	2580
VDFNTPRPSTVE	G3X939|SL9A3_MOUSE	44.99	12	339	NA	274
VDFNTPRPSTVEA	G3X939|SL9A3_MOUSE	47.86	13	8460	302	9720
VDFNTPRPSTVEAS	G3X939|SL9A3_MOUSE	46.14	14	544	NA	621
VDGYFPSSVKPSVT	Q61730|IL1AP_MOUSE	36.97	14	155	NA	NA
VDHAYVTSIGRLIG	Q9R0A1|CLCN2_MOUSE	40.8	14	87.2	NA	120
VDISIRENIWKAPEPVEIREN(+15.00)ST	Q9R100|CAD17_MOUSE	38.22	23	518	NA	NA
VDKEFYLFPTVFDENE	Q61147|CERU_MOUSE	48.91	16	1740	NA	416
VDKEFYLFPTVFDENES	Q61147|CERU_MOUSE	49.69	17	598	NA	NA
VDLGGSYVGPTQNRILR	Q8BW75|AOFB_MOUSE	30.79	17	84.8	NA	NA
VDLRFSTSQSLPASQ	P28665|MUG1_MOUSE	40.69	15	1070	NA	NA
VDLRFSTSQSLPASQT	P28665|MUG1_MOUSE	40.72	16	3300	NA	1090
VDLRFSTSQSLPASQTR	P28665|MUG1_MOUSE	39.52	17	84.7	NA	NA
VDLYIM(+15.99)HYPVPM(+15.99)KSGDI	Q8VC28|AK1CD_MOUSE	36.4	17	343	NA	NA
VDLYTAKGLFRAAVPSGASTG	P17183|ENOG_MOUSE:P17182|ENOA_M	49.78	21	384	NA	NA
VDPTPDPNTAYASYPSASVEN	O55101|SNG2_MOUSE	49.94	21	528	NA	292
VDPTPDPNTAYASYPSASVENY	O55101|SNG2_MOUSE	49.94	22	348	NA	423
VDPTPDPNTAYASYPSASVENYQ	O55101|SNG2_MOUSE	49.95	23	1900	NA	1970
VDPTPDPNTAYASYPSASVENYQQPP	O55101|SNG2_MOUSE	49.95	26	1580	NA	1560
VDQIYHLASPASPP	Q91XL3|UXS1_MOUSE	29.36	14	10400	NA	NA
VDRVLKSPVASIVYE	Q8BP47|SYNC_MOUSE	29.72	15	242	NA	NA
VDRYDAPGIAFYPG	Q9D771|PACC1_MOUSE	46.59	14	794	NA	794
VDVFSDGPTAQPSLGPT	P17426|AP2A1_MOUSE	45.63	17	200	NA	141
VDVFYSSGIPATAR	Q91VN0|LRP5_MOUSE	42.39	14	455	NA	211
VDVFYSSGIPATARP	Q91VN0|LRP5_MOUSE	49.07	15	18000	572	12800
VDVFYSSGIPATARPY	Q91VN0|LRP5_MOUSE	49.87	16	21200	861	16900
VDVFYSSGIPATARPYRP	Q91VN0|LRP5_MOUSE	49.93	18	8340	NA	7250
VEISDSAPSAALVKDVT	Q5PR69|CRACD_MOUSE	49.36	17	178	NA	NA
VENPEYLAPRAGTAS	P70424|ERBB2_MOUSE	48.27	15	692	NA	639
VENPEYLAPRAGTASQ	P70424|ERBB2_MOUSE	47.28	16	721	NA	690
VENPEYLAPRAGTASQP	P70424|ERBB2_MOUSE	49.33	17	1320	NA	1740
VENPEYLAPRAGTASQPH	P70424|ERBB2_MOUSE	49.93	18	18000	NA	13100
VENPEYLAPRAGTASQPHP	P70424|ERBB2_MOUSE	49.91	19	93200	670	83400
VENPEYLAPRAGTASQPHPS	P70424|ERBB2_MOUSE	48.78	20	259	NA	199
VEPGNFIAATSLYSPER	Q80XN0|BDH_MOUSE	48.15	17	379	NA	319
VEPLTPSGAVPNQAQ	P70424|ERBB2_MOUSE	46.91	15	1110	NA	716
VEPLTPSGAVPNQAQM(+15.99)R	P70424|ERBB2_MOUSE	46.19	17	356	NA	235
VEPLTPSGAVPNQAQMR	P70424|ERBB2_MOUSE	49.92	17	82.2	NA	181
VEPYEVHNPVPLIVG	P05555|ITAM_MOUSE	46.8	15	1720	316	929
VEQ(+15.00)ERRREQ(+15.00)ERIHRER	D3YXK2|SAFB1_MOUSE	27.74	32	569	NA	NA
VEQPSTSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	48.71	22	1380	NA	1950
VEYAVRGPIVQRA	Q8QZR5|ALAT1_MOUSE	37.67	13	116	NA	108
VEYAVRGPIVQRALE	Q8QZR5|ALAT1_MOUSE	49.89	15	6900	NA	6770
VEYAVRGPIVQRALEL	Q8QZR5|ALAT1_MOUSE	48.83	16	15300	NA	22500
VEYHFLSPYVSPR	Q62351|TFR1_MOUSE	47.71	13	2540	NA	1390
VEYHFLSPYVSPRE	Q62351|TFR1_MOUSE	45.04	14	974	NA	128
VEYHFLSPYVSPRES	Q62351|TFR1_MOUSE	46.21	15	121	NA	NA
VEYHFLSPYVSPRESP	Q62351|TFR1_MOUSE	48.86	16	1380	NA	523
VEYHFLSPYVSPRESPF	Q62351|TFR1_MOUSE	49.65	17	472	NA	61.8
VFDVTAPNTFKT	P51150|RAB7A_MOUSE	42.7	12	268	NA	265
VFDVTAPNTFKTL	P51150|RAB7A_MOUSE	49.33	13	73.3	NA	NA
VFDVTAPNTFKTLD	P51150|RAB7A_MOUSE	49.05	14	4600	96.3	4020
VFDVTAPNTFKTLDS	P51150|RAB7A_MOUSE	48.6	15	1250	NA	1050
VFENYEASKAYSSVD	Q9D306|MGT4C_MOUSE	49.83	15	10200	513	5750
VFENYEASKAYSSVDE	Q9D306|MGT4C_MOUSE	49.93	16	7080	319	2560
VFIYHGSPTGIITKPT	Q61739|ITA6_MOUSE	44.03	16	119	NA	NA
VFVAPAVTPVK	P70158|ASM3A_MOUSE	44.22	11	11300	269	8030
VFVAPAVTPVKG	P70158|ASM3A_MOUSE	41.99	12	7590	162	6160
VFVAPAVTPVKGVL	P70158|ASM3A_MOUSE	49.43	14	348	NA	NA
VFYSSGIPATARP	Q91VN0|LRP5_MOUSE	48.7	13	450	NA	387
VFYSSGIPATARPY	Q91VN0|LRP5_MOUSE	42.38	14	224	NA	160
VGDIFSNPEAVLAK	Q3TPX4|EXOC5_MOUSE	45.08	14	162	NA	58.7
VGDLYTDPQIHTEKG	O08796|EF2K_MOUSE	41.57	15	65	NA	NA
VGETFHASQPSLTVDG	Q62432|SMAD2_MOUSE	45.82	16	3930	NA	3340
VGFIFKSGKITSIVK	O08992|SDCB1_MOUSE	48.83	15	57.2	NA	NA
VGGERFEAPEALFQ	P61161|ARP2_MOUSE	42.51	14	362	NA	NA
VGGERFEAPEALFQP	P61161|ARP2_MOUSE	46.41	15	1070	NA	868
VGGERFEAPEALFQPH	P61161|ARP2_MOUSE	49.34	16	18200	220	16100
VGGERFEAPEALFQPHL	P61161|ARP2_MOUSE	49.15	17	92.8	NA	NA
VGINIFTNSKIHKPR	Q61838|PZP_MOUSE	49.82	15	117	NA	97.5
VGINYQPPTVVPG	P68369|TBA1A_MOUSE:P68373|TBA1C_	40.1	13	159	NA	287
VGINYQPPTVVPGG	P68369|TBA1A_MOUSE:P68373|TBA1C_	37.18	14	289	NA	357
VGINYQPPTVVPGGDL	P68369|TBA1A_MOUSE:P68373|TBA1C_	46.53	16	5440	NA	5780
VGPDYAHAEARKSP	A2ARP1|VIP1_MOUSE:Q6ZQB6|VIP2_M	46.76	14	249	NA	95.5

VGPDYAHAEARKSPA	A2ARP1|VIP1_MOUSE:Q6ZQB6|VIP2_M	47.31	15	1350	NA	1730
VGPDYAHAEARKSPAL	A2ARP1|VIP1_MOUSE:Q6ZQB6|VIP2_M	49.65	16	6660	NA	5160
VGTIRYM(+15.99)APEVLEGAVN	O35607|BMPR2_MOUSE	49.05	17	845	NA	651
VGTKRYM(+15.99)APEVLDET	Q61271|ACV1B_MOUSE:P37172|ACVR1	46.18	15	499	NA	NA
VGTKRYM(+15.99)APEVLDETIN	Q61271|ACV1B_MOUSE	49.86	17	30100	NA	9270
VGTKRYMAPEVLDE	Q61271|ACV1B_MOUSE:Q61288|ACVL1	32.86	14	139	NA	NA
VGTKRYMAPEVLDESL	P36895|BMR1A_MOUSE	29.76	16	1060	NA	3040
VGTKRYMAPEVLDESLN	P36895|BMR1A_MOUSE	41.53	17	1110	NA	890
VGTKRYMAPEVLDET	Q61271|ACV1B_MOUSE:P37172|ACVR1	43.53	15	490	NA	NA
VGTKRYMAPEVLDETIN	Q61271|ACV1B_MOUSE	49.8	17	16600	NA	23500
VGTRRYM(+15.99)APEVLEGAIN	P27038|AVR2A_MOUSE:P27040|AVR2B	25.47	17	24900	NA	14500
VGTRRYMAPEVLEGA	P27038|AVR2A_MOUSE:P27040|AVR2B	25.51	15	44.3	NA	NA
VGTRRYMAPEVLEGAI	P27038|AVR2A_MOUSE:P27040|AVR2B	26.4	16	560	NA	1600
VGTRRYMAPEVLEGAIN	P27038|AVR2A_MOUSE:P27040|AVR2B	45.08	17	21200	NA	22500
VGVTFYHAATGSLPFRP	Q9WUN2|TBK1_MOUSE	49.92	17	131	NA	NA
VHERHFM(+15.99)APGVRRVPV	Q6Q2Z6|ACOT5_MOUSE:Q32Q92|ACOT	25.7	16	135	NA	NA
VHERHFMAPGVRRVPV	Q6Q2Z6|ACOT5_MOUSE:Q32Q92|ACOT	43.04	16	121	NA	540
VHLRVFQPLPHEN	Q62426|CYTB_MOUSE	38.78	13	97.5	NA	NA
VHSVAIVGAPFSRGQKKLGVEY	O08691|ARGI2_MOUSE	33.02	22	64.6	NA	NA
VILPEETPTASASADTP	E9Q7D5|ARHG5_MOUSE	49.92	17	1330	NA	1100
VILPEETPTASASADTPH	E9Q7D5|ARHG5_MOUSE	49.9	18	5000	NA	3880
VILYYTEPGSHVSR	O35206|COFA1_MOUSE	47.74	14	861	116	560
VILYYTEPGSHVSRE	O35206|COFA1_MOUSE	47.32	15	203	NA	148
VILYYTEPGSHVSREA	O35206|COFA1_MOUSE	49.46	16	1350	296	910
VIPELNGKLTGM(+15.99)AFRVPTPNVS	P16858|G3P_MOUSE	49.38	22	645	NA	NA
VIPELNGKLTGM(+15.99)AFRVPTPNVS\	P16858|G3P_MOUSE	49.87	25	9850	NA	7830
VIPSRYSSPTTIAT	Q9DBM2|ECHP_MOUSE	41.74	14	439	NA	NA
VIPSRYSSPTTIATVM	Q9DBM2|ECHP_MOUSE	49.89	16	3300	NA	9800
VIPSRYSSPTTIATVM(+15.99)	Q9DBM2|ECHP_MOUSE	48.01	16	10800	568	15900
VIPSRYSSPTTIATVM(+15.99)S	Q9DBM2|ECHP_MOUSE	48.25	17	813	NA	908
VIPSRYSSPTTIATVMS	Q9DBM2|ECHP_MOUSE	49.39	17	47.2	NA	366
VITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.93	17	16400	802	21600
VITNQYNSPTGLYSSENI	O70400|PDLI1_MOUSE	49.94	18	1010	NA	1700
VITNQYNSPTGLYSSENIS	O70400|PDLI1_MOUSE	49.93	19	1690	NA	2840
VITNQYNSPTGLYSSENISN	O70400|PDLI1_MOUSE	49.94	20	146	NA	NA
VKAAKPKKAAKSPAKAKAP	P43277|H13_MOUSE	35.51	19	102	NA	NA
VKAAKPKKAAKSPAKAKAPKAKASKPKA	P43277|H13_MOUSE	49.95	28	1820	1980	1920
VKAAKPKKAAKSPAKAKAPKAKASKPKA	P43277|H13_MOUSE	49.84	29	596	NA	NA
VKAKKVAK	P43275|H11_MOUSE	27.91	8	277	NA	NA
VKASKPKKA	P10922|H10_MOUSE	36.36	9	1460	939	1120
VKDSELSPPTSAPSL	Q9WUU8|TNIP1_MOUSE	32.57	15	722	NA	720
VKDSELSPPTSAPSLVS	Q9WUU8|TNIP1_MOUSE	48.43	17	9100	NA	7310
VKKVATPKKAAKPKKAASKAPS(+79.97)	P10922|H10_MOUSE	26.13	29	4110	NA	NA
VKM(+15.99)EYFRPNIVVSG	Q922Q1|MARC2_MOUSE	30.64	14	426	NA	141
VKMEYFRPNIVVSG	Q922Q1|MARC2_MOUSE	45.76	14	352	NA	NA
VKPKAAKPKTSKPKAAK	P43274|H14_MOUSE	36.66	17	1210	NA	NA
VKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.38	16	2480	NA	NA
VKPKASKAKVTKPKTPAKPKKAAPK	P43275|H11_MOUSE	49.91	25	538	NA	NA
VKPQAIKPKM(+15.99)PKGPKLKRLAFIA	P47915|RL29_MOUSE	49.95	32	2220	NA	NA
VKPQAIKPKMPKGPKLKRLAFIAHPKLGK	P47915|RL29_MOUSE	49.95	32	4550	NA	NA
VKPVKASKPKKAK	P10922|H10_MOUSE	48.45	13	274	144	782
VKSASKAVKPKAAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	28	1190	NA	NA
VKSKASKPKVTKPKTAKPK	P43276|H15_MOUSE	49.95	19	1040	NA	NA
VKSKASKPKVTKPKTAKPKAAKAK	P43276|H15_MOUSE	49.95	24	632	NA	1140
VKSKASKPKVTKPKTAKPKAAKAKK	P43276|H15_MOUSE	49.95	25	2500	NA	2550
VKSKASKPKVTKPKTAKPKAAKAKKA	P43276|H15_MOUSE	49.95	26	888	635	1390
VKSKASKPKVTKPKTAKPKAAKAKKAVS	P43276|H15_MOUSE	49.95	30	3880	1130	3590
VKSKASKPKVTKPKTAKPKAAKAKKAVS	P43276|H15_MOUSE	49.95	31	33400	9920	9410
VKVSWRSPVPNKQH	Q64487|PTPRD_MOUSE	42.17	14	209	NA	194
VKVSWRSPVPNKQHG	Q64487|PTPRD_MOUSE	49.14	15	6070	NA	4490
VKVTFNSALAQKEAK	O89051|ITM2B_MOUSE	49.59	15	497	NA	332
VKVTFNSALAQKEAKK	O89051|ITM2B_MOUSE	49.89	16	15600	587	9600
VKVTFNSALAQKEAKKD	O89051|ITM2B_MOUSE	49.78	17	2200	NA	905
VKVTFNSALAQKEAKKDEPK	O89051|ITM2B_MOUSE	49.65	20	410	NA	217
VLIPYQGPSSDYVVV	O88307|SORL_MOUSE	49.84	15	1970	NA	1030
VLIPYQGPSSDYVVVK	O88307|SORL_MOUSE	49.82	16	2720	173	1450
VLLPPYDDATAVPSTAKEPPPP	Q91XQ6|LAP4B_MOUSE	49.95	22	9600	NA	9960
VLNRLKVGLQVVAVKAPGFGDNRKNQL	P63038|CH60_MOUSE	49.03	28	1670	NA	3770
VLPNIQAVLLPKKTESHHK	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	47.45	19	63	516	569
VLPNIQAVLLPKKTESHHKAK	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	49.55	21	561	NA	1160
VLPTYDASKVTASGPG	Q80X90|FLNB_MOUSE	49.56	16	2090	NA	1180
VLRIINEPTAAAIAYG	P17879|HS71B_MOUSE:P16627|HS71L_	49.81	16	1500	NA	1110
VLRYNITHPVVNDADAS	Q8BZW8|NHLC2_MOUSE	29.54	17	306	NA	NA
VLVFDVTAPNTFKTLD	P51150|RAB7A_MOUSE	49.25	16	1070	NA	1140
VLVFDVTAPNTFKTLDS	P51150|RAB7A_MOUSE	49.4	17	289	NA	233
VLVTWTPPRARIAG	P11276|FINC_MOUSE	27.89	14	312	NA	288
VLVTWTPPRARIAGYR	P11276|FINC_MOUSE	48.37	16	9410	NA	10900

VM(+15.99)RIINEPTAAAIAYG	P20029|BIP_MOUSE	48.87	16	372	NA	NA
VMRIINEPTAAAIAYG	P20029|BIP_MOUSE	48.57	16	223	NA	344
VNFVDPAASSSADD	P55012|S12A2_MOUSE	49.66	14	303	NA	63
VNGKKFTAPHILIAT	P47791|GSHR_MOUSE	36.07	15	311	NA	NA
VNGKKFTAPHILIATGG	P47791|GSHR_MOUSE	46.62	17	3570	NA	4370
VNKAVDYPPVANAGP	Q8K135|K319L_MOUSE	48.3	15	650	NA	647
VNKAVDYPPVANAGPN	Q8K135|K319L_MOUSE	49.32	16	2510	NA	3030
VNKAVDYPPVANAGPNQ	Q8K135|K319L_MOUSE	49.88	17	11200	NA	13000
VNPFVGPLTNRIG	Q8R090|VMAT1_MOUSE	39.63	13	5480	NA	2560
VNPFVGPLTNRIGYH	Q8R090|VMAT1_MOUSE	36.17	15	761	NA	401
VNVDFNTPRPST	G3X939|SL9A3_MOUSE	45.51	12	1150	NA	1820
VNVDFNTPRPSTVE	G3X939|SL9A3_MOUSE	47.06	14	2300	NA	2860
VNVDFNTPRPSTVEA	G3X939|SL9A3_MOUSE	49.48	15	31200	1850	41600
VNVDFNTPRPSTVEAS	G3X939|SL9A3_MOUSE	48.52	16	1370	NA	1840
VNVDYSKL	Q62425|NDUA4_MOUSE	32.34	8	393	NA	NA
VNVQPYSGSPANFAVY	P50431|GLYC_MOUSE	49.88	16	401	NA	467
VNVQPYSGSPANFAVYT	P50431|GLYC_MOUSE	49.94	17	7990	NA	7660
VNWYAPLVAPISK	Q80VA0|GALT7_MOUSE	49.52	13	98.5	NA	NA
VNWYAPLVAPISKD	Q80VA0|GALT7_MOUSE	48.66	14	96.5	NA	NA
VPAQSTFWRPQTQEERPH	Q8C708|CP054_MOUSE	43.78	18	159	NA	236
VPDDLLYSFPVVIKN	P14152|MDHC_MOUSE	49.85	15	814	NA	442
VPDDLLYSFPVVIKNK	P14152|MDHC_MOUSE	49.92	16	38100	323	29800
VPDDLLYSFPVVIKNKT	P14152|MDHC_MOUSE	49.94	17	33900	290	27700
VPDDLLYSFPVVIKNKTW	P14152|MDHC_MOUSE	49.9	18	151	NA	80.8
VPDSYKSAVPFKIL	A2A8L5|PTPRF_MOUSE	48.85	14	234	NA	187
VPDSYKSAVPFKILY	A2A8L5|PTPRF_MOUSE	49.39	15	3800	NA	2850
VPDSYKSAVPFKILYN	A2A8L5|PTPRF_MOUSE	47.65	16	246	NA	544
VPESLLTPRLAPSKP	P97927|LAMA4_MOUSE	40.98	15	214	NA	197
VPESLLTPRLAPSKPF	P97927|LAMA4_MOUSE	46.83	16	422	NA	299
VPFDAATLHTSTAM(+15.99)AAQHG	P13020|GELS_MOUSE	49.58	19	186	NA	NA
VPFETRGPHINNSVH	Q8K296|MTMR3_MOUSE	49.67	15	26100	NA	28000
VPFETRGPHINNSVHM	Q8K296|MTMR3_MOUSE	49.33	16	1930	NA	3860
VPFETRGPHINNSVHM(+15.99)	Q8K296|MTMR3_MOUSE	46.7	16	3820	NA	4710
VPFWAHAGNAIPSADQ	Q9D0F3|LMAN1_MOUSE	27.2	16	692	NA	530
VPFYVRGPNVEAG	Q8CFG0|SULF2_MOUSE	44.92	13	86.3	NA	115
VPFYVRGPNVEAGSL	Q8CFG0|SULF2_MOUSE	49.09	15	1310	NA	1410
VPFYVRGPNVEAGSLN	Q8CFG0|SULF2_MOUSE	49.59	16	347	NA	332
VPFYVRGPNVEAGSLNP	Q8CFG0|SULF2_MOUSE	48.6	17	481	NA	806
VPFYVRGPNVEAGSLNPH	Q8CFG0|SULF2_MOUSE	49.89	18	5450	79.9	5330
VPGTSTSATLTGLTR	P11276|FINC_MOUSE	49.34	15	2190	813	193
VPIVEPEVLPDG	Q91Y97|ALDOB_MOUSE	40.1	12	230	NA	NA
VPIVEPEVLPDGDH	Q91Y97|ALDOB_MOUSE	49.46	14	3330	NA	1470
VPIVEPEVLPDGDHD	Q91Y97|ALDOB_MOUSE	49.33	15	926	NA	NA
VPIVEPEVLPDGDHDLE	Q91Y97|ALDOB_MOUSE	49.32	17	21.5	NA	NA
VPIYEGYALPHAILR	P63260|ACTG_MOUSE:P60710|ACTB_M	49.25	15	2290	40.7	1660
VPKHEYTYPYVDSSD	Q924S7|SPRE2_MOUSE	33.06	15	830	NA	100
VPKHEYTYPYVDSSDF	Q924S7|SPRE2_MOUSE	49.91	16	8440	NA	10500
VPKHEYTYPYVDSSDFG	Q924S7|SPRE2_MOUSE	49.93	17	13500	NA	9590
VPKPAPQPYTFPASLSTIN	Q04207|TF65_MOUSE	49.6	19	129	NA	NA
VPNVHGALAPLAIPSAAA	P17225|PTBP1_MOUSE	28.72	18	201	NA	NA
VPNVHGALAPLAIPSAAAA	P17225|PTBP1_MOUSE	37.19	19	60.7	NA	NA
VPNVHGALAPLAIPSAAAAA	P17225|PTBP1_MOUSE	29.64	20	255	NA	NA
VPNYKLITPAVVSER	P62852|RS25_MOUSE	45.67	15	254	NA	175
VPNYKLITPAVVSERL	P62852|RS25_MOUSE	48.53	16	554	NA	436
VPNYKLITPAVVSERLK	P62852|RS25_MOUSE	49.8	17	53	NA	NA
VPPAGGGDPEAPAPAPAAERPP	Q68FL4|SAHH3_MOUSE	49.94	22	7820	NA	22200
VPPAGGGDPEAPAPAPAAERPPA	Q68FL4|SAHH3_MOUSE	49.93	23	6290	NA	8990
VPPAGGGDPEAPAPAPAAERPPAPGPG	Q68FL4|SAHH3_MOUSE	49.94	27	4740	NA	9480
VPPDQYYWAPLAQHER	P30999|CTND1_MOUSE	48.77	16	2060	NA	3910
VPPDQYYWAPLAQHERG	P30999|CTND1_MOUSE	49.75	17	4640	NA	6560
VPPEAYVPPRAVEPQPP	P97873|LOXL1_MOUSE	49.6	17	10800	537	12000
VPPFLQPEVM(+15.99)GVSK	P02666	42.44	14	3670	NA	NA
VPPFLQPEVMGVSK	P02666	44.69	14	727	NA	NA
VPPLIPSSQQKPEVLPSATKPQPPPP	P39447|ZO1_MOUSE	25.58	26	253	NA	NA
VPPSVSPSPATAFSG	Q3UPH1|PRRC1_MOUSE	49.79	15	448	NA	301
VPPSVSPSPATAFSGPP	Q3UPH1|PRRC1_MOUSE	49.49	17	3050	NA	3470
VPPVFTQPTANIM(+15.99)PS	P97789|XRN1_MOUSE	39.08	15	719	NA	277
VPQNQGDLEYQMSTTARAK	Q02257|PLAK_MOUSE	49.93	19	423	NA	831
VPQNQGDLEYQMSTTARAKR	Q02257|PLAK_MOUSE	47.56	20	200	NA	794
VPQSQAQPATAPQAAAAQEPG	Q3UHJ0|AAK1_MOUSE	49.94	21	746	NA	1920
VPSAYQKTVPIEAVTS	Q60598|SRC8_MOUSE	45.17	16	205	NA	158
VPSGLFIPSM(+15.99)AIGAIA	P51791|CLCN3_MOUSE	48.12	16	4880	NA	2000
VPSGLFIPSM(+15.99)AIGAIAG	P51791|CLCN3_MOUSE	42.69	17	211	NA	NA
VPSGLFIPSM(+15.99)AIGAIAGR	P51791|CLCN3_MOUSE	35.93	18	378	NA	141
VPTGHKLPSPLIM(+15.99)SPGPIYAVDG	Q8VHF2|CDHR5_MOUSE	49.28	23	439	NA	465
VPTGHKLPSPLIM(+15.99)SPGPIYAVDG	Q8VHF2|CDHR5_MOUSE	49.95	24	1770	NA	1940
VPTGHKLPSPLIM(+15.99)SPGPIYAVDG	Q8VHF2|CDHR5_MOUSE	49.94	25	1790	NA	1450

VPTGHKLPSPLIMSPGPIYAVDGD	Q8VHF2|CDHR5_MOUSE	49.95	24	274	NA	1330
VPTGHKLPSPLIMSPGPIYAVDGDQ	Q8VHF2|CDHR5_MOUSE	49.94	25	337	NA	1270
VPTPSKTQQGLYQAPGPNPQFQ	Q61140|BCAR1_MOUSE	26.25	22	69.5	NA	NA
VPTVPLLPPQVNQS	Q99JX3|GORS2_MOUSE	46.04	14	834	NA	339
VPTVPLLPPQVNQSLA	Q99JX3|GORS2_MOUSE	49.02	16	4880	NA	2840
VPTVPLLPPQVNQSLAS	Q99JX3|GORS2_MOUSE	49.33	17	1240	NA	998
VPTVPLLPPQVNQSLASM(+15.99)PP	Q99JX3|GORS2_MOUSE	49.88	20	4060	NA	1770
VPVIVEKAPKARIGDL	Q9DCD6|GBRAP_MOUSE	49.88	16	612	NA	454
VPVPEGPDKGDRPHTYFGPETSASK	P70277|SIA7B_MOUSE	49.94	25	1170	NA	1070
VPVPEGPDKGDRPHTYFGPETSASKFK	P70277|SIA7B_MOUSE	49.95	27	322	NA	1730
VPVQAPQVPEAIEKGD	Q8VDP3|MICA1_MOUSE	48.91	16	210	NA	134
VPWNFHEPQPGQYE	P23780|BGAL_MOUSE	49.61	14	5250	NA	2720
VPWNFHEPQPGQYEF	P23780|BGAL_MOUSE	49.8	15	804	NA	366
VPWNFHEPQPGQYEFS	P23780|BGAL_MOUSE	49.92	16	339	NA	NA
VPYPFQWGM(+15.99)PTVSAAGVI	Q9EPR4|S23A2_MOUSE	49.63	18	772	NA	858
VQAFTHAPAALEADRG	Q8BK64|AHSA1_MOUSE	41.94	16	250	NA	951
VQFNYPQASVTDVT	Q61703|ITIH2_MOUSE	47.96	14	2650	NA	740
VQFPYVTPAPHEPVK	Q9D074|MGRN1_MOUSE	48.52	15	140	NA	402
VQFTYQQPQPLSVEPR	B2RXS4|PLXB2_MOUSE	49.86	16	6840	NA	5940
VQGDTEGRLEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	49.95	23	492	NA	360
VQIFFVNPAGEVSAPS	Q8R1X6|SPART_MOUSE	48.16	16	309	NA	NA
VQIYHNPTANSF	P70460|VASP_MOUSE	41.61	12	185	NA	NA
VQIYHNPTANSFR	P70460|VASP_MOUSE	47.39	13	2200	NA	2510
VQIYHNPTANSFRV	P70460|VASP_MOUSE	48.37	14	338	NA	174
VQKLFVDKIREYKSKRQ	P97450|ATP5J_MOUSE	48.53	17	117	NA	NA
VQKLFVDKIREYKSKRQA	P97450|ATP5J_MOUSE	39.4	18	940	NA	NA
VQLVQANSPASLVGLRFG	O08992|SDCB1_MOUSE	46.42	18	37.2	NA	NA
VQPYSGSPANFAVYT	P50431|GLYC_MOUSE	49.53	15	1030	NA	NA
VQWNDPGAQYSLVN	Q9R100|CAD17_MOUSE	49.69	14	946	NA	393
VQWNDPGAQYSLVNK	Q9R100|CAD17_MOUSE	49.58	15	483	NA	409
VQWNDPGAQYSLVNKE	Q9R100|CAD17_MOUSE	49.77	16	209	NA	NA
VRIDQYQGADAVGLEE	Q8CDN6|TXNL1_MOUSE	47.4	16	435	NA	224
VRTDMAGPKATKSPEE	P48758|CBR1_MOUSE	49.36	16	829	NA	206
VRYTQKAPQVSTP	P07724|ALBU_MOUSE	44.19	13	1680	NA	NA
VRYTQKAPQVSTPT	P07724|ALBU_MOUSE	47.94	14	1500	NA	76.2
VRYTQKAPQVSTPTL	P07724|ALBU_MOUSE	49.82	15	51900	2380	58300
VRYTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.92	16	18200	50.1	17100
VRYTQKAPQVSTPTLVE	P07724|ALBU_MOUSE	49.44	17	975	NA	7700
VRYTQKAPQVSTPTLVEA	P07724|ALBU_MOUSE	49.93	18	1850	NA	2640
VRYTQKAPQVSTPTLVEAA	P07724|ALBU_MOUSE	49.05	19	264	NA	NA
VSGAQEM(+15.99)VSSSVSSAKETV	Q9DBG5|PLIN3_MOUSE	49.92	19	332	NA	189
VSGAQEM(+15.99)VSSSVSSAKETVA	Q9DBG5|PLIN3_MOUSE	48.91	20	609	NA	444
VSGAQEMVSSSVSSAKETV	Q9DBG5|PLIN3_MOUSE	49.93	19	135	NA	NA
VSGAQEMVSSSVSSAKETVA	Q9DBG5|PLIN3_MOUSE	49.91	20	228	NA	837
VSGRHKFRPSFPASSPYVT	O89023|TPP1_MOUSE	29.66	19	142	NA	NA
VSHDYKGSTSHSLP	E9Q414|APOB_MOUSE	36.51	14	16700	NA	13200
VSHDYKGSTSHSLPY	E9Q414|APOB_MOUSE	46.48	15	42200	NA	40600
VSHDYKGSTSHSLPYE	E9Q414|APOB_MOUSE	47.08	16	10800	NA	7410
VSHTYGDPHVNLVIG	Q80T32|AGRD1_MOUSE	49.58	15	6650	NA	2790
VSM(+15.99)EYESSVAKFPVT	Q09199|B4GN2_MOUSE	29.48	15	356	NA	NA
VSNHRFFGPDAEISQPP	Q8R3L2|TCF25_MOUSE	31.46	17	537	NA	NA
VSNVLSQPLAQAAVKL	Q9DBG6|RPN2_MOUSE	30.07	16	374	NA	165
VSPTDFKNPTINN	Q9CQY8|T4S20_MOUSE	48.18	13	204	NA	515
VSPTDFKNPTINNM(+15.99)VS	Q9CQY8|T4S20_MOUSE	49.78	16	269	NA	441
VSPYVSGEIQKAEIK	Q9D8C4|IN35_MOUSE	47.03	15	340	NA	307
VSSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	46.72	13	43700	810	17600
VSSVEAPSVSPARH	Q8BUJ9|LRP12_MOUSE	44.2	14	1270	NA	128
VSSVEAPSVSPARHQ	Q8BUJ9|LRP12_MOUSE	46.43	15	10900	NA	113
VSTLIWAAPRLQSEVA	Q9CX00|IST1_MOUSE	36.41	16	452	NA	679
VSTLIWAAPRLQSEVAE	Q9CX00|IST1_MOUSE	37.11	17	52.4	NA	NA
VSWQEKQPEASISQ	E9PYK3|PARP4_MOUSE	49.18	14	356	NA	234
VSWQEKQPEASISQT	E9PYK3|PARP4_MOUSE	49.33	15	450	NA	606
VSWQEKQPEASISQTE	E9PYK3|PARP4_MOUSE	49.87	16	976	NA	1430
VSWRSPVPNKQHG	Q64487|PTPRD_MOUSE	28.28	13	148	NA	NA
VTDATETTITISWR	P11276|FINC_MOUSE	37.6	14	901	270	462
VTERVYAPTSTLVDQ	O55111|DSG2_MOUSE	47.59	15	84.8	NA	95.5
VTERVYAPTSTLVDQH	O55111|DSG2_MOUSE	49.84	16	66.3	NA	NA
VTFNSALAQKEAKK	O89051|ITM2B_MOUSE	49.5	14	904	NA	359
VTFYHAATGSLPF	Q9WUN2|TBK1_MOUSE	40.38	13	104	NA	NA
VTFYHAATGSLPFR	Q9WUN2|TBK1_MOUSE	49.6	14	54.9	NA	NA
VTGGAASKLSKIRVVRKSIAR	Q6ZWV7|RL35_MOUSE	38.9	21	242	NA	NA
VTGPPIFNPVANEVYLN	Q07113|MPRI_MOUSE	49.57	17	240	NA	NA
VTKKVAKSPKKAKVT	P15864|H12_MOUSE	39.15	15	5110	NA	2130
VTKKVAKSPKKAKVTKPKKVK	P15864|H12_MOUSE	49.95	21	2210	NA	3720
VTKKVAKSPKKAKVTKPKKVKSA	P15864|H12_MOUSE	49.95	23	431	NA	1040
VTKKVAKSPKKAKVTKPKKVKSASKAVK	P15864|H12_MOUSE	49.95	31	337	NA	375
VTQFHPPHIEIQ	P01887|B2MG_MOUSE	44.84	12	20600	NA	5470

VTQFHPPHIEIQM	P01887|B2MG_MOUSE	48.9	13	344	NA	564
VTQFHPPHIEIQM(+15.99)	P01887|B2MG_MOUSE	48.49	13	620	NA	2360
VTQFHPPHIEIQM(+15.99)L	P01887|B2MG_MOUSE	49.32	14	16800	NA	6150
VTQFHPPHIEIQM(+15.99)LK	P01887|B2MG_MOUSE	47.05	15	2550	NA	1640
VTQFHPPHIEIQM(+15.99)LKN	P01887|B2MG_MOUSE	28.36	16	121	NA	NA
VTQFHPPHIEIQML	P01887|B2MG_MOUSE	42.55	14	361000	NA	478000
VTQFHPPHIEIQMLK	P01887|B2MG_MOUSE	48.76	15	571	NA	894
VTQFHPPHIEIQMLKNG	P01887|B2MG_MOUSE	45.07	17	202	NA	420
VTTDHISPAGNIARNSP	P28271|ACOHC_MOUSE	48.81	17	433	NA	971
VTTDHISPAGNIARNSPA	P28271|ACOHC_MOUSE	49.62	18	1210	NA	499
VTYEWAPPVQNQAL	P47226|TES_MOUSE	32.72	14	119	NA	NA
VTYEWAPPVQNQALAR	P47226|TES_MOUSE	44.75	16	435	NA	524
VVDNVSSPETIVVFNG	Q8CAS9|PARP9_MOUSE	45.27	16	607	NA	464
VVKAKKVAK	P43275|H11_MOUSE	37.65	9	1350	NA	NA
VVKPVPITSPAVSKVTST	Q8CI51|PDLI5_MOUSE	49.94	18	433	NA	NA
VVKPVPITSPAVSKVTSTT	Q8CI51|PDLI5_MOUSE	49.85	19	105	NA	NA
VVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.94	16	3890	2650	4520
VVLVYRPGLPNALDG	Q8R4P9|MRP7_MOUSE	46.51	15	58.1	NA	NA
VVPPFLQPEVM(+15.99)GVSK	P02666	49.34	15	1560	NA	NA
VVPPFLQPEVMGVSK	P02666	36.07	15	105	NA	NA
VVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	33.99	13	247	NA	NA
VVVPPFLQPEVM(+15.99)GVSK	P02666	42.06	16	498	NA	NA
VVVPPFLQPEVMGVSK	P02666	25.62	16	141	NA	NA
VVWDYFTQLSNNAK	P06728|APOA4_MOUSE	49.73	14	155	NA	106
VVWDYFTQLSNNAKE	P06728|APOA4_MOUSE	49.72	15	2250	NA	1860
VVWDYFTQLSNNAKEA	P06728|APOA4_MOUSE	49.86	16	1390	NA	1330
VVWDYFTQLSNNAKEAV	P06728|APOA4_MOUSE	49.72	17	428	NA	319
VVYSYKASQPDELTI	Q3USJ8|FCSD2_MOUSE	45.38	15	705	NA	1180
VWDYFTQLSNNAKE	P06728|APOA4_MOUSE	48.63	14	317	NA	252
VWDYFTQLSNNAKEA	P06728|APOA4_MOUSE	49.54	15	123	NA	70
VYLIQGTQVYVFLTK	Q91X72|HEMO_MOUSE	49.62	15	3160	1610	2500
VYLLVVNHPDSSSTVE	P52430|PON1_MOUSE	48.27	16	1240	NA	1570
VYPAYASVKAIESPS	Q9JM62|REEP6_MOUSE	49.9	15	3250	NA	2020
VYPAYASVKAIESPSK	Q9JM62|REEP6_MOUSE	49.78	16	1370	NA	NA
VYPTPAYTIPFYTPIPNG	O08573|LEG9_MOUSE	49.69	18	332	NA	277
VYTYGKPVPGLVT	Q61838|PZP_MOUSE	47.02	13	1280	NA	1360
VYTYGKPVPGLVTL	Q61838|PZP_MOUSE	48.57	14	205	NA	131
WDYFTQLSNNAKE	P06728|APOA4_MOUSE	48.67	13	681	NA	511
WDYFTQLSNNAKEA	P06728|APOA4_MOUSE	49.45	14	1190	NA	314
WDYFTQLSNNAKEAV	P06728|APOA4_MOUSE	49.32	15	322	NA	333
WEDVSSTPFAAVTPEK	Q60805|MERTK_MOUSE	49.43	16	66.4	NA	79
WGIDPYDQPNAIYIER	O88307|SORL_MOUSE	49.9	16	147	NA	NA
WGIDPYDQPNAIYIERH	O88307|SORL_MOUSE	49.94	17	749	NA	436
WKALYTDPKSSETA	Q920A5|RISC_MOUSE	36.51	14	201	NA	151
WKALYTDPKSSETAA	Q920A5|RISC_MOUSE	40.77	15	1650	NA	1750
WKALYTDPKSSETAAF	Q920A5|RISC_MOUSE	48.48	16	661	NA	441
WKALYTDPKSSETAAFV	Q920A5|RISC_MOUSE	29.4	17	94.3	NA	NA
WNDPGAQYSLVN	Q9R100|CAD17_MOUSE	45.74	12	53.1	NA	NA
WNDPGAQYSLVNK	Q9R100|CAD17_MOUSE	48.9	13	315	NA	134
WNDPGAQYSLVNKE	Q9R100|CAD17_MOUSE	49.83	14	2400	NA	2060
WNDPGAQYSLVNKEK	Q9R100|CAD17_MOUSE	49.84	15	4210	NA	1760
WPENQWRPPLPDNYPE	P09470|ACE_MOUSE	49.94	16	10100	NA	7180
WQGGVYASPSIAGSRP	Q8R0X7|SGPL1_MOUSE	49.73	16	171	NA	480
WQGGVYASPSIAGSRPG	Q8R0X7|SGPL1_MOUSE	49.82	17	7080	217	5520
WQQKSTGPQVILAKEPKA	Q99MZ6|MYO7B_MOUSE	48.2	18	188	NA	NA
WSIENVSFGSGGALLQK	Q99KQ4|NAMPT_MOUSE	49.81	17	136	127	NA
WTYNPAAVSKVAPA	Q80SY4|MIB1_MOUSE	48.83	14	682	NA	423
WVRTDM(+15.99)AGPKATKSPEE	P48758|CBR1_MOUSE	45.83	17	6820	NA	NA
WVRTDMAGPKATKSPE	P48758|CBR1_MOUSE	39.03	16	669	NA	732
WVRTDMAGPKATKSPEE	P48758|CBR1_MOUSE	49.92	17	12800	NA	6310
WVYDTPGSSIVTE	O70577|S22A2_MOUSE:O08966|S22A1_	25.39	13	87.2	NA	NA
Y(+42.01)(+79.97)WTDWEEDPKDS(+79.	Q91ZX7|LRP1_MOUSE	25.72	17	1800	NA	NA
Y(+42.01)LN(+15.00)IYVPAHAHEGSN	Q8BK48|EST2E_MOUSE	29.79	15	280	NA	324
Y(+42.01)LN(+15.00)IYVPAHAHEGSNL	Q8BK48|EST2E_MOUSE	36.8	16	127	NA	NA
YAFSPPRGLLSK	Q91WC9|DGLB_MOUSE	48.74	12	498	NA	293
YAFSPPRGLLSKSL	Q91WC9|DGLB_MOUSE	48.86	14	342	NA	257
YAKKIFLAPKPAPL	Q9Z1T1|AP3B1_MOUSE	49.55	14	1380	NA	695
YAKKIFLAPKPAPLLE	Q9Z1T1|AP3B1_MOUSE	48.75	16	223	NA	179
YAVRGPIVQRALE	Q8QZR5|ALAT1_MOUSE	47.25	13	5620	NA	4100
YAVRGPIVQRALEL	Q8QZR5|ALAT1_MOUSE	46.97	14	6380	NA	5620
YAVYETPTAH	Q9QZ06|TOLIP_MOUSE	31.07	10	318	NA	NA
YAVYETPTAHN	Q9QZ06|TOLIP_MOUSE	40.34	11	238	NA	209
YAVYETPTAHNG	Q9QZ06|TOLIP_MOUSE	41.99	12	425	NA	336
YAVYETPTAHNGA	Q9QZ06|TOLIP_MOUSE	43.26	13	359	NA	NA
YAVYETPTAHNGAK	Q9QZ06|TOLIP_MOUSE	45.64	14	544	NA	333
YAVYETPTAHNGAKN	Q9QZ06|TOLIP_MOUSE	46.74	15	524	NA	321
YAVYETPTAHNGAKNP	Q9QZ06|TOLIP_MOUSE	49.6	16	6440	NA	2760

YAVYETPTAHNGAKNPR	Q9QZ06|TOLIP_MOUSE	49.78	17	13000	324	9990
YDDATAVPSTAKEPPPP	Q91XQ6|LAP4B_MOUSE	47.11	17	583	NA	NA
YDHNFPYKDPVAALYEDG	P16301|LCAT_MOUSE	45.99	18	433	NA	NA
YDKYFTNPQISQGVPG	Q3U0J8|TBD2B_MOUSE	48.4	16	1010	NA	1090
YDVKAPAM(+15.99)FNIRNIGK	P97351|RS3A_MOUSE	42.91	16	192	576	369
YEAFYQRSFAEKAYE	Q6T3U4|NPCL1_MOUSE	45.64	15	801	NA	53
YEAFYQRSFAEKAYES	Q6T3U4|NPCL1_MOUSE	49.64	16	3560	NA	1600
YEGPETHTSL	P14483|HB2A_MOUSE	36.44	10	391	NA	304
YEGPETHTSLR	P14483|HB2A_MOUSE	48.09	11	466	NA	401
YEKLAEPTVSYSSYR	Q04592|PCSK5_MOUSE	39.32	15	175	NA	232
YEPPAPAPAPLPPP	O35609|SCAM3_MOUSE	47.96	14	1680	NA	1390
YEWAPPVQNQALAR	P47226|TES_MOUSE	38.12	14	22.9	NA	NA
YEYVSPEQLSGFDK	Q80TA1|EPT1_MOUSE	43.75	14	254	NA	111
YFEKTHEQLTPLVRSAGTS	P09813|APOA2_MOUSE	49.87	19	423	NA	NA
YFIEKVIPSTANSN	E9Q7P9|CDHR2_MOUSE	49.32	14	228	NA	114
YFIEKVIPSTANSNN	E9Q7P9|CDHR2_MOUSE	47.03	15	192	NA	159
YFYQM(+15.99)AKIHPEPG	Q3UZZ6|ST1D1_MOUSE	47.89	13	522	NA	331
YFYQMAKIHPEPG	Q3UZZ6|ST1D1_MOUSE	49.76	13	1190	NA	881
YGARYVGSM(+15.99)VADVHR	P70695|F16P2_MOUSE	48.67	15	102	NA	NA
YGIPFAAPTALASRDG	Q91VX2|UBAP2_MOUSE	47.89	16	1760	NA	1300
YGIPFAAPTALASRDGN	Q91VX2|UBAP2_MOUSE	42.88	17	585	NA	508
YGPYSGAYPAGTQV	Q9QZC7|PKHB2_MOUSE	44.38	14	146	NA	NA
YGPYSGAYPAGTQVV	Q9QZC7|PKHB2_MOUSE	48.64	15	146	NA	NA
YGQPPTGYSTPTAPQAYSQPVQ	Q61545|EWS_MOUSE	49.81	22	49.9	NA	868
YHDTSYKPPAGRTAAPE	Q69ZQ1|MYORG_MOUSE	49.53	17	558	NA	741
YHDYYITSTSNGSLE	P52795|EFNB1_MOUSE	48.78	15	287	NA	657
YHLEYVSSELRKSLQ	E9Q414|APOB_MOUSE	48.8	15	1180	NA	1270
YIEGYVPSQADVAVFE	O70251|EF1B_MOUSE	39.57	16	1520	NA	1570
YIFIPSSIRDYLML	P70277|SIA7B_MOUSE	44.87	14	203	NA	NA
YIM(+15.99)QYIAAITNPSQRA	Q5SYD0|MYO1D_MOUSE	48.38	16	367	NA	404
YIQTPLPSRAIVG	O89093|CCL20_MOUSE	37.04	13	488	NA	235
YISVFKGSGC(+57.02)WS(+79.97)SV	Q61847|MEP1B_MOUSE	37.8	14	588	NA	454
YIWQGSQASQDE	Q62468|VILI_MOUSE	46.34	12	189	NA	NA
YIYFHKAPSPEKAEEE	Q61024|ASNS_MOUSE	41.99	16	251	NA	992
YKKELEEQLGPVAEETR	P08226|APOE_MOUSE	36.54	17	1010	NA	NA
YKKELEEQLGPVAEETRAR	P08226|APOE_MOUSE	48.5	19	217	NA	NA
YKKSPVYKNPTPGSSE	Q99PG0|AAAD_MOUSE	34.71	16	160	NA	117
YKKSPVYKNPTPGSSEL	Q99PG0|AAAD_MOUSE	43.11	17	182	NA	NA
YKKSPVYKNPTPGSSELAQ	Q99PG0|AAAD_MOUSE	42.27	19	167	NA	NA
YKPFQNPVPNQSP	P16382|IL4RA_MOUSE	43.44	13	191	NA	162
YKPFQNPVPNQSPS	P16382|IL4RA_MOUSE	49.57	14	11500	NA	13800
YKSFVQNYPVVSIEDPF	P17182|ENOA_MOUSE	49.94	17	148	NA	293
YKSFVQNYPVVSIEDPFD	P17182|ENOA_MOUSE	49.95	18	354	NA	264
YKTYFQGSLPARAAYQ	P52760|RIDA_MOUSE	38.75	16	221	NA	161
YKVIPKSKFVLVKF	P57759|ERP29_MOUSE	49.85	14	2130	NA	1070
YKYSFKGPHLVQSDG	Q9D0F3|LMAN1_MOUSE	37.01	15	299	NA	NA
YLAVFDGPSTNSR	Q9JLB4|CUBN_MOUSE	35.15	13	198	NA	95.9
YLAVFDGPSTNSRL	Q9JLB4|CUBN_MOUSE	32.25	14	39.6	NA	NA
YLLAALGGNSSPSAKDIKK	P99027|RLA2_MOUSE	49.4	19	118	NA	NA
YLLSQSSPAPLTAAE	Q91YR1|TWF1_MOUSE	49.12	15	279	NA	189
YLLSQSSPAPLTAAEE	Q91YR1|TWF1_MOUSE	49.89	16	2240	NA	1320
YLLVVNHPDSSSTVE	P52430|PON1_MOUSE	47.19	15	1890	NA	1960
YLNEYGAPDAGGLE	Q8BFR4|GNS_MOUSE	46.46	14	96.5	NA	NA
YLNIYTPAHAHEG	Q91WG0|EST2C_MOUSE	45.91	13	2670	NA	1750
YLNIYTPAHAHEGS	Q91WG0|EST2C_MOUSE	40.97	14	489	NA	346
YLNIYTPAHAHEGSN	Q91WG0|EST2C_MOUSE	48.67	15	18800	197	17000
YLNIYTPAHAHEGSNL	Q91WG0|EST2C_MOUSE	48.7	16	15600	132	14100
YLNIYTPAHAHEGSNLP	Q91WG0|EST2C_MOUSE	49.8	17	6480	NA	6590
YLNIYTPAHAHEGSNLPV	Q91WG0|EST2C_MOUSE	49.89	18	43500	NA	23400
YLNIYTPTHAQEGSNLPV	Q8QZR3|EST2A_MOUSE	40.38	18	169	NA	NA
YLNIYVPAHAHE	Q8BK48|EST2E_MOUSE	38.6	12	282	NA	200
YLNIYVPAHAHEG	Q8BK48|EST2E_MOUSE	45.58	13	20400	436	16400
YLNIYVPAHAHEGS	Q8BK48|EST2E_MOUSE	46.91	14	3470	NA	3870
YLNIYVPAHAHEGSN	Q8BK48|EST2E_MOUSE	48.99	15	132000	5110	129000
YLNIYVPAHAHEGSNL	Q8BK48|EST2E_MOUSE	48.5	16	101000	2360	82600
YLNIYVPAHAHEGSNLP	Q8BK48|EST2E_MOUSE	49.39	17	38900	NA	38400
YLNIYVPAHAHEGSNLPV	Q8BK48|EST2E_MOUSE	49.91	18	90800	2390	102000
YLPYKSPGINVD	Q9JHJ8|ICOSL_MOUSE	39.9	12	159	NA	75.3
YLPYKSPGINVDSS	Q9JHJ8|ICOSL_MOUSE	49.11	14	1320	NA	1170
YLPYKSPGINVDSSY	Q9JHJ8|ICOSL_MOUSE	42.8	15	76.4	NA	NA
YLVYQEPIPTAQLV	P49722|PSA2_MOUSE	49.43	14	689	NA	426
YNFVTPLTHM(+15.99)VVT	A6X935|ITIH4_MOUSE	43.08	13	916	NA	592
YNFVTPLTHM(+15.99)VVTKP	A6X935|ITIH4_MOUSE	44.18	15	5000	NA	7450
YNFVTPLTHM(+15.99)VVTKPE	A6X935|ITIH4_MOUSE	48.13	16	488	NA	344
YNFVTPLTHMVVT	A6X935|ITIH4_MOUSE	44.19	13	394	NA	541
YNFVTPLTHMVVTKP	A6X935|ITIH4_MOUSE	49.5	15	5320	NA	9000
YNFVTPLTHMVVTKPE	A6X935|ITIH4_MOUSE	43.53	16	67.8	NA	373

YNPEAM(+15.99)VAPSVLSNIQ	Q3UQN2|FCHO2_MOUSE	49.29	16	175	NA	242
YNPEAMVAPSVLSNIQ	Q3UQN2|FCHO2_MOUSE	48.36	16	122	NA	570
YNSQITAPYADRVT	O88792|JAM1_MOUSE	46.68	14	295	NA	200
YNSQITAPYADRVTF	O88792|JAM1_MOUSE	48.36	15	1810	NA	1610
YNSQITAPYADRVTFS	O88792|JAM1_MOUSE	49.81	16	3610	53	3770
YNTASNKTRLSRTPGNRIVYLYTKKVGK	Q9D1R9|RL34_MOUSE	47.84	30	563	NA	3510
YNTASNKTRLSRTPGNRIVYLYTKKVGK	Q9D1R9|RL34_MOUSE	48.93	31	1610	12500	2050
YNTASNKTRLSRTPGNRIVYLYTKKVGK	Q9D1R9|RL34_MOUSE	49.95	32	5200	8910	7760
YPAGSPGYNPPQM(+15.99)NTL	Q8K419|LEG4_MOUSE	48.88	16	1030	NA	507
YPAGSPGYNPPQM(+15.99)NTLP	Q8K419|LEG4_MOUSE	49.54	17	4680	NA	3580
YPAGSPGYNPPQM(+15.99)NTLPV	Q8K419|LEG4_MOUSE	49.71	18	7120	NA	5360
YPAGSPGYNPPQM(+15.99)NTLPVM(+1	Q8K419|LEG4_MOUSE	49.87	19	619	NA	NA
YPAGSPGYNPPQMNTLP	Q8K419|LEG4_MOUSE	47.42	17	6710	NA	730
YPAGSPGYNPPQMNTLPV	Q8K419|LEG4_MOUSE	49.86	18	2570	NA	4730
YPAGSPGYNPPQMNTLPVM(+15.99)	Q8K419|LEG4_MOUSE	48.24	19	220	NA	47.6
YPAYASVKAIESPS	Q9JM62|REEP6_MOUSE	49.39	14	3790	NA	2840
YPAYASVKAIESPSK	Q9JM62|REEP6_MOUSE	49.86	15	1310	NA	498
YPAYASVKAIESPSKE	Q9JM62|REEP6_MOUSE	47.11	16	78.2	NA	NA
YPDDYQYYPPGVRPDS	Q7TQG1|PKHA6_MOUSE	48.71	16	88.1	NA	NA
YPDKKVTFSSGYVNLSPEN	P06684|CO5_MOUSE	44.12	19	9470	NA	9420
YPDKKVTFSSGYVNLSPENK	P06684|CO5_MOUSE	44.82	20	138	NA	668
YPENFAPSFPHGSPG	Q3UDK1|TRAD1_MOUSE	49.68	15	4920	NA	3610
YPFDFRGARILSGQDE	O55026|ENTP2_MOUSE	31	16	6030	NA	NA
YPGSPPPGGYGQPSVLPGGYP	Q8BJZ3|LFG3_MOUSE	49.54	21	1900	NA	1640
YPGSPPPGGYGQPSVLPGGYPA	Q8BJZ3|LFG3_MOUSE	44.03	22	5540	NA	NA
YPLAFGVPAALM(+15.99)A	Q9JIP7|S15A1_MOUSE	40.03	13	165	NA	NA
YPLAFGVPAALM(+15.99)AVA	Q9JIP7|S15A1_MOUSE	46.9	15	400	NA	NA
YPNFAGPQAALANK	Q8BJW6|EIF2A_MOUSE	46.4	14	143	NA	118
YPNFAGPQAALANKS	Q8BJW6|EIF2A_MOUSE	46.57	15	211	NA	179
YPNPTLDHYKEPSAIFQLPY	Q60677|ITAE_MOUSE	28.43	20	538	NA	NA
YPNPTLDHYKEPSAIFQLPYE	Q60677|ITAE_MOUSE	26.63	21	129	NA	NA
YPNSFSAPEQQRSALE	P24270|CATA_MOUSE	45.77	16	306	NA	NA
YPNTPYISPVASYS	Q3UPL0|SC31A_MOUSE	46.5	14	115	NA	NA
YPNTPYISPVASYSG	Q3UPL0|SC31A_MOUSE	49.15	15	489	NA	NA
YPNTPYISPVASYSGQP	Q3UPL0|SC31A_MOUSE	49.76	17	9670	58.6	9960
YPNTPYISPVASYSGQPQ	Q3UPL0|SC31A_MOUSE	49.93	18	6360	NA	7780
YPPPYPPAAFQGPSDHAAY	Q9JJ00|PLS1_MOUSE	45.83	19	1060	NA	508
YPPPYPPAAFQGPSDHAAYPI	Q9JJ00|PLS1_MOUSE	49.92	21	8690	NA	4770
YPPPYPPAAFQGPSDHAAYPIP	Q9JJ00|PLS1_MOUSE	48.23	22	3030	NA	1610
YPPPYPPAAFQGPSDHAAYPIPQ	Q9JJ00|PLS1_MOUSE	49.66	23	6710	NA	2110
YPPSGPTYRGPVPWHT	Q9WV54|ASAH1_MOUSE	45.4	16	1070	NA	2410
YPPSGPTYRGPVPWHTIN	Q9WV54|ASAH1_MOUSE	46.08	18	36300	NA	50100
YPSQASIYSPPAAAAAA	P70297|STAM1_MOUSE	48.75	17	647	NA	467
YPSQASIYSPPAAAAAAA	P70297|STAM1_MOUSE	49.91	18	23600	141	27200
YPSQASIYSPPAAAAAAAA	P70297|STAM1_MOUSE	49.91	19	68100	1350	67600
YPSSPPVVNTVKG	Q8VCT4|EST1D_MOUSE	44.28	13	1680	NA	488
YPTAYPAAAPAYNPS	Q8BGZ2|F168A_MOUSE	46.87	15	691	NA	NA
YPTPAYTIPFYT(+79.97)PIPN(+15.00)	O08573|LEG9_MOUSE	31.32	16	282	NA	NA
YPTPAYTIPFYTPIPN	O08573|LEG9_MOUSE	49.52	16	8220	NA	5970
YPTPAYTIPFYTPIPN(+15.00)GL	O08573|LEG9_MOUSE	45.08	18	133	NA	NA
YPTPAYTIPFYTPIPNG	O08573|LEG9_MOUSE	49.68	17	60700	2150	71100
YPTPAYTIPFYTPIPNGLYP	O08573|LEG9_MOUSE	49.94	20	1550	NA	3520
YPTPAYTIPFYTPIPNGLYPS	O08573|LEG9_MOUSE	49.94	21	33400	99.2	36500
YPTPAYTIPFYTPIPNGLYPSK	O08573|LEG9_MOUSE	49.94	22	201	NA	NA
YPVVPVHLDGTF	O35291|RNAS2_MOUSE:P97425|ECP2_	43.04	12	2790	1020	859
YPYLGPSTLRDRP	P97390|VPS45_MOUSE	38.74	13	690	NA	NA
YQLSIHKNPNASEPK	Q8VDN2|AT1A1_MOUSE	41.5	15	511	NA	329
YQLSIHKNPNASEPKH	Q8VDN2|AT1A1_MOUSE	47.08	16	407	NA	274
YQLYFQEPGVAEAE	P34914|HYES_MOUSE	49.85	14	898	NA	534
YQLYFQEPGVAEAELEK	P34914|HYES_MOUSE	49.68	17	106	NA	150
YRPSFVHPGAATVPT	Q9DCP9|DAZP2_MOUSE	30.89	15	392	NA	NA
YSFKAARALLDHRK	Q9WTN3|SRBP1_MOUSE	49.12	14	482	NA	257
YSIVSAPAAQKVREL	Q8BH86|GLUCM_MOUSE	49.13	15	655	NA	491
YSKYSAPRLPAAL	P97432|NBR1_MOUSE	49.44	13	234	NA	83.7
YSKYSAPRLPAALE	P97432|NBR1_MOUSE	49.82	14	538	NA	500
YSKYSAPRLPAALEQ	P97432|NBR1_MOUSE	49.83	15	1550	NA	1430
YSLQLTEPTANELG	Q9Z1P8|ANGL4_MOUSE	44.18	14	78.7	NA	NA
YSLQLTEPTANELGAT	Q9Z1P8|ANGL4_MOUSE	37.12	16	242	NA	NA
YSRKALYKRKYSAAKTKVEKKKKKEK	P47911|RL6_MOUSE	49.95	26	763	1140	2040
YSRKALYKRKYSAAKTKVEKKKKKEKVL	P47911|RL6_MOUSE	49.95	28	2020	NA	NA
YSRKALYKRKYSAAKTKVEKKKKKEKVL	P47911|RL6_MOUSE	49.95	29	6330	NA	3790
YSTSYSGPYPAAAPP	Q9WVH9|FBLN5_MOUSE	32.62	15	1350	NA	NA
YSTYKTPVPETNIPG	Q60855|RIPK1_MOUSE	39.15	15	1660	NA	1240
YSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.75	15	89.6	310	NA
YTAKGLFRAAVPSGAST	P17183|ENOG_MOUSE:P17182|ENOA_M	48.05	17	248	NA	806
YTAKGLFRAAVPSGASTG	P17183|ENOG_MOUSE:P17182|ENOA_M	49.48	18	1080	NA	651
YTDIQEPM(+15.99)LNAAQEQ	Q9QZM0|UBQL2_MOUSE:Q8R317|UBQL	49.18	15	472	NA	137

YTDPKSSETAAF	Q920A5|RISC_MOUSE	37.35	12	711	NA	1170
YTDPKSSETAAFV	Q920A5|RISC_MOUSE	30.97	13	705	NA	376
YTGYPTAYPAAAPAYNPS	Q8BGZ2|F168A_MOUSE	49.91	18	63.1	NA	106
YTHEYKGPKADLKKD	Q8BU14|SEC62_MOUSE	48.97	15	935	NA	978
YTIHWNGPAPRTTFL	Q5FWI3|CEIP2_MOUSE	36.01	15	80.6	NA	NA
YTIPFYTPIPN	O08573|LEG9_MOUSE	41.64	11	6530	NA	NA
YTIPFYTPIPNG	O08573|LEG9_MOUSE	47.61	12	89000	1960	77900
YTIPFYTPIPNGL	O08573|LEG9_MOUSE	47.57	13	4320	NA	1340
YTIPFYTPIPNGLY	O08573|LEG9_MOUSE	47.35	14	774	NA	145
YTIPFYTPIPNGLYP	O08573|LEG9_MOUSE	49.15	15	29600	373	23700
YTIPFYTPIPNGLYPS	O08573|LEG9_MOUSE	49.66	16	25600	938	19400
YTIPFYTPIPNGLYPSK	O08573|LEG9_MOUSE	49.93	17	426	NA	483
YTPYYVAPEVLGPE	Q3UMW7|MAPK3_MOUSE:P49138|MAP	48.89	14	265	NA	146
YTPYYVAPEVLGPEK	Q3UMW7|MAPK3_MOUSE:P49138|MAP	49.65	15	1280	NA	NA
YTQKAPQVSTP	P07724|ALBU_MOUSE	36.62	11	206	NA	139
YTQKAPQVSTPT	P07724|ALBU_MOUSE	47.88	12	750	NA	487
YTQKAPQVSTPTL	P07724|ALBU_MOUSE	46.93	13	1580	NA	816
YTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.7	14	995	NA	755
YTQKAPQVSTPTLVE	P07724|ALBU_MOUSE	49.63	15	1000	NA	1320
YTQKAPQVSTPTLVEA	P07724|ALBU_MOUSE	49.9	16	621	NA	540
YTYGKPVPGHVKI	P28665|MUG1_MOUSE	29.75	13	43.9	NA	NA
YVASYLLAALGGNSSPSAKDIKK	P99027|RLA2_MOUSE	49.94	23	1170	NA	92.6
YVDPTPDPNTAYASYPSASVENYQQPP	O55101|SNG2_MOUSE	41.66	27	579	NA	2060
YVPWNFHEPQPGQYE	P23780|BGAL_MOUSE	49.9	15	598	NA	280
YVTQFHPPHIE	P01887|B2MG_MOUSE	44.43	11	1180	NA	796
YVTQFHPPHIEIQ	P01887|B2MG_MOUSE	48.71	13	184000	2180	141000
YVTQFHPPHIEIQM	P01887|B2MG_MOUSE	48.76	14	7900	NA	16200
YVTQFHPPHIEIQM(+15.99)	P01887|B2MG_MOUSE	49.73	14	40300	677	34700
YVTQFHPPHIEIQM(+15.99)L	P01887|B2MG_MOUSE	49.73	15	266000	1040	209000
YVTQFHPPHIEIQM(+15.99)LK	P01887|B2MG_MOUSE	49.91	16	52300	NA	36700
YVTQFHPPHIEIQM(+15.99)LKN	P01887|B2MG_MOUSE	49.92	17	14100	NA	10400
YVTQFHPPHIEIQM(+15.99)LKNG	P01887|B2MG_MOUSE	49.72	18	7440	NA	3090
YVTQFHPPHIEIQML	P01887|B2MG_MOUSE	49.59	15	39500	NA	72000
YVTQFHPPHIEIQMLK	P01887|B2MG_MOUSE	49.49	16	15300	NA	38900
YVTQFHPPHIEIQMLKN	P01887|B2MG_MOUSE	49.83	17	4510	NA	9160
YVTQFHPPHIEIQMLKNG	P01887|B2MG_MOUSE	49.43	18	3030	NA	4920
YVTQFHPPHIEIQMLKNGK	P01887|B2MG_MOUSE	49.93	19	700	NA	366
YVTQFHPPHIEIQMLKNGKK	P01887|B2MG_MOUSE	40.57	20	167	NA	NA
YVYIAELLAHK	P52430|PON1_MOUSE	40.93	11	214	NA	NA
YYFYQM(+15.99)AKIHPEPG	Q3UZZ6|ST1D1_MOUSE	49.76	14	116	NA	NA
YYFYQMAKIHPEPG	Q3UZZ6|ST1D1_MOUSE	49.84	14	280	NA	438
YYLPYKSPGINVDS	Q9JHJ8|ICOSL_MOUSE	49.47	14	305	NA	202
YYLPYKSPGINVDSS	Q9JHJ8|ICOSL_MOUSE	49.48	15	5650	NA	4580
YYLPYKSPGINVDSSY	Q9JHJ8|ICOSL_MOUSE	49.89	16	1440	NA	1250
YYLVYQEPIPTAQLV	P49722|PSA2_MOUSE	49.86	15	1060	NA	831
YYLVYQEPIPTAQLVQ	P49722|PSA2_MOUSE	49.66	16	95.6	NA	NA
YYNEVHSPSVAVEM(+15.99)G	Q99KC8|VMA5A_MOUSE	35.77	15	371	NA	NA
YYRYM(+15.99)NPAIVAPDG	Q3UQ44|IQGA2_MOUSE	26.64	14	57	NA	NA
YYYFYQM(+15.99)AKIHPEPG	Q3UZZ6|ST1D1_MOUSE	49.88	15	313	NA	208
YYYFYQMAKIHPEPG	Q3UZZ6|ST1D1_MOUSE	49.75	15	642	NA	901

5-KO_CAD						
Peptide	Accession	X.10LgP	Length	Area.1	Area.3	Area.5
A(+42.01)ATPKKAKKPKVVKVKPVK	P10922|H10_MOUSE	49.95	19	6310	4450	3690
A(+42.01)N(+15.00)DTGAKKKKKQKKK	O70310|NMT1_MOUSE	43.24	16	NA	994	NA
A(+42.01)PKAKASKPKASKPKATKAKKA	P43277|H13_MOUSE	41.18	27	NA	604	NA
A(+42.01)SKRALVILAKGAE	Q99LX0|PARK7_MOUSE	29.71	14	536	94	1390
AAAGAKKAKSP	P43274|H14_MOUSE	35.21	11	2190	2920	3580
AAAGAKKAKSPKKAKATKAKKAPK	P43274|H14_MOUSE	49.95	24	NA	3710	2280
AAAKKTVKTPKKPKKPAVSKK	P43275|H11_MOUSE	49.95	21	764	301	509
AAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	43.16	17	NA	4630	NA
AAGAKKAKSPKKAKATKAKKAPKSPAKA	P43274|H14_MOUSE	49.95	29	NA	1120	NA
AAGVKKVAKSPKKAKAAAKPKKAAKSPA	P43276|H15_MOUSE	49.95	31	315	376	1400
AAGVKKVAKSPKKAKAAAKPKKAAKSPA	P43276|H15_MOUSE	48.95	32	NA	1550	2110
AAKPKKAAKSPAKAKAPKAKASKP	P43277|H13_MOUSE	28.08	24	NA	286	NA
AAKPKTSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.95	22	NA	1750	1780
AAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	17	20900	861	3560
AAKSPAKPKA	P43276|H15_MOUSE	42.21	10	NA	5070	4480
AALRPLVKPKIVKKRTKKFIRHQSDR	P17932|RL32P_MOUSE:P62911|RL32_M	48.95	26	NA	836	777
ADPSAFAAAAPAAAATT	P14869|RLA0_MOUSE	48.62	17	6470	620	5020
AFKKTKKEVKKVATPKKAAKPKK	P10922|H10_MOUSE	49.56	23	66.4	732	NA
AGLQFPVGR	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	40.73	9	NA	171	NA
AKAAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	48.95	19	NA	4450	6380
AKASKPKASKPKATKAKKAAP	P43277|H13_MOUSE	48.66	21	NA	408	1530
AKASKPKASKPKATKAKKAAPR	P43277|H13_MOUSE	48.93	22	NA	184	824
AKKAAPRKK	P43277|H13_MOUSE	38.79	9	2090	1950	NA
AKKPAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.95	20	1600	1550	1120
AKKTVKTPKKPKKPAVSKK	P43275|H11_MOUSE	49.94	19	456	401	NA
AKKVAAKKK	P15864|H12_MOUSE	42.65	9	5880	543	673
AKPKKAAKSPAKPKA	P43276|H15_MOUSE	46.33	15	NA	242	686
AKPKKAAPK	P43275|H11_MOUSE	37.64	9	3120	603	NA
AKSPAKPKA	P43276|H15_MOUSE	35.32	9	NA	492	962
AKSPKKAK	P15864|H12_MOUSE:P43276|H15_MOU	38.45	8	269	85.9	NA
AKSPKKAKAAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	48.95	25	NA	548	543
AKTVKPKAKSSAKR	P10922|H10_MOUSE	49.8	14	539	484	1230
ALRAPRKKIHRRVLKKNPLK	Q9D8E6|RL4_MOUSE	39.85	20	NA	1460	1340
ALRAPRKKIHRRVLKKNPLKNLR	Q9D8E6|RL4_MOUSE	43.23	23	NA	521	NA
APAAAATTAAPAAAAAPAK	P14869|RLA0_MOUSE	49.89	19	7290	135	NA
APETRSQVTPSVPSEALDDS	Q7TQH7|LRP10_MOUSE	49.93	20	12000	213	9320
APGPSHTVAAPQAAAAAAL	Q80U93|NU214_MOUSE	49.31	19	4130	74.1	4350
APKAKASKPKASKPKATKAKKAAPRKK	P43277|H13_MOUSE	43.18	27	411	887	NA
APKKGSKKAISKAQKKDGKKRKR	Q64475|H2B1B_MOUSE	43.25	23	NA	2370	NA
APKKGSKKAISKAQKKDGKKRKRSR	Q64475|H2B1B_MOUSE	43.24	25	NA	3150	NA
APKKGSKKAVTKAQKKDGKKRKR	Q8CGP0|H2B3B_MOUSE:Q8CGP2|H2B1	43.25	23	NA	2850	NA
APKKGSKKAVTKAQKKDGKKRKRSR	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	48.95	25	NA	3150	NA
APM(+15.99)YYRGAQAAIV	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	45.29	13	4700	57.2	2450
APM(+15.99)YYRGAQAAIVV	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	37.79	14	22400	2590	17500
APM(+15.99)YYRGAQAAIVVY	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	49.55	15	79700	13700	62300
APM(+15.99)YYRGAQAAIVVYD	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	49.61	16	118000	12500	81100
APPLPIKTPIPTPSTLP	Q7TQH7|LRP10_MOUSE	49.88	17	8360	142	11300
APSTM(+15.99)KIKIIAPPERKY	P63260|ACTG_MOUSE:P60710|ACTB_M	47.96	17	NA	114	NA
AQ(+15.00)KKDGKKRKRSRKESYSIYVY	Q64524|H2B2E_MOUSE	43.25	31	NA	498	NA
AQKKDGKKRKRSRKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.25	23	NA	16800	NA
AQKKDGKKRKRSRKESYSVYVYKVL	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.24	25	NA	2200	81.6
AQKKDGKKRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	48.95	26	NA	16400	375
AQKKDGKKRKRSRKESYSVYVYKVLKQ	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	49.95	31	23600	251000	24000
ASKPKASKPKATKAKKAAPR	P43277|H13_MOUSE	48.95	20	NA	192	NA
ASKPKATKAKKAAPR	P43277|H13_MOUSE	48.93	15	333	1000	4030
ASKPKKAK	P10922|H10_MOUSE	39.67	8	NA	939	685
ASKPKKAKTVKPK	P10922|H10_MOUSE	42.22	13	NA	85.7	NA
ASKPKKAKTVKPKAK	P10922|H10_MOUSE	49.84	15	NA	1260	1100
ASKPKKAKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.95	25	4010	2260	NA
ASKPKVTKPKTAKPKAAKAKKAVSKKK	P43276|H15_MOUSE	49.95	27	8160	8190	3110
ASLVYENASAIM(+15.99)AHE	E9Q0N2|PTPRH_MOUSE	48.34	15	1170	53.1	855
ATKAKKAAPR	P43277|H13_MOUSE	43.09	10	685	2220	3420
ATNPIITPVAQENQ	P08226|APOE_MOUSE	45.99	14	17500	548	12300
ATPKKTAKKTPKKAKKPA	P43277|H13_MOUSE	49.94	18	2240	3320	5610
AVTKAQKKDGKKRKRSRKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.24	27	NA	1610	NA
DARSYTAAVANRAK	Q91XS1|MTMR4_MOUSE	47.02	14	25400	896	19800
DARSYTAAVANRAKGGG	Q91XS1|MTMR4_MOUSE	49.93	17	86000	2710	49900
DFPSVVVVGLGKRS	Q9CPY7|AMPL_MOUSE	47.93	14	350	91.6	351
DFSALESQLQDTQELLQEENR	Q8VDD5|MYH9_MOUSE	49.93	21	NA	83.8	NA
DGELTYENVQVSPVPGGPPG	P21855|CD72_MOUSE	49.53	20	1840	208	785
DGKKRKRSRKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	47.03	19	NA	2320	NA
DGKKRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	43.25	22	NA	2650	NA
DGKKRKRSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.95	27	23700	38500	3300
DGNHTLFH	P43023|CX6A2_MOUSE:P43024|CX6A1_	43.1	8	987	312	737
DM(+15.99)RQTVAVGVIKAVDKKAAGAG	P10126|EF1A1_MOUSE	49.95	23	1490	965	2150
DPKSKSKKKKS(+79.97)LKKKKDKEKKE	O08784|TCOF_MOUSE	42.21	33	NA	2530	NA
DPSAFAAAAPAAAATT	P14869|RLA0_MOUSE	49.72	16	2180	73.1	1340
DPTPDPNTAYASYPSASVEN	O55101|SNG2_MOUSE	49.93	20	14900	126	13300
DQYVKLEEQRRHRQRLEKDKKRKKKEK	O54774|AP3D1_MOUSE	43.21	31	NA	543	NA

DQYVKLEEQRRHRQRLEKDKKRKKKEK	O54774|AP3D1_MOUSE	43.13	32	NA	962	NA
DSGKDKKKKTKKIKEKYID	P11499|HS90B_MOUSE	43.24	19	NA	433	NA
DSGKDKKKKTKKIKEKYIDQ	P11499|HS90B_MOUSE	49.53	20	NA	2160	NA
DSLVHSSPHVALSHVD	Q9WV91|FPRP_MOUSE	49.86	16	7980	50.4	6710
DSPNKLYTLVTYVPVTTFK	P62900|RL31_MOUSE	48.91	19	NA	29.9	637
DSPQ(+15.00)KKTKNKKKKNKKK	Q3UZ39|LRRF1_MOUSE	37.75	17	NA	189	NA
DTEGRLEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	49.89	20	9600	47.9	9180
DTGAKKKKKQKKK	O70310|NMT1_MOUSE	48.91	14	NA	3030	2190
DTGAKKKKKQKKKKEKG	O70310|NMT1_MOUSE	48.9	18	NA	1790	NA
DVAIFARGPQAHLVH	P24823|PPBN_MOUSE:P24822|PPBI_M(	49	15	12200	313	11600
DVAIFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_M(	49.62	16	22200	711	18600
DVVYALKRQGRTLYGFGG	P62806|H4_MOUSE	26.2	18	NA	899	NA
EDGGGWWYNR	Q8K0E8|FIBB_MOUSE	42.94	10	9100	2480	371
EDIEVAPPKAHEVR	P00329|ADH1_MOUSE	48.37	14	21300	237	9970
EDVAIFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_M(	46.36	17	12600	232	11700
EDYVELPPSVSQAAKSPP	P26955|IL3RB_MOUSE	34.96	18	2340	209	388
EDYVELPPSVSQAAKSPPG	P26955|IL3RB_MOUSE	42.01	19	2130	190	1280
EEKPVPAAPVPSPVAPAPVP	P97825|JUPI1_MOUSE	49.94	20	20000	457	17600
EEKPVPAAPVPSPVAPAPVPS	P97825|JUPI1_MOUSE	49.94	21	6170	30.2	4210
EGFGHLSPTGTTEFWLGNEK	Q8VCM7|FIBG_MOUSE	49.93	20	7100	1540	733
EKPVPAAPVPSPVAPAPVP	P97825|JUPI1_MOUSE	49.94	19	11900	184	12100
ELEEQLGPVAEETR	P08226|APOE_MOUSE	47.71	14	28300	3310	13700
ENIWKAPEPVEIRE	Q9R100|CAD17_MOUSE	48.23	14	38100	200	9150
ENIWKAPEPVEIREN(+15.00)ST	Q9R100|CAD17_MOUSE	49.33	17	49500	127	12000
ENPIYKSAVTTVVNPK	P09055|ITB1_MOUSE	49.91	16	11800	209	12500
EPENPEYNTGYAVVAYR	Q64282|IFIT1_MOUSE	49.94	17	3630	117	3230
ESKEAFQEALAAAGDK	P10639|THIO_MOUSE	49.87	16	5340	56.9	4870
EVSSVEAPSVSPA	Q8BUJ9|LRP12_MOUSE	42.19	13	10200	42.6	7820
EVSSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	48.43	14	106000	3030	72800
FTAQWIAPSVQLTGYR	P11276|FINC_MOUSE	48.5	16	4380	43.9	4260
G(+42.01)KEKTHINIVVIGHVDSGKS	P62631|EF1A2_MOUSE:P10126|EF1A1_	37.52	20	NA	1550	2900
GAAAKKTVKTPKKPKKPAVSKK	P43275|H11_MOUSE	49.95	22	859	549	500
GAKAAKPK	A2APF3|CTCFL_MOUSE	28.53	8	NA	193	NA
GAKKAKSPKKAKATKAKKAPKSPAKAK	P43274|H14_MOUSE	48.95	27	NA	2380	737
GAKKKKKKQKKKK	O70310|NMT1_MOUSE	42.42	13	NA	7810	NA
GAKKKKKKQKKKKE	O70310|NMT1_MOUSE	48.95	14	NA	1830	NA
GAKKKKKKQKKKKEK	O70310|NMT1_MOUSE	48.93	15	NA	6740	NA
GAKKTVKKTPKKAKKPAAAGVKKVAKSI	P43276|H15_MOUSE	49.95	32	158	2400	2940
GDGNHTLFH	P43023|CX6A2_MOUSE:P43024|CX6A1_	39.23	9	576	256	334
GDLSQHATPLPTPAVLPG	O88746|TOM1_MOUSE	49.39	18	33100	833	13800
GDTEGRLEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	49.94	21	23700	1070	23400
GENPIYKSAVTTVVNPK	P09055|ITB1_MOUSE	49.83	17	7600	120	9660
GGEDVAIFARGPQAHLVHG	P24822|PPBI_MOUSE	48.84	19	6710	137	7420
GGKKGAKKKVVDPFSKK	P97351|RS3A_MOUSE	43.25	17	NA	233	NA
GGKRKPYHKKRKY	P62242|RS8_MOUSE	39.54	13	NA	3790	NA
GIKLESGEQSD	O08784|TCOF_MOUSE	41.77	11	233	158	438
GISRDNWHKRRKTGGKRKPYHKKR	P62242|RS8_MOUSE	47.95	24	NA	1970	3160
GISRDNWHKRRKTGGKRKPYHKKRKY	P62242|RS8_MOUSE	48.84	26	NA	3640	3260
GISRDNWHKRRKTGGKRKPYHKKRKYE	P62242|RS8_MOUSE	47.35	27	NA	1100	1800
GISRDNWHKRRKTGGKRKPYHKKRKYE	P62242|RS8_MOUSE	48.48	29	NA	5790	27100
GISRDNWHKRRKTGGKRKPYHKKRKYE	P62242|RS8_MOUSE	49.94	32	NA	5620	31700
GKDKKKKTKKIKEKYIDQ	P11499|HS90B_MOUSE	43.25	18	NA	202	NA
GKKRKRSRKESYSVYVY	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	36.08	17	NA	2580	NA
GKKRKRSRKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	47.74	18	7380	94000	4270
GKKRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	48.95	21	NA	1840	326
GKKRKRSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.44	26	10200	117000	29300
GKNKRLTKGGKKGAKKKVVDPFSK	P97351|RS3A_MOUSE	48.95	24	NA	2110	4000
GKNKRLTKGGKKGAKKKVVDPFSKK	P97351|RS3A_MOUSE	48.95	25	NA	3480	3210
GKNKRLTKGGKKGAKKKVVDPFSKKDW	P97351|RS3A_MOUSE	48.95	28	NA	582	4650
GLQFPVGR	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	39.06	8	NA	119	NA
GNRIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	43.25	17	NA	232	NA
GPDGRFVM(+15.99)GPTVAPSQ	Q05BQ1|TUTLA_MOUSE	44.67	16	31200	1070	21100
GPDGRFVM(+15.99)GPTVAPSQE	Q05BQ1|TUTLA_MOUSE	44.48	17	8610	80	5570
GPDGRFVM(+15.99)GPTVAPSQEK	Q05BQ1|TUTLA_MOUSE	49.44	18	105000	2280	98700
GPDGRFVM(+15.99)GPTVAPSQEKL	Q05BQ1|TUTLA_MOUSE	49.88	19	57600	1550	20700
GPLIVSGPDGAPAKGDG	Q8VBW1|SC6A8_MOUSE	47.74	17	15300	194	15200
GRFTYQNAAAQPETGPG	Q9QZM4|TR10B_MOUSE	48.32	17	22300	200	14000
GRLEVVTDPTTNAGYV	Q9R100|CAD17_MOUSE	49.9	16	3750	38.3	3240
GRLEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	49.93	17	31900	415	34800
GSKKAISKAQKKDGKKRKRSRKESYSV	Q64475|H2B1B_MOUSE	43.25	31	NA	6620	NA
GSKKAVTKAQKKDGKKRKRSRKESY	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.24	25	NA	1150	NA
GSKKAVTKAQKKDGKKRKRSRKESYSV	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.25	31	NA	19700	NA
GSLFLKTPKIVSSKD	P06151|LDHA_MOUSE	49.91	15	15000	130	10900
GSLFLKTPKIVSSKDY	P06151|LDHA_MOUSE	49.85	16	12200	116	9930
GTNM(+15.99)YNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	49.84	17	8090	253	7800
GTSRHPGPL	P23150|HA2J_MOUSE:P14434|HA2B_M(	41.86	9	10700	644	6880
GVKKVAKSPKKAKAAAKPKKAAKSPAKI	P43276|H15_MOUSE	48.93	30	NA	812	993
GVLPNIQAVLLPKKTESHHK	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	48.82	20	NA	886	1500
GVLPNIQAVLLPKKTESHHKAK	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	49.94	22	2900	10300	6150
GVLPNIQAVLLPKKTESHHKAKGK	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	42.87	24	NA	260	NA
GVSSQETAGIGASAHLVNFK	Q99KQ4|NAMPT_MOUSE	49.55	20	2540	1850	2510

HEVVVIAPEASIHIK	Q63886|UD11_MOUSE	49.42	15	7140	84.6	2430
HGTDDGVVWM(+15.99)NWK	Q8K0E8|FIBB_MOUSE	47.78	13	656	145	NA
HINIVVIGH	P62631|EF1A2_MOUSE:P10126|EF1A1_	43.13	9	109	324	470
HKRRKTGGKRKPYHKKR	P62242|RS8_MOUSE	29.27	17	NA	543	NA
HLKIVYRRFRHGFREGTTPKPKR	Q9D823|RL37_MOUSE	48.89	23	8700	12200	5560
HLKIVYRRFRHGFREGTTPKPKRA	Q9D823|RL37_MOUSE	49.56	24	9660	4100	685
HLQLAIRN	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	37.48	8	386	1000	194
HLQLAIRND	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	42.59	9	1760	1920	302
IEDIEVAPPKAHEVR	P00329|ADH1_MOUSE	47.48	15	17800	188	16200
IEKVIPSTANSNNL	E9Q7P9|CDHR2_MOUSE	44.74	14	15300	239	8440
IFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_M	48.05	13	45900	1060	29000
IILLLLILL	P11627|L1CAM_MOUSE	25.3	9	NA	165	NA
IILLLLLII	Q03146|DDR1_MOUSE	25.3	9	NA	165	NA
IKLESGEQSD	O08784|TCOF_MOUSE	43	10	NA	612	348
ILLLLLIIL	Q6R5P0|TLR11_MOUSE	25.3	9	NA	165	NA
ILVRYTQKAPQVSTPTL	P07724|ALBU_MOUSE	49.94	17	11400	250	14800
ILVRYTQKAPQVSTPTLVE	P07724|ALBU_MOUSE	49.36	19	6020	94.9	7850
IPGTNM(+15.99)YNTDRANPVLD	E9Q7P9|CDHR2_MOUSE	49.85	17	142000	5480	93800
IPGTNM(+15.99)YNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	49.91	19	356000	10900	224000
IPGTNM(+15.99)YNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	49.87	20	65100	1940	44500
IQRLVTPRVLQ(+15.00)HKRR	P62754|RS6_MOUSE	34.55	15	NA	710	NA
IRPFFPQQ	Q8K0E8|FIBB_MOUSE	39.65	8	1460	156	NA
ISKAQKKDGKKRKRSRKESYSVYVYK	Q64475|H2B1B_MOUSE	43.25	26	NA	4340	NA
ITQVQWNDPGAQYSLVNK	Q9R100|CAD17_MOUSE	49.94	18	9350	315	11100
IVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	43.23	14	NA	441	166
IVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	48.4	15	NA	575	194
K(+42.01)KRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.36	20	885	2770	NA
K(+42.01)KTKKEVKKVATPKKAAKPKK	P10922|H10_MOUSE	46.67	21	658	1600	NA
K(+42.01)N(+15.00)KRLTKGGKKGAKKK	P97351|RS3A_MOUSE	43.25	24	NA	643	NA
K(+42.01)N(+15.00)KRLTKGGKKGAKKK	P97351|RS3A_MOUSE	40.6	25	NA	322	NA
K(+42.01)PKVVKVKPVKASKPKKAKTVK	P10922|H10_MOUSE	49.71	26	2820	4260	2230
K(+42.01)TQKKEGRKRKRC(+57.02)RKE	P70696|H2B1A_MOUSE	31.32	32	NA	1300	NA
KAAKKTPKKAKKPA	P15864|H12_MOUSE	40.9	14	NA	3930	NA
KAAKPKKTAAKKK	P43274|H14_MOUSE	43.21	13	NA	1880	NA
KAAKSPAKPKA	P43276|H15_MOUSE	42.89	11	NA	5580	NA
KAAKSPAKPKAVKSKASK	P43276|H15_MOUSE	40.27	18	NA	2930	5340
KAISKAQKKDGKKRKRSRKESYSVYVY	Q64475|H2B1B_MOUSE	27	27	NA	3360	NA
KAISKAQKKDGKKRKRSRKESYSVYVYK	Q64475|H2B1B_MOUSE	43.2	28	NA	1010	NA
KAKAAAKPKKAA	P43276|H15_MOUSE	25.49	12	NA	543	NA
KAKAAAKPKKAAK	P43276|H15_MOUSE	49.29	13	290	233	NA
KAKAAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	48.88	20	NA	15300	12800
KAKATKAKKAPKSPAKAKTVK	P43274|H14_MOUSE	49.43	21	2780	3830	4710
KAKKKPAATPKKAKKPKVVKVKPVKASK	P10922|H10_MOUSE	49.95	33	1730	1470	1200
KAKKPAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.95	21	2440	1910	2140
KAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	22	2180	2210	6890
KAKSPKKAK	P43274|H14_MOUSE	35.06	9	NA	173	284
KAKTVKPKA	P43274|H14_MOUSE:P10922|H10_MOU	41.72	9	186	359	1310
KAKTVKPKAKSSAK	P10922|H10_MOUSE	48.59	14	477	519	947
KAPEPVEIRE	Q9R100|CAD17_MOUSE	37.51	10	7270	106	4430
KAQKKDGKKRKRSRKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	42.88	24	NA	4900	NA
KAQKKDGKKRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	39.29	27	NA	503	NA
KAQKKDGKKRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	48.95	32	1850	68300	4550
KASKPKATKAKKAAPRK	P43277|H13_MOUSE	42.17	17	NA	802	4120
KASKPKKAK	P10922|H10_MOUSE	41.9	9	5370	3520	NA
KAVTKAQKKDGKKR	Q8CGP0|H2B3B_MOUSE:Q8CGP2|H2B1	36.7	14	NA	348	NA
KAVTKAQKKDGKKRKRSRKESYSVYVY	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.25	28	NA	19200	NA
KAVTKVQKKDGKKRKRSRKESYSVYVY	Q64525|H2B2B_MOUSE	27.09	28	NA	456	NA
KDGKKRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	39.95	23	NA	1920	NA
KDGKKRKRSRKESYSVYVYKVLKQVHP	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	43.25	28	4700	10800	1780
KELEEQLGPVAEETR	P08226|APOE_MOUSE	48.95	15	53600	2230	37800
KELEEQLGPVAEETRA	P08226|APOE_MOUSE	49.63	16	37300	2070	29400
KESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	42.24	10	NA	968	NA
KFYKGKKYKPLDLRPKKT	Q6ZWV7|RL35_MOUSE	49.94	18	1220	1850	2460
KFYKGKKYKPLDLRPKKTR	Q6ZWV7|RL35_MOUSE	49.95	19	1500	7630	5510
KFYKGKKYKPLDLRPKKTRA	Q6ZWV7|RL35_MOUSE	48.93	20	NA	133	261
KFYKGKKYKPLDLRPKKTRAM(+15.99)R	Q6ZWV7|RL35_MOUSE	49.95	23	NA	10300	1930
KFYKGKKYKPLDLRPKKTRAMRR	Q6ZWV7|RL35_MOUSE	49.95	23	631	6760	5610
KGSKKAISKAQKKDGKKRKR	Q64475|H2B1B_MOUSE	43.25	20	NA	3070	NA
KGSKKAISKAQKKDGKKRKRSRKESY	Q64475|H2B1B_MOUSE	43.11	26	NA	2380	NA
KGSKKAISKAQKKDGKKRKRSRKESYSV	Q64475|H2B1B_MOUSE	42.08	32	NA	49600	2660
KGSKKALTKAQKKDGKKRKRSRKESYS	Q64478|H2B1H_MOUSE	43.25	32	NA	14300	NA
KGSKKAVTKAQKKDGKKRKRSR	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.25	22	NA	29500	NA
KGSKKAVTKAQKKDGKKRKRSRKESY	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.25	26	NA	3930	NA
KGSKKAVTKAQKKDGKKRKRSRKESYS	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.25	29	NA	1680	NA
KGSKKAVTKAQKKDGKKRKRSRKESYS	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	42.52	31	NA	4830	NA
KGSKKAVTKAQKKDGKKRKRSRKESYS	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	48.62	32	NA	151000	3860
KGSKKAVTKVQKKDGKKRKRSRKESYS	Q64525|H2B2B_MOUSE	43.25	32	NA	5410	NA
KKAAKKTPKKAKKPA	P15864|H12_MOUSE	48.65	15	NA	91.9	3860
KKAAPRKK	P43277|H13_MOUSE	42.36	8	NA	303	NA
KKAGAPKV	Q9DBJ3|BI2L1_MOUSE	27.51	8	NA	2570	NA
KKAKATKAKKAPKSPAK	P43274|H14_MOUSE	49.94	17	251	26.3	295

KKAKATKAKKAPKSPAKAK	P43274|H14_MOUSE	49.95	19	4410	2030	1870
KKAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	23	7790	3290	6130
KKAKSPKKAK	P43274|H14_MOUSE	43.25	10	NA	701	1770
KKAKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.95	21	1100	1200	NA
KKAKVTKPKKVKSASKAVKPKAAKPK	P15864|H12_MOUSE	48.67	26	NA	830	1550
KKAPKSPAK	P43274|H14_MOUSE	26.97	9	NA	708	NA
KKDGKKRKR	Q8CGP0|H2B3B_MOUSE:Q8CGP2|H2B1	25.78	9	NA	1630	NA
KKDGKKRKRSRK	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	41.73	12	NA	5730	NA
KKDGKKRKRSRKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.2	21	NA	13500	NA
KKDGKKRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.25	24	NA	3300	NA
KKDGKKRKRSRKESYSVYVYKVLKQVH	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.95	29	6630	40200	6410
KKELEEQLGPVAEETR	P08226|APOE_MOUSE	49.9	16	14200	178	20300
KKELEEQLGPVAEETRAR	P08226|APOE_MOUSE	49.04	18	12500	221	11500
KKGSKKAISKAQKKDGKKR	Q64475|H2B1B_MOUSE	48.91	19	NA	1580	NA
KKGSKKALTKAQKKDGKKRKRSRKESY	Q64478|H2B1H_MOUSE	43.25	33	NA	13400	NA
KKGSKKAVTKAQKKDGKKR	Q8CGP0|H2B3B_MOUSE:Q8CGP2|H2B1	43.25	19	NA	456	NA
KKGSKKAVTKAQKKDGKKRKRSRKESY	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.25	27	NA	3260	NA
KKGSKKAVTKAQKKDGKKRKRSRKESY	Q64524|H2B2E_MOUSE	43.25	33	NA	2760	NA
KKGSKKAVTKAQKKDGKKRKRSRKESY	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	48.95	30	NA	6020	NA
KKGSKKAVTKAQKKDGKKRKRSRKESY	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	49.04	33	842	74400	14300
KKGSKKAVTKVQKKDGKKRKR	Q64525|H2B2B_MOUSE	48.95	21	NA	903	NA
KKGSKKAVTKVQKKDGKKRKRSRKESY	Q64525|H2B2B_MOUSE	43.25	33	NA	6670	NA
KKKKKKKP	Q99L45|IF2B_MOUSE	42.41	9	NA	5930	16300
KKKKKTGRAK	P62862|RS30_MOUSE	35.58	10	NA	741	NA
KKKKKTGRAKRR	P62862|RS30_MOUSE	39.85	12	NA	1980	2540
KKKKVDPRKDQAAKDRLKKRIRKL	Q9Z2Q5|RM40_MOUSE	25.47	24	NA	214	NA
KKPAATPKKAKKPKVVKVKPVKAS(+79.	P10922|H10_MOUSE	41.14	27	67.2	266	NA
KKPAATPKKAKKPKVVKVKPVKASKPKK	P10922|H10_MOUSE	43.25	30	NA	1130	NA
KKPAKAAAPRKKP	P43275|H11_MOUSE	40.62	13	NA	1000	264
KKPKKTAGAAAKKTVK	P43275|H11_MOUSE	26.07	16	NA	73.3	NA
KKPRTKAPKIQ(+15.00)RLVTPRVLQHKF	P62754|RS6_MOUSE	35.22	32	NA	8370	NA
KKPRTKAPKIQRLV	P62754|RS6_MOUSE	25.54	14	NA	4820	NA
KKSTKKTPKKA	P43274|H14_MOUSE	28.42	11	NA	204	NA
KKTPKKAKKPAA	P15864|H12_MOUSE:P43276|H15_MOU	48.89	12	845	624	1130
KKTVKTPKKPKKPAVSKK	P43275|H11_MOUSE	43.22	18	NA	328	NA
KKVAKSPAKAKAVKPK	P43275|H11_MOUSE	40.75	16	452	401	208
KKVAKSPKKAKVTKPKKVKSASKAVKPK	P15864|H12_MOUSE	48.94	28	NA	1830	537
KKVAKSPKKAKVTKPKKVKSASKAVKPK	P15864|H12_MOUSE	49.95	29	539	542	1390
KKVATPKKAAKPKKA	P10922|H10_MOUSE	40.53	15	NA	206	NA
KKVS(+79.97)KS(+79.97)PKKVKAAKPK	P43277|H13_MOUSE	25.68	16	NA	138	NA
KNLDYVATSIHEAVT	P05201|AATC_MOUSE	49.61	15	15700	414	11300
KNLDYVATSIHEAVTK	P05201|AATC_MOUSE	49.86	16	18500	514	13500
KPAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.94	18	5370	4520	5380
KPAAAGVKKVAKSPKKAKA	P43276|H15_MOUSE	48.94	19	NA	572	993
KPKAAKPK	P15864|H12_MOUSE:P43274|H14_MOU	41.71	8	727	186	NA
KPKAAKPKKT(+79.97)AAKKK	P43274|H14_MOUSE	38.57	15	NA	478	NA
KPKAAKPKTSKPKAAKPK	P43274|H14_MOUSE	48.84	18	NA	861	1090
KPKAAKPKTSKPKAAKPKKTAAKK	P43274|H14_MOUSE	48.93	24	2590	818	1390
KPKAAKPKVAKAKKVAAKK	P15864|H12_MOUSE	39.8	19	NA	349	NA
KPKAKKAG	P43277|H13_MOUSE	28.39	8	NA	191	NA
KPKAKSSAK	P10922|H10_MOUSE	25.36	9	NA	84.1	NA
KPKAKSSAKRASK	P10922|H10_MOUSE	33.97	13	1870	1110	NA
KPKASKAKVTKPKTPAKPKKA	P43275|H11_MOUSE	38.49	21	NA	1080	1760
KPKASKPKATKAKKAAP	P43277|H13_MOUSE	34.67	17	NA	181	NA
KPKASKPKATKAKKAAPRK	P43277|H13_MOUSE	43.24	19	NA	7170	NA
KPKKAAKSPAKPKA	P43276|H15_MOUSE	43.25	14	NA	95.5	NA
KPKKAKTVKPKAKSSAKRASK	P10922|H10_MOUSE	43.13	21	NA	919	NA
KPKKAKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.95	23	1300	1910	NA
KPKTPAKPKKAAP	P43275|H11_MOUSE	42.7	13	NA	149	376
KPKTSKPKAAKPK	P43274|H14_MOUSE	42.61	13	596	1370	NA
KPKTSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.95	20	NA	8700	NA
KPKVVKAKKVAKS(+79.97)PAKAKAVKP	P43275|H11_MOUSE	43.06	28	NA	228	NA
KPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.91	19	193	834	602
KPPSYNVATTLPSYD	Q8R0W6|NFIP1_MOUSE	43.91	15	2680	54.8	3050
KPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	49.04	16	24400	922	25000
KPPSYNVATTLPSYDEA	Q8R0W6|NFIP1_MOUSE	49.3	17	3730	27.3	5630
KPTVTVVSPLPNDSIN	Q8VD58|EVI2B_MOUSE	49.21	16	480	96.6	165
KPTVTVVSPLPNDSINPQ	Q8VD58|EVI2B_MOUSE	49.94	18	2890	905	1680
KPTVTVVSPLPNDSINPQP	Q8VD58|EVI2B_MOUSE	49.94	19	6290	1700	3750
KPVKASKPKKAKTVKPKA	P10922|H10_MOUSE	49.22	18	979	1420	NA
KRKRSRKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	38.69	16	NA	1960	NA
KRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.23	19	NA	198	NA
KRKRSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.95	24	3080	3870	NA
KRSRKESY(+79.97)SIY(+79.97)VYKVLK	Q64524|H2B2E_MOUSE	43.08	22	NA	45.6	NA
KRSRKESY(+79.97)SIYVY(+79.97)KVLK	Q64524|H2B2E_MOUSE	39.13	22	NA	45.6	NA
KRSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.95	22	6810	8360	1960
KSPKKAKVTKPKK	P15864|H12_MOUSE	49.93	13	13200	2230	1390
KSTKKTPKKAKKP	P43274|H14_MOUSE	48.9	13	NA	4490	NA
KSTKKTPKKAKKPA	P43274|H14_MOUSE	49.94	14	6320	2030	2300
KSTKKTPKKAKKPAA	P43274|H14_MOUSE	49.87	15	420	1330	2010
KSTKKTPKKAKKPAAAAGAKKAK	P43274|H14_MOUSE	49.68	23	NA	1500	NA

KSTKKTPKKAKKPAAAAGAKKAKSPKKA	P43274|H14_MOUSE	48.95	29	NA	2680	NA
KTPKKAKKPAAAGVKKVAKS(+79.97)PK	P43276|H15_MOUSE	40.07	25	NA	400	NA
KTRLSRTPGNRIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	49.47	25	NA	4170	820
KTRLSRTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	43.25	26	354	1850	NA
KTSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	43.25	18	NA	1720	NA
KTSKSPKKPKVVKAKKVAK	P43275|H11_MOUSE	49.95	19	3840	3710	2830
KTVKKTPKK	P43276|H15_MOUSE	29.11	9	NA	94.5	NA
KTVKKTPKKAKKPA	P43276|H15_MOUSE	49.95	14	6350	2180	2660
KTVKKTPKKAKKPAAAGVKK	P43276|H15_MOUSE	49	20	660	533	277
KTVKKTPKKAKKPAAAGVKKVAKSPKKA	P43276|H15_MOUSE	49.95	29	1680	696	1660
KTVKPKAAKPKTSKPKAAKPKKTAAKK	P43274|H14_MOUSE	48.95	27	NA	1870	2220
KTVKTPKKPKKPAVSKK	P43275|H11_MOUSE	49.49	17	489	401	NA
KVAKSPAKAK	P43275|H11_MOUSE	31.15	10	2830	922	NA
KVAKSPKKAK	P15864|H12_MOUSE:P43276|H15_MOU	42.43	10	846	243	471
KVAKSPKKAKAAAKPKKAAK	P43276|H15_MOUSE	49.94	20	1690	1300	1060
KVAKSPKKAKAAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	47.05	27	NA	1310	1750
KVKAAKPKKAAKSPAKAKAPKAKASKPK	P43277|H13_MOUSE	49.93	29	203	1140	NA
KVKPVKASKPKKAK	P10922|H10_MOUSE	49.94	14	369	495	1060
KVQKKDGKKRKRSRKESYSVYVYKVLK	Q64525|H2B2B_MOUSE	43.24	32	NA	2850	NA
KVTFNSALAQKEAKK	O89051|ITM2B_MOUSE	49.81	15	26000	513	20700
LAPM(+15.99)YYRGAQAAIVVYD	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	46.89	17	3720	172	3730
LEEQLGPVAEETR	P08226|APOE_MOUSE	42.59	13	3480	102	1690
LEEQLGPVAEETRA	P08226|APOE_MOUSE	44.96	14	2720	120	2540
LEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	45.42	15	9360	142	7570
LIIIILIIL	Q8VGI1|O1E16_MOUSE	25.3	9	NA	165	NA
LIILLLILL	P10404|ENV1_MOUSE	25.3	9	NA	165	NA
LLILILLLL	P09803|CADH1_MOUSE	25.3	9	NA	165	NA
LLLLLILLL	Q69ZN7|MYOF_MOUSE	25.3	9	NA	165	NA
LLLLLLLLL	Q91W27|TIP39_MOUSE:Q91Y57|SIG12_	25.3	9	NA	165	NA
LNIYVPAHAHEGSN	Q8BK48|EST2E_MOUSE	45.01	14	15700	194	12000
LNIYVPAHAHEGSNLPV	Q8BK48|EST2E_MOUSE	49.79	17	13500	76.9	10200
LPDDINVYATTAANPKESS	O89017|LGMN_MOUSE	49.94	19	5130	179	3320
LPPYDDATAVPSTAKEPPP	Q91XQ6|LAP4B_MOUSE	49.93	19	179000	2600	185000
LPPYDDATAVPSTAKEPPPP	Q91XQ6|LAP4B_MOUSE	49.93	20	951000	19800	927000
LPSPLIM(+15.99)SPGPIYAVDG	Q8VHF2|CDHR5_MOUSE	49.93	17	9110	63.4	7480
LQDEIDAALPNKAP	Q64464|CP3AD_MOUSE	48.9	14	10400	79.4	6980
LQDEIDAALPNKAPA	Q64464|CP3AD_MOUSE	48.31	15	12900	171	8150
LQDEIDAALPNKAPAT	Q64464|CP3AD_MOUSE	49.32	16	11400	191	7590
LRKFYKGKKYKPLDLRPKKTR	Q6ZWV7|RL35_MOUSE	49.95	21	199	225	365
LRKFYKGKKYKPLDLRPKKTRAM(+15.9	Q6ZWV7|RL35_MOUSE	43.25	25	NA	216	NA
LRPLVKPKIVKKRTKKFIRHQSDR	P17932|RL32P_MOUSE:P62911|RL32_M	48.95	24	NA	1260	1080
LRRQPKYPRKSAPRRNKLDHYAIIKF	P62751|RL23A_MOUSE	49.95	26	8320	629	3370
LSRTPGNRIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	48.94	22	NA	4600	3140
LSRTPGNRIVYLYTKKVGKAPKSA	Q9D1R9|RL34_MOUSE	28.84	24	NA	217	NA
LVAYYTLIGASGQR	P01027|CO3_MOUSE	46.28	14	558	399	NA
LVRYTQKAPQVSTPT	P07724|ALBU_MOUSE	49.82	15	23100	541	17000
LVRYTQKAPQVSTPTL	P07724|ALBU_MOUSE	49.89	16	59000	3760	72100
LVRYTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.92	17	54100	2330	59400
LVRYTQKAPQVSTPTLVE	P07724|ALBU_MOUSE	49.89	18	10800	87.3	12800
M(+15.99)GPTELLIEM(+15.99)EDWK	Q8K0E8|FIBB_MOUSE	37.54	14	NA	155	NA
M(+15.99)QKEITALA	P63260|ACTG_MOUSE:P60710|ACTB_M	25.59	9	146	469	NA
MQKEITALA	P63260|ACTG_MOUSE:P60710|ACTB_M	29.18	9	261	113	319
NIYVPAHAHEGSN	Q8BK48|EST2E_MOUSE	42.66	13	4460	171	564
NIYVPAHAHEGSNL	Q8BK48|EST2E_MOUSE	46.18	14	35100	629	22100
NKTRLSRTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	48.94	27	296	1110	2230
NPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	45.33	12	159	268	668
NPRTPQDSPM(+15.99)YPVVPVHLDGTF	P97425|ECP2_MOUSE	49.94	22	230	102	336
NTASNKTRLSRTPGNRIVYLYTKKVGKA	Q9D1R9|RL34_MOUSE	47.14	30	NA	274	373
P(+42.01)KKGSKKALTKAQ(+15.00)KKD	Q64478|H2B1H_MOUSE	42.33	33	NA	4040	NA
PAAAAGAKKAKSPKKAK	P43274|H14_MOUSE	48.89	17	NA	3370	631
PAAAGVKKVAKSPKKA	P43276|H15_MOUSE	43.22	16	NA	293	NA
PAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.94	17	22200	21600	21100
PAAAGVKKVAKSPKKAKA	P43276|H15_MOUSE	49.94	18	4660	3740	4460
PAAAGVKKVAKSPKKAKAA	P43276|H15_MOUSE	49.93	19	1300	2230	2900
PAAAGVKKVAKSPKKAKAAAKPK	P43276|H15_MOUSE	43.25	23	NA	695	NA
PAATPKKAKKPKVVKVKP	P10922|H10_MOUSE	43.08	18	NA	905	NA
PAATPKKAKKPKVVKVKPVKASKPKKA	P10922|H10_MOUSE	48.94	27	272	410	373
PAATPKKAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	28	3610	2560	4120
PAKAKAPKAKASKPKA	P43277|H13_MOUSE	49.92	16	9900	6200	4320
PAKPKKAAP	P43275|H11_MOUSE	30.88	9	NA	408	1180
PAKPKKAAPK	P43275|H11_MOUSE	47.5	10	888	512	864
PAKPKKAAPKK	P43275|H11_MOUSE	49.3	11	699	927	571
PAKSAPAPKKGSKKAVTKVQ(+15.00)KK	Q64525|H2B2B_MOUSE	42.39	27	NA	205	NA
PAPKKGSKKAISKAQKKDGKKRKRSR	Q64475|H2B1B_MOUSE	43.25	26	NA	16100	NA
PAPKKGSKKAVTKAQKKDGKKRKR	Q8CGP0|H2B3B_MOUSE:Q8CGP2|H2B1	49.95	24	NA	5250	8640
PAPKKGSKKAVTKAQKKDGKKRKRSR	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	49.95	26	1700	8460	11400
PAVSKKTSKSPKKPKVVKAKKVAK	P43275|H11_MOUSE	49.95	24	12500	4070	3600
PKAAKAKKAVSKKK	P43276|H15_MOUSE	49.94	14	6710	1350	NA
PKAAKPKKTAAKKK	P43274|H14_MOUSE	49.66	14	17300	8850	4000
PKAAKPKTSKPKAAKPKK	P43274|H14_MOUSE	49.94	18	869	61.1	NA
PKAAKPKTSKPKAAKPKKT	P43274|H14_MOUSE	49.94	19	804	1560	3100

PKAAKPKVAKAKKVAAKK	P15864|H12_MOUSE	49.94	18	9290	1350	3100
PKAAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	19	41200	6630	5690
PKAKASKPKA	P43277|H13_MOUSE	41.21	10	124	2330	1040
PKAKASKPKASKPKATKAKKAAPR	P43277|H13_MOUSE	48.95	24	NA	408	449
PKAKSSAKR	P10922|H10_MOUSE	42.93	9	1940	2080	3110
PKAKSSAKRASKKK	P10922|H10_MOUSE	46.46	14	27900	2950	8100
PKASKAKVTKP	P43275|H11_MOUSE	27.83	11	NA	517	NA
PKASKPKATKAKKA	P43277|H13_MOUSE	43.24	14	608	588	3260
PKASKPKATKAKKAAPR	P43277|H13_MOUSE	49.77	17	2920	3630	6580
PKASKPKATKAKKAAPRK	P43277|H13_MOUSE	49.94	18	3010	1100	2670
PKASKPKATKAKKAAPRKK	P43277|H13_MOUSE	49.95	19	9430	7170	4220
PKATKAKKAAPRK	P43277|H13_MOUSE	48.02	13	1640	5030	6390
PKATKAKKAAPRKK	P43277|H13_MOUSE	49.94	14	27500	27600	17100
PKGKKAKGKKVAPAPAVVKK	P12970|RL7A_MOUSE	43.25	20	NA	320	NA
PKGKKAKGKKVAPAPAVVKKQEAKKVV	P12970|RL7A_MOUSE	49.92	32	1420	157	NA
PKKAAKPK	P10922|H10_MOUSE	41.96	8	NA	186	NA
PKKAAKSPAKPKA	P43276|H15_MOUSE	49.02	13	2340	6100	5560
PKKAAPKKK	P43275|H11_MOUSE	42.75	9	5630	606	NA
PKKAKKPA	P15864|H12_MOUSE:P43276|H15_MOU	40.95	8	5530	5630	NA
PKKAKKPAA	P15864|H12_MOUSE:P43276|H15_MOU	38.24	9	NA	1810	577
PKKAKKPAAAGVKK	P43276|H15_MOUSE	48.64	14	301	203	176
PKKAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	24	NA	964	1870
PKKAKTVKPKAK	P10922|H10_MOUSE	45.78	12	NA	782	232
PKKAKTVKPKAKSSAKR	P10922|H10_MOUSE	49.94	17	203	460	372
PKKAKTVKPKAKSSAKRASKK	P10922|H10_MOUSE	49.95	21	5660	405	2440
PKKGSKKAVTKAQKKDGKKRKR	Q8CGP0|H2B3B_MOUSE:Q8CGP2|H2B1	42.54	22	NA	1940	NA
PKKGSKKAVTKAQKKDGKKRKRSR	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	48.95	24	NA	5940	2140
PKKNKHKRKK	P62983|RS27A_MOUSE	43.25	10	NA	2210	NA
PKKPKVVKAKKVAK	P43275|H11_MOUSE	49.95	14	8250	2680	2840
PKKPKVVKAKKVAKSPAK	P43275|H11_MOUSE	48.95	18	NA	126	152
PKKPKVVKAKKVAKSPAKAK	P43275|H11_MOUSE	43.22	20	NA	99	NA
PKKTAAKKK	P43274|H14_MOUSE	37.03	9	NA	1050	1060
PKKTAKKTPKKAKKPAAAAGAKKVS(+7	P43277|H13_MOUSE	32.53	27	NA	1070	NA
PKTAKPKAAKAKKAVSKK	P43276|H15_MOUSE	49.94	18	718	105	NA
PKTAKPKAAKAKKAVSKKK	P43276|H15_MOUSE	49.95	19	1960	137	NA
PKTPAKPKK	P43275|H11_MOUSE	41.84	9	NA	185	791
PKTPAKPKKA	P43275|H11_MOUSE	36.88	10	494	528	NA
PKTPAKPKKAAPKKK	P43275|H11_MOUSE	48.83	15	9220	1050	4150
PKTSKPKAAKPKKT	P43274|H14_MOUSE	47.32	14	1310	646	1890
PKTSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.95	19	8780	5000	4610
PKVAKAKKVAAKKK	P15864|H12_MOUSE	49.94	14	22100	4050	6120
PKVVKAKKVAKSPAKAK	P43275|H11_MOUSE	49.86	17	973	1590	843
PKVVKVKPVKASKPKKA	P10922|H10_MOUSE	49.95	17	1720	1270	NA
PKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.94	18	7680	6720	9460
PVKASKPKKAKTVKPKA	P10922|H10_MOUSE	49.95	17	1390	227	1740
PVKASKPKKAKTVKPKAK	P10922|H10_MOUSE	49.94	18	861	4280	3110
PVKASKPKKAKTVKPKAKSSAKR	P10922|H10_MOUSE	49.95	23	710	417	3920
QDGSVDFGR	Q8K0E8|FIBB_MOUSE	42.32	9	279	72.8	NA
QEKKKKKTGRAKR	P62862|RS30_MOUSE	42.27	13	NA	724	NA
QKKDGKKRKRGRKESYSIYVYKVLKQVH	Q8CGP0|H2B3B_MOUSE:Q9D2U9|H2B3	48.95	30	NA	453	1310
QKKDGKKRKRSRKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.25	22	NA	994	NA
QKKDGKKRKRSRKESYSVYVYKVL	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.14	24	NA	331	NA
QKKDGKKRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	43.19	25	NA	728	NA
QKKDGKKRKRSRKESYSVYVYKVLKQV	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.95	30	20700	99700	1240
QPSTSSLAAPTVEAAA	Q91ZP6|NFIP2_MOUSE	45.93	16	7240	93.2	4790
QPSTSSLAAPTVEAAAS	Q91ZP6|NFIP2_MOUSE	48.58	17	72000	3110	61100
QPSTSSLAAPTVEAAASA	Q91ZP6|NFIP2_MOUSE	49.39	18	82000	4570	61400
QPSTSSLAAPTVEAAASAP	Q91ZP6|NFIP2_MOUSE	49.72	19	78200	2610	89900
QPSTSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	49.77	20	231000	8860	248000
QYVVRKPLNKEGKKPRTKAPKIQRLVTP	P62754|RS6_MOUSE	42.28	29	NA	430	NA
R(+42.01)KRGRKESYSIYVYKVLKQVHP	Q8CGP0|H2B3B_MOUSE:Q9D2U9|H2B3	49.39	23	723	5430	NA
RENIWKAPEPVEIREN(+15.00)ST	Q9R100|CAD17_MOUSE	49.91	18	53900	593	23400
RFTYQNAAAQPETGPG	Q9QZM4|TR10B_MOUSE	48.73	16	10600	197	9630
RFVNVVPTFGKKKGPNA	P62862|RS30_MOUSE	40.69	17	NA	128	NA
RIKRFLAKKQKQNRPIPQ	Q9CQD0|RL39L_MOUSE:P62892|RL39_	49.94	18	285	121	NA
RIVYLYTKKVGKAP	Q9D1R9|RL34_MOUSE	48.4	14	NA	651	797
RIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	49.94	16	282	1090	218
RKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.22	11	NA	257	NA
RKQHSLLKRLRKAKKEAPPM(+15.99)EK	P62843|RS15_MOUSE	42.17	31	NA	436	NA
RLTKHEEKLKTKKQQRKERLYPLR	Q6ZWV7|RL35_MOUSE	43.24	24	NA	1740	NA
RLTKHEEKLKTKKQQRKERLYPLRKYAV	Q6ZWV7|RL35_MOUSE	26.68	30	NA	419	NA
RRQPKYPRKSAPRRNKLDHYAIIKF	P62751|RL23A_MOUSE	49.85	25	5900	247	4230
RTLYGFGG	P62806|H4_MOUSE	41.03	8	NA	370	379
RTPGNRIVYLYTKKVGKAP	Q9D1R9|RL34_MOUSE	49.94	19	402	2030	3390
RTPGNRIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	49.95	20	700	6680	2800
RTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	49.95	21	1910	2640	1080
S(+42.01)GRGKQGGKARAKAKSRSSRA	Q8BFU2|H2A3_MOUSE:Q64522|H2A2B_	43.25	29	NA	2180	NA
S(+42.01)GRGKQGGKARAKAKSRSSRA	Q8BFU2|H2A3_MOUSE:Q64522|H2A2B_	39.62	31	NA	4230	NA
S(+42.01)GRGKQGGKARAKAKTRSSRA	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	49.94	29	3790	50400	3350
S(+42.01)GRGKQGGKARAKAKTRSSRA	C0HKE3|H2A1D_MOUSE:C0HKE7|H2A1	49.94	31	2830	3660	NA
S(+42.01)GRGKQGGKARAKAKTRSSRA	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	43.24	32	2530	19000	2330

S(+42.01)KSPKKPKVVKAKKVAKSPAK	P43275|H11_MOUSE	49.94	21	2290	221	1560
S(+42.01)SRGGKKKSTKTSRSAKAGVIF	Q9QZQ8|H2AY_MOUSE	43.23	26	NA	893	NA
S(+42.01)VQVVSAAAAAKVPEVE	Q68FL4|SAHH3_MOUSE	49.84	17	2690	137	3370
SAPAPKKGSKKAISKAQKKDGKKRKR	Q64475|H2B1B_MOUSE	49.95	26	8450	21000	NA
SAPAPKKGSKKAISKAQKKDGKKRKRSI	Q64475|H2B1B_MOUSE	43.25	28	NA	16000	NA
SAPAPKKGSKKAVTKAQKKDGKKR	Q8CGP0|H2B3B_MOUSE:Q6ZWY9|H2B	49.95	24	11100	1810	NA
SAPAPKKGSKKAVTKAQKKDGKKRKR	Q8CGP0|H2B3B_MOUSE:Q6ZWY9|H2B	49.95	26	9760	2820	32900
SASKAVKPKAAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	26	11500	2420	723
SDTIKPDVN	P35700|PRDX1_MOUSE	41.53	9	224	164	261
SEAEQKKGKARRPVPRRT(+79.97)VPKI	E9PZM4|CHD2_MOUSE	27.21	25	NA	1400	NA
SEVKKKKKKKRK	Q8K363|DDX18_MOUSE	48.9	12	NA	5730	881
SGDGVTHTVPIYEG	P63260|ACTG_MOUSE:P60710|ACTB_M	32.82	14	479	109	NA
SGDGVTHTVPIYEGYAL	P63260|ACTG_MOUSE:P60710|ACTB_M	38.23	17	NA	113	NA
SGFTNTM(+15.99)RVVPVP	P52480|KPYM_MOUSE	43.73	13	21600	14100	15400
SGKDKKKKTKK	P11499|HS90B_MOUSE	47.09	11	NA	91.5	NA
SGKDKKKKTKKIKEKYIDQ	P11499|HS90B_MOUSE	49.56	19	161	1080	795
SGNFRPANPNWGVFS	E9PV24|FIBA_MOUSE	49.02	15	7300	39.7	6670
SGRFTYQNAAAQPETGPG	Q9QZM4|TR10B_MOUSE	48.94	18	10500	266	589
SKAKVTKPKTPAKPKKAAPKK	P43275|H11_MOUSE	49.95	21	69.2	222	211
SKAKVTKPKTPAKPKKAAPKKK	P43275|H11_MOUSE	49.95	22	7630	1850	443
SKASKPKVTKPKTAKPKAAKAKKAVSKK	P43276|H15_MOUSE	49.95	29	45900	12400	1620
SKAVKPKAAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	24	5860	340	1400
SKKAVTKAQKKDGKKRKRSRKESYSVY	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B	43.25	30	NA	3130	NA
SKKKKKKKKP	Q99L45|IF2B_MOUSE	43.23	10	16100	12700	15400
SKKKKKKKKPFM(+15.99)	Q99L45|IF2B_MOUSE	49.94	12	3370	2990	NA
SKPKAAKPKKTAAKK	P43274|H14_MOUSE	42.88	15	NA	1300	NA
SKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.95	16	2920	2240	NA
SKPKASKPKATKAKKAAPRKK	P43277|H13_MOUSE	49.67	21	NA	1860	NA
SKPKATKAKKAAPRK	P43277|H13_MOUSE	49.91	15	30000	9690	3560
SKPKATKAKKAAPRKK	P43277|H13_MOUSE	49.95	16	82800	45900	27600
SLVSKGTLVQTK	P43276|H15_MOUSE:P43274|H14_MOU	48.4	12	617	83.3	739
SLVSKGTLVQTKG	P43276|H15_MOUSE:P43274|H14_MOU	48.53	13	1050	137	1550
SLVSKGTLVQTKGTGASGSFKLNKK	P43276|H15_MOUSE:P43274|H14_MOU	49.95	25	5780	413	15700
SPKKAKAAAKPKKAAK	P43276|H15_MOUSE	49.82	16	12300	7490	3530
SPKKAKAAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	48.95	23	NA	900	2490
SPKKAKATKAKKAPK	P43274|H14_MOUSE	49.92	15	8380	1300	5720
SPKKAKATKAKKAPKSPAKAK	P43274|H14_MOUSE	49.95	21	1130	8700	3400
SPKKPKVVKAKKVAK	P43275|H11_MOUSE	49.95	15	19100	6790	6130
SPKKVKAAKPKKAAKSPAK	P43277|H13_MOUSE	41.41	19	NA	373	NA
SPM(+15.99)YPVVPVHLDGTF	P97425|ECP2_MOUSE:P97426|ECP1_M	46.83	15	281	135	258
SPQKKTKNKKKKNKKKK	Q3UZ39|LRRF1_MOUSE	43.25	17	NA	6500	NA
SPTVHFTPAEISRSVFE	Q9QXH4|ITAX_MOUSE	44.26	17	931	35.1	299
SQPSKADKKQKKKVDRKGGQSN	Q0VG18|SIM24_MOUSE	47.52	22	NA	1750	1900
SRAGLQFPVGRVH	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	41.91	13	NA	102	NA
SRKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B	42.23	12	NA	962	NA
SRTPGNRIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	49.85	21	134	634	1630
SRTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	49.66	22	741	691	2150
SSRAGLQFPVGRVHRLLR	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	34.2	18	NA	2350	NA
STKKTPKKAKKPA	P43274|H14_MOUSE	49.9	13	2760	2920	8380
STKKTPKKAKKPAA	P43274|H14_MOUSE	48.76	14	NA	370	596
STKKTPKKAKKPAAAAGAKKAK	P43274|H14_MOUSE	49.95	22	1050	952	2460
SVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2	49.84	14	1550	9630	1160
SYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B	42.88	8	NA	140	NA
T(+42.01)VKPKAAKPKTSKPKAAKPKKT/	P43274|H14_MOUSE	49.95	27	2200	9550	7980
TAKGLFRAAVPSGAST	P17183|ENOG_MOUSE:P17182|ENOA_M	49.77	16	30600	762	32900
TAKGLFRAAVPSGASTG	P17183|ENOG_MOUSE:P17182|ENOA_M	49.8	17	16500	149	17100
TAKKSTKKTPKKAKKPA	P43274|H14_MOUSE	49.95	17	14400	4180	16400
TAKKSTKKTPKKAKKPAA	P43274|H14_MOUSE	48.95	18	2140	956	3730
TAKPKAAKAKKAVSKKK	P43276|H15_MOUSE	49.94	17	7330	6910	256
TEAAVLLFYR	O88310|ITL1A_MOUSE:Q80ZA0|ITL1B_M	36.52	10	NA	27.1	NA
TKAKKAAPR	P43277|H13_MOUSE	36.49	9	NA	281	551
TKAQKKDGKKRKRSRKESYSVYVYKVL	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B	49.95	33	4140	13000	1910
TKHEEKLKTKKQQRKERLYPLRKYAVKA	Q6ZWV7|RL35_MOUSE	38.98	28	NA	837	NA
TKKVAKSPKKAKVTKPKKVKSASKAVKP	P15864|H12_MOUSE	49.95	29	NA	330	NA
TLQVLRPGLVVVH	Q9D3D9|ATPD_MOUSE	48.12	13	461	380	1990
TM(+15.99)SKKKKKKKK	Q99L45|IF2B_MOUSE	43.06	11	NA	419	994
TM(+15.99)SKKKKKKKKP	Q99L45|IF2B_MOUSE	49.28	12	4090	27800	32000
TMSKKKKKKKKP	Q99L45|IF2B_MOUSE	48.95	12	NA	2970	17200
TNPIITPVAQENQ	P08226|APOE_MOUSE	46.63	13	4150	110	2360
TPAKPKKAAP	P43275|H11_MOUSE	42.66	10	NA	240	2630
TPFQFRAASPVEE	Q3UKC1|TAXB1_MOUSE	47.8	13	9120	276	11200
TPFQFRAASPVEEL	Q3UKC1|TAXB1_MOUSE	48.36	14	8210	188	10400
TPKKAAKKTPKKAKKPA	P15864|H12_MOUSE	49.95	17	3710	350	1410
TPKKAAKKTPKKAKKPAA	P15864|H12_MOUSE	49.95	18	2730	968	3340
TPKKAKKPA	P15864|H12_MOUSE:P43276|H15_MOU	42.49	9	NA	5570	3140
TPKKAKKPAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	48.95	24	NA	227	123
TPKKAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	25	3860	2290	789
TPKKNKHKRKK	P62983|RS27A_MOUSE	43.25	11	NA	1120	NA
TPKKTAKKTPKKAKKPA	P43277|H13_MOUSE	49.95	17	12600	6380	8900
TPVFVHAGPFANIAHGNS	Q922D8|C1TC_MOUSE:Q3V3R1|C1TM_	49.93	18	29400	91.8	28500
TRLSRTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	37.02	25	NA	292	NA

TSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.94	17	4940	5990	5590
TVKKTPKKAKKPA	P43276|H15_MOUSE	49.92	13	1930	315	NA
TVKPKAAKPKTSKPKAAKP	P43274|H14_MOUSE	47.92	19	NA	200	2240
TVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.94	17	19600	3220	5040
V(+42.01)KSASKAVKPKAAKPKVAKAK	P15864|H12_MOUSE	43.25	21	NA	1190	1900
VAIFARGPQAHLVH	P24823|PPBN_MOUSE:P24822|PPBI_M	47.36	14	185000	8330	143000
VAIFARGPQAHLVHGV	P24823|PPBN_MOUSE:P24822|PPBI_M	49.7	16	35500	338	25500
VAIFARGPQAHLVHGVQ	P24823|PPBN_MOUSE:P24822|PPBI_M	49.92	17	263000	10100	214000
VAKSPKKAK	P15864|H12_MOUSE:P43276|H15_MOU	42.02	9	NA	939	1120
VAKSPKKAKAAAKPK	P43276|H15_MOUSE	46.19	15	NA	114	NA
VAKSPKKAKAAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	49.95	26	1280	2440	3340
VAKVTGGAASKLSKIRVVRKSIAR	Q6ZWV7|RL35_MOUSE	49.94	24	1560	10000	4300
VARYRPRAPIIAVTRNPQ	P52480|KPYM_MOUSE	49.93	18	70900	924	58800
VATNPIITPVAQENQ	P08226|APOE_MOUSE	48.17	15	11100	747	9570
VEPYEVHNPVPLIVG	P05555|ITAM_MOUSE	46.8	15	1720	316	929
VFDVTAPNTFKTLD	P51150|RAB7A_MOUSE	49.05	14	4600	96.3	4020
VKAAKPKKAAKSPAKAKAPKAKASKPKA	P43277|H13_MOUSE	49.95	28	1820	1980	1920
VKASKPKKA	P10922|H10_MOUSE	36.36	9	1460	939	1120
VKKVAKSPKKAK	P43276|H15_MOUSE	48.95	12	NA	209	NA
VKPVKASKPKKAK	P10922|H10_MOUSE	48.45	13	274	144	782
VKSKASKPKVTKPKTAKPKAAKAKKA	P43276|H15_MOUSE	49.95	26	888	635	1390
VKSKASKPKVTKPKTAKPKAAKAKKAVS	P43276|H15_MOUSE	49.95	30	3880	1130	3590
VKSKASKPKVTKPKTAKPKAAKAKKAVS	P43276|H15_MOUSE	49.95	31	33400	9920	9410
VKVTFNSALAQKEAKK	O89051|ITM2B_MOUSE	49.89	16	15600	587	9600
VLPNIQAVLLPKKTESHHK	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	47.45	19	63	516	569
VLTVINQTQKENLRKFYKGKKYKPLDLRI	Q6ZWV7|RL35_MOUSE	48.95	33	NA	3390	4160
VPFYVRGPNVEAGSLNPH	Q8CFG0|SULF2_MOUSE	49.89	18	5450	79.9	5330
VQAVSSSKER	P43275|H11_MOUSE	27.8	10	NA	452	NA
VQKKDGKKRKRSRKESYSVYVYKVLKQ	Q64525|H2B2B_MOUSE	43.24	31	NA	2500	NA
VRYTQKAPQVSTPTL	P07724|ALBU_MOUSE	49.82	15	51900	2380	58300
VRYTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.92	16	18200	50.1	17100
VSSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	46.72	13	43700	810	17600
VTDATETTITISWR	P11276|FINC_MOUSE	37.6	14	901	270	462
VTKAQKKDGKKRKRSRKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.25	26	NA	4700	NA
VTKAQKKDGKKRKRSRKESYSVYVYKV	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.01	28	NA	1380	268
VTKAQKKDGKKRKRSRKESYSVYVYKV	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.22	29	NA	1760	147
VTKKVAKSPKKAKVTKPKKVKSASKAVK	P15864|H12_MOUSE	49.91	30	NA	504	NA
VVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.94	16	3890	2650	4520
VVRKPLNKEGKKPRTKAPKIQRLVTPR	P62754|RS6_MOUSE	43.25	27	NA	355	NA
VYKVLKQVHPD	Q8CGP0|H2B3B_MOUSE:Q8CGP2|H2B1	43.22	11	NA	187	NA
VYLIQGTQVYVFLTK	Q91X72|HEMO_MOUSE	49.62	15	3160	1610	2500
VYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	46.18	13	NA	1440	NA
WSIENVSFGSGGALLQK	Q99KQ4|NAMPT_MOUSE	49.81	17	136	127	NA
YDVKAPAM(+15.99)FNIRNIGK	P97351|RS3A_MOUSE	42.91	16	192	576	369
YLNIYTPAHAHEGSN	Q91WG0|EST2C_MOUSE	48.67	15	18800	197	17000
YLNIYVPAHAHEG	Q8BK48|EST2E_MOUSE	45.58	13	20400	436	16400
YLNIYVPAHAHEGSNLPV	Q8BK48|EST2E_MOUSE	49.91	18	90800	2390	102000
YNSQITAPYADRVTFS	O88792|JAM1_MOUSE	49.81	16	3610	53	3770
YNTASNKTRLSRTPGNRIVYLYTKKVGK	Q9D1R9|RL34_MOUSE	48.93	31	1610	12500	2050
YNTASNKTRLSRTPGNRIVYLYTKKVGK	Q9D1R9|RL34_MOUSE	49.95	32	5200	8910	7760
YPVVPVHLDGTF	O35291|RNAS2_MOUSE:P97425|ECP2_	43.04	12	2790	1020	859
YSRKALYKRKYSAAKTKVEKKKKK	P47911|RL6_MOUSE	48.92	24	NA	453	NA
YSRKALYKRKYSAAKTKVEKKKKKEK	P47911|RL6_MOUSE	49.95	26	763	1140	2040
YSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.75	15	89.6	310	NA

5-WT-AAD						
Peptide	Accession	X.10LgP	Length	Area.1	Area.3	Area.5
A(+42.01)AKKRKIKTIKKC(+57.02)	E9PYK3|PARP4_MOUSE	25.42	13	NA	NA	1960
A(+42.01)ATPKKAKKPKVVKVKPVK	P10922|H10_MOUSE	49.95	19	6310	4450	3690
A(+42.01)AYKLVLIRHG	Q9DBJ1|PGAM1_MOUSE	43.23	11	NA	NA	85.1
A(+42.01)GYEYVSPEQLSG	Q80TA1|EPT1_MOUSE	30.88	13	303	NA	436
A(+42.01)GYEYVSPEQLSGFDKY	Q80TA1|EPT1_MOUSE	49.92	17	545	NA	415
A(+42.01)SKRALVILAKGAE	Q99LX0|PARK7_MOUSE	29.71	14	536	94	1390
AAAAAAVAAAAAAAAA	Q3TSG4|ALKB5_MOUSE	28.69	16	NA	NA	506
AAAGAKKAKSP	P43274|H14_MOUSE	35.21	11	2190	2920	3580
AAAGAKKAKSPKKAKATKAKKAPK	P43274|H14_MOUSE	49.95	24	NA	3710	2280
AAAKKTVKTPKKPKKPAVSKK	P43275|H11_MOUSE	49.95	21	764	301	509
AAEEFKVPAATSAIIT	P61961|UFM1_MOUSE	49.64	16	2400	NA	1250
AAGAKKAKSP	P43274|H14_MOUSE	28.62	10	NA	NA	413
AAGVFSNPAVRTAAA	O35609|SCAM3_MOUSE	39.57	15	538	NA	664
AAGVKKVAKSPKKAKAAAKPKKAAKSPA	P43276|H15_MOUSE	48.95	32	NA	1550	2110
AAIPGTNM(+15.99)YNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	47.67	22	398	NA	190
AAIPGTNMYNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	39.51	22	122	NA	235
AAKPKTSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.95	22	NA	1750	1780
AAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	17	20900	861	3560
AALRPLVKPKIVKKRTKKFIRHQSDR	P17932|RL32P_MOUSE:P62911|RL32_M	48.95	26	NA	836	777
AALYSFKAARALLDHR	Q9WTN3|SRBP1_MOUSE	48.1	16	387	NA	316
AAPAAAATTAAPAAAAAPAKAEAKEE	P14869|RLA0_MOUSE	49.95	26	910	NA	172
AAPQQAAAPEPTSAFNPR	E9Q555|RN213_MOUSE	49.35	18	788	NA	1050
AASAYYNPGNPHNVYM(+15.99)PT	P97765|WBP2_MOUSE	49.89	18	3450	NA	1650
AASAYYNPGNPHNVYMPT	P97765|WBP2_MOUSE	49.94	18	506	NA	1750
AASTIYGPHTLSAYIQ	Q9JHE3|ASAH2_MOUSE	48.79	16	3460	NA	1640
AATPKKTAKKTPKKAKKPA	P43277|H13_MOUSE	49.95	19	NA	NA	688
AAVTKKVAKSPKKAKVTKPKK	P15864|H12_MOUSE	48.95	21	NA	NA	306
AAVTKKVAKSPKKAKVTKPKKVK	P15864|H12_MOUSE	49.94	23	NA	NA	239
ADASFVAAIPSTQVV	Q62178|SEM4A_MOUSE	27.43	15	2980	NA	1070
ADFHYAASKALRVPA	Q80TA9|EPG5_MOUSE	49.9	15	5790	NA	9540
ADFSYRGPAGSIEQGPY	Q99LI2|CLCC1_MOUSE	49.63	17	802	NA	752
ADGREVSSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	32.18	18	152	NA	62.5
ADKEFHAPLIIDE	Q91YN5|UAP1_MOUSE	41.83	13	722	NA	111
ADKEFHAPLIIDEN	Q91YN5|UAP1_MOUSE	46.95	14	2100	NA	616
ADKEFHAPLIIDENG	Q91YN5|UAP1_MOUSE	48.49	15	12000	NA	6000
ADTKHYYESEALTIPSK	Q06770|CBG_MOUSE	47.04	17	NA	NA	155
AEEFKVPAATSAIIT	P61961|UFM1_MOUSE	49.29	15	725	NA	207
AEEFKVPAATSAIITN	P61961|UFM1_MOUSE	49.67	16	1580	NA	1220
AEEFKVPAATSAIITNDG	P61961|UFM1_MOUSE	37.89	18	1220	NA	634
AEELVKDSELSPPTSAPSLVS	Q9WUU8|TNIP1_MOUSE	40.85	21	332	NA	250
AEPSYRGSEPEPEY	Q60598|SRC8_MOUSE	29.73	14	151	NA	351
AERLKPYVAAQVDVLPD	A2A8L5|PTPRF_MOUSE	49.49	17	245	NA	575
AERLKPYVAAQVDVLPDT	A2A8L5|PTPRF_MOUSE	49.94	18	505	NA	1670
AFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MO	48.33	13	13500	87.4	11200
AGEQSWIQALPSVAKEEK	Q8BH86|GLUCM_MOUSE	48.91	18	508	NA	370
AGGGDPEAPAPAPAAERPP	Q68FL4|SAHH3_MOUSE	49.53	19	487	NA	106
AGKLQDQGPDVLLAKVS	A6X935|ITIH4_MOUSE	49.87	17	727	NA	1290
AGKVRGQTPKVAKQEKKKKKTGRAKR	P62862|RS30_MOUSE	46.98	26	NA	NA	4460
AGNDLSFIHPKALSGLK	A2ARI4|LGR4_MOUSE	47.63	17	NA	NA	154
AGNDLSFIHPKALSGLKE	A2ARI4|LGR4_MOUSE	44.92	18	601	NA	594
AGNFYVPAEPKLA	P14148|RL7_MOUSE	40.25	13	NA	NA	150
AGNFYVPAEPKLAFVI	P14148|RL7_MOUSE	42.99	16	351	NA	376
AGTRYSAPANLYVR	Q64487|PTPRD_MOUSE:A2A8L5|PTPRF	41.56	14	1090	NA	1050
AHELRYQVPGAVPAK	Q9Z280|PLD1_MOUSE	49.87	15	13300	NA	8350
AHELRYQVPGAVPAKVQ	Q9Z280|PLD1_MOUSE	48.68	17	79.1	NA	224
AHELRYQVPGAVPAKVQL	Q9Z280|PLD1_MOUSE	49.57	18	47.7	NA	53.5
AIFARGPQAHLVH	P24823|PPBN_MOUSE:P24822|PPBI_MO	48.18	13	2390	NA	1270
AIFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_MO	48.85	14	14300	NA	8530
AIKNNSFYGPEVKIEKG	Q00519|XDH_MOUSE	46.46	17	88.2	NA	94.8
AILVRYTQKAPQVSTP	P07724|ALBU_MOUSE	49.72	16	139	NA	168
AILVRYTQKAPQVSTPTLVE	P07724|ALBU_MOUSE	49.94	20	506	NA	871
AIPGTNM(+15.99)YNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	49.78	20	2200	NA	2160
AIPGTNM(+15.99)YNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	49.94	21	3420	NA	2990
AIPGTNMYNTDRANPV	E9Q7P9|CDHR2_MOUSE	29.35	16	NA	NA	98.3
AIPGTNMYNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	29.87	20	874	NA	2380
AIPGTNMYNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	49.93	21	1300	NA	2410
AISKAQKKDGKKR	Q64475|H2B1B_MOUSE	42.3	13	NA	NA	130
AITSYSIPESIKSLE	Q91Y74|SIA4C_MOUSE	31.38	15	1240	NA	908
AKAAAKPKKAAKSPAKP	P43276|H15_MOUSE	31.36	17	NA	NA	340
AKASKPKASKPKATKAKKAAP	P43277|H13_MOUSE	48.66	21	NA	408	1530
AKASKPKASKPKATKAKKAAPR	P43277|H13_MOUSE	48.93	22	NA	184	824
AKGLFRAAVPSGAST	P17183|ENOG_MOUSE:P17182|ENOA_M	48.43	15	5860	NA	6230
AKKAAPRK	P43277|H13_MOUSE	29.46	8	1120	NA	697
AKKPAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.95	20	1600	1550	1120
AKKRKKKSYTTPKKNKHKRKK	P62983|RS27A_MOUSE	49.95	21	4190	68400	4020
AKKRKKKSYTTPKKNKHKRKKVKLAVL	P62983|RS27A_MOUSE	49.95	27	4690	4190	8760
AKKRKKKSYTTPKKNKHKRKKVKLAVLK	P62983|RS27A_MOUSE	49.95	28	8370	24200	18100
AKKRKKKSYTTPKKNKHKRKKVKLAVLK	P62983|RS27A_MOUSE	49.95	29	10600	3020	18400
AKKRKKKSYTTPKKNKHKRKKVKLAVLK	P62983|RS27A_MOUSE	49.95	31	4430	10600	8230

AKKRKKKSYTTPKKNKHKRKKVKLAVLK	P62983|RS27A_MOUSE	49.94	33	757	NA	282
AKKVAAKKK	P15864|H12_MOUSE	42.65	9	5880	543	673
AKKVAKSPAK	P43275|H11_MOUSE	29.38	10	NA	NA	1940
AKPKAVKS(+79.97)KAS(+79.97)KPKV	P43276|H15_MOUSE	25.67	15	NA	NA	114
AKPKKAAKSPAKPKA	P43276|H15_MOUSE	46.33	15	NA	242	686
AKPKKAASKAP	P10922|H10_MOUSE	29.59	11	NA	NA	2510
AKPKKAASKAPSKK	P10922|H10_MOUSE	27.24	14	NA	NA	159
AKPKTSKPKAAKPKK	P43274|H14_MOUSE	35.51	15	NA	NA	644
AKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	16	3040	NA	334
AKPSGYNPPISILGIL	Q61739|ITA6_MOUSE	36.77	16	468	NA	669
AKPSGYNPPISILGILE	Q61739|ITA6_MOUSE	32.41	17	NA	NA	945
AKPVSQM(+15.99)RMATPLLM(+15.99)R	P04441|HG2A_MOUSE	36.34	18	397	NA	14300
AKPVSQM(+15.99)RMATPLLMRPM	P04441|HG2A_MOUSE	46.07	18	NA	NA	13400
AKPVSQM(+15.99)RMATPLLMRPM(+15	P04441|HG2A_MOUSE	49.55	18	17300	NA	14800
AKPVSQMRM(+15.99)ATPLLMRP	P04441|HG2A_MOUSE	36.94	17	1130	NA	679
AKPVSQMRM(+15.99)ATPLLMRPM	P04441|HG2A_MOUSE	42.97	18	3490	NA	288
AKPVSQMRMATPLLM(+15.99)RPM	P04441|HG2A_MOUSE	48.42	18	NA	NA	21900
AKPVSQMRMATPLLM(+15.99)RPM(+15	P04441|HG2A_MOUSE	45.33	18	12400	NA	11800
AKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	49.41	18	301	NA	11400
AKPVSQMRMATPLLMRPM(+15.99)	P04441|HG2A_MOUSE	49.8	18	6530	NA	21900
AKRAGAAKAKKPAGAAKKPK	P43274|H14_MOUSE	25.4	20	NA	NA	403
AKSPKKAKAAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	48.95	25	NA	548	543
AKSSAKRASKK	P10922|H10_MOUSE	30.87	11	NA	NA	802
AKTVKPKAAKPKTSKPKAAKPKKTAAKK	P43274|H14_MOUSE	49.95	29	1140	NA	304
AKTVKPKAK	P10922|H10_MOUSE	29.8	9	NA	NA	1310
AKTVKPKAKSSAKR	P10922|H10_MOUSE	49.8	14	539	484	1230
AKVELVPPTPAEIPT	Q9CPQ8|ATP5L_MOUSE	28.48	15	397	NA	284
AKVTKPKTPAKPKKAAP	P43275|H11_MOUSE	46.78	17	NA	NA	2020
ALAVAGAPIALSAVG	Q8VC49|IF27B_MOUSE	48.26	15	3170	NA	2880
ALAVAGAPVALSAVG	Q8VC49|IF27B_MOUSE	46.3	15	1200	NA	953
ALIQYFSPYVSADM(+15.99)H	Q99LD4|CSN1_MOUSE	39.98	15	281	NA	87.8
ALKAKKAVLKGVHSHKKKKIRTSPTFRR	P62751|RL23A_MOUSE	48.95	29	NA	524	742
ALKAKKAVLKGVHSHKKKKIRTSPTFRR	P62751|RL23A_MOUSE	48.95	30	NA	10300	3590
ALKAKKAVLKGVHSHKKKKIRTSPTFRR	P62751|RL23A_MOUSE	48.75	31	NA	2100	933
ALKAKKAVLKGVHSHKKKKIRTSPTFRR	P62751|RL23A_MOUSE	48.95	33	272	3610	1930
ALLSPYSYSTTAVVSNPQ	P07309|TTHY_MOUSE	49.47	18	237	NA	414
ALRAPRKKIHRRVLKKNPLK	Q9D8E6|RL4_MOUSE	39.85	20	NA	1460	1340
ALRNYEYYASHVPESVKN	Q9Z0S1|BPNT1_MOUSE	49.18	18	690	NA	262
ALYSFKAARALLDHR	Q9WTN3|SRBP1_MOUSE	49.45	15	3770	NA	2820
ALYSFKAARALLDHRK	Q9WTN3|SRBP1_MOUSE	49.89	16	10700	NA	5770
AM(+15.99)LQVLGPKPALPEG	P13020|GELS_MOUSE	49.41	15	3260	NA	1970
ANVVWDYFTQLSNNAKEA	P06728|APOA4_MOUSE	49.84	18	188	NA	352
ANVVWDYFTQLSNNAKEAV	P06728|APOA4_MOUSE	46.18	19	NA	NA	309
APAAAATTAAPAAAAAPAKAEAKEE	P14869|RLA0_MOUSE	49.95	25	1420	NA	83
APAEAQAAM(+15.99)EEPVVQPSVVDR	Q9DBG5|PLIN3_MOUSE	49.93	21	1050	NA	748
APAEAQAAMEEPVVQPSVVDR	Q9DBG5|PLIN3_MOUSE	49.95	21	241	NA	734
APAIDIFSTPSSSNSTS	Q7M6Y3|PICAL_MOUSE	48.95	17	291	NA	354
APAIDIFSTPSSSNSTSK	Q7M6Y3|PICAL_MOUSE	48.63	18	6410	67.7	7340
APAIDIFSTPSSSNSTSKLPN	Q7M6Y3|PICAL_MOUSE	48.93	21	756	NA	1280
APAQM(+15.99)AYPTAYPSFPG	Q7TN29|SMAP2_MOUSE	46.68	16	1720	NA	1220
APAQMAYPTAYPSFPG	Q7TN29|SMAP2_MOUSE	31.9	16	495	NA	1040
APAVTPVK	P70158|ASM3A_MOUSE	30.12	8	1960	NA	3650
APDAWDYSQGFVNEEMIR	Q9DCN2|NB5R3_MOUSE	49.89	18	132	NA	154
APDFVFYAPRLRINK	P26043|RADI_MOUSE:P26040|EZRI_MC	36.66	15	419	NA	387
APDRTEEIKTPEPLEEGPA	Q6EDY6|CARL1_MOUSE	48.91	19	2600	NA	3140
APDTRFVAPGAL	Q3U2C5|RN149_MOUSE	29.47	12	613	80.2	466
APDTRFVAPGALG	Q3U2C5|RN149_MOUSE	41.65	13	16000	2460	9780
APDTRFVAPGALGNAP	Q3U2C5|RN149_MOUSE	49.44	16	10600	224	10600
APDTRFVAPGALGNAPW	Q3U2C5|RN149_MOUSE	49.57	17	4780	151	4320
APETRSQVTPSVPSEALD	Q7TQH7|LRP10_MOUSE	49.9	18	560	NA	314
APETRSQVTPSVPSEALDDS	Q7TQH7|LRP10_MOUSE	49.93	20	12000	213	9320
APETRSQVTPSVPSEALDDST	Q7TQH7|LRP10_MOUSE	49.94	21	3310	NA	2310
APETRSQVTPSVPSEALDDSTG	Q7TQH7|LRP10_MOUSE	49.93	22	225	NA	197
APFDWEGAQASQAL	Q91W98|S15A4_MOUSE	45.55	14	561	NA	368
APFFTPNAAPAE	Q80TA9|EPG5_MOUSE	38.82	12	591	NA	532
APGGYVAPKAVWL	Q9DBG3|AP2B1_MOUSE	46.44	13	192	NA	189
APGHYTYSSPHSGSIH	O09114|PTGDS_MOUSE	49.88	16	1010	NA	413
APGKKVIYSQPSTRSEGEF	O88792|JAM1_MOUSE	49.6	19	6480	NA	4320
APGLAFTTPVVASAAPV	Q80VC9|CAMP3_MOUSE	42.06	17	553	NA	676
APGM(+15.99)HTYSQPYSSRSRL	Q9ET43|CLD12_MOUSE	30.66	17	246	NA	334
APGMHTYSQPYSSRSR	Q9ET43|CLD12_MOUSE	48.19	16	4370	NA	4290
APGMHTYSQPYSSRSRL	Q9ET43|CLD12_MOUSE	29.43	17	NA	NA	214
APGMHTYSQPYSSRSRLS	Q9ET43|CLD12_MOUSE	48.21	18	739	NA	891
APGNAYFGPGSGSIVL	Q60997|DMBT1_MOUSE	46.48	16	NA	NA	473
APGPSHTVAAPQAAAAAAL	Q80U93|NU214_MOUSE	49.31	19	4130	74.1	4350
APGPSQPAVLQPSVEPAQ	Q9ERN0|SCAM2_MOUSE	48.84	18	574	NA	1130
APGPSQPAVLQPSVEPAQPTPQ	Q9ERN0|SCAM2_MOUSE	49.94	22	6130	NA	7890
APGPYQAAAGPSVVPTAPPT	Q9JLJ0|LITAF_MOUSE	49.4	20	231	NA	177
APGRDLHYQNPHSNAVGNP	Q01279|EGFR_MOUSE	35.94	19	3080	NA	2620
APINAFIGGLAAQEVM(+15.99)K	Q02053|UBA1_MOUSE	47.69	17	518	NA	175
APISSHTAPRPNPTPA	Q6PB44|PTN23_MOUSE	45.55	16	20800	NA	17000

APISSHTAPRPNPTPALP	Q6PB44|PTN23_MOUSE	49.67	18	4970	NA	1360
APISSHTAPRPNPTPALPQ	Q6PB44|PTN23_MOUSE	49.9	19	2000	NA	1860
APLNVQFSSPLPGEAVK	Q80X90|FLNB_MOUSE	49.92	17	2410	NA	3010
APLNVQFSSPLPGEAVKD	Q80X90|FLNB_MOUSE	49.94	18	11600	554	12600
APM(+15.99)DAFSGSRAVLSGPA	Q8K010|OPLA_MOUSE	49.33	17	816	NA	256
APM(+15.99)YYRGAQAA	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	41.71	11	1230	NA	1150
APM(+15.99)YYRGAQAAIV	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	45.29	13	4700	57.2	2450
APM(+15.99)YYRGAQAAIVV	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	37.79	14	22400	2590	17500
APM(+15.99)YYRGAQAAIVVY	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	49.55	15	79700	13700	62300
APM(+15.99)YYRGAQAAIVVYD	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	49.61	16	118000	12500	81100
APMDAFSGSRAVLSGPA	Q8K010|OPLA_MOUSE	49.89	17	420	NA	588
APMYYRGAQAA	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	45.76	11	1100	NA	1670
APMYYRGAQAAIVVY	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	47.63	15	28000	NA	57100
APMYYRGAQAAIVVYD	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	49.47	16	39800	NA	79400
APNLHFHNPNPEIPA	P19096|FAS_MOUSE	37.01	15	337	NA	827
APNYYPNSFSAPEQQRSALE	P24270|CATA_MOUSE	28.86	20	NA	NA	194
APPAEKAPAKKKAAKKPAGVRR	P15864|H12_MOUSE	49.95	22	NA	NA	1540
APPAGSLYSSPVNSSAP	Q99LI8|HGS_MOUSE	48.45	17	4650	NA	3740
APPLPIKTPIPTPST	Q7TQH7|LRP10_MOUSE	49.89	15	11900	169	12500
APPLPIKTPIPTPSTL	Q7TQH7|LRP10_MOUSE	49.86	16	1740	NA	1290
APPLPIKTPIPTPSTLP	Q7TQH7|LRP10_MOUSE	49.88	17	8360	142	11300
APQQAAAPEPTSAFNPR	E9Q555|RN213_MOUSE	49.22	17	5010	NA	4170
APQVSTPTLVEAARNLG	P07724|ALBU_MOUSE	49.84	17	161	NA	104
APRPFGSVSSPKVTSIPSPS	Q8CI51|PDLI5_MOUSE	44.78	20	191	NA	425
APSKKPKATPVKKAKKKPA	P10922|H10_MOUSE	48.95	19	NA	NA	861
APSKLPSNSVYAGTVPSRVPA	Q8VCF0|MAVS_MOUSE	34.83	21	NA	NA	145
APSNYLNNPYVRKAL	P16675|PPGB_MOUSE	49.53	15	876	NA	564
APSNYLNNPYVRKALHIPE	P16675|PPGB_MOUSE	47.55	19	51800	NA	22400
APSTMKIKIIAPPERKY	P63260|ACTG_MOUSE:P60710|ACTB_M	47.87	17	NA	NA	642
APSTRVITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.95	22	1320	NA	2300
APSTRVITNQYNSPTGLYSSENIS	O70400|PDLI1_MOUSE	49.94	24	67.7	NA	321
APSWHASVPTRAGPD	O88839|ADA15_MOUSE	36.12	15	1630	NA	2160
APTAAIPGTNMYNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	39.86	25	NA	NA	257
APTSALGPKASPAP	Q8K0V4|CNOT3_MOUSE	41.73	14	748	NA	357
APTSALGPKASPAPS	Q8K0V4|CNOT3_MOUSE	43.76	15	2350	NA	1590
APVFYTPQAYAAIPS	Q5YD48|A1CF_MOUSE	48.83	15	873	NA	996
APVPSPVAPAPVPSR	P97825|JUPI1_MOUSE	49.36	15	163	NA	124
APVPSPVAPAPVPSRRNPPG	P97825|JUPI1_MOUSE	35.94	20	96.7	NA	301
APVVFSTPQATQM(+15.99)NTPS	Q6NZJ6|IF4G1_MOUSE	49.8	17	712	NA	764
APWQWSGPASHNSLPA	G3X9J0|SI1L3_MOUSE	46.07	16	321	NA	600
APYGARYVGSM(+15.99)VADIH	Q9QXD6|F16P1_MOUSE	48.08	16	809	NA	470
APYGARYVGSM(+15.99)VADIHRT	Q9QXD6|F16P1_MOUSE	49.93	18	2420	NA	2450
APYGARYVGSMVADIH	Q9QXD6|F16P1_MOUSE	25.49	16	NA	NA	260
APYGARYVGSMVADIHR	Q9QXD6|F16P1_MOUSE	49.92	17	3920	NA	7950
APYGARYVGSMVADIHRT	Q9QXD6|F16P1_MOUSE	49.88	18	2340	NA	3870
APYQGPDAAPGALD	P57780|ACTN4_MOUSE	36.29	14	1000	NA	643
AQAAM(+15.99)EEPVVQPSVVDR	Q9DBG5|PLIN3_MOUSE	49.72	17	542	NA	365
AQAAMEEPVVQPSVVD	Q9DBG5|PLIN3_MOUSE	48.21	16	199	NA	561
AQKKDGKKRKRSRKESYSVYVYKVL	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.24	25	NA	2200	81.6
AQKKDGKKRKRSRKESYSVYVYKVLK	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	48.95	26	NA	16400	375
AQPPEYTFPSGSGAHFP	Q2TBE6|P4K2A_MOUSE	47.51	17	5350	NA	4950
AQPPEYTFPSGSGAHFPQ	Q2TBE6|P4K2A_MOUSE	49.88	18	10700	NA	10800
AQPVLQYGNPYSAQETRDG	Q3UKC1|TAXB1_MOUSE	48.95	19	NA	NA	114
AQRAGYKAAIVHNVD	O54965|RNF13_MOUSE	47.44	15	NA	NA	220
AQSPYINPIIPFTGPI	O08573|LEG9_MOUSE	47.73	16	482	NA	462
AQTAYSANPASQAFV	O08992|SDCB1_MOUSE	48.45	15	NA	NA	256
AQTAYSANPASQAFVL	O08992|SDCB1_MOUSE	47.46	16	NA	NA	1340
AQYVLTSPEASSRFG	O70362|PHLD_MOUSE	27.85	15	252	NA	132
ARDNMFSGSKINYTENR	P06745|G6PI_MOUSE	49.15	17	931	NA	967
ARM(+15.99)APYQGPDAAPGALD	P57780|ACTN4_MOUSE	42.14	17	680	NA	536
ARM(+15.99)PYTNAVIHEVQ	P24456|CP2DA_MOUSE:P24457|CP2DB	39.71	14	1440	NA	409
ARMAPYQGPDAAPGALD	P57780|ACTN4_MOUSE	39.97	17	224	NA	581
ARMPYTNAVIHEVQ	P24456|CP2DA_MOUSE:P24457|CP2DB	43.42	14	1840	NA	533
ARMPYTNAVIHEVQR	P24456|CP2DA_MOUSE:P24457|CP2DB	46.83	15	4840	NA	4500
ARQQVRSPVTNIAR	P84091|AP2M1_MOUSE	48.69	14	11000	NA	11400
ARQQVRSPVTNIARTS	P84091|AP2M1_MOUSE	45.75	16	4610	NA	4370
ARVLEMVEPLVTRTRDR	Q61268|APOC4_MOUSE	25.39	17	NA	NA	256
ARYIYGKPVQGVAYT	P01029|CO4B_MOUSE	47.97	15	233	NA	107
ARYIYGKPVQGVAYTR	P01029|CO4B_MOUSE	49.82	16	782	NA	1300
ARYRPRAPIIAVTRNPQ	P52480|KPYM_MOUSE	46.28	17	249	NA	680
ASAYYNPGNPHNVY	P97765|WBP2_MOUSE	46.05	14	214	NA	227
ASAYYNPGNPHNVYM(+15.99)PT	P97765|WBP2_MOUSE	49.85	17	9780	55.7	4990
ASDPKYATPQVIQAPGPR	O54967|ACK1_MOUSE	49.81	18	685	NA	1480
ASERYVPTYSVPALQ	Q9D956|MALD3_MOUSE	28.49	15	488	NA	390
ASGQIFISPDSLLGVEK	Q9D871|CEA18_MOUSE	32.32	17	NA	NA	43.9
ASIYSPPAAAAAAA	P70297|STAM1_MOUSE	46.37	14	1280	NA	997
ASKAKVTKPKTPAKPKKA	P43275|H11_MOUSE	41.12	18	NA	NA	472
ASKPKASKPKATKAKKAAPRKK	P43277|H13_MOUSE	49.95	22	745	NA	1910
ASKPKATKAKKAAP	P43277|H13_MOUSE	29.88	14	NA	NA	357
ASKPKATKAKKAAPR	P43277|H13_MOUSE	48.93	15	333	1000	4030
ASKPKATKAKKAAPRKK	P43277|H13_MOUSE	49.94	17	8790	NA	14100

ASKPKKAK	P10922|H10_MOUSE	39.67	8	NA	939	685
ASKPKKAKTVKPKAK	P10922|H10_MOUSE	49.84	15	NA	1260	1100
ASKPKKAKTVKPKAKSSAKR	P10922|H10_MOUSE	49.95	20	NA	NA	2060
ASKPKVTKPKTAKPKAAKAKKAVSKKK	P43276|H15_MOUSE	49.95	27	8160	8190	3110
ASLVYENASAIM(+15.99)AHE	E9Q0N2|PTPRH_MOUSE	48.34	15	1170	53.1	855
ASLVYENASAIM(+15.99)AHES	E9Q0N2|PTPRH_MOUSE	49.55	16	535	NA	641
ASLVYENASAIMAH	E9Q0N2|PTPRH_MOUSE	38.87	14	NA	NA	94.7
ASLVYENASAIMAHE	E9Q0N2|PTPRH_MOUSE	48.66	15	926	NA	1260
ASLVYENASAIMAHESE	E9Q0N2|PTPRH_MOUSE	49.74	17	940	NA	1380
ASPAPSTRVITNQYNSPTGLYSSENISN	O70400|PDLI1_MOUSE	48.94	28	NA	NA	966
ASPAPSTRVITNQYNSPTGLYSSENISNF	O70400|PDLI1_MOUSE	43.32	31	NA	NA	73.7
ASPELTSPLANQSL	Q8CHY3|DYM_MOUSE	36.39	14	406	NA	263
ASPPPYAAYATPTPEVYGYG	Q9QZC7|PKHB2_MOUSE	49.88	20	558	NA	1080
ASVATNPIITPVAQENQ	P08226|APOE_MOUSE	49.68	17	944	NA	738
ASYEFVQRL	Q9JHU4|DYHC1_MOUSE	36.33	9	315	NA	115
ATDDVFSPSHAIPIET	Q91ZH7|ABHD3_MOUSE	49.25	16	3120	NA	2160
ATGFYKTPNLGYSFE	Q00519|XDH_MOUSE	48.88	15	NA	NA	293
ATKAKKAAP	P43277|H13_MOUSE	30.6	9	NA	NA	2140
ATKAKKAAPR	P43277|H13_MOUSE	43.09	10	685	2220	3420
ATKAKKAPKSPAKAK	P43274|H14_MOUSE	47.61	15	928	NA	1990
ATKAKKAPKSPAKAKTVKPKAAKPK	P43274|H14_MOUSE	48.4	25	NA	NA	351
ATLEIKGPQADLID	Q8CAS9|PARP9_MOUSE	30.54	14	378	NA	326
ATLEIKGPQADLIDA	Q8CAS9|PARP9_MOUSE	36.61	15	940	NA	579
ATLPPVSPPKAALSVDE	Q6NZJ6|IF4G1_MOUSE	25.72	17	NA	NA	456
ATNPIITPVAQENQ	P08226|APOE_MOUSE	45.99	14	17500	548	12300
ATPAPSAPAAASATSPSPAPSSGNG	Q9JKV1|ADRM1_MOUSE	48.9	25	NA	NA	94
ATPKKTAKKTPKKAKKPA	P43277|H13_MOUSE	49.94	18	2240	3320	5610
ATPSTNPFVAATGPSAASSTNPFQ	Q8K2K6|AGFG1_MOUSE	49.94	24	140	NA	491
ATSYGQPPTGYSTPTAPQAYSQPVQ	Q61545|EWS_MOUSE	48.95	25	NA	NA	140
ATVSWRAPTAQVES	Q80YX1|TENA_MOUSE	47.89	14	1650	NA	998
ATVSWRAPTAQVESFR	Q80YX1|TENA_MOUSE	49.92	16	3790	NA	2370
ATYKLSAPWVEQEGP	P14432|HA1T_MOUSE	49.21	15	954	NA	1040
ATYKLSAPWVEQEGPE	P14432|HA1T_MOUSE	49.9	16	8980	87.9	8400
AVDALASSHPLSSPA	P97449|AMPN_MOUSE	46.09	15	1660	NA	336
AVDALASSHPLSSPAD	P97449|AMPN_MOUSE	48.26	16	606	NA	105
AVDVFFPPEAQNDF	Q68FD5|CLH1_MOUSE	36.93	14	1140	NA	515
AVDVFFPPEAQNDFP	Q68FD5|CLH1_MOUSE	45.27	15	1550	NA	1280
AVDVFFPPEAQNDFPV	Q68FD5|CLH1_MOUSE	48.1	16	3140	NA	3990
AVEQPSTSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	47.53	23	244	NA	405
AVGKVIPELNGKLTGM(+15.99)AFRVPTI	P16858|G3P_MOUSE	49.86	29	3670	NA	11200
AVGKVIPELNGKLTGMAFRVPTPNVSVV	P16858|G3P_MOUSE	49.95	29	2590	NA	13800
AVKSKYKASIAALEAK	Q8VDD5|MYH9_MOUSE	49.91	16	2720	NA	1780
AVKVSWRSPVPNKQHG	Q64487|PTPRD_MOUSE	44.17	16	1090	NA	1530
AVYHTSSM(+15.99)LPAPP	P70665|SIAE_MOUSE	27.35	13	980	NA	361
AYTIPFYTPIPNG	O08573|LEG9_MOUSE	43.21	13	641	NA	712
AYTIPFYTPIPNGLYPS	O08573|LEG9_MOUSE	25.85	17	NA	NA	85.3
C(+57.02)(+42.01)RHNY(+79.97)EGPETH	P14483|HB2A_MOUSE	40.18	15	13300	NA	12400
C(+57.02)RHN(+15.00)YEGPETHTSL	P14483|HB2A_MOUSE	28.92	14	NA	NA	87.6
DAPAEAQAAMEEPVVQPSVVD	Q9DBG5|PLIN3_MOUSE	31.04	21	NA	NA	145
DAPAEAQAAMEEPVVQPSVVDR	Q9DBG5|PLIN3_MOUSE	49.95	22	66.3	NA	85
DARSYAAAVANRA	Q8K296|MTMR3_MOUSE	35.36	13	NA	NA	395
DARSYAAAVANRAKG	Q8K296|MTMR3_MOUSE	44.6	15	764	NA	1290
DARSYAAAVANRAKGGG	Q8K296|MTMR3_MOUSE	47.77	17	9720	NA	6500
DARSYTAAVANRAK	Q91XS1|MTMR4_MOUSE	47.02	14	25400	896	19800
DARSYTAAVANRAKG	Q91XS1|MTMR4_MOUSE	46.53	15	10400	155	5790
DARSYTAAVANRAKGG	Q91XS1|MTMR4_MOUSE	48.38	16	17600	420	13400
DARSYTAAVANRAKGGG	Q91XS1|MTMR4_MOUSE	49.93	17	86000	2710	49900
DATLYVPSAPLSGP	Q60928|GGT1_MOUSE	40.12	14	1220	NA	720
DATLYVPSAPLSGPV	Q60928|GGT1_MOUSE	43.86	15	668	NA	476
DDAPRAVFPSIVG	P63260|ACTG_MOUSE:P60710|ACTB_M	28.93	13	917	NA	160
DDDVYRAPPIDRSILPT	Q8BGD9|IF4B_MOUSE	48.64	17	752	NA	130
DDFEPYLSPQARPNN	Q91YT7|YTHD2_MOUSE	49.04	15	712	NA	398
DDGHGGYKPFQNPVPNQSPS	P16382|IL4RA_MOUSE	48.76	20	951	NA	3800
DDHKLSLDELHRKYG	Q8VDN2|AT1A1_MOUSE	46.07	15	228	NA	173
DDIEADHVG	P14434|HA2B_MOUSE:P01910|HA2K_M	30.37	9	976	NA	379
DDLLYSFPVVIKNK	P14152|MDHC_MOUSE	46.34	14	NA	NA	65.1
DDLNFFNQKKKKKKTKK	Q99L45|IF2B_MOUSE	47.34	17	NA	NA	76.5
DEAKERASFITPVPGGVG	Q922D8|C1TC_MOUSE	44.62	18	538	NA	1340
DEAKERASFITPVPGGVGP	Q922D8|C1TC_MOUSE	26.3	19	NA	NA	38
DEATRYLAPTIL	P47740|AL3A2_MOUSE	40.22	12	538	NA	218
DEATRYLAPTILT	P47740|AL3A2_MOUSE	35.65	13	650	NA	216
DEATRYLAPTILTDVDPN	P47740|AL3A2_MOUSE	49.55	18	28900	NA	8640
DEFEPPIVKGVKPAKAAPAAPASE	P09405|NUCL_MOUSE	35.7	24	NA	NA	517
DEGERYIAPTVLVDVQE	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	49.7	17	5880	NA	4310
DEIDAALPNKAP	Q64464|CP3AD_MOUSE	42.01	12	1900	NA	1150
DEIDAALPNKAPAT	Q64464|CP3AD_MOUSE	46.73	14	1050	NA	702
DEIQRYQKPVVAAIQ	Q9DBM2|ECHP_MOUSE	44.34	15	NA	NA	162
DEIQRYQKPVVAAIQG	Q9DBM2|ECHP_MOUSE	49.74	16	3490	NA	6140
DEPKRSVAFKKTKKEVKKVATPKKAAKP	P10922|H10_MOUSE	49.79	32	NA	NA	497
DESGFPKPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	49.94	22	5220	NA	1410
DFHYAASKALRVPA	Q80TA9|EPG5_MOUSE	49.75	14	143	NA	620

DFKDEQRRLKKLRGKGKPRKGEGKRAT	Q9D2R8|RT33_MOUSE	49.2	30	NA	NA	8120
DFKPSYGTPAPGFSSM	P23249|MOV10_MOUSE	37.26	16	NA	NA	132
DFKPSYGTPAPGFSSM(+15.99)	P23249|MOV10_MOUSE	48.28	16	498	NA	610
DFLAGGVAAAISKTAVAPIERVK	P51881|ADT2_MOUSE	45.94	23	NA	NA	121
DFPSVVVVGLGKRS	Q9CPY7|AMPL_MOUSE	47.93	14	350	91.6	351
DFPSVVVVGLGKRSAG	Q9CPY7|AMPL_MOUSE	48.37	16	696	520	1390
DGAAAVLLARRSKA	Q8VCH0|THIKB_MOUSE:Q921H8|THIKA	36.06	14	NA	NA	1530
DGDSVVFAGPAGNSVETR	Q8R146|ACPH_MOUSE	49.37	18	3990	NA	2920
DGDSYRSPWSNKYD	P47757|CAPZB_MOUSE	49.7	14	782	NA	362
DGDSYRSPWSNKYDPP	P47757|CAPZB_MOUSE	49.88	16	44700	310	38500
DGDSYRSPWSNKYDPPL	P47757|CAPZB_MOUSE	49.16	17	50900	551	46300
DGEQAPPLPIKTPIPTPST	Q7TQH7|LRP10_MOUSE	49.93	19	650	NA	592
DGKGM(+15.99)NPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.87	21	121	NA	167
DGLLSYTAPVGQTM(+15.99)QL	Q03146|DDR1_MOUSE	47.41	16	3690	NA	2380
DGLLSYTAPVGQTMQL	Q03146|DDR1_MOUSE	49.58	16	299	NA	322
DGNHTLFH	P43023|CX6A2_MOUSE:P43024|CX6A1_	43.1	8	987	312	737
DGNHTLFHNPHVNPL	P43023|CX6A2_MOUSE:P43024|CX6A1_	47.14	15	347	NA	815
DGNHTLFHNPHVNPLPT	P43023|CX6A2_MOUSE:P43024|CX6A1_	49.33	17	6930	NA	7530
DGNHTLFHNPHVNPLPTG	P43023|CX6A2_MOUSE:P43024|CX6A1_	49.31	18	2420	NA	4170
DGPSTSSAHLAPVASSSVSYDPRKP	Q8CB77|ELOA1_MOUSE	49.65	25	185	NA	1140
DGPSTSSAHLAPVASSSVSYDPRKPA	Q8CB77|ELOA1_MOUSE	48.17	26	372	NA	559
DGQINYQAASPDEGAL	Q148W0|AT8B1_MOUSE	43.54	16	476	NA	251
DGREVSSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	47.51	17	964	NA	894
DGREVSSVEAPSVSPARH	Q8BUJ9|LRP12_MOUSE	36.59	18	NA	NA	99.8
DGRFVM(+15.99)GPTVAPSQEK	Q05BQ1|TUTLA_MOUSE	47.49	16	297	NA	238
DGRFVMGPTVAPSQ	Q05BQ1|TUTLA_MOUSE	43.37	14	85.4	NA	143
DGRFVMGPTVAPSQEK	Q05BQ1|TUTLA_MOUSE	39.47	16	NA	NA	291
DGTVPFWAHAGNAIPSADQ	Q9D0F3|LMAN1_MOUSE	25.93	19	595	NA	264
DHLTYGISGPNASYF	E9Q7P9|CDHR2_MOUSE	49.66	15	516	NA	211
DHNFPYKDPVAALYED	P16301|LCAT_MOUSE	48.71	16	4920	NA	1450
DHNFPYKDPVAALYEDG	P16301|LCAT_MOUSE	49.84	17	4500	NA	1860
DHNPLYPGSPPPGGYGQPSVLPGGYPA	Q8BJZ3|LFG3_MOUSE	49.95	27	4280	NA	1270
DHVDFSQPEPHTVL	Q9QUR8|SEM7A_MOUSE	49.82	14	1420	NA	694
DHVDFSQPEPHTVLF	Q9QUR8|SEM7A_MOUSE	49.76	15	10100	NA	6740
DHVDFSQPEPHTVLFH	Q9QUR8|SEM7A_MOUSE	49.89	16	2080	NA	374
DIFGSPVTATAPLAHPNKP	Q6PGH2|JUPI2_MOUSE	48.93	19	NA	NA	338
DIFIGPKAEEHR	P61164|ACTZ_MOUSE	37.23	12	2250	NA	1250
DIFIGPKAEEHRG	P61164|ACTZ_MOUSE	39.87	13	4490	NA	2810
DIKAIAKD	Q91YX5|LGAT1_MOUSE	26.33	8	NA	NA	1530
DIKSFITSIANKN	Q8CHR6|DPYD_MOUSE	47.94	13	169	NA	230
DIPGVRFKVVKVANVSLLALYKGKKERP	P62267|RS23_MOUSE	48.42	28	NA	NA	123
DIPGVRFKVVKVANVSLLALYKGKKERP	P62267|RS23_MOUSE	49.95	29	1300	NA	3600
DIPGVRFKVVKVANVSLLALYKGKKERP	P62267|RS23_MOUSE	49.81	30	3540	NA	3040
DIYQAPSADSADH	P26361|CFTR_MOUSE	32.26	13	1430	NA	435
DIYQAPSADSADHL	P26361|CFTR_MOUSE	37.08	14	676	NA	567
DKEFHAPLIIDENG	Q91YN5|UAP1_MOUSE	47.1	14	1360	NA	287
DKIYFAFPLANHR	Q3UUQ7|PGAP1_MOUSE	43	13	NA	NA	61.1
DKIYFAFPLANHRK	Q3UUQ7|PGAP1_MOUSE	44.84	14	312	NA	115
DLEYQMSTTARAKR	Q02257|PLAK_MOUSE	31	14	188	NA	419
DLFIGPKAEEHR	Q8R5C5|ACTY_MOUSE	37.23	12	2250	NA	1250
DLFIGPKAEEHRG	Q8R5C5|ACTY_MOUSE	39.87	13	4490	NA	2810
DLLTQYSTPEGSSVPI	E9Q414|APOB_MOUSE	36.91	16	124	NA	421
DLLYSFPVVIKNK	P14152|MDHC_MOUSE	48.48	13	3320	NA	1630
DLNFFNQKKKKKKTKK	Q99L45|IF2B_MOUSE	45.45	16	306	NA	304
DLNFRNPAVQEEIK	Q91WV7|SLC31_MOUSE	46	14	3360	NA	942
DLPTTFQGATASTSYG	Q9JJZ4|UB2J1_MOUSE	32.28	16	131	NA	272
DLQHGSLFLKTPKIVSSKDY	P06151|LDHA_MOUSE	49.89	20	565	NA	588
DLRHAFSPVASVESA	P29699|FETUA_MOUSE	49.4	15	644	NA	654
DLSQHATPLPTPAVLPG	O88746|TOM1_MOUSE	49.82	17	5450	NA	2560
DM(+15.99)FKASLVIPSKD	Q8BJD1|ITIH5_MOUSE	38.05	13	495	NA	159
DM(+15.99)RQTVAVGVIKAVDKK	P10126|EF1A1_MOUSE	35.21	17	NA	NA	117
DM(+15.99)RQTVAVGVIKAVDKKAAGAC	P10126|EF1A1_MOUSE	49.95	23	1490	965	2150
DMFKASLVIPSKD	Q8BJD1|ITIH5_MOUSE	43.28	13	205	NA	170
DMRQTVAVGVIKAVDKKAAGAGK	P10126|EF1A1_MOUSE	49.94	23	808	NA	2570
DNDNIFLSPLSISTA	P32261|ANT3_MOUSE	48.5	15	2110	278	1180
DNIFLSPLSISTA	P32261|ANT3_MOUSE	47.47	13	1390	NA	114
DNYRFAHTNIESLV	P27773|PDIA3_MOUSE	48.19	14	140	NA	90.9
DPAGGQYLTVSAAKAPGGK	Q91V88|NPNT_MOUSE	49.78	19	508	NA	337
DPAGPNFEYAEAPSRLSPDDA	P11152|LIPL_MOUSE	49.67	21	1760	NA	225
DPETGVFTAPLAGRYL	Q99K41|EMIL1_MOUSE	49.1	16	1150	NA	578
DPEVFSQPKVLPSAIPI	Q91YD3|DCP1A_MOUSE	49.92	17	304	NA	208
DPGESKSYSYSEVLPTEGPPS	Q8BHT7|RGP1_MOUSE	46.69	21	788	NA	427
DPGFGAPAASQVAS	Q6IRU5|CLCB_MOUSE	43.68	14	NA	NA	256
DPGFGAPAASQVASAQPG	Q6IRU5|CLCB_MOUSE	47.89	18	848	NA	966
DPGFRSPSTQVANNSHQPPP	Q6A037|N4BP1_MOUSE	47.55	20	3840	NA	6620
DPIQKYLTPQMATS	Q6P9J9|ANO6_MOUSE	47.6	14	510	NA	644
DPIQKYLTPQMATSIT	Q6P9J9|ANO6_MOUSE	49.84	16	39300	106	30500
DPKLTYHGFTLEDAASPK	Q62312|TGFR2_MOUSE	47.44	18	2230	NA	1580
DPKTQEFILNSPTVTSIK	Q9R0H0|ACOX1_MOUSE	49.87	18	240	NA	490
DPKYATPQVIQAPG	O54967|ACK1_MOUSE	45.51	14	991	NA	921
DPKYATPQVIQAPGP	O54967|ACK1_MOUSE	49.75	15	608	NA	540

DPKYATPQVIQAPGPR	O54967|ACK1_MOUSE	49.6	16	1420	NA	1430
DPLHYSIVSAPAAQKVRE	Q8BH86|GLUCM_MOUSE	49.92	18	351	NA	133
DPLHYSIVSAPAAQKVREL	Q8BH86|GLUCM_MOUSE	49.94	19	1210	NA	886
DPNTAYASYPSASVEN	O55101|SNG2_MOUSE	48.53	16	109	NA	106
DPNTAYASYPSASVENYQQPP	O55101|SNG2_MOUSE	49.94	21	201	NA	588
DPPASVVVGPVVVPR	P29699|FETUA_MOUSE	49.52	15	1170	NA	615
DPPASVVVGPVVVPRGL	P29699|FETUA_MOUSE	49.89	17	1600	NA	1560
DPPVKTKFGYHIIMVEGRK	Q9CWW6|PIN4_MOUSE	30.57	19	NA	NA	111
DPSAFAAAAPAAAAT	P14869|RLA0_MOUSE	46.7	15	2730	NA	2550
DPSAFAAAAPAAAATT	P14869|RLA0_MOUSE	49.72	16	2180	73.1	1340
DPSGKVSHTYGDPHVNLVIG	Q80T32|AGRD1_MOUSE	49.94	20	2330	NA	696
DPSLGIYNSPYIIPG	P18894|OXDA_MOUSE	45.37	15	NA	NA	170
DPSLGIYNSPYIIPGS	P18894|OXDA_MOUSE	49.57	16	505	NA	626
DPSLGIYNSPYIIPGSKT	P18894|OXDA_MOUSE	49.77	18	6420	NA	7180
DPSM(+15.99)VSAYM(+15.99)YPTGAPG	Q99LI8|HGS_MOUSE	48.07	19	507	NA	162
DPSMVSAYMYPTGAPGAQA	Q99LI8|HGS_MOUSE	48.59	19	NA	NA	102
DPTFHTPLDLYAY	Q07797|LG3BP_MOUSE	41.5	13	1260	NA	533
DPTFHTPLDLYAYA	Q07797|LG3BP_MOUSE	40.9	14	924	NA	401
DPTNPFRFPNIGVEK	O35598|ADA10_MOUSE	41.39	15	NA	NA	200
DPTPDPNTAYASYPSASVE	O55101|SNG2_MOUSE	49.62	19	2690	NA	2270
DPTPDPNTAYASYPSASVEN	O55101|SNG2_MOUSE	49.93	20	14900	126	13300
DPTPDPNTAYASYPSASVENYQ	O55101|SNG2_MOUSE	49.95	22	6320	NA	5260
DPTRIYDTALALWIPS	Q8K177|KCP3_MOUSE	25.16	16	NA	NA	687
DPTTAFQAPDVGQAL	A2ASQ1|AGRIN_MOUSE	48.6	15	6170	247	3110
DPTTAFQAPDVGQALL	A2ASQ1|AGRIN_MOUSE	49.77	16	1440	NA	1070
DPTTAFQAPDVGQALLQ	A2ASQ1|AGRIN_MOUSE	49.82	17	1530	NA	471
DPYDQPNAIYIERH	O88307|SORL_MOUSE	49.77	14	741	NA	612
DPYQRYHTPTPRDE	Q91XT4|SC16B_MOUSE	35.35	14	710	NA	585
DQARMPYTNAVIHEVQ	P24456|CP2DA_MOUSE:P24457|CP2DB	49.43	16	682	NA	1090
DQLFSGPLPGRLPV	Q60805|MERTK_MOUSE	48.86	14	NA	NA	282
DQLFSGPLPGRLPVNHRPFS	Q60805|MERTK_MOUSE	49.02	20	1210	NA	168
DQNLRPYQGGKANILGYN	Q6XQH0|G3ST2_MOUSE	44.83	18	132	NA	180
DQRDLISNHEQLPILG	P04441|HG2A_MOUSE	40.02	16	109	NA	391
DQTVVEPNIAIQSVTR	Q8BM96|AGRG7_MOUSE	47.97	16	61.4	NA	60
DRDSLVHSSPHVALSHVD	Q9WV91|FPRP_MOUSE	49.94	18	2410	NA	2120
DRDSLVHSSPHVALSHVDT	Q9WV91|FPRP_MOUSE	49.78	19	310	NA	620
DRKIVYEGPELNHAF	Q91ZX7|LRP1_MOUSE	49.92	15	4070	NA	2670
DRKIVYEGPELNHAFG	Q91ZX7|LRP1_MOUSE	49.94	16	323000	12800	342000
DRPHTYFGPETSASK	P70277|SIA7B_MOUSE	48.47	15	9900	177	7540
DRPHTYFGPETSASKFK	P70277|SIA7B_MOUSE	49.93	17	21100	NA	13500
DRQVWSGSKAAGAPP	Q8K2C7|OS9_MOUSE	43.54	15	2870	NA	789
DRYVASLAARNK	Q00560|IL6RB_MOUSE	36.31	12	174	NA	101
DRYYTPTISRERA	Q9R1P3|PSB2_MOUSE	46.2	13	822	NA	750
DSGGFYISPRSTFSSLQ	P08103|HCK_MOUSE	45.52	17	400	NA	116
DSGNFRPANPNWG	E9PV24|FIBA_MOUSE	47.95	13	479	NA	416
DSIVLPSGPVAHLALHG	Q8K0B3|LRC66_MOUSE	28.35	17	184	NA	135
DSKSKSDASTPPSPKVTYKAPVPTGEV	P35564|CALX_MOUSE	40.81	28	NA	NA	3380
DSLIKATIAGGGVIPHIHKSLIGKKGQQK	Q3THW5|H2AV_MOUSE:P0C0S6|H2AZ_	49.68	29	NA	NA	81.9
DSLVHSSPHVALSH	Q9WV91|FPRP_MOUSE	47.36	14	272	NA	896
DSLVHSSPHVALSHV	Q9WV91|FPRP_MOUSE	47.46	15	NA	NA	39.8
DSLVHSSPHVALSHVD	Q9WV91|FPRP_MOUSE	49.86	16	7980	50.4	6710
DSNFGAPSASVAAAP	O35643|AP1B1_MOUSE	44.89	15	758	NA	511
DSNFGAPSASVAAAPA	O35643|AP1B1_MOUSE	42.82	16	1300	NA	1150
DSNFGAPSASVAAAPAP	O35643|AP1B1_MOUSE	42.35	17	3050	NA	3040
DSNFGAPSASVAAAPAPA	O35643|AP1B1_MOUSE	49.82	18	713	NA	2930
DSNFGAPSASVAAAPAPAR	O35643|AP1B1_MOUSE	49.89	19	1950	NA	1220
DSNFGAPSASVAAAPAPARL	O35643|AP1B1_MOUSE	48.93	20	NA	NA	167
DSPDVVYSPETIEAR	Q9JHU9|INO1_MOUSE	44.41	15	819	NA	469
DSPNKLYTLVTYVPVTTFK	P62900|RL31_MOUSE	48.91	19	NA	29.9	637
DSRTNTAYVGSAILSEET	Q9QZC7|PKHB2_MOUSE	47.93	18	172	NA	267
DSSKNVFLSPMSISSA	Q60854|SPB6_MOUSE	28.51	16	NA	NA	68.4
DSSKNVFLSPMSISSAL	Q60854|SPB6_MOUSE	48.08	17	NA	NA	57.2
DSSSPATRKEYHTGKAVTSKGDKEL	E9PV24|FIBA_MOUSE	48.93	25	NA	NA	356
DSSSPATRKEYHTGKAVTSKGDKELLIG	E9PV24|FIBA_MOUSE	49.95	31	670	NA	90.2
DSVTTDHISPAGNIA	P28271|ACOHC_MOUSE	45.98	15	304	NA	112
DSVTTDHISPAGNIARNSP	P28271|ACOHC_MOUSE	49.78	19	240	NA	55.9
DSVTTDHISPAGNIARNSPA	P28271|ACOHC_MOUSE	49.89	20	6390	NA	4610
DSVVFAGPAGNSVE	Q8R146|ACPH_MOUSE	41.56	14	993	NA	589
DSVVFAGPAGNSVETR	Q8R146|ACPH_MOUSE	41	16	773	NA	400
DSYRSPWSNKYDPP	P47757|CAPZB_MOUSE	49.79	14	3960	NA	3660
DSYRSPWSNKYDPPL	P47757|CAPZB_MOUSE	49.69	15	294	NA	627
DTGENPIYKSAVTTVVNPK	P09055|ITB1_MOUSE	49.3	19	94.1	NA	679
DTIEFRGPNGLLV	Q9DCN2|NB5R3_MOUSE	44.54	13	613	NA	243
DTKVVFLSPAVPEEP	B2RXS4|PLXB2_MOUSE	49.26	15	302	NA	81.5
DTKVVFLSPAVPEEPEA	B2RXS4|PLXB2_MOUSE	49.85	17	115	NA	74.3
DTSSKVIQSVANYAKG	Q99KY4|GAK_MOUSE	47	16	NA	NA	163
DTSYKPPAGRTAAPE	Q69ZQ1|MYORG_MOUSE	44.25	15	843	NA	468
DTVPLEEPKVISAFSGK	Q4U2R1|HERC2_MOUSE	49.13	17	515	NA	220
DTVTFYKVIPKSKFVLVKF	P57759|ERP29_MOUSE	49.41	19	278	NA	119
DTYQSYSSPSPRVSRFK	Q60997|DMBT1_MOUSE	43.04	17	NA	NA	681
DVAIFARGPQAHLVH	P24823|PPBN_MOUSE:P24822|PPBI_M(	49	15	12200	313	11600

DVAIFARGPQAHLVHGVQ	P24823|PPBN_MOUSE:P24822|PPBI_M(	49.57	18	21200	NA	19700
DVGGAYVGPTQNRIL	Q64133|AOFA_MOUSE	35.68	15	265	NA	158
DVRRAFLGPFAHKEG	Q62177|SEM3B_MOUSE	45.72	15	NA	NA	409
DVRRAFLGPFAHKEGP	Q62177|SEM3B_MOUSE	47.46	16	364	NA	6440
DVRRAFLGPFAHKEGPT	Q62177|SEM3B_MOUSE	48.69	17	12200	NA	9620
DVVKAAKKFVS	Q9DB77|QCR2_MOUSE	44.7	11	266	NA	496
DVYVFLGPEPKSVVQ	P70699|LYAG_MOUSE	36.4	15	244	NA	128
DWPTFLNPNVDKAGPA	Q61508|ECM1_MOUSE	47.06	16	375	NA	379
DWQGGVYASPSIAGSRPG	Q8R0X7|SGPL1_MOUSE	49.79	18	452	NA	364
DYLAVFDGPSTNSRL	Q9JLB4|CUBN_MOUSE	45.7	15	952	NA	522
DYSAPNPIKVTHR	Q8CFG0|SULF2_MOUSE	46.79	13	407	NA	966
EAAASAYYNPGNPHNVYM(+15.99)PT	P97765|WBP2_MOUSE	49.92	20	350	NA	398
EAAASAYYNPGNPHNVYMPT	P97765|WBP2_MOUSE	48.9	20	NA	NA	229
EAASTIYGPHTLSAYIQ	Q9JHE3|ASAH2_MOUSE	49.32	17	768	NA	378
EAGAYDGPRTADGIV	P27773|PDIA3_MOUSE	40.17	15	429	NA	246
EANQWKQSLVQATEEN	A6X935|ITIH4_MOUSE	49.84	16	NA	NA	116
EAQAAM(+15.99)EEPVVQPSVVDR	Q9DBG5|PLIN3_MOUSE	49.75	18	351	NA	190
EAQAAMEEPVVQPSVVDR	Q9DBG5|PLIN3_MOUSE	48.9	18	NA	NA	112
EATRYLAPTILTDVDPN	P47740|AL3A2_MOUSE	49.88	17	6520	46.4	2810
EATSQELVRAPTAALSPEPQDSKEDVK	D3YXK2|SAFB1_MOUSE:Q80YR5|SAFB	35.16	27	NA	NA	233
EDIEVAPPKAHEVR	P00329|ADH1_MOUSE	48.37	14	21300	237	9970
EDIEVAPPKAHEVRI	P00329|ADH1_MOUSE	45.77	15	453	NA	165
EDIEVAPPKAHEVRIK	P00329|ADH1_MOUSE	49.9	16	6870	NA	4540
EDLSYQSSLASWNYN	Q8R0I0|ACE2_MOUSE	49.28	15	1100	NA	559
EDNVFEAPTLVKVF	Q61490|CD166_MOUSE	49.63	14	908	NA	277
EDRRYNPPIIHQGFQ	P27784|CCL6_MOUSE	44.03	15	18900	NA	21000
EDVAIFARGPQAHLVH	P24823|PPBN_MOUSE:P24822|PPBI_M(	48.56	16	4270	NA	4150
EDVAIFARGPQAHLVHGVQ	P24823|PPBN_MOUSE:P24822|PPBI_M(	49.45	19	11100	NA	7170
EEAAAEITRKLEKQEKKRLKKEKKR	Q9D6Z1|NOP56_MOUSE	44.06	25	394	NA	345
EEAGAYDGPRTADGIVS	P27773|PDIA3_MOUSE	48.82	17	615	NA	171
EEEYSAPLPTPAPS	P97467|AMD_MOUSE	48.78	14	338	NA	182
EEEYYAEPGVTEAEPV	Q6P6J9|TXD15_MOUSE	49.7	16	1670	NA	586
EEIEVAPPKAHEVR	P28474|ADHX_MOUSE	45.2	14	2500	NA	1440
EEKPVPAAPVPSPVAPAP	P97825|JUPI1_MOUSE	49.84	18	1140	NA	1000
EEKPVPAAPVPSPVAPAPV	P97825|JUPI1_MOUSE	49.94	19	3210	NA	2400
EEKPVPAAPVPSPVAPAPVPS	P97825|JUPI1_MOUSE	49.94	21	6170	30.2	4210
EEKPVPAAPVPSPVAPAPVPSRRNPPG	P97825|JUPI1_MOUSE	49.93	27	2960	NA	4800
EEKPVPAAPVPSPVAPAPVPSRRNPPG	P97825|JUPI1_MOUSE	49.95	29	1180	NA	197
EELKGHLTPRANEL	P06728|APOA4_MOUSE	36.14	14	207	NA	300
EELKGHLTPRANELKAT	P06728|APOA4_MOUSE	47.29	17	NA	NA	748
EELVITPLPSGDVA	Q8BXQ2|PIGT_MOUSE	29.72	14	322	NA	67.4
EEPPVFSRPTVSASYPPY	Q61187|TS101_MOUSE	45.49	18	3080	NA	8940
EETAFQTPKPSQTPSVPP	Q8VCB1|NDC1_MOUSE	38.07	18	3770	NA	2920
EEYSAPLPTPAPS	P97467|AMD_MOUSE	48.19	13	1490	NA	1470
EFQAWKSPGASLL	Q8VC30|TKFC_MOUSE	48.25	13	130	NA	128
EFVVIAPAAHSDA	Q80UJ7|RB3GP_MOUSE	29.67	13	650	NA	351
EGDIFIGPKAEEHR	P61164|ACTZ_MOUSE	36.57	14	1460	NA	1580
EGDIFIGPKAEEHRG	P61164|ACTZ_MOUSE	47.98	15	4010	NA	2630
EGDLFIGPKAEEHRG	Q8R5C5|ACTY_MOUSE	47.98	15	4010	NA	2630
EGERYIAPTVLVD	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	36.71	13	1450	NA	461
EGERYIAPTVLVDVQ	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	46.83	15	3370	NA	2750
EGKEVRYPVILNAREK	Q6ZQB6|VIP2_MOUSE	40.49	16	753	NA	667
EGRLEVVTDPTTNAG	Q9R100|CAD17_MOUSE	47.29	15	345	NA	214
EGRLEVVTDPTTNAGYV	Q9R100|CAD17_MOUSE	49.88	17	422	NA	496
EGRLEVVTDPTTNAGYVKIK	Q9R100|CAD17_MOUSE	49.93	20	107	NA	714
EHGDKKGKKAKKER	Q8VDN2|AT1A1_MOUSE	47.81	14	NA	NA	646
EIQDWSASSPHSAAYV	Q80SY4|MIB1_MOUSE	49.87	16	632	NA	358
EISHLIEPLASAARAE	P26039|TLN1_MOUSE	46.83	16	127	NA	308
EISYTGSRPASNMV	P28666|MUG2_MOUSE:P28665|MUG1_M	49.32	14	1580	NA	1180
EKEDRRYNPPIIHQGFQ	P27784|CCL6_MOUSE	37.61	17	NA	NA	1150
EKFGFQAPNVTFLHG	Q91WU5|AS3MT_MOUSE	47.58	15	244	NA	157
EKPVPAAPVPSPVAPAP	P97825|JUPI1_MOUSE	48.19	17	2440	NA	2790
EKPVPAAPVPSPVAPAPV	P97825|JUPI1_MOUSE	49.83	18	3960	NA	3880
EKPVPAAPVPSPVAPAPVP	P97825|JUPI1_MOUSE	49.94	19	11900	184	12100
EKPVPAAPVPSPVAPAPVPS	P97825|JUPI1_MOUSE	49.94	20	3590	NA	4190
EKPVPAAPVPSPVAPAPVPSRRNPP	P97825|JUPI1_MOUSE	49.94	25	1330	NA	1960
EKPVPAAPVPSPVAPAPVPSRRNPPG	P97825|JUPI1_MOUSE	49.93	26	1580	NA	1280
EKTHEQLTPLVRSAGTS	P09813|APOA2_MOUSE	49.67	17	1670	NA	964
EKYVTSAPMPEPGAPG	P01872|IGHM_MOUSE	49.81	16	1440	NA	1260
ELDQLFSGPLPGRLP	Q60805|MERTK_MOUSE	45	15	1290	NA	549
ELDQLFSGPLPGRLPV	Q60805|MERTK_MOUSE	46.5	16	1200	NA	633
ELDQLFSGPLPGRLPVN	Q60805|MERTK_MOUSE	48.87	17	1220	NA	238
ELEEQLGPVAEETR	P08226|APOE_MOUSE	47.71	14	28300	3310	13700
ELEEQLGPVAEETRAR	P08226|APOE_MOUSE	40.78	16	12800	NA	390
ELKGHLTPRANEL	P06728|APOA4_MOUSE	46.94	13	241	NA	292
ELKGHLTPRANELKA	P06728|APOA4_MOUSE	29.49	15	2240	NA	1460
ELKGHLTPRANELKAT	P06728|APOA4_MOUSE	32.24	16	NA	NA	378
ELVAPRANTLK	O54782|MA2B2_MOUSE	26.16	11	264	NA	280
ELVAPRANTLKF	O54782|MA2B2_MOUSE	30.81	12	89.2	NA	38.5
EM(+15.99)ESYDEAIANLQR	Q9WUD1|CHIP_MOUSE	46.25	14	595	NA	304
EMNLMHAPQVADAILG	Q68FD5|CLH1_MOUSE	41.43	16	NA	NA	150

ENGNFKIVTDPKTNEGIL	P55292|DSC2_MOUSE	46.06	18	NA	NA	53.3
ENIWKAPEPVEIR	Q9R100|CAD17_MOUSE	48.58	13	6340	NA	4240
ENIWKAPEPVEIRE	Q9R100|CAD17_MOUSE	48.23	14	38100	200	9150
ENIWKAPEPVEIREN(+15.00)ST	Q9R100|CAD17_MOUSE	49.33	17	49500	127	12000
ENLRKFYKGKKYKPLDLRPKKTR	Q6ZWV7|RL35_MOUSE	48.95	23	NA	NA	171
ENLYPYLGPSTLRDRPQ	P97390|VPS45_MOUSE	28.7	17	893	NA	1080
ENPEYLAPRAGTASQPH	P70424|ERBB2_MOUSE	49.86	17	21600	52.9	4970
ENPEYLAPRAGTASQPHP	P70424|ERBB2_MOUSE	49.76	18	31300	NA	29500
ENPIYKSAVTTVVN	P09055|ITB1_MOUSE	49.07	14	385	NA	503
ENPIYKSAVTTVVNPK	P09055|ITB1_MOUSE	49.91	16	11800	209	12500
EPAGPAGRAASAPEAAQAEEDR	Q9JJX7|TYDP2_MOUSE	49.84	22	1470	NA	1030
EPEAM(+15.99)LQVLGPKPALPEG	P13020|GELS_MOUSE	49.92	18	5050	NA	3390
EPEAMLQVLGPKPALPEGTE	P13020|GELS_MOUSE	49.91	20	NA	NA	260
EPENPEYNTGYAVVAYR	Q64282|IFIT1_MOUSE	49.94	17	3630	117	3230
EPEVDYRTVTVNTEQ	Q6PDN3|MYLK_MOUSE	48.99	15	587	NA	314
EPEVDYRTVTVNTEQK	Q6PDN3|MYLK_MOUSE	45.12	16	2190	NA	1940
EPEVDYRTVTVNTEQKV	Q6PDN3|MYLK_MOUSE	27.79	17	NA	NA	200
EPEYATPIVERHL	Q9D4J3|DCBD1_MOUSE	45.67	13	NA	NA	490
EPFFYSKYSAPRLPAAL	P97432|NBR1_MOUSE	49.94	17	309	NA	68.5
EPGNFIAATSLYSPER	Q80XN0|BDH_MOUSE	43.21	16	211	NA	158
EPPPAYEPPAPAPA	O35609|SCAM3_MOUSE	42.31	14	8350	NA	3190
EPPPAYEPPAPAPAP	O35609|SCAM3_MOUSE	46.08	15	1630	NA	2760
EPPPAYEPPAPAPAPLPP	O35609|SCAM3_MOUSE	49.94	18	96400	1840	184000
EPPPAYEPPAPAPAPLPPP	O35609|SCAM3_MOUSE	49.93	19	1610000	19500	1530000
EPPPAYEPPAPAPAPLPPPS	O35609|SCAM3_MOUSE	49.9	20	14700	NA	22300
EPPPYQEPRPRGTPP	Q03146|DDR1_MOUSE	30.93	15	4440	NA	9410
EPPPYQEPRPRGTPPH	Q03146|DDR1_MOUSE	32.65	16	NA	NA	504
EPPSDLDFFSPRPVPAAS	Q8BMI3|GGA3_MOUSE	49.94	18	19400	NA	18500
EPSKLKRSYSSPDITQALQE	Q80U87|UBP8_MOUSE	48.53	20	3360	NA	5740
EPSVFNGPEVTM(+15.99)LKD	Q8BHN3|GANAB_MOUSE	38.29	15	1870	NA	293
EPYGARYVGSM(+15.99)VADVHR	P70695|F16P2_MOUSE	49.89	17	24300	NA	23100
EPYTFSHPNKG	Q5U462|CDCP1_MOUSE	45.79	11	890	NA	930
EQAPPLPIKTPIPTPST	Q7TQH7|LRP10_MOUSE	48.6	17	NA	NA	87.8
EQAQEQAQEQVQPKPLES	P06728|APOA4_MOUSE	49.93	18	2750	NA	2290
EQIYYAGPVNNPGLDVP	O88188|LY86_MOUSE	47.8	17	7420	520	1400
EQPDLNFRNPAVQEE	Q91WV7|SLC31_MOUSE	44.81	15	735	NA	509
EQPDLNFRNPAVQEEIK	Q91WV7|SLC31_MOUSE	28.31	17	NA	NA	28100
EQTYVISAPKILRVG	P06684|CO5_MOUSE	48.41	15	NA	NA	357
EQTYVISAPKILRVGS	P06684|CO5_MOUSE	48.75	16	24.9	NA	401
ERASFITPVPGGVG	Q922D8|C1TC_MOUSE	46.2	14	8260	185	8330
ERASFITPVPGGVGP	Q922D8|C1TC_MOUSE	48.42	15	3090	NA	2750
ERASFITPVPGGVGPM	Q922D8|C1TC_MOUSE	49.74	16	536	NA	1620
ERASFITPVPGGVGPM(+15.99)	Q922D8|C1TC_MOUSE	49.73	16	4480	NA	3510
ERPVAQDVALV	Q8C0Z1|F234A_MOUSE	29.48	11	NA	NA	136
ESEEEYSAPLPTPAPS	P97467|AMD_MOUSE	49.9	16	1790	NA	1300
ESEPYTFSHPNK	Q5U462|CDCP1_MOUSE	48.28	12	1130	NA	582
ESEPYTFSHPNKG	Q5U462|CDCP1_MOUSE	47.86	13	4520	NA	1610
ESEPYTFSHPNKGE	Q5U462|CDCP1_MOUSE	49.4	14	2430	NA	241
ESEPYTFSHPNKGEI	Q5U462|CDCP1_MOUSE	49.87	15	1160	NA	1240
ESKEAFQEALAAAGDK	P10639|THIO_MOUSE	49.87	16	5340	56.9	4870
ESLRMKLPKSAKPVSQMRMATPLLMRP	P04441|HG2A_MOUSE	48.85	28	NA	NA	499
ESPEQIRAPSGIITSPG	Q8BUJ9|LRP12_MOUSE	48.01	17	351	NA	334
ESVAPYGGPSSSPAEEG	P10493|NID1_MOUSE	48.72	17	567	NA	261
ETDSVVSSVTTKAKGVA	Q9JJX6|P2RX4_MOUSE	45.76	17	1270	NA	751
ETELDQLFSGPLPGRLPVN	Q60805|MERTK_MOUSE	49.9	19	102	NA	117
ETNEAQPPGPAPSDDAPL	Q3U9N9|MOT10_MOUSE	29.41	18	1170	NA	514
EVDRYDAPGIAFYPG	Q9D771|PACC1_MOUSE	49.15	15	7520	NA	4320
EVKAFFESHPAPSAER	Q11011|PSA_MOUSE	49.77	16	874	NA	456
EVPDSYKSAVPFKILY	A2A8L5|PTPRF_MOUSE	49.93	16	1930	NA	1910
EVPNYKLITPAVVSERLK	P62852|RS25_MOUSE	49.91	18	NA	NA	197
EVRRVPPRFS(+79.97)IPP	Q64487|PTPRD_MOUSE	25.65	13	NA	NA	172000
EVSSPITLQALVQ	E9Q414|APOB_MOUSE	42.33	13	487	NA	162
EVSSVEAPSVSPA	Q8BUJ9|LRP12_MOUSE	42.19	13	10200	42.6	7820
EVSSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	48.43	14	106000	3030	72800
EVSSVEAPSVSPARH	Q8BUJ9|LRP12_MOUSE	48.69	15	13800	NA	2180
EWKDYKAGFGNLERE	P12804|FGL2_MOUSE	42.56	15	NA	NA	1890
EYFVFRPGTIEQAVEE	Q9DBS2|TPRGL_MOUSE	40.03	16	NA	NA	354
EYSGSVANEAN	E9Q414|APOB_MOUSE	39.43	11	1430	NA	1410
EYSGSVANEANVY	E9Q414|APOB_MOUSE	46.37	13	663	NA	1210
EYVAPEVILNKG	Q61410|KGP2_MOUSE	30.85	12	92.3	NA	126
FAAEEFKVPAATSAIITN	P61961|UFM1_MOUSE	49.78	18	1390	NA	1450
FAAEEFKVPAATSAIITNDG	P61961|UFM1_MOUSE	49.92	20	656	NA	542
FAAGVFSNPAVRTAAAN	O35609|SCAM3_MOUSE	49.38	17	414	NA	488
FAAPFFIVRHQLLKK	P17665|COX7C_MOUSE	36.01	15	1600	NA	907
FDALLINPRASDSPID	Q9R111|GUAD_MOUSE	42.4	16	394	NA	64.8
FDFAGPAIHGSAV	Q60930|VDAC2_MOUSE	37.71	13	357	NA	217
FDGYRSPLPTNESQP	Q8CCN5|BCAS3_MOUSE	48.41	15	2220	NA	2070
FDPGFRSPSTQVAN	Q6A037|N4BP1_MOUSE	49.28	14	515	NA	389
FDPGFRSPSTQVANNS	Q6A037|N4BP1_MOUSE	47.63	16	1390	NA	1080
FDPTTAFQAPDVGQAL	A2ASQ1|AGRIN_MOUSE	47.13	16	622	NA	287
FDPTTAFQAPDVGQALLQ	A2ASQ1|AGRIN_MOUSE	49.82	18	169	NA	259

FEKTHEQLTPLVRSAG	P09813|APOA2_MOUSE	49.52	16	687	NA	670
FGNIYSTPLALQM	O88968|TCO2_MOUSE	46.27	13	65.2	NA	212
FGNIYSTPLALQM(+15.99)LM(+15.99)	O88968|TCO2_MOUSE	49.69	15	5640	NA	4220
FGNIYSTPLALQMLM(+15.99)	O88968|TCO2_MOUSE	49.63	15	685	NA	791
FGNSEFDPPGPNVATTT	Q9Z1D1|EIF3G_MOUSE	49.88	17	1070	NA	863
FGPYYTEPVIAGLD	Q9R1P1|PSB3_MOUSE	45.5	14	252	NA	138
FHFPYDYPNLQTAQL	Q3TCT4|ENTP7_MOUSE	49.31	15	742	NA	401
FIEKVIPSTANSN	E9Q7P9|CDHR2_MOUSE	47.34	13	1410	NA	654
FIEKVIPSTANSNN	E9Q7P9|CDHR2_MOUSE	48.31	14	1440	NA	632
FIEKVIPSTANSNNL	E9Q7P9|CDHR2_MOUSE	48.89	15	5770	NA	3500
FIEKVIPSTANSNNLF	E9Q7P9|CDHR2_MOUSE	47.94	16	537	NA	299
FIVNTNVPRASVPE	P34884|MIF_MOUSE	48.9	14	301	NA	270
FKPSYGTPAPGFSS	P23249|MOV10_MOUSE	30.57	14	NA	NA	91.7
FNNQAYHSPATALAIVD	Q8R420|ABCA3_MOUSE	48.82	17	4930	NA	6370
FNNQAYHSPATALAIVDN	Q8R420|ABCA3_MOUSE	49.29	18	2230	NA	2150
FNPVSTPVALPTPALSPS	Q9Z1T1|AP3B1_MOUSE	48.56	18	NA	NA	115
FPGSVIDPPAVNLAAQN	O88738|BIRC6_MOUSE	45.25	17	282	NA	309
FPIKWTAPEAALYG	P39688|FYN_MOUSE:Q04736|YES_MOU	43.69	14	372	NA	309
FPKPPSYNVATTLPSY	Q8R0W6|NFIP1_MOUSE	46.13	16	2250	NA	1550
FPKPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	49.92	18	474000	18000	304000
FPKPPSYNVATTLPSYDEA	Q8R0W6|NFIP1_MOUSE	49.9	19	247000	NA	213000
FPKPPSYNVATTLPSYDEAE	Q8R0W6|NFIP1_MOUSE	49.94	20	8290	NA	5400
FPTDYPFKPPKVAFTTR	P61079|UB2D3_MOUSE:P62838|UB2D2_	49.93	17	6610	NA	7150
FPWQVFFNHPRASGALI	Q8CG14|CS1A_MOUSE	33.29	17	NA	NA	223
FPYEGPAPLEAIAN	Q8R4G6|MGT5A_MOUSE:Q765H6|MGT5	46.07	14	2950	NA	1510
FPYVTPAPH	Q9D074|MGRN1_MOUSE	39.58	9	580	NA	845
FPYVTPAPHEP	Q9D074|MGRN1_MOUSE	46.72	11	10200	NA	10600
FPYVTPAPHEPVK	Q9D074|MGRN1_MOUSE	48.13	13	142000	6760	167000
FPYVTPAPHEPVKT	Q9D074|MGRN1_MOUSE	49.65	14	29100	639	31200
FPYVTPAPHEPVKTL	Q9D074|MGRN1_MOUSE	49.53	15	785	NA	2590
FQFKTNPPAVTFELT	Q9R100|CAD17_MOUSE	46.96	15	NA	NA	289
FRPAHQAPM(+15.99)AQTTIH	O08573|LEG9_MOUSE	48.4	15	8610	NA	7170
FRPAHQAPM(+15.99)AQTTIHM	O08573|LEG9_MOUSE	48.01	16	NA	NA	289
FRPAHQAPMAQTTIHM	O08573|LEG9_MOUSE	47.5	16	NA	NA	273
FRVNFVDPAASSSA	P55012|S12A2_MOUSE	49.67	14	224	NA	209
FRVNFVDPAASSSAD	P55012|S12A2_MOUSE	49.06	15	4420	NA	4900
FRVNFVDPAASSSADD	P55012|S12A2_MOUSE	49.92	16	23600	644	23800
FRVNFVDPAASSSADDS	P55012|S12A2_MOUSE	49.87	17	3830	NA	3250
FRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MO	47.84	12	5120	NA	4390
FRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MO	45.26	14	553	NA	161
FSEYRYPVATFQPS	Q8CGK5|INLR1_MOUSE	36.14	14	273	NA	214
FSPIIHFPHPSRTEQ	P0C7W3|TOR2X_MOUSE:Q8R1J9|TOR2	26.36	15	NA	NA	239
FSSEVYTFPVPERH	P09803|CADH1_MOUSE	49.08	14	382	NA	517
FSSEVYTFPVPERHLE	P09803|CADH1_MOUSE	49.87	16	506	NA	952
FSSEVYTFPVPERHLER	P09803|CADH1_MOUSE	47.09	17	547	NA	574
FTAQWIAPSVQLTGYR	P11276|FINC_MOUSE	48.5	16	4380	43.9	4260
FTVHWVAPRAPITG	P11276|FINC_MOUSE	48.86	14	913	NA	1130
FTYQQPQPLSVEP	B2RXS4|PLXB2_MOUSE	47.74	13	400	NA	269
FVAPAVTPVKG	P70158|ASM3A_MOUSE	45.22	11	14100	NA	14500
FVAPAVTPVKGVL	P70158|ASM3A_MOUSE	49.51	13	5200	NA	4280
FYSKYSAPRLPAAL	P97432|NBR1_MOUSE	49.84	14	5520	NA	5430
FYSKYSAPRLPAALE	P97432|NBR1_MOUSE	49.88	15	7180	12.9	6590
FYSKYSAPRLPAALEQ	P97432|NBR1_MOUSE	49.93	16	5370	NA	4840
FYTPIPNGLYPS	O08573|LEG9_MOUSE	45.41	12	897	NA	765
G(+42.01)FPKPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	29.08	19	2630	NA	1780
G(+42.01)KEKTHINIVVIGHVDSGKS	P62631|EF1A2_MOUSE:P10126|EF1A1_	37.52	20	NA	1550	2900
G(+42.01)N(+15.00)PLNSVFVAPAVTPVI	P70158|ASM3A_MOUSE	49	17	824	NA	755
G(+42.01)N(+15.00)PLNSVFVAPAVTPVI	P70158|ASM3A_MOUSE	49.58	18	872	NA	1120
G(+42.01)PRIRGN(+15.00)VYIHPTAKVA	Q922H4|GMPPA_MOUSE	42.72	19	NA	NA	207
GAAAKKTVKTPKKPKKPAVSKK	P43275|H11_MOUSE	49.95	22	859	549	500
GAKKTVKKTPKKAKKP	P43276|H15_MOUSE	49.94	16	36900	NA	7610
GAKKTVKKTPKKAKKPA	P43276|H15_MOUSE	49.95	17	3010	NA	7160
GAKKTVKKTPKKAKKPAAAGVKKVAKSI	P43276|H15_MOUSE	49.95	32	158	2400	2940
GALLLNAPVVSITQGR	O09046|OXLA_MOUSE	41.19	16	497	NA	219
GAQEMVSSSVSSAKETV	Q9DBG5|PLIN3_MOUSE	42.56	17	197	NA	288
GAQEMVSSSVSSAKETVA	Q9DBG5|PLIN3_MOUSE	38.65	18	NA	NA	116
GARYVGSMVADVHR	P70695|F16P2_MOUSE	42.14	14	178	NA	153
GAVIFNFPGTRNEVIP	Q9D304|RN128_MOUSE	45.03	16	1300	NA	431
GAVIFNFPGTRNEVIPM	Q9D304|RN128_MOUSE	49.7	17	5730	NA	7450
GDATLYVPSAPLSGP	Q60928|GGT1_MOUSE	41.75	15	1960	NA	315
GDATLYVPSAPLSGPV	Q60928|GGT1_MOUSE	40.43	16	861	NA	671
GDEKKGPLIVSGPDGAPAK	Q8VBW1|SC6A8_MOUSE	30.78	19	NA	NA	109
GDGNHTLFH	P43023|CX6A2_MOUSE:P43024|CX6A1_	39.23	9	576	256	334
GDGNHTLFHNPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	47.29	21	1330	664	2170
GDIFIGPKAEEHRG	P61164|ACTZ_MOUSE	36.78	14	1210	NA	822
GDKIIYQAASPDEGAL	P70704|AT8A1_MOUSE	36.66	16	NA	NA	127
GDKKGKKAKKER	Q8VDN2|AT1A1_MOUSE	45.72	12	NA	NA	845
GDLEYQM(+15.99)STTARAK	Q02257|PLAK_MOUSE	41.35	14	396	NA	143
GDLEYQM(+15.99)STTARAKR	Q02257|PLAK_MOUSE	35.15	15	2090	NA	1030
GDLEYQMSTTARAKR	Q02257|PLAK_MOUSE	44.19	15	6180	NA	6540
GDLEYQMSTTARAKRV	Q02257|PLAK_MOUSE	37.1	16	253	NA	438

GDLSQHATPLPTPAVLPG	O88746|TOM1_MOUSE	49.39	18	33100	833	13800
GDQTVVEPNIAIQSVTR	Q8BM96|AGRG7_MOUSE	44.7	17	1380	NA	1260
GDQTVVEPNIAIQSVTRD	Q8BM96|AGRG7_MOUSE	43.44	18	NA	NA	163
GDRPHTYFGPETSASKF	P70277|SIA7B_MOUSE	49.72	17	151	NA	372
GDRPHTYFGPETSASKFK	P70277|SIA7B_MOUSE	49.94	18	1230	NA	1930
GDSNFGAPSASVAA	O35643|AP1B1_MOUSE	36.51	14	399	NA	446
GDSNFGAPSASVAAAP	O35643|AP1B1_MOUSE	44.21	16	8740	NA	8330
GDSNFGAPSASVAAAPA	O35643|AP1B1_MOUSE	46.93	17	3880	NA	2970
GDSVVFAGPAGNSVETR	Q8R146|ACPH_MOUSE	48.01	17	108	NA	89.4
GDSYRSPWSNKYDPP	P47757|CAPZB_MOUSE	48.43	15	5500	NA	4520
GDSYRSPWSNKYDPPL	P47757|CAPZB_MOUSE	46.96	16	6760	NA	6070
GDTEGRLEVVTDPTTNAG	Q9R100|CAD17_MOUSE	49.61	18	1630	NA	1300
GDTEGRLEVVTDPTTNAGYV	Q9R100|CAD17_MOUSE	48.49	20	NA	NA	1530
GDTEGRLEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	49.94	21	23700	1070	23400
GDTEGRLEVVTDPTTNAGYVKIK	Q9R100|CAD17_MOUSE	49.94	23	220	NA	1050
GDTIEFRGPNGLLVYQ	Q9DCN2|NB5R3_MOUSE	48.61	16	1620	NA	882
GDTIEFRGPNGLLVYQG	Q9DCN2|NB5R3_MOUSE	49.54	17	9470	NA	6890
GELVYEAPETIAAEPPP	O88738|BIRC6_MOUSE	47.52	17	431	NA	496
GELYTFNTPSGTAGVE	Q9QYY0|GAB1_MOUSE	40.29	16	80	NA	28.5
GENPIYKSAVTTVVNPK	P09055|ITB1_MOUSE	49.83	17	7600	120	9660
GEPEAMLQVLGPKPALPEG	P13020|GELS_MOUSE	49.71	19	NA	NA	795
GEPKEVVKPVPITSPAVSKVTSTT	Q8CI51|PDLI5_MOUSE	32.11	24	NA	NA	176
GERFEAPEALFQP	P61161|ARP2_MOUSE	47.82	13	624	NA	154
GERYIAPTVLVDVQE	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	48.43	15	NA	NA	961
GEVKAFFESHPAPSAER	Q11011|PSA_MOUSE	49.82	17	401	NA	356
GFHFPYDYPNLQTAQ	Q3TCT4|ENTP7_MOUSE	48.39	15	274	NA	185
GFPYEGPAPLEAIA	Q8R4G6|MGT5A_MOUSE:Q765H6|MGT5	45.44	14	2170	NA	1470
GFPYEGPAPLEAIANG	Q8R4G6|MGT5A_MOUSE:Q765H6|MGT5	47.6	16	461	NA	308
GFTNTMRVVPVP	P52480|KPYM_MOUSE	37	12	617	NA	1150
GGASALLIEKL	Q8QZT1|THIL_MOUSE	27.88	11	468	NA	460
GGDPEAPAPAPAAERPPAPGPG	Q68FL4|SAHH3_MOUSE	49.93	22	288	NA	224
GGEDVAIFARGPQAHLVH	P24822|PPBI_MOUSE	47.48	18	3770	NA	3510
GGEDVAIFARGPQAHLVHG	P24822|PPBI_MOUSE	48.84	19	6710	137	7420
GGEDVAIFARGPQAHLVHGVQ	P24822|PPBI_MOUSE	49.47	21	8230	NA	6720
GGEPEAMLQVLGPKPALPEGTE	P13020|GELS_MOUSE	40.54	22	NA	NA	267
GGERFEAPEALFQPH	P61161|ARP2_MOUSE	47.24	15	519	NA	396
GGGASALLIEKL	Q8QZT1|THIL_MOUSE	29.53	12	157	NA	235
GGGDPEAPAPAPAAERPP	Q68FL4|SAHH3_MOUSE	48.78	18	912	NA	1980
GGGSVRIGSGGVFRAPSIHGGSGGR	P19001|K1C19_MOUSE	36.78	25	NA	NA	2800
GGLPDYSAPNPIK	Q8CFG0|SULF2_MOUSE	48.02	13	4790	181	4790
GGLPDYSAPNPIKVT	Q8CFG0|SULF2_MOUSE	49.89	15	6100	290	7490
GGVFRAPSIHGGSG	P19001|K1C19_MOUSE	37.98	14	NA	NA	487
GGVLPNIQAVLLPKKTESHHKAK	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	29.83	23	NA	NA	418
GGVYASPSIAGSRP	Q8R0X7|SGPL1_MOUSE	44.84	14	363	NA	154
GGYKFSAPVVPSSFN	Q9EPL8|IPO7_MOUSE	47.71	15	714	NA	1080
GGYKPFQNPVPNQSPS	P16382|IL4RA_MOUSE	49.82	16	1130	NA	3090
GGYRYPRALEEEV	Q8K3K8|OPTN_MOUSE	29.14	13	12200	NA	5720
GIDPYDQPNAIYIE	O88307|SORL_MOUSE	42.53	14	4110	NA	2140
GIDPYDQPNAIYIER	O88307|SORL_MOUSE	49.38	15	66300	3900	52900
GIDPYDQPNAIYIERH	O88307|SORL_MOUSE	49.67	16	40800	992	33800
GIDPYDQPNAIYIERHE	O88307|SORL_MOUSE	49.93	17	1080	NA	731
GIEGRYATALYSAASKEKKL	Q9DB20|ATPO_MOUSE	48.5	20	NA	NA	617
GIPFAAPTALASRDG	Q91VX2|UBAP2_MOUSE	39.27	15	296	NA	250
GIPVYRFVLPANAFA	Q08857|CD36_MOUSE	39.76	15	9570	122	3800
GISRDNWHKRRKTGGKRKPYHKKRKY	P62242|RS8_MOUSE	48.84	26	NA	3640	3260
GISRDNWHKRRKTGGKRKPYHKKRKYE	P62242|RS8_MOUSE	47.35	27	NA	1100	1800
GISRDNWHKRRKTGGKRKPYHKKRKYE	P62242|RS8_MOUSE	48.48	29	NA	5790	27100
GISRDNWHKRRKTGGKRKPYHKKRKYE	P62242|RS8_MOUSE	49.94	32	NA	5620	31700
GKEFQFLNPNPVPEDL	Q8R0K2|TRI31_MOUSE	49.75	16	1040	NA	1030
GKFM(+15.99)KPGKVVLVLAGRYSGRKA	P61358|RL27_MOUSE	49.92	29	26900	NA	9180
GKFMKPGKVVLVLAGRYSGR	P61358|RL27_MOUSE	28.88	20	NA	NA	457
GKFMKPGKVVLVLAGRYSGRKA	P61358|RL27_MOUSE	45.5	22	NA	NA	711
GKGM(+15.99)NPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.88	20	344	NA	155
GKGM(+15.99)NPPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	49.94	21	431	NA	220
GKGMNPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	28.85	20	NA	NA	152
GKGMNPPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	33.24	21	NA	NA	102
GKKAKGKKVAPAPAVVKKQEAKKVVNP	P12970|RL7A_MOUSE	49.95	33	1690	NA	2230
GKKRKRSRKESYSVYVYK	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	47.74	18	7380	94000	4270
GKKRKRSRKESYSVYVYKVLKQ	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.94	22	84.6	NA	348
GKKRKRSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.44	26	10200	117000	29300
GKKRKRSRKESYSVYVYKVLKQVHPDT	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	45.71	32	1620	NA	126
GKLQDQGPDVLLAKVS	A6X935|ITIH4_MOUSE	45.79	16	184	NA	355
GKLTGMAFRVPTPNVS	P16858|G3P_MOUSE:Q64467|G3PT_MO	48.77	16	244	NA	620
GKLTGMAFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MO	49.94	19	7490	NA	17800
GKLTGMAFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MO	39.34	21	NA	NA	798
GKNKRLTKGGKKGAKKKVVDPFS	P97351|RS3A_MOUSE	45.86	23	NA	NA	721
GKNKRLTKGGKKGAKKKVVDPFSK	P97351|RS3A_MOUSE	48.95	24	NA	2110	4000
GKNKRLTKGGKKGAKKKVVDPFSKK	P97351|RS3A_MOUSE	48.95	25	NA	3480	3210
GKNKRLTKGGKKGAKKKVVDPFSKKD	P97351|RS3A_MOUSE	48.95	26	NA	NA	1770
GKNKRLTKGGKKGAKKKVVDPFSKKDW	P97351|RS3A_MOUSE	42.65	27	NA	NA	781
GKNKRLTKGGKKGAKKKVVDPFSKKDW	P97351|RS3A_MOUSE	48.95	28	NA	582	4650

GKNKRLTKGGKKGAKKKVVDPFSKKDW	P97351|RS3A_MOUSE	25.74	31	NA	NA	303
GKNKRLTKGGKKGAKKKVVDPFSKKDW	P97351|RS3A_MOUSE	48.95	33	250	NA	11100
GKTAWVGSLASGVGL	Q7TM99|MOT9_MOUSE	41.55	15	283	NA	250
GKVFIYHGSPTGIITKP	Q61739|ITA6_MOUSE	49.59	17	352	NA	141
GKYTYGKPVPGHVK	P28665|MUG1_MOUSE	49.88	14	6920	NA	1790
GKYTYGKPVPGHVKI	P28665|MUG1_MOUSE	49.94	15	52600	80.2	18800
GLPDYSAPNPIK	Q8CFG0|SULF2_MOUSE	47.58	12	10700	739	12300
GLPDYSAPNPIKV	Q8CFG0|SULF2_MOUSE	46.2	13	605	NA	662
GLPDYSAPNPIKVT	Q8CFG0|SULF2_MOUSE	49.87	14	12100	NA	14100
GLPDYSAPNPIKVTH	Q8CFG0|SULF2_MOUSE	49.53	15	92000	3850	83700
GLVPIVEPEVLPDG	Q91Y97|ALDOB_MOUSE	44.76	14	801	NA	207
GLVPIVEPEVLPDGDH	Q91Y97|ALDOB_MOUSE	48.76	16	3860	NA	1330
GLYEYLQPLGTPSQES	Q571I9|A16A1_MOUSE	38.76	16	364	NA	161
GLYQYLHSRAHNASRP	Q6PDG8|MON1A_MOUSE	25.81	16	NA	NA	80.4
GM(+15.99)AFRVPTPNVSV	P16858|G3P_MOUSE:Q64467|G3PT_MC	46.17	13	2060	NA	1330
GM(+15.99)AFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	48.51	14	7420	NA	8010
GM(+15.99)AFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.31	16	1630	NA	979
GM(+15.99)NPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.56	18	2920	NA	1890
GMAFRVPTPNVS	P16858|G3P_MOUSE:Q64467|G3PT_MC	43.13	12	333	NA	325
GMAFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.6	14	3070	NA	4350
GMAFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.83	16	579	NA	785
GMNPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.84	18	341	NA	807
GN(+15.00)PLN(+15.00)SVFVAPAVTPVI	P70158|ASM3A_MOUSE	44.09	17	1010	NA	1070
GN(+15.00)PLN(+15.00)SVFVAPAVTPVI	P70158|ASM3A_MOUSE	36.12	18	641	NA	810
GN(+15.00)PLN(+15.00)SVFVAPAVTPVI	P70158|ASM3A_MOUSE	42.57	20	NA	NA	146
GNDLSFIHPKALSGLKE	A2ARI4|LGR4_MOUSE	40.38	17	1240	NA	1240
GNFKIVTDPKTNEGIL	P55292|DSC2_MOUSE	48.74	16	4570	NA	3130
GNIYIYNGPVLGGTR	P50284|TNR3_MOUSE	44.33	15	4620	53.7	5830
GNKGFFVQPTVFSNVT	O35945|AL1A7_MOUSE:P24549|AL1A1_	48.96	16	3520	NA	1520
GNPLNSVFVAPAVTPVKG	P70158|ASM3A_MOUSE	49.88	18	4540	NA	5290
GNPLNSVFVAPAVTPVKGV	P70158|ASM3A_MOUSE	49.9	19	146	NA	350
GNPLNSVFVAPAVTPVKGVL	P70158|ASM3A_MOUSE	49.92	20	2550	NA	4580
GNSEFDPPGPNVATTT	Q9Z1D1|EIF3G_MOUSE	45.36	16	1920	NA	1310
GNVYIHPTAKVAPSA	Q922H4|GMPPA_MOUSE	47.3	15	823	NA	489
GPAGPGAVEGPNPASSPDA	Q99MS7|EH1L1_MOUSE	49.2	19	1070	NA	619
GPDGKGM(+15.99)NPPSYYTQPVPVPN	Q9JLJ0|LITAF_MOUSE	49.9	21	1370	NA	1210
GPDGKGM(+15.99)NPPSYYTQPVPVPN	Q9JLJ0|LITAF_MOUSE	49.94	22	554	NA	737
GPDGKGM(+15.99)NPPSYYTQPVPVPN	Q9JLJ0|LITAF_MOUSE	49.94	23	16800	404	16700
GPDGKGMNPPSYYTQPVPVPN	Q9JLJ0|LITAF_MOUSE	47.68	21	NA	NA	719
GPDGKGMNPPSYYTQPVPVPNA	Q9JLJ0|LITAF_MOUSE	48.94	22	NA	NA	399
GPDGRFVM(+15.99)GPTVAPSQ	Q05BQ1|TUTLA_MOUSE	44.67	16	31200	1070	21100
GPDGRFVM(+15.99)GPTVAPSQEK	Q05BQ1|TUTLA_MOUSE	49.44	18	105000	2280	98700
GPDGRFVMGPTVAPS	Q05BQ1|TUTLA_MOUSE	41.23	15	108	NA	261
GPDGRFVMGPTVAPSQ	Q05BQ1|TUTLA_MOUSE	48.47	16	14200	NA	20200
GPDGRFVMGPTVAPSQE	Q05BQ1|TUTLA_MOUSE	49.11	17	4000	NA	6170
GPDGRFVMGPTVAPSQEK	Q05BQ1|TUTLA_MOUSE	49.66	18	51300	NA	89100
GPDGRFVMGPTVAPSQEKL	Q05BQ1|TUTLA_MOUSE	49.94	19	22200	NA	42500
GPDYAHAEARKSPAL	A2ARP1|VIP1_MOUSE:Q6ZQB6|VIP2_M	49.59	15	149	NA	113
GPGLGYLSSHIANVE	P13020|GELS_MOUSE	49.33	15	209	NA	305
GPGLGYLSSHIANVER	P13020|GELS_MOUSE	49.69	16	1120	NA	1690
GPGLYYVDSEGNRISG	O55234|PSB5_MOUSE	41.4	16	964	NA	716
GPKPFSAPKPQTSP	P40124|CAP1_MOUSE	48.51	14	2570	NA	1260
GPKPFSAPKPQTSPS	P40124|CAP1_MOUSE	49.85	15	43500	1420	8390
GPKPFSAPKPQTSPSPK	P40124|CAP1_MOUSE	49.93	17	65300	3810	54000
GPKPFSAPKPQTSPSPKP	P40124|CAP1_MOUSE	49.91	18	111000	6820	77500
GPKPFSAPKPQTSPSPKPA	P40124|CAP1_MOUSE	49.93	19	2570	NA	1760
GPLIVSGPDGAPAKG	Q8VBW1|SC6A8_MOUSE	47.42	15	1750	NA	1750
GPLIVSGPDGAPAKGDG	Q8VBW1|SC6A8_MOUSE	47.74	17	15300	194	15200
GPLIVSGPDGAPAKGDGP	Q8VBW1|SC6A8_MOUSE	49.03	18	623	NA	1210
GPM(+15.99)AKFIQSTPSKSL	Q9D309|FAM3B_MOUSE	49.48	15	1590	NA	1540
GPM(+15.99)AKFIQSTPSKSLL	Q9D309|FAM3B_MOUSE	49.76	16	3580	NA	3940
GPMAKFIQSTPSKS	Q9D309|FAM3B_MOUSE	49.13	14	121	NA	387
GPMAKFIQSTPSKSL	Q9D309|FAM3B_MOUSE	49.72	15	1550	NA	2330
GPMAKFIQSTPSKSLLF	Q9D309|FAM3B_MOUSE	49.81	17	1010	NA	2500
GPNFEYAEAPSRLSPDD	P11152|LIPL_MOUSE	45.7	17	1750	NA	246
GPPIFNPVANEVY	Q07113|MPRI_MOUSE	47.64	13	286	NA	241
GPPIFNPVANEVYLN	Q07113|MPRI_MOUSE	49.32	15	1880	NA	1660
GPPPYHESLAGASQPPY	Q9D7I0|SHSA5_MOUSE	48.92	17	5470	NA	4210
GPRAFSSRSFTSGPGARISSSSF	P11679|K2C8_MOUSE	27.43	23	NA	NA	374
GPRGPPPAGLLQ	P06345|HB2S_MOUSE:P06346|HB2F_M	27.81	12	3460	NA	1890
GPSAPATPAAEAKAAEAAASAYYNPG	P97765|WBP2_MOUSE	49.8	26	1470	NA	723
GPSAPATPAAEAKAAEAAASAYYNPGN	P97765|WBP2_MOUSE	49.77	29	NA	NA	157
GPSQPAVLQPSVEPAQP	Q9ERN0|SCAM2_MOUSE	49.31	17	1070	NA	1480
GPSQPAVLQPSVEPAQPTP	Q9ERN0|SCAM2_MOUSE	49.86	19	3250	NA	4460
GPSQPAVLQPSVEPAQPTPQ	Q9ERN0|SCAM2_MOUSE	49.76	20	984	NA	1530
GPSQPRQYNNPIGLYSAET	Q9JKS4|LDB3_MOUSE	47.66	19	841	NA	917
GPSRGQYYGGSLPNVNQ	Q68ED7|CRTC1_MOUSE	29.62	17	48.7	NA	42.7
GPTYRGPVPWHT	Q9WV54|ASAH1_MOUSE	34.63	12	380	NA	868
GPTYRGPVPWHTIN	Q9WV54|ASAH1_MOUSE	44.64	14	13100	114	17100
GPVHNTLMSPQVSSSQG	Q3U2P1|SC24A_MOUSE	45.26	17	728	NA	2210
GPVTPLSPSVLPSLPQ	Q6NS82|RETR2_MOUSE	44.83	16	739	NA	434

GPYQAAAGPSVVPTAPP	Q9JLJ0|LITAF_MOUSE	48.95	17	288	NA	314
GPYYTEPVIAGLDPK	Q9R1P1|PSB3_MOUSE	49.65	15	643	NA	330
GQNAWFLPAQADIVAT	P10852|4F2_MOUSE	42.77	16	NA	NA	223
GQPPTGYSTPTAPQAYSQPV	Q61545|EWS_MOUSE	47.88	20	NA	NA	1000
GQPPTGYSTPTAPQAYSQPVQ	Q61545|EWS_MOUSE	48.85	21	NA	NA	5180
GQPPTGYSTPTAPQAYSQPVQGYGTGT	Q61545|EWS_MOUSE	48.51	29	NA	NA	92.4
GRDKYEPAAVSEHGDK	Q8VDN2|AT1A1_MOUSE	49.32	16	2040	NA	1340
GREVSSVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	36.64	16	114	NA	260
GREVSSVEAPSVSPARHQ	Q8BUJ9|LRP12_MOUSE	48.91	18	321	NA	390
GRFTYQNAAAQPETGPG	Q9QZM4|TR10B_MOUSE	48.32	17	22300	200	14000
GRFVM(+15.99)GPTVAPSQ	Q05BQ1|TUTLA_MOUSE	39.68	13	2210	NA	1190
GRFVM(+15.99)GPTVAPSQEK	Q05BQ1|TUTLA_MOUSE	46.74	15	8810	NA	3260
GRFVM(+15.99)GPTVAPSQEKL	Q05BQ1|TUTLA_MOUSE	44.91	16	906	NA	246
GRFVMGPTVAPSQ	Q05BQ1|TUTLA_MOUSE	36.08	13	1230	NA	1230
GRFVMGPTVAPSQE	Q05BQ1|TUTLA_MOUSE	45.23	14	257	NA	336
GRFVMGPTVAPSQEK	Q05BQ1|TUTLA_MOUSE	48.49	15	4750	NA	4970
GRFVMGPTVAPSQEKL	Q05BQ1|TUTLA_MOUSE	45.26	16	164	NA	438
GRIEHLYKNPQAHIEGNM	Q8K0C9|GMDS_MOUSE	32.61	18	117	NA	379
GRIEHLYKNPQAHIEGNM(+15.99)	Q8K0C9|GMDS_MOUSE	49.93	18	505	NA	387
GRKFVYAGSNSGVVQAPL	O09126|SEM4D_MOUSE	28.35	18	204	153	289
GRLEVVTDPTTNAG	Q9R100|CAD17_MOUSE	48.44	14	2180	NA	1400
GRLEVVTDPTTNAGYVKIK	Q9R100|CAD17_MOUSE	49.93	19	267	NA	354
GRLSYLPATTEPALPIPG	Q9JIA7|SPHK2_MOUSE	39.85	18	883	NA	741
GRPITPVYTVAPNVQRIPTAG	Q91WT8|RBM47_MOUSE	49.93	21	NA	NA	228
GRRASHTAPQVLFSHREPP	Q9CVB6|ARPC2_MOUSE	43.86	19	2130	NA	2200
GSDIFAAPAPQSTAT	Q8K2K6|AGFG1_MOUSE	45.42	15	1230	NA	1670
GSDM(+15.99)FKASLVIPSK	Q8BJD1|ITIH5_MOUSE	31.3	14	82.3	NA	85.2
GSDM(+15.99)FKASLVIPSKD	Q8BJD1|ITIH5_MOUSE	48.49	15	11700	2210	5020
GSDM(+15.99)FKASLVIPSKDK	Q8BJD1|ITIH5_MOUSE	46.93	16	9800	1590	4880
GSDM(+15.99)FKASLVIPSKDKA	Q8BJD1|ITIH5_MOUSE	36.87	17	2350	NA	874
GSDMFKASLVIPSK	Q8BJD1|ITIH5_MOUSE	44.23	14	182	NA	233
GSDMFKASLVIPSKD	Q8BJD1|ITIH5_MOUSE	48.44	15	5480	108	4270
GSDMFKASLVIPSKDK	Q8BJD1|ITIH5_MOUSE	49.2	16	6190	NA	6600
GSDMFKASLVIPSKDKA	Q8BJD1|ITIH5_MOUSE	48.86	17	1360	NA	1460
GSFVYKGGKIYKVPS	P50396|GDIA_MOUSE:Q61598|GDIB_M(	48.44	15	144	NA	103
GSGFAAPFFIVRHQLLKK	P17665|COX7C_MOUSE	48.82	18	386	NA	298
GSGGVFRAPSIHGGSG	P19001|K1C19_MOUSE	45.91	16	2100	118	7250
GSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	49.67	19	3650	222	6610
GSILWSQPLPSLPGGPPS	Q8C0Z1|F234A_MOUSE	49.76	18	1790	NA	1020
GSLFLKTPKIVSSKD	P06151|LDHA_MOUSE	49.91	15	15000	130	10900
GSLSTYLPSQPAPG	P47878|IBP3_MOUSE	38.5	14	1330	NA	1340
GSPGYNPPQM(+15.99)NTLP	Q8K419|LEG4_MOUSE	38.24	14	540	NA	252
GSPNYAAPEVISGRL	Q5EG47|AAPK1_MOUSE:Q8BRK8|AAPK	43.44	15	986	NA	1190
GSTLWSSPLPEEA	Q8BYI8|F234B_MOUSE	41.69	13	153	NA	84.1
GSTLWSSPLPEEAQDV	Q8BYI8|F234B_MOUSE	46.59	16	142	NA	56.7
GSVLWERPVAQDVALV	Q8C0Z1|F234A_MOUSE	49.94	16	236	NA	215
GSVRIGSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	46.53	24	337	NA	1010
GSVTYIAPPGNYD	P50516|VATA_MOUSE	27.88	13	206	NA	174
GTAKVLQPSAARNK	Q9EQK5|MVP_MOUSE	27.83	14	272	NA	294
GTATAKKSTKKTPKKA	P43274|H14_MOUSE	49.94	16	NA	NA	986
GTATAKKSTKKTPKKAKKPA	P43274|H14_MOUSE	49.95	20	8900	NA	4020
GTATAKKSTKKTPKKAKKPAAA	P43274|H14_MOUSE	48.39	22	NA	NA	1130
GTDRKIVYEGPELNHAFG	Q91ZX7|LRP1_MOUSE	49.83	18	4760	NA	65000
GTGGGSVRIGSGGVFRAPSIHGGSGGR	P19001|K1C19_MOUSE	48.91	27	NA	NA	6680
GTGGGSVRIGSGGVFRAPSIHGGSGGR	P19001|K1C19_MOUSE	49.94	28	15200	NA	18000
GTGGLPDYSAPNPIKVTHR	Q8CFG0|SULF2_MOUSE	49.77	19	1330	NA	2300
GTIRYM(+15.99)APEVLEGAV	O35607|BMPR2_MOUSE	47.94	15	829	NA	368
GTIRYM(+15.99)APEVLEGAVN	O35607|BMPR2_MOUSE	46.04	16	1550	NA	708
GTIRYMAPEVLEG	O35607|BMPR2_MOUSE	29.71	13	NA	NA	62.4
GTIRYMAPEVLEGAVN	O35607|BMPR2_MOUSE	47.11	16	302	NA	433
GTKRYMAPEVLDETIN	Q61271|ACV1B_MOUSE	47.76	16	5140	NA	5090
GTLVQTKGTGAAGSFKLNKKAESKAITT	P43275|H11_MOUSE	47.34	29	NA	NA	103
GTNM(+15.99)YNTDRANPVLDL	E9Q7P9|CDHR2_MOUSE	39.12	16	260	NA	214
GTNM(+15.99)YNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	49.84	17	8090	253	7800
GTNM(+15.99)YNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	49.92	18	1040	NA	944
GTNMYNTDRANPVL	E9Q7P9|CDHR2_MOUSE	44.37	14	NA	NA	80.2
GTNMYNTDRANPVLD	E9Q7P9|CDHR2_MOUSE	48.59	15	1480	NA	2640
GTNMYNTDRANPVLDL	E9Q7P9|CDHR2_MOUSE	47.7	16	NA	NA	150
GTPDYIAPEIIAYQP	P63318|KPCG_MOUSE:P20444|KPCA_M	35.78	15	69.1	NA	96.3
GTPDYIAPEILLGQK	Q02111|KPCT_MOUSE	36.17	15	NA	NA	570
GTPDYIAPEILQG	P28867|KPCD_MOUSE	32.16	13	899	NA	416
GTPDYIAPEILQGLK	P28867|KPCD_MOUSE	45.34	15	733	NA	570
GTPDYISPEVLKSQGG	P70336|ROCK2_MOUSE:P70335|ROCK1	28.82	16	NA	NA	99.5
GTPEFVAPEVINYEPI	Q6PDN3|MYLK_MOUSE	47.28	16	1930	NA	1190
GTPEYLAPEIILSKG	P68181|KAPCB_MOUSE:P05132|KAPCA	49.35	15	57800	2170	50000
GTPEYLAPEIILSKGY	P68181|KAPCB_MOUSE:P05132|KAPCA	49.52	16	69.1	NA	95.4
GTPEYLAPEIILSKGYN	P68181|KAPCB_MOUSE:P05132|KAPCA	46.36	17	6070	NA	5720
GTPEYLAPEVIQSKG	Q922R0|PRKX_MOUSE	40.07	15	110	NA	208
GTPEYVAPEVILNKG	Q61410|KGP2_MOUSE	48.3	15	14300	255	11200
GTRRYMAPEVLEGAI	P27038|AVR2A_MOUSE:P27040|AVR2B	28.2	15	204	NA	640
GTRRYMAPEVLEGAIN	P27038|AVR2A_MOUSE:P27040|AVR2B	25.59	16	4750	NA	5130

GTSRHPGPL	P23150|HA2J_MOUSE:P14434|HA2B_M(	41.86	9	10700	644	6880
GVAYEAPSLATGYG	P99026|PSB4_MOUSE	48.37	14	186	NA	178
GVFRAPSIHGGSG	P19001|K1C19_MOUSE	32.58	13	142	NA	1300
GVFRAPSIHGGSGGR	P19001|K1C19_MOUSE	30.59	15	361	NA	674
GVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	42.81	16	1080	NA	440
GVFSNPAVRTAAAN	O35609|SCAM3_MOUSE	44.9	14	370	NA	263
GVKKVAKSPKKAKAAAKPKKAAKSPAKI	P43276|H15_MOUSE	48.93	30	NA	812	993
GVPDDLLYSFPVVIKNK	P14152|MDHC_MOUSE	49.9	17	789	NA	1120
GVPTVPLLPPQVNQSLAS	Q99JX3|GORS2_MOUSE	37.6	18	NA	NA	220
GVPTVPLLPPQVNQSLASM(+15.99)PP	Q99JX3|GORS2_MOUSE	48.1	21	254	NA	566
GVPTVPLLPPQVNQSLASMPP	Q99JX3|GORS2_MOUSE	25.74	21	NA	NA	130
GVPVQAPQVPEAIEK	Q8VDP3|MICA1_MOUSE	48.11	15	391	NA	1170
GVPVQAPQVPEAIEKGD	Q8VDP3|MICA1_MOUSE	49.73	17	890	NA	209
GVSSEFYSQPGALPPPP	Q91XT4|SC16B_MOUSE	48.64	17	180	NA	165
GVSSQETAGIGASAHLVNFK	Q99KQ4|NAMPT_MOUSE	49.55	20	2540	1850	2510
GVYASPSIAGSRPG	Q8R0X7|SGPL1_MOUSE	46.29	14	3880	NA	1970
GVYTYGKPVPGLVTL	Q61838|PZP_MOUSE	49.68	15	4600	NA	5510
GVYTYGKPVPGLVTLR	Q61838|PZP_MOUSE	49.91	16	1330	NA	1020
GYAVYETPTAH	Q9QZ06|TOLIP_MOUSE	38.11	11	299	NA	348
GYAVYETPTAHN	Q9QZ06|TOLIP_MOUSE	39.39	12	666	NA	441
GYAVYETPTAHNG	Q9QZ06|TOLIP_MOUSE	39.3	13	1080	NA	764
GYAVYETPTAHNGA	Q9QZ06|TOLIP_MOUSE	44.95	14	328	NA	254
GYAVYETPTAHNGAK	Q9QZ06|TOLIP_MOUSE	45.75	15	1880	NA	525
GYAVYETPTAHNGAKNP	Q9QZ06|TOLIP_MOUSE	49.86	17	13700	NA	6850
GYAVYETPTAHNGAKNPR	Q9QZ06|TOLIP_MOUSE	49.92	18	24800	408	22800
GYKPFQNPVPNQSP	P16382|IL4RA_MOUSE	45.58	14	NA	NA	906
GYKPFQNPVPNQSPS	P16382|IL4RA_MOUSE	49.59	15	20200	890	33200
GYKPFQNPVPNQSPSS	P16382|IL4RA_MOUSE	49.49	16	1700	NA	1300
GYPTAYPAAAPAYNPS	Q8BGZ2|F168A_MOUSE	46.91	16	3930	56.1	3340
HAAHFAQAFPNAEWQPS	Q9DCS2|MTL26_MOUSE	43.46	17	616	NA	531
HARQQVRSPVTNIA	P84091|AP2M1_MOUSE	26.27	14	455	NA	436
HARQQVRSPVTNIAR	P84091|AP2M1_MOUSE	47.15	15	3810	NA	4240
HDLRHAFSPVASVESAS	P29699|FETUA_MOUSE	49.89	17	13200	NA	10300
HDLRHAFSPVASVESASG	P29699|FETUA_MOUSE	49.93	18	2670	NA	1830
HDLRHAFSPVASVESASGET	P29699|FETUA_MOUSE	49.59	20	2590	NA	1230
HDLRHAFSPVASVESASGETLHSPK	P29699|FETUA_MOUSE	49.95	25	533	NA	128
HDSKIKFPLPHRVLRRQHKPRFTTKRPN	P62717|RL18A_MOUSE	43.88	29	NA	NA	264
HDTSYKPPAGRTAAP	Q69ZQ1|MYORG_MOUSE	38.41	15	1270	NA	842
HDTSYKPPAGRTAAPE	Q69ZQ1|MYORG_MOUSE	49.6	16	5840	NA	5570
HDYKGSTSHSLPY	E9Q414|APOB_MOUSE	46.91	13	1680	NA	898
HDYKGSTSHSLPYE	E9Q414|APOB_MOUSE	37.38	14	1180	NA	857
HELRYQVPGAVPAK	Q9Z280|PLD1_MOUSE	49.69	14	3470	NA	2960
HGAIVDGPVPITIEV	Q9R100|CAD17_MOUSE	47.17	15	636	NA	508
HGLELEEPPLVLAAANV	O35522|PSB9_MUSMB:P28076|PSB9_M	45.14	17	974	NA	344
HGSLFLKTPKIVSSKD	P06151|LDHA_MOUSE	49.91	16	2950	NA	2230
HGSLFLKTPKIVSSKDY	P06151|LDHA_MOUSE	49.94	17	2380	NA	2110
HHPADFTPAVHASLDK	P01942|HBA_MOUSE	49.93	16	1050	NA	1410
HKYIYKSPELPRIL	Q99LR1|ABD12_MOUSE	49.88	14	NA	NA	69.1
HLKIVYRRFRHGFREGTTPKPKR	Q9D823|RL37_MOUSE	48.89	23	8700	12200	5560
HLQLAIRN	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	37.48	8	386	1000	194
HLQLAIRND	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	42.59	9	1760	1920	302
HLRFNYPEVQKVMPR	Q6XQH0|G3ST2_MOUSE	49.77	15	4970	NA	4590
HLRFSAPQIENEPE	Q61190|I10R2_MOUSE	49.18	14	10700	NA	8060
HLRFSAPQIENEPET	Q61190|I10R2_MOUSE	48.83	15	393	NA	380
HNPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	39.01	13	NA	NA	176
HNYEGPETHTSL	P14483|HB2A_MOUSE	48.17	12	9200	2730	4350
HNYEGPETHTSLR	P14483|HB2A_MOUSE	49.57	13	22500	3730	14600
HNYEGPETHTSLRR	P14483|HB2A_MOUSE	44.81	14	NA	NA	44300
HPAPGRDLHYQNPHSNAVGNP	Q01279|EGFR_MOUSE	45.39	21	3750	NA	3320
HPDRFAYPIPHTTRPP	O70589|CSKP_MOUSE	49.77	16	9910	NA	7140
HPIQWNAPEPSHIT	P11276|FINC_MOUSE	36.16	14	NA	NA	377
HPIQWNAPEPSHITK	P11276|FINC_MOUSE	49.45	15	4220	NA	5800
HPQTYYYAVAVVKK	Q921I1|TRFE_MOUSE	49.81	14	NA	NA	177
HPQTYYYAVAVVKKG	Q921I1|TRFE_MOUSE	49.27	15	325	NA	681
HPQTYYYAVAVVKKGTDF	Q921I1|TRFE_MOUSE	49.88	18	188	NA	192
HPSSHVFM(+15.99)PPSPSTTPPH	Q571K4|TAB3_MOUSE	41.4	18	4590	NA	3060
HPSSHVFMPPSPSTTPP	Q571K4|TAB3_MOUSE	48.42	17	206	NA	747
HPSSHVFMPPSPSTTPPH	Q571K4|TAB3_MOUSE	48.12	18	623	NA	1040
HQQYTFVNPSVLSLSPI	P70207|PLXA2_MOUSE	48.93	17	NA	NA	288
HRDPYATSVGHLIEK	Q923U0|TM1L1_MOUSE	49.42	15	322	NA	151
HRNGIKKPRSQRYESLKGVDPKFL	P47915|RL29_MOUSE	33.69	24	NA	NA	1020
HTIAYLTPLPQPNR	Q91VS7|MGST1_MOUSE	45.72	14	3410	NA	1260
HTLFHNPHVNPL	P43023|CX6A2_MOUSE:P43024|CX6A1_	42.03	12	335	NA	155
HTLFHNPHVNPLP	P43023|CX6A2_MOUSE:P43024|CX6A1_	48.51	13	1780	160	2210
HTLFHNPHVNPLPT	P43023|CX6A2_MOUSE:P43024|CX6A1_	49.64	14	8410	662	7000
HTLFHNPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	47.07	17	324	NA	654
HVPTLQVLRPGLVVVH	Q9D3D9|ATPD_MOUSE	46.92	16	968	NA	3900
HYQSFQYPTTAGTFR	Q3V3F6|MPZL3_MOUSE	47.51	15	127	NA	104
I(+42.01)HVC(+57.02)LPSQFKC(+57.02)T	Q91ZX7|LRP1_MOUSE	28.76	20	NA	NA	1110
I(+42.01)PGTN(+15.00)MYNTDRANPVLI	E9Q7P9|CDHR2_MOUSE	37.29	17	281	NA	492
I(+42.01)TQ(+15.00)VQWNDPGAQYSLV	Q9R100|CAD17_MOUSE	33.35	17	NA	NA	64.9

I(+42.01)TQ(+15.00)VQWNDPGAQYSLV	Q9R100|CAD17_MOUSE	28.73	18	NA	NA	89.4
IAEDYFMAKAIADRG	O88693|CEGT_MOUSE	49.71	15	225	NA	298
IAFLSPKVDPS	Q9CQU3|RER1_MOUSE	26.3	11	555	NA	336
IAFLSPKVDPSL	Q9CQU3|RER1_MOUSE	36.75	12	287	NA	195
IDAVYEAPQEEKAVF	P33434|MMP2_MOUSE	47.11	15	418	NA	209
IDIFARPTAGFITG	P57787|MOT4_MOUSE	41.14	14	179	NA	198
IDPYDQPNAIYIER	O88307|SORL_MOUSE	49.37	14	10100	372	6190
IDPYDQPNAIYIERH	O88307|SORL_MOUSE	49.67	15	3110	NA	2490
IDPYDQPNAIYIERHEP	O88307|SORL_MOUSE	40.2	17	160	NA	174
IDTTIAYPKAEPID	Q91YX5|LGAT1_MOUSE	44.45	14	2940	NA	2130
IDWTYRPPSSSRTESI	Q3V3F6|MPZL3_MOUSE	30.89	16	NA	NA	2890
IEDIEVAPPKAHEVRIK	P00329|ADH1_MOUSE	49.93	17	7350	NA	5670
IEEIEVAPPKAHEVR	P28474|ADHX_MOUSE	43.14	15	2750	NA	2700
IEEIEVAPPKAHEVRIK	P28474|ADHX_MOUSE	49.09	17	367	NA	537
IEFRGPNGLLVYQ	Q9DCN2|NB5R3_MOUSE	35.95	13	268	NA	146
IEFRGPNGLLVYQGK	Q9DCN2|NB5R3_MOUSE	49.01	15	1550	NA	1130
IEHLYKNPQAHIEG	Q8K0C9|GMDS_MOUSE	49.63	14	5350	NA	4420
IEHLYKNPQAHIEGN	Q8K0C9|GMDS_MOUSE	49.83	15	1370	NA	1180
IEHLYKNPQAHIEGNM	Q8K0C9|GMDS_MOUSE	49.94	16	2530	NA	4550
IEHLYKNPQAHIEGNM(+15.99)	Q8K0C9|GMDS_MOUSE	49.91	16	6660	NA	2880
IEKVIPSTANSN	E9Q7P9|CDHR2_MOUSE	37.67	12	5560	NA	3020
IEKVIPSTANSNN	E9Q7P9|CDHR2_MOUSE	41.06	13	3540	NA	1760
IEKVIPSTANSNNL	E9Q7P9|CDHR2_MOUSE	44.74	14	15300	239	8440
IENDPGFGAPAASQVASAQPG	Q6IRU5|CLCB_MOUSE	49.11	21	464	NA	1020
IESKEAFQEALAAAGDK	P10639|THIO_MOUSE	49.86	17	3020	NA	3000
IESKEAFQEALAAAGDKL	P10639|THIO_MOUSE	49.92	18	397	NA	286
IEVAPPKAHEVRIK	P28474|ADHX_MOUSE:P00329|ADH1_M	37.3	14	2000	NA	1680
IEVSSPITLQALV	E9Q414|APOB_MOUSE	48.35	13	184	NA	85.5
IEVSSPITLQALVQ	E9Q414|APOB_MOUSE	48.6	14	3460	NA	1100
IFARGPQAHLVH	P24823|PPBN_MOUSE:P24822|PPBI_M	44.42	12	6120	NA	4310
IFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_M	48.05	13	45900	1060	29000
IFARGPQAHLVHGVQ	P24823|PPBN_MOUSE:P24822|PPBI_M	48.76	15	3320	NA	2120
IFIYNASKPQNLE	Q921R7|S35A5_MOUSE	37	13	138	NA	202
IGDSNFGAPSASVAAAP	O35643|AP1B1_MOUSE	35.17	17	942	NA	188
IGDSNFGAPSASVAAAPA	O35643|AP1B1_MOUSE	49.69	18	4660	46.9	4110
IGDSNFGAPSASVAAAPAP	O35643|AP1B1_MOUSE	49.64	19	14600	377	15400
IGDTIEFRGPNGLLVYQ	Q9DCN2|NB5R3_MOUSE	31.07	17	NA	NA	522
IGDTIEFRGPNGLLVYQG	Q9DCN2|NB5R3_MOUSE	49.89	18	5150	NA	5430
IGDTIEFRGPNGLLVYQGK	Q9DCN2|NB5R3_MOUSE	49.88	19	5880	NA	10400
IGGDPFAAPQVVPAFAS	Q80WC7|AGFG2_MOUSE	47.94	17	341	NA	360
IGSGGVFRAPSIHGGSG	P19001|K1C19_MOUSE	48.87	17	467	NA	7630
IGSGGVFRAPSIHGGSGG	P19001|K1C19_MOUSE	33.43	18	NA	NA	182
IGSGGVFRAPSIHGGSGGR	P19001|K1C19_MOUSE	49.8	19	6220	475	14800
IGSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	49.94	20	12100	608	12000
IGSGIFVSPKGVLE	Q9QXW9|LAT2_MOUSE	40.22	14	2280	NA	1770
IGSGIFVSPKGVLEN	Q9QXW9|LAT2_MOUSE	47.66	15	2500	NA	1780
IGSGIFVSPKGVLENA	Q9QXW9|LAT2_MOUSE	48.32	16	3080	NA	2830
IIDTTIAYPKAEPID	Q91YX5|LGAT1_MOUSE	48.6	15	1630	NA	1020
IIGSGIFVSPKGVLENAG	Q9QXW9|LAT2_MOUSE	47.05	18	NA	NA	572
IKETDYNGFPVLVSRDS	Q61418|CLCN4_MOUSE	49.91	17	1400	NA	1450
IKIAWESPQGQVSR	P11276|FINC_MOUSE	48.45	14	3340	NA	1430
IKNNSFYGPEVKIEKGDL	Q00519|XDH_MOUSE	49.85	18	1930	NA	1650
IKVNVIPPLAQATIN	Q8C165|P20D1_MOUSE	47.51	15	NA	NA	287
IKVYWDAPSPAPD	Q8K385|FRRS1_MOUSE	48.73	13	1620	NA	873
IKVYWDAPSPAPDH	Q8K385|FRRS1_MOUSE	49.9	14	2590	NA	2490
IKVYWDAPSPAPDHIR	Q8K385|FRRS1_MOUSE	40.99	16	NA	NA	2400
ILDARSYTAAVANRAKGGG	Q91XS1|MTMR4_MOUSE	49.69	19	1250	NA	892
ILDRYYTPTISRER	Q9R1P3|PSB2_MOUSE	49.28	14	2880	NA	2750
ILDRYYTPTISRERA	Q9R1P3|PSB2_MOUSE	47.9	15	8910	NA	6230
ILPEETPTASASADTPH	E9Q7D5|ARHG5_MOUSE	38.02	17	155	NA	50
ILVRYTQKAPQVSTP	P07724|ALBU_MOUSE	49.91	15	824	NA	644
ILVRYTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.94	18	19300	NA	22000
INDYKGAVIVVSHDAR	Q6P542|ABCF1_MOUSE	49.48	16	90.6	NA	282
INETSYNGFPVIM(+15.99)SKES	P51791|CLCN3_MOUSE	49.66	17	900	NA	567
INETSYNGFPVIM(+15.99)SKESQ	P51791|CLCN3_MOUSE	49.93	18	1800	NA	1330
INETSYNGFPVIMSKE	P51791|CLCN3_MOUSE	49.87	16	740	NA	1240
INETSYNGFPVIMSKES	P51791|CLCN3_MOUSE	49.89	17	482	NA	940
INETSYNGFPVIMSKESQ	P51791|CLCN3_MOUSE	49.6	18	904	NA	1330
INFDFPKL	P54823|DDX6_MOUSE	27.84	8	234	NA	66.4
INMKQYASPM(+15.99)PTQTDV	Q69ZW3|EHBP1_MOUSE	37.37	16	NA	NA	92.4
INPDNVATPIAASFG	Q8BYR8|S41A2_MOUSE	47.61	15	1480	NA	400
INPDNVATPIAASFGD	Q8BYR8|S41A2_MOUSE	47.61	16	472	NA	286
INRLDNYDAPDIANIAIS	Q68FD5|CLH1_MOUSE	48.36	18	NA	NA	347
INYQPPTVVPGGDL	P68369|TBA1A_MOUSE:P68373|TBA1C	43.97	14	3820	NA	2620
IPAYPAGSPGYNPPQM(+15.99)NTL	Q8K419|LEG4_MOUSE	49.91	19	434	NA	468
IPAYPAGSPGYNPPQM(+15.99)NTLP	Q8K419|LEG4_MOUSE	49.89	20	2950	NA	3010
IPAYPAGSPGYNPPQM(+15.99)NTLPVM	Q8K419|LEG4_MOUSE	49.95	22	465	NA	372
IPAYPAGSPGYNPPQMNTL	Q8K419|LEG4_MOUSE	48.82	19	322	NA	900
IPAYPAGSPGYNPPQMNTLPVM(+15.99	Q8K419|LEG4_MOUSE	49.49	22	104	NA	288
IPENYNSAM(+15.99)PFKILY	Q64487|PTPRD_MOUSE	48.92	15	617	NA	174
IPENYNSAMPFKILY	Q64487|PTPRD_MOUSE	48.68	15	293	NA	510

IPEPAHAYAQPQTTTPLPT	P47941|CRKL_MOUSE	49.77	19	237	NA	279
IPEQSFYTKPLPGIIM(+15.99)	P58021|TM9S2_MOUSE	49.8	16	678	NA	570
IPEQSFYTKPLPGIIM(+15.99)G	P58021|TM9S2_MOUSE	49.93	17	2860	NA	2090
IPEQSFYTKPLPGIIMG	P58021|TM9S2_MOUSE	49.86	17	209	NA	922
IPFYTPIPN	O08573|LEG9_MOUSE	30.12	9	NA	NA	41.3
IPFYTPIPNG	O08573|LEG9_MOUSE	34.95	10	23600	682	21700
IPFYTPIPNGLY	O08573|LEG9_MOUSE	47.9	12	1450	NA	855
IPFYTPIPNGLYP	O08573|LEG9_MOUSE	46.71	13	20400	913	26600
IPFYTPIPNGLYPS	O08573|LEG9_MOUSE	47.45	14	89400	3720	56700
IPFYTPIPNGLYPSK	O08573|LEG9_MOUSE	49.01	15	898	NA	631
IPGTNM(+15.99)YNTDRANPVLDL	E9Q7P9|CDHR2_MOUSE	47.66	18	14900	NA	9740
IPGTNM(+15.99)YNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	49.87	20	65100	1940	44500
IPGTNMYNTDRANPV	E9Q7P9|CDHR2_MOUSE	49.88	15	2760	NA	2010
IPGTNMYNTDRANPVL	E9Q7P9|CDHR2_MOUSE	49.78	16	7240	NA	8530
IPGTNMYNTDRANPVLDL	E9Q7P9|CDHR2_MOUSE	48.22	18	NA	NA	4720
IPGTNMYNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	49.92	19	146000	NA	182000
IPGTNMYNTDRANPVLDLPT	E9Q7P9|CDHR2_MOUSE	49.92	20	23500	NA	37300
IPIRWTAPEAIAFRK	Q60629|EPHA5_MOUSE:P54761|EPHB4	44.29	15	NA	NA	178
IPIRWTAPEAIAH	Q60750|EPHA1_MOUSE	47.68	13	1440	NA	1770
IPIRWTAPEAIQYRK	P54763|EPHB2_MOUSE	49	15	149	NA	199
IPIRWTAPEAISY	Q03145|EPHA2_MOUSE	37.22	13	822	NA	1060
IPIRWTAPEAISYR	Q03145|EPHA2_MOUSE	47.98	14	2150	NA	2670
IPIRWTAPEAISYRK	Q03145|EPHA2_MOUSE	48.01	15	7200	64.8	9010
IPM(+15.99)YDAAQALKTNPE	Q6EDY6|CARL1_MOUSE	47.95	15	220	NA	149
IPM(+15.99)YSIITPNVLRLE	P01027|CO3_MOUSE	41.83	15	586	NA	433
IPM(+15.99)YSIITPNVLRLESE	P01027|CO3_MOUSE	47.77	17	2630	NA	1680
IPMYSIITPNVLRLES	P01027|CO3_MOUSE	46.92	16	1050	NA	2110
IPMYSIITPNVLRLESE	P01027|CO3_MOUSE	44.91	17	927	NA	1120
IPQAERYQEALPTVAN	P30999|CTND1_MOUSE	46.38	16	2720	NA	2610
IPQAERYQEALPTVANS	P30999|CTND1_MOUSE	47.33	17	416	NA	991
IPQAERYQEALPTVANST	P30999|CTND1_MOUSE	48.85	18	3600	NA	4770
IPSNPALKTPMVAVSEDL	Q8R5K2|UBP33_MOUSE	48.93	18	NA	NA	279
IPSPSSAFTPAHAATSSH	Q8CI51|PDLI5_MOUSE	49.86	18	1860	NA	1070
IPSPSSAFTPAHAATSSHA	Q8CI51|PDLI5_MOUSE	49.94	19	16700	NA	13200
IPSRYSSPTTIATVM(+15.99)	Q9DBM2|ECHP_MOUSE	45.3	15	4700	134	5630
IPSSVPATFAPSPTPAVVSS	Q9DBG3|AP2B1_MOUSE	48.88	20	NA	NA	350
IPSSVPATFAPSPTPAVVSSG	Q9DBG3|AP2B1_MOUSE	49.93	21	165	NA	911
IPVKTLKYSIDPSVVNISDEM(+15.99)	Q8BTY2|S4A7_MOUSE	49.95	21	545	NA	283
IPYQGPSSDYVVVK	O88307|SORL_MOUSE	48.98	14	356	NA	303
IQASVATNPIITPVAQEN	P08226|APOE_MOUSE	49.47	18	168	NA	110
IQEPYTFPAILKSV	Q8BFR4|GNS_MOUSE	49.68	14	956	NA	666
IQLSFSQPKAHEAS	Q5PT54|NTCP5_MOUSE	42.49	14	713	NA	426
IQLSFSQPKAHEASVA	Q5PT54|NTCP5_MOUSE	49.13	16	3030	NA	2130
IREFYSASVAEDA	E9Q7P9|CDHR2_MOUSE	47.87	13	2940	36	2600
IRENIWKAPEPVEI	Q9R100|CAD17_MOUSE	46.97	14	NA	NA	226
IRENIWKAPEPVEIREN(+15.00)ST	Q9R100|CAD17_MOUSE	49.91	19	20200	NA	16100
IRLPYTASSGLM(+15.99)AP	Q9R1Q9|VAS1_MOUSE	49.43	14	354	NA	138
IRLPYTASSGLM(+15.99)APR	Q9R1Q9|VAS1_MOUSE	48.55	15	5010	NA	3900
IRLPYTASSGLM(+15.99)APRE	Q9R1Q9|VAS1_MOUSE	49.69	16	4100	NA	2920
IRLPYTASSGLMAPR	Q9R1Q9|VAS1_MOUSE	48.88	15	657	NA	3610
IRLPYTASSGLMAPRE	Q9R1Q9|VAS1_MOUSE	49.8	16	494	NA	1590
IRPSVYQPVPASSYSPS	Q9JKS4|LDB3_MOUSE	49.93	17	143	NA	164
IRPSVYQPVPASSYSPSPG	Q9JKS4|LDB3_MOUSE	49.93	19	1010	NA	484
IRYM(+15.99)APEVLEGAVN	O35607|BMPR2_MOUSE	39.91	14	501	NA	167
IRYMAPEVLEGAVN	O35607|BMPR2_MOUSE	39.92	14	NA	NA	151
ISKQEYDESGPSIVH	P63260|ACTG_MOUSE:P60710|ACTB_M	45.94	15	448	NA	521
ISKQEYDESGPSIVHR	P63260|ACTG_MOUSE:P60710|ACTB_M	49.88	16	914	NA	697
ISKQEYDESGPSIVHRK	P63260|ACTG_MOUSE:P60710|ACTB_M	48.66	17	510	NA	474
ISLLYTEPGASQTQTG	P39061|COIA1_MOUSE	35.74	16	NA	NA	181
ISLNTYTPTKILPTPP	Q6ZQB6|VIP2_MOUSE	40.82	16	231	NA	276
ISQIFSQAM(+15.99)AARSINRP	P34914|HYES_MOUSE	28.66	17	5770	NA	6490
ISQIFSQAM(+15.99)AARSINRPM	P34914|HYES_MOUSE	29.47	18	NA	NA	273
ISQIFSQAM(+15.99)AARSINRPM(+15.99	P34914|HYES_MOUSE	29.48	18	NA	NA	102
ISQIFSQAMAARSIN	P34914|HYES_MOUSE	46.79	15	1140	NA	1610
ISQIFSQAMAARSINR	P34914|HYES_MOUSE	36.69	16	4420	NA	5500
ISSDENAPSVIKSVED	Q62469|ITA2_MOUSE	48.23	16	1680	NA	1110
ISYTGSRPASN	P28666|MUG2_MOUSE:P28665|MUG1_M	44.61	11	1050	NA	388
ISYTGSRPASNMV	P28666|MUG2_MOUSE:P28665|MUG1_M	48.47	13	478	NA	387
ITDENWLSPRPASGPS	P97305|NFAC3_MOUSE	28.87	16	260	NA	385
ITNNQDFRGSAGAPSVENV	P49443|PPM1A_MOUSE	48.46	19	108	NA	222
ITNQYNSPTGLYS	O70400|PDLI1_MOUSE	46.48	13	2940	NA	2600
ITNQYNSPTGLYSS	O70400|PDLI1_MOUSE	49.22	14	2690	NA	1900
ITNQYNSPTGLYSSE	O70400|PDLI1_MOUSE	49.64	15	4200	NA	4460
ITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.66	16	86900	4640	82400
ITNQYNSPTGLYSSENI	O70400|PDLI1_MOUSE	49.9	17	2350	NA	2560
ITNQYNSPTGLYSSENIS	O70400|PDLI1_MOUSE	49.86	18	515	NA	438
ITPSYVAFTPEGER	P20029|BIP_MOUSE	47.93	14	2180	NA	2080
ITPSYVAFTPEGERL	P20029|BIP_MOUSE	47.22	15	6820	161	6540
ITPSYVAFTPEGERLI	P20029|BIP_MOUSE	46.62	16	4170	NA	2660
ITQVQWNDPGAQYS	Q9R100|CAD17_MOUSE	49.81	14	156	NA	159
ITQVQWNDPGAQYSL	Q9R100|CAD17_MOUSE	49.88	15	NA	NA	162

ITQVQWNDPGAQYSLV	Q9R100|CAD17_MOUSE	49.49	16	267	NA	667
ITQVQWNDPGAQYSLVN	Q9R100|CAD17_MOUSE	49.94	17	21900	NA	30000
ITQVQWNDPGAQYSLVNKEK	Q9R100|CAD17_MOUSE	49.44	20	229	NA	161
ITTDYNSPEAGNIF	B2RXV4|FLVC1_MOUSE	47.91	14	27800	160	11700
ITYSYAGARAPM(+15.99)GQG	Q7TQH7|LRP10_MOUSE	48.16	15	1310	NA	551
IVLGYNGSLPNGDRG	Q8C669|PELI1_MOUSE	48.39	15	394	NA	421
IVSHDYKGSTSHSLP	E9Q414|APOB_MOUSE	40.44	15	9760	NA	9550
IVSHDYKGSTSHSLPYE	E9Q414|APOB_MOUSE	49.81	17	15900	NA	13500
IVTDYTLAEAEAALQK	Q9ES64|USH1C_MOUSE	40	16	NA	NA	94.9
IVTERVYAPTSTLVDQ	O55111|DSG2_MOUSE	49.83	16	558	NA	1160
IVTERVYAPTSTLVDQHY	O55111|DSG2_MOUSE	49.93	18	670	NA	348
IVYEGPELNHAFG	Q91ZX7|LRP1_MOUSE	47.68	13	5780	NA	3370
IVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	48.4	15	NA	575	194
IYIYNGPVLGGTR	P50284|TNR3_MOUSE	40.31	13	648	NA	898
IYVPAHAHEGSNLPV	Q8BK48|EST2E_MOUSE	27.87	15	NA	NA	35.4
IYYHASRAIPFG	Q9ET30|TM9S3_MOUSE	38.11	12	NA	NA	72.4
K(+42.01)KTKKPAKAAAPRK	P43275|H11_MOUSE	34.28	14	467	NA	798
K(+42.01)N(+15.00)KRLTKGGKKGAKK	P97351|RS3A_MOUSE	27.82	15	NA	NA	1710
K(+42.01)N(+15.00)KRLTKGGKKGAKKK	P97351|RS3A_MOUSE	27.9	16	NA	NA	9870
K(+42.01)N(+15.00)KRLTKGGKKGAKKK	P97351|RS3A_MOUSE	35.78	27	NA	NA	596
K(+42.01)PKVVKVKPVKASKPKKAKTVK	P10922|H10_MOUSE	49.71	26	2820	4260	2230
K(+42.01)PVKASKPKKAKTVKPKAK	P10922|H10_MOUSE	37.79	19	NA	NA	3690
K(+42.01)TVKPKAAKPKTSKPKAAKPKK	P43274|H14_MOUSE	37.26	27	NA	NA	3550
K(+42.01)VQKKDGKKRKRSRKESYSVY	Q64525|H2B2B_MOUSE	25.67	32	NA	NA	1130
KAAGTATAKKSTKKTPKKAKKPA	P43274|H14_MOUSE	48.95	23	NA	NA	456
KAAKKTPKKAKKPAA	P15864|H12_MOUSE	37.03	15	NA	NA	531
KAAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	18	2230	NA	233
KAAKSPAKPKAVKSKASK	P43276|H15_MOUSE	40.27	18	NA	2930	5340
KAKAAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	48.88	20	NA	15300	12800
KAKAPKAKASKPKA	P43277|H13_MOUSE	46.36	14	818	NA	393
KAKATKAKKAPKSPAKAK	P43274|H14_MOUSE	49.68	18	NA	NA	3470
KAKATKAKKAPKSPAKAKTVK	P43274|H14_MOUSE	49.43	21	2780	3830	4710
KAKKAVLKGVHSHKKKIRTSPTFRRPK	P62751|RL23A_MOUSE	48.95	28	NA	1310	3280
KAKKAVLKGVHSHKKKIRTSPTFRRPK	P62751|RL23A_MOUSE	48.95	33	NA	NA	439
KAKKKPAATPKKAKKPKVVKVKPVKASK	P10922|H10_MOUSE	49.95	33	1730	1470	1200
KAKKPAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.95	21	2440	1910	2140
KAKKPAGATPKKPK	P43276|H15_MOUSE	30.73	14	NA	NA	188
KAKKPKVVKVKPVKASKPKKAKT(+79.9	P10922|H10_MOUSE	37.19	25	NA	NA	262
KAKKPKVVKVKPVKASKPKKAKTVKPK	P10922|H10_MOUSE	43.75	27	NA	NA	863
KAKKPKVVKVKPVKASKPKKAKTVKPKA	P10922|H10_MOUSE	48.95	29	NA	NA	285
KAKSPKKAKATKAKKAPK	P43274|H14_MOUSE	48.95	18	NA	NA	1160
KAKSPKKAKATKAKKAPKSPAKAK	P43274|H14_MOUSE	49.95	24	NA	NA	2950
KAKTVKPKA	P43274|H14_MOUSE:P10922|H10_MOU	41.72	9	186	359	1310
KAKTVKPKAK	P10922|H10_MOUSE	42.68	10	290	NA	633
KAKTVKPKAKSSAKRASKK	P10922|H10_MOUSE	49.94	19	5680	NA	1780
KAKVTKPKTPAKPKKA	P43275|H11_MOUSE	31.06	16	3380	NA	1010
KAPEPVEIR	Q9R100|CAD17_MOUSE	38.44	9	777	NA	491
KAPKAKASKPKASK	P43277|H13_MOUSE	32.52	14	NA	NA	159
KASKPKATKAKKAAPRK	P43277|H13_MOUSE	42.17	17	NA	802	4120
KASKPKKAKTVKPKAK	P10922|H10_MOUSE	49.94	16	510	183	976
KASKPKKAKTVKPKAKSSAKR	P10922|H10_MOUSE	48.95	21	NA	NA	443
KASKPKKAKTVKPKAKSSAKRASKK	P10922|H10_MOUSE	48.95	25	NA	NA	642
KASPKKAA	Q9CR57|RL14_MOUSE	25.54	8	NA	NA	140
KATKAKKAAPRKK	P43277|H13_MOUSE	49.93	13	NA	NA	815
KAVDYPPVANAGP	Q8K135|K319L_MOUSE	37.71	13	NA	NA	129
KAVDYPPVANAGPNQ	Q8K135|K319L_MOUSE	48.7	15	3250	NA	3410
KAVGKVIPELNGKLTGM(+15.99)AFRVP	P16858|G3P_MOUSE	49.9	30	1550	NA	2760
KAVGKVIPELNGKLTGMAFRVPTPNVSV	P16858|G3P_MOUSE	48.95	30	1640	NA	19600
KDESGFPKPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	46.07	23	2040	NA	894
KDESGFPKPPSYNVATTLPSYDEA	Q8R0W6|NFIP1_MOUSE	49.63	24	3070	NA	2310
KDGKKRKRSRKESYSVYVYKVLKQVHP	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	43.25	28	4700	10800	1780
KDSELSPPTSAPSLVS	Q9WUU8|TNIP1_MOUSE	43.58	16	319	NA	171
KEDRRYNPPIIHQGFQD	P27784|CCL6_MOUSE	35.5	17	NA	NA	1820
KEFQFLNPNPVPE	Q8R0K2|TRI31_MOUSE	25.74	13	NA	NA	165
KELEEQLGPVAEETRA	P08226|APOE_MOUSE	49.63	16	37300	2070	29400
KERASFITPVPGGVG	Q922D8|C1TC_MOUSE	39.86	15	583	NA	706
KERASFITPVPGGVGP	Q922D8|C1TC_MOUSE	45.82	16	719	NA	1180
KERASFITPVPGGVGPM(+15.99)	Q922D8|C1TC_MOUSE	49.36	17	310	NA	385
KEVDRYDAPGIAFYPG	Q9D771|PACC1_MOUSE	36.93	16	944	NA	1530
KFYKGKKYKPLDLRPKK	Q6ZWV7|RL35_MOUSE	49.94	17	272	NA	388
KFYKGKKYKPLDLRPKKT	Q6ZWV7|RL35_MOUSE	49.94	18	1220	1850	2460
KFYKGKKYKPLDLRPKKTR	Q6ZWV7|RL35_MOUSE	49.95	19	1500	7630	5510
KFYKGKKYKPLDLRPKKTRA	Q6ZWV7|RL35_MOUSE	48.93	20	NA	133	261
KFYKGKKYKPLDLRPKKTRAM(+15.99)R	Q6ZWV7|RL35_MOUSE	49.95	23	NA	10300	1930
KGFEVDAPLANALA	Q6PDE7|GGT6_MOUSE	49.43	14	562	NA	434
KGFEVDAPLANALAI	Q6PDE7|GGT6_MOUSE	48.69	15	1630	NA	1400
KGFEVDAPLANALAIQ	Q6PDE7|GGT6_MOUSE	47.35	16	186	NA	104
KGGKKKKQVLKFTL	P67984|RL22_MOUSE	36.71	14	NA	NA	186
KGIPVYRFVLPANAFA	Q08857|CD36_MOUSE	49.75	16	1080	NA	253
KGKPELRKKVHPAVVIRQRKSYRRKDG	P62830|RL23_MOUSE	40.4	27	NA	NA	1780
KGPLIVSGPDGAPAKG	Q8VBW1|SC6A8_MOUSE	49.17	16	494	NA	654

KGPLIVSGPDGAPAKGDG	Q8VBW1|SC6A8_MOUSE	49.86	18	13300	NA	13200
KGPLIVSGPDGAPAKGDGP	Q8VBW1|SC6A8_MOUSE	48.9	19	NA	NA	269
KGSKKAISKAQKKDGKKRKRSRKESYS	Q64475|H2B1B_MOUSE	42.08	32	NA	49600	2660
KGSKKAVTKAQKKDGKKRKRSRKESYS	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	48.62	32	NA	151000	3860
KHPDRFAYPIPHTTRPP	O70589|CSKP_MOUSE	49.33	17	8080	NA	7180
KHPDRFAYPIPHTTRPPK	O70589|CSKP_MOUSE	49.91	18	424	NA	280
KHQLLRVKRKVT	Q6P5U7|NWD2_MOUSE	26.22	12	NA	NA	4490
KIQASVATNPIITPVAQENQ	P08226|APOE_MOUSE	49.87	20	118	NA	105
KIVYEGPELNHA	Q91ZX7|LRP1_MOUSE	48.02	12	630	NA	629
KIVYEGPELNHAF	Q91ZX7|LRP1_MOUSE	49.66	13	460	NA	625
KKAAAPPKK	E9Q5C9|NOLC1_MOUSE	28.54	9	NA	NA	2190
KKAAKKTPKKAKKPA	P15864|H12_MOUSE	48.65	15	NA	91.9	3860
KKAAKSPAKPK	P43276|H15_MOUSE	30.07	11	NA	NA	48.7
KKAKATKAKKAPKSPAK	P43274|H14_MOUSE	49.94	17	251	26.3	295
KKAKATKAKKAPKSPAKAK	P43274|H14_MOUSE	49.95	19	4410	2030	1870
KKAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	23	7790	3290	6130
KKAKKPKVVKVKPVKASKPKKAKTVKP	P10922|H10_MOUSE	48.93	27	NA	NA	863
KKAKSPKKAK	P43274|H14_MOUSE	43.25	10	NA	701	1770
KKAKVTKPKKVKSASKAVKPKAAKPK	P15864|H12_MOUSE	48.67	26	NA	830	1550
KKEKPMKKFYS(+79.97)ES(+79.97)EEE	Q9Z1T1|AP3B1_MOUSE	28.92	16	NA	NA	2590
KKELEEQLGPVAEETR	P08226|APOE_MOUSE	49.9	16	14200	178	20300
KKELEEQLGPVAEETRAR	P08226|APOE_MOUSE	49.04	18	12500	221	11500
KKELEEQLGPVAEETRARL	P08226|APOE_MOUSE	47.06	19	NA	NA	439
KKGPLIVSGPDGAPAKGDG	Q8VBW1|SC6A8_MOUSE	49.86	19	80.7	NA	131
KKGSKKAISKAQKKDGKKRKRSR	Q64475|H2B1B_MOUSE	38.15	23	NA	NA	1640
KKGSKKAITKAQKKDGKKRKR	Q9D2U9|H2B3A_MOUSE	48.93	21	NA	NA	2610
KKKKKKKP	Q99L45|IF2B_MOUSE	33.67	8	NA	NA	1450
KKKKKTGRAKRR	P62862|RS30_MOUSE	39.85	12	NA	1980	2540
KKKKTKKIKEKYIDQ	P11499|HS90B_MOUSE	48	15	NA	NA	269
KKKKYEPPVPTRVGKK	P62192|PRS4_MOUSE	47.95	16	1550	NA	1040
KKLQDEIDAALPNKAP	Q64464|CP3AD_MOUSE	36.68	16	475	NA	404
KKLQDEIDAALPNKAPAT	Q64464|CP3AD_MOUSE	49.28	18	714	NA	874
KKPAAAAGAKKAKS(+79.97)PKKAKATK	P43274|H14_MOUSE	25.74	29	NA	NA	208
KKPAAAKK	Q99K28|ARFG2_MOUSE	25.66	8	NA	NA	309
KKPAKAAAPRKKP	P43275|H11_MOUSE	40.62	13	NA	1000	264
KKPAVSKKTSKSPKKPKVVKAKKVAKS(	P43275|H11_MOUSE	48.67	32	NA	NA	2790
KKPFVYTQGQAVLNR	Q8VCT3|AMPB_MOUSE	49.42	15	907	NA	1070
KKPFVYTQGQAVLNRA	Q8VCT3|AMPB_MOUSE	49.08	16	483	NA	483
KKPKKAAGTATAKKSTKKTPKKAKKPA	P43274|H14_MOUSE	48.95	27	NA	NA	31800
KKPKKPAVSKKT(+79.97)SK	P43275|H11_MOUSE	30.01	14	NA	NA	501
KKPVPIPK	A2ASS6|TITIN_MOUSE	29.55	8	NA	NA	389
KKSPVYKNPTPGSSELA	Q99PG0|AAAD_MOUSE	40.79	17	788	NA	536
KKTKNKKKKNKK	Q3UZ39|LRRF1_MOUSE	45.27	12	NA	NA	4110
KKTKNKKKKNKKK	Q3UZ39|LRRF1_MOUSE	47.74	13	NA	NA	2310
KKVAKSPKKAKAAAKPKKAAKSPAK	P43276|H15_MOUSE	41	25	NA	NA	1120
KKVAKSPKKAKVTKPKKVKS	P15864|H12_MOUSE	49.94	20	380	NA	935
KKVAKSPKKAKVTKPKKVKSASKAVKPK	P15864|H12_MOUSE	48.94	28	NA	1830	537
KKVHPKGKKPKKAKP	P47911|RL6_MOUSE	48.95	15	NA	NA	3610
KKVTFSSGYVNLSPEN	P06684|CO5_MOUSE	49.49	16	544	NA	220
KLFQTQPQPANANAV	P29699|FETUA_MOUSE	46.92	15	NA	NA	109
KLLEAKGPVTDVAYSHD	O88342|WDR1_MOUSE	49.88	17	3720	NA	1890
KLPKSAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	27.78	23	NA	NA	219
KLPSPLIM(+15.99)SPGPIYAVDGD	Q8VHF2|CDHR5_MOUSE	49.91	19	347	NA	210
KLPSPLIM(+15.99)SPGPIYAVDGDQ	Q8VHF2|CDHR5_MOUSE	49.95	20	197	NA	114
KLPSPLIMSPGPIYAVDGD	Q8VHF2|CDHR5_MOUSE	48.9	19	NA	NA	178
KLPSPLIMSPGPIYAVDGDQ	Q8VHF2|CDHR5_MOUSE	48.84	20	NA	NA	175
KLQDEIDAALPNKAP	Q64464|CP3AD_MOUSE	43.75	15	2430	NA	2020
KLQDEIDAALPNKAPA	Q64464|CP3AD_MOUSE	49.36	16	3840	NA	2780
KLQDEIDAALPNKAPAT	Q64464|CP3AD_MOUSE	49.76	17	4010	NA	3770
KLQDQGPDVLLAKVS	A6X935|ITIH4_MOUSE	47.58	15	NA	NA	332
KLTGM(+15.99)AFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MO	49.91	18	12700	93.4	9300
KLTGMAFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MO	49.92	18	3860	NA	9710
KNLDYVATSIHEAVTK	P05201|AATC_MOUSE	49.86	16	18500	514	13500
KNNSFYGPEVKIEK	Q00519|XDH_MOUSE	48.47	14	1130	NA	1110
KNNSFYGPEVKIEKG	Q00519|XDH_MOUSE	49.39	15	19900	162	12600
KNNSFYGPEVKIEKGDL	Q00519|XDH_MOUSE	49.21	17	2100	NA	1230
KPAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.94	18	5370	4520	5380
KPAAAGVKKVAKSPKKAKA	P43276|H15_MOUSE	48.94	19	NA	572	993
KPAQTPVLTSPAPADSTPG	P54728|RD23B_MOUSE	49.91	19	366	NA	815
KPAVSKKTSKSPKKPKVVKAKKVAK	P43275|H11_MOUSE	49.95	25	1520	NA	456
KPFQNPVPNQSP	P16382|IL4RA_MOUSE	33.46	12	288	NA	769
KPFTIEDIEVAPPKAHEVRIK	P00329|ADH1_MOUSE	49.94	21	504	NA	266
KPIDYYTETKILQERA	Q9R1J0|NSDHL_MOUSE	49.84	16	1380	NA	1120
KPIDYYTETKILQERAV	Q9R1J0|NSDHL_MOUSE	49.91	17	558	NA	374
KPKAAKPKKTAAKK	P43274|H14_MOUSE	37.9	14	NA	NA	214
KPKAAKPKTSKPKAAKPK	P43274|H14_MOUSE	48.84	18	NA	861	1090
KPKAAKPKTSKPKAAKPKKTAA	P43274|H14_MOUSE	44.2	22	NA	NA	776
KPKAKKTG	P43276|H15_MOUSE	35.25	8	NA	NA	685
KPKAKKTGAAKAKKPA	P43276|H15_MOUSE	43.15	16	1170	NA	1080
KPKASKAKVTKPKTPAKPK	P43275|H11_MOUSE	45.09	19	NA	NA	447
KPKASKAKVTKPKTPAKPKKA	P43275|H11_MOUSE	38.49	21	NA	1080	1760

KPKASKPKA	P43277|H13_MOUSE	29.3	9	1910	NA	475
KPKAVKS(+79.97)KAS(+79.97)K	P43276|H15_MOUSE	25.42	11	NA	NA	119
KPKFQEHIIQAPKPVEAIKRPSP	Q9D1P4|CHRD1_MOUSE	49.89	23	129	NA	189
KPKGQLPDYTSPVVLPYSR	P32233|DRG1_MOUSE	49.58	19	121	NA	270
KPKKAKPH	P47911|RL6_MOUSE	40.93	8	395	NA	341
KPKQDSQFEFKGPQAAQEQD	Q6RHR9|MAGI1_MOUSE	49.92	20	1580	NA	1320
KPKQDSQFEFKGPQAAQEQDF	Q6RHR9|MAGI1_MOUSE	49.19	21	461	NA	558
KPKTAKPKAA	P43276|H15_MOUSE	27.76	10	NA	NA	471
KPKTPAKPKKAAP	P43275|H11_MOUSE	42.7	13	NA	149	376
KPKTSKPKAAKPKKTAAKK	P43274|H14_MOUSE	48.71	19	NA	NA	975
KPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.91	19	193	834	602
KPLSVFKGPLLHISPA	Q9CWP6|MSPD2_MOUSE	29.59	16	956	NA	1230
KPPLGSLRFAPPQPAEPWS	Q8VCT4|EST1D_MOUSE:Q91WU0|EST1	49.79	19	2000	NA	3760
KPPSYNVATTLPSYD	Q8R0W6|NFIP1_MOUSE	43.91	15	2680	54.8	3050
KPPSYNVATTLPSYDE	Q8R0W6|NFIP1_MOUSE	49.04	16	24400	922	25000
KPRGEFHTPVTVAGPH	Q8JZQ5|AOC1_MOUSE	49.79	16	28900	706	21900
KPSGYNPPISILGIL	Q61739|ITA6_MOUSE	36.81	15	1700	NA	1590
KPSGYNPPISILGILE	Q61739|ITA6_MOUSE	41.28	16	860	NA	290
KPSPIYISSYSSPARE	Q68FH0|PKP4_MOUSE	45.16	16	615	NA	56.2
KPSPIYISSYSSPAREQ	Q68FH0|PKP4_MOUSE	49.61	17	4120	NA	3220
KPSPIYISSYSSPAREQN	Q68FH0|PKP4_MOUSE	47.58	18	1370	NA	1050
KPSTFAYPAPLEVP	Q3TXS7|PSMD1_MOUSE	43.47	14	655	NA	312
KPSTFAYPAPLEVPK	Q3TXS7|PSMD1_MOUSE	49.78	15	3110	NA	2320
KPSTFAYPAPLEVPKE	Q3TXS7|PSMD1_MOUSE	49.93	16	678	NA	440
KPTVTVVSPLPNDS	Q8VD58|EVI2B_MOUSE	41.65	14	284	NA	118
KPTVTVVSPLPNDSIN	Q8VD58|EVI2B_MOUSE	49.21	16	480	96.6	165
KPTVTVVSPLPNDSINPQ	Q8VD58|EVI2B_MOUSE	49.94	18	2890	905	1680
KPTVTVVSPLPNDSINPQP	Q8VD58|EVI2B_MOUSE	49.94	19	6290	1700	3750
KPVKASKPKKAKTVKPKAKSSAKRA	P10922|H10_MOUSE	32.21	25	NA	NA	1150
KPVPAAPVPSPVAPAPVPSRRNPPG	P97825|JUPI1_MOUSE	49.94	25	807	NA	423
KPVPITSPAVSKVTST	Q8CI51|PDLI5_MOUSE	48.42	16	149	NA	436
KPVSQM(+15.99)RMATPLLM(+15.99)RP	P04441|HG2A_MOUSE	42.79	17	14700	NA	226000
KPVSQM(+15.99)RMATPLLMRPM	P04441|HG2A_MOUSE	49.16	17	20500	NA	179000
KPVSQMRM(+15.99)ATPLLMRPM(+15.9	P04441|HG2A_MOUSE	47.76	17	380000	NA	386000
KPVSQMRMATPLLMRP	P04441|HG2A_MOUSE	45.52	16	NA	NA	17700
KPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	49.04	17	17600	NA	236000
KRKFVMKPPQVVRVGTK	Q99L45|IF2B_MOUSE	49.9	17	NA	NA	223
KRKKKSYTTPKKN	P62983|RS27A_MOUSE	48.84	13	NA	3140	2530
KRKKKSYTTPKKNKHKR	P62983|RS27A_MOUSE	48.95	17	NA	3120	6300
KRKKKSYTTPKKNKHKRK	P62983|RS27A_MOUSE	48.95	18	NA	61400	23900
KRKKKSYTTPKKNKHKRKKVKLAVLKY	P62983|RS27A_MOUSE	49.94	27	NA	1850	13700
KRKKKSYTTPKKNKHKRKKVKLAVLKYY	P62983|RS27A_MOUSE	49.64	29	NA	7200	11300
KRKKKSYTTPKKNKHKRKKVKLAVLKYY	P62983|RS27A_MOUSE	48.95	31	NA	NA	1690
KRNPRQINWTVLYRRKHKKGQSEEIQKI	Q8BP67|RL24_MOUSE	48.78	29	NA	NA	1250
KRQQLYIASRSAVAQ	Q62177|SEM3B_MOUSE	38.33	15	1090	NA	1090
KRSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2I	49.95	22	6810	8360	1960
KRYMAPEVLDETIN	Q61271|ACV1B_MOUSE	47.99	14	357	NA	205
KSFVGPTPAPAPAPR	Q501J7|PHAR4_MOUSE	38.3	15	NA	NA	190
KSFVQNYPVVSIED	P17182|ENOA_MOUSE	49.5	14	470	NA	242
KSFVQNYPVVSIEDP	P17182|ENOA_MOUSE	49.13	15	98.5	NA	451
KSFVQNYPVVSIEDPF	P17182|ENOA_MOUSE	49.94	16	19600	411	18700
KSFVQNYPVVSIEDPFD	P17182|ENOA_MOUSE	49.92	17	5750	NA	3830
KSGGKAKKKKWSKGKVR	P62852|RS25_MOUSE	48.94	17	NA	NA	2360
KSKTVYEGPFASRSLS	Q60680|IKKA_MOUSE	44.07	16	1180	NA	761
KSKTVYEGPFASRSLSD	Q60680|IKKA_MOUSE	47.2	17	NA	NA	905
KSPAKAKAVKPKASKA	P43275|H11_MOUSE	26.31	16	NA	NA	166
KSPAKAKTVKPKAAKPKTSKPKAAKPK	P43274|H14_MOUSE	40.64	27	NA	NA	581
KSPKKVKAAKP	P43277|H13_MOUSE	37.29	11	NA	NA	95.5
KSPVYKNPTPGSSEL	Q99PG0|AAAD_MOUSE	49.58	15	6600	NA	761
KSTKKTPKKAKKPA	P43274|H14_MOUSE	49.94	14	6320	2030	2300
KSTKKTPKKAKKPAA	P43274|H14_MOUSE	49.87	15	420	1330	2010
KTHDLYIQSHISENRE	Q9R111|GUAD_MOUSE	49.94	16	1570	NA	1190
KTITYESSQVDPGADL	Q9WV92|E41L3_MOUSE	48.78	16	5320	210	4760
KTKNSEEFAAAMSRYELK	E9Q414|APOB_MOUSE	47.18	18	NA	NA	74.9
KTPEIVAPESAHAAF	Q8R0X7|SGPL1_MOUSE	49.75	15	635	NA	226
KTPEIVAPESAHAAFD	Q8R0X7|SGPL1_MOUSE	46.03	16	397	NA	237
KTPEIVAPESAHAAFDK	Q8R0X7|SGPL1_MOUSE	49.48	17	339	NA	329
KTPESFLGPNAALVDL	Q80VP1|EPN1_MOUSE	45.09	16	454	NA	419
KTPESFLGPNAALVDLD	Q80VP1|EPN1_MOUSE	49.58	17	11200	NA	9480
KTPESFLGPNAALVDLDS	Q80VP1|EPN1_MOUSE	49.69	18	1780	NA	1950
KTPIETTAPTAAIPGTN	E9Q7P9|CDHR2_MOUSE	48.79	17	208	NA	213
KTPKKAKKPA	P15864|H12_MOUSE:P43276|H15_MOU	49.09	10	1920	NA	1010
KTQYISPNLNPN	P97499|TEP1_MOUSE	46.7	12	4790	NA	5130
KTQYISPNLNPND	P97499|TEP1_MOUSE	48.31	13	2910	111	8450
KTQYISPNLNPNDV	P97499|TEP1_MOUSE	48.87	14	1700	NA	1280
KTQYISPNLNPNDVT	P97499|TEP1_MOUSE	49.78	15	2240	NA	1610
KTSKSPKKPKVVKAKKVAK	P43275|H11_MOUSE	49.95	19	3840	3710	2830
KTVKKTPKKAKKPAAAGVKK	P43276|H15_MOUSE	49	20	660	533	277
KTVKKTPKKAKKPAAAGVKKVAKSPKKA	P43276|H15_MOUSE	49.95	29	1680	696	1660
KVAKSPAKAKAVKPKA	P43275|H11_MOUSE	49.77	16	1380	NA	3320
KVAKSPKKAK	P15864|H12_MOUSE:P43276|H15_MOU	42.43	10	846	243	471

KVAKSPKKAKAAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	47.05	27	NA	1310	1750
KVEYHFLSPYVSPR	Q62351|TFR1_MOUSE	41.35	14	408	NA	497
KVEYHFLSPYVSPRE	Q62351|TFR1_MOUSE	46.16	15	356	NA	241
KVEYHFLSPYVSPRESP	Q62351|TFR1_MOUSE	49.49	17	478	NA	257
KVGINYQPPTVVPGGDL	P68369|TBA1A_MOUSE:P68373|TBA1C_	32.52	17	NA	NA	284
KVIPELNGKLTGM(+15.99)AFRVPTPNVS	P16858|G3P_MOUSE	49.93	26	783	NA	2560
KVIPELNGKLTGMAFRVPTPNVSVVD	P16858|G3P_MOUSE	48.94	26	2260	NA	5230
KVIPKSKFVLVKF	P57759|ERP29_MOUSE	49.82	13	576	NA	125
KVKPVKASKPKKA	P10922|H10_MOUSE	29.34	13	NA	NA	96.7
KVLPTYDASKVTASGPG	Q80X90|FLNB_MOUSE	49.51	17	2980	NA	2360
KVTFNSALAQKEA	O89051|ITM2B_MOUSE	46.58	13	802	NA	350
KVTFNSALAQKEAKK	O89051|ITM2B_MOUSE	49.81	15	26000	513	20700
KVYIYHSSSGGLL	Q62470|ITA3_MOUSE	49.12	13	314	NA	345
KWKALYTDPKSSETA	Q920A5|RISC_MOUSE	45.6	15	NA	NA	163
KWKALYTDPKSSETAAF	Q920A5|RISC_MOUSE	47.7	17	NA	NA	638
KYNFVTPLTHM(+15.99)VVTKP	A6X935|ITIH4_MOUSE	49.62	16	4020	NA	3160
KYNFVTPLTHMVVT	A6X935|ITIH4_MOUSE	48.86	14	25.8	NA	99.3
KYTYGKPVPGHVK	P28665|MUG1_MOUSE	48.79	13	45400	1290	26400
L(+42.01)RKSGKNAKITIRRKKKVQIPVS	P39447|ZO1_MOUSE	46.73	23	NA	NA	912
LALIYGTPRAATVKA	Q9DBC7|KAP0_MOUSE:P12849|KAP1_M	48.7	15	22300	NA	20800
LALIYGTPRAATVKAK	Q9DBC7|KAP0_MOUSE:P12849|KAP1_M	49.67	16	5160	NA	4430
LALM(+15.99)YNTPRAATIIA	P12367|KAP2_MOUSE	49.11	15	1180	NA	664
LANM(+15.99)ISEPRISYGND	P12023|A4_MOUSE	41.15	15	NA	NA	120
LAPFFTPNAAPA	Q80TA9|EPG5_MOUSE	37.39	12	NA	NA	329
LAPM(+15.99)YYRGAQAAIVV	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	41.61	15	447	NA	370
LAPMYYRGAQAAIVV	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	41.21	15	150	NA	183
LAPMYYRGAQAAIVVY	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	27.88	16	NA	NA	173
LAPMYYRGAQAAIVVYD	P61021|RAB5B_MOUSE:Q9CQD1|RAB5	45.94	17	326	NA	3210
LAQVYGAPQLQVEK	P27808|MGAT1_MOUSE	48.79	14	319	NA	196
LAQVYGAPQLQVEKV	P27808|MGAT1_MOUSE	49.78	15	465	NA	245
LAVAGAPIALSAVG	Q8VC49|IF27B_MOUSE	47.99	14	1240	NA	954
LAVAGAPVALSAVG	Q8VC49|IF27B_MOUSE	37.95	14	307	NA	200
LDARSYAAAVANRAKGGG	Q8K296|MTMR3_MOUSE	45.14	18	NA	NA	185
LDARSYTAAVANRAK	Q91XS1|MTMR4_MOUSE	46.46	15	503	NA	912
LDARSYTAAVANRAKG	Q91XS1|MTMR4_MOUSE	38.59	16	NA	NA	105
LDARSYTAAVANRAKGGG	Q91XS1|MTMR4_MOUSE	49.45	18	6650	NA	5590
LDEFYSDPHAVAGAL	Q3UIA2|RHG17_MOUSE	38.03	15	89.5	NA	144
LDHYIYEAEEANLGPG	P02469|LAMB1_MOUSE	49.26	16	2460	NA	1040
LDIDSEPVAARSTSI	P53657|KPYR_MOUSE	47.63	15	629	NA	611
LDIDSEPVAARSTSII	P53657|KPYR_MOUSE	49.29	16	823	NA	815
LDIKSFITSIANKN	Q8CHR6|DPYD_MOUSE	49.38	14	347	NA	200
LDIKSFITSIANKNYYG	Q8CHR6|DPYD_MOUSE	49.87	17	91.6	NA	379
LDLLDLAPEPRYAHIPV	Q09200|B4GN1_MOUSE	29.92	17	498	NA	257
LDLSQYHAVAVRRVLN	Q8BND5|QSOX1_MOUSE	30.76	16	NA	NA	199
LDQLFSGPLPGRLP	Q60805|MERTK_MOUSE	47.53	14	5790	NA	3390
LDQLFSGPLPGRLPV	Q60805|MERTK_MOUSE	48.82	15	21500	NA	12900
LDRDSLVHSSPHVALSHVD	Q9WV91|FPRP_MOUSE	49.89	19	527	NA	993
LDRDSLVHSSPHVALSHVDT	Q9WV91|FPRP_MOUSE	48.85	20	592	NA	128
LDRYYTPTISRER	Q9R1P3|PSB2_MOUSE	49.19	13	1860	NA	2050
LDRYYTPTISRERA	Q9R1P3|PSB2_MOUSE	39.44	14	5080	NA	6390
LDYHFVTPLTSLT	Q61702|ITIH1_MOUSE	39.33	13	317	NA	257
LDYWTYPGSLTTPPL	P00920|CAH2_MOUSE	38.94	15	NA	NA	119
LEAYYSSPQDLPYPDPA	Q61316|HSP74_MOUSE	49.49	17	663	NA	393
LEDFYGSPIPSVSLKL	Q9Z0M6|AGRE5_MOUSE	49.64	16	1210	NA	384
LEEQLGPVAEETR	P08226|APOE_MOUSE	42.59	13	3480	102	1690
LEEQLGPVAEETRA	P08226|APOE_MOUSE	44.96	14	2720	120	2540
LEEQLGPVAEETRAR	P08226|APOE_MOUSE	48.42	15	2980	NA	1230
LEISYTGSRPASNM(+15.99)	P28666|MUG2_MOUSE:P28665|MUG1_M	45.71	14	1210	NA	219
LEISYTGSRPASNM(+15.99)V	P28666|MUG2_MOUSE:P28665|MUG1_M	48.69	15	11200	NA	2060
LEISYTGSRPASNMV	P28666|MUG2_MOUSE:P28665|MUG1_M	49.38	15	3300	NA	2860
LERESKVVVPPLPGKAF	O70492|SNX3_MOUSE	42.09	17	227	NA	126
LERFYDPM(+15.99)AGSVFL	P06795|MDR1B_MOUSE:P21447|MDR1A	49.19	14	587	NA	130
LERKLKKERKKEEKKRLR	Q9CXL3|CG050_MOUSE	30.54	18	NA	NA	4790
LEVVTDPTTNAG	Q9R100|CAD17_MOUSE	42.88	12	520	NA	340
LEVVTDPTTNAGY	Q9R100|CAD17_MOUSE	46.64	13	145	NA	92.1
LEVVTDPTTNAGYV	Q9R100|CAD17_MOUSE	49.3	14	1390	NA	980
LEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	45.42	15	9360	142	7570
LFLTAAAQPLKAKTD	Q8VC30|TKFC_MOUSE	49.29	15	NA	NA	222
LFTQYFQSM(+15.99)TDYGKD	P09813|APOA2_MOUSE	48.52	15	861	NA	361
LGFPYEGPAPLEAIANG	Q8R4G6|MGT5A_MOUSE	49.66	17	1440	NA	695
LGVAYEAPSLATGYG	P99026|PSB4_MOUSE	47.32	15	810	NA	807
LGYAVYETPTAHNGAKNPR	Q9QZ06|TOLIP_MOUSE	49.88	19	1700	NA	2500
LIEVSSPITLQAL	E9Q414|APOB_MOUSE	44.92	13	NA	NA	62
LIEVSSPITLQALVQ	E9Q414|APOB_MOUSE	49.89	15	144	NA	212
LIIQWNGPESNRM(+15.99)E	Q62468|VILI_MOUSE	49.09	14	457	NA	115
LIRLPYTASSGLM(+15.99)APRE	Q9R1Q9|VAS1_MOUSE	49.45	17	426	NA	338
LIRLPYTASSGLM(+15.99)APREV	Q9R1Q9|VAS1_MOUSE	49.93	18	NA	NA	112
LISNHEQLPILG	P04441|HG2A_MOUSE	28.9	12	NA	NA	137
LIVSHDYKGSTSHSLP	E9Q414|APOB_MOUSE	29.29	16	NA	NA	673
LIVSHDYKGSTSHSLPY	E9Q414|APOB_MOUSE	49.86	17	715	NA	858
LIVSHDYKGSTSHSLPYE	E9Q414|APOB_MOUSE	44.72	18	676	NA	822

LIYGTPRAATVKA	Q9DBC7|KAP0_MOUSE:P12849|KAP1_M	47.26	13	4360	NA	3640
LKRSYSSPDITQALQ	Q80U87|UBP8_MOUSE	49.73	15	3690	NA	6540
LKRSYSSPDITQALQE	Q80U87|UBP8_MOUSE	49.77	16	4360	NA	3890
LKYHFVTPLTSMVVTKP	Q61704|ITIH3_MOUSE	42.35	17	NA	NA	62.2
LKYNFVTPLTHM(+15.99)VVT	A6X935|ITIH4_MOUSE	49.87	15	1410	NA	719
LKYNFVTPLTHMVVT	A6X935|ITIH4_MOUSE	49.81	15	307	NA	803
LKYSIDPSVVNISDEM(+15.99)	Q8BTY2|S4A7_MOUSE	49.05	16	464	NA	175
LLKDFRTPLSHAANR	Q08ED0|B2L15_MOUSE	49.64	15	1470	NA	1460
LLLLLLLLLLL	Q80YA8|CRUM2_MOUSE:Q8BLH5|TSP5	25.99	12	NA	NA	72.9
LLPPYDDATAVPSTAKEPPPP	Q91XQ6|LAP4B_MOUSE	49.94	21	5140	NA	7510
LLTQYSTPEGSSVPI	E9Q414|APOB_MOUSE	48.47	15	1160	NA	10400
LLVVNHPDSSSTVE	P52430|PON1_MOUSE	46.36	14	109	NA	504
LM(+15.99)PFRQPITTIVGKP	Q80W94|MOGT2_MOUSE	32.79	15	180	NA	97.8
LMPFRQPITTIVGKP	Q80W94|MOGT2_MOUSE	28.52	15	NA	NA	137
LMPFRQPITTIVGKPI	Q80W94|MOGT2_MOUSE	46.14	16	NA	NA	127
LNFRNPAVQEEIKE	Q91WV7|SLC31_MOUSE	42.14	14	457	NA	136
LNIYVPAHAHEGS	Q8BK48|EST2E_MOUSE	36.2	13	412	NA	312
LNIYVPAHAHEGSNLP	Q8BK48|EST2E_MOUSE	48.06	16	5460	NA	2710
LNLAYIGAVPHSGIE	P48441|IDUA_MOUSE	37.82	15	442	NA	286
LNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	48.92	14	872	NA	1180
LNSVFVAPAVTPVKG	P70158|ASM3A_MOUSE	49.13	15	562	NA	629
LNVLRIINEPTAAAIAYG	P17879|HS71B_MOUSE:P16627|HS71L_	49.91	18	469	NA	427
LNVQFSSPLPGEAVK	Q80X90|FLNB_MOUSE	49.22	15	190	NA	206
LPADPPASVVVGPVVVPRGLS	P29699|FETUA_MOUSE	49.88	21	105	NA	197
LPDDINVYATTAANPKE	O89017|LGMN_MOUSE	44.51	17	766	NA	231
LPDDINVYATTAANPKES	O89017|LGMN_MOUSE	49.94	18	763	NA	568
LPDDINVYATTAANPKESS	O89017|LGMN_MOUSE	49.94	19	5130	179	3320
LPDDINVYATTAANPKESSY	O89017|LGMN_MOUSE	49.94	20	285	NA	170
LPDIYGWPVASDN	Q61391|NEP_MOUSE	44.95	13	877	NA	260
LPDIYGWPVASDNWD	Q61391|NEP_MOUSE	49.89	15	658	NA	202
LPDIYGWPVASDNWDQ	Q61391|NEP_MOUSE	49.8	16	3380	NA	1140
LPDYSAPNPIK	Q8CFG0|SULF2_MOUSE	42.07	11	1400	NA	1600
LPDYSAPNPIKV	Q8CFG0|SULF2_MOUSE	47.76	12	NA	NA	46.1
LPDYSAPNPIKVTH	Q8CFG0|SULF2_MOUSE	49.82	14	22700	849	30000
LPDYSAPNPIKVTHR	Q8CFG0|SULF2_MOUSE	49.87	15	23700	1080	32500
LPETFRRPQIDPAVEG	Q7TN29|SMAP2_MOUSE	25.66	16	NA	NA	5630
LPFGAYTNPFATPAQ	Q80WC7|AGFG2_MOUSE	47.5	15	1070	NA	998
LPFGAYTNPFATPAQAQ	Q80WC7|AGFG2_MOUSE	47.88	17	2350	NA	3080
LPGPSQPRQYNNPIGLYSAET	Q9JKS4|LDB3_MOUSE	49.94	21	13700	NA	12000
LPGPSQPRQYNNPIGLYSAETL	Q9JKS4|LDB3_MOUSE	49.53	22	507	NA	474
LPIPERYLSPDATVSTE	Q640N1|AEBP1_MOUSE	49.81	17	2960	NA	1590
LPKSAKPVSQM(+15.99)RM(+15.99)ATP	P04441|HG2A_MOUSE	38.26	22	NA	NA	688
LPKSAKPVSQM(+15.99)RMATPLLMRPM	P04441|HG2A_MOUSE	46.72	22	57.2	NA	4100
LPKSAKPVSQM(+15.99)RMATPLLMRPM	P04441|HG2A_MOUSE	46.87	22	2620	NA	4040
LPKSAKPVSQMRM(+15.99)ATPLLM(+15	P04441|HG2A_MOUSE	42.74	22	NA	NA	2910
LPKSAKPVSQMRM(+15.99)ATPLLMRPM	P04441|HG2A_MOUSE	49.11	22	2620	NA	3960
LPKSAKPVSQMRMATPLLM(+15.99)RPM	P04441|HG2A_MOUSE	49.85	22	1200	NA	5270
LPKSAKPVSQMRMATPLLM(+15.99)RPM	P04441|HG2A_MOUSE	45.05	22	1350	NA	4970
LPKSAKPVSQMRMATPLLMRP	P04441|HG2A_MOUSE	48.87	21	NA	NA	355
LPKSAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	48.93	22	NA	NA	4440
LPKSAKPVSQMRMATPLLMRPM(+15.99	P04441|HG2A_MOUSE	49.94	22	1200	NA	5270
LPLPEQAQEQAQEQAQEQVQPKPLES	P06728|APOA4_MOUSE	49.95	26	306	NA	80.8
LPLRSQFKGPAPRETKD	Q9JM76|ARPC3_MOUSE	37.43	17	1600	NA	3000
LPLRSQFKGPAPRETKDT	Q9JM76|ARPC3_MOUSE	43.99	18	1970	NA	5190
LPPASLPESTPVPSSSPP	Q6PB44|PTN23_MOUSE	49.74	18	1440	NA	4640
LPPASLPESTPVPSSSPPP	Q6PB44|PTN23_MOUSE	49.91	19	16800	NA	23600
LPPHVYSTPQPSLPP	Q3UPH1|PRRC1_MOUSE	49.78	15	175000	2250	172000
LPPHVYSTPQPSLPPVQ	Q3UPH1|PRRC1_MOUSE	49.78	17	53500	703	59200
LPPHVYSTPQPSLPPVQP	Q3UPH1|PRRC1_MOUSE	49.71	18	13500	NA	16900
LPPHVYSTPQPSLPPVQPS	Q3UPH1|PRRC1_MOUSE	49.93	19	34700	NA	42300
LPPHVYSTPQPSLPPVQPSAPPP	Q3UPH1|PRRC1_MOUSE	49.95	23	18800	NA	25700
LPPVSPPKAALSVDE	Q6NZJ6|IF4G1_MOUSE	49.84	15	3660	NA	2230
LPPYDDATAVPSTA	Q91XQ6|LAP4B_MOUSE	27.81	14	2330	NA	1300
LPPYDDATAVPSTAK	Q91XQ6|LAP4B_MOUSE	42.34	15	731	NA	940
LPPYDDATAVPSTAKEPPP	Q91XQ6|LAP4B_MOUSE	49.93	19	179000	2600	185000
LPPYDDATAVPSTAKEPPPP	Q91XQ6|LAP4B_MOUSE	49.93	20	951000	19800	927000
LPPYDDATAVPSTAKEPPPPY	Q91XQ6|LAP4B_MOUSE	49.84	21	349	NA	81.6
LPQDPTFHTPLDLYA	Q07797|LG3BP_MOUSE	49.71	15	1160	NA	570
LPQDPTFHTPLDLYAYAR	Q07797|LG3BP_MOUSE	49.93	18	96600	439	47800
LPQEKYVTSAPM(+15.99)PEPG	P01872|IGHM_MOUSE	49.86	16	17900	201	8160
LPQEKYVTSAPM(+15.99)PEPGAPG	P01872|IGHM_MOUSE	49.94	19	27100	641	13300
LPQEKYVTSAPMPEPGAPG	P01872|IGHM_MOUSE	49.92	19	6830	NA	12100
LPQLIEVSSPITLQAL	E9Q414|APOB_MOUSE	49.56	16	364	NA	279
LPSNSVYAGTVPSRVPA	Q8VCF0|MAVS_MOUSE	46.24	17	728	NA	1060
LPSNSVYAGTVPSRVPAS	Q8VCF0|MAVS_MOUSE	46.84	18	NA	NA	92.2
LPSPLIM(+15.99)SPGPIYAVDG	Q8VHF2|CDHR5_MOUSE	49.93	17	9110	63.4	7480
LPSPLIM(+15.99)SPGPIYAVDGDQ	Q8VHF2|CDHR5_MOUSE	49.94	19	7620	NA	4930
LPSPLIMSPGPIYAVDG	Q8VHF2|CDHR5_MOUSE	49.76	17	2480	NA	4120
LPSPLIMSPGPIYAVDGD	Q8VHF2|CDHR5_MOUSE	49.94	18	5730	NA	10100
LPSPLIMSPGPIYAVDGDQ	Q8VHF2|CDHR5_MOUSE	49.94	19	2930	NA	4740
LPSQVPFETRGPHINNSVH	Q8K296|MTMR3_MOUSE	49.59	19	750	NA	1130

LPSQVPFETRGPHINNSVHM(+15.99)	Q8K296|MTMR3_MOUSE	35.93	20	342	NA	291
LPTTFQGATASTSYG	Q9JJZ4|UB2J1_MOUSE	41.35	15	1130	NA	524
LPVKWTAPEAIRT	Q922K9|FRK_MOUSE	49.2	13	416	NA	737
LPVKWTAPEAIRTN	Q922K9|FRK_MOUSE	49.09	14	1370	NA	1350
LPVKWTAPEAIRTNK	Q922K9|FRK_MOUSE	49.5	15	3390	NA	2280
LPVKWTAPEAIRTNKF	Q922K9|FRK_MOUSE	49.74	16	819	NA	756
LPVNHRPFSAPHSSRDQLPPP	Q60805|MERTK_MOUSE	47.61	21	593	NA	1070
LPYKPSTVVIPR	Q9Z0S5|CLD15_MOUSE	37.07	12	131	NA	28.5
LPYKSPGINVD	Q9JHJ8|ICOSL_MOUSE	36.52	11	364	NA	442
LPYKSPGINVDS	Q9JHJ8|ICOSL_MOUSE	47.8	12	881	NA	273
LPYKSPGINVDSS	Q9JHJ8|ICOSL_MOUSE	49.19	13	1960	NA	1390
LPYSFLTFPYVEEAIK	P70274|SEPP1_MOUSE	41.46	16	743	NA	715
LPYVQYFGGVSALSKQQ	P15535|B4GT1_MOUSE	44.11	17	420	NA	216
LPYVSWQEKQPEASISQ	E9PYK3|PARP4_MOUSE	49.93	17	567	NA	426
LPYVSWQEKQPEASISQTE	E9PYK3|PARP4_MOUSE	49.94	19	2240	NA	2250
LQDEIDAALPNKAP	Q64464|CP3AD_MOUSE	48.9	14	10400	79.4	6980
LQDEIDAALPNKAPA	Q64464|CP3AD_MOUSE	48.31	15	12900	171	8150
LQDEIDEALPNKAPP	Q64459|CP3AB_MOUSE	48.47	15	700	NA	318
LQEPQPAGSQPLLANSPL	Q8R1U2|CGRE1_MOUSE	49.84	18	333	NA	1170
LQEPQPAGSQPLLANSPLQ	Q8R1U2|CGRE1_MOUSE	48.63	19	NA	NA	63
LQKQPYFGAVVGRVAN	Q8K157|GALM_MOUSE	49.63	16	264	NA	166
LQKQPYFGAVVGRVANR	Q8K157|GALM_MOUSE	49.86	17	2330	NA	2070
LQKTQYISPNLNPN	P97499|TEP1_MOUSE	49.62	14	2530	NA	1660
LQKTQYISPNLNPNDV	P97499|TEP1_MOUSE	44.25	16	NA	NA	591
LQSINFLGGQPAAAPYPG	Q8K419|LEG4_MOUSE	46.69	18	684	NA	1070
LQSTDYGNFLANEASPL	P51863|VA0D1_MOUSE	49.82	17	418	NA	848
LRDMYSKSSAAM(+15.99)STY	Q05020|APOC2_MOUSE	27.24	15	326	NA	547
LRDMYSKSSAAMSTYA	Q05020|APOC2_MOUSE	28.49	16	386	NA	548
LRDNYRFAHTNIESLV	P27773|PDIA3_MOUSE	32.12	16	1540	NA	1230
LRGGAKKRKKKSYT(+79.97)TPKKNKHK	P62983|RS27A_MOUSE	25.4	26	NA	NA	130
LRHAFSPVASVESAS	P29699|FETUA_MOUSE	48.56	15	75	NA	142
LRKFYKGKKYKPLDLRPKKTR	Q6ZWV7|RL35_MOUSE	49.95	21	199	225	365
LRNYEYYASHVPESVK	Q9Z0S1|BPNT1_MOUSE	49.72	16	3500	NA	3800
LRPKKTRAM(+15.99)RRRLTKHEEKLKT	Q6ZWV7|RL35_MOUSE	48.95	30	NA	NA	2160
LRPLVKPKIVKKRTKKFIRHQSDR	P17932|RL32P_MOUSE:P62911|RL32_M	48.95	24	NA	1260	1080
LRPVTIFGPIADVAREK	P39447|ZO1_MOUSE	49.91	17	130	NA	141
LRRQPKYPRKSAPRRNKLDHYAIIKF	P62751|RL23A_MOUSE	49.95	26	8320	629	3370
LSDIYQAPSADSADH	P26361|CFTR_MOUSE	46.83	15	2360	NA	2150
LSDIYQAPSADSADHL	P26361|CFTR_MOUSE	47.07	16	1280	NA	2390
LSKRNPRQINWTVLYRRKHKKG	Q8BP67|RL24_MOUSE	38.85	22	NA	NA	169
LSKRNPRQINWTVLYRRKHKKGQSEEIC	Q8BP67|RL24_MOUSE	27.52	31	NA	NA	1120
LSLAEAKPQVLSSQEE	Q91X58|ZFN2B_MOUSE	44.24	16	166	NA	68.1
LSLLYNVPAVAEEIQ	P12023|A4_MOUSE	48.78	15	10300	213	4910
LSLLYNVPAVAEEIQD	P12023|A4_MOUSE	49.55	16	6990	160	5470
LSLLYNVPAVAEEIQDE	P12023|A4_MOUSE	49.93	17	4090	NA	1400
LSQHATPLPTPAVLPG	O88746|TOM1_MOUSE	49.03	16	624	NA	660
LSRFTSGVPSFVLD	Q9R097|SPIT1_MOUSE	38.23	14	3910	NA	3010
LSRFTSGVPSFVLDTE	Q9R097|SPIT1_MOUSE	47.08	16	926	NA	909
LSRTPGNRIVYLYTKKVGKAP	Q9D1R9|RL34_MOUSE	46.56	21	NA	NA	779
LSRTPGNRIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	48.94	22	NA	4600	3140
LSRTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	49.95	23	1090	NA	2910
LSTKYDAPFVFAEVN	P21981|TGM2_MOUSE	38.7	15	NA	NA	180
LSVTWSIPVSQQSR	Q03145|EPHA2_MOUSE	37.02	14	134	NA	186
LSYIGPSVNK	O35604|NPC1_MOUSE	27.5	10	NA	NA	613
LSYIQTPLPSRAIV	O89093|CCL20_MOUSE	49	14	134	NA	215
LSYIQTPLPSRAIVG	O89093|CCL20_MOUSE	48.57	15	6550	1050	5030
LTEAYQVPDASVSSM(+15.99)H	P58242|ASM3B_MOUSE	45.37	16	742	NA	295
LTGGYRYPRALEEEV	Q8K3K8|OPTN_MOUSE	29.39	15	32300	1770	85700
LTGM(+15.99)AFRVPTPNVS	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.48	14	3440	NA	2260
LTGM(+15.99)AFRVPTPNVSV	P16858|G3P_MOUSE:Q64467|G3PT_MC	36.4	15	84.8	NA	93.9
LTGM(+15.99)AFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	48.99	16	632	NA	335
LTGM(+15.99)AFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.9	18	9310	NA	9500
LTGMAFRVPTPNVS	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.65	14	7420	NA	4580
LTGMAFRVPTPNVSV	P16858|G3P_MOUSE:Q64467|G3PT_MC	48.65	15	NA	NA	301
LTGMAFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.8	16	272	NA	459
LTGMAFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.86	17	25000	NA	43000
LTGMAFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.93	19	2870	NA	5690
LTNDRYVASLAARNK	Q00560|IL6RB_MOUSE	46.89	15	405	NA	696
LTNDRYVASLAARNKVG	Q00560|IL6RB_MOUSE	47.76	17	530	NA	724
LTQYSTPEGSSVPI	E9Q414|APOB_MOUSE	44.1	14	274	NA	989
LTTSSYSNPTIGYENR	Q07797|LG3BP_MOUSE	49.76	16	292	NA	166
LTVNKAVDYPPVANAGP	Q8K135|K319L_MOUSE	46.9	17	137	NA	165
LTVNKAVDYPPVANAGPNQ	Q8K135|K319L_MOUSE	49.94	19	1700	NA	1880
LTYISPSAAIFQA	Q9WVL3|S12A7_MOUSE	39.83	13	337	NA	264
LVFDVTAPNTFKT	P51150|RAB7A_MOUSE	47.55	13	213	NA	256
LVFDVTAPNTFKTLDS	P51150|RAB7A_MOUSE	43.78	16	290	NA	262
LVKDSELSPPTSAPSLVS	Q9WUU8|TNIP1_MOUSE	45.14	18	NA	NA	1300
LVLYFKLRPKKTPAVK	Q78IK2|ATPMK_MOUSE	28.17	16	NA	NA	641
LVNPFVGPLTNRIG	Q8R090|VMAT1_MOUSE	40.45	14	2540	NA	1110
LVNPFVGPLTNRIGYH	Q8R090|VMAT1_MOUSE	44.1	16	742	NA	240
LVPIVEPEVLPDGDH	Q91Y97|ALDOB_MOUSE	49.47	15	5770	63	2940

LVRYTQKAPQVSTPT	P07724|ALBU_MOUSE	49.82	15	23100	541	17000
LVRYTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.92	17	54100	2330	59400
LVRYTQKAPQVSTPTLVEA	P07724|ALBU_MOUSE	48.57	19	NA	NA	1480
LVTPHQPAVLESET	P15261|INGR1_MOUSE	29.69	14	NA	NA	158
LVYENASAIMAHE	E9Q0N2|PTPRH_MOUSE	46.58	13	61.3	NA	200
LVYENASAIMAHESE	E9Q0N2|PTPRH_MOUSE	48.23	15	NA	NA	33.8
LYLNIYTPAHAHEGSNLPV	Q91WG0|EST2C_MOUSE	35.41	19	NA	NA	237
LYPENFAPSFPHGSPG	Q3UDK1|TRAD1_MOUSE	44.95	16	239	NA	78.9
M(+15.99)AFRVPTPNVSV	P16858|G3P_MOUSE:Q64467|G3PT_MC	44.88	12	445	NA	320
M(+15.99)AFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	46.22	13	917	NA	538
M(+15.99)AFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MC	47.73	15	348	NA	146
M(+15.99)APYQGPDAAPGAL	P57780|ACTN4_MOUSE	33.19	14	661	NA	415
M(+15.99)APYQGPDAAPGALD	P57780|ACTN4_MOUSE	40.44	15	1350	NA	809
M(+15.99)KLPKSAKPVSQMRMATPLLM(	P04441|HG2A_MOUSE	31.12	24	NA	NA	882
M(+15.99)LQVLGPKPALPEG	P13020|GELS_MOUSE	46.24	14	248	NA	77.5
M(+15.99)PIPM(+15.99)YDAAQALKTNPE	Q6EDY6|CARL1_MOUSE	47.53	17	5190	NA	4140
M(+15.99)PIPMYDAAQALKTNPE	Q6EDY6|CARL1_MOUSE	49.71	17	2970	NA	3800
M(+15.99)PIYPSNQPQVHVISG	Q99N10|M4A8_MOUSE	46.23	16	871	NA	497
M(+15.99)SLDYHFVTPLTSLT	Q61702|ITIH1_MOUSE	41.84	15	1440	NA	991
M(+15.99)YSTYKTPVPETNIPG	Q60855|RIPK1_MOUSE	28.93	16	1250	NA	855
M(+42.01)(+15.99)DETSPLVSPER	Q2TBE6|P4K2A_MOUSE	38.86	12	2240	NA	1250
M(+42.01)(+15.99)DETSPLVSPERAQPP	Q2TBE6|P4K2A_MOUSE	48.54	16	15000	NA	14900
M(+42.01)(+15.99)DETSPLVSPERAQPP	Q2TBE6|P4K2A_MOUSE	43.6	17	1340	NA	1440
M(+42.01)(+15.99)NPPSYYTQPVPVPNA	Q9JLJ0|LITAF_MOUSE	28.92	17	NA	NA	97
M(+42.01)DETSPLVSPER	Q2TBE6|P4K2A_MOUSE	45.58	12	156	NA	737
M(+42.01)DETSPLVSPERAQPP	Q2TBE6|P4K2A_MOUSE	49.22	16	2080	NA	4250
M(+42.01)DFSRQSFHRSLSSSSQGPAL	Q9D312|K1C20_MOUSE	28.88	21	NA	NA	179
MAFRVPTPNVSV	P16858|G3P_MOUSE:Q64467|G3PT_MC	45.3	12	374	NA	253
MAFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	48.89	14	30600	368	30700
MAPYQGPDAAPGAL	P57780|ACTN4_MOUSE	35.95	14	79.7	NA	304
MAPYQGPDAAPGALD	P57780|ACTN4_MOUSE	41.48	15	538	NA	783
MEEKPVPAAPVPSPVAPAPVP	P97825|JUPI1_MOUSE	45.31	21	NA	NA	71.4
MEELKGHLTPRANELK	P06728|APOA4_MOUSE	48.43	16	176	NA	152
MIPAHDSPLAALAFDAS	Q80W47|WIPI2_MOUSE	37.08	17	346	NA	355
MKLPKSAKPVSQM(+15.99)RMATPLLMF	P04441|HG2A_MOUSE	48.82	24	NA	NA	938
MKLPKSAKPVSQMRMATPLLM(+15.99)F	P04441|HG2A_MOUSE	48.95	24	NA	NA	2930
MKLPKSAKPVSQMRMATPLLM(+15.99)F	P04441|HG2A_MOUSE	46.92	24	215	NA	849
MLQVLGPKPALPEG	P13020|GELS_MOUSE	46.94	14	134	NA	270
MNPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.23	17	121	NA	559
MNPPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	48.19	18	140	NA	401
MPIPM(+15.99)YDAAQALKTNPE	Q6EDY6|CARL1_MOUSE	49.04	17	2050	NA	5800
MPTSPKPLLQSPKPSPSARPS	Q6EDY6|CARL1_MOUSE	48.94	21	NA	NA	164
MPYTNAVIHEVQR	P24456|CP2DA_MOUSE:P24457|CP2DB	40.68	13	NA	NA	64.9
MQKEITALA	P63260|ACTG_MOUSE:P60710|ACTB_M	29.18	9	261	113	319
MRYVASYLLAALGGNSSPSAKDIKK	P99027|RLA2_MOUSE	49.95	25	14500	NA	4780
MSLDYHFVTPLTSLT	Q61702|ITIH1_MOUSE	42.45	15	446	NA	593
MSPEEVAPSPRASPA	Q8CH72|TRI32_MOUSE	41.3	15	876	NA	1230
N(+15.00)GNPLNSVFVAPAVTPVKG	P70158|ASM3A_MOUSE	41.94	19	NA	NA	273
N(+42.01)(+15.00)HTLFHNPHVNPLPTGY	P43023|CX6A2_MOUSE:P43024|CX6A1_	33.83	18	NA	NA	1050
N(+42.01)(+15.00)IYIYNGPVLGGTR	P50284|TNR3_MOUSE	30.53	14	NA	NA	5830
N(+42.01)(+15.00)KGFFVQPTVFSNVTD	O35945|AL1A7_MOUSE:P24549|AL1A1_	27.82	16	NA	NA	99.5
N(+42.01)(+15.00)PPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	40.67	16	2580	NA	2810
NATDDVFSPSHAIPIETA	Q91ZH7|ABHD3_MOUSE	49.64	18	452	NA	165
NDAFVLKTPSAAYL	P13020|GELS_MOUSE	47.75	14	NA	NA	68.4
NDDDVYRAPPIDRSILPT	Q8BGD9|IF4B_MOUSE	49.93	18	517	NA	330
NDIIRAPTIEQMKD	P63085|MK01_MOUSE	32.32	14	NA	NA	157
NDLSFIHPKALSGLKE	A2ARI4|LGR4_MOUSE	49.76	16	1620	NA	836
NDNDNIFLSPLSISTA	P32261|ANT3_MOUSE	47.09	16	137	NA	242
NDPGAQYSLVN	Q9R100|CAD17_MOUSE	38.39	11	271	NA	381
NDPGAQYSLVNK	Q9R100|CAD17_MOUSE	46.08	12	620	NA	399
NDPGFGAPAASQVAS	Q6IRU5|CLCB_MOUSE	46.97	15	813	NA	874
NDPGFGAPAASQVASA	Q6IRU5|CLCB_MOUSE	48.69	16	1330	NA	1170
NDVRRAFLGPFAHKEGPT	Q62177|SEM3B_MOUSE	36.22	18	NA	NA	458
NEPSVFNGPEVTM(+15.99)LKD	Q8BHN3|GANAB_MOUSE	49.88	16	829	NA	536
NFRPAHQAPM(+15.99)AQTTIH	O08573|LEG9_MOUSE	49.21	16	2540	NA	2050
NFRPAHQAPMAQTTIH	O08573|LEG9_MOUSE	49.91	16	2260	NA	2890
NFRPAHQAPMAQTTIHMV	O08573|LEG9_MOUSE	48	18	NA	NA	66.7
NGKLTGMAFRVPTPNVSVVD	P16858|G3P_MOUSE	35.85	20	NA	NA	290
NGLVPIVEPEVLPDG	Q91Y97|ALDOB_MOUSE	49.46	15	777	NA	234
NGN(+15.00)PLNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	45.48	18	NA	NA	805
NGNPLNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	49.94	18	872	NA	1120
NHLRFNYPEVQKV	Q6XQH0|G3ST2_MOUSE	38	13	394	NA	171
NHLRFNYPEVQKVMPR	Q6XQH0|G3ST2_MOUSE	49.92	16	17800	NA	17700
NHRSPVATPTPTMSLPE	Q61805|LBP_MOUSE	45.41	17	NA	NA	732
NHTLFHNPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	49.75	18	2600	1540	5410
NIPYFETSAKEAIN	P51150|RAB7A_MOUSE	41.24	14	NA	NA	191
NIYDLVAPFPSAPN	P09470|ACE_MOUSE	45.77	14	969	NA	117
NIYIYNGPVLGGTRGPG	P50284|TNR3_MOUSE	47.05	17	290	NA	250
NIYTPAHAHEGSNLPV	Q91WG0|EST2C_MOUSE	49.66	16	3870	NA	911
NIYVPAHAHEGSN	Q8BK48|EST2E_MOUSE	42.66	13	4460	171	564
NIYVPAHAHEGSNLP	Q8BK48|EST2E_MOUSE	45.73	15	8700	NA	8770

NIYVPAHAHEGSNLPV	Q8BK48|EST2E_MOUSE	49.66	16	35800	423	29900
NKTRLSRTPGNRIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	48.87	26	NA	NA	1640
NKTRLSRTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	48.94	27	296	1110	2230
NLAVGSPSAAEAPG	Q03157|APLP1_MOUSE	44.02	14	2350	NA	2620
NLAVGSPSAAEAPGS	Q03157|APLP1_MOUSE	48.46	15	380	NA	590
NLAVGSPSAAEAPGSAQ	Q03157|APLP1_MOUSE	46.73	17	566	NA	435
NLRKMGAPEAGMAEYL	P09528|FRIH_MOUSE	46.97	16	196	NA	472
NM(+15.99)DLYLSPVAQSQEF	Q91XS1|MTMR4_MOUSE	48.81	15	614	NA	350
NNQAYHSPATALAIVDN	Q8R420|ABCA3_MOUSE	49.1	17	1200	NA	1430
NNQDFRGSAGAPSVENV	P49443|PPM1A_MOUSE	48.38	17	638	NA	722
NNSFYGPEVKIEKG	Q00519|XDH_MOUSE	48.53	14	5180	NA	3550
NNSFYGPEVKIEKGDL	Q00519|XDH_MOUSE	49.93	16	1840	NA	701
NNSIMSNPVAGLVIG	Q9DBP0|NPT2B_MOUSE	49.14	15	546	NA	433
NNYALFLSPRAQQASWQ	E9Q414|APOB_MOUSE	47.68	17	262	NA	647
NPDKNIVFSPLSISAA	Q03734|SPA3M_MOUSE:Q91WP6|SPA3	46.52	16	413	NA	536
NPEGAVFTWEPSTGKDAVQKK	P01878|IGHA_MOUSE	49.69	21	185	NA	509
NPEYLAPRAGTAS	P70424|ERBB2_MOUSE	36.95	13	147	NA	73.6
NPEYLAPRAGTASQPH	P70424|ERBB2_MOUSE	49.19	16	4890	NA	582
NPEYLAPRAGTASQPHP	P70424|ERBB2_MOUSE	49.91	17	34100	460	12100
NPIITPVAQENQ	P08226|APOE_MOUSE	46.21	12	603	NA	234
NPIYKSAVTTVVNPK	P09055|ITB1_MOUSE	49.13	15	84.5	NA	133
NPLLKQYQGPTGDSSAT	P51912|AAAT_MOUSE	41.26	17	4830	NA	4120
NPLNSVFVAPAVT	P70158|ASM3A_MOUSE	42.92	13	73.7	NA	99.7
NPLNSVFVAPAVTP	P70158|ASM3A_MOUSE	48.57	14	1240	NA	1910
NPLNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	49.93	16	381000	26400	413000
NPLNSVFVAPAVTPVKGV	P70158|ASM3A_MOUSE	49.94	18	41200	NA	44400
NPPSYYTQPVPV	Q9JLJ0|LITAF_MOUSE	48.89	12	244	NA	274
NPPSYYTQPVPVP	Q9JLJ0|LITAF_MOUSE	39.31	13	450	NA	702
NPPSYYTQPVPVPN	Q9JLJ0|LITAF_MOUSE	49.22	14	49100	2750	49800
NPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	49.7	16	231000	17200	241000
NPPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	49.82	17	30200	1160	27300
NPPSYYTQPVPVPNANAI	Q9JLJ0|LITAF_MOUSE	49.72	18	134	NA	120
NPQIQHFSPTVAPAVRT	Q6VGS5|DAPLE_MOUSE	40.67	17	NA	NA	214
NPRPQASAYSPAAAASPAPS	Q9JKS4|LDB3_MOUSE	49.41	20	246	NA	365
NPSWVAEPIPHSAVQS	Q8K0B3|LRC66_MOUSE	48.26	16	186	NA	178
NPTDAYLDAM(+15.99)M(+15.99)NEAPG	Q3THE2|ML12B_MOUSE	49.63	18	903	NA	699
NPTDAYLDAMM(+15.99)NEAPGPI	Q3THE2|ML12B_MOUSE	49.57	18	206	NA	227
NPTDAYLDAMMNEAPGPI	Q3THE2|ML12B_MOUSE	48.43	18	NA	NA	271
NPTLPYKRPIPG	O54891|LEG6_MOUSE:Q8K419|LEG4_M	48.11	12	407	NA	556
NPTLPYKRPIPGGL	O54891|LEG6_MOUSE:Q8K419|LEG4_M	48.07	14	1390	NA	348
NPTLPYKRPIPGGLSV	O54891|LEG6_MOUSE:Q8K419|LEG4_M	47.76	16	1620	NA	1250
NPTLPYKRPIPGGLSVG	O54891|LEG6_MOUSE:Q8K419|LEG4_M	28.84	17	NA	NA	171
NPVVIPEPPNPIPSYSEVV	Q99N10|M4A8_MOUSE	49.94	19	784	NA	158
NPYSTSYSGPYPAAAPPVP	Q9WVH9|FBLN5_MOUSE	49.88	19	10400	NA	10200
NPYSTSYSGPYPAAAPPVPA	Q9WVH9|FBLN5_MOUSE	49.93	20	10300	251	7810
NQAYHSPATALAIV	Q8R420|ABCA3_MOUSE	46.86	14	1270	NA	1680
NQAYHSPATALAIVD	Q8R420|ABCA3_MOUSE	45.76	15	9630	NA	10400
NQAYHSPATALAIVDN	Q8R420|ABCA3_MOUSE	41.76	16	724	NA	644
NQDPEVFSQPKVLPSAIPI	Q91YD3|DCP1A_MOUSE	48.01	19	NA	NA	145
NQLEALVGPEANVGPYG	O09159|MA2B1_MOUSE	49.61	17	1080	NA	643
NQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	48.94	14	500	NA	242
NRLDNYDAPDIANIAI	Q68FD5|CLH1_MOUSE	47.4	16	NA	NA	701
NRLDNYDAPDIANIAIS	Q68FD5|CLH1_MOUSE	49.64	17	379	NA	439
NRLKVGLQVVAVKAPGFGDNRKNQLK	P63038|CH60_MOUSE	29.96	26	NA	NA	160
NRPAFMPSEGRMVSDIN	P57780|ACTN4_MOUSE:Q7TPR4|ACTN1	48.04	17	NA	NA	467
NSEEFAAAM(+15.99)SRYELK	E9Q414|APOB_MOUSE	49.52	15	379	NA	433
NSEEFAAAMSRYELK	E9Q414|APOB_MOUSE	49.73	15	1230	NA	1620
NSEFDPPGPNVATTT	Q9Z1D1|EIF3G_MOUSE	49.47	15	991	NA	742
NSIM(+15.99)SNPVAGLVIG	Q9DBP0|NPT2B_MOUSE	47.47	14	1610	NA	1130
NSIMSNPVAGLVIG	Q9DBP0|NPT2B_MOUSE	46.42	14	536	NA	624
NSNSYGIPEPAHAYA	P47941|CRKL_MOUSE	48.41	15	285	NA	783
NSNSYGIPEPAHAYAQPQ	P47941|CRKL_MOUSE	49.7	18	944	NA	1590
NSQPEILER	P14483|HB2A_MOUSE:P01921|HB2D_M	30.65	9	675	NA	360
NSVFVAPAVTPVK	P70158|ASM3A_MOUSE	47.66	13	7410	262	7870
NSVFVAPAVTPVKG	P70158|ASM3A_MOUSE	47.86	14	2370	45.8	2420
NVDFNTPRPST	G3X939|SL9A3_MOUSE	41.75	11	187	NA	372
NVDFNTPRPSTVEA	G3X939|SL9A3_MOUSE	48.86	14	4010	37.6	6690
NVKQFIAPETSEGVS	Q9EPS3|GLCE_MOUSE	43.66	15	753	NA	743
NVLRIINEPTAAAIAY	P17879|HS71B_MOUSE:P16627|HS71L_	48.82	16	117	NA	85.5
NVLRIINEPTAAAIAYG	P17879|HS71B_MOUSE:P16627|HS71L_	49.93	17	5460	NA	4410
NVM(+15.99)RIINEPTAAAIAYG	P20029|BIP_MOUSE	49.41	17	302	NA	267
NVMRIINEPTAAAIAYG	P20029|BIP_MOUSE	45.88	17	NA	NA	344
NVQFNYPQASVT	Q61703|ITIH2_MOUSE	36.46	12	111	NA	57.3
NVQFNYPQASVTD	Q61703|ITIH2_MOUSE	48.24	13	9280	340	7920
NVQFNYPQASVTDV	Q61703|ITIH2_MOUSE	48.4	14	1210	NA	927
NVQFNYPQASVTDVT	Q61703|ITIH2_MOUSE	49.62	15	65800	3480	14600
NVQFNYPQASVTDVTQ	Q61703|ITIH2_MOUSE	49.74	16	737	NA	521
NVQFSSPLPGEAVK	Q80X90|FLNB_MOUSE	43.04	14	375	NA	457
NVQPYSGSPANFAVYT	P50431|GLYC_MOUSE	48.71	16	633	NA	137
NVSSLEGARALIAEAT	P19096|FAS_MOUSE	40.97	16	NA	NA	80.9
NVTELNEPLSNEERNL	P61982|1433G_MOUSE	47.81	16	299	NA	269

NVVWDYFTQLSNNAKEA	P06728|APOA4_MOUSE	49.94	17	1250	NA	1150
NWIQYKEGFGHLSPT	Q8VCM7|FIBG_MOUSE	49.16	15	279	NA	522
NWIQYKEGFGHLSPTG	Q8VCM7|FIBG_MOUSE	49.78	16	741	NA	1030
NYALFLSPRAQQASWQ	E9Q414|APOB_MOUSE	48.09	16	311	NA	643
NYEGPETHTSLRR	P14483|HB2A_MOUSE	28.37	13	2840	NA	1790
NYEYYASHVPESVK	Q9Z0S1|BPNT1_MOUSE	49.43	14	9230	117	5770
NYEYYASHVPESVKN	Q9Z0S1|BPNT1_MOUSE	49.93	15	2620	NA	1620
P(+42.01)SQ(+15.00)PAVLQPSVEPAQP	Q9ERN0|SCAM2_MOUSE	30.39	18	NA	NA	4460
PAAAAGAKKAKSPKKAK	P43274|H14_MOUSE	48.89	17	NA	3370	631
PAAAGVKKVAKSPKK	P43276|H15_MOUSE	47.64	15	755	NA	681
PAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.94	17	22200	21600	21100
PAAAGVKKVAKSPKKAKA	P43276|H15_MOUSE	49.94	18	4660	3740	4460
PAAAGVKKVAKSPKKAKAAAKPKKAAK	P43276|H15_MOUSE	49.95	27	1900	NA	854
PAATPKKAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	28	3610	2560	4120
PAGAAKKPKKAAGTATAKKSTKKTPKKA	P43274|H14_MOUSE	49.95	32	NA	NA	1080
PAGAAKKPKKATGAATPKKTAKKTPKKA	P43277|H13_MOUSE	49.95	32	1610	NA	2450
PAGGGDPEAPAPAPAAERPP	Q68FL4|SAHH3_MOUSE	49.25	20	556	NA	566
PAKAKAPKAKASKPKA	P43277|H13_MOUSE	49.92	16	9900	6200	4320
PAKAKAPKAKASKPKASKPKATKAKKAA	P43277|H13_MOUSE	48.95	30	NA	NA	588
PAKAKTVKPKAAKPKTSKPKAAKP	P43274|H14_MOUSE	48.83	24	NA	NA	805
PAKKAKSPT	Q52KI8|SRRM1_MOUSE	27.81	9	NA	NA	897
PAKKKT(+79.97)T(+79.97)KKA	P43276|H15_MOUSE	27.8	10	NA	NA	111
PAKPKKAAPK	P43275|H11_MOUSE	47.5	10	888	512	864
PAKPKKAAPKKK	P43275|H11_MOUSE	30.95	12	NA	NA	281
PAPAPPAPIPPP	Q5I1X5|IASPP_MOUSE	38.6	12	5460	NA	12100
PAPKKGSKKAVTKAQKKDGKKRKR	Q8CGP0|H2B3B_MOUSE:Q8CGP2|H2B1	49.95	24	NA	5250	8640
PAPSTRVITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.95	23	754	NA	980
PAVTPVKG	P70158|ASM3A_MOUSE	32.21	8	785	NA	2160
PAYTIPFYTPIPNG	O08573|LEG9_MOUSE	49.21	14	863	NA	480
PAYTIPFYTPIPNGLYPS	O08573|LEG9_MOUSE	49.94	18	566	NA	424
PAYTIPFYTPIPNGLYPSKS	O08573|LEG9_MOUSE	34.93	20	NA	NA	226
PC(+57.02)LQVYAPEVS(+79.97)PESIM(	Q9ESY9|GILT_MOUSE	46.1	16	435	NA	137
PEAPAPAPAAERPP	Q68FL4|SAHH3_MOUSE	28.92	14	NA	NA	158
PELNHAFG	Q91ZX7|LRP1_MOUSE	32.78	8	61.6	NA	437
PFYTPIPNG	O08573|LEG9_MOUSE	28.58	9	4080	NA	2250
PFYTPIPNGL	O08573|LEG9_MOUSE	29.9	10	91.6	NA	540
PHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	41.51	11	52.1	NA	179
PIQKYLTPQM(+15.99)ATSIT	Q6P9J9|ANO6_MOUSE	29.99	15	1440	NA	950
PIQKYLTPQMATSIT	Q6P9J9|ANO6_MOUSE	48.82	15	204	NA	243
PKAAKPKK	P43274|H14_MOUSE	27.42	8	NA	NA	3940
PKAAKPKKTAAKKK	P43274|H14_MOUSE	49.66	14	17300	8850	4000
PKAAKPKTSKPKAAKP	P43274|H14_MOUSE	48.93	16	NA	1040	4200
PKAAKPKTSKPKAAKPKKT	P43274|H14_MOUSE	49.94	19	804	1560	3100
PKAAKPKVAKAKKV	P15864|H12_MOUSE	38.34	14	NA	NA	504
PKAAKPKVAKAKKVAAK	P15864|H12_MOUSE	49.95	17	723	NA	611
PKAAKPKVAKAKKVAAKK	P15864|H12_MOUSE	49.94	18	9290	1350	3100
PKAKASKPKA	P43277|H13_MOUSE	41.21	10	124	2330	1040
PKAKSSAKR	P10922|H10_MOUSE	42.93	9	1940	2080	3110
PKAKSSAKRAS	P10922|H10_MOUSE	41.87	11	NA	NA	243
PKASKAKVTKPKTPAKP	P43275|H11_MOUSE	48.57	17	NA	NA	487
PKASKAKVTKPKTPAKPKKAAP	P43275|H11_MOUSE	48.95	22	NA	NA	4370
PKASKAKVTKPKTPAKPKKAAPKKK	P43275|H11_MOUSE	49.95	25	1800	NA	536
PKASKPKATKAK	P43277|H13_MOUSE	36.2	12	NA	NA	336
PKASKPKATKAKKA	P43277|H13_MOUSE	43.24	14	608	588	3260
PKASKPKATKAKKAAP	P43277|H13_MOUSE	41.79	16	NA	2340	4210
PKASKPKATKAKKAAPR	P43277|H13_MOUSE	49.77	17	2920	3630	6580
PKASKPKATKAKKAAPRKK	P43277|H13_MOUSE	49.95	19	9430	7170	4220
PKATKAKKA	P43277|H13_MOUSE	30.23	9	428	NA	717
PKATKAKKAAPR	P43277|H13_MOUSE	48.05	12	NA	NA	1060
PKATKAKKAAPRK	P43277|H13_MOUSE	48.02	13	1640	5030	6390
PKATKAKKAAPRKK	P43277|H13_MOUSE	49.94	14	27500	27600	17100
PKATPVKKAKKKPAA	P10922|H10_MOUSE	26.26	15	NA	NA	1010
PKKAAKKT	P15864|H12_MOUSE	26.52	8	NA	NA	110
PKKAAKPKK	P10922|H10_MOUSE	30.66	9	NA	NA	1730
PKKAAKSPAKPKA	P43276|H15_MOUSE	49.02	13	2340	6100	5560
PKKAAPKK	P43275|H11_MOUSE	29.66	8	NA	NA	463
PKKAASKAPS(+79.97)K	P10922|H10_MOUSE	27.84	11	NA	NA	841
PKKAKAAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	48.95	22	NA	NA	856
PKKAKKPAA	P15864|H12_MOUSE:P43276|H15_MOU	38.24	9	NA	1810	577
PKKAKKPAAAAGAKKAKS(+79.97)P	P43274|H14_MOUSE	27.19	19	NA	NA	814
PKKAKKPAAAGVKK	P43276|H15_MOUSE	48.64	14	301	203	176
PKKAKKPAAAGVKKVAKSPKKAK	P43276|H15_MOUSE	49.95	23	271	NA	258
PKKAKTVKP	P10922|H10_MOUSE	38.79	9	NA	NA	1290
PKKAKTVKPKAK	P10922|H10_MOUSE	45.78	12	NA	782	232
PKKAKTVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.95	22	11700	NA	3200
PKKTAGAKKTVKKTPKKAKKPA	P43276|H15_MOUSE	49.95	22	2050	NA	546
PKKTAKKTPKKAKK	P43277|H13_MOUSE	38.95	14	NA	NA	475
PKKTAKKTPKKAKKPA	P43277|H13_MOUSE	49.95	16	688	NA	554
PKKVGPKP	Q7TSA6|PRSR3_MOUSE	29.47	8	NA	NA	102
PKPKVPAK	A2ASS6|TITIN_MOUSE	27.77	8	NA	NA	543
PKSKVKRRN(+15.00)LTRLPKPKQ	Q7TQE7|MACA2_MOUSE	25.49	18	NA	NA	3440

PKTPAKPKK	P43275|H11_MOUSE	41.84	9	NA	185	791
PKTPAKPKKAAP	P43275|H11_MOUSE	41.92	12	181	NA	1260
PKTPAKPKKAAPKK	P43275|H11_MOUSE	45.36	14	2180	NA	2160
PKTPAKPKKAAPKKK	P43275|H11_MOUSE	48.83	15	9220	1050	4150
PKTSKPKAAKPK	P43274|H14_MOUSE	43.2	12	NA	NA	285
PKTSKPKAAKPKKTAAK	P43274|H14_MOUSE	48.67	17	121	NA	187
PKTSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.95	19	8780	5000	4610
PKVAKAKKVAAKKK	P15864|H12_MOUSE	49.94	14	22100	4050	6120
PKVVKAKKVAKSPAK	P43275|H11_MOUSE	49.93	15	2740	1640	2200
PKVVKAKKVAKSPAKAK	P43275|H11_MOUSE	49.86	17	973	1590	843
PKVVKAKKVAKSPAKAKAVKPKA	P43275|H11_MOUSE	48.95	23	NA	NA	694
PLNSVFVAPAVTPVK	P70158|ASM3A_MOUSE	49.85	15	4810	NA	4840
PLPPLPEYGGKVR	Q9CQQ7|AT5F1_MOUSE	37.69	13	NA	NA	56.2
PMFIVNTNVPRASVPE	P34884|MIF_MOUSE	49.56	16	253	NA	358
PPALQEPQPAGSQPLLANSPL	Q8R1U2|CGRE1_MOUSE	49.91	21	212	NA	201
PPAPAPAPLPPP	O35609|SCAM3_MOUSE	39.5	12	5460	NA	12100
PPAYEPPAPAPAPLPPP	O35609|SCAM3_MOUSE	49.87	17	31900	NA	12900
PPHVQFTYQQPQPLSVEPR	B2RXS4|PLXB2_MOUSE	49.94	19	15800	77.6	9070
PPSYYTQPVPVPN	Q9JLJ0|LITAF_MOUSE	43.18	13	3460	48	2800
PPSYYTQPVPVPNA	Q9JLJ0|LITAF_MOUSE	48.35	14	1790	NA	1820
PPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	48.39	15	26400	1030	24300
PPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	49.43	16	2890	NA	2410
PPYDDATAVPSTAKEPPPP	Q91XQ6|LAP4B_MOUSE	49.88	19	9680	NA	2840
PPYTIVYFPVRGR	P19157|GSTP1_MOUSE	39.52	13	NA	NA	155
PQASVTDVT	Q61703|ITIH2_MOUSE	32.17	9	NA	NA	5960
PQLIEVSSPITLQAL	E9Q414|APOB_MOUSE	49.65	15	308	NA	241
PRGPPPAGLLQ	P06345|HB2S_MOUSE:P06346|HB2F_M	29.51	11	2860	NA	1530
PRTPQDSPM(+15.99)YPVVPVHLDGTF	P97425|ECP2_MOUSE:P97426|ECP1_M	49.94	21	192	NA	221
PSTSSLAAPTVEAAAS	Q91ZP6|NFIP2_MOUSE	46.7	16	389	NA	107
PSTSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	49.02	19	629	NA	518
PTFHTPLDLYAYAR	Q07797|LG3BP_MOUSE	46.39	14	692	NA	361
PTPAYTIPFYTPIPNG	O08573|LEG9_MOUSE	47.2	16	5110	NA	1970
PTPAYTIPFYTPIPNGLYP	O08573|LEG9_MOUSE	49.68	19	483	NA	318
PTPAYTIPFYTPIPNGLYPS	O08573|LEG9_MOUSE	49.86	20	2710	NA	1130
PTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	31.01	11	633	NA	3920
PVKASKPKKAKTVKP	P10922|H10_MOUSE	48.85	15	964	196	3850
PVKASKPKKAKTVKPK	P10922|H10_MOUSE	48.92	16	145	NA	653
PVKASKPKKAKTVKPKA	P10922|H10_MOUSE	49.95	17	1390	227	1740
PVKASKPKKAKTVKPKAK	P10922|H10_MOUSE	49.94	18	861	4280	3110
PVKASKPKKAKTVKPKAKSSAKR	P10922|H10_MOUSE	49.95	23	710	417	3920
PVKASKPKKAKTVKPKAKSSAKRASKK	P10922|H10_MOUSE	49.95	27	1500	NA	3580
PVQFPYVTPAPHEPVK	Q9D074|MGRN1_MOUSE	48.63	16	162	NA	54.9
PVSQM(+15.99)RMATPLLM(+15.99)RPM	P04441|HG2A_MOUSE	44.92	16	256	NA	879
PVSQM(+15.99)RMATPLLMRPM	P04441|HG2A_MOUSE	40.68	16	NA	NA	362
PVSQM(+15.99)RMATPLLMRPM(+15.99	P04441|HG2A_MOUSE	31.31	16	181	NA	643
PVSQMRMATPLLM(+15.99)RPM(+15.99	P04441|HG2A_MOUSE	44.57	16	1040	NA	1160
PVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	48.59	16	NA	NA	724
PVSQMRMATPLLMRPM(+15.99)	P04441|HG2A_MOUSE	47.39	16	NA	NA	1160
PVSQMRMATPLLMRPM(+15.99)S	P04441|HG2A_MOUSE	44.27	17	372	NA	307
PVSQMRMATPLLMRPMS	P04441|HG2A_MOUSE	48.74	17	NA	NA	173
PVVPVHLDGTF	O35291|RNAS2_MOUSE:P97425|ECP2_	47.39	11	2190	NA	1940
PYDQPNAIYIER	O88307|SORL_MOUSE	44.12	12	131	NA	212
Q(+42.01)(+15.00)DGEQAPPLPIKTPIPTI	Q7TQH7|LRP10_MOUSE	44.84	20	284	NA	400
Q(+42.01)(+15.00)PSTSSLAAPTVEAAAS	Q91ZP6|NFIP2_MOUSE	25.61	18	NA	NA	568
QASIYSPPAAAAAA	P70297|STAM1_MOUSE	39.04	14	NA	NA	111
QASIYSPPAAAAAAA	P70297|STAM1_MOUSE	48.73	15	12500	NA	11400
QASIYSPPAAAAAAAA	P70297|STAM1_MOUSE	49.02	16	3910	NA	3580
QDPEVFSQPKVLPSAIP	Q91YD3|DCP1A_MOUSE	49.89	17	1730	NA	1630
QDPEVFSQPKVLPSAIPI	Q91YD3|DCP1A_MOUSE	49.94	18	1230	NA	1270
QDPTFHTPLDLYAYAR	Q07797|LG3BP_MOUSE	49.85	16	1270	NA	384
QDQAYKAPVVVEGKV	P56974|NRG2_MOUSE	49.23	15	385	NA	141
QEFILNSPTVTSIK	Q9R0H0|ACOX1_MOUSE	41.69	14	361	NA	654
QEFILNSPTVTSIKW	Q9R0H0|ACOX1_MOUSE	43.68	15	NA	NA	68.3
QEYSGSVANEAN	E9Q414|APOB_MOUSE	43.41	12	701	NA	1060
QGGVYASPSIAGSRP	Q8R0X7|SGPL1_MOUSE	45.45	15	540	NA	321
QGGVYASPSIAGSRPG	Q8R0X7|SGPL1_MOUSE	47.02	16	10100	NA	6540
QINWTVLYRRKHKKGQSEEIQKKR	Q8BP67|RL24_MOUSE	45.25	24	NA	NA	270
QKAEASSPVPYLSPET	P39447|ZO1_MOUSE	49.43	16	3460	NA	3070
QKKDGKKRKRGRKESYSIYVYKVLKQVI	Q8CGP0|H2B3B_MOUSE:Q9D2U9|H2B3	48.95	30	NA	453	1310
QKQPYFGAVVGRVA	Q8K157|GALM_MOUSE	46.6	14	478	NA	208
QKQPYFGAVVGRVANR	Q8K157|GALM_MOUSE	33.81	16	1320	NA	998
QKTQYISPNLNPN	P97499|TEP1_MOUSE	46.92	13	2560	NA	1870
QKTQYISPNLNPND	P97499|TEP1_MOUSE	48.04	14	3050	NA	2750
QKTQYISPNLNPNDV	P97499|TEP1_MOUSE	47.74	15	1810	NA	803
QKTQYISPNLNPNDVT	P97499|TEP1_MOUSE	49.83	16	773	NA	432
QLAFKQPSSAYAAF	P01027|CO3_MOUSE	32.06	14	NA	NA	20.3
QLDEYSSSVANFLQA	Q91VE0|S27A4_MOUSE	47.47	15	1570	NA	877
QLDEYSSSVANFLQAR	Q91VE0|S27A4_MOUSE	49.9	16	380	NA	227
QLEALVGPEANVGP	O09159|MA2B1_MOUSE	42	14	612	NA	168
QLEALVGPEANVGPY	O09159|MA2B1_MOUSE	48.88	15	1000	NA	263
QLEALVGPEANVGPYG	O09159|MA2B1_MOUSE	49.85	16	2990	NA	1300

QNAWFLPAQADIVATK	P10852|4F2_MOUSE	49.76	16	2370	NA	1820
QNHGYTIPVVNIEVSPF	E9Q414|APOB_MOUSE	49.73	17	943	NA	1490
QPDLNFRNPAVQEEIK	Q91WV7|SLC31_MOUSE	49.94	16	132000	NA	89800
QPDLNFRNPAVQEEIKE	Q91WV7|SLC31_MOUSE	49.66	17	50900	NA	40100
QPPEYTFPSGSGAHFP	Q2TBE6|P4K2A_MOUSE	49.87	16	7160	NA	6660
QPPEYTFPSGSGAHFPQ	Q2TBE6|P4K2A_MOUSE	38.68	17	2380	NA	2120
QPSTSSLAAPTVEAA	Q91ZP6|NFIP2_MOUSE	41.87	15	2810	NA	2110
QPSTSSLAAPTVEAAA	Q91ZP6|NFIP2_MOUSE	45.93	16	7240	93.2	4790
QPSTSSLAAPTVEAAASA	Q91ZP6|NFIP2_MOUSE	49.39	18	82000	4570	61400
QPSTSSLAAPTVEAAASAP	Q91ZP6|NFIP2_MOUSE	49.72	19	78200	2610	89900
QPTGPPPYHESLAGASQPP	Q9D7I0|SHSA5_MOUSE	48.26	19	48700	NA	48300
QPTGPPPYHESLAGASQPPY	Q9D7I0|SHSA5_MOUSE	49.26	20	14800	NA	15600
QPTGPPPYHESLAGASQPPYN	Q9D7I0|SHSA5_MOUSE	49.58	21	724	NA	637
QPVLQYGNPYSAQETRDG	Q3UKC1|TAXB1_MOUSE	49.94	18	396	NA	363
QQLAFKQPSSAYAA	P01027|CO3_MOUSE	49.11	14	1560	NA	873
QQLAFKQPSSAYAAF	P01027|CO3_MOUSE	49.78	15	6320	164	7560
QQLAFKQPSSAYAAFNN	P01027|CO3_MOUSE	49.94	17	167	NA	126
QQVRSPVTNIAR	P84091|AP2M1_MOUSE	45.48	12	457	NA	456
QSINFLGGQPAAAPYP	Q8K419|LEG4_MOUSE	41.8	16	377	NA	378
QSINFLGGQPAAAPYPG	Q8K419|LEG4_MOUSE	37.4	17	NA	NA	2120
QSTDYGNFLANEASP	P51863|VA0D1_MOUSE	46.42	15	292	NA	236
QVQWNDPGAQYSLVN	Q9R100|CAD17_MOUSE	49.86	15	5830	NA	2670
QVQWNDPGAQYSLVNK	Q9R100|CAD17_MOUSE	49.91	16	2460	NA	1900
QVQWNDPGAQYSLVNKE	Q9R100|CAD17_MOUSE	49.94	17	512	NA	552
QWNDPGAQYSLVNKE	Q9R100|CAD17_MOUSE	49.75	15	231	NA	129
QYPNFAGPQAALANK	Q8BJW6|EIF2A_MOUSE	28.94	15	NA	NA	211
QYPNFAGPQAALANKS	Q8BJW6|EIF2A_MOUSE	48.9	16	860	NA	562
R(+42.01)PVQ(+15.00)FPYVTPAPHEPVI	Q9D074|MGRN1_MOUSE	48.73	17	579	NA	1310
RAGYKAAIVHNVDS	O54965|RNF13_MOUSE	48	14	693	NA	334
RASIYQSVVINTSKE	P97872|FMO5_MOUSE	48.97	15	4950	NA	4120
RATPAPSAPAAASATSPSPAPS	Q9JKV1|ADRM1_MOUSE	42.86	22	NA	NA	134
RDNM(+15.99)FSGSKINYTENR	P06745|G6PI_MOUSE	47.74	16	NA	NA	344
RDNMFSGSKINYTENR	P06745|G6PI_MOUSE	49.51	16	775	NA	966
RDPYATSVGHLIEK	Q923U0|TM1L1_MOUSE	45.89	14	168	NA	129
REFYSASVAEDA	E9Q7P9|CDHR2_MOUSE	39.54	12	594	NA	747
RENIWKAPEPVE	Q9R100|CAD17_MOUSE	37.08	12	473	NA	159
RENIWKAPEPVEIR	Q9R100|CAD17_MOUSE	49.68	14	13600	NA	11000
RENIWKAPEPVEIRE	Q9R100|CAD17_MOUSE	49.61	15	70200	653	50300
REVSSVEAPSVSPA	Q8BUJ9|LRP12_MOUSE	38.08	14	470	NA	645
REVSSVEAPSVSPARH	Q8BUJ9|LRP12_MOUSE	48.04	16	186	NA	323
REVSSVEAPSVSPARHQ	Q8BUJ9|LRP12_MOUSE	49.75	17	1500	NA	1610
REVSSVEAPSVSPARHQL	Q8BUJ9|LRP12_MOUSE	44.73	18	NA	NA	186
RFVNVVPTFG	P62862|RS30_MOUSE	29.6	10	NA	NA	300
RHKYIYKSPELPRIL	Q99LR1|ABD12_MOUSE	49.91	15	4900	NA	2240
RHNYEGPETHTSL	P14483|HB2A_MOUSE	47.89	13	20800	3910	13500
RHNYEGPETHTSLR	P14483|HB2A_MOUSE	49.05	14	53400	3850	53100
RIEHLYKNPQAHIEG	Q8K0C9|GMDS_MOUSE	49.79	15	776	NA	823
RIEHLYKNPQAHIEGN	Q8K0C9|GMDS_MOUSE	26.27	16	318	NA	216
RIGSGGVFRAPSIHGGSGGR	P19001|K1C19_MOUSE	48.87	20	NA	NA	1310
RIGSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	48.19	21	836	NA	2820
RIKRFLAKKQKQNRPIPQWIRM(+15.99)I	P62892|RL39_MOUSE	43.67	23	739	NA	1580
RINAWNSPTLPIYEPG	O70475|UGDH_MOUSE	36.81	16	96.9	NA	90.5
RIPSAVGYQPTLATD	P56480|ATPB_MOUSE	40.83	15	NA	48.8	197
RIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	48.92	15	NA	2430	601
RIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	49.94	16	282	1090	218
RKAAGGAKRKTSGPPVSELITKAVAASK	P43274|H14_MOUSE	48.95	30	NA	NA	636
RKATGPPVSELITKAVSASKERG	P43276|H15_MOUSE	48.95	23	NA	NA	164
RKFYKGKKYKPLDLRPKKTR	Q6ZWV7|RL35_MOUSE	48.89	20	NA	NA	163
RKIVYEGPELNH	Q91ZX7|LRP1_MOUSE	43.47	12	175	NA	164
RKIVYEGPELNHA	Q91ZX7|LRP1_MOUSE	49.25	13	3620	NA	2800
RKIVYEGPELNHAFG	Q91ZX7|LRP1_MOUSE	49.91	15	407000	17700	350000
RKRSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.95	23	8610	NA	282
RLEVVTDPTTNAGYVK	Q9R100|CAD17_MOUSE	49.45	16	3220	NA	2120
RLPYTASSGLM(+15.99)APRE	Q9R1Q9|VAS1_MOUSE	48.89	15	3350	NA	2860
RLPYTASSGLMAPR	Q9R1Q9|VAS1_MOUSE	45.5	14	332	NA	352
RLPYTASSGLMAPRE	Q9R1Q9|VAS1_MOUSE	47.44	15	353	NA	196
RM(+15.99)APYQGPDAAPGAL	P57780|ACTN4_MOUSE	42.25	15	649	NA	532
RM(+15.99)APYQGPDAAPGALD	P57780|ACTN4_MOUSE	44.52	16	NA	NA	1430
RM(+15.99)KLPKSAKPVSQMRMATPLLM	P04441|HG2A_MOUSE	43.44	25	NA	NA	565
RM(+15.99)KLPKSAKPVSQMRMATPLLM	P04441|HG2A_MOUSE	48.78	25	NA	NA	289
RMAPYQGPDAAPG	P57780|ACTN4_MOUSE	49.01	13	383	NA	322
RMAPYQGPDAAPGAL	P57780|ACTN4_MOUSE	47.54	15	188	NA	383
RMAPYQGPDAAPGALD	P57780|ACTN4_MOUSE	49.39	16	701	NA	1080
RMKLPKSAKPVSQM(+15.99)RMATPLLM	P04441|HG2A_MOUSE	46.87	25	NA	NA	1390
RMKLPKSAKPVSQM(+15.99)RMATPLLM	P04441|HG2A_MOUSE	39.99	25	NA	NA	389
RMKLPKSAKPVSQMRMATPLLM(+15.99	P04441|HG2A_MOUSE	38.69	25	NA	NA	762
RNPRQINWTVLYRRKHKKGQSEEIQK	Q8BP67|RL24_MOUSE	27.82	26	NA	NA	1620
RNPRQINWTVLYRRKHKKGQSEEIQKKK	Q8BP67|RL24_MOUSE	48.81	28	1070	NA	4480
RNPRQINWTVLYRRKHKKGQSEEIQKKK	Q8BP67|RL24_MOUSE	38.11	29	NA	NA	1170
RNVNIFKFIIPNIVK	P06151|LDHA_MOUSE	49.71	15	NA	NA	207
RNVQFNYPQASVTD	Q61703|ITIH2_MOUSE	49.72	14	3200	NA	2650

RNVQFNYPQASVTDV	Q61703|ITIH2_MOUSE	49.57	15	338	NA	501
RNVQFNYPQASVTDVT	Q61703|ITIH2_MOUSE	49.85	16	26500	1230	31000
RNVQFNYPQASVTDVTQ	Q61703|ITIH2_MOUSE	49.92	17	118	NA	115
RNYEYYASHVPESVK	Q9Z0S1|BPNT1_MOUSE	49.79	15	12400	NA	11700
RNYSYEKL	Q02257|PLAK_MOUSE	27.88	8	NA	NA	200
RPDAEYWNSQPEIL	P14483|HB2A_MOUSE:P01921|HB2D_M	47.92	14	3370	214	2370
RPDAEYWNSQPEILE	P14483|HB2A_MOUSE:P01921|HB2D_M	48.91	15	14100	485	6790
RPDAEYWNSQPEILER	P14483|HB2A_MOUSE:P01921|HB2D_M	49.76	16	44800	2110	30900
RPDAEYWNSQPEILERT	P14483|HB2A_MOUSE:P01921|HB2D_M	49.07	17	2350	NA	1020
RPEPWGPSWDAAPTPGPAPWG	Q9D956|MALD3_MOUSE	42.17	21	632	NA	763
RPGPREPPPYQEPRPRGTPPH	Q03146|DDR1_MOUSE	48.04	21	1010	NA	1450
RPHTYFGPETSASK	P70277|SIA7B_MOUSE	45.86	14	NA	NA	217
RPHTYFGPETSASKF	P70277|SIA7B_MOUSE	48.53	15	558	NA	479
RPKQESYKHADIKVAPP	Q6Q473|CLA4A_MOUSE	46.84	17	342	NA	178
RPLYTHEYKGPKADLKKDEK	Q8BU14|SEC62_MOUSE	49.87	20	NA	NA	297
RPSFFKDFRPPYVKADHG	Q8BK48|EST2E_MOUSE	49.94	18	375	NA	393
RPVQFPYVTPAPHEP	Q9D074|MGRN1_MOUSE	49.75	15	18300	222	38200
RPVQFPYVTPAPHEPVK	Q9D074|MGRN1_MOUSE	49.92	17	208000	9070	191000
RPVQFPYVTPAPHEPVKT	Q9D074|MGRN1_MOUSE	49.92	18	20600	92.1	28400
RPVQFPYVTPAPHEPVKTL	Q9D074|MGRN1_MOUSE	49.93	19	264	NA	844
RPVTIFGPIADVAREK	P39447|ZO1_MOUSE	49.37	16	1510	NA	1740
RPVVILGPVADIAMKK	Q9QXY1|ZO3_MOUSE	49.87	16	NA	NA	62
RQLDEYSSSVANFL	Q91VE0|S27A4_MOUSE	49.2	14	386	NA	184
RQLDEYSSSVANFLQ	Q91VE0|S27A4_MOUSE	48.65	15	199	NA	173
RQLDEYSSSVANFLQA	Q91VE0|S27A4_MOUSE	48.18	16	NA	NA	1150
RQLDEYSSSVANFLQAR	Q91VE0|S27A4_MOUSE	49.92	17	298	NA	237
RQPKYPRKSAPRRNKLDHYAIIKF	P62751|RL23A_MOUSE	49.93	24	2890	NA	1390
RQQLYIASRSAVAQIA	Q62177|SEM3B_MOUSE	36.47	16	779	NA	828
RQQVRSPVTNIAR	P84091|AP2M1_MOUSE	37.35	13	NA	NA	1020
RRASHTAPQVLFSHREPP	Q9CVB6|ARPC2_MOUSE	40.56	18	1980	NA	1450
RRPYRRRRFPPYYM(+15.99)RRPYARR	P62960|YBOX1_MOUSE	25.65	30	NA	1400	3630
RRPYRRRRFPPYYMRRPYARRPQYSNF	P62960|YBOX1_MOUSE	36.34	30	NA	NA	19800
RSAHQVARYRPRAPIIAVTRNPQ	P52480|KPYM_MOUSE	49.49	23	64.6	NA	238
RSESYHAGLPM(+15.99)EPDYPG	Q32NZ6|TMC5_MOUSE	43.57	17	1220	NA	287
RSFFWNVAPGAESAVAS	P57716|NICA_MOUSE	41.05	17	536	NA	1280
RSPHPYQLPQALAPHVD	O89023|TPP1_MOUSE	49.93	17	395	NA	429
RSQVTPSVPSEALDD	Q7TQH7|LRP10_MOUSE	48.57	15	562	NA	282
RSQVTPSVPSEALDDS	Q7TQH7|LRP10_MOUSE	49.2	16	457	NA	281
RSQVTPSVPSEALDDST	Q7TQH7|LRP10_MOUSE	49.8	17	273	NA	98.2
RSRKESYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.95	21	997	NA	466
RSYAAAVANRAKGGG	Q8K296|MTMR3_MOUSE	38.96	15	NA	NA	135
RSYSSPDITQALQ	Q80U87|UBP8_MOUSE	45.84	13	1060	NA	949
RSYSSPDITQALQE	Q80U87|UBP8_MOUSE	45.03	14	2800	NA	2310
RSYSSPDITQALQEE	Q80U87|UBP8_MOUSE	46.43	15	819	NA	518
RSYTAAVANRA	Q91XS1|MTMR4_MOUSE	36.52	11	301	NA	308
RSYTAAVANRAK	Q91XS1|MTMR4_MOUSE	41.48	12	NA	NA	906
RSYTAAVANRAKGG	Q91XS1|MTMR4_MOUSE	45.62	14	NA	NA	530
RSYTAAVANRAKGGG	Q91XS1|MTMR4_MOUSE	47.23	15	2530	NA	2300
RTFQYQDSLPSLPVPA	Q9DC50|OCTC_MOUSE	26.36	16	NA	NA	1280
RTGAKGPILSIYFR	Q9D8I3|GLOD5_MOUSE	30.75	14	NA	NA	141
RTPGNRIVYLYTKKVGKAP	Q9D1R9|RL34_MOUSE	49.94	19	402	2030	3390
RTPGNRIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	49.95	20	700	6680	2800
RTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	49.95	21	1910	2640	1080
RTTTWQRPTAEYVR	Q9DBH0|WWP2_MOUSE	31.03	14	445	NA	539
RTTTWQRPTAEYVRNY	Q9DBH0|WWP2_MOUSE	49.31	16	332	NA	426
RVEAQSSPVPAYAWY	Q9D2Z1|CEA20_MOUSE	48.14	15	503	NA	1120
RVEAQSSPVPAYAWYLP	Q9D2Z1|CEA20_MOUSE	47.56	17	171	NA	636
RVITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.93	18	3560	NA	4950
RVPKKKKMPENFMPPVPITSPIMNPSG	Q3UPL0|SC31A_MOUSE	48.94	27	NA	NA	292
RVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.56	13	128	NA	131
RVQIYHNPTANSFR	P70460|VASP_MOUSE	46.65	14	2570	NA	3170
RVQIYHNPTANSFRV	P70460|VASP_MOUSE	47.8	15	NA	NA	2300
RYIAPTVLVDVQ	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	38.48	12	105	NA	232
RYIAPTVLVDVQE	Q80VQ0|AL3B1_MOUSE:E9Q3E1|AL3B2	43.03	13	363	NA	703
RYKPSPERYAAAPHPLLSFDPH	G3X9J0|SI1L3_MOUSE	47.99	22	NA	NA	247
RYM(+15.99)APEVLDEHIR	Q61288|ACVL1_MOUSE	29.57	13	NA	NA	83.5
RYM(+15.99)APEVLDESLN	P36895|BMR1A_MOUSE	44.92	13	485	NA	211
RYM(+15.99)APEVLDETIN	Q61271|ACV1B_MOUSE	48.68	13	5310	18.6	3170
RYM(+15.99)APEVLDETIQ	P37172|ACVR1_MOUSE	36.94	13	733	NA	375
RYMAPEVLDET	Q61271|ACV1B_MOUSE:P37172|ACVR1	37.09	11	78.3	NA	63.6
RYMAPEVLDETIN	Q61271|ACV1B_MOUSE	48.1	13	1880	NA	2590
RYMAPEVLDETIQ	P37172|ACVR1_MOUSE	43.41	13	182	NA	352
RYRPRAPIIAVTRNPQ	P52480|KPYM_MOUSE	46.53	16	1250	NA	4710
RYTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.93	15	4780	NA	7310
RYTQKAPQVSTPTLVEA	P07724|ALBU_MOUSE	49.88	17	2450	NA	1610
S(+42.01)AEREAAEAATVAAATEA	Q62465|VAT1_MOUSE	37.36	18	740	NA	455
S(+42.01)AEREAAEAATVAAATEAG	Q62465|VAT1_MOUSE	40.23	19	1040	NA	946
S(+42.01)ETAPAETAAPAPVEKSPAK	P43276|H15_MOUSE	36.85	20	NA	NA	92.1
S(+42.01)ETAPVAQAASTA	P43275|H11_MOUSE	32.69	13	2210	NA	1510
S(+42.01)ETAPVAQAASTATEKPA	P43275|H11_MOUSE	49.91	18	3010	NA	5870
S(+42.01)ETAPVAQAASTATEKPAA	P43275|H11_MOUSE	49.89	19	3410	NA	1660

S(+42.01)ETAPVAQAASTATEKPAAAKK	P43275|H11_MOUSE	43.76	26	557	NA	660
S(+42.01)GRGKQGGKARAKAKSR	Q8BFU2|H2A3_MOUSE:Q64522|H2A2B_	43.25	17	NA	NA	811
S(+42.01)GRGKQGGKARAKAKTRSSRA	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	49.94	29	3790	50400	3350
S(+42.01)GRGKQGGKARAKAKTRSSRA	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	43.24	32	2530	19000	2330
S(+42.01)ILYVSPHPDAFPS	Q9Z1Q9|SYVC_MOUSE	42.27	14	292	NA	382
S(+42.01)IRVTQKSYKM(+15.99)STSGPF	P11679|K2C8_MOUSE	48.95	25	390	NA	3540
S(+42.01)IRVTQKSYKM(+15.99)STSGPF	P11679|K2C8_MOUSE	48.88	29	NA	NA	1390
S(+42.01)IRVTQKSYKMSTSGPRAFSSR	P11679|K2C8_MOUSE	49.94	26	1550	NA	707
S(+42.01)IRVTQKSYKMSTSGPRAFSSR	P11679|K2C8_MOUSE	38.1	29	7120	NA	2820
S(+42.01)KPPPKPVKPGQVKVFRALYTF	Q62422|OSTF1_MOUSE	49.91	22	611	NA	355
S(+42.01)KSPKKPKVVKAKKVAKSPAK	P43275|H11_MOUSE	49.94	21	2290	221	1560
S(+42.01)PKKVKAAKPKKAAKSPAK	P43277|H13_MOUSE	49.9	19	3910	NA	3100
S(+42.01)SKKAKTKTTKKRPQRATSNVF	Q3THE2|ML12B_MOUSE	48.39	25	913	NA	683
S(+42.01)SKKAKTKTTKKRPQRATSNVF	Q3THE2|ML12B_MOUSE	29.71	25	NA	NA	594
S(+42.01)SNGTDAPAEAQAAM(+15.99)E	Q9DBG5|PLIN3_MOUSE	49.94	27	475	NA	214
S(+42.01)VQVVSAAAAAKVPEV	Q68FL4|SAHH3_MOUSE	48.4	16	1190	118	1820
S(+42.01)VQVVSAAAAAKVPEVELK	Q68FL4|SAHH3_MOUSE	48.91	19	NA	NA	809
S(+42.01)YGPLDM(+15.99)YRNPGPSGF	Q9ER00|STX12_MOUSE	36.88	19	905	NA	5420
S(+42.01)YKPIAPAPSSTPG	Q9CPY4|CDKA2_MOUSE	28.8	14	207	NA	136
S(+42.01)YTPGQPVTAVVQR	Q9DBG9|TX1B3_MOUSE	44.6	14	519	NA	460
SAAPAPAPAAAPAPAPAAQAVG	Q9Z1W9|STK39_MOUSE	28.85	22	NA	NA	51.3
SAGTRYSAPANLYVR	Q64487|PTPRD_MOUSE:A2A8L5|PTPRF	48.91	15	197	NA	227
SAKPVSQM(+15.99)RMATPLLMRPM	P04441|HG2A_MOUSE	29.75	19	NA	NA	6940
SAKPVSQM(+15.99)RMATPLLMRPMS	P04441|HG2A_MOUSE	29.76	20	606	NA	1670
SAKPVSQMRM(+15.99)ATPLLMRPM	P04441|HG2A_MOUSE	42.29	19	1460	NA	4680
SAKPVSQMRMATPLLM(+15.99)RPM(+1	P04441|HG2A_MOUSE	49.75	19	7660	NA	11000
SAKPVSQMRMATPLLMRPM	P04441|HG2A_MOUSE	48.93	19	NA	NA	8090
SAKPVSQMRMATPLLMRPM(+15.99)	P04441|HG2A_MOUSE	49.86	19	2600	NA	10500
SAKPVSQMRMATPLLMRPM(+15.99)SM	P04441|HG2A_MOUSE	38.87	21	NA	NA	1410
SANVFRSPSPLRAGPL	Q9CSB4|PAR3L_MOUSE	44.73	16	NA	NA	80.1
SAPAPKKGSKKAVTKAQKKDGKKRKR	Q8CGP0|H2B3B_MOUSE:Q6ZWY9|H2B1	49.95	26	9760	2820	32900
SAPAPKKGSKKAVTKAQKKDGKKRKRS	Q6ZWY9|H2B1C_MOUSE:Q64524|H2B2	48.95	29	NA	NA	4030
SAPAPKKGSKKAVTKAQKKDGKKRKRS	Q6ZWY9|H2B1C_MOUSE:Q64524|H2B2	48.49	30	NA	NA	5150
SAQSPYINPIIPFTGPI	O08573|LEG9_MOUSE	49.83	17	408	NA	409
SASKAVKPKAAKPKVAKAKK	P15864|H12_MOUSE	48.95	20	NA	NA	3630
SASKTEAPAAAKSLTSPL	Q9QY76|VAPB_MOUSE	48.85	18	1930	NA	1850
SASNLITPSVVAIVGPQ	Q8BJ51|MFS11_MOUSE	30.5	17	NA	NA	22.8
SDHTYQSALLSGSDEE	Q8VCZ2|TM45B_MOUSE	36.04	16	NA	NA	451
SDIYQAPSADSADHL	P26361|CFTR_MOUSE	44.4	15	712	NA	657
SDM(+15.99)FKASLVIPSKD	Q8BJD1|ITIH5_MOUSE	38.56	14	1220	NA	332
SDMFKASLVIPSKD	Q8BJD1|ITIH5_MOUSE	47.43	14	528	NA	345
SDPKYATPQVIQAPGP	O54967|ACK1_MOUSE	48.51	16	1860	NA	1790
SDPKYATPQVIQAPGPR	O54967|ACK1_MOUSE	49.82	17	12600	NA	15500
SDSGNFRPANPNWG	E9PV24|FIBA_MOUSE	48.16	14	464	NA	561
SDSGNFRPANPNWGVF	E9PV24|FIBA_MOUSE	48.28	16	433	NA	632
SDSGNFRPANPNWGVFS	E9PV24|FIBA_MOUSE	49.89	17	886	NA	1090
SDSGNFRPANPNWGVFSE	E9PV24|FIBA_MOUSE	49.94	18	144	NA	111
SDTIKPDVN	P35700|PRDX1_MOUSE	41.53	9	224	164	261
SEEEYSAPLPTPAP	P97467|AMD_MOUSE	49.34	14	1070	NA	1070
SEEEYSAPLPTPAPS	P97467|AMD_MOUSE	49.9	15	8700	60.2	6230
SEPEYATPIVERH	Q9D4J3|DCBD1_MOUSE	42.77	13	1250	NA	1240
SEPEYATPIVERHL	Q9D4J3|DCBD1_MOUSE	49.06	14	1280	NA	1170
SEPEYATPIVERHLL	Q9D4J3|DCBD1_MOUSE	48	15	NA	NA	999
SEPFFYSKYSAPRLPAALEQ	P97432|NBR1_MOUSE	48.92	20	102	NA	349
SEPYTFSHPNKGEIG	Q5U462|CDCP1_MOUSE	49.76	15	7410	NA	1840
SESEPYTFSHPNKGEIG	Q5U462|CDCP1_MOUSE	49.58	17	640	NA	532
SESSFNSPQGVAIADN	Q8BZW8|NHLC2_MOUSE	41.28	16	241	NA	174
SEVYTFPVPERH	P09803|CADH1_MOUSE	46.45	12	508	NA	93
SFFWNVAPGAESAVA	P57716|NICA_MOUSE	36.2	15	1210	NA	1070
SFFWNVAPGAESAVAS	P57716|NICA_MOUSE	37.89	16	2040	NA	1840
SFPAAQQTVFTIHPSHVQPAYTTPPH	O70305|ATX2_MOUSE	42.97	26	NA	NA	213
SFRNPLAK	P17182|ENOA_MOUSE	28.9	8	NA	NA	56
SFTSGPGARISS	P11679|K2C8_MOUSE	37.97	12	NA	NA	165
SFVQNYPVVSIEDPF	P17182|ENOA_MOUSE	49.84	15	585	NA	650
SGAQEM(+15.99)VSSSVSSAKETV	Q9DBG5|PLIN3_MOUSE	48.77	18	NA	NA	283
SGAQEMVSSSVSSAKETVA	Q9DBG5|PLIN3_MOUSE	49.9	19	78.9	NA	114
SGAVIFNFPGTRNEVIP	Q9D304|RN128_MOUSE	29.58	17	NA	NA	441
SGAVIFNFPGTRNEVIPM	Q9D304|RN128_MOUSE	49.92	18	980	NA	2050
SGAVIFNFPGTRNEVIPM(+15.99)	Q9D304|RN128_MOUSE	49.94	18	7180	NA	1910
SGDEKKGPLIVSGPDGAPAKGDG	Q8VBW1|SC6A8_MOUSE	48.31	23	1940	NA	866
SGFAAPFFIVRHQLLKK	P17665|COX7C_MOUSE	43.52	17	3850	NA	2460
SGFTNTM(+15.99)RVVPVP	P52480|KPYM_MOUSE	43.73	13	21600	14100	15400
SGFTNTMRVVPVP	P52480|KPYM_MOUSE	47.62	13	16800	NA	24700
SGGTSRHPGPL	P23150|HA2J_MOUSE:P14434|HA2B_M	36.29	11	1100	NA	648
SGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	45.15	18	1140	NA	874
SGIFVSPKGVLENAG	Q9QXW9|LAT2_MOUSE	40.34	15	309	NA	180
SGKDKKKKTKKIKEKYID	P11499|HS90B_MOUSE	48.93	18	NA	NA	222
SGKDKKKKTKKIKEKYIDQ	P11499|HS90B_MOUSE	49.56	19	161	1080	795
SGNFRPANPNWG	E9PV24|FIBA_MOUSE	40.33	12	575	NA	1700
SGNFRPANPNWGVF	E9PV24|FIBA_MOUSE	49.32	14	1730	NA	2440
SGPKPFSAPKPQTSPSP	P40124|CAP1_MOUSE	45.96	17	7240	189	13300

SGPKPFSAPKPQTSPSPK	P40124|CAP1_MOUSE	49.86	18	12300	690	16300
SGPKPFSAPKPQTSPSPKPA	P40124|CAP1_MOUSE	49.94	20	12300	244	6210
SGPMAKFIQSTPSKSL	Q9D309|FAM3B_MOUSE	48.36	16	NA	NA	188
SGPMAKFIQSTPSKSLLF	Q9D309|FAM3B_MOUSE	48.05	18	NA	NA	43.8
SGPVTPLSPSVLPSLPQ	Q6NS82|RETR2_MOUSE	43.72	17	526	NA	315
SGQIFISPDSLLGVEK	Q9D871|CEA18_MOUSE	44.81	16	2880	NA	1080
SGRFTYQNAAAQPETGPG	Q9QZM4|TR10B_MOUSE	48.94	18	10500	266	589
SGRHKFRPSFPASSP	O89023|TPP1_MOUSE	29.45	15	668	NA	252
SGRHKFRPSFPASSPYVT	O89023|TPP1_MOUSE	38.43	18	348	NA	96.7
SGVSLAALKK	P15864|H12_MOUSE:P43275|H11_MOU	33.72	10	NA	NA	92.5
SGVSLAALKKALAAAGYDVEKNNSRIKL(	P15864|H12_MOUSE:P43274|H14_MOU	48.9	31	NA	NA	7640
SHDYKGSTSHSLPYE	E9Q414|APOB_MOUSE	32.47	15	1160	NA	910
SHPPAHFQSPPTPFIPFTSPLPLPPAPPC	Q9D6N5|NC2A_MOUSE	48.93	31	NA	NA	2450
SHRAVYVGVHVPFSKE	Q8BTY2|S4A7_MOUSE	49.68	16	60	NA	156
SHRDPYATSVGHLIE	Q923U0|TM1L1_MOUSE	49.27	15	1150	NA	899
SHRDPYATSVGHLIEK	Q923U0|TM1L1_MOUSE	49.76	16	1340	NA	1010
SHRDPYATSVGHLIEKA	Q923U0|TM1L1_MOUSE	49.84	17	421	NA	295
SIASFKDPKISTSLP	Q61233|PLSL_MOUSE	47.26	15	1040	NA	580
SILDRYYTPTISRE	Q9R1P3|PSB2_MOUSE	36.93	14	433	NA	355
SILDRYYTPTISRER	Q9R1P3|PSB2_MOUSE	45.21	15	7440	NA	7850
SILDRYYTPTISRERAV	Q9R1P3|PSB2_MOUSE	47.18	17	626	NA	179
SILWSQPLPSLPGGPP	Q8C0Z1|F234A_MOUSE	49.66	16	3530	NA	2530
SINFLGGQPAAAPY	Q8K419|LEG4_MOUSE	45.57	14	180	NA	98.8
SINFLGGQPAAAPYPG	Q8K419|LEG4_MOUSE	49.26	16	10700	NA	7350
SIPAWTGPEIPESGPS	Q8K4G1|LTBP4_MOUSE	48.71	16	850	NA	232
SKADKKQKKKVDRK	Q0VG18|SIM24_MOUSE	48.63	14	NA	NA	1170
SKAPSKKPKATPVKKAKKKPA	P10922|H10_MOUSE	49.95	21	NA	NA	1230
SKASKPKVTKPKTAKPKAAKAKK	P43276|H15_MOUSE	49.95	23	NA	NA	1620
SKASKPKVTKPKTAKPKAAKAKKAVSKK	P43276|H15_MOUSE	49.95	28	1260	NA	1750
SKASKPKVTKPKTAKPKAAKAKKAVSKK	P43276|H15_MOUSE	49.95	29	45900	12400	1620
SKAVKPKAAKP	P15864|H12_MOUSE	33.85	11	NA	NA	275
SKAVKPKAAKPKVAKAKKVAAKK	P15864|H12_MOUSE	49.95	23	461	NA	336
SKAVKPKAAKPKVAKAKKVAAKKK	P15864|H12_MOUSE	49.95	24	5860	340	1400
SKKKKKFRTPSFLKKNKK	Q9QYB5|ADDG_MOUSE	49.7	18	NA	NA	1920
SKKKKKFRTPSFLKKNKKK	Q9QYB5|ADDG_MOUSE	49.95	19	1240	4710	2560
SKKKKKFRTPSFLKKNKKKEK	Q9QYB5|ADDG_MOUSE	49.67	21	NA	NA	748
SKKKKKKKKP	Q99L45|IF2B_MOUSE	43.23	10	16100	12700	15400
SKLLYKTSVVKKAAAR	Q9JJY3|NSMA2_MOUSE	49.91	16	384	NA	338
SKLVNNSPLPQSVVF	Q61703|ITIH2_MOUSE	46.03	15	101	NA	151
SKNVFLSPM(+15.99)SISSA	Q60854|SPB6_MOUSE	43.03	14	426	NA	232
SKNVFLSPM(+15.99)SISSAL	Q60854|SPB6_MOUSE	48.01	15	907	NA	369
SKNVFLSPMSISSA	Q60854|SPB6_MOUSE	47.24	14	357	NA	319
SKNVFLSPMSISSAL	Q60854|SPB6_MOUSE	38.4	15	230	NA	638
SKPKATKAKKAAPR	P43277|H13_MOUSE	49.9	14	2620	NA	3680
SKPKVTKPKTAKPKAAKAKKAVSKKK	P43276|H15_MOUSE	49.95	26	2010	NA	551
SKRNPRQINWTVLYRRKHKKGQSEEIQI	Q8BP67|RL24_MOUSE	48.45	30	NA	NA	658
SKTVYEGPFASRSLS	Q60680|IKKA_MOUSE	42.67	15	863	NA	814
SLDKFLASVSTVLTSKYR	P01942|HBA_MOUSE	49.69	18	NA	NA	295
SLESFLGPRANTEDLP	Q8BSF4|PISD_MOUSE	36.14	16	1850	NA	647
SLFLKTPKIVSSKD	P06151|LDHA_MOUSE	49.89	14	680	NA	331
SLFLKTPKIVSSKDY	P06151|LDHA_MOUSE	48.34	15	282	NA	275
SLHLRFSAPQIENEP	Q61190|I10R2_MOUSE	47.84	15	1280	NA	760
SLHLRFSAPQIENEPET	Q61190|I10R2_MOUSE	49.88	17	2280	NA	2210
SLKYNFVTPLTHM(+15.99)VVT	A6X935|ITIH4_MOUSE	49.86	16	1520	NA	1730
SLKYNFVTPLTHM(+15.99)VVTKP	A6X935|ITIH4_MOUSE	49.94	18	23500	481	21700
SLKYNFVTPLTHM(+15.99)VVTKPE	A6X935|ITIH4_MOUSE	49.94	19	705	NA	570
SLKYNFVTPLTHMVVT	A6X935|ITIH4_MOUSE	49.93	16	401	NA	1580
SLKYNFVTPLTHMVVTKPE	A6X935|ITIH4_MOUSE	49.94	19	324	NA	699
SLLYNVPAVAEEIQ	P12023|A4_MOUSE	48.97	14	1710	NA	924
SLPESTPVPSSSPP	Q6PB44|PTN23_MOUSE	29.16	14	446	NA	278
SLPESTPVPSSSPPP	Q6PB44|PTN23_MOUSE	48.72	15	1120	NA	400
SLPPHVYSTPQPSLPPVQPSAPPP	Q3UPH1|PRRC1_MOUSE	49.94	24	1230	NA	3830
SLPQLPPTVLPVE	Q99LJ1|FUCO_MOUSE	29.59	13	3670	NA	1530
SLRDLESPNVDSSPSPP	Q8K0B3|LRC66_MOUSE	49.9	17	773	NA	727
SLRFAPPQPAEPWS	Q8VCT4|EST1D_MOUSE:Q91WU0|EST1	49.65	14	239	NA	208
SLVHSSPHVALSHVD	Q9WV91|FPRP_MOUSE	49.31	15	294	NA	445
SLVHSSPHVALSHVDT	Q9WV91|FPRP_MOUSE	25.95	16	NA	NA	59.4
SLVSKGTLVQTK	P43276|H15_MOUSE:P43274|H14_MOU	48.4	12	617	83.3	739
SLVSKGTLVQTKGTGASGSFKLNK	P43276|H15_MOUSE:P43274|H14_MOU	49.95	24	1400	NA	1420
SLVSKGTLVQTKGTGASGSFKLNKK	P43276|H15_MOUSE:P43274|H14_MOU	49.95	25	5780	413	15700
SLVSKGTLVQTKGTGASGSFKLNKKA	P43276|H15_MOUSE:P43274|H14_MOU	49.95	26	308	NA	312
SLVSKGTLVQTKGTGASGSFKLNKKAAS	P43276|H15_MOUSE:P43274|H14_MOU	49.92	28	974	NA	2880
SLVSKGTLVQTKGTGASGSFKLNKKAAS	P43276|H15_MOUSE:P43274|H14_MOU	48.01	29	412	NA	998
SNDTTVLLPPYDDATAVPSTAKEPPPP	Q91XQ6|LAP4B_MOUSE	49.88	27	492	NA	680
SNHEQLPILG	P04441|HG2A_MOUSE	28.48	10	711	NA	319
SNIKIYNTPSASYLEV	P13595|NCAM1_MOUSE	45.52	16	177	NA	254
SNIYDLVAPFPSAPN	P09470|ACE_MOUSE	48.49	15	806	NA	39.1
SNIYDLVAPFPSAPNID	P09470|ACE_MOUSE	49.61	17	667	NA	2020
SNKTRLSRTPGNRIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	29.78	27	NA	NA	2230
SNMTYEKL	Q3UPW2|ELF3_MOUSE	28.64	8	NA	NA	341
SNNSIMSNPVAGLVIG	Q9DBP0|NPT2B_MOUSE	47.94	16	282	NA	684

SNPSYNYEIVNRAS	Q9JHU4|DYHC1_MOUSE	47.68	14	NA	NA	164
SPAEYAGPEGSYFG	P43406|ITAV_MOUSE	41.82	14	313	NA	291
SPAKAKAVKPKASKAKVTKPKTPAKPKK	P43275|H11_MOUSE	44.33	31	NA	NA	594
SPAPSTRVITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.95	24	4860	60.4	8050
SPAPSTRVITNQYNSPTGLYSSENIS	O70400|PDLI1_MOUSE	49.95	26	1040	NA	2500
SPAPSTRVITNQYNSPTGLYSSENISN	O70400|PDLI1_MOUSE	48.95	27	149	NA	923
SPATRKEYHTGKAVTSKG	E9PV24|FIBA_MOUSE	49.94	18	508	NA	633
SPATRKEYHTGKAVTSKGDK	E9PV24|FIBA_MOUSE	49.94	20	1510	NA	2520
SPAVAAAQAPAPTPALPP	P54728|RD23B_MOUSE	49.88	18	10300	NA	11700
SPAVAAAQAPAPTPALPPT	P54728|RD23B_MOUSE	49.88	19	11300	NA	11800
SPAVAAAQAPAPTPALPPTS	P54728|RD23B_MOUSE	38.46	20	1200	NA	1010
SPDSLLGVEK	Q9D871|CEA18_MOUSE	26.34	10	NA	NA	1320
SPDVDVISPTTQPSPT	Q9D8N1|CK024_MOUSE	43.08	16	781	NA	363
SPDVDVISPTTQPSPTLPT	Q9D8N1|CK024_MOUSE	46.41	19	1030	NA	823
SPDVVYSPETIEAR	Q9JHU9|INO1_MOUSE	41.51	14	500	NA	381
SPDVVYSPETIEARYE	Q9JHU9|INO1_MOUSE	43.08	16	2150	NA	1860
SPEQIRAPSGIITSPG	Q8BUJ9|LRP12_MOUSE	32.58	16	NA	NA	472
SPGFSSEVYTFPVPERHLE	P09803|CADH1_MOUSE	48.94	19	743	NA	1720
SPGFSSEVYTFPVPERHLER	P09803|CADH1_MOUSE	40.07	20	2580	NA	4480
SPGLKPASQQKAEASSPVPYLSPETTPA	P39447|ZO1_MOUSE	47.8	29	NA	NA	38.1
SPGTLTASGVVSGPAAAPAAQHL	P46938|YAP1_MOUSE	48.6	23	NA	NA	55.9
SPGYNPPQM(+15.99)NTLPV	Q8K419|LEG4_MOUSE	43.14	14	2460	NA	2040
SPGYNPPQMNTL	Q8K419|LEG4_MOUSE	41.9	12	NA	NA	144
SPGYNPPQMNTLP	Q8K419|LEG4_MOUSE	36.25	13	288	NA	726
SPGYNPPQMNTLPV	Q8K419|LEG4_MOUSE	48.43	14	736	NA	1290
SPHPYQLPQALAPH	O89023|TPP1_MOUSE	49.64	14	624	NA	767
SPHPYQLPQALAPHVD	O89023|TPP1_MOUSE	49.41	16	5100	NA	4470
SPIKLPFFYSEPVNVLN	E9Q414|APOB_MOUSE	49.94	17	635	NA	307
SPIKLPFFYSEPVNVLNG	E9Q414|APOB_MOUSE	49.94	18	127	NA	262
SPKKAKAAAKPKKAAK	P43276|H15_MOUSE	49.82	16	12300	7490	3530
SPKKAKAAAKPKKAAKSPAKPKA	P43276|H15_MOUSE	48.95	23	NA	900	2490
SPKKAKATKAKKAPK	P43274|H14_MOUSE	49.92	15	8380	1300	5720
SPKKAKATKAKKAPKSPAK	P43274|H14_MOUSE	49.94	19	788	NA	251
SPKKPKVVKAKKVAK	P43275|H11_MOUSE	49.95	15	19100	6790	6130
SPKPLLQSPKPSPSARP	Q6EDY6|CARL1_MOUSE	44.95	17	NA	NA	212
SPKPLLQSPKPSPSARPS	Q6EDY6|CARL1_MOUSE	49.84	18	1400	NA	831
SPLSISAALALVSLGAK	Q03734|SPA3M_MOUSE:P07759|SPA3K	48.13	17	181	NA	177
SPNYAAPEVISGRL	Q5EG47|AAPK1_MOUSE:Q8BRK8|AAPK	45.9	14	1480	NA	1220
SPPESESEPYTFSHPNK	Q5U462|CDCP1_MOUSE	49.73	17	225	NA	345
SPPESESEPYTFSHPNKGEIG	Q5U462|CDCP1_MOUSE	48.83	21	1510	NA	5950
SPPHVQFTYQQPQPL	B2RXS4|PLXB2_MOUSE	47.2	15	285	NA	1090
SPPHVQFTYQQPQPLS	B2RXS4|PLXB2_MOUSE	49.9	16	2940	NA	3120
SPPHVQFTYQQPQPLSVE	B2RXS4|PLXB2_MOUSE	49.86	18	982	NA	1500
SPPHVQFTYQQPQPLSVEP	B2RXS4|PLXB2_MOUSE	49.92	19	4100	NA	3980
SPPHVQFTYQQPQPLSVEPR	B2RXS4|PLXB2_MOUSE	49.95	20	292000	10900	299000
SPPPGGYGQPSVLPGGY	Q8BJZ3|LFG3_MOUSE	27.83	17	NA	NA	318
SPPPYAAYATPTPEVY	Q9QZC7|PKHB2_MOUSE	49.51	16	5320	NA	6070
SPPPYAAYATPTPEVYG	Q9QZC7|PKHB2_MOUSE	49.57	17	79400	1110	15700
SPPPYSSITVEAPTTSDTDV	Q91ZP6|NFIP2_MOUSE	49.83	20	231	NA	262
SPPPYSSITVEAPTTSDTDVY	Q91ZP6|NFIP2_MOUSE	49.37	21	1090	NA	1550
SPPQFQETPPLVLEVKE	Q05BQ1|TUTLA_MOUSE	49.91	17	2370	NA	2210
SPPVTRVSPVPSPSQP	Q8VDP3|MICA1_MOUSE	43.29	16	55.7	NA	105
SPRPGSDSGNFRPANPNWG	E9PV24|FIBA_MOUSE	37.71	19	NA	NA	2360
SPRPGSDSGNFRPANPNWGVFS	E9PV24|FIBA_MOUSE	48.1	22	271	NA	1280
SPRTATLEIKGPQADLIDAV	Q8CAS9|PARP9_MOUSE	25.88	20	94	NA	117
SPSHLLTEPKASSSKESL	Q8BRN9|C2D1B_MOUSE	39.61	18	NA	NA	460
SPSTDNM(+15.99)VNVDFNTPRPST	G3X939|SL9A3_MOUSE	47.53	19	NA	NA	89.7
SPTVHFTPAEISRSVFE	Q9QXH4|ITAX_MOUSE	44.26	17	931	35.1	299
SPVPYLSPETTPA	P39447|ZO1_MOUSE	42.76	13	NA	NA	1040
SPVPYLSPETTPAS	P39447|ZO1_MOUSE	46.56	14	970	NA	1140
SPVYKNPTPGSSEL	Q99PG0|AAAD_MOUSE	48.58	14	499	NA	440
SPYINPIIPFTGP	O08573|LEG9_MOUSE	37.84	13	1380	NA	2250
SPYSSGFNSPSSTPVRPP	Q8CI08|SLAI2_MOUSE	49.04	18	1740	NA	1920
SQASIYSPPAAAAAAAA	P70297|STAM1_MOUSE	49.37	17	448	NA	340
SQFEFKGPQAAQEQD	Q6RHR9|MAGI1_MOUSE	49.87	15	2650	NA	1970
SQPAAYVAQPATAAAYASQPA	Q8C2Q3|RBM14_MOUSE	41.02	21	56.4	NA	736
SQPAVLQPSVEPAQPTP	Q9ERN0|SCAM2_MOUSE	46.43	17	NA	NA	271
SQPLPSLPGGPP	Q8C0Z1|F234A_MOUSE	38.31	12	349	NA	290
SQPSKADKKQKKKVDRKGGQS	Q0VG18|SIM24_MOUSE	32.2	21	NA	NA	707
SQPSKADKKQKKKVDRKGGQSN	Q0VG18|SIM24_MOUSE	47.52	22	NA	1750	1900
SQRAGLQFPVGRIHRHLKSR	P0C0S6|H2AZ_MOUSE	48.59	20	NA	NA	391
SRPVQFPYVTPAPHEPVK	Q9D074|MGRN1_MOUSE	49.64	18	131	NA	227
SRTPGNRIVYLYTKKVGKAPK	Q9D1R9|RL34_MOUSE	49.85	21	134	634	1630
SRTPGNRIVYLYTKKVGKAPKS	Q9D1R9|RL34_MOUSE	49.66	22	741	691	2150
SRTPGNRIVYLYTKKVGKAPKSA	Q9D1R9|RL34_MOUSE	48.77	23	NA	NA	468
SRVQIYHNPTANSF	P70460|VASP_MOUSE	48.23	14	143	NA	375
SRVQIYHNPTANSFR	P70460|VASP_MOUSE	45.21	15	5730	NA	7280
SRVQIYHNPTANSFRV	P70460|VASP_MOUSE	49.93	16	8940	NA	8390
SSENYISPRTLTSQS	Q9WV66|MARH7_MOUSE	35.81	15	719	NA	1010
SSEVYTFPVPERH	P09803|CADH1_MOUSE	48.29	13	4540	NA	5790
SSEVYTFPVPERHL	P09803|CADH1_MOUSE	46.26	14	NA	NA	558

SSEVYTFPVPERHLE	P09803|CADH1_MOUSE	49.8	15	22100	451	25100
SSEVYTFPVPERHLER	P09803|CADH1_MOUSE	45.7	16	1430	NA	1330
SSGIYKAAFPLHD	Q6P9J9|ANO6_MOUSE	48.33	13	277	NA	83.2
SSIASFKDPKISTSLPV	Q61233|PLSL_MOUSE	49.88	17	5370	567	4610
SSIASFKDPKISTSLPVLD	Q61233|PLSL_MOUSE	40.19	19	NA	NA	311
SSKNVFLSPM(+15.99)SISSA	Q60854|SPB6_MOUSE	45.9	15	307	NA	389
SSKNVFLSPM(+15.99)SISSAL	Q60854|SPB6_MOUSE	48.08	16	708	NA	290
SSKNVFLSPMSISSA	Q60854|SPB6_MOUSE	42.68	15	225	NA	1210
SSKNVFLSPMSISSAL	Q60854|SPB6_MOUSE	48.44	16	235	NA	665
SSLAAPTVEAAAS	Q91ZP6|NFIP2_MOUSE	38.07	13	169	NA	297
SSM(+15.99)NYTGPRTNLGYLG	Q32NZ6|TMC5_MOUSE	49.89	16	6640	128	4390
SSMNYTGPRTNLG	Q32NZ6|TMC5_MOUSE	44.03	13	239	NA	376
SSMNYTGPRTNLGYL	Q32NZ6|TMC5_MOUSE	48.63	15	5210	NA	10200
SSNRYGASVPIPVPTQ	O70405|ULK1_MOUSE	36.95	16	NA	NA	103
SSPAVAAAQAPAPTPALPPT	P54728|RD23B_MOUSE	48.63	20	NA	NA	453
SSRSFTSGPGARISSSSF	P11679|K2C8_MOUSE	43.6	18	719	NA	1070
SSSNYHSFVPSSASVD	Q811P8|RHG32_MOUSE	45.01	16	417	NA	525
STDYGNFLANEASP	P51863|VA0D1_MOUSE	49.69	14	860	NA	568
STDYGNFLANEASPL	P51863|VA0D1_MOUSE	49.28	15	4600	NA	1830
STKKTPKKAKKP	P43274|H14_MOUSE	48.49	12	1410	NA	729
STKKTPKKAKKPA	P43274|H14_MOUSE	49.9	13	2760	2920	8380
STPFQFRAASPVEE	Q3UKC1|TAXB1_MOUSE	47.79	14	1020	NA	1130
STPFQFRAASPVEEL	Q3UKC1|TAXB1_MOUSE	47.14	15	915	NA	1240
STPFQFRAASPVEELL	Q3UKC1|TAXB1_MOUSE	49.7	16	797	NA	1870
STPFQFRAASPVEELLT	Q3UKC1|TAXB1_MOUSE	48.49	17	302	NA	514
STRVITNQYNSPTGLYSSENI	O70400|PDLI1_MOUSE	49.54	21	41	NA	147
STRVITNQYNSPTGLYSSENIS	O70400|PDLI1_MOUSE	49.95	22	451	NA	1060
STRVITNQYNSPTGLYSSENISN	O70400|PDLI1_MOUSE	47.74	23	NA	NA	88.2
STSSLAAPTVEAAAS	Q91ZP6|NFIP2_MOUSE	41.21	15	1340	NA	1240
STSSLAAPTVEAAASA	Q91ZP6|NFIP2_MOUSE	41.07	16	924	NA	538
STSSLAAPTVEAAASAP	Q91ZP6|NFIP2_MOUSE	40.14	17	1310	NA	1650
STSYSGPYPAAAPP	Q9WVH9|FBLN5_MOUSE	40.73	14	584	NA	185
SVAAYVSARTMPEAKA	P15208|INSR_MOUSE	44.07	16	NA	NA	259
SVASQAPQSLPAISQPP	Q99LI8|HGS_MOUSE	32.16	17	715	NA	603
SVATNPIITPVAQENQ	P08226|APOE_MOUSE	49.48	16	3000	NA	2650
SVEAPSVSPAR	Q8BUJ9|LRP12_MOUSE	36.87	11	6500	NA	3210
SVEAPSVSPARHQ	Q8BUJ9|LRP12_MOUSE	38.4	13	NA	NA	423
SVFVAPAVTPVKGV	P70158|ASM3A_MOUSE	48.84	14	12300	448	11200
SVFVAPAVTPVKGVL	P70158|ASM3A_MOUSE	49.66	15	15500	NA	11400
SVGSIGPLPNLDLEE	O55111|DSG2_MOUSE	47	15	1010	NA	240
SVHAVFSAPAIPSGTG	Q8BMS2|SPON2_MOUSE	47.06	16	71.6	NA	33.9
SVHTYVGGLPEVSVIS	Q61592|GAS6_MOUSE	27.83	16	160	NA	167
SVLYLASPLASYVSG	Q9WV68|DECR2_MOUSE	49.42	15	415	NA	239
SVPAGGAVAVSAAPGSAAPAAGSAPAA	P99027|RLA2_MOUSE	27.9	27	NA	NA	111
SVPATFAPSPTPAVVS	Q9DBG3|AP2B1_MOUSE	49.11	16	2450	NA	264
SVPNVHGALAPLAIPSAAAAA	P17225|PTBP1_MOUSE	42.26	21	515	NA	671
SVPPSVSPSPATAFSG	Q3UPH1|PRRC1_MOUSE	49.65	16	1400	NA	1410
SVRIGSGGVFRAPSIHGGSGGR	P19001|K1C19_MOUSE	28.68	22	NA	NA	345
SVRIGSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	49.85	23	377	NA	1090
SVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.84	14	1550	9630	1160
SYLGPDVNQAL	Q6T3U4|NPCL1_MOUSE	44.89	11	265	NA	190
SYLYPLATNIPN	Q9DBX3|SUSD2_MOUSE	48.32	12	315	NA	221
SYPSQASIYSPPAAAAAAAA	P70297|STAM1_MOUSE	49.76	20	672	NA	1210
SYSVYVYKVLKQVHPD	Q8CGP2|H2B1P_MOUSE:Q64525|H2B2E	49.42	16	156	572	234
T(+42.01)PAPKKGSKKAITKAQKKDGKK	Q9D2U9|H2B3A_MOUSE	46.88	24	NA	NA	613
T(+42.01)SYSYRQTSAM(+15.99)SSFG	P19001|K1C19_MOUSE	48.9	15	640	NA	605
T(+42.01)SYSYRQTSAMSSFG	P19001|K1C19_MOUSE	25.65	15	NA	NA	65.7
T(+42.01)VKPKAAKPKTSKPKAAKPKKT/	P43274|H14_MOUSE	49.95	27	2200	9550	7980
TAKGLFRAAVPSGA	P17183|ENOG_MOUSE:P17182|ENOA_M	40.37	14	178	NA	319
TAKGLFRAAVPSGAS	P17183|ENOG_MOUSE:P17182|ENOA_M	49.2	15	2120	NA	2540
TAKGLFRAAVPSGAST	P17183|ENOG_MOUSE:P17182|ENOA_M	49.77	16	30600	762	32900
TAKGLFRAAVPSGASTG	P17183|ENOG_MOUSE:P17182|ENOA_M	49.8	17	16500	149	17100
TAKGLFRAAVPSGASTGI	P17183|ENOG_MOUSE:P17182|ENOA_M	46.73	18	NA	NA	171
TAKKSTKKTPKKAKKPAA	P43274|H14_MOUSE	48.95	18	2140	956	3730
TAKPKAAKAKKAVSKKK	P43276|H15_MOUSE	49.94	17	7330	6910	256
TASNKTRLSRTPGNRIVYLYTKKVGKAP	Q9D1R9|RL34_MOUSE	30.88	30	NA	NA	437
TATAKKSTKKTPKKAKKP	P43274|H14_MOUSE	42.94	18	NA	NA	318
TATAKKSTKKTPKKAKKPA	P43274|H14_MOUSE	49.95	19	7140	NA	3760
TATYKLSAPWVEQEGP	P14432|HA1T_MOUSE	48.68	16	342	NA	375
TATYKLSAPWVEQEGPE	P14432|HA1T_MOUSE	49.9	17	3000	NA	4060
TDANYRQPILVAL	P14246|GTR2_MOUSE	36.95	13	365	NA	264
TDDVFSPSHAIPIE	Q91ZH7|ABHD3_MOUSE	43.02	14	419	NA	163
TDSVVSSVTTKAKGVA	Q9JJX6|P2RX4_MOUSE	47.86	16	153	NA	86.6
TEDNVFEAPTLVKVF	Q61490|CD166_MOUSE	49.17	15	74.6	NA	105
TEEQYQDFEARYVQAK	O70228|ATP9A_MOUSE	45.24	16	174	NA	206
TELDQLFSGPLPGRLPVN	Q60805|MERTK_MOUSE	49.88	18	191	NA	201
TFPQYETSSATTSPFFKPP	Q9QZS3|NUMB_MOUSE	43.78	19	NA	NA	297
TFTDVAPRGVESGQR	Q8JZQ5|AOC1_MOUSE	38.41	15	691	NA	391
TGGGSVRIGSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	49.94	27	1680	NA	2700
TGGLPDYSAPNPIKVTHR	Q8CFG0|SULF2_MOUSE	49.33	18	527	NA	1390
TGGYRYPRALEEEV	Q8K3K8|OPTN_MOUSE	40.34	14	23400	NA	23300

TGLDFHSPRIA	Q9JLB4|CUBN_MOUSE	40.11	11	563	NA	623
TGM(+15.99)AFRVPTPNVS	P16858|G3P_MOUSE:Q64467|G3PT_MC	47.58	13	10700	152	6960
TGM(+15.99)AFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.84	15	44100	605	35100
TGM(+15.99)AFRVPTPNVSVVDL	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.92	17	19400	463	13900
TGM(+15.99)AFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.85	18	5300	NA	2900
TGMAFRVPTPNVSVV	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.87	15	12600	NA	32200
TGMAFRVPTPNVSVVD	P16858|G3P_MOUSE:Q64467|G3PT_MC	49.84	16	362000	6200	478000
TGMAFRVPTPNVSVVDLT	P16858|G3P_MOUSE:Q64467|G3PT_MC	48.96	18	408000	NA	358000
TGPDGKGM(+15.99)NPPSYYTQPVPVP	Q9JLJ0|LITAF_MOUSE	49.95	24	715	NA	1050
TGPDGKGM(+15.99)NPPSYYTQPVPVP	Q9JLJ0|LITAF_MOUSE	49.35	25	1410	NA	1790
TGPDGKGMNPPSYYTQPVPVPNAN	Q9JLJ0|LITAF_MOUSE	43.55	24	NA	NA	408
TGPDGKGMNPPSYYTQPVPVPNANA	Q9JLJ0|LITAF_MOUSE	49.72	25	NA	NA	576
TGPKYIHL	Q60805|MERTK_MOUSE	30.49	8	NA	NA	84.2
TGPPPYHESLAGASQPP	Q9D7I0|SHSA5_MOUSE	37.69	17	2410	NA	7340
TGPPPYHESLAGASQPPY	Q9D7I0|SHSA5_MOUSE	37.6	18	NA	NA	812
TGSILWSQPLPSLPGGPP	Q8C0Z1|F234A_MOUSE	48.9	18	NA	NA	310
TGVPTVPLLPPQVNQSLA	Q99JX3|GORS2_MOUSE	45.28	18	499	NA	433
TGYPTAYPAAAPAYNPS	Q8BGZ2|F168A_MOUSE	49.3	17	3410	NA	2050
THDLYIQSHISENR	Q9R111|GUAD_MOUSE	49.8	14	2740	NA	1300
THDLYIQSHISENREE	Q9R111|GUAD_MOUSE	49.84	16	12900	NA	6820
TIEDIEVAPPKAHEVR	P00329|ADH1_MOUSE	49.21	16	1480	NA	1320
TIEDIEVAPPKAHEVRIK	P00329|ADH1_MOUSE	49.82	18	640	NA	513
TIEFRGPNGLLVYQ	Q9DCN2|NB5R3_MOUSE	40.1	14	1760	NA	1300
TIEFRGPNGLLVYQG	Q9DCN2|NB5R3_MOUSE	47.34	15	3190	NA	2560
TIPFYTPIPN	O08573|LEG9_MOUSE	27.84	10	944	NA	685
TIPFYTPIPNG	O08573|LEG9_MOUSE	40.06	11	30800	NA	31000
TIPFYTPIPNGL	O08573|LEG9_MOUSE	29.57	12	977	NA	473
TIPFYTPIPNGLY	O08573|LEG9_MOUSE	44.88	13	681	NA	361
TIPFYTPIPNGLYP	O08573|LEG9_MOUSE	48.38	14	12800	477	16900
TIPFYTPIPNGLYPS	O08573|LEG9_MOUSE	47.16	15	20300	521	11300
TIRYM(+15.99)APEVLEGAV	O35607|BMPR2_MOUSE	35.92	14	405	NA	259
TIRYM(+15.99)APEVLEGAVN	O35607|BMPR2_MOUSE	48.85	15	1870	NA	606
TIRYMAPEVLEGAV	O35607|BMPR2_MOUSE	43.62	14	115	NA	184
TIRYMAPEVLEGAVN	O35607|BMPR2_MOUSE	46.7	15	324	NA	337
TITSWYSPDAKFQK	Q9QZI9|SERC3_MOUSE	41.63	14	244	NA	254
TKKFRFEEPVVLPDLS	Q01705|NOTC1_MOUSE	27.13	16	623	NA	792
TKKFRFEEPVVLPDLSD	Q01705|NOTC1_MOUSE	43.87	17	741	NA	411
TKNLDYVATSIHEAVT	P05201|AATC_MOUSE	49.25	16	85.7	NA	160
TKPKTPAKPKKAAPK	P43275|H11_MOUSE	41.23	15	NA	NA	242
TKRYM(+15.99)APEVLDETIN	Q61271|ACV1B_MOUSE	49.1	15	3670	NA	1110
TKRYMAPEVLDETIN	Q61271|ACV1B_MOUSE	49.5	15	5200	NA	1670
TKRYMAPEVLDETIQ	P37172|ACVR1_MOUSE	42.46	15	109	NA	236
TLFHNPHVNPLPTGYE	P43023|CX6A2_MOUSE:P43024|CX6A1_	48.01	16	720	300	1580
TLKYPIEHGIITNW	P68134|ACTS_MOUSE:P68033|ACTC_M	28.61	14	NA	NA	132
TLPPVSPPKAALSVDE	Q6NZJ6|IF4G1_MOUSE	49.93	16	1720	NA	1490
TLQVLRPGLVVVH	Q9D3D9|ATPD_MOUSE	48.12	13	461	380	1990
TLQVLRPGLVVVHTE	Q9D3D9|ATPD_MOUSE	46.98	15	NA	NA	129
TLTGAFGILASH	Q9D3D9|ATPD_MOUSE	32.19	12	NA	NA	123
TM(+15.99)SKKKKKKK	Q99L45|IF2B_MOUSE	43.06	11	NA	419	994
TM(+15.99)SKKKKKKKP	Q99L45|IF2B_MOUSE	49.28	12	4090	27800	32000
TMSKKKKKKKP	Q99L45|IF2B_MOUSE	48.95	12	NA	2970	17200
TMSKKKKKKKPF	Q99L45|IF2B_MOUSE	27.42	13	NA	NA	458
TNDRYVASLAARNK	Q00560|IL6RB_MOUSE	43.92	14	5000	457	4220
TNDRYVASLAARNKVG	Q00560|IL6RB_MOUSE	48.55	16	5300	991	4290
TNLHYSAPLPASLDT	Q91X84|CRTC3_MOUSE	43.36	15	244	NA	195
TNM(+15.99)YNTDRANPVLDLP	E9Q7P9|CDHR2_MOUSE	49.64	16	1100	NA	516
TNNQDFRGSAGAPSVENV	P49443|PPM1A_MOUSE	49.84	18	728	NA	818
TNPIITPVAQENQ	P08226|APOE_MOUSE	46.63	13	4150	110	2360
TNTAYVGSAILSEE	Q9QZC7|PKHB2_MOUSE	44.12	14	816	NA	1320
TNTAYVGSAILSEET	Q9QZC7|PKHB2_MOUSE	47.43	15	4510	546	5360
TNVKQFIAPETSEGVS	Q9EPS3|GLCE_MOUSE	41.85	16	205	NA	325
TPAAEAKAAEAAASAYY	P97765|WBP2_MOUSE	40.88	17	NA	NA	657
TPAAPTSALGPKASPAP	Q8K0V4|CNOT3_MOUSE	38.51	17	167	NA	151
TPAAPTSALGPKASPAPSH	Q8K0V4|CNOT3_MOUSE	49.58	19	1710	NA	1040
TPAKPKKAAP	P43275|H11_MOUSE	42.66	10	NA	240	2630
TPAKPKKAAPK	P43275|H11_MOUSE	38.25	11	NA	NA	1030
TPAKPKKAAPKKK	P43275|H11_MOUSE	49.84	13	1370	NA	376
TPAPSAPAAASATSPSPAPSSGN	Q9JKV1|ADRM1_MOUSE	33.74	23	NA	NA	136
TPAPSAPAAASATSPSPAPSSGNG	Q9JKV1|ADRM1_MOUSE	48.76	24	289	NA	532
TPATNEAPQATVFPK	P14434|HA2B_MOUSE:P01910|HA2K_M	49.01	15	694	NA	528
TPAYTIPFYTPIPNG	O08573|LEG9_MOUSE	48.4	15	49900	1510	36800
TPAYTIPFYTPIPNGL	O08573|LEG9_MOUSE	49.61	16	2300	NA	711
TPAYTIPFYTPIPNGLYPS	O08573|LEG9_MOUSE	49.9	19	30700	315	43400
TPDPNTAYASYPSASVE	O55101|SNG2_MOUSE	49.43	17	1780	NA	2120
TPDPNTAYASYPSASVENY	O55101|SNG2_MOUSE	49.81	19	668	NA	1010
TPDPNTAYASYPSASVENYQ	O55101|SNG2_MOUSE	49.93	20	183	NA	221
TPDPNTAYASYPSASVENYQQPP	O55101|SNG2_MOUSE	49.9	23	190	NA	366
TPDYIAPEIIAYQP	P63318|KPCG_MOUSE:P20444|KPCA_M	42.65	14	122	NA	171
TPDYIAPEIIAYQPY	P63318|KPCG_MOUSE:P20444|KPCA_M	49.76	15	1200	NA	582
TPDYIAPEILQG	P28867|KPCD_MOUSE	38.31	12	655	NA	378
TPDYIAPEILQGLK	P28867|KPCD_MOUSE	43.09	14	877	NA	717

TPESFLGPNAALVNLD	Q8CHU3|EPN2_MOUSE	49.7	16	128	NA	52.4
TPEVYGYGPYSGAYPAGTQVV	Q9QZC7|PKHB2_MOUSE	48.92	21	NA	NA	72.6
TPEYLAPEIILSK	P68181|KAPCB_MOUSE:P05132|KAPCA	47.55	13	4350	NA	3450
TPEYLAPEIILSKGYN	P68181|KAPCB_MOUSE:P05132|KAPCA	48.33	16	745	NA	509
TPEYVAPEVILNK	Q61410|KGP2_MOUSE	48.3	13	2970	NA	2030
TPEYVAPEVILNKGHD	Q61410|KGP2_MOUSE	48	16	622	NA	537
TPFQFRAASPVE	Q3UKC1|TAXB1_MOUSE	43.25	12	182	NA	291
TPFQFRAASPVEE	Q3UKC1|TAXB1_MOUSE	47.8	13	9120	276	11200
TPFQFRAASPVEEL	Q3UKC1|TAXB1_MOUSE	48.36	14	8210	188	10400
TPFQFRAASPVEELL	Q3UKC1|TAXB1_MOUSE	49.8	15	9830	NA	9110
TPGGPRIRGNVYIHPTAKVAPS	Q922H4|GMPPA_MOUSE	49.89	22	12600	460	19800
TPIETTAPTAAIPGTN	E9Q7P9|CDHR2_MOUSE	48.78	16	1810	NA	703
TPIPNGLYP	O08573|LEG9_MOUSE	28.07	9	NA	NA	1610
TPIPNGLYPS	O08573|LEG9_MOUSE	28.51	10	531	NA	3030
TPKKAAKKTPKKAKKPA	P15864|H12_MOUSE	49.95	17	3710	350	1410
TPKKAAKKTPKKAKKPAA	P15864|H12_MOUSE	49.95	18	2730	968	3340
TPKKAKKPA	P15864|H12_MOUSE:P43276|H15_MOU	42.49	9	NA	5570	3140
TPKKAKKPAA	P15864|H12_MOUSE:P43276|H15_MOU	38.52	10	NA	NA	1140
TPKKAKKPKVVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.95	25	3860	2290	789
TPKKTAKKTPKKAKKPA	P43277|H13_MOUSE	49.95	17	12600	6380	8900
TPLLRNVQFNYPQASVTDVT	Q61703|ITIH2_MOUSE	48.92	20	NA	NA	103
TPPPAAAPIPAPSTEE	O54774|AP3D1_MOUSE	45.86	16	1520	NA	1120
TPPPAAAPIPAPSTEELA	O54774|AP3D1_MOUSE	48.34	18	702	NA	92.5
TPPSPKVTYKAPVPTG	P35564|CALX_MOUSE	47.67	16	1590	NA	2400
TPPSPKVTYKAPVPTGEV	P35564|CALX_MOUSE	47.62	18	735	NA	2040
TPQSPTYTPSSPSYSPS	P08775|RPB1_MOUSE	43.03	17	125	NA	128
TPRDYFFALAHTVRDH	Q8CI94|PYGB_MOUSE	44.5	16	1130	NA	722
TPRVLSQAPSPLYSVEF	P70699|LYAG_MOUSE	49.52	17	556	NA	330
TPSAAYLWVGAGASEAEKT	P13020|GELS_MOUSE	47.3	19	2360	NA	1800
TPSPAPTYSPSPAPAYTPS	Q9JKS4|LDB3_MOUSE	49.87	19	828	NA	695
TPSPAPTYSPSPAPAYTPSP	Q9JKS4|LDB3_MOUSE	49.89	20	4350	NA	4230
TPTPEVYG	Q9QZC7|PKHB2_MOUSE	28.82	8	NA	NA	4160
TPTPEVYGYGPYSGAYPAGTQ	Q9QZC7|PKHB2_MOUSE	49.73	21	260	NA	150
TPTPEVYGYGPYSGAYPAGTQV	Q9QZC7|PKHB2_MOUSE	49.9	22	164	NA	144
TPTSFTAQWIAPSVQLTGYR	P11276|FINC_MOUSE	49.6	20	309	NA	569
TPTVSSYTPPQPSYSQPP	Q8VDM6|HNRL1_MOUSE	33.87	18	478	NA	779
TPTVSSYTPPQPSYSQPPY	Q8VDM6|HNRL1_MOUSE	40.43	19	295	NA	398
TPVFVHAGPFANIAHG	Q922D8|C1TC_MOUSE:Q3V3R1|C1TM_	49.8	16	5310	NA	5210
TPVFVHAGPFANIAHGN	Q922D8|C1TC_MOUSE:Q3V3R1|C1TM_	49.89	17	9490	NA	7750
TPVFVHAGPFANIAHGNS	Q922D8|C1TC_MOUSE:Q3V3R1|C1TM_	49.93	18	29400	91.8	28500
TPVKKAKKKPAATPKKAKKPKV	P10922|H10_MOUSE	40.99	22	NA	NA	903
TPVKKKAKKTGAAAGKR	P43277|H13_MOUSE	47.74	17	NA	NA	5280
TPVPLYSVPATHLAVT	Q91XT4|SC16B_MOUSE	42	16	28.2	NA	139
TPVPLYSVPATHLAVTS	Q91XT4|SC16B_MOUSE	49.92	17	610	NA	614
TPVPLYSVPATHLAVTSG	Q91XT4|SC16B_MOUSE	49.88	18	345	NA	455
TPVPLYSVPATHLAVTSGA	Q91XT4|SC16B_MOUSE	48.81	19	NA	NA	217
TPVPLYSVPATHLAVTSGAS	Q91XT4|SC16B_MOUSE	48.78	20	NA	NA	319
TPYSTPQMSPATTPA	Q6PAR5|GAPD1_MOUSE	28.53	15	156	NA	156
TPYYVAPEVLGPE	Q3UMW7|MAPK3_MOUSE:P49138|MAP	48.17	13	600	NA	603
TPYYVAPEVLGPEK	Q3UMW7|MAPK3_MOUSE:P49138|MAP	45.89	14	2060	NA	1330
TQEFILNSPTVTSIK	Q9R0H0|ACOX1_MOUSE	32.28	15	NA	NA	285
TQQLAFKQPSSAYAA	P01027|CO3_MOUSE	47.04	15	NA	NA	161
TQQLAFKQPSSAYAAFN	P01027|CO3_MOUSE	49.92	17	1770	44.8	3240
TQVQWNDPGAQYSL	Q9R100|CAD17_MOUSE	49.1	14	354	NA	228
TQVQWNDPGAQYSLV	Q9R100|CAD17_MOUSE	49.85	15	16000	NA	6830
TQVQWNDPGAQYSLVNK	Q9R100|CAD17_MOUSE	49.93	17	2480	NA	1690
TRRYMAPEVLEGAIN	P27038|AVR2A_MOUSE:P27040|AVR2B	27.28	15	NA	NA	2020
TRSQVTPSVPSEALDD	Q7TQH7|LRP10_MOUSE	49.66	16	189	NA	291
TRSQVTPSVPSEALDDS	Q7TQH7|LRP10_MOUSE	49.66	17	808	NA	544
TSDIFGSPVTATAPLA	Q6PGH2|JUPI2_MOUSE	48.82	16	265	NA	301
TSKPKAAKPK	P43274|H14_MOUSE	35.22	10	NA	NA	483
TSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.94	17	4940	5990	5590
TSKWSYLYPLATNIPN	Q9DBX3|SUSD2_MOUSE	49.82	16	4660	NA	7580
TSLSSGPLPTFPLEQLVNKS	Q62468|VILI_MOUSE	49.93	20	457	NA	145
TSLSSGPLPTFPLEQLVNKSVE	Q62468|VILI_MOUSE	49.94	22	298	NA	316
TSQELVRAPTAALSPEPQD	D3YXK2|SAFB1_MOUSE:Q80YR5|SAFB	48.78	19	NA	NA	133
TSSLAAPTVEAAA	Q91ZP6|NFIP2_MOUSE	30.45	13	280	NA	365
TSSLAAPTVEAAASA	Q91ZP6|NFIP2_MOUSE	48.67	15	1970	NA	1740
TSSLAAPTVEAAASAP	Q91ZP6|NFIP2_MOUSE	47.95	16	2140	NA	971
TSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	48.97	17	1420	NA	481
TSSYSNPTIGYEN	Q07797|LG3BP_MOUSE	47.97	13	5250	234	1260
TSSYSNPTIGYENR	Q07797|LG3BP_MOUSE	49.16	14	17800	483	7790
TSSYSNPTIGYENRV	Q07797|LG3BP_MOUSE	49.7	15	3060	85.9	1980
TSWTYNPAAVSKVAPA	Q80SY4|MIB1_MOUSE	49.79	16	903	NA	907
TTGQLFFPEVNKNH	P11911|CD79A_MOUSE	47.37	14	968	NA	185
TTHSFGNPSISVSTQQPPK	Q8BFW7|LPP_MOUSE	36.73	19	74.2	NA	189
TTSSYSNPTIGYEN	Q07797|LG3BP_MOUSE	48.67	14	2140	85.5	583
TTSSYSNPTIGYENR	Q07797|LG3BP_MOUSE	49.31	15	11300	364	2710
TTTNLEQPQVIPSQG	Q9DBG3|AP2B1_MOUSE	47.26	15	423	NA	386
TTTTNLEQPQVIPSQGDL	Q9DBG3|AP2B1_MOUSE	42.21	18	197	NA	119
TVDVVLTPLVAEALDR	A2AAE1|BLTP1_MOUSE	25.74	16	678	NA	644

TVHWVAPRAPITG	P11276|FINC_MOUSE	43.78	13	231	NA	199
TVIHFNNPKVQASL	Q9CQH7|BT3L4_MOUSE:Q64152|BTF3_	49.76	14	564	NA	430
TVIHFNNPKVQASLA	Q64152|BTF3_MOUSE	49.9	15	11400	136	13300
TVIHFNNPKVQASLS	Q9CQH7|BT3L4_MOUSE	49.88	15	1930	NA	2340
TVINQTQKENLRKFYKGKKYKPLDLRPK	Q6ZWV7|RL35_MOUSE	49.94	31	1660	NA	3140
TVKPKAAKPKTSKPKAAKP	P43274|H14_MOUSE	47.92	19	NA	200	2240
TVKPKAAKPKTSKPKAAKPKK	P43274|H14_MOUSE	49.95	21	1920	NA	3340
TVKPKAAKPKTSKPKAAKPKKT	P43274|H14_MOUSE	49.95	22	877	NA	1550
TVKPKAAKPKTSKPKAAKPKKTAAK	P43274|H14_MOUSE	48.95	25	NA	NA	915
TVKPKAAKPKTSKPKAAKPKKTAAKKK	P43274|H14_MOUSE	49.95	27	4600	NA	2220
TVKPKAKSSAKRASKKK	P10922|H10_MOUSE	49.94	17	19600	3220	5040
TVKSFVGPTPAPAPAP	Q501J7|PHAR4_MOUSE	47.89	16	500	NA	548
TVKSFVGPTPAPAPAPR	Q501J7|PHAR4_MOUSE	49.6	17	1780	NA	2710
TVLVEPTVSLIKGPD	Q9JLB9|NECT3_MOUSE	26.54	15	855	NA	234
TVNKAVDYPPVANAGPN	Q8K135|K319L_MOUSE	48.46	17	NA	NA	77.8
TVNKAVDYPPVANAGPNQ	Q8K135|K319L_MOUSE	49.91	18	3260	NA	3280
TVTVLVEPTVSLIKGPD	Q9JLB9|NECT3_MOUSE	36.86	17	47.4	NA	81.6
TYHDLRHAFSPVASVESASGET	P29699|FETUA_MOUSE	49.7	22	820	NA	277
TYHDLRHAFSPVASVESASGETLHSPK	P29699|FETUA_MOUSE	49.95	27	NA	NA	298
TYPYYTPTGEPVFGG	Q91ZJ9|HYAL1_MOUSE	35.38	15	489	NA	479
TYQSYSSPSPRVSRF	Q60997|DMBT1_MOUSE	29.81	15	NA	NA	909
TYQSYSSPSPRVSRFK	Q60997|DMBT1_MOUSE	44.71	16	2790	NA	5320
TYVISAPKILRVG	P06684|CO5_MOUSE	49.7	13	602	NA	554
TYVISAPKILRVGS	P06684|CO5_MOUSE	49.86	14	511	NA	459
TYVISAPKILRVGSS	P06684|CO5_MOUSE	49.18	15	293	NA	447
V(+42.01)DYHAANQAYQYGPN	P57780|ACTN4_MOUSE	35.95	15	NA	NA	98.2
VADFHYAASKALRVPA	Q80TA9|EPG5_MOUSE	49.89	16	1450	NA	2490
VADKEFHAPLIIDEN	Q91YN5|UAP1_MOUSE	48.62	15	2280	NA	930
VAIFARGPQAHLVHG	P24823|PPBN_MOUSE:P24822|PPBI_M(	48.65	15	576000	30700	346000
VAIFARGPQAHLVHGVQ	P24823|PPBN_MOUSE:P24822|PPBI_M(	49.92	17	263000	10100	214000
VAKSPAKAKAVKPKA	P43275|H11_MOUSE	47.33	15	NA	NA	1080
VAKSPKKAKAAAKPKKAAKSPAK	P43276|H15_MOUSE	49.29	23	2760	NA	976
VAKVTGGAASKLSKIRVVRKSIAR	Q6ZWV7|RL35_MOUSE	49.94	24	1560	10000	4300
VAPAVTPVK	P70158|ASM3A_MOUSE	31.34	9	469	NA	1220
VARYRPRAPIIAVTR	P52480|KPYM_MOUSE	36.6	15	3090	NA	5530
VARYRPRAPIIAVTRNP	P52480|KPYM_MOUSE	45.56	17	21200	NA	12500
VARYRPRAPIIAVTRNPQ	P52480|KPYM_MOUSE	49.93	18	70900	924	58800
VARYRPRAPIIAVTRNPQT	P52480|KPYM_MOUSE	49.59	19	1600	NA	1180
VASYLLAALGGNSSPSAKDIKK	P99027|RLA2_MOUSE	48.65	22	656	NA	171
VATNPIITPVAQEN	P08226|APOE_MOUSE	43.88	14	183	NA	146
VATNPIITPVAQENQ	P08226|APOE_MOUSE	48.17	15	11100	747	9570
VAVNWYAPLVAPISK	Q80VA0|GALT7_MOUSE	49.77	15	178	NA	316
VAVNWYAPLVAPISKD	Q80VA0|GALT7_MOUSE	49.71	16	354	NA	559
VDEIQRYQKPVVAAIQ	Q9DBM2|ECHP_MOUSE	48.81	16	NA	NA	103
VDEIQRYQKPVVAAIQG	Q9DBM2|ECHP_MOUSE	46.67	17	1670	NA	4210
VDEIQRYQKPVVAAIQGVA	Q9DBM2|ECHP_MOUSE	38.96	19	NA	NA	124
VDFDFAGPAIHGSA	Q60930|VDAC2_MOUSE	46.11	14	530	NA	312
VDFDFAGPAIHGSAV	Q60930|VDAC2_MOUSE	48.84	15	3350	NA	2580
VDFNTPRPSTVE	G3X939|SL9A3_MOUSE	44.99	12	339	NA	274
VDFNTPRPSTVEA	G3X939|SL9A3_MOUSE	47.86	13	8460	302	9720
VDFNTPRPSTVEAS	G3X939|SL9A3_MOUSE	46.14	14	544	NA	621
VDKEFYLFPTVFDENE	Q61147|CERU_MOUSE	48.91	16	1740	NA	416
VDLRFSTSQSLPASQT	P28665|MUG1_MOUSE	40.72	16	3300	NA	1090
VDLYIMHYPVPMKSGDN	Q8VC28|AK1CD_MOUSE	48.7	17	NA	NA	155
VDPTPDPNTAYASYPSASVEN	O55101|SNG2_MOUSE	49.94	21	528	NA	292
VDPTPDPNTAYASYPSASVENY	O55101|SNG2_MOUSE	49.94	22	348	NA	423
VDPTPDPNTAYASYPSASVENYQ	O55101|SNG2_MOUSE	49.95	23	1900	NA	1970
VDPTPDPNTAYASYPSASVENYQQPP	O55101|SNG2_MOUSE	49.95	26	1580	NA	1560
VDRYDAPGIAFYPG	Q9D771|PACC1_MOUSE	46.59	14	794	NA	794
VDVFYSSGIPATAR	Q91VN0|LRP5_MOUSE	42.39	14	455	NA	211
VDVFYSSGIPATARP	Q91VN0|LRP5_MOUSE	49.07	15	18000	572	12800
VDVFYSSGIPATARPY	Q91VN0|LRP5_MOUSE	49.87	16	21200	861	16900
VDVFYSSGIPATARPYRP	Q91VN0|LRP5_MOUSE	49.93	18	8340	NA	7250
VENPEYLAPRAGTAS	P70424|ERBB2_MOUSE	48.27	15	692	NA	639
VENPEYLAPRAGTASQ	P70424|ERBB2_MOUSE	47.28	16	721	NA	690
VENPEYLAPRAGTASQP	P70424|ERBB2_MOUSE	49.33	17	1320	NA	1740
VENPEYLAPRAGTASQPH	P70424|ERBB2_MOUSE	49.93	18	18000	NA	13100
VENPEYLAPRAGTASQPHPS	P70424|ERBB2_MOUSE	48.78	20	259	NA	199
VEPGNFIAATSLYSPER	Q80XN0|BDH_MOUSE	48.15	17	379	NA	319
VEPLTPSGAVPNQAQ	P70424|ERBB2_MOUSE	46.91	15	1110	NA	716
VEPLTPSGAVPNQAQM(+15.99)R	P70424|ERBB2_MOUSE	46.19	17	356	NA	235
VEPLTPSGAVPNQAQMR	P70424|ERBB2_MOUSE	49.92	17	82.2	NA	181
VEPYEVHNPVPLIVG	P05555|ITAM_MOUSE	46.8	15	1720	316	929
VEQPSTSSLAAPTVEAAASAPA	Q91ZP6|NFIP2_MOUSE	48.71	22	1380	NA	1950
VEYAVRGPIVQRA	Q8QZR5|ALAT1_MOUSE	37.67	13	116	NA	108
VEYAVRGPIVQRALEL	Q8QZR5|ALAT1_MOUSE	48.83	16	15300	NA	22500
VEYHFLSPYVSPR	Q62351|TFR1_MOUSE	47.71	13	2540	NA	1390
VEYHFLSPYVSPRE	Q62351|TFR1_MOUSE	45.04	14	974	NA	128
VEYHFLSPYVSPRESP	Q62351|TFR1_MOUSE	48.86	16	1380	NA	523
VFDVTAPNTFKT	P51150|RAB7A_MOUSE	42.7	12	268	NA	265
VFDVTAPNTFKTLDS	P51150|RAB7A_MOUSE	48.6	15	1250	NA	1050

VFENYEASKAYSSVD	Q9D306|MGT4C_MOUSE	49.83	15	10200	513	5750
VFVAPAVTPVKG	P70158|ASM3A_MOUSE	41.99	12	7590	162	6160
VFYSSGIPATARP	Q91VN0|LRP5_MOUSE	48.7	13	450	NA	387
VFYSSGIPATARPY	Q91VN0|LRP5_MOUSE	42.38	14	224	NA	160
VGDIFSNPEAVLAK	Q3TPX4|EXOC5_MOUSE	45.08	14	162	NA	58.7
VGETFHASQPSMTVDG	Q8BUN5|SMAD3_MOUSE	27.79	16	NA	NA	144
VGGERFEAPEALFQP	P61161|ARP2_MOUSE	46.41	15	1070	NA	868
VGGERFEAPEALFQPH	P61161|ARP2_MOUSE	49.34	16	18200	220	16100
VGGRFQSPGTQSSRPI	Q571I9|A16A1_MOUSE	44.39	16	NA	NA	353
VGINIFTNSKIHKPR	Q61838|PZP_MOUSE	49.82	15	117	NA	97.5
VGINYQPPTVVPG	P68369|TBA1A_MOUSE:P68373|TBA1C_	40.1	13	159	NA	287
VGINYQPPTVVPGG	P68369|TBA1A_MOUSE:P68373|TBA1C_	37.18	14	289	NA	357
VGINYQPPTVVPGGDL	P68369|TBA1A_MOUSE:P68373|TBA1C_	46.53	16	5440	NA	5780
VGLGFPYEGPAPLEAIANG	Q8R4G6|MGT5A_MOUSE	42.09	19	NA	NA	331
VGPDYAHAEARKSP	A2ARP1|VIP1_MOUSE:Q6ZQB6|VIP2_M	46.76	14	249	NA	95.5
VGPDYAHAEARKSPA	A2ARP1|VIP1_MOUSE:Q6ZQB6|VIP2_M	47.31	15	1350	NA	1730
VGPGIVIDKKT(+79.97)RKKMKKAHKKSH	Q9CQJ5|PRR13_MOUSE	43.01	28	NA	NA	210
VGPRYTNL	P63085|MK01_MOUSE	27.51	8	NA	NA	252
VGRDKYEPAAVSEHGDK	Q8VDN2|AT1A1_MOUSE	48.69	17	NA	NA	201
VGTIRYM(+15.99)APEVLEGAVN	O35607|BMPR2_MOUSE	49.05	17	845	NA	651
VGTKRYM(+15.99)APEVLDETIN	Q61271|ACV1B_MOUSE	49.86	17	30100	NA	9270
VGTKRYMAPEVLDESL	P36895|BMR1A_MOUSE	29.76	16	1060	NA	3040
VGTKRYMAPEVLDETIN	Q61271|ACV1B_MOUSE	49.8	17	16600	NA	23500
VGTRRYM(+15.99)APEVLEGAIN	P27038|AVR2A_MOUSE:P27040|AVR2B	25.47	17	24900	NA	14500
VGTRRYMAPEVLEGAI	P27038|AVR2A_MOUSE:P27040|AVR2B	26.4	16	560	NA	1600
VGTRRYMAPEVLEGAIN	P27038|AVR2A_MOUSE:P27040|AVR2B	45.08	17	21200	NA	22500
VHERHFMAPGVRRVPV	Q6Q2Z6|ACOT5_MOUSE:Q32Q92|ACOT	43.04	16	121	NA	540
VHERHFMAPGVRRVPVR	Q6Q2Z6|ACOT5_MOUSE:Q32Q92|ACOT	48.53	17	NA	NA	296
VIGHALGPSPIPA	Q9WV38|GTR5_MOUSE	35.17	13	NA	NA	2050
VILYYTEPGSHVSR	O35206|COFA1_MOUSE	47.74	14	861	116	560
VILYYTEPGSHVSRE	O35206|COFA1_MOUSE	47.32	15	203	NA	148
VILYYTEPGSHVSREA	O35206|COFA1_MOUSE	49.46	16	1350	296	910
VINQTQKENLRKFYKGKKYKPLDLRPKK	Q6ZWV7|RL35_MOUSE	35.76	30	NA	NA	351
VIPELNGKLTGM(+15.99)AFRVPTPNVSV	P16858|G3P_MOUSE	49.87	25	9850	NA	7830
VIPELNGKLTGMAFRVPTPNVSVVD	P16858|G3P_MOUSE	48.76	25	NA	NA	8460
VIPELNGKLTGMAFRVPTPNVSVVDL	P16858|G3P_MOUSE	48.9	26	NA	NA	251
VIPELNGKLTGMAFRVPTPNVSVVDLT	P16858|G3P_MOUSE	48.94	27	NA	NA	522
VIPSRYSSPTTIATVM(+15.99)S	Q9DBM2|ECHP_MOUSE	48.25	17	813	NA	908
VIQAAFRTPATTASSPV	P25799|NFKB1_MOUSE	42.17	17	NA	NA	141
VITNQYNSPTGLYSSEN	O70400|PDLI1_MOUSE	49.93	17	16400	802	21600
VITNQYNSPTGLYSSENI	O70400|PDLI1_MOUSE	49.94	18	1010	NA	1700
VITNQYNSPTGLYSSENIS	O70400|PDLI1_MOUSE	49.93	19	1690	NA	2840
VKAAKPKKAAKSPAKAKAPKAK	P43277|H13_MOUSE	49.94	22	NA	NA	719
VKAAKPKKAAKSPAKAKAPKAKASKPK	P43277|H13_MOUSE	48.83	27	NA	NA	563
VKAAKPKKAAKSPAKAKAPKAKASKPKA	P43277|H13_MOUSE	49.95	28	1820	1980	1920
VKAAKPKKAAKSPAKAKAPKAKASKPKA	P43277|H13_MOUSE	35.69	32	NA	NA	93.9
VKASKPKKA	P10922|H10_MOUSE	36.36	9	1460	939	1120
VKDGYQMAQPVFAPK	P09581|CSF1R_MOUSE	27.83	15	NA	NA	79
VKDSELSPPTSAPSL	Q9WUU8|TNIP1_MOUSE	32.57	15	722	NA	720
VKDSELSPPTSAPSLVS	Q9WUU8|TNIP1_MOUSE	48.43	17	9100	NA	7310
VKM(+15.99)EYFRPNIVVSG	Q922Q1|MARC2_MOUSE	30.64	14	426	NA	141
VKPKAAKP	P15864|H12_MOUSE:P43274|H14_MOU	25.67	8	NA	NA	172
VKPKASKAKVTK	P43275|H11_MOUSE	29.73	12	NA	NA	38.4
VKPVKASKPKKAK	P10922|H10_MOUSE	48.45	13	274	144	782
VKSKASKPKVTKPKTAKPKAAKAK	P43276|H15_MOUSE	49.95	24	632	NA	1140
VKSKASKPKVTKPKTAKPKAAKAKK	P43276|H15_MOUSE	49.95	25	2500	NA	2550
VKSKASKPKVTKPKTAKPKAAKAKKA	P43276|H15_MOUSE	49.95	26	888	635	1390
VKSKASKPKVTKPKTAKPKAAKAKKAVS	P43276|H15_MOUSE	48.95	29	NA	NA	1000
VKSKASKPKVTKPKTAKPKAAKAKKAVS	P43276|H15_MOUSE	49.95	30	3880	1130	3590
VKVKPVKASKPKKAK	P10922|H10_MOUSE	48.76	15	NA	NA	6680
VKVSWRSPVPNK	Q64487|PTPRD_MOUSE	27.89	12	NA	NA	67.9
VKVSWRSPVPNKQ	Q64487|PTPRD_MOUSE	29.16	13	NA	NA	263
VKVSWRSPVPNKQH	Q64487|PTPRD_MOUSE	42.17	14	209	NA	194
VKVSWRSPVPNKQHG	Q64487|PTPRD_MOUSE	49.14	15	6070	NA	4490
VKVTFNSALAQKEAK	O89051|ITM2B_MOUSE	49.59	15	497	NA	332
VKVTFNSALAQKEAKK	O89051|ITM2B_MOUSE	49.89	16	15600	587	9600
VLIPYQGPSSDYVVVK	O88307|SORL_MOUSE	49.82	16	2720	173	1450
VLKLKGPRAANSFNPN	E9Q555|RN213_MOUSE	49.76	16	NA	NA	800
VLNRLKVGLQVVAVKAPGFGDNRKNQL	P63038|CH60_MOUSE	49.03	28	1670	NA	3770
VLPGPSQPRQYNNPIGLYSAETL	Q9JKS4|LDB3_MOUSE	46.35	23	NA	NA	38
VLPNIQAVLLPKKTESHHK	C0HKE3|H2A1D_MOUSE:Q8BFU2|H2A3	47.45	19	63	516	569
VLPNIQAVLLPKKTESHHKA	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	44.53	20	NA	NA	84
VLPNIQAVLLPKKTESHHKAK	C0HKE7|H2A1N_MOUSE:C0HKE3|H2A1	49.55	21	561	NA	1160
VLPTYDASKVTASGPG	Q80X90|FLNB_MOUSE	49.56	16	2090	NA	1180
VLRIINEPTAAAIAYG	P17879|HS71B_MOUSE:P16627|HS71L_	49.81	16	1500	NA	1110
VLVFDVTAPNTFKTLD	P51150|RAB7A_MOUSE	49.25	16	1070	NA	1140
VLVFDVTAPNTFKTLDS	P51150|RAB7A_MOUSE	49.4	17	289	NA	233
VLVTWTPPRARIAG	P11276|FINC_MOUSE	27.89	14	312	NA	288
VMRIINEPTAAAIAYG	P20029|BIP_MOUSE	48.57	16	223	NA	344
VNFVDPAASSSADD	P55012|S12A2_MOUSE	49.66	14	303	NA	63
VNKAVDYPPVANAGP	Q8K135|K319L_MOUSE	48.3	15	650	NA	647

VNKAVDYPPVANAGPNQ	Q8K135|K319L_MOUSE	49.88	17	11200	NA	13000
VNKNYLYLSPSGNTSPPG	Q62393|TPD52_MOUSE	48.47	18	NA	NA	103
VNPFVGPLTNRIG	Q8R090|VMAT1_MOUSE	39.63	13	5480	NA	2560
VNVDFNTPRPSTVEA	G3X939|SL9A3_MOUSE	49.48	15	31200	1850	41600
VNVQPYSGSPANFAVYT	P50431|GLYC_MOUSE	49.94	17	7990	NA	7660
VPAQSTFWRPQTQEERPH	Q8C708|CP054_MOUSE	43.78	18	159	NA	236
VPDDLLYSFPVVIKN	P14152|MDHC_MOUSE	49.85	15	814	NA	442
VPDDLLYSFPVVIKNKT	P14152|MDHC_MOUSE	49.94	17	33900	290	27700
VPDSYKSAVPFKILY	A2A8L5|PTPRF_MOUSE	49.39	15	3800	NA	2850
VPDSYKSAVPFKILYN	A2A8L5|PTPRF_MOUSE	47.65	16	246	NA	544
VPEGPDKGDRPHTYFGPETSASK	P70277|SIA7B_MOUSE	47.97	23	NA	NA	351
VPESLLTPRLAPSKP	P97927|LAMA4_MOUSE	40.98	15	214	NA	197
VPFDAATLHTSTAMAAQHG	P13020|GELS_MOUSE	47.7	19	NA	NA	118
VPFETRGPHINNSVH	Q8K296|MTMR3_MOUSE	49.67	15	26100	NA	28000
VPFETRGPHINNSVHM(+15.99)	Q8K296|MTMR3_MOUSE	46.7	16	3820	NA	4710
VPFWAHAGNAIPSADQ	Q9D0F3|LMAN1_MOUSE	27.2	16	692	NA	530
VPFYVRGPNVEAG	Q8CFG0|SULF2_MOUSE	44.92	13	86.3	NA	115
VPFYVRGPNVEAGSL	Q8CFG0|SULF2_MOUSE	49.09	15	1310	NA	1410
VPFYVRGPNVEAGSLN	Q8CFG0|SULF2_MOUSE	49.59	16	347	NA	332
VPFYVRGPNVEAGSLNP	Q8CFG0|SULF2_MOUSE	48.6	17	481	NA	806
VPFYVRGPNVEAGSLNPH	Q8CFG0|SULF2_MOUSE	49.89	18	5450	79.9	5330
VPIYEGYALPHAILR	P63260|ACTG_MOUSE:P60710|ACTB_M	49.25	15	2290	40.7	1660
VPKHEYTYPYVDSSDFG	Q924S7|SPRE2_MOUSE	49.93	17	13500	NA	9590
VPNYKLITPAVVSER	P62852|RS25_MOUSE	45.67	15	254	NA	175
VPNYKLITPAVVSERL	P62852|RS25_MOUSE	48.53	16	554	NA	436
VPPAGGGDPEAPAPAPAAERPPAPGPG	Q68FL4|SAHH3_MOUSE	49.94	27	4740	NA	9480
VPPDQYYWAPLAQHER	P30999|CTND1_MOUSE	48.77	16	2060	NA	3910
VPPDQYYWAPLAQHERG	P30999|CTND1_MOUSE	49.75	17	4640	NA	6560
VPPSVSPSPATAFSG	Q3UPH1|PRRC1_MOUSE	49.79	15	448	NA	301
VPPSVSPSPATAFSGPP	Q3UPH1|PRRC1_MOUSE	49.49	17	3050	NA	3470
VPQNQGDLEYQMSTTARAK	Q02257|PLAK_MOUSE	49.93	19	423	NA	831
VPQNQGDLEYQMSTTARAKR	Q02257|PLAK_MOUSE	47.56	20	200	NA	794
VPQSQAQPATAPQAAAAQEPG	Q3UHJ0|AAK1_MOUSE	49.94	21	746	NA	1920
VPSAYQKTVPIEAVT	Q60598|SRC8_MOUSE	28.46	15	NA	NA	145
VPSAYQKTVPIEAVTS	Q60598|SRC8_MOUSE	45.17	16	205	NA	158
VPSGLFIPSM(+15.99)AIGAIA	P51791|CLCN3_MOUSE	48.12	16	4880	NA	2000
VPSGLFIPSM(+15.99)AIGAIAGR	P51791|CLCN3_MOUSE	35.93	18	378	NA	141
VPTGHKLPSPLIM(+15.99)SPGPIYAVDG	Q8VHF2|CDHR5_MOUSE	49.28	23	439	NA	465
VPTGHKLPSPLIM(+15.99)SPGPIYAVDG	Q8VHF2|CDHR5_MOUSE	49.94	25	1790	NA	1450
VPTGHKLPSPLIMSPGPIYAVDG	Q8VHF2|CDHR5_MOUSE	39.07	23	NA	NA	455
VPTGHKLPSPLIMSPGPIYAVDGDQ	Q8VHF2|CDHR5_MOUSE	49.94	25	337	NA	1270
VPTVPLLPPQVNQS	Q99JX3|GORS2_MOUSE	46.04	14	834	NA	339
VPTVPLLPPQVNQSLAS	Q99JX3|GORS2_MOUSE	49.33	17	1240	NA	998
VPTVPLLPPQVNQSLASM(+15.99)PP	Q99JX3|GORS2_MOUSE	49.88	20	4060	NA	1770
VPTVPLLPPQVNQSLASMPP	Q99JX3|GORS2_MOUSE	48.19	20	NA	NA	1020
VPVIVEKAPKARIGDL	Q9DCD6|GBRAP_MOUSE	49.88	16	612	NA	454
VPVPEGPDKGDRPHTYFGPETSASKF	P70277|SIA7B_MOUSE	49.93	26	NA	NA	87.4
VPVPEGPDKGDRPHTYFGPETSASKFK	P70277|SIA7B_MOUSE	49.95	27	322	NA	1730
VPVQAPQVPEAIEK	Q8VDP3|MICA1_MOUSE	46.81	14	NA	NA	240
VPVQAPQVPEAIEKGD	Q8VDP3|MICA1_MOUSE	48.91	16	210	NA	134
VPWNFHEPQPGQYE	P23780|BGAL_MOUSE	49.61	14	5250	NA	2720
VPWNFHEPQPGQYEF	P23780|BGAL_MOUSE	49.8	15	804	NA	366
VPYPFQWGM(+15.99)PTVSAAGVI	Q9EPR4|S23A2_MOUSE	49.63	18	772	NA	858
VQAFTHAPAALEADRG	Q8BK64|AHSA1_MOUSE	41.94	16	250	NA	951
VQFTYQQPQPLSVEPR	B2RXS4|PLXB2_MOUSE	49.86	16	6840	NA	5940
VQIYHNPTANSFR	P70460|VASP_MOUSE	47.39	13	2200	NA	2510
VQIYHNPTANSFRV	P70460|VASP_MOUSE	48.37	14	338	NA	174
VQWNDPGAQYSLVN	Q9R100|CAD17_MOUSE	49.69	14	946	NA	393
VQWNDPGAQYSLVNK	Q9R100|CAD17_MOUSE	49.58	15	483	NA	409
VREGFKTPFAVASTR	Q19LI2|A1BG_MOUSE	46.81	15	NA	NA	6280
VRIGSGGVFRAPSIHGGSGGRG	P19001|K1C19_MOUSE	49.44	22	NA	NA	759
VRTDMAGPKATKSPEE	P48758|CBR1_MOUSE	49.36	16	829	NA	206
VRYTQKAPQVSTPT	P07724|ALBU_MOUSE	47.94	14	1500	NA	76.2
VRYTQKAPQVSTPTL	P07724|ALBU_MOUSE	49.82	15	51900	2380	58300
VRYTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.92	16	18200	50.1	17100
VRYTQKAPQVSTPTLVE	P07724|ALBU_MOUSE	49.44	17	975	NA	7700
VSGAQEM(+15.99)VSSSVSSAKETVA	Q9DBG5|PLIN3_MOUSE	48.91	20	609	NA	444
VSGAQEMVSSSVSSAKETVA	Q9DBG5|PLIN3_MOUSE	49.91	20	228	NA	837
VSGDEKKGPLIVSGPDGAPAKGDG	Q8VBW1|SC6A8_MOUSE	46.92	24	NA	NA	836
VSGRHKFRPSFPASSPYV	O89023|TPP1_MOUSE	32.28	18	NA	NA	315
VSHDYKGSTSHSLP	E9Q414|APOB_MOUSE	36.51	14	16700	NA	13200
VSHDYKGSTSHSLPY	E9Q414|APOB_MOUSE	46.48	15	42200	NA	40600
VSHDYKGSTSHSLPYE	E9Q414|APOB_MOUSE	47.08	16	10800	NA	7410
VSHTYGDPHVNLVIG	Q80T32|AGRD1_MOUSE	49.58	15	6650	NA	2790
VSPTDFKNPTIN	Q9CQY8|T4S20_MOUSE	26.69	12	NA	NA	89.3
VSPTDFKNPTINN	Q9CQY8|T4S20_MOUSE	48.18	13	204	NA	515
VSPTDFKNPTINNM(+15.99)VS	Q9CQY8|T4S20_MOUSE	49.78	16	269	NA	441
VSPYVSGEIQKAEIK	Q9D8C4|IN35_MOUSE	47.03	15	340	NA	307
VSSVEAPSVSPARH	Q8BUJ9|LRP12_MOUSE	44.2	14	1270	NA	128
VSSVEAPSVSPARHQ	Q8BUJ9|LRP12_MOUSE	46.43	15	10900	NA	113
VSTLIWAAPRLQSEVA	Q9CX00|IST1_MOUSE	36.41	16	452	NA	679

VSWQEKQPEASISQ	E9PYK3|PARP4_MOUSE	49.18	14	356	NA	234
VSWQEKQPEASISQT	E9PYK3|PARP4_MOUSE	49.33	15	450	NA	606
VTDATETTITISWR	P11276|FINC_MOUSE	37.6	14	901	270	462
VTFYKVIPKSKFVLVKF	P57759|ERP29_MOUSE	49.95	17	NA	NA	112
VTKAQKKDGKKRKRSRKESYSVYVYKV	Q8CGP2|H2B1P_MOUSE:Q6ZWY9|H2B1	43.22	29	NA	1760	147
VTKKVAKSPKKAKVTKPKKVKS	P15864|H12_MOUSE	49.95	22	NA	NA	584
VTKKVAKSPKKAKVTKPKKVKSA	P15864|H12_MOUSE	49.95	23	431	NA	1040
VTKKVAKSPKKAKVTKPKKVKSASKAVK	P15864|H12_MOUSE	49.95	31	337	NA	375
VTKPKTPAKPKKAAP	P43275|H11_MOUSE	48.91	15	NA	NA	438
VTQFHPPHIEIQ	P01887|B2MG_MOUSE	44.84	12	20600	NA	5470
VTQFHPPHIEIQM	P01887|B2MG_MOUSE	48.9	13	344	NA	564
VTQFHPPHIEIQML	P01887|B2MG_MOUSE	42.55	14	361000	NA	478000
VTTDHISPAGNIARNSPA	P28271|ACOHC_MOUSE	49.62	18	1210	NA	499
VTYEWAPPVQNQALAR	P47226|TES_MOUSE	44.75	16	435	NA	524
VVDNVSSPETIVVFNG	Q8CAS9|PARP9_MOUSE	45.27	16	607	NA	464
VVKVKPVKASKPKKAK	P10922|H10_MOUSE	49.94	16	3890	2650	4520
VVWDYFTQLSNNAKE	P06728|APOA4_MOUSE	49.72	15	2250	NA	1860
VVWDYFTQLSNNAKEA	P06728|APOA4_MOUSE	49.86	16	1390	NA	1330
VVWDYFTQLSNNAKEAV	P06728|APOA4_MOUSE	49.72	17	428	NA	319
VVYSYKASQPDELTI	Q3USJ8|FCSD2_MOUSE	45.38	15	705	NA	1180
VWDYFTQLSNNAKE	P06728|APOA4_MOUSE	48.63	14	317	NA	252
VYLIQGTQVYVFLTK	Q91X72|HEMO_MOUSE	49.62	15	3160	1610	2500
VYLLVVNHPDSSSTVE	P52430|PON1_MOUSE	48.27	16	1240	NA	1570
VYPAYASVKAIESPS	Q9JM62|REEP6_MOUSE	49.9	15	3250	NA	2020
VYPTPAYTIPFYTPIPNG	O08573|LEG9_MOUSE	49.69	18	332	NA	277
VYTYGKPVPGLVTL	Q61838|PZP_MOUSE	48.57	14	205	NA	131
WDYFTQLSNNAKE	P06728|APOA4_MOUSE	48.67	13	681	NA	511
WDYFTQLSNNAKEA	P06728|APOA4_MOUSE	49.45	14	1190	NA	314
WEAATPAVAETPDIK	P97461|RS5_MOUSE	42.58	15	NA	NA	142
WGIDPYDQPNAIYIERH	O88307|SORL_MOUSE	49.94	17	749	NA	436
WKALYTDPKSSETAAF	Q920A5|RISC_MOUSE	48.48	16	661	NA	441
WNDPGAQYSLVNKE	Q9R100|CAD17_MOUSE	49.83	14	2400	NA	2060
WNDPGAQYSLVNKEK	Q9R100|CAD17_MOUSE	49.84	15	4210	NA	1760
WPENQWRPPLPDNYPE	P09470|ACE_MOUSE	49.94	16	10100	NA	7180
WQGGVYASPSIAGSRPG	Q8R0X7|SGPL1_MOUSE	49.82	17	7080	217	5520
WTTGAWKNPHVQQAAQN	Q9JKD3|SCAM5_MOUSE	48.26	17	NA	NA	353
WTYNPAAVSKVAPA	Q80SY4|MIB1_MOUSE	48.83	14	682	NA	423
WVRTDMAGPKATKSPE	P48758|CBR1_MOUSE	39.03	16	669	NA	732
WVRTDMAGPKATKSPEE	P48758|CBR1_MOUSE	49.92	17	12800	NA	6310
YAFSPPRGLLSK	Q91WC9|DGLB_MOUSE	48.74	12	498	NA	293
YAFSPPRGLLSKSL	Q91WC9|DGLB_MOUSE	48.86	14	342	NA	257
YAKKIFLAPKPAPL	Q9Z1T1|AP3B1_MOUSE	49.55	14	1380	NA	695
YAVRGPIVQRALE	Q8QZR5|ALAT1_MOUSE	47.25	13	5620	NA	4100
YAVRGPIVQRALEL	Q8QZR5|ALAT1_MOUSE	46.97	14	6380	NA	5620
YAVYETPTAHNG	Q9QZ06|TOLIP_MOUSE	41.99	12	425	NA	336
YAVYETPTAHNGAK	Q9QZ06|TOLIP_MOUSE	45.64	14	544	NA	333
YAVYETPTAHNGAKN	Q9QZ06|TOLIP_MOUSE	46.74	15	524	NA	321
YAVYETPTAHNGAKNPR	Q9QZ06|TOLIP_MOUSE	49.78	17	13000	324	9990
YDKYFTNPQISQGVPG	Q3U0J8|TBD2B_MOUSE	48.4	16	1010	NA	1090
YDVKAPAM(+15.99)FNIRNIGK	P97351|RS3A_MOUSE	42.91	16	192	576	369
YEGPETHTSLR	P14483|HB2A_MOUSE	48.09	11	466	NA	401
YEKLAEPTVSYSSYR	Q04592|PCSK5_MOUSE	39.32	15	175	NA	232
YEPPAPAPAPLPPP	O35609|SCAM3_MOUSE	47.96	14	1680	NA	1390
YFIEKVIPSTANSN	E9Q7P9|CDHR2_MOUSE	49.32	14	228	NA	114
YFIEKVIPSTANSNN	E9Q7P9|CDHR2_MOUSE	47.03	15	192	NA	159
YFYQM(+15.99)AKIHPEPG	Q3UZZ6|ST1D1_MOUSE	47.89	13	522	NA	331
YFYQMAKIHPEPG	Q3UZZ6|ST1D1_MOUSE	49.76	13	1190	NA	881
YGIPFAAPTALASRDG	Q91VX2|UBAP2_MOUSE	47.89	16	1760	NA	1300
YGIPFAAPTALASRDGN	Q91VX2|UBAP2_MOUSE	42.88	17	585	NA	508
YGQPPTGYSTPTAPQAYSQPVQ	Q61545|EWS_MOUSE	49.81	22	49.9	NA	868
YHDTSYKPPAGRTAAPE	Q69ZQ1|MYORG_MOUSE	49.53	17	558	NA	741
YHDYYITSTSNGSLE	P52795|EFNB1_MOUSE	48.78	15	287	NA	657
YHLEYVSSELRKSLQ	E9Q414|APOB_MOUSE	48.8	15	1180	NA	1270
YIEGYVPSQADVAVFE	O70251|EF1B_MOUSE	39.57	16	1520	NA	1570
YIMQYIAAITNPSQR	Q5SYD0|MYO1D_MOUSE	44.67	15	NA	NA	193
YIMQYIAAITNPSQRA	Q5SYD0|MYO1D_MOUSE	47.46	16	NA	NA	650
YISVFKGSGC(+57.02)WS(+79.97)SV	Q61847|MEP1B_MOUSE	37.8	14	588	NA	454
YIYFHKAPSPEKAEEE	Q61024|ASNS_MOUSE	41.99	16	251	NA	992
YKAPVPTGEVY	P35564|CALX_MOUSE	44.67	11	NA	NA	78.6
YKAPVPTGEVYF	P35564|CALX_MOUSE	46.98	12	NA	NA	117
YKKSPVYKNPTPGSSE	Q99PG0|AAAD_MOUSE	34.71	16	160	NA	117
YKPFQNPVPNQSPS	P16382|IL4RA_MOUSE	49.57	14	11500	NA	13800
YKRTKAALTIIRYYRRYKVKS	Q5SYD0|MYO1D_MOUSE	25.56	21	NA	NA	97.4
YKSFVQNYPVVSIEDPF	P17182|ENOA_MOUSE	49.94	17	148	NA	293
YKSFVQNYPVVSIEDPFD	P17182|ENOA_MOUSE	49.95	18	354	NA	264
YKTYFQGSLPARAAYQ	P52760|RIDA_MOUSE	38.75	16	221	NA	161
YLAVFDGPSTNSR	Q9JLB4|CUBN_MOUSE	35.15	13	198	NA	95.9
YLLSQSSPAPLTAAE	Q91YR1|TWF1_MOUSE	49.12	15	279	NA	189
YLLSQSSPAPLTAAEE	Q91YR1|TWF1_MOUSE	49.89	16	2240	NA	1320
YLLVVNHPDSSSTVE	P52430|PON1_MOUSE	47.19	15	1890	NA	1960
YLNIYTPAHAHEG	Q91WG0|EST2C_MOUSE	45.91	13	2670	NA	1750

YLNIYTPAHAHEGSN	Q91WG0|EST2C_MOUSE	48.67	15	18800	197	17000
YLNIYTPAHAHEGSNL	Q91WG0|EST2C_MOUSE	48.7	16	15600	132	14100
YLNIYTPAHAHEGSNLP	Q91WG0|EST2C_MOUSE	49.8	17	6480	NA	6590
YLNIYTPAHAHEGSNLPV	Q91WG0|EST2C_MOUSE	49.89	18	43500	NA	23400
YLNIYVPAHAHE	Q8BK48|EST2E_MOUSE	38.6	12	282	NA	200
YLNIYVPAHAHEG	Q8BK48|EST2E_MOUSE	45.58	13	20400	436	16400
YLNIYVPAHAHEGS	Q8BK48|EST2E_MOUSE	46.91	14	3470	NA	3870
YLNIYVPAHAHEGSNL	Q8BK48|EST2E_MOUSE	48.5	16	101000	2360	82600
YLNIYVPAHAHEGSNLP	Q8BK48|EST2E_MOUSE	49.39	17	38900	NA	38400
YLNIYVPAHAHEGSNLPV	Q8BK48|EST2E_MOUSE	49.91	18	90800	2390	102000
YLVYQEPIPTAQLV	P49722|PSA2_MOUSE	49.43	14	689	NA	426
YNFVTPLTHM(+15.99)VVT	A6X935|ITIH4_MOUSE	43.08	13	916	NA	592
YNFVTPLTHM(+15.99)VVTKPE	A6X935|ITIH4_MOUSE	48.13	16	488	NA	344
YNFVTPLTHMVVT	A6X935|ITIH4_MOUSE	44.19	13	394	NA	541
YNFVTPLTHMVVTKPE	A6X935|ITIH4_MOUSE	43.53	16	67.8	NA	373
YNPTLPYKRPIPGGLS	O54891|LEG6_MOUSE:Q8K419|LEG4_M	41.26	16	NA	NA	402
YNSQITAPYADRVT	O88792|JAM1_MOUSE	46.68	14	295	NA	200
YNSQITAPYADRVTF	O88792|JAM1_MOUSE	48.36	15	1810	NA	1610
YNSQITAPYADRVTFS	O88792|JAM1_MOUSE	49.81	16	3610	53	3770
YNTASNKTRLSRTPGNRIVYLYTKKVGK	Q9D1R9|RL34_MOUSE	47.84	30	563	NA	3510
YNTASNKTRLSRTPGNRIVYLYTKKVGK	Q9D1R9|RL34_MOUSE	48.93	31	1610	12500	2050
YPAGSPGYNPPQM(+15.99)NTLP	Q8K419|LEG4_MOUSE	49.54	17	4680	NA	3580
YPAGSPGYNPPQM(+15.99)NTLPV	Q8K419|LEG4_MOUSE	49.71	18	7120	NA	5360
YPAYASVKAIESPSK	Q9JM62|REEP6_MOUSE	49.86	15	1310	NA	498
YPENFAPSFPHGSPG	Q3UDK1|TRAD1_MOUSE	49.68	15	4920	NA	3610
YPNFAGPQAALANK	Q8BJW6|EIF2A_MOUSE	46.4	14	143	NA	118
YPNFAGPQAALANKS	Q8BJW6|EIF2A_MOUSE	46.57	15	211	NA	179
YPNTPYISPVASYSGQP	Q3UPL0|SC31A_MOUSE	49.76	17	9670	58.6	9960
YPNTPYISPVASYSGQPQ	Q3UPL0|SC31A_MOUSE	49.93	18	6360	NA	7780
YPPPYPPAAFQGPSDHAAY	Q9JJ00|PLS1_MOUSE	45.83	19	1060	NA	508
YPPPYPPAAFQGPSDHAAYPI	Q9JJ00|PLS1_MOUSE	49.92	21	8690	NA	4770
YPPPYPPAAFQGPSDHAAYPIPQ	Q9JJ00|PLS1_MOUSE	49.66	23	6710	NA	2110
YPPSGPTYRGPVPWHT	Q9WV54|ASAH1_MOUSE	45.4	16	1070	NA	2410
YPQASVTDVT	Q61703|ITIH2_MOUSE	30.54	10	NA	NA	809
YPSQASIYSPPAAAAAA	P70297|STAM1_MOUSE	48.75	17	647	NA	467
YPSQASIYSPPAAAAAAA	P70297|STAM1_MOUSE	49.91	18	23600	141	27200
YPSQASIYSPPAAAAAAAA	P70297|STAM1_MOUSE	48.02	20	NA	NA	243
YPSSPPVVNTVKG	Q8VCT4|EST1D_MOUSE	44.28	13	1680	NA	488
YPTPAYTIPFYTPIPN	O08573|LEG9_MOUSE	49.52	16	8220	NA	5970
YPTPAYTIPFYTPIPNG	O08573|LEG9_MOUSE	49.68	17	60700	2150	71100
YPTPAYTIPFYTPIPNGL	O08573|LEG9_MOUSE	48.74	18	NA	NA	22000
YPTPAYTIPFYTPIPNGLY	O08573|LEG9_MOUSE	49.88	19	NA	NA	406
YPTPAYTIPFYTPIPNGLYP	O08573|LEG9_MOUSE	49.94	20	1550	NA	3520
YPTPAYTIPFYTPIPNGLYPS	O08573|LEG9_MOUSE	49.94	21	33400	99.2	36500
YPVVPVHLDGTF	O35291|RNAS2_MOUSE:P97425|ECP2_	43.04	12	2790	1020	859
YQLSIHKNPNASEPKH	Q8VDN2|AT1A1_MOUSE	47.08	16	407	NA	274
YQLYFQEPGVAEAE	P34914|HYES_MOUSE	49.85	14	898	NA	534
YQLYFQEPGVAEAELEK	P34914|HYES_MOUSE	49.68	17	106	NA	150
YSFKAARALLDHRK	Q9WTN3|SRBP1_MOUSE	49.12	14	482	NA	257
YSIVSAPAAQKVREL	Q8BH86|GLUCM_MOUSE	49.13	15	655	NA	491
YSKYSAPRLPAALE	P97432|NBR1_MOUSE	49.82	14	538	NA	500
YSKYSAPRLPAALEQ	P97432|NBR1_MOUSE	49.83	15	1550	NA	1430
YSRKALYKRKYSAAKTKVEKKKKKEKVL	P47911|RL6_MOUSE	49.95	29	6330	NA	3790
YSSQPAAYVAQPATAAAYASQPA	Q8C2Q3|RBM14_MOUSE	48.47	23	NA	NA	191
YSTYKTPVPETNIPG	Q60855|RIPK1_MOUSE	39.15	15	1660	NA	1240
YTAKGLFRAAVPSGAST	P17183|ENOG_MOUSE:P17182|ENOA_M	48.05	17	248	NA	806
YTAKGLFRAAVPSGASTG	P17183|ENOG_MOUSE:P17182|ENOA_M	49.48	18	1080	NA	651
YTDIQEPM(+15.99)LNAAQEQ	Q9QZM0|UBQL2_MOUSE:Q8R317|UBQL	49.18	15	472	NA	137
YTDIQEPMLNAAQEQ	Q9QZM0|UBQL2_MOUSE:Q8R317|UBQL	45.43	15	NA	NA	220
YTDPKSSETAAF	Q920A5|RISC_MOUSE	37.35	12	711	NA	1170
YTGYPTAYPAAAPAYNPS	Q8BGZ2|F168A_MOUSE	49.91	18	63.1	NA	106
YTIPFYTPIPNGL	O08573|LEG9_MOUSE	47.57	13	4320	NA	1340
YTIPFYTPIPNGLY	O08573|LEG9_MOUSE	47.35	14	774	NA	145
YTIPFYTPIPNGLYP	O08573|LEG9_MOUSE	49.15	15	29600	373	23700
YTQKAPQVSTP	P07724|ALBU_MOUSE	36.62	11	206	NA	139
YTQKAPQVSTPT	P07724|ALBU_MOUSE	47.88	12	750	NA	487
YTQKAPQVSTPTL	P07724|ALBU_MOUSE	46.93	13	1580	NA	816
YTQKAPQVSTPTLV	P07724|ALBU_MOUSE	49.7	14	995	NA	755
YTQKAPQVSTPTLVEA	P07724|ALBU_MOUSE	49.9	16	621	NA	540
YVDPTPDPNTAYASYPSASVENYQQPP	O55101|SNG2_MOUSE	41.66	27	579	NA	2060
YVIGHALGPSPIPA	Q9WV38|GTR5_MOUSE	41.26	14	NA	NA	428
YVPWNFHEPQPGQYE	P23780|BGAL_MOUSE	49.9	15	598	NA	280
YVTQFHPPHIE	P01887|B2MG_MOUSE	44.43	11	1180	NA	796
YVTQFHPPHIEIQ	P01887|B2MG_MOUSE	48.71	13	184000	2180	141000
YVTQFHPPHIEIQM(+15.99)	P01887|B2MG_MOUSE	49.73	14	40300	677	34700
YVTQFHPPHIEIQM(+15.99)L	P01887|B2MG_MOUSE	49.73	15	266000	1040	209000
YVTQFHPPHIEIQM(+15.99)LKN	P01887|B2MG_MOUSE	49.92	17	14100	NA	10400
YVTQFHPPHIEIQML	P01887|B2MG_MOUSE	49.59	15	39500	NA	72000
YVTQFHPPHIEIQMLK	P01887|B2MG_MOUSE	49.49	16	15300	NA	38900
YVTQFHPPHIEIQMLKN	P01887|B2MG_MOUSE	49.83	17	4510	NA	9160
YVTQFHPPHIEIQMLKNG	P01887|B2MG_MOUSE	49.43	18	3030	NA	4920

YVTQFHPPHIEIQMLKNGK	P01887|B2MG_MOUSE	49.93	19	700	NA	366
YYFYQMAKIHPEPG	Q3UZZ6|ST1D1_MOUSE	49.84	14	280	NA	438
YYLPYKSPGINVDS	Q9JHJ8|ICOSL_MOUSE	49.47	14	305	NA	202
YYLPYKSPGINVDSS	Q9JHJ8|ICOSL_MOUSE	49.48	15	5650	NA	4580
YYLPYKSPGINVDSSY	Q9JHJ8|ICOSL_MOUSE	49.89	16	1440	NA	1250
YYLVYQEPIPTAQLV	P49722|PSA2_MOUSE	49.86	15	1060	NA	831
YYYFYQM(+15.99)AKIHPEPG	Q3UZZ6|ST1D1_MOUSE	49.88	15	313	NA	208
YYYFYQMAKIHPEPG	Q3UZZ6|ST1D1_MOUSE	49.75	15	642	NA	901

Table S5 Information of peptides identified in IEC MHCII immunopeptidome (Independent replicate experiment for Fig. 2d)