

Supplemental Table 1

Accession number	Symbol	Protein	Conf	Sequence	Modifications	Cleavages	dMass	Prec MW	Prec m/z	Theor MW	Theor m/z	Theor z	Area 114	Area 115	Area 116	Area 117				
IPIIPI00131622.1	DPL	doppel	99	HDCFWLER	ITRAQ4plex@N-term; Pyridylethyl(C)@2		-0.03	1353.61	452.21	1353.64	452.22	3	6.0	89.0	3.4	1.6				
			99	VAENRPGAF	ITRAQ4plex@N-term	cleaved F-I@C-term	0.00	1103.58	552.80	1103.58	552.80	2	0.7	94.7	1.7	2.9				
			99	VLPSSGGQITEAR	ITRAQ4plex@N-term		-0.01	1457.79	729.90	1457.80	729.91	2	0.1	98.1	1.2	0.6				
			99	LDIDFGAEGNR	ITRAQ4plex@N-term		-0.02	1349.65	675.83	1349.67	675.84	2	1.3	94.3	2.6	1.7				
			99	VLPSSGGQITEAR	ITRAQ4plex@N-term; Ala->Val@12		0.01	1485.84	496.29	1485.83	496.28	3	1.6	89.9	2.4	6.0				
			99	VLPSSGGQITEARVAENRPGAFIKQGR	ITRAQ4plex@N-term; Asn->His@17; Lys->Glu@24	missed R-V@13; missed K-Q@24	0.00	3005.59	752.41	3005.59	752.41	4	3.9	89.9	4.1	2.1				
			99	VLPSSGGQITEAR	ITRAQ4plex@N-term; Deamidated(O)@8; Dimethyl(R)@13		0.06	1486.87	496.63	1486.81	496.61	3	1.0	91.2	4.4	3.3				
			99	KVLPSGGQITEAR	ITRAQ4plex@N-term; ITRAQ4plex(K)@1	missed K-V@1	-0.02	1729.97	577.66	1729.99	577.67	3	1.7	91.0	4.1	3.2				
			99	KLDIDFGAEGNR	ITRAQ4plex@N-term; ITRAQ4plex(K)@1	missed K-L@1	-0.04	1621.83	541.62	1621.87	541.63	3	2.4	87.6	6.3	3.7				
			99	KVLPSGGQITEAR	ITRAQ4plex@N-term; ITRAQ4plex(K)@1; HexNac(T)@11	missed K-V@1	0.02	1933.09	645.37	1933.07	645.36	3	2.5	92.2	3.3	2.0				
			99	VAENRPGAFIK	ITRAQ4plex@N-term; ITRAQ4plex(K)@11		0.96	1489.83	497.62	1488.97	497.30	3	0.0	99.4	0.0	0.6				
			99	VAENRPGAFIK	ITRAQ4plex@N-term; Lys->Arg@11		-0.05	1372.72	687.37	1372.77	687.39	2	1.0	95.6	1.5	1.6				
92	KVLPSGGQITEAR	ITRAQ4plex@N-term; Lys->Gln@1	missed K-V@1	0.05	1585.90	529.64	1585.85	529.63	3	3.5	89.0	3.8	3.7							
													Average:	2.0	92.5	3.0	2.5			
													StDev:	1.7	3.7	1.6	1.5			
IPIIPI00120793.1	PRNP	prion protein	99	HVAGAAAAGAVVGLGGYMLGSMSR	ITRAQ4plex@N-term	cleaved R-P@C-term	0.03	2474.29	825.77	2474.26	825.76	3	7.0	25.9	55.7	11.5				
			96	QHTVTTTTK	Gln->pyro-Gln@N-term; ITRAQ4plex(K)@9		0.02	1142.62	572.32	1142.61	572.31	2	2.2	24.0	61.0	12.8				
			99	PMIHFGNDWEDR	ITRAQ4plex@N-term	cleaved R-P@N-term	0.06	1659.82	554.28	1659.76	554.26	3	6.1	26.8	55.3	11.8				
			97	ESQAYYDGR	ITRAQ4plex@N-term		0.00	1231.56	616.79	1231.56	616.79	2	3.4	11.5	76.4	8.6				
			99	VVEQMVCVTQYQK	ITRAQ4plex@N-term; Pyridylethyl(C)@6; ITRAQ4plex(K)@12		-0.09	1847.86	616.96	1847.95	616.99	3	1.1	14.2	76.9	7.7				
																Average:	4.0	20.5	65.1	10.5
													StDev:	2.5	7.1	10.8	2.2			
IPIIPI00226455.1	SPRN	shadoo	99	ICLLGGTLGALELRP	ITRAQ4plex@N-term; Pyridylethyl(C)@2		-0.01	2000.19	667.74	2000.20	667.74	3	0.0	6.9	32.4	60.7				
			99	VAAAGAAAGAAAGVAGLATGSGWR	ITRAQ4plex@N-term		-0.04	2198.13	733.72	2198.17	733.73	3	0.0	21.6	18.3	60.1				
			99	YGSLSLR	ITRAQ4plex@N-term		0.00	825.45	413.73	825.45	413.73	2	0.8	2.3	23.2	73.8				
			99	VAAAGAAAGAAAGVAGLATGSGWR	ITRAQ4plex@N-term; Oxidation(W)@24		-0.01	2214.15	739.06	2214.16	739.06	3	8.0	13.4	15.0	63.5				
			99	VAAAGAAAGAAAGVAGLATGSGWR	ITRAQ4plex@N-term; Val->Asn@14		0.05	2213.19	738.74	2213.14	738.72	3	7.1	12.9	15.4	64.7				
99	VAAAGAAAGAAAGVAGLATGSGWR	ITRAQ4plex@N-term; Val->Met@14		0.07	2230.21	744.41	2230.14	744.39	3	1.4	11.1	18.8	68.7							
													Average:	2.9	11.4	20.5	65.2			
													StDev:	3.7	6.5	6.5	5.2			
IPIIPI00469000.4	SLC39A6	ZIP6	99	ESASSSEVTSVAVNAVSEGTR	ITRAQ4plex@N-term		0.01	2274.08	759.03	2274.07	759.03	3	3.7	29.2	35.9	31.2				
			95	AGMIVK	ITRAQ4plex@N-term; Dehydrated(T)@4; ITRAQ4plex(K)@6		-0.03	975.48	438.75	975.51	438.76	2	31.1	2.2	31.1	31.9	34.8			
			99	YDSQLSSNEEK	ITRAQ4plex@N-term; Lys->Gln@11		0.06	1442.69	722.35	1442.63	722.32	2	3.7	29.2	30.5	36.6				
													Average:	3.2	29.9	32.8	34.2			
													StDev:	0.8	1.1	2.8	2.8			
IPIIPI00273801.3	SLC39A10	ZIP10	99	QSTEESTIGR	ITRAQ4plex@N-term		0.03	1250.65	626.33	1250.62	626.32	2	2.3	39.3	15.7	42.7				
			98	NYLGVEEEEK	ITRAQ4plex@N-term; Lys->Gln@9		0.07	1223.65	612.83	1223.58	612.80	2	2.5	33.2	17.7	46.5				
													Average:	2.4	36.3	16.7	44.6			
													StDev:	0.2	4.3	1.4	2.7			
IPIIPI00110850.1	ACTB	actin	99	AGFAGDDAPR	ITRAQ4plex@N-term		0.02	1119.56	560.79	1119.54	560.78	2	27.5	13.1	37.0	22.4				
			99	AVFPSVGR	ITRAQ4plex@N-term	cleaved R-P@C-term	-0.02	1088.63	545.32	1088.65	545.33	2	27.2	13.0	27.9	31.9				
			99	AVFPSVGRPR	ITRAQ4plex@N-term		-0.01	1341.79	448.27	1341.80	448.27	3	24.9	19.8	33.3	22.0				
			99	AVFPSVGRPR	ITRAQ4plex@N-term; Deamidated(R)@9		-0.03	1342.76	448.59	1342.78	448.60	3	25.5	14.2	33.8	26.5				
			84	AVFPSVGRPR	ITRAQ4plex@N-term; Dimethyl(R)@11		0.01	1369.85	457.62	1369.83	457.62	3	28.8	16.8	32.9	21.5				
			99	DLTDYLMK	ITRAQ4plex@N-term; ITRAQ4plex(K)@8		0.00	1285.68	643.85	1285.68	643.85	2	18.2	23.6	37.5	20.7				
			99	DLTDYLMK	ITRAQ4plex@N-term; Lys->Gln@8		0.02	1141.57	571.79	1141.54	571.78	2	10.6	8.5	30.5	50.4				
			99	DLYANTVLSGGTMYPGIADR	ITRAQ4plex@N-term		0.13	2358.29	787.10	2358.16	787.06	3	11.0	29.3	30.3	29.4				
			99	DLYANTVLSGGTMYPGIADR	ITRAQ4plex@N-term; Dimethyl(R)@21		-0.02	2386.23	796.42	2386.20	796.41	3	30.1	18.6	0.0	51.3				
			99	DLYANTVLSGGTMYPGIADR	ITRAQ4plex@N-term; Leu->Pro@2		-0.02	2342.12	781.71	2342.13	781.72	3	5.7	28.2	29.4	36.7				
			99	DSYVGDEAQS	ITRAQ4plex@N-term; Dehydrated(S)@2; Lys->Gln@11		0.04	1323.61	662.81	1323.57	662.79	2	29.3	8.9	29.6	32.2				
			99	DSYVGDEAQS	ITRAQ4plex@N-term; ITRAQ4plex(K)@11		0.04	1485.76	496.26	1485.72	496.25	3	22.5	29.7	31.8	16.0				
			99	DSYVGDEAQS	ITRAQ4plex@N-term; Lys->Arg@11		0.04	1369.67	685.84	1369.62	685.82	2	21.7	10.8	31.2	36.4				
			99	DSYVGDEAQS	ITRAQ4plex@N-term; Lys->Gln@11		0.04	1341.62	671.82	1341.58	671.80	2	21.6	9.4	33.0	35.9				
			87	DSYVGDEAQS	ITRAQ4plex@N-term; Ser->Asp@10; ITRAQ4plex(K)@11		-0.01	1513.72	505.58	1513.71	505.58	3	28.7	17.7	34.1	21.6				
			92	DSYVGDEAQS	ITRAQ4plex@N-term; Ser->Val@10; ITRAQ4plex(K)@11		0.01	1497.76	500.26	1497.76	500.26	3	27.3	25.1	28.8	18.8				
			99	DSYVGDEAQS	ITRAQ4plex@N-term; ITRAQ4plex(K)@11	missed K-R@11	0.04	1641.86	548.29	1641.82	548.28	3	17.9	32.4	44.2	5.5				
			96	DSYVGDEAQS	ITRAQ4plex@N-term; Lys->Gln@11	missed K-R@11	0.08	1497.76	500.26	1497.68	500.23	3	19.9	30.0	36.4	16.4				
			80	EITALPSTMK	Glu->pyro-Glu@N-term; ITRAQ4plex(K)@11		0.06	1286.76	644.39	1286.70	644.36	2	25.0	12.1	33.5	29.5				
			89	EITALPSTMK	ITRAQ4plex@N-term; Lys->Arg@11		0.01	1332.73	667.37	1332.72	667.37	2	19.8	11.4	33.8	35.0				
			89	EITALPSTMK	ITRAQ4plex@N-term; Lys->Gln@11		0.07	1304.75	653.38	1304.68	653.35	2	23.7	19.2	32.7	27.4				
			99	EITALPSTMKI	ITRAQ4plex@N-term; Lys->Ala@11; Ile->Ala@12	cleaved I-K@C-term; missed K-I@11	0.01	1318.70	660.36	1318.69	660.35	2	18.0	8.7	28.2	45.1				
			99	GYSFTTAAER	ITRAQ4plex@N-term		0.00	1275.63	638.82	1275.62	638.82	2	13.6	14.7	36.8	34.9				
			99	GYSFTTAAER	ITRAQ4plex@N-term; Dimethyl(R)@10		0.05	1303.71	652.86	1303.65	652.83	2	22.5	6.8	32.6	38.0				
			99	HQGVVMGMQK	ITRAQ4plex@N-term; ITRAQ4plex(K)@11		0.00	1458.77	487.26	1458.77	487.26	3	14.5	30.6	37.5	17.4				
			90	HQGVVMGMQK	ITRAQ4plex@N-term; Lys->Arg@11		0.03	1342.70	448.57	1342.67	448.56	3	11.4	13.7	34.2	40.7				
			99	HQGVVMGMQK	ITRAQ4plex@N-term; Lys->Gln@11		0.05	1314.68	439.23	1314.63	439.22	3	14.2	22.0	31.8	32.0				
			99	KDLYANTVLSGGTMYPGIADR	ITRAQ4plex@N-term; ITRAQ4plex(K)@1		0.04	2630.40	658.61	2630.36	658.60	4	12.5	33.2	28.5	25.8				
			99	LDLAGRDLTDYLMK	ITRAQ4plex@N-term; ITRAQ4plex(K)@14	missed R-D@6	0.01	1911.05	638.02	1911.04	638.02	3	40.6	15.9	32.7	10.8				
			99	MTQIMFETFNTPAMYVAIQVLSYASGR	ITRAQ4plex@N-term		0.07	3396.77	850.20	3396.70	850.18	4	8.9	52.0	28.3	10.8				
			99	QYDESGPSVHR	ITRAQ4plex@N-term		0.04	1659.84	554.29	1659.80	554.27	3	6.6	42.9	29.0	21.5				
			99	SYELPDGOVITIGNER	ITRAQ4plex@N-term		-0.02	1933.97	645.66	1933.99	645.67	3	11.2	41.0	30.4	17.5				
			99	SYELPDGOVITIGNER	ITRAQ4plex@N-term; Asn->Arg@14		0.01	1976.05	659.69	1976.04	659.69	3	18.3	20.0	36.3	25.4				
			99	SYELPDGOVITIGNER	ITRAQ4plex@N-term; Asp->Pro@6		-0.08	1915.93	639.65	1916.01	639.68	3	5.5	16.6	32.5	45.4				
			99	SYELPDGOVITIGNER	ITRAQ4plex@N-term; Deamidated(N)@14; Glu->Arg@15		0.02	1962.05	655.02	1962.03	655.02	3	20.0	23.6	28.9	27.5				
			99	SYELPDGOVITIGNER	ITRAQ															