

A8MYE6 Integrin beta

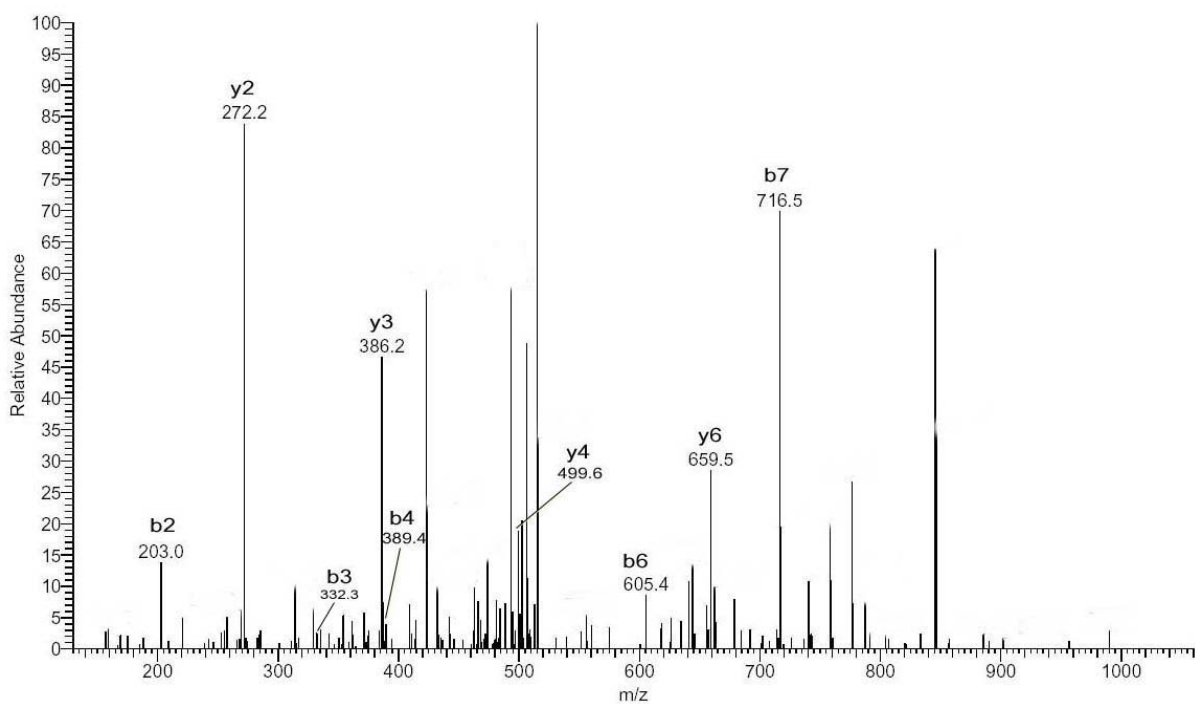
MH+ (Da): 1047.7857

b ions

y ions

b1	T	102.1			
b2	TT	203.2	y9	TTEGCLNPR	991.1
b3	TTE	332.3	y8	TEGCLNPR	890
b4	TTEG	389.39	y7	EGCLNPR	788.9
b5	TTEGC	492.53	y6	GCLNPR	659.8
b6	TTEGCL	605.69	y5	CLNPR	602.7
b7	TTEGCLN	719.79	y4	LNPR	499.6
b8	TTEGCLNP	816.91	y3	NPR	386.4
b9	TTEGCLNPR	973.1	y2	PR	272.3
			y1	R	175.2

The detected ions were shown in bold.



Q9P273 Teneurin-3

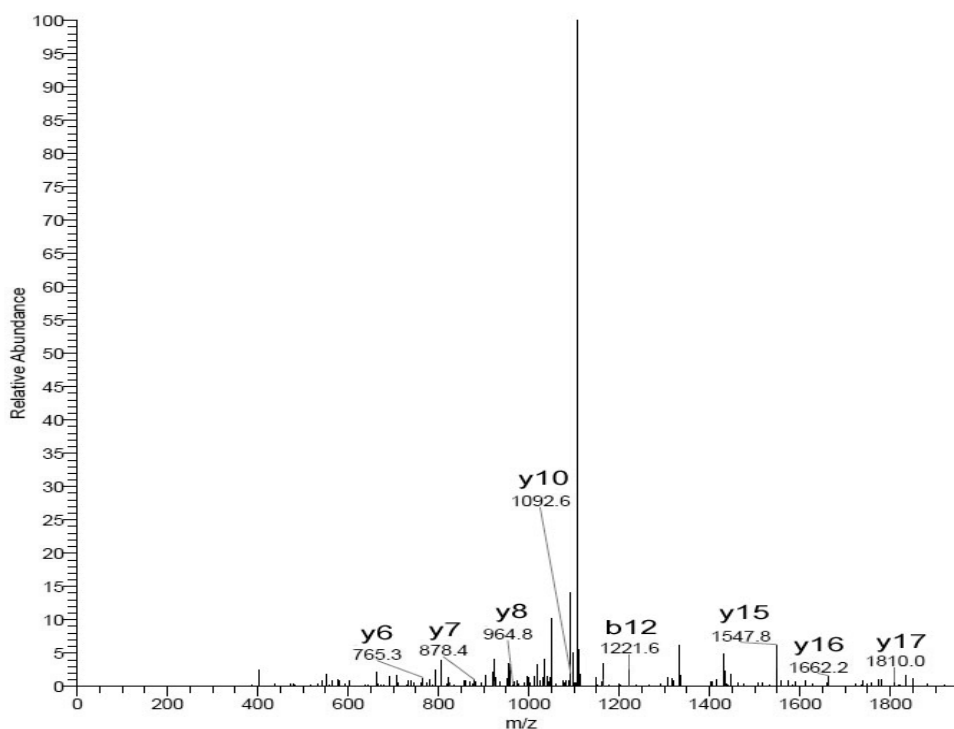
MH+
(Da): 2254.3396

b ions

y ions

b1	Q	129.15			
b2	QD	244.23	y21	QDGMFDLVANGGASLTLVFER	2257.52
b3	QDG	301.29	y20	DGMFDLVANGGASLTLVFER	2129.39
b4	QDGM	448.48	y19	GMFDLVANGGASLTLVFER	2014.3
b5	QDGMF	595.66	y18	MFDLVANGGASLTLVFER	1957.24
b6	QDGMFD	710.74	y17	FDLVANGGASLTLVFER	1810.05
b7	QDGMFDL	823.9	y16	DLVANGGASLTLVFER	1662.88
b8	QDGMFDLV	923.04	y15	LVANGGASLTLVFER	1547.79
b9	QDGMFDLVA	994.12	y14	VANGGASLTLVFER	1434.63
b10	QDGMFDLVAN	1108.22	y13	ANGGASLTLVFER	1335.49
b11	QDGMFDLVANG	1165.27	y12	NGGASLTLVFER	1264.42
b12	QDGMFDLVANGG	1222.32	y11	GGASLTLVFER	1150.31
b13	QDGMFDLVANGGA	1293.4	y10	GASLTLVFER	1093.26
b14	QDGMFDLVANGGAS	1380.48	y9	ASLTLVFER	1036.21
b15	QDGMFDLVANGGASL	1493.64	y8	SLTLVFER	965.13
b16	QDGMFDLVANGGASLT	1594.74	y7	LTLVFER	878.05
b17	QDGMFDLVANGGASLTL	1707.9	y6	TLVFER	764.89
b18	QDGMFDLVANGGASLTLV	1807.04	y5	LVFER	663.79
b19	QDGMFDLVANGGASLTLVF	1954.21	y4	VFER	550.63
b20	QDGMFDLVANGGASLTLVFE	2083.33	y3	FER	451.49
b21	QDGMFDLVANGGASLTLVFER	2239.52	y2	ER	304.32
			y1	R	175.2

The detected ions were shown in bold.



Q92828 **Coronin-2A**

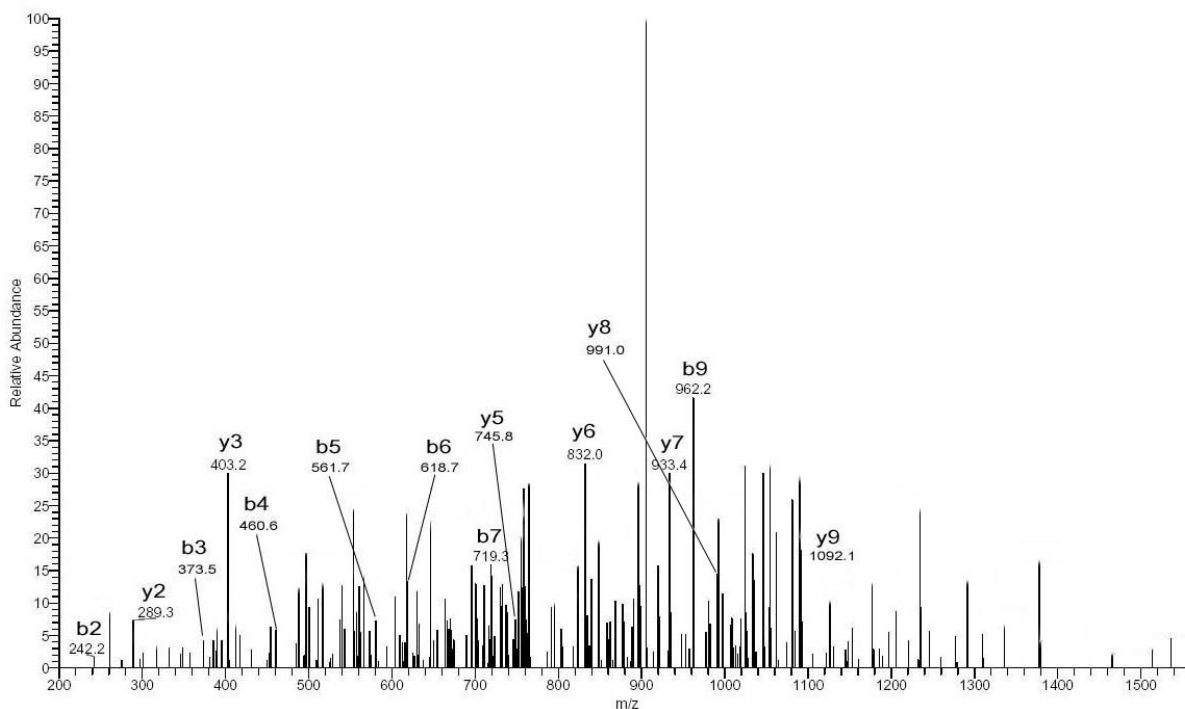
MH+
(Da): 1550.6224

b ions

y ions

b1	K	129.19	y13	KLMSTGTSRWNNR	1551.76
b2	KL	242.35	y12	LMSTGTSRWNNR	1423.58
b3	KLM	373.54	y11	MSTGTSRWNNR	1310.42
b4	KLMS	460.62	y10	STGTSRWNNR	1179.23
b5	KLMST	561.72	y9	TGTSRWNNR	1092.15
b6	KLMSTG	618.78	y8	GTSRWNNR	991.05
b7	KLMSTGT	719.88	y7	TSRWNNR	933.99
b8	KLMSTGTS	806.96	y6	SRWNNR	832.89
b9	KLMSTGTSR	963.15	y5	RWNNR	745.81
b10	KLMSTGTSRW	1149.36	y4	WNNR	589.62
b11	KLMSTGTSRWN	1263.46	y3	NNR	403.41
b12	KLMSTGTSRWNN	1377.57	y2	NR	289.31
b13	KLMSTGTSRWNNR	1533.76	y1	R	175.2

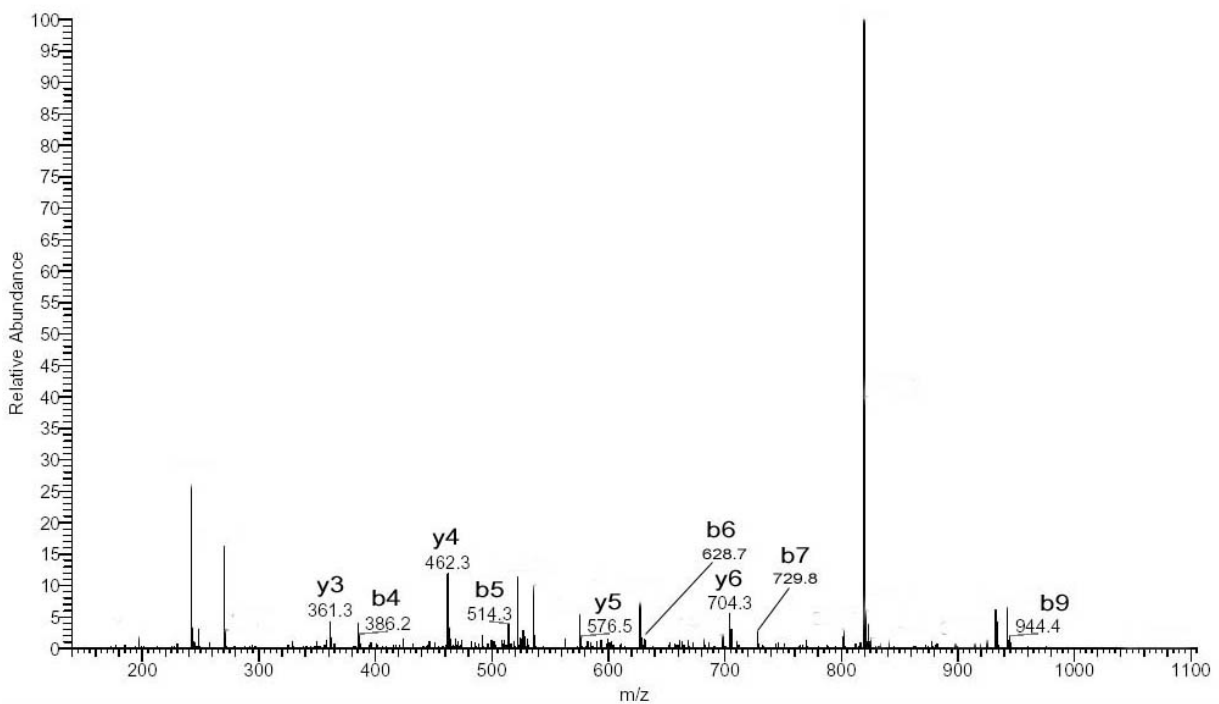
The detected ions were shown in bold.



Q8TC23 C19orf2 protein MH+
 (Da): 1088.1358
 b ions y ions

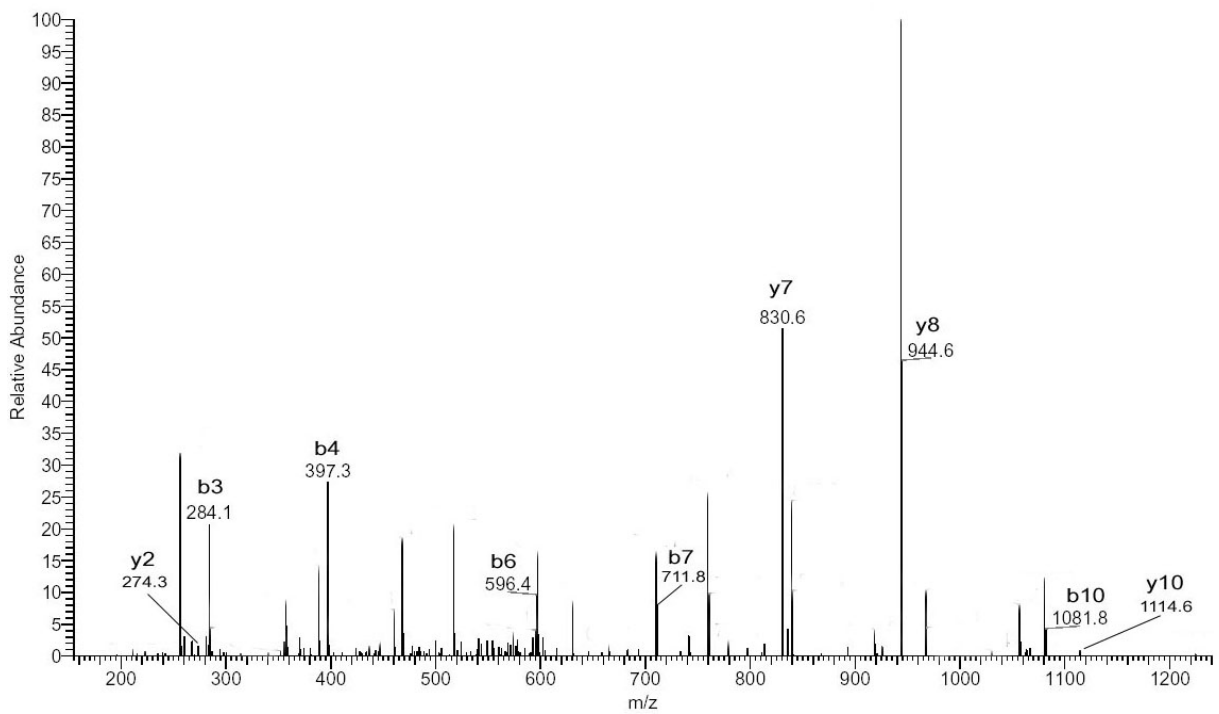
b1	I	114.17			
b2	IN	228.28	y10	INTGKNTTLK	1090.26
b3	INT	329.38	y9	NTGKNTTLK	977.1
b4	INTG	386.44	y8	TGKNTTLK	862.99
b5	INTGK	514.61	y7	GKNTTLK	761.89
b6	INTGKN	628.71	y6	KNTTLK	704.84
b7	INTGKNT	729.82	y5	NTTLK	576.66
b8	INTGKNTT	830.92	y4	TTLK	462.56
b9	INTGKNTTL	944.08	y3	TLK	361.45
b10	INTGKNTTLK	1072.26	y2	LK	260.35
			y1	K	147.19

The detected ions were shown in bold.



P11532 Isoform 4 of Dystrophin		MH+ 1226.9591			
b ions		(Da): y ions			
b1	L	114.17	y11	LAVLKADLEKK	1227.51
b2	LA	185.25	y10	AVLKADLEKK	1114.35
b3	LAV	284.39	y9	VLKADLEKK	1043.27
b4	LAVL	397.55	y8	LKADLEKK	944.14
b5	LAVLK	525.72	y7	KADLEKK	830.98
b6	LAVLKA	596.8	y6	ADLEKK	702.81
b7	LAVLKAD	711.89	y5	DLEKK	631.73
b8	LAVLKADL	825.05	y4	LEKK	516.64
b9	LAVLKADLE	954.16	y3	EKK	403.48
b10	LAVLKADLEK	1082.34	y2	KK	274.36
b11	LAVLKADLEKK	1210.51	y1	K	146.19

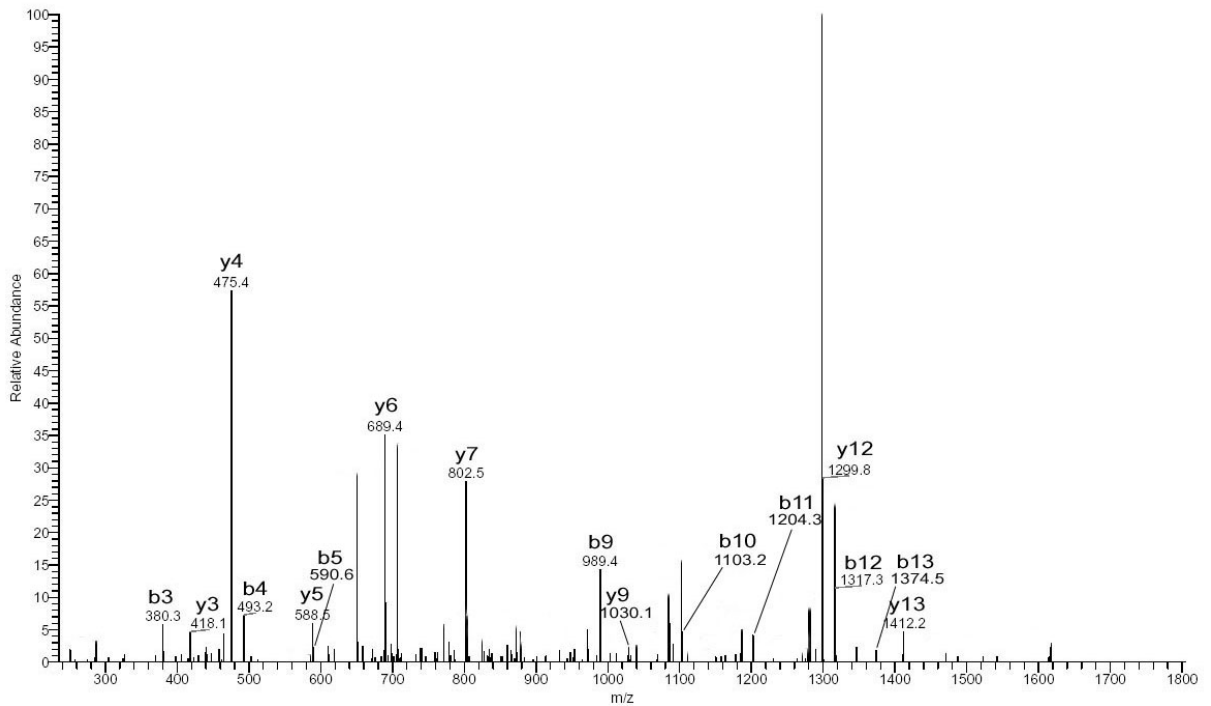
The detected ions were shown in bold.



Q562R1 **hypothetical protein** **MH+**
LOC345651 **LOC345651** **(Da):** **1791.0197**
b ions y ions

b1	S	88.09	y16	SYELPDGQVITIGNER	1791.95
b2	SY	251.27	y15	YELPDGQVITIGNER	1704.87
b3	SYE	380.38	y14	ELPDGQVITIGNER	1541.69
b4	SYEL	493.54	y13	LPDGQVITIGNER	1412.58
b5	SYELP	590.66	y12	PDGQVITIGNER	1299.42
b6	SYELPD	705.75	y11	DGQVITIGNER	1202.3
b7	SYELPDG	762.8	y10	GQVITIGNER	1087.21
b8	SYELPDGQ	890.93	y9	QVITIGNER	1030.16
b9	SYELPDGQV	990.06	y8	VITIGNER	902.03
b10	SYELPDGQVI	1103.22	y7	ITIGNER	802.9
b11	SYELPDGQVIT	1204.33	y6	TIGNER	689.74
b12	SYELPDGQVITI	1317.49	y5	IGNER	588.63
b13	SYELPDGQVITIG	1374.54	y4	IGNER	475.47
b14	SYELPDGQVITIGN	1488.64	y3	NER	418.42
b15	SYELPDGQVITIGNE	1617.76	y2	ER	304.32
b16	SYELPDGQVITIGNER	1773.95	y1	R	175.2

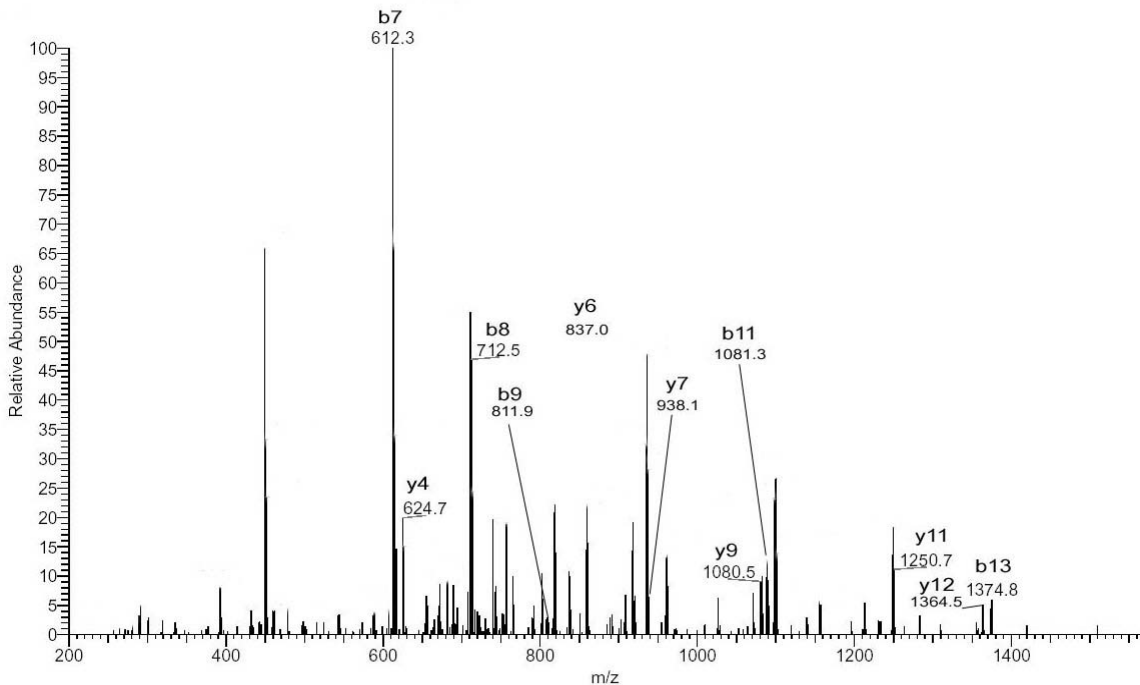
The detected ions were shown in bold.



Q6ZWC4 none MH+
 (Da): 1546.8087
 b ions y ions

b1	A	72.09	y14	ALNLGAATVLRHR	1548.83
b2	AL	185.25	y13	LNLGAATVLRHR	1477.75
b3	ALN	299.36	y12	NLGAATVLRHR	1364.59
b4	ALNL	412.52	y11	LGAATVLRHR	1250.48
b5	ALNLG	469.57	y10	GAATVLRHR	1137.33
b6	ALNLGA	540.65	y9	AATVLRHR	1080.27
b7	ALNLGAA	611.73	y8	ATVLRHR	1009.19
b8	ALNLGAAT	712.83	y7	TVLRHR	938.12
b9	ALNLGAATV	811.96	y6	VLRRHR	837.01
b10	ALNLGAATVL	925.12	y5	LRRHR	737.88
b11	ALNLGAATVLR	1081.31	y4	RRHR	624.72
b12	ALNLGAATVLRR	1237.5	y3	RHR	468.53
b13	ALNLGAATVLRHR	1374.64	y2	HR	312.34
b14	ALNLGAATVLRHR	1530.83	y1	R	175.2

The detected ions were shown in bold.

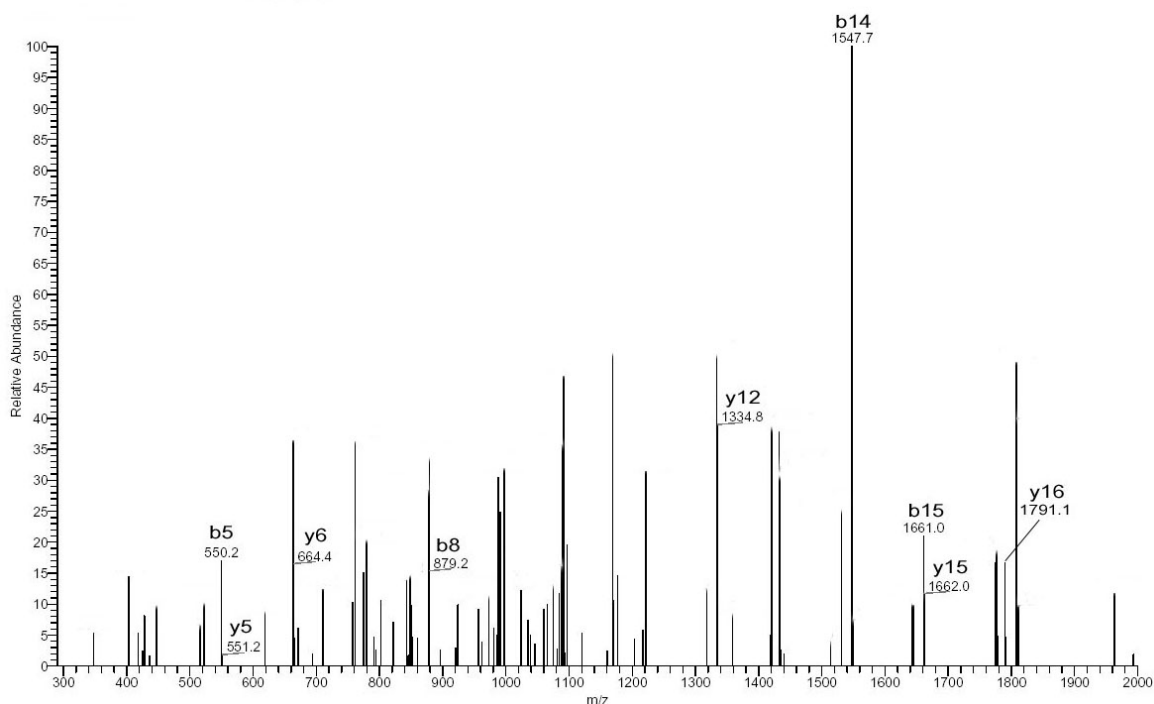


Q9NSA0
Isoform 1 of Solute carrier
family 22 member 11

MH+
(Da): 2210.0904

b ions			y ions		
b1	I	114. 17	y20	INGHKEAKNLTIEVLMSSVK	2212. 6
b2	IN	228. 28	y19	NGHKEAKNLTIEVLMSSVK	2099. 45
b3	ING	285. 33	y18	GHKEAKNLTIEVLMSSVK	1985. 34
b4	INGH	422. 47	y17	HKEAKNLTIEVLMSSVK	1928. 29
b5	INGHK	550. 65	y16	KEAKNLTIEVLMSSVK	1791. 15
b6	INGHKE	679. 76	y15	EAKNLTIEVLMSSVK	1662. 97
b7	INGHKEA	750. 84	y14	AKNLTIEVLMSSVK	1533. 86
b8	INGHKEAK	879. 01	y13	KNLTIEVLMSSVK	1462. 78
b9	INGHKEAKN	993. 12	y12	NLTIEVLMSSVK	1334. 61
b10	INGHKEAKNL	1106. 28	y11	LTIEVLMSSVK	1220. 5
b11	INGHKEAKNLT	1207. 38	y10	TIEVLMSSVK	1107. 34
b12	INGHKEAKNLTIE	1320. 54	y9	IEVLMSSVK	1006. 24
b13	INGHKEAKNLTIE	1449. 66	y8	EVLMSVK	893. 08
b14	INGHKEAKNLTIEV	1548. 79	y7	VLMSVK	763. 96
b15	INGHKEAKNLTIEVL	1661. 95	y6	LMSSVK	664. 83
b16	INGHKEAKNLTIEVLM	1793. 14	y5	MSSVK	551. 67
b17	INGHKEAKNLTIEVLMSS	1880. 22	y4	SSVK	420. 48
b18	INGHKEAKNLTIEVLMSS	1967. 3	y3	SVK	333. 4
b19	INGHKEAKNLTIEVLMSSV	2066. 43	y2	VK	246. 32
b20	INGHKEAKNLTIEVLMSSVK	2194. 6	y1	K	147. 19

The detected ions were shown in bold.

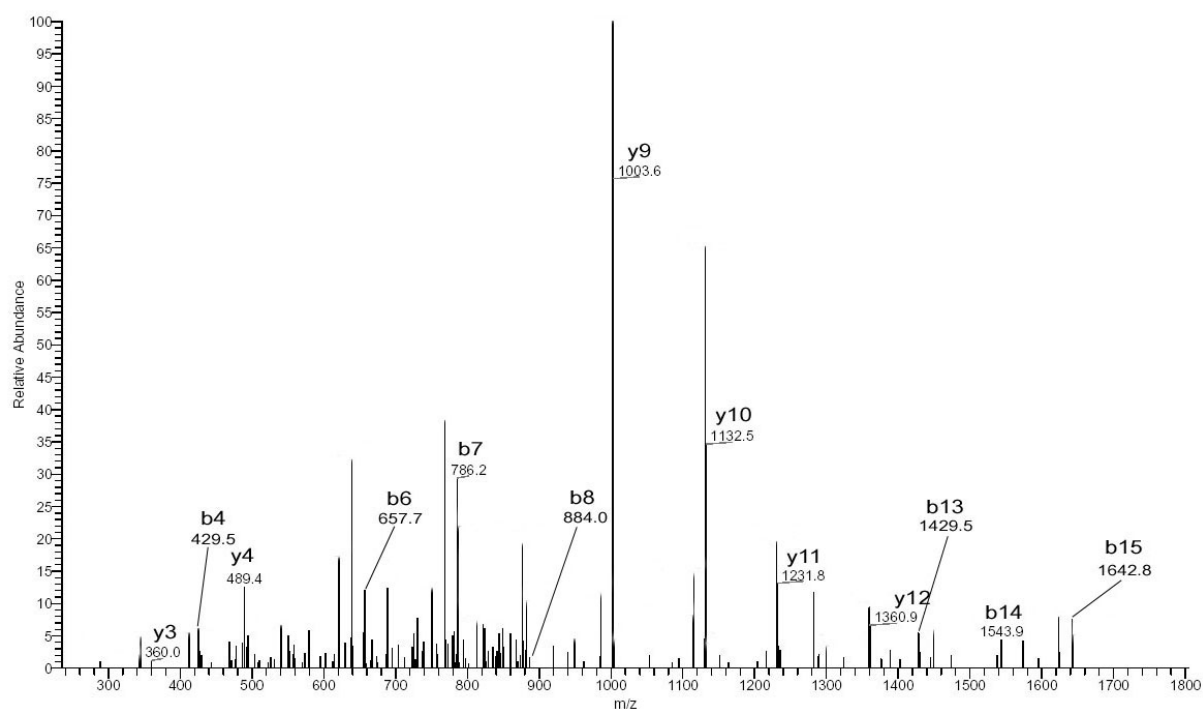


**UBC;UBB ubiquitin
and ribosomal protein
P62979 S27a precursor**

MH+
(Da): 1788.1465

b ions			y ions		
b1	T	102.12	y16	TITLEVEPSDTIENVK	1788.98
b2	TI	215.28	y15	ITLEVEPSDTIENVK	1687.88
b3	TIT	316.38	y14	TLEVEPSDTIENVK	1574.72
b4	TITL	429.54	y13	LEVEPSDTIENVK	1473.61
b5	TITLE	558.66	y12	EVEPSDTIENVK	1360.45
b6	TITLEV	657.79	y11	VEPSDTIENVK	1231.34
b7	TITLEVE	786.91	y10	EPSDTIENVK	1132.2
b8	TITLEVEP	884.02	y9	PSDTIENVK	1003.09
b9	TITLEVEPS	971.1	y8	SDTIENVK	905.97
b10	TITLEVEPSD	1086.19	y7	DTIENVK	818.89
b11	TITLEVEPSDT	1187.3	y6	TIENVK	703.81
b12	TITLEVEPSDTI	1300.46	y5	IENVK	602.7
b13	TITLEVEPSDTIE	1429.57	y4	ENVK	489.54
b14	TITLEVEPSDTIEN	1543.68	y3	NVK	360.43
b15	TITLEVEPSDTIENV	1642.81	y2	VK	246.32
b16	TITLEVEPSDTIENVK	1770.98	y1	K	147.19

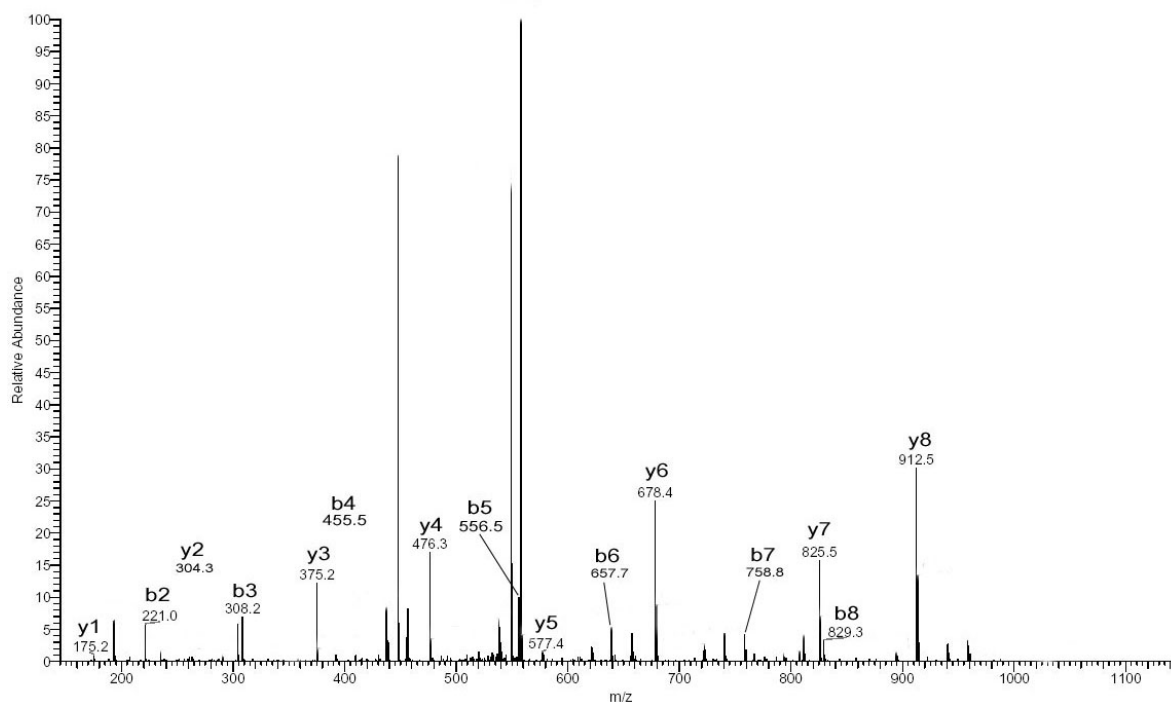
The detected ions were shown in bold.



P60709 **Actin, cytoplasmic 1** MH+
 (Da): 1132.7391
 b ions y ions

b1	G	58.07			
b2	GY	221.24	y10	GYSFTTTAER	1133.2
b3	GYS	308.32	y9	YSFTTTAER	1076.14
b4	GYSF	455.5	y8	SFTTTAER	912.97
b5	GYSFT	556.6	y7	FTTTAER	825.89
b6	GYSFTT	657.71	y6	TTTAER	678.71
b7	GYSFTTT	758.81	y5	TTAER	577.61
b8	GYSFTTTA	829.89	y4	TAER	476.5
b9	GYSFTTTAE	959.01	y3	AER	375.4
b10	GYSFTTTAER	1115.2	y2	ER	304.32
			y1	R	175.2

The detected ions were shown in bold.



**Probable G-protein
coupled receptor 179**
A8MWI1 precursor

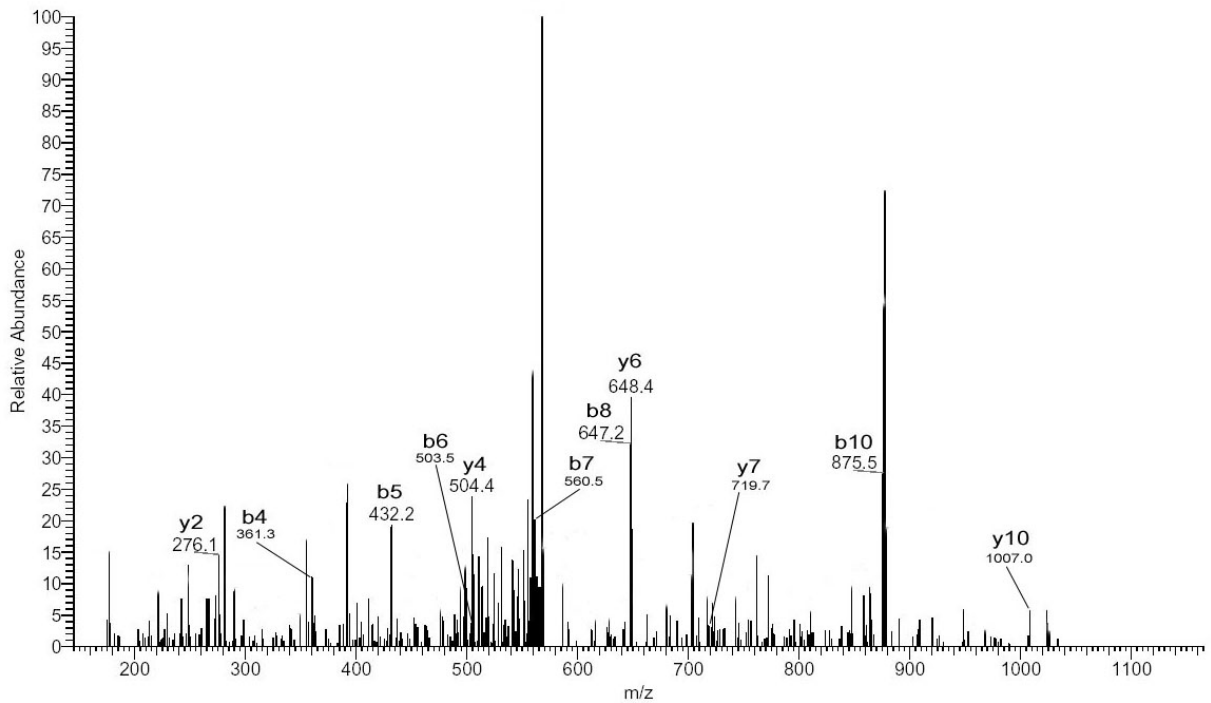
MH+
(Da): 1150.9204

b ions

y ions

b1	G	58.07	y12	GSSEAAGSVETR	1151.17
b2	GS	145.15	y11	SSEAAGSVETR	1094.12
b3	GSS	232.22	y10	SEAAGSVETR	1007.04
b4	GSSE	361.34	y9	EAAGSVETR	919.96
b5	GSSEA	432.42	y8	AAGSVETR	790.84
b6	GSSEAA	503.5	y7	AGSVETR	719.76
b7	GSSEAAG	560.55	y6	GSVETR	648.69
b8	GSSEAAGS	647.63	y5	SVETR	591.63
b9	GSSEAAGSV	746.76	y4	VETR	504.56
b10	GSSEAAGSVE	875.87	y3	ETR	405.42
b11	GSSEAAGSVET	976.98	y2	TR	276.31
b12	GSSEAAGSVETR	1133.17	y1	R	175.2

The detected ions were shown in bold.



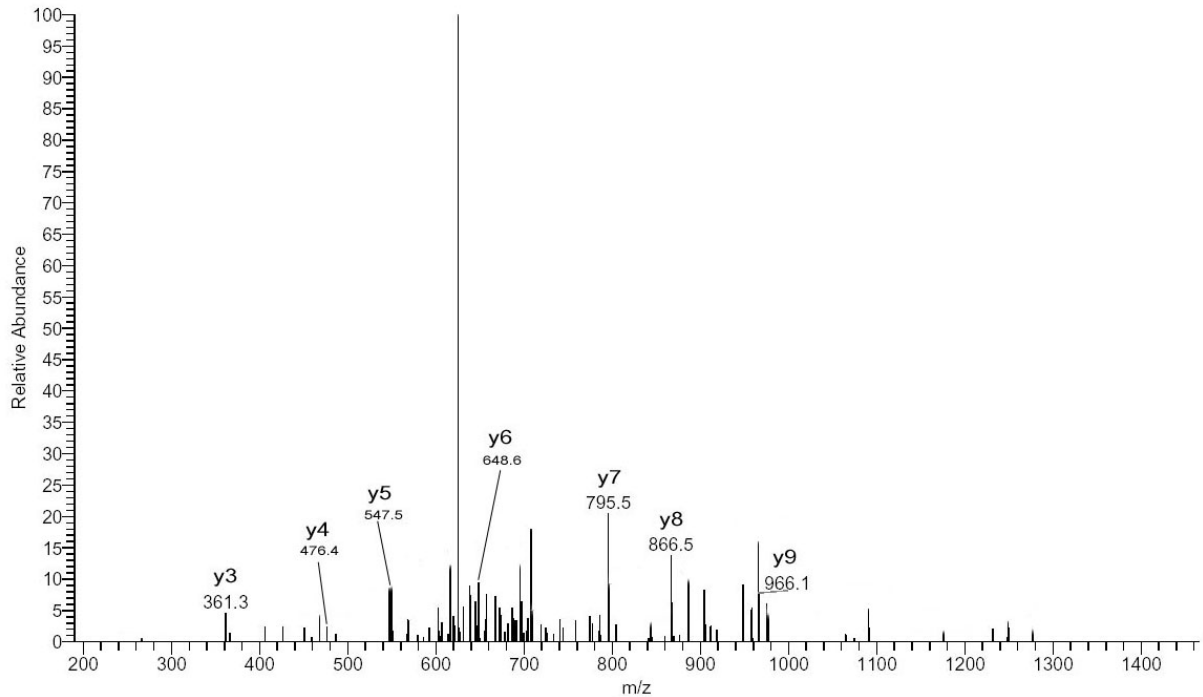
**heat shock 70kDa
protein 9,
mitochondrial
precursor**

P38646
b ions

MH+
(Da): 1450.7788
y ions

b1	T	102.12	y14	TTPSVVAFTADGER	1451.57
b2	TT	203.23	y13	TPSVVAFTADGER	1350.46
b3	TTP	300.34	y12	PSVVAFTADGER	1249.36
b4	TTPS	387.42	y11	SVVAFTADGER	1152.24
b5	TTPSV	486.55	y10	VVAFTADGER	1065.16
b6	TTPSVV	585.69	y9	VAFTADGER	966.03
b7	TTPSVVA	656.76	y8	AFTADGER	866.9
b8	TTPSVVAF	803.94	y7	FTADGER	795.82
b9	TTPSVVAFT	905.05	y6	TADGER	648.64
b10	TTPSVVAFTA	976.12	y5	ADGER	547.54
b11	TTPSVVAFTAD	1091.21	y4	DGER	476.46
b12	TTPSVVAFTADG	1148.27	y3	GER	361.37
b13	TTPSVVAFTADGE	1277.38	y2	ER	304.32
b14	TTPSVVAFTADGER	1433.57	y1	R	175.2

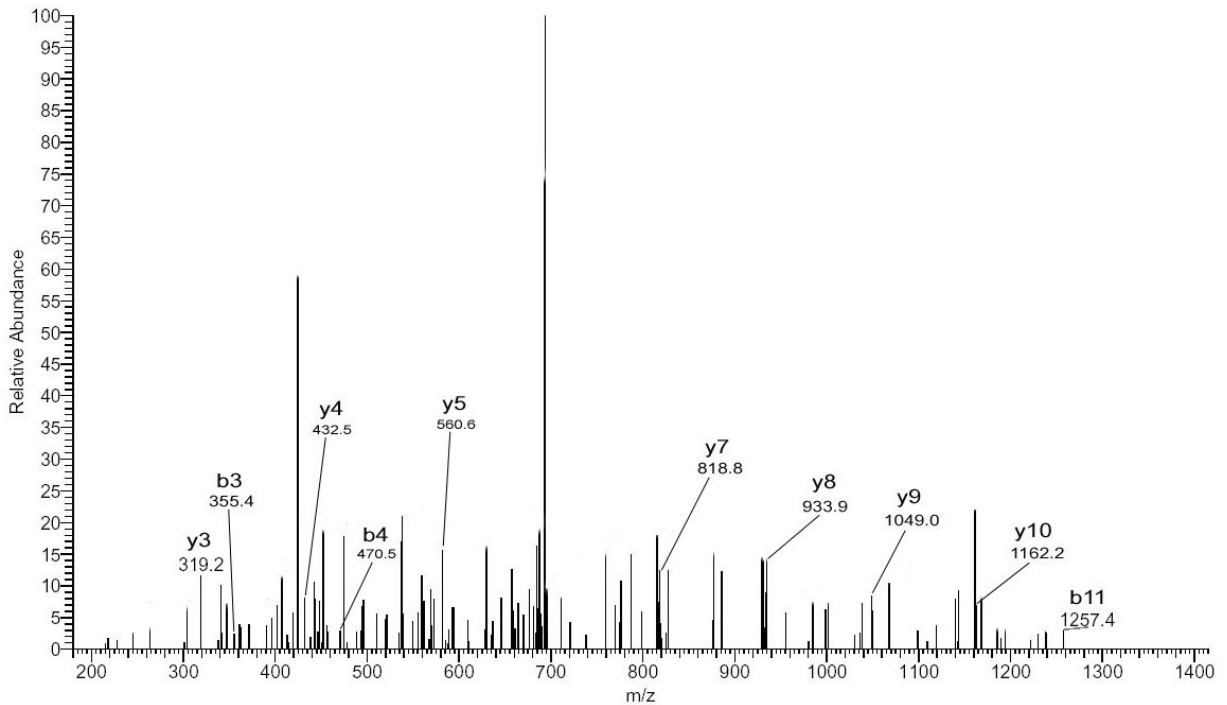
The detected ions were shown in bold.



Q9BSJ8 **Isoform 1 of Protein** MH+
FAM62A (Da): 1402.3521
b ions y ions

b1	Q	129.15	y12	QLLDDEEQLTAK	1403.52
b2	QL	242.31	y11	LLDDEEQLTAK	1275.39
b3	QLL	355.46	y10	LDDEEQLTAK	1162.23
b4	QLLD	470.55	y9	DDEEQLTAK	1049.07
b5	QLLDD	585.64	y8	DEEQLTAK	933.98
b6	QLLDDE	714.76	y7	EEQLTAK	818.89
b7	QLLDDEE	843.87	y6	EQLTAK	689.78
b8	QLLDDEEQ	972	y5	QLTAK	560.66
b9	QLLDDEEQL	1085.16	y4	LTAK	432.53
b10	QLLDDEEQLT	1186.27	y3	TAK	319.37
b11	QLLDDEEQLTA	1257.35	y2	AK	218.27
b12	QLLDDEEQLTAK	1385.52	y1	K	147.19

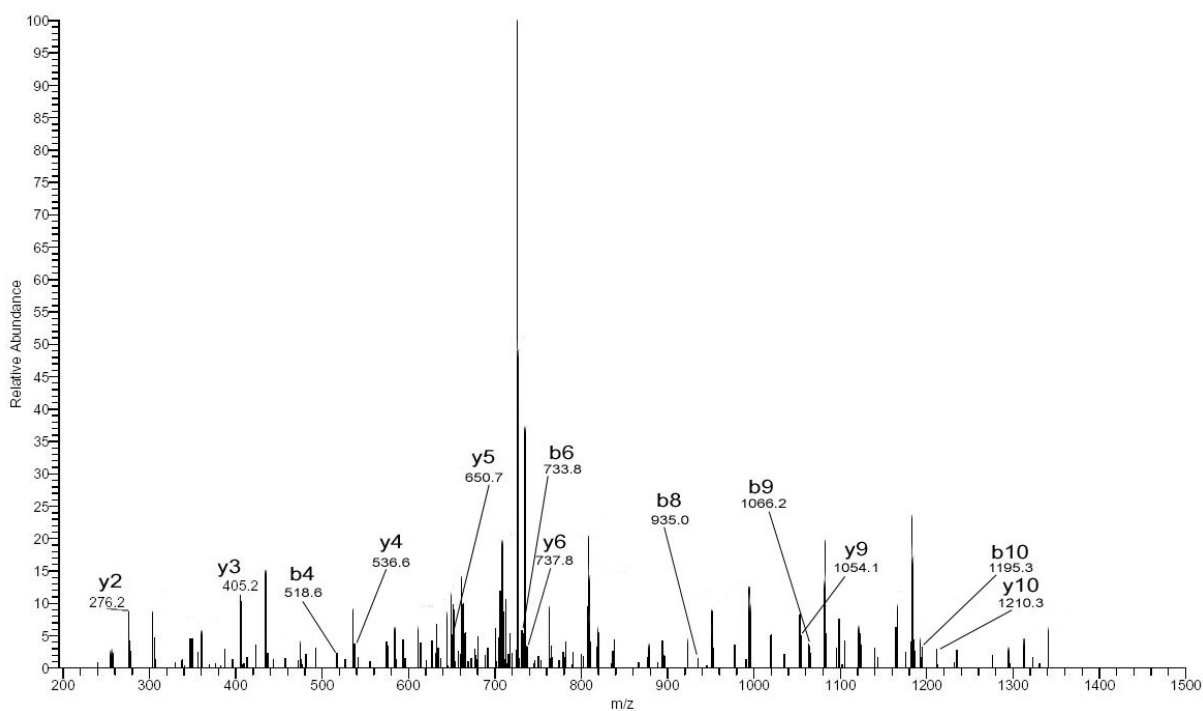
The detected ions were shown in bold.



Q7Z5G9 ELMO2 protein MH+
 (Da): 1484.9090
 b ions y ions

b1	M	132. 21	y12	MERTQSSNMETR	1470. 61
b2	ME	261. 32	y11	ERTQSSNMETR	1339. 41
b3	MER	417. 51	y10	RTQSSNMETR	1210. 3
b4	MERT	518. 62	y9	TQSSNMETR	1054. 11
b5	MERTQ	646. 75	y8	QSSNMETR	953. 01
b6	MERTQS	733. 82	y7	SSNMETR	824. 88
b7	MERTQSS	820. 9	y6	SNMETR	737. 8
b8	MERTQSSN	935. 01	y5	NMETR	650. 72
b9	MERTQSSNM	1066. 2	y4	METR	536. 62
b10	MERTQSSNME	1195. 31	y3	ETR	405. 42
b11	MERTQSSNMET	1296. 42	y2	TR	276. 31
b12	MERTQSSNMETR	1452. 61	y1	R	175. 2

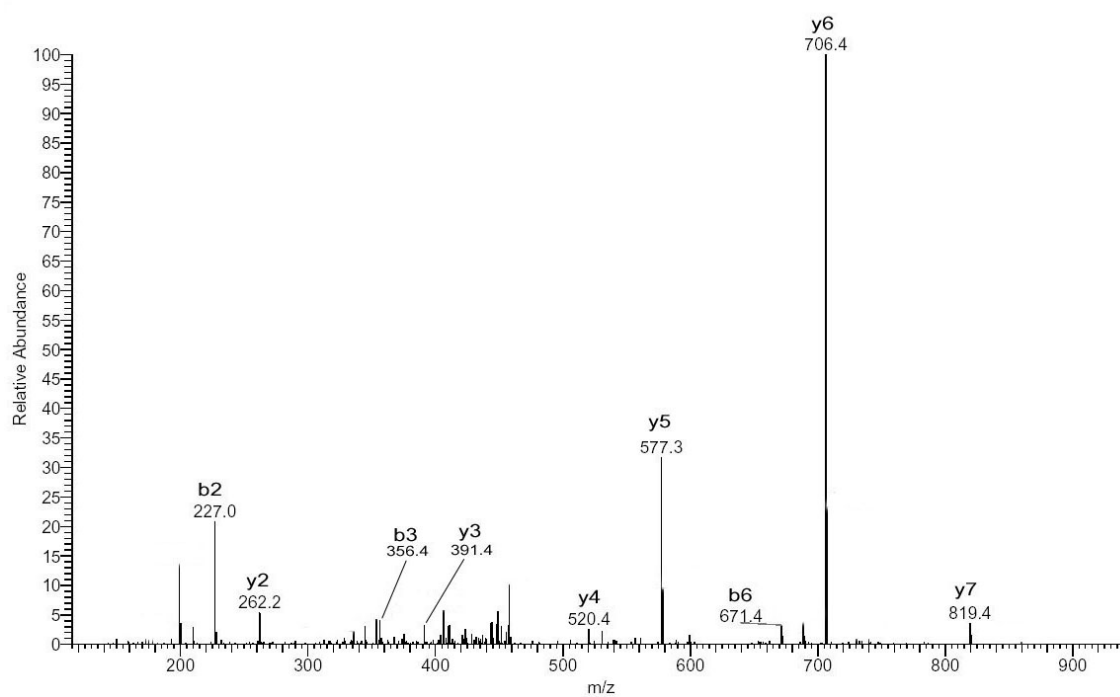
The detected ions were shown in bold.



P41219 **Isoform 1 of** MH+ 1309.9330
Peripheralin (Da):
b ions y ions

b1	L	114.17	y8	LLEGEESR	933
b2	LL	227.33	y7	LEGEESR	819.84
b3	LLE	356.45	y6	EGEESR	706.68
b4	LLEG	413.5	y5	GEESR	577.56
b5	LLEGE	542.62	y4	EESR	520.51
b6	LLEGEE	671.73	y3	ESR	391.4
b7	LLEGEES	758.81	y2	SR	262.28
b8	LLEGEESR	915	y1	R	175.2

The detected ions were shown in bold.



**ATP synthase subunit
alpha, mitochondrial
precursor**

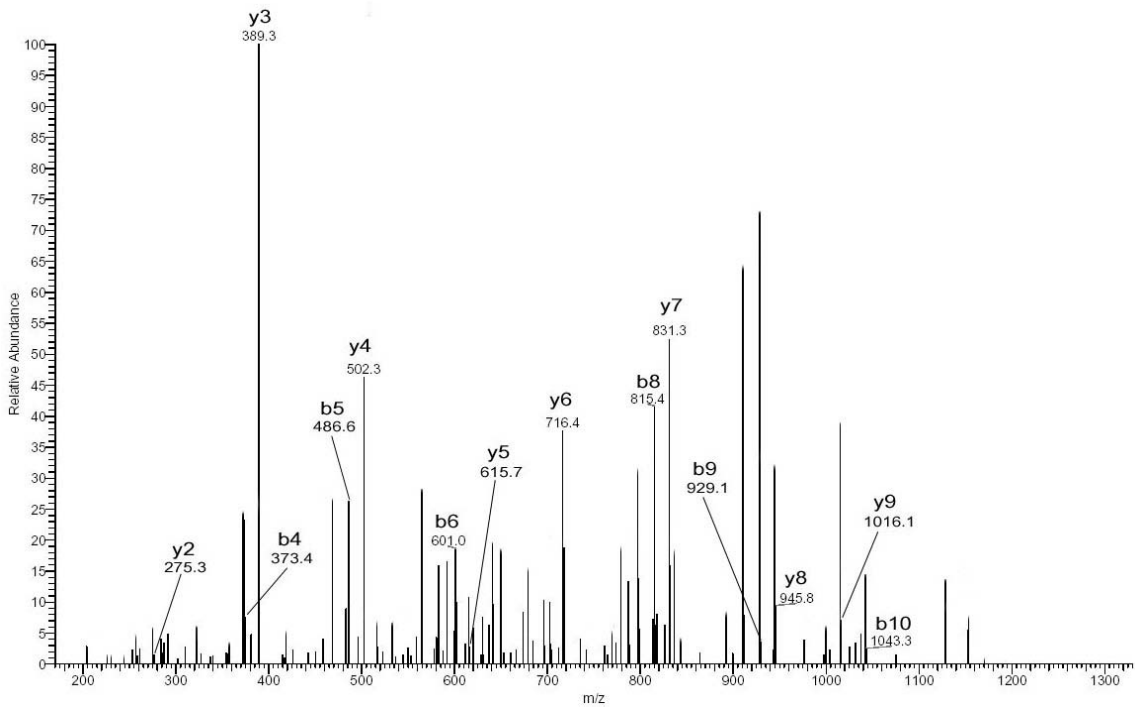
MH+
(Da): 1316.9060

P25705
b ions

y ions

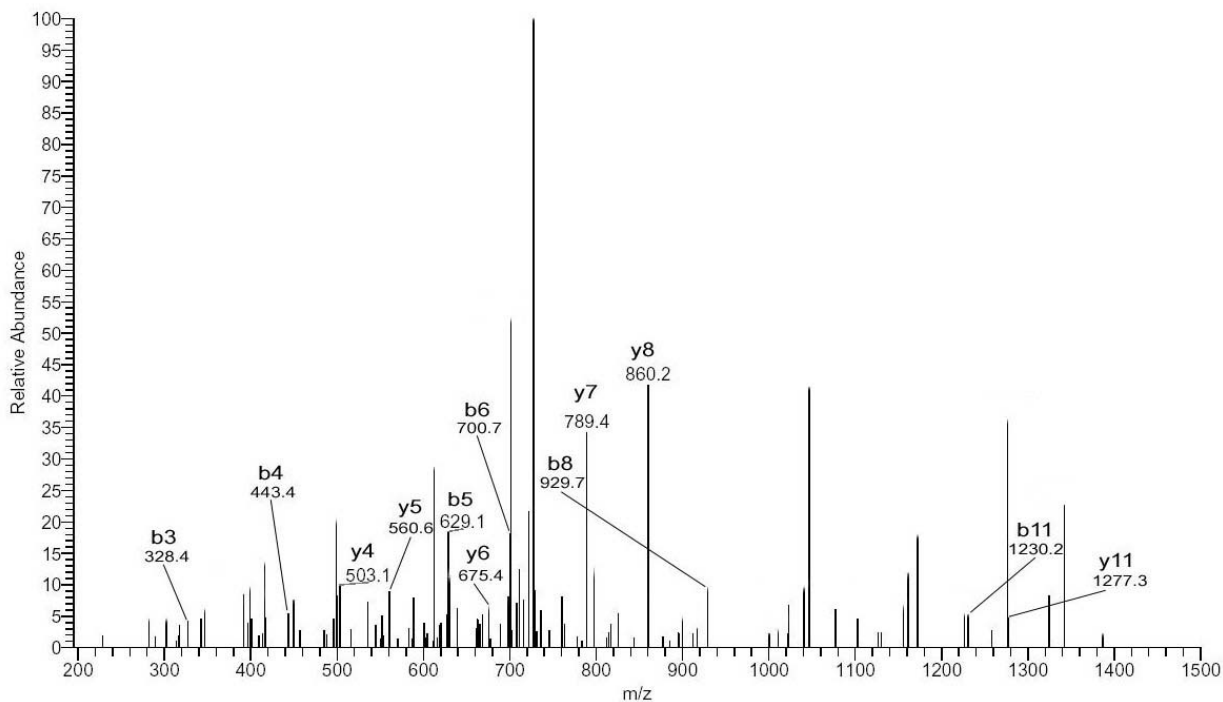
b1	T	102.12	y12	TSIAIDTIINQK	1317.52
b2	TS	189.2	y11	SIAIDTIINQK	1216.41
b3	TSI	302.36	y10	IAIDTIINQK	1129.33
b4	TSIA	373.44	y9	AIDTIINQK	1016.17
b5	TSIAI	486.6	y8	IDTIINQK	945.1
b6	TSIAID	601.68	y7	DTIINQK	831.94
b7	TSIAIDT	702.79	y6	TIINQK	716.85
b8	TSIAIDTI	815.95	y5	IINQK	615.74
b9	TSIAIDTII	929.11	y4	INQK	502.58
b10	TSIAIDTIIN	1043.21	y3	NQK	389.42
b11	TSIAIDTIINQ	1171.34	y2	QK	275.32
b12	TSIAIDTIINQK	1299.52	y1	K	147.19

The detected ions were shown in bold.



B4DGP8		Calnexin precursor		MH+	(Da):	1488.7949
b ions			y ions			
b1	I	114.17	y13	IVDDWANDGWGLK	1489.62	
b2	IV	213.31	y12	VDDWANDGWGLK	1376.46	
b3	IVD	328.4	y11	DDWANDGWGLK	1277.33	
b4	IVDD	443.48	y10	DWANDGWGLK	1162.24	
b5	IVDDW	629.7	y9	WANDGWGLK	1047.15	
b6	IVDDWA	700.78	y8	ANDGWGLK	860.94	
b7	IVDDWAN	814.88	y7	NDGWGLK	789.86	
b8	IVDDWAND	929.97	y6	DGWGLK	675.75	
b9	IVDDWANDG	987.02	y5	GWGLK	560.67	
b10	IVDDWANDGW	1173.23	y4	WGLK	503.61	
b11	IVDDWANDGWG	1230.29	y3	GLK	317.4	
b12	IVDDWANDGWGL	1343.45	y2	LK	260.35	
b13	IVDDWANDGWGLK	1471.62	y1	K	147.19	

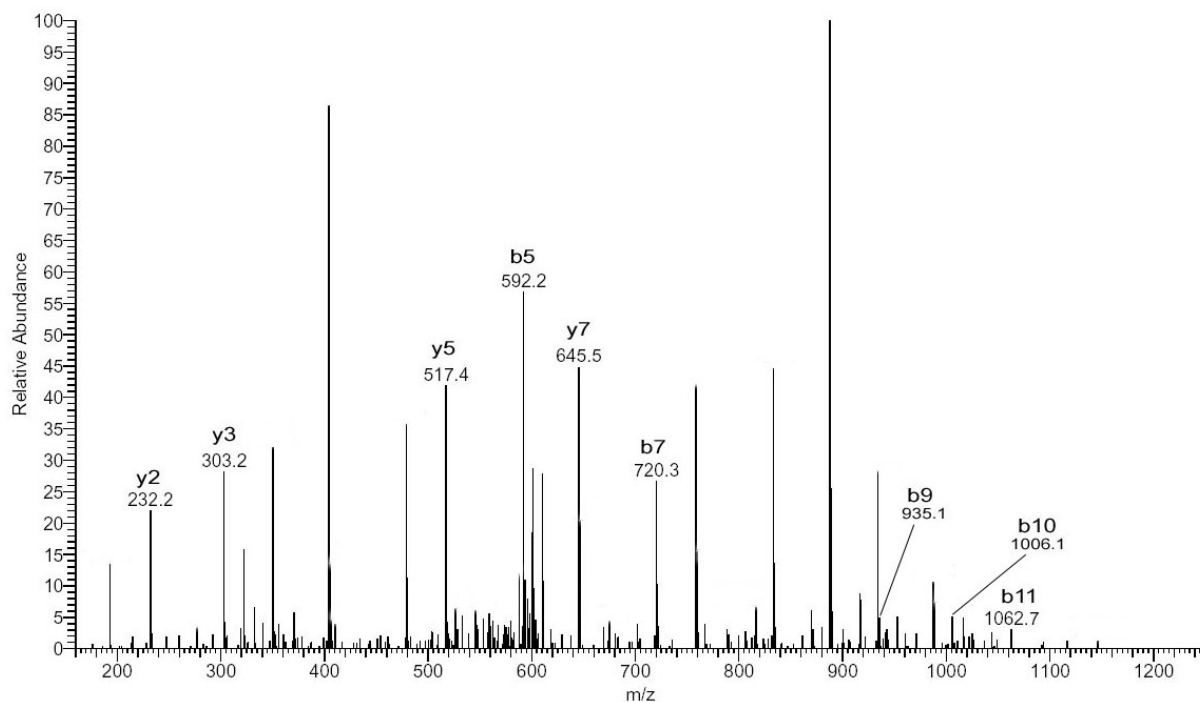
The detected ions were shown in bold.



Isoform 1 of
AT-hook-containing
Q7Z591 transcription factor MH+
(Da): 1236.9160

b ions			y ions		
b1	P	98.13	y12	PLPRQGATLAGR	1237.44
b2	PL	211.29	y11	LPRQGATLAGR	1140.32
b3	PLP	308.41	y10	PRQGATLAGR	1027.16
b4	PLPR	464.6	y9	RQGATLAGR	930.05
b5	PLPRQ	592.73	y8	QGATLAGR	773.86
b6	PLPRQG	649.78	y7	GATLAGR	645.73
b7	PLPRQGA	720.86	y6	ATLAGR	588.68
b8	PLPRQGAT	821.96	y5	TLAGR	517.6
b9	PLPRQGATL	935.12	y4	LAGR	416.49
b10	PLPRQGATLA	1006.2	y3	AGR	303.33
b11	PLPRQGATLAG	1063.25	y2	GR	232.25
b12	PLPRQGATLAGR	1219.44	y1	R	175.2

The detected ions were shown in bold.



Integrin beta-2		MH+			
P05107	precursor	(Da):	1090.0657		
b ions			y ions		
b1	A	72.09	y10	ALNEITESGR	1090.17
b2	AL	185.25	y9	LNEITESGR	1019.09
b3	ALN	299.36	y8	NEITESGR	905.93
b4	ALNE	428.47	y7	EITESGR	791.83
b5	ALNEI	541.63	y6	ITESGR	662.71
b6	ALNEIT	642.74	y5	TESGR	549.55
b7	ALNEITE	771.85	y4	ESGR	448.45
b8	ALNEITES	858.93	y3	SGR	319.33
b9	ALNEITESG	915.98	y2	GR	232.25
b10	ALNEITESGR	1072.17	y1	R	175.2

The detected ions were shown in bold.

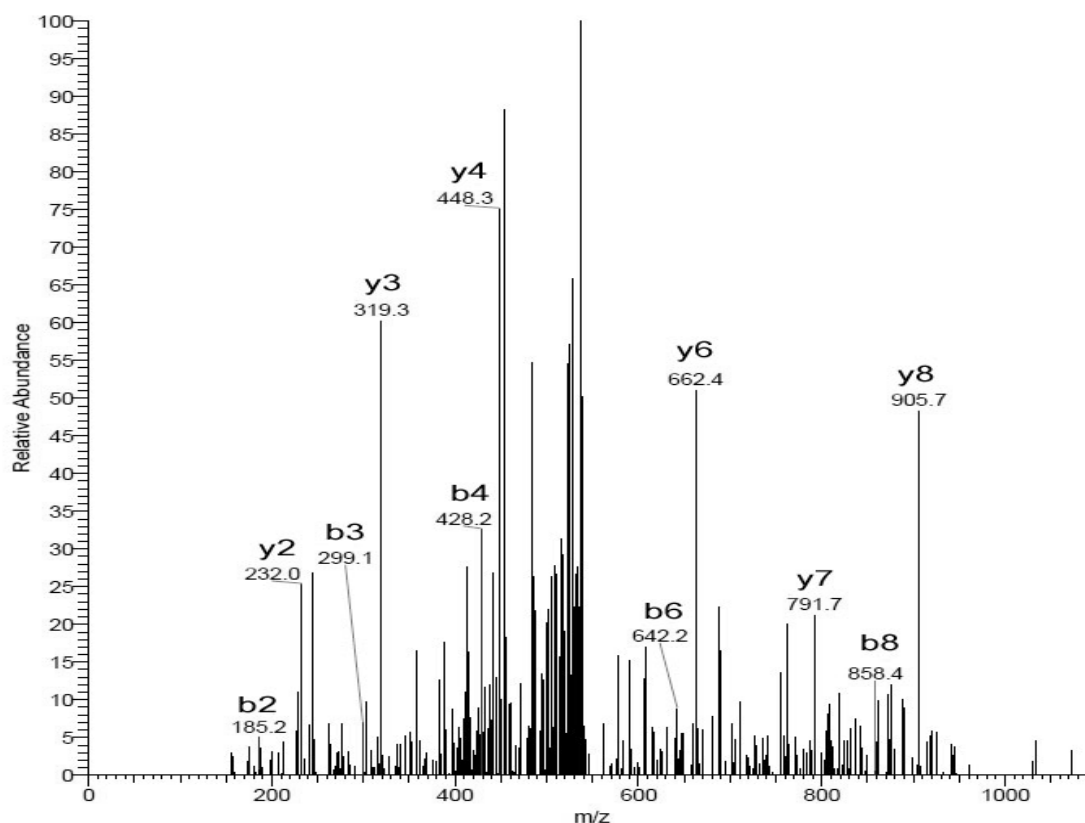


Figure S3

The MS/MS spectra for single-peptide-based identifications. The detected b and y ions used in the protein identification were labeled in the MS/MS spectra. The unlabeled peaks are a, c, x or z ions generated in mass spectrometer.