

Supplementary Table 1: List of peptides identified by SILAC

	NCBI Accession number	Protein Description	Peptide Sequence	Peptide modifications	Protein Mass [Da]	h/w protein intensity ratio*	h/w protein StDev	h/w protein intensity ratio*	h/w protein StDev	Mass charge ratio	Measured mass	Mascot calculated mass [Da]	Uncalibrated mass error [Da]	Charge	Peptide Score	Left flanking AA	Right flanking AA	Sequence coverage	No. of peptides assigned to protein
1	gi 4506903	Splicing factor, arginine/serine-rich 9	VEFPR	1Arg10	25526	2.718	1.188	9.337	3.581	329.20	656.39	656.35	0.034	2	32	R	T	19	5
			VEFPR							324.20	646.38	646.34	0.037	2	30	R	T		
			VEFPR	1Arg6						327.21	652.40	652.36	0.034	2	30	R	T		
			IYVGNLPTDVR	1Arg10						628.89	1255.77	1255.68	0.087	2	38	R	E		
			EKDLEDFYK							650.37	1298.72	1298.64	0.077	2	51	R	Y		
			DLEDLFYK							521.80	1041.59	1041.50	0.085	2	41	K	Y		
			DQVGMVEYLR	1Arg10						574.82	1147.62	1147.56	0.059	2	41	K	K		
2	gi 5901926	Cleavage and polyadenylation specific factor 5	YIQQTKPLTLER	1Arg10	26211	2.673	1.478	4.811	3.070	500.64	1498.90	1498.84	0.058	3	39	K	T	40	9
			TNLYPLNTYFTGTK							873.47	1744.92	1744.90	0.014	2	54	R	E		
			SQTGWPR	1Arg10						421.23	840.45	840.41	0.034	2	30	R	G		
			LPGGELNPGDEVEGLK							876.94	1751.86	1751.86	-0.002	2	73	K	R		
			LMTIELGR	1Arg10						471.79	941.56	941.52	0.032	2	53	R	O		
			LMTIELGR	1Arg6						469.79	937.56	937.54	0.027	2	30	R	O		
			LFLVQLQEK							559.35	1116.69	1116.65	0.031	2	53	R	A		
			KFLVQLQEK							415.95	1244.82	1244.75	0.070	3	45	K	A		
			GVTQFGNK							425.74	849.47	849.43	0.038	2	30	R	Y		
			ALFAVPK							373.24	744.47	744.45	0.017	2	51	K	N		
3	gi 7706322	Homeobox prox 1	NHSSDWPK		28068	1.131	0.141	2.000	0.301	361.87	1082.58	1082.51	0.061	3	33	R	F	44	9
			NFVWLEDDK							646.35	1290.89	1290.85	0.012	2	37	R	I		
			NAEPLNLDVNNPDFK							605.00	1811.97	1811.96	0.030	3	82	K	A		
			LLHIEELR	1Arg10						344.89	1031.64	1031.61	0.055	3	33	R	E		
			INEAIVAVQAIADPK							833.00	1663.99	1663.91	0.106	2	79	K	T		
			ILVQER	1Arg10						384.26	766.50	766.41	0.042	2	31	R	L		
			HILGFDTGDAVLNEAAQILR							718.41	2152.22	2151.96	0.030	3	65	K	L		
			EGLPVALDK							471.29	940.56	940.34	0.031	2	67	K	H		
			AGVMALANLQIQR	1Arg6						507.32	1518.93	1518.89	0.071	3	39	K	H		
			AGVMALANLQIQR	1Arg10						762.45	1522.88	1522.86	0.049	2	73	K	H		
4	gi 13376429	NEFA interacting nuclear protein	LTVKPIETK		28895	1.463	0.071	3.836	0.947	343.56	1027.67	1027.63	0.039	3	30	K	N	12	3
			IVSSIFR	1Arg10						416.25	830.49	830.49	0.005	2	50	K	T		
			GLDEDETNFLDEVSR	1Arg10						874.88	1747.76	1747.78	-0.022	2	67	R	Q		
5	gi 30410796	Proteasome activator subunit 3 isoform 2	TVSEEAASYLDQISR	1Arg10	30867	1.248	0.173	2.554	0.370	560.30	1677.89	1677.81	0.082	3	66	R	Y	30	8
			TVSEEAASYLDQISR							558.99	1667.95	1667.80	0.145	3	36	R	Y		
			TVSEEAASYLDQISR	1Arg6						559.00	1673.97	1673.82	0.152	3	30	R	Y		
			SNQQLVDIEK							643.86	1285.71	1285.69	0.022	2	65	K	V		
			MWVQLLIPR	1Met(ox) 1Arg10						591.39	1180.76	1180.67	0.092	2	51	K	I		
			MWVQLLIPR	1Arg10						583.39	1164.77	1164.67	0.098	2	47	K	I		
			LLIEK							308.24	614.47	614.40	0.067	2	30	R	C		
			LLLEDSFLK							539.36	1076.70	1076.61	0.087	2	61	K	E		
			LIISLR	1Arg10						427.28	852.55	852.53	0.022	2	39	R	N		
			LIISLR							422.30	842.59	842.52	0.065	2	49	R	N		
			LIISLR	1Arg6						425.31	848.61	848.54	0.066	2	30	R	N		
			KLLEDSFLK							402.63	1204.86	1204.71	0.150	3	54	K	E		
			ITSEAEDEVANFFPK							840.99	1679.96	1679.84	0.115	2	89	R	K		
6	gi 16905517	FUS interacting protein (serine/arginine-rich) 1	YLRPNTSLFVR	2Arg10	31300	1.900	0.000	5.140	0.000	494.97	1481.89	1481.52	0.03	3	49	R	N	5	1
			YLRPNTSLFVR							498.31	1491.90	1491.61	0.136	3	30	R	N		
7	gi 14110414	heterogeneous nuclear ribonucleoprotein D	LDPITGR	1Arg10	32942	1.516	0.000	4.332	0.000	391.24	780.46	780.44	0.050	2	38	K	S	12.5	4
			KYHNVLGSK							349.22	1044.63	1044.57	0.020	3	33	K	C		
			IFVGGSLPDTPEEK							744.88	1487.75	1487.75	-0.005	2	67	K	I		
			DLKDYFSK							339.19	1014.55	1014.50	0.039	3	37	K	F		
8	gi 49472822	Eukaryotic translation initiation factor 3, subunit 4	VTNLSEDTIR	1Arg6	35611	1.121	0.000	2.210	0.000	520.79	1039.57	1039.52	0.120	2	31	R	E	3	1
			VTNLSEDTIR	1Arg10						522.79	1043.56	1043.51	0.126	2	63	R	E		
9	gi 55956919	Heterogeneous nuclear ribonucleoprotein AB	VLDQK		35945	3.619	0.000	8.010	0.000	301.70	601.38	601.34	0.035	2	30	K	E	24	8
			MFVGGSLWSDTSK							664.33	1326.64	1326.63	0.016	2	76	K	K		
			KFHTVSGSK							495.79	989.56	989.53	0.026	2	57	K	C		
			IFVGGSLNPEATEEK							752.40	1502.78	1502.76	0.020	2	83	K	I		
			GFGLFLK							464.79	927.56	927.52	0.041	2	42	R	D		
			EYVQQQYSGGGR	1Arg10						755.36	1508.70	1508.69	0.013	2	56	K	G		
			EYVQQQYSGGGR	1Arg6						753.36	1504.71	1504.70	0.009	2	45	K	G		
			EYVQQQYSGGGR							750.34	1498.67	1498.68	-0.012	2	32	K	G		
			DYFTK							337.20	672.39	672.31	0.079	2	30	K	F		
			DLKDYFTK							515.28	1028.54	1028.52	0.020	2	49	K	F		
10	gi 4502923	Calponin 3	HLVDPK		36391	1.001	0.000	3.389	0.000	386.72	771.42	771.39	0.024	2	30	R	M	9.1	3
			GPSYGLSAEVK							594.28	1186.55	1186.53	0.026	2	55	K	N		
			GASQAGMLAPGTR	1Arg10						613.81	1225.61	1225.61	0.002	2	71	K	R		
			GASQAGMLAPGTR	1Met(ox) 1Arg10						621.82	1241.62	1241.61	0.012	2	32	K	R		
11	gi 11034845	Chromosome 20 Open reading frame 77	LTFYLANDVIQNSK		36877	1.494	0.312	1.953	0.268	580.34	1737.99	1737.93	0.063	3	53	K	R	19	5
			LLNIWQER	1Arg10						541.31	1080.60	1080.60	0.007	2	43	R	S		
			LAALEDR	1Arg10						463.75	925.48	925.47	0.003	2	57	R	R		
			IASLPEVDDVSLLEK							590.35	1768.01	1767.96	0.053	3	75	K	I		
			EFESVLDVAFSHVAR	1Arg10						572.65	1714.94	1714.86	0.083	3	55	R	E		
12	gi 14043072	Heterogeneous nuclear ribonucleoprotein A2/B1	TLETVPLER	1Arg10	37407	3.150	1.430	10.230	5.053	534.32	1066.62	1066.59	0.030	2	58	K	K	53	16
			RGFQVTFDDHPVDK	1Arg10						621.32	1860.94	1860.87	0.071	3	43	K	I		
			QEMQEVQSSR	1Arg10						607.79	1213.56	1213.53	0.036	2	59	R	S		
			NYEQWQK							544.26	1086.51	1086.48	0.032	2	39	R	L		
			LFVGGIKEDTTEHILR	1Arg10						473.27	1889.05	1888.97	0.086	4	45	K	D		
	</																		

		GGGGNFGPGGPNFR	1Arg10							694.32	1386.63	1386.63	-0.003	2	76	R	G		
		GFGVTFDDHDPVKLQK								570.08	2276.28	2276.15	0.134	4	42	R	Y		
		GFGVTFDDHDPVVK								848.38	1694.75	1694.76	-0.010	2	89	R	I		
		GFGVTFDDHDPVVK								848.38	1694.75	1694.76	-0.005	2	85	R	I		
		EESGKPGAHVTVK								669.86	1337.70	1337.69	0.005	2	49	R	K		
		EDTEEHHLR	1Arg10							588.28	1174.55	1174.52	0.026	2	33	K	D		
		EDTEEHHLR	1Arg10							588.29	1174.57	1174.52	0.045	2	55	K	D		
		EDTEEHHLR	1Arg6							586.29	1170.56	1170.54	0.025	2	30	K	D		
		DYFEYEGK								525.74	1049.46	1049.43	0.028	2	33	R	I		
13	gj34740329	Heterogeneous nuclear ribonucleoprotein A3	1Arg10	39571	1.799	0.432	6.086	2.518		667.61	1999.79	1999.76	0.038	3	45	R	R	22.4	7
		ISSGGYGGYGGSSGGSGYGR								431.31	860.60	860.55	0.055	2	60	K	E		
		KIFVGGIK								622.82	1243.62	1243.60	0.016	2	74	K	Q		
		IETIEVMEDR	1Arg10							630.82	1259.62	1259.59	0.022	2	50	K	Q		
		IETIEVMEDR	1Met(ox) 1Arg10							571.95	1712.83	1712.77	0.067	3	48	R	I		
		GFAFVTFDDHDTVVK								589.78	1177.54	1177.51	0.030	2	66	K	D		
		EDTEEYNLR	1Arg10							460.94	1379.81	1379.74	0.066	3	48	R	K		
		EDSVKPSAHLTVK								525.24	1048.47	1048.49	-0.019	2	33	R	I		
		DYFEYEGK								486.27	970.52	970.48	0.040	2	50	R	V	12	5
14	gj13899354	RNA binding motif protein 4B	1Arg10	40124	2.896	0.716	9.408	3.749		470.30	938.58	938.56	0.027	2	40	K	E		
		SLFEQYQK								554.78	1107.54	1107.52	0.022	2	67	R	R		
		LFIGNLPR								493.25	984.49	984.48	0.018	2	54	R	S		
		GLDNTEFGQK								492.26	982.51	982.50	0.017	2	61	R	G		
		EATEQER	1Arg10							1236.15	2470.28	2470.13	0.145	2	81	K	S	14.5	3
		AEDAENR	1Arg10							1365.23	2728.44	2728.31	0.138	2	30	R	E		
15	gj21361320	TRK-fused gene	1Arg10	43421	1.112	0.000	2.353	0.000		451.26	900.51	900.47	0.043	2	30	K	R		
		NVMSAFGLTDDQVSPSPAEADR								551.82	1101.62	1101.58	0.039	2	43	R	V	14.5	5
		LLDSLEPGEPEPSTNIPENDVDGR								921.46	1840.91	1840.88	0.025	2	85	R	A		
		AQLGEDIR								887.93	1773.84	1773.73	0.101	2	50	K	L		
		VHIEIGPDGR	1Arg10	49198	1.815	0.319	5.591	0.915		355.22	708.43	708.38	0.044	2	31	R	E		
		STGEAFVQFASQIEAK								669.69	2006.06	2005.98	0.082	3	30	R	V		
		HTGPNSPDTANGFVFR	1Arg10							935.94	1869.87	1869.77	0.106	2	57	R	I	29	10
		FVYTR	1Arg10							890.95	1779.89	1779.79	0.099	2	30	R	I		
		ATENDIYNFSPNLNPR								507.03	1518.07	1517.93	0.138	3	83	R	G		
17	gj14165435	Heterogeneous nuclear ribonucleoprotein K	phospho (Y), 1Arg10	50944	1.762	0.155	3.732	0.241		858.04	1714.07	1713.98	0.095	2	32	R	K		
		TDYNASVSPDSSGPER								351.25	700.48	700.45	0.028	2	35	R	N		
		TDYNASVSPDSSGPER								863.87	2586.60	2586.58	0.219	3	50	R	Q		
		LLIHSLAGGIQVK								670.92	1339.83	1339.80	0.030	2	87	K	G		
		ILLSADIEITGELK								635.31	1268.61	1268.58	0.033	2	57	K	I		
		ILLOS								639.71	1916.11	1916.03	0.085	3	45	R	D		
		IIITGTQDQIQNAQYLLQNSVK								504.26	1006.51	1006.44	0.067	2	38	R	R		
		IILDISEPIK								437.27	872.53	872.50	0.032	2	47	K	G		
		IDPLEGSEDR	1Arg10							419.27	836.52	836.49	0.021	2	33	R	G	1	1
		GSYDGLGGPIITQVTIPK								424.25	846.48	846.43	0.031	2	30	R	G		
		GGDLMAYDR	1Arg10							345.71	689.40	689.37	0.031	2	33	K	R	25	8
		DLAGSIQK								749.88	1497.74	1497.66	0.083	2	50	K	E		
18	gj5031703	RasGAP SH3-domain binding protein	1Arg10	52164	1.123	0.000	2.215	0.000		1717.89	1433.76	1433.68	0.075	2	31	K	E		
		INIPQR	1Arg10							1195.95	3584.82	3584.82	0.200	3	34	R	Q		
		VSFATR	1Arg10	53394	2.179	0.219	5.007	0.866		710.61	1419.65	1419.65	0.013	2	76	K	A		
		TGQPMNLYTDR	1Arg10							446.29	890.56	890.45	0.108	2	42	K	V		
		TGQPMNLYTDR	1Met(ox) 1Arg10							755.03	2262.08	2261.97	0.101	3	60	K	R		
		HDSECDNSDNTIFVQGLGENVTIESVADYFK								1127.06	2252.10	2251.97	0.131	2	46	K	R		
		GEATVSDPDPBAK								632.33	1893.97	1893.93	0.048	3	32	K	V		
		EFSGNPIK								511.77	1021.52	1021.49	0.032	2	73	K	E		
		APKPDGPGGGPGGSHMGGNYGDDR	1Arg10							470.77	939.53	939.45	0.078	2	38	R	K	12.5	6
		APKPDGPGGGPGGSHMGGNYGDDR								525.34	1048.66	1048.59	0.066	2	58	R	G		
		AAIDVFDGKFEFSGNPIK								861.96	1721.91	1721.82	0.084	2	105	K	A		
		LAIDVFDGK								351.74	701.47	701.41	0.063	2	30	R	E		
		TEIDLSIK	1Arg10	59797	4.914	2.761	29.801	9.129		499.28	996.54	996.51	0.029	2	50	R	G		
		LLNAENR	1Arg10							698.43	2092.27	2092.06	0.210	3	37	R	T		
		LFGGFNSSDVTSPQR	1Arg10							872.99	1743.97	1743.87	0.104	2	55	K	L	17.5	7
		GTLFVR	1Arg10							600.81	1199.61	1199.55	0.066	2	73	R	E		
		EVLDQVER	1Arg10							977.99	1953.96	1953.84	0.121	2	43	K	T		
		AGPLAGGVITTFVALYDYESR	1Arg6							1083.06	2164.10	2163.97	0.136	2	86	R	E		
		AGPLAGGVITTFVALYDYESR	1Arg6							431.74	861.46	861.40	0.052	2	44	K	V		
		TOTPPVSPAPQTEER	1Arg10	61549	2.481	1.485	4.892	2.642		453.76	905.51	905.46	0.050	2	37	R	E		
		QDSAAVFDYK								675.36	2023.06	2022.97	0.090	3	35	R	L		
		NASTFEDVTQVSSAYOK	phospho (Y)							1016.040	2030.070	2029.950	0.007	2	45	K	T	3	1
		GPVSGTEPEPVYSMEAADYR	1Arg10							351.25	700.49	700.45	0.038	2	62	K	G	9.7	8
		FGVMDR	1Arg10							380.23	758.45	758.42	0.029	2	42	R	I		
		ANFENLAK								479.30	956.59	956.55	0.038	2	50	R	G		
		AKTQTPPVSPAPQTEER	1Arg10							1027.48	2052.96	2052.91	0.128	2	65	K	R		
22,000	gj40254978	FIP1-like 1	phospho (Y)	66535	0.000	0.000	0.000	0.000		539.33	1076.64	1076.59	0.065	2	56	R	C		
		TGLIIGK								579.82	1157.57	1157.57	0.058	2	48	R	Q		
		OLIEEK								506.80	1011.59	1011.57	0.020	2	34	K	D		
		LLDQIVEK								494.76	987.51	987.43	0.078	2	35	K	K		
		IGDGDATSLNSNDYGYGGQK	phospho (Y)							329.24	656.47	656.42	0.044	2	55	K	G		
		IAQITGPPDR	1Arg10							825.06	2472.16	2472.03	0.135	3	55	R	S	13.1	4
		GTPOQIDYAR	1Arg10							862.									

26	gj 5031579	A-kinase anchor protein 8	AGLVIGK SNPGTFMR	1Arg10	76061	2.088	0.000	5.509	0.000	329.24	656.47	656.42	0.044	2	55	K	G		
			LAAEQFK							460.25	918.49	918.43	0.060	2	32	R	S	2.1	2
27	gj 4826998	Splicing factor proline/glutamine rich	NLSPYVSNLEELLEAFSQFGPIER FGQGGAGPVGGGGPR FGQGGAGPVGGGGPR	1Arg10	76102	1.618	0.425	3.073	0.980	403.75	905.48	805.43	0.048	2	32	R	K		6.5
			AVVIVDDR	1Arg10						676.38	1350.74	1350.67	0.078	2	35	R	G		
			TASGVADEDALTLEEEQQQR	1Arg10	78720	1.32	0.000	3.715	0.000	671.38	1340.74	1340.71	0.106	2	36	R	G		
28	gj 38044290	zinc finger, CCHC domain containing 8	SVTYDLISK	1Arg10						448.78	895.54	895.50	0.039	2	32	R	G		
			VALSEPOFER	1Arg10	90194	1.994	0.000	5.396	0.000	1157.62	2313.22	2313.80	0.038	2	47	R	R	4.1	2
			EVAFNNFLTDAK	1Arg10						456.76	911.51	911.49	0.021	2	39	K	L		
29	gj 33383233	Arsenate resistance protein ARS2 isoform b	VGEFVLSSEER VGEFVLSSEER	1Arg10	90194	1.994	0.000	5.396	0.000	568.33	1134.65	1134.59	0.059	2	37	R	R	2.9	2
			SSLGQASASETEDTVSVSK	1Arg10	100165	1.405	0.000	2.996	0.000	758.42	1514.82	1514.74	0.049	2	58	R	L	6.4	3
			LAQQQAALLMQQEER	1Met(ox) 1Arg10						662.872	1323.7398	1323.6545	0.0853746	2	69	R	L		
			GSSYGVSTFESYK							657.8584	1313.7022	1313.6462	0.0560746	2	36	R	L		
31	gj 20127479	RNA binding motif protein 10	GLOLSHGVQAR	1Arg10	103469	2.305	0.212	7.188	0.573	971.0134	1940.0122	1939.8858	0.1264746	2	58	R	K		
			GDPTGAGPEASLEPGADSVSMQAFSR	1Arg10						892.0159	1782.0172	1781.8969	0.1203746	2	30	K	A		
			ELSQGLLPLPOPYQAQGVLSAQLSQGSEPSSENANDTII	1Arg10						683.36	1364.70	1364.61	0.090	2	31	R	E	14	5
			AOPGAAPGYQGSAAESSQGTAAANSQSYTIMSPAVLK	1Arg10						595.85	1189.69	1189.62	0.066	2	34	R	E		
			VFLDDR	1Arg10	106122	2.200	0.000	5.500	0.000	1272.66	2543.31	2543.15	0.164	2	40	K	A		
			SIFDHIK							1108.38	4429.49	4429.26	0.229	4	63	R	N		
			LLASTLVHSVK							1256.69	3767.04	3766.81	0.227	3	35	R	S		
			DTFEHDPSEIDFNK							386.76	771.51	771.45	0.043	2	35	R	G	4.5	4
			SPSELFQAQHVITIVHHVK		108789	1.209	0.000	5.143	0.000	430.26	858.51	858.46	0.120	2	30	R	L		
33	gj 4827040	Thyroid hormone receptor associated protein 3	SIFHQIQAQSQR	1Arg10						389.93	1166.77	1166.70	0.020	3	51	R	K		
			LDIERRK	2Arg6						637.31	1908.90	1908.80	0.020	3	30	K	S		
			GSFSDTGLQDGK							511.31	2041.19	2041.11	0.037	3	41	R	E	5	4
			TLEPOELAR	1Arg10	111851	0.818	0.000	2.160	0.000	513.96	1538.86	1538.81	0.120	3	31	R	S		
			ISLAPTDVK							471.33	940.65	940.62	0.090	2	33	R	K		
			FNEENYGVK							570.80	1139.59	1139.51	0.081	2	56	K	M		
34	gj 27262645	Ataxin 2 related protein	DGSLASNPYSGDLTK	1Arg10						533.83	1085.66	1085.57	0.086	2	48	R	I	2.5	3
			SPAVATSTAAPPPSPPLPSK		114730	1.313	1.113	6.621	2.100	472.31	942.60	942.54	0.060	2	46	K	E		
			RYPSSISSPOK	1Arg10						550.29	1098.57	1098.50	0.075	2	42	K	T		
			QRPGATAEGR	1Arg10						654.50	1959.13	1959.30	0.096	3	32	K	S	12	9
			NPDSAVHSPTK							673.89	1345.76	1345.71	0.106	2	34	R	D		
			IFTASNSSVPLPAENVTITAGQR	1Arg10						439.94	1316.79	1316.17	0.037	3	58	K	L		
			IDLAVLLGK							693.88	1385.74	1385.66	0.020	2	42	K	R		
			GGSTTGSQFLEQFK							828.15	2481.43	2481.31	0.121	3	37	K	I		
			GGSTTGSQFLEQFK							471.33	940.65	940.60	0.062	2	64	R	T		
			FPLDYYSIFPPTPTPLTGR	1Arg10						743.91	1485.80	1485.71	0.048	2	38	K	T		
			DGSLASNPYSGDLTK							743.91	1485.80	1485.78	0.030	2	38	K	T		
			VLAAGLGGGGGSSVLSGLSDPR	1Arg10	140169	1.511	1.023	3.7624	1.853	765.08	2292.21	2292.17	0.043	3	35	R	D		
			TVNATGSSAAGSSDKPSDPR	1Arg10						762.91	1523.81	1523.71	0.084	2	65	R	F		
			TVLWNPEDLPLPIK							390.72	779.43	779.41	0.112	2	30	K	C	13	10
			QQTSSRPASVGLSSSLGDPDR	2Arg10						861.83	2582.46	2582.4	0.042	3	71	R	T		
			IPSLFEIWRPTGQLAEK	1Arg10						671.35	2011.04	2010.96	0.035	3	30	K	V		
			DVTLSPKPSAR	1Arg10						923.08	1844.14	1844.1	0.042	2	36	R	Q		
			AVNIFLDPLPGHPLRDR	2Arg10						778.43	2332.27	2315.1256	0.116	3	30	R	L		
			AVNIFLDPLPGHPLR	2Arg10						669.74	2006.2	2006.15	0.016	3	34	K	L		
			ALPTSKPEGLHSSPVGPSSSK							615.67	1229.73	1229.69	0.067	2	30	K	T		
			DLTEYLSR	1Arg10	46409	4.128	2.285	9.993	5.218	666.4	1996.19	1996.14	0.024	3	68	K	S		
			GFQVLFK							540.34	1617.99	1617.95	0.048	3	30	K	D		
			GFQVLFK							538.3	2149.18	2149.09	0.023	3	30	R	G		
			KDLTEYLSR	1Arg10						503.76	1005.50	1005.50	0.00	2	40	K	F	15.5	7
			LLESR	1Arg10						457.77	913.52	913.51	0.01	2	43	R	D		
			MFIGGLSWDTSK	1Met(ox)						457.78	913.55	913.51	0.05	2	38	R	D		
			MFIGGLSWDTSK							567.81	1133.61	1133.60	0.01	2	36	K	F		
			VFIGGLSPDTSEEQIK							314.20	626.38	626.36	0.02	2	31	K	Y		
			YHQIGSGK							679.34	1356.66	1356.64	0.02	2	62	K	K		
										671.33	1340.65	1340.64	0.01	2	80	K	K		
										853.43	1704.85	1704.86	-0.01	2	88	K	E		
										445.24	888.46	888.45	0.02	2	30	R	C		

PS: * "w" refers to the Arg0, "i" refers to the Arg6 and "h" refers to the Arg10