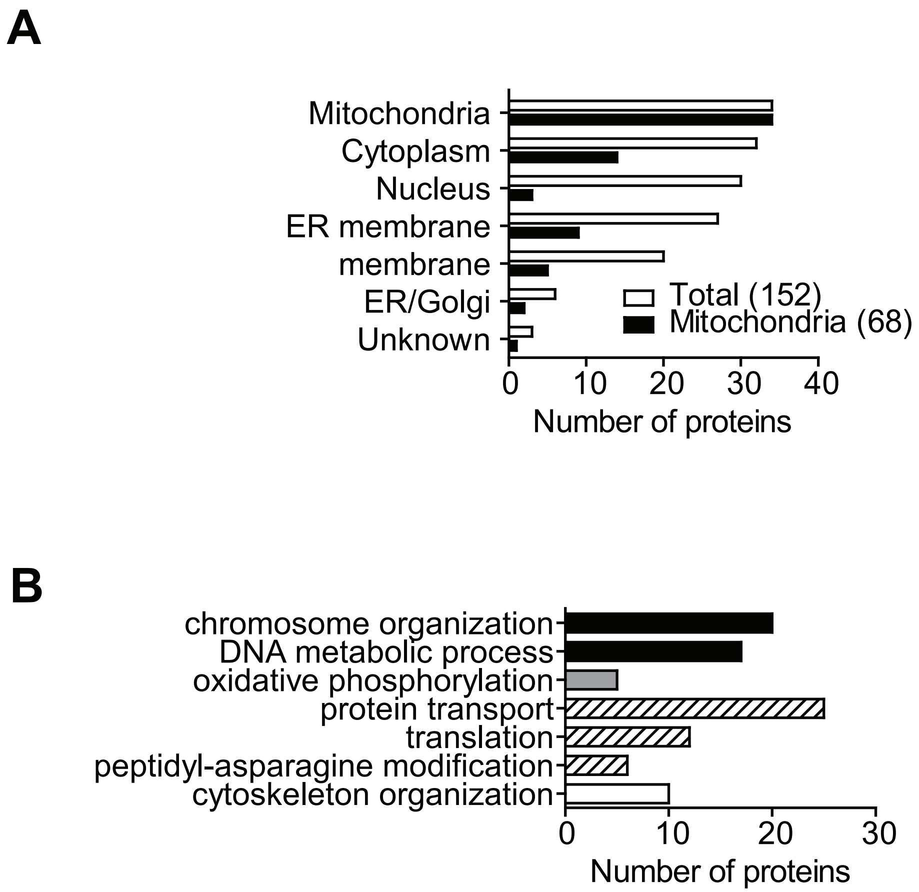


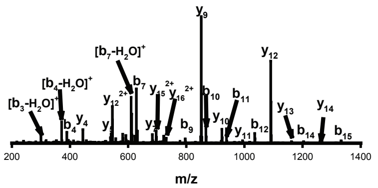
Supplementary Figure S1. (A) Categories of intracellular locations in Supplementary Table S1A. The numbers of proteins in various locations were compared between the 152 D-loop DNA binding proteins (Total) and 68 mitochondrial proteins predicted in Figure 1D (Mitochondria).
(B) Numbers of proteins in 7 cellular processes in Figure 2.

Supplementary Figure S2-1

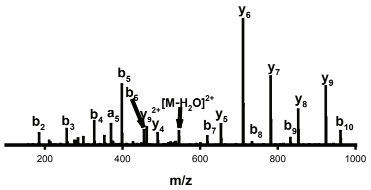
H1 Histone family, member 2 (Coverage : 44.1 %, Hit : 25)

MSETAP**AAPAAAPPAEKAPVKKK**AAKKAGGTPR**KASGPPVSELITK**AVAASKER**SGVSLAALKKALAAAGYDVEKNNS**
RIKLGLKSLVSK**GTLVQTKGTGASGSFK**LNKKAASGEAKPKVKKAGGTKPKKPVGAAKKPK**KAAGGATPK**KSAKKTPK
KAK**KPAAATVTKK**VAKSPKKAKVAKPKKAAKSAAKAVKPKAAKPKVVKPKKAAPKKK

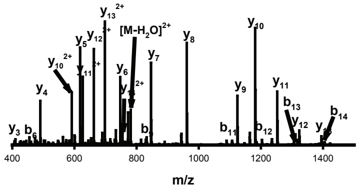
SETAPAAPAAAPPAEK (Xcorr=3.97)



ALAAAGYDVEK (Xcorr=3.69)



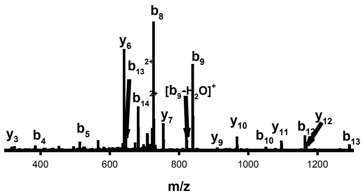
ALAAAGYDVEKNNSR (Xcorr=4.61



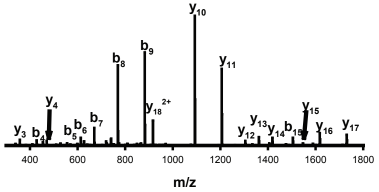
H2A Histone family, member A (Coverage : 61.5 %, Hit : 16)

MSGRGKQGGKARAKAKSRSSR**AGLQFPVGR**V**HRLLRKGNYSERVGAGAPVYLAAVLEYLTAEILELAGNAAR**DNKKTR
IIPRHLQLAIR**NDEELNKLLGRVTIAQGGVLPNIQAVLLPK**KTESHHKAKG

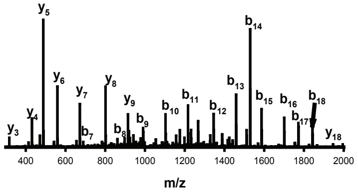
VTIAQGGVLPNIQAVLLPK(Xcorr=4.99)



V]TIAQGGVLPNIQAVLLPK(Xcorr=4.73)



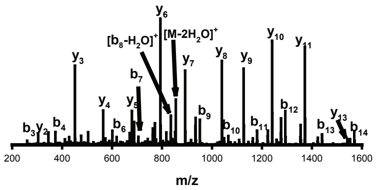
AVLEYLTAEILELAGNAAR(Xcorr=5.24)



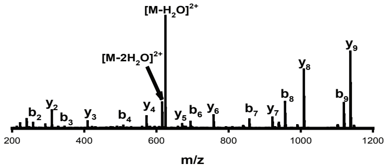
H2B Histone family, member J (Coverage : 53.1 %, Hit : 12)

MPDPAKSAPAPKKGSKKAVTKAQKKDGKKRKRSR**KESYSVYVYK**VLK**QVHPDTGISSKAMGIMNSFVNDIFER**IAGEA
SR**LAHYNKR**STITSR**EIQTAVRLLLPGELAKHAVSEGTK**AVTKYTSSK

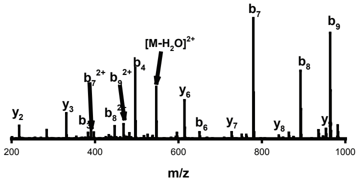
AMGIMNSFVNDIFER (Xcorr=5.07)



KESYSVYVYK (Xcorr=3.46)



RLLLPGELAK (Xcorr=3.14)

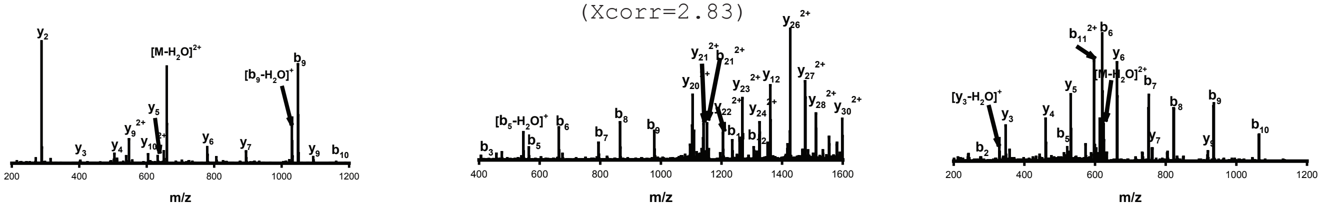


Supplemetary Figure S2-2

H3 histone (Coverage : 36.2 %, Hit : 6)

LAMARTKQTARKSTGGKAPRKQLATKAARKSAPATGGVKKPHRYRPGTVALREIRRYQK**STELLIR**KLPFQRLVR**EIAQDFKTDLRFQSSAVMALQEACEAYLVGLFEDTNLCAIHAK**RVTIMPKDIQLARRIRGERA

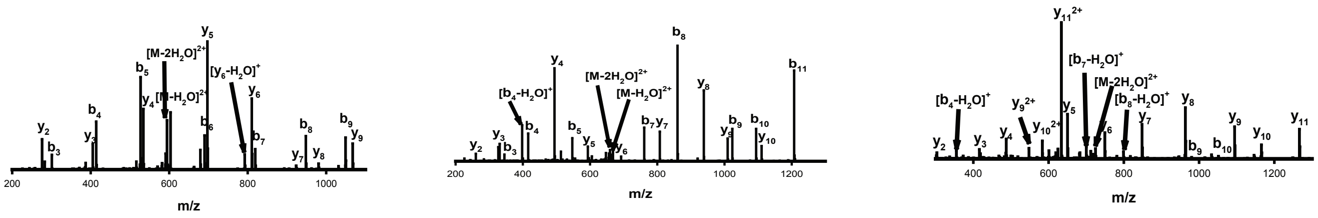
EIAQDFKTDLR(Xcorr=2.83)   F]QSSAVMALQEACEAYLVGLFEDTNLCAIHAK (Xcorr=2.83)   FQSSAVMALQEA(Xcorr=3.60)



H4 histone (Coverage : 54.9%, Hit : 12)

SGRGKGGKGLGKGGAKRHRKVLR**DNIQGITKPAIR**RLARRGGVKR**ISGLIYEETRGV**LK**VFLENVIRDAVTYTEHAKRKTVTAMDVVYALKR**QGRTLYGFGG

I]SGLIYEETR (Xcorr=3.77)   T]VTAMDVVYALK (Xcorr=3.93)   TVTAMDVVYALKR (Xcorr=3.58)



Supplementary Figure S2. Representative histone proteins identified by LC/MS/MS experiments. The portion of identified protein sequence was indicated in bold. Some of annotated MS/MS spectra were also shown along with their Xcorr values.

Supplementary Table S1A. Proteins identified by μHPLC and MS/MS

serial #	IPI No.	AC	EntrezID	Gene_Symbol	열1	Cov	# unique peptides (total peptides)	localization	functional category	Protein group
1	IPI00453473.6	A2VCL0	8294	HIST1H4B;HIST1H4J	Histone H4	65	31 (31)	nucleus	DNA binding	
2	IPI00550239.4	P07305	3005	H1F0	Histone H1.0	20.6	7 (7)	nucleus	DNA binding	
3	IPI00783271.1	A0PJE3	10128	LRPPRC	Leucine-rich PPR motif-containing pr	4.2	5 (5)	mitochondria	DNA binding	
4	IPI00021924.1	Q92522	8971	H1FX	Histone H1x	17.8	3 (3)	nucleus	DNA binding	
5	IPI00008529.1	P05387	6181	RPLP2	60S acidic ribosomal protein P2	28.7	2 (2)	cytoplasm	RNA binding	
6	IPI00024976.5	Q53GB0	56993	TOMM22	Mitochondrial import receptor Tom2	23.2	2 (2)	mitochondria	protein transport	
7	IPI00221222.7	P53999	10923	SUB1	Activated RNA polymerase II transcri	18.9	2 (2)	nucleus	DNA binding	
8	IPI00425902.4	P43308	6746	SSR2 cDNA FLJ5630	Translocon-associated protein subun	15.3	2 (2)	ER membrane	protein transport	
9	IPI00007188.5	O43350	292	SLC25A5	ADP/ATP translocase 2	14.4	2 (2)	mitochondria	transport	
10	IPI00025974.3	P59074	128866	CHMP4B	Protein CGI-301	11.2	2 (2)	cytoplasm	protein transport	
11	IPI00029744.1	A4D1U3	6742	SSBP1	Single-stranded DNA binding protei	10.1	2 (2)	mitochondria	DNA binding	
12	IPI00396321.1	Q96AG4	55379	LRRC59	Leucine-rich repeat-containing protei	7.2	2 (2)	ER membrane	DNA binding	
13	IPI00027107.5	O15276	7284	TUFM	Elongation factor Tu, mitochondrial	4.6	2 (2)	mitochondria	nucleotide binding	
14	IPI00328170.9	Q13724	7841	GCS1	Mannosyl-oligosaccharide glucosidas	4.4	2 (2)	ER membrane	metabolism	
15	IPI00297492.2	P46977	3703	STT3A	Dolichyl-diphosphooligosaccharide--	4.3	2 (2)	ER membrane	metabolism	
16	IPI00026970.4	Q0VGA3	11198	SUPT16H	SUPT16H protein	3.1	2 (2)	membrane	DNA binding	
17	IPI00166865.3	Q7Z3D5	493856	CISD2	CDGSH iron sulfur domain-containin	22.2	1 (1)	mitochondria	ion binding	
18	IPI00018855.1	P27449	527	ATP6V0C	V-type proton ATPase 16 kDa protec	20	1 (1)	membrane	transport	
19	IPI00386294.2	A2A3M0	100188893	TOMM6	Prickle-like protein 4	18.9	1 (1)	mitochondria	protein transport	
20	IPI00220835.7	P38390	10952	SEC61B	Sec61 beta subunit	15.6	1 (1)	ER membrane	protein transport	
21	IPI00021785.2	P10606	1329	COX5B	Cytochrome c oxidase subunit 5B, mi	14	1 (1)	mitochondria	Electron transport	
22	IPI00739464.1	Q562Z7	71	ACT	Actin-like protein	10.5	1 (1)	cytoplasm	protein transport	
23	IPI00220739.3	O00264	10857	PGRMC1	Membrane-associated progesterone	10.3	1 (1)	ER membrane	signal transduction	
24	IPI00220362.5	P61604	3336	HSPE1	10 kDa heat shock protein, mitochon	9.8	1 (1)	mitochondria	protein folding	
25	IPI00009407.8	P61803	1603	DAD1	Dolichyl-diphosphooligosaccharide--	8.8	1 (1)	ER membrane	metabolism	
26	IPI00024920.1	P30049	513	ATP5D	ATP synthase subunit delta, mitocho	8.3	1 (1)	mitochondria	Electron transport	
27	IPI00009368.4	Q9H9B4	94081	SFXN1	Sideroflexin-1	7.5	1 (1)	mitochondria	transport	
28	IPI00009235.2	Q549M4	6747	SSR3 cDNA FLJ5206	Translocon-associated protein subun	7.1	1 (1)	ER membrane	protein transport	
29	IPI00016339.4	P51148	5878	RAB5C	Ras-related protein Rab-5C	5.6	1 (1)	membrane	nucleotide binding	
30	IPI00006865.3	Q96IW7	26984	SEC22B	Vesicle-trafficking protein SEC22a	4.7	1 (1)	ER membrane	protein transport	
31	IPI00784154.1	P10809	3329	HSPD1	60 kDa heat shock protein, mitochon	4.4	1 (1)	mitochondria	protein folding	
32	IPI00798360.1	P82979	84324	CIP29	Nuclear protein Hcc-1	4.3	1 (1)	nucleus	DNA binding	
33	IPI00257903.4	Q4VXJ7	79956	ERMP1	Endoplasmic reticulum metallopeptid	2.9	1 (1)	ER membrane	metabolism	
34	IPI00298281.3	P11047	3915	LAMC1	Laminin subunit gamma-1	2.3	1 (1)	membrane	signal transduction	
35	IPI00015911.1	P09622	1738	DLD	Dihydrolipoyl dehydrogenase, mitoch	2.2	1 (1)	mitochondria	Electron transport	
36	IPI00328715.4	Q05DH2	92140	MTDH	MTDH protein	1.9	1 (1)	membrane	protein binding	
37	IPI00017592.1	O95202	3954	LETM1	LETM1 and EF-hand domain-containi	1.6	1 (1)	mitochondria	ion binding	
38	IPI00031522.2	P40939	3030	HADHA	Trifunctional enzyme subunit alpha,	1.6	1 (1)	mitochondria	metabolism	
39	IPI00218922.5	O95380	11231	SEC63	Translocation protein SEC63 homolo	1.1	1 (1)	ER membrane	protein transport	
40	IPI00007858.1	O95252	8735	MYH13	Myosin-13	0.8	1 (1)	cytoplasm	protein binding	
41	IPI00024284.4	P98160	3339	HSPG2	Basement membrane-specific hepara	0.5	1 (1)	membrane	signal transduction	

42	IPI00019502.3	O60805	4627	MYH9	Myosin-9	19.7	6 (39)	cytoplasm	nucleotide binding	Isoform 2 of Myosin-9(IPI00395772); FLJ00279 protein (Fragment)(IPI00742780); Isoform 1 of Myosin-10(IPI00397526); Isoform 2 of Myosin-10(IPI00479307); Isoform 3 of Myosin-10(IPI00790503); smooth muscle myosin heavy chain 11 isoform SM2A(IPI00024870); smooth muscle myosin heavy chain 11 isoform SM2B(IPI00744256); 1 Myosin-11(IPI00020501); smooth muscle myosin heavy chain 11 isoform SM1B(IPI00743857); 228 kDa protein(IPI00873792); Myosin heavy chain 11 smooth muscle isoform(IPI00873982); MYH9 protein(IPI00556012); Isoform 5 of Myosin-14(IPI00029818); Isoform 4 of Myosin-14(IPI00607778); Isoform 1 of Myosin-14(IPI00337335); MYH14 variant
43	IPI00016801.1	P00367	2746	GLUD1	Glutamate dehydrogenase 1, mitoch	46.1	1 (33)	mitochondria	metabolism	cDNA FLJ16138 fis, clone BRALZ2017531, highly similar to Glutamate dehydrogenase 1, mitochondrial(IPI00872742); Glutamate dehydrogenase 1 variant (Fragment)(IPI00746092); Glutamate dehydrogenase 2, mitochondrial(IPI00027146); similar
44	IPI00217465.5	P16403	3006	HIST1H1C	Histone H1.2	51.2	9 (27)	nucleus	DNA binding	Histone H1.4(IPI00217467); Histone H1.3(IPI00217466); Histone H1.1(IPI00217469); Histone H1t(IPI00419983); Histone H1.5(IPI00217468); Histone H1 gene (Fragment)(IPI00815867);
45	IPI00081836.3	A3KPC7	8329	HIST1H2AH	Histone H2A RuleBase RU000527V2	72.7	0 (25)	nucleus	DNA binding	Histone H2A type 1-J(IPI00552873); Histone H2A type 1(IPI00291764); Histone H2A type 2-A(IPI00216457); Histone H2A.x(IPI00219037); Histone H2A type 1-C(IPI00216456); Histone H2A type 1-D(IPI00255316); Isoform 1 of Histone H2A.J(IPI00220855); Histone H2A type 2-C(IPI00339274); cDNA, FLJ92409, highly similar to Homo sapiens histone 1, H2ad (HIST1H2AD), mRNA(IPI00902514); Histone H2A type 2-B(IPI00216730); Histone H2A type 1-B/E(IPI00026272); Histone H2A type 3(IPI00031562); Isoform 2 of Histone H2A.J(IPI00102165); Histone H2A type 1-A(IPI00045109); Isoform 1 of Core histone macro-H2A.1(IPI00744148); H2A histone family, member Y isoform 2(IPI00059366); Isoform 2 of Core histone macro-H2A.1(IPI00304171); 13 kDa protein(IPI00249267); Histone H2A.V(IPI00018278); Histone H2A.Z(IPI00218448); H2A histone family, member V isoform 2(IPI00141938); H2A histone family, member V isoform 3(IPI00398798); Core histone macro-
46	IPI00021439.1	Q75MN2	60	ACTB	Actin, cytoplasmic 1	56.3	0 (23)	cytoplasm	structure	Actin, cytoplasmic 2(IPI00021440); cDNA FLJ52842, highly similar to Actin, cytoplasmic 1(IPI00894365); Beta actin variant (Fragment)(IPI00894498); cDNA FLJ43573 fis, clone RECTM2001691, highly similar to Actin, cytoplasmic 2(IPI00794523); Actin, alpha skeletal muscle(IPI00021428); Actin, alpha cardiac muscle 1(IPI00023006); cDNA FLJ39583 fis, clone SKMUS2004897, highly similar to ACTIN, ALPHA SKELETAL MUSCLE(IPI00878173); Actin, gamma-enteric smooth muscle(IPI00025416); Actin, aortic smooth muscle(IPI00008603); Putative uncharacterized protein ACTA1(IPI00514530); ACTA2 protein (Fragment)(IPI00816229); cDNA FLJ51195, highly similar to Actin, gamma-enteric smooth muscle(IPI00914623); Actin alpha 1 skeletal muscle protein(IPI00414057); 16 kDa protein(IPI00796881); 22 kDa protein(IPI00790339); Beta-actin-like protein 2(IPI00003269); 11 kDa protein(IPI00894523); 11 kDa protein(IPI00893981); 9 kDa protein(IPI00893604); ACTB protein

47	IPI00003935.6	A3KMC7	8349	HIST2H2BE	Histone H2B type 2-E	53.2	0 (18)	nucleus	DNA binding	Histone H2B type 1-L(IPI00018534); histone cluster 1, H2bg(IPI00020101); Histone H2B type 1-O(IPI00152785); Histone H2B type 1-D(IPI00152906); Histone H2B type 1-B(IPI00220403); Histone H2B type 1-H(IPI00303133); Histone H2B type 2-F(IPI00329665); Histone H2B type 1-J(IPI00515061); Histone H2B type 1-M(IPI00554798); cDNA FLJ56780, highly similar to Histone H2B type 2-F(IPI00419833); cDNA FLJ56787, highly similar to Histone H2B type 2-F(IPI00646240); Histone H2B type 1-N(IPI00794461); Histone H2B type 3-B(IPI00166293); Histone H2B type F-S(IPI00477495); Histone H2B(IPI00816252); Histone H2B(IPI00815755); Histone H2B(IPI00787441); Histone H2B type 1-A(IPI00465363); Putative histone H2B type 2-D(IPI00746251);
48	IPI00449049.5	P09874	142	PARP1	Poly [ADP-ribose] polymerase 1	21.8	15 (17)	nucleus	DNA binding	PARP1 protein (Fragment)(IPI00896487); Poly (ADP-ribose) polymerase family, member 1(IPI00477173); Poly (ADP-ribose) polymerase family, member 1(IPI00478427);
49	IPI00296337.2	P78527	5591	PRKDC	DNA-dependent protein kinase catal	5.8	1 (16)	nucleus	DNA binding	similar to DNA dependent protein kinase catalytic subunit(IPI00786995); Isoform 2 of DNA-dependent protein kinase catalytic subunit(IPI00376215);
50	IPI00007765.5	P38646	3313	HSPA9	Stress-70 protein, mitochondrial	27.8	13 (14)	mitochondria	protein folding	HSPA5 protein(IPI00003362); cDNA FLJ59163, highly similar to Heat shock cognate 71 kDa protein(IPI00910870); Isoform 2 of Heat shock cognate 71 kDa protein(IPI00037070); Heat shock 70 kDa protein 1L(IPI00301277); Heat shock 70 kDa protein 1(IPI00304925); cDNA FLJ54392, highly similar to Heat shock 70 kDa protein 1(IPI00845339); Heat shock 70kDa protein 1-like variant(IPI00893099); Isoform 1 of Heat shock cognate 71 kDa protein(IPI00003865); cDNA FLJ56386, highly similar to Heat shock 70 kDa protein 1L(IPI00643152); cDNA FLJ54389, highly similar to Heat shock 70 kDa protein 1(IPI00647012); cDNA FLJ40505 fis, clone TESTI2045562, highly similar to HEAT SHOCK-RELATED 70 kDa PROTEIN 2(IPI00902596); cDNA FLJ53752, highly similar to Heat shock 70 kDa protein 1(IPI00909073); cDNA FLJ54407, highly similar to Heat shock 70 kDa protein 1(IPI00910482); cDNA FLJ54408, highly similar to Heat shock 70 kDa protein
51	IPI00383680.3	P04844	6185	RPN2	Dolichyl-diphosphooligosaccharide--	30.4	0 (10)	ER/Golgi	metabolism	Dolichyl-diphosphooligosaccharide--protein glycosyltransferase subunit 2(IPI00844076); Ribophorin II(IPI00028635); cDNA, FLJ96923, highly similar to Homo sapiens ribophorin II (RPN2), mRNA(IPI00872681); Putative uncharacterized protein RPN2(IPI00552972); Ribophorin II(IPI00552307); Ribophorin
52	IPI00303476.1	P06576	506	ATP5B	ATP synthase subunit beta, mitochon	27.4	4 (10)	mitochondria	Electron transport	17 kDa protein(IPI00791498); 13 kDa protein(IPI00792534); 15 kDa protein(IPI00790847); 12 kDa protein(IPI00793271);
53	IPI00604713.3	Q07065	10970	CKAP4	Cytoskeleton-associated protein 4	17.6	0 (9)	ER membrane	DNA binding	Similar to cytoskeleton-associated protein 4 (Fragment)(IPI00883950); Isoform 1 of Cytoskeleton-associated protein 4(IPI00141318); 8 kDa protein(IPI00790467); ZFYVE19 protein variant (Fragment)(IPI00555885); Isoform 3 of Zinc finger FYVE domain-containing protein 19(IPI00102875); Isoform 2 of Zinc finger FYVE domain-containing protein 19(IPI00329053); Isoform 1 of Zinc finger FYVE domain-containing protein
54	IPI00871391.1	O43594	7520	XRCC5	Ku86 autoantigen related protein 1	17.7	0 (9)	cytoplasm	DNA binding	ATP-dependent DNA helicase 2 subunit 2(IPI00220834);
55	IPI00465070.7	A0PJT7	8350	HIST1H3J;HIST1H3B	Histone H3.1	50.7	1 (8)	nucleus	DNA binding	Histone H3.2(IPI00171611); Histone H3.1t(IPI00216402); cDNA FLJ52843, highly similar to Histone H3.3(IPI00909530); cDNA FLJ57905, moderately similar to Histone H3.3(IPI00477080); Histone H3.3(IPI00219038); Histone H3(IPI00455457); Histone H3 (Fragment)(IPI00874018); 13 kDa protein(IPI00793280); Histone H3-like(IPI00419884); 11 kDa protein(IPI00792719); similar to

56	IPI00220573.4	P19105	10627	MRCL3	Myosin regulatory light chain MRLC3	35.1	0 (7)	cytoplasm	protein binding	Myosin regulatory light chain MRLC2(IPI00033494); Myosin regulatory light chain MRCL3 variant(IPI00604523); 13 kDa protein(IPI00642780); Myosin regulatory light chain(IPI00719669); Myosin regulatory light polypeptide 9(IPI00220278); similar to myosin:SUBUNIT=regulatory light chain(IPI00376572); similar to myosin:SUBUNIT=regulatory light chain(IPI00888438); myosin regulatory light chain 9 isoform b(IPI00030929); similar to
57	IPI00604476.1	P38378	29927	SEC61A1	Sec61 alpha 1 subunit	19.4	0 (7)	ER membrane	protein transport	cDNA FLJ59739, highly similar to Protein transport protein Sec61 subunit alpha isoform 1(IPI00218466);
58	IPI00455383.4	Q00610	1213	CLTC	Clathrin heavy chain 1	9.5	0 (6)	mitochondria	signal transduction	Isoform 1 of Clathrin heavy chain 1(IPI00024067);
59	IPI00792677.1	P68363	10376	TUBA1B	Tubulin alpha-1B chain	18.3	0 (6)	cytoplasm	structure	Tubulin alpha-1C chain(IPI00218343); Tubulin alpha-1B chain(IPI00387144); TUBA1B protein(IPI00793930); 29 kDa protein(IPI00478908); TUBA1C protein(IPI00166768); Isoform 2 of Tubulin alpha-3C/D chain(IPI00218345); Tubulin alpha-2 chain (Alpha-tubulin 2). Isoform 2(IPI00895775); Isoform 1 of Tubulin alpha-3C/D chain(IPI00179709); Tubulin alpha-3E chain(IPI00410402); Tubulin alpha-1A chain(IPI00180675); cDNA FLJ53765, highly similar to Tubulin alpha chain(IPI00909762); cDNA FLJ32385 fis, clone SKMUS1000110, highly similar to Tubulin alpha-8 chain(IPI00792478); Putative uncharacterized protein TUBA4A(IPI00794663); Tubulin alpha-4A chain(IPI00007750); Tubulin alpha-8 chain(IPI00646909); 52 kDa protein(IPI00791613); Putative uncharacterized protein DKFZp686L04275 (Fragment)(IPI00793953); Putative tubulin-like protein alpha-4B(IPI00017454); 19 kDa protein(IPI00795002);
60	IPI00413611.1	O43256	7150	TOP1	DNA topoisomerase 1	7.8	0 (6)	cytoplasm	DNA binding	99 kDa protein(IPI00902597);
61	IPI00299024.9	O43596	10409	BASP1	Brain acid soluble protein 1	41.4	1 (6)	membrane	protein transport	cDNA FLJ51212, moderately similar to Brain acid soluble protein 1(IPI00908521);
62	IPI00514204.3	P02545	4000	LMNA	Lamin-A/C	12.7	0 (5)	nucleus	structure	Rhabdomyosarcoma antigen MU-RMS-40.12(IPI00655812); Isoform C of Lamin-A/C(IPI00216952); Progerin(IPI00644087); Isoform ADelta10 of Lamin-A/C(IPI00216953); Isoform A of Lamin-A/C(IPI00021405); Lamin A/C(IPI00514817); Lamin A/C(IPI00514320); cDNA FLJ56081, highly similar to Lamin-
63	IPI00414101.4	P11388	7153	TOP2A	DNA topoisomerase 2-alpha	3.9	0 (5)	nucleus	DNA binding	Isoform 3 of DNA topoisomerase 2-alpha(IPI00218753); Isoform 1 of DNA topoisomerase 2-alpha(IPI00478232); DNA topoisomerase 2 (Fragment)(IPI00178667); Isoform 4 of DNA topoisomerase 2-alpha(IPI00879004); Isoform Beta-1 of DNA topoisomerase 2-beta(IPI00217709); Isoform Beta-2 of DNA topoisomerase 2-
64	IPI00413922.7	Q561V9	4637	MYL6B	Myosin light polypeptide 6	43.3	0 (5)	cytoplasm	protein binding	13 kDa protein(IPI00795576); 16 kDa protein(IPI00796366); Isoform Non-muscle of Myosin light polypeptide 6(IPI00335168); Isoform Smooth muscle of Myosin light polypeptide 6(IPI00789605); Myosin light chain 6B(IPI00027255); cDNA FLJ60058, highly similar to Myosin light chain 1, slow-twitch muscle A isoform(IPI00909366); 8 kDa protein(IPI00795944); 10 kDa protein(IPI00796500); 11 kDa protein(IPI00797626); 13 kDa protein(IPI00793089); 13 kDa protein(IPI00792530); 17 kDa
65	IPI00470805.2	A1Z5I6	9656	MDC1	Mediator of DNA damage checkpoin	7.8	0 (5)	nucleus	protein binding	Isoform 1 of Mediator of DNA damage checkpoint protein 1(IPI00552897); 227 kDa protein(IPI00641106); Isoform 5 of Mediator of DNA damage checkpoint protein 1(IPI00895837); Isoform 3 of Mediator of DNA damage checkpoint protein
66	IPI00218200.7	P51572	10134	BCAP31	B-cell receptor-associated protein 31	19.8	1 (5)	ER membrane	protein transport	16 kDa protein(IPI00640444); 20 kDa protein(IPI00646739); 21 kDa protein(IPI00639976); 21 kDa protein(IPI00641554); 21 kDa protein(IPI00642984);
67	IPI00014230.1	Q07021	708	C1QBP	Complement component 1 Q subcor	30.5	1 (5)	mitochondria	protein binding	20 kDa protein(IPI00796075); 16 kDa protein(IPI00796630);
68	IPI00790831.1	P20700	4001	LMNB1	Lamin-B1	15.8	0 (5)	nucleus	structure	Lamin-B1(IPI00217975);

69	IPI00893179.1	P12956	2547	XRCC6	ATP-dependent DNA helicase 2 subu	7.9	0 (4)	cytoplasm	DNA binding	Putative uncharacterized protein(IPI00889791); ATP-dependent DNA helicase 2 subunit 1(IPI00644712); X-ray repair complementing defective repair in Chinese hamster cells 6(IPI00893062); hypothetical LOC389901(IPI00888181);
70	IPI00643708.1	Q00059	7019	TFAM	Transcription factor A, mitochondrial	13.2	0 (4)	mitochondria	DNA binding	Transcription factor A, mitochondrial(IPI00020928); Putative uncharacterized protein TFAM(IPI00644515);
71	IPI00643414.2	O14874	10295	BCKDK	[3-methyl-2-oxobutanoate dehydrog	15.3	0 (4)	mitochondria	metabolism	[3-methyl-2-oxobutanoate dehydrogenase [lipoamide]] kinase, mitochondrial(IPI00298612); BCKDK protein(IPI00062344); FLJ60500, highly similar to 3-methyl-2-oxobutanoate
72	IPI00795527.1	P62988	7316	RPS27A;UBC;UBB	Ubiquitin	35.7	0 (3)	cytoplasm	metabolism	21 kDa protein(IPI00794925); 39 kDa protein(IPI00792712); ubiquitin C(IPI00798127); UBC protein(IPI00793729); ubiquitin B precursor(IPI00719280); Ubiquitin C splice variant(IPI00784990); cDNA FLJ51326, highly similar to Homo sapiens ubiquitin B (UBB), mRNA(IPI00796007); 18 kDa protein(IPI00794211); 18 kDa protein(IPI00796600); 25 kDa protein(IPI00790633); 19 kDa protein(IPI00797400); 19 kDa protein(IPI00793810); 16 kDa protein(IPI00789823); 30 kDa protein(IPI00789107); 44 kDa protein(IPI00743241); 44 kDa protein(IPI00743650); 44 kDa protein(IPI00744274); 26 kDa protein(IPI00794205); 12 kDa protein(IPI00798155); 12 kDa protein(IPI00793330); Similar to Ribosomal protein S27a(IPI00418813); ubiquitin and ribosomal protein L40 precursor(IPI00456429); ubiquitin and ribosomal protein S27a precursor(IPI00179330); Ubiquitin C(IPI00792139);
73	IPI00216134.3	O15513	7168	TPM1	Alpha-tropomyosin	11.3	0 (3)	cytoplasm	structure	Tropomyosin 1 alpha variant 6(IPI00384369); cDNA FLJ52936, weakly similar to Tropomyosin alpha-4 chain(IPI00910322); Isoform 1 of Tropomyosin alpha-4 chain(IPI00010779); Putative uncharacterized protein DKFZp686J1372(IPI00642042); Isoform 3 of Tropomyosin alpha-3 chain(IPI00218320); tropomyosin 3 isoform 5(IPI00477649); Isoform 2 of Tropomyosin alpha-3 chain(IPI00218319); Tropomyosin 3(IPI00382894); tropomyosin 3 isoform 4(IPI00479185); Isoform 2 of Tropomyosin alpha-1 chain(IPI00745267); Tropomyosin isoform(IPI00018853); Isoform 3 of Tropomyosin alpha-1 chain(IPI00216135); Isoform 4 of Tropomyosin alpha-1 chain(IPI00296039); CDNA FLJ26372 fis, clone HRT06233(IPI00442894); Tropomyosin 3(IPI00854592); cDNA FLJ35371 fis, clone SKMUS2001740, highly similar to TROPOMYOSIN ALPHA CHAIN, SKELETAL MUSCLE TYPE(IPI00645055); Isoform 3 of Tropomyosin beta chain(IPI00218820); tropomyosin 1 alpha chain isoform 2(IPI00000230); Isoform 1 of Tropomyosin beta
74	IPI00005614.6	O60837	6711	SPTBN1	Spectrin beta chain, brain 1	2	0 (3)	cytoplasm	structure	276 kDa protein(IPI00871932); Isoform 2 of Spectrin beta chain, brain 1(IPI00333015); Isoform Short of Spectrin beta chain, brain 1(IPI00328230);
75	IPI00909642.1	P21333	2316	FLNA	Filamin-A	2.4	0 (3)	cytoplasm	structure	Filamin A, alpha(IPI00644576); Isoform 2 of Filamin-A(IPI00302592); Isoform 1 of Filamin-A(IPI00333541);
76	IPI00005996.1	Q1M182	8091	HMGA2	HMGA2f	37.6	0 (3)	nucleus	DNA binding	6 kDa protein(IPI00793762); HMGA2d(IPI00759667); HMGA2c'(IPI00902434); high mobility group AT-hook 2 isoform b(IPI00845492); HMGA2e(IPI00759481);
77	IPI00790304.1	P21796	7416	VDAC1	Voltage-dependent anion-selective c	20.7	0 (3)	mitochondria	transport	Voltage-dependent anion-selective channel protein 1(IPI00216308); Similar to Voltage-dependent anion-selective channel protein 1(IPI00847300); cDNA FLJ57715, highly similar to
78	IPI00744706.2	Q13186	6709	SPTAN1	Spectrin alpha chain, brain	1.3	0 (3)	cytoplasm	protein binding	Isoform 3 of Spectrin alpha chain, brain(IPI00843765); Isoform 1 of Spectrin alpha chain, brain(IPI00844215); Isoform 2 of Spectrin alpha chain, brain(IPI00871535); Putative uncharacterized protein SPTAN1(IPI00879810); Putative uncharacterized protein
79	IPI00020984.2	P27824	821	CANX cDNA FLJ555	Calnexin	4	1 (3)	ER membrane	protein folding	Calnexin (Fragment)(IPI00383227); 32 kDa protein(IPI00477719);

80	IPI00017334.1	P35232	5245	PHB	Prohibitin	13.6	0 (3)	mitochondria	DNA binding	Prohibitin variant (Fragment)(IPI00791634); 23 kDa protein(IPI00793658); Putative uncharacterized protein PHB(IPI00793442);
81	IPI00383539.4	O75390	1431	CS cDNA FLJ38537	Citrate synthase, mitochondrial	13.3	0 (3)	mitochondria	metabolism	48 kDa protein(IPI00793839); Citrate synthase, mitochondrial(IPI00025366); 9 kDa protein(IPI00795682); 12 kDa protein(IPI00791211); 16 kDa protein(IPI00791780); 16 kDa protein(IPI00795080); 7 kDa protein(IPI00792509); 30 kDa
82	IPI00025874.2	P04843	6184	RPN1	Dolichyl-diphosphooligosaccharide--	7.6	2 (3)	ER/Golgi	metabolism	5 kDa protein(IPI00793589);
83	IPI00297084.7	O43244	1650	DDOST	Dolichyl-diphosphooligosaccharide--	9	1 (3)	ER membrane	metabolism	cDNA FLJ52929, highly similar to Dolichyl-diphosphooligosaccharide--proteinglycosyltransferase 48 kDa subunit(IPI00910419);
84	IPI00297211.1	O60264	8467	SMARCA5	SWI/SNF-related matrix-associated a	3.4	2 (3)	nucleus	DNA binding	SWI/SNF related, matrix associated, actin dependent regulator of chromatin, subfamily a, member 1(IPI00647510); Isoform 2 of Probable global transcription activator SNF2L1(IPI00646130); Isoform 1 of Probable global transcription activator
85	IPI00027252.6	P35232	11331	PHB2	Prohibitin	12.7	1 (3)	mitochondria	DNA binding	cDNA FLJ56579, highly similar to Prohibitin-2(IPI00797822);
86	IPI00646719.1	Q53G00	84061	MAGT1	Magnesium transporter protein 1	14.8	0 (2)	ER membrane	transport	hypothetical protein(IPI00515117); cDNA FLJ56344, highly similar to Implantation-associated protein(IPI00301202);
87	IPI00908762.1	Q08380	3959	cDNA FLJ53509	Galectin-3-binding protein	6.1	0 (2)	unknown	signal transduction	cDNA FLJ54583, highly similar to Galectin-3-binding protein(IPI00902654); similar to lectin, galactoside-binding, soluble, 3 binding protein(IPI00887555); Galectin-3-binding
88	IPI00414005.2	P05023	476	ATP1A1	Sodium/potassium-transporting ATPa	4.1	0 (2)	membrane	transport	Potassium-transporting ATPase alpha chain 1(IPI00218919); ATPase, Na+/K+ transporting, alpha 1 polypeptide(IPI00646182); Isoform Long of Sodium/potassium-transporting ATPase subunit alpha-1(IPI00006482); cDNA FLJ53737, highly similar to Sodium/potassium-transporting ATPase alpha-2 chain(IPI00911028); ATPase, Na+/K+ transporting, alpha 2 (+) polypeptide(IPI00640401); Sodium/potassium-transporting ATPase subunit alpha-3(IPI00302840); Sodium/potassium-transporting ATPase subunit alpha-2(IPI00003021); Na+/K+-ATPase alpha 3
89	IPI00186338.1	O75531	8815	LOC645870	Barrier-to-autointegration factor	44.2	0 (2)	nucleus	unknown	Barrier-to-autointegration factor(IPI00026087);
90	IPI00019385.3	P51571	6748	SSR4	Translocon-associated protein subun	22.8	1 (2)	ER membrane	protein transport	Protein(IPI00646864); Putative uncharacterized protein SSR4(IPI00647421);
91	IPI00398982.1	P07437	203068	TUBB	Tubulin beta chain	24.5	0 (2)	cytoplasm	structure	cDNA FLJ53012, highly similar to Tubulin beta-7 chain(IPI00909140); cDNA FLJ52029, highly similar to Tubulin beta-7 chain(IPI00908398); Tubulin, beta(IPI00647896); cDNA FLJ11352 fis, clone HEMBA1000020, highly similar to Tubulin beta-2C chain(IPI00911016); Tubulin, beta polypeptide(IPI00645452); Tubulin beta chain(IPI00011654); Tubulin beta-2C chain(IPI00007752); Tubulin beta-2A chain(IPI00013475); Tubulin beta-2B chain(IPI00031370); cDNA FLJ56903, highly similar to Tubulin beta-7 chain(IPI00910813); cDNA FLJ52536, highly similar to Tubulin beta-4 chain(IPI00909781); cDNA FLJ52847, highly similar to Tubulin beta-6 chain(IPI00647682); 35 kDa protein(IPI00644620); cDNA FLJ53341, highly similar to Tubulin beta-4 chain(IPI00910742); cDNA FLJ53063, highly similar to Tubulin beta-7 chain(IPI00908770); cDNA FLJ77784(IPI00640115); 43 kDa protein(IPI00643158); 46 kDa protein(IPI00641706); cDNA FLJ52712, highly similar to Tubulin beta-6 chain(IPI00908469);
92	IPI00552772.2	Q15K36	81502	HM13	Signal peptide peptidase beta	10.7	0 (2)	ER membrane	signal transduction	Isoform 1 of Minor histocompatibility antigen H13(IPI00152441); Isoform 3 of Minor histocompatibility antigen H13(IPI00220688); Isoform 4 of Minor histocompatibility antigen H13(IPI00329296);
93	IPI00879747.1	O75477	10613	ERLIN1	Erlin-1	15.6	0 (2)	ER membrane	unknown	ER lipid raft associated 1(IPI00007940); Isoform 1 of Erlin-2(IPI00026942); 15 kDa protein(IPI00793890); Isoform 2 of Erlin-2(IPI00386655); Isoform 3 of Erlin-2(IPI00384365);
94	IPI00329025.1	Q8N5M9	84522	JAGN1	Protein jagunal homolog 1	18	0 (2)	ER membrane	transport	GL009(IPI00387005);

95	IPI00913922.1	A0JLU0	6949	TCOF1	TCOF1 protein	2.1	0 (2)	nucleus	DNA binding	Isoform 2 of Treacle protein(IPI00298696); Treacher Collins-Franceschetti syndrome 1 isoform a(IPI00165041); Treacher Collins-Franceschetti syndrome 1 isoform e(IPI00914061); Isoform 1 of Treacle protein(IPI00815731); Isoform 3 of Treacle
96	IPI00887976.1	P62906	4736	RPL10A	60S ribosomal protein L10a	21.8	0 (2)	cytoplasm	metabolism	60S ribosomal protein L10a(IPI00412579); 25 kDa protein(IPI00827508);
97	IPI00386010.1	P52815	6182	MRPL12 5C5	39S ribosomal protein L12, mitochon	14	0 (2)	mitochondria	RNA binding	39S ribosomal protein L12, mitochondrial(IPI00005537);
98	IPI00329352.3	P78421	23420	NOMO1;NOMO3	Nodal modulator 1	4.5	0 (2)	membrane	protein binding	Isoform 2 of Nodal modulator 2(IPI00333985); Nodal modulator 3(IPI00872411); 139 kDa protein(IPI00413732); Isoform 1 of Nodal modulator 2(IPI00465432); nodal modulator 2(IPI00888809);
99	IPI00830089.1	P08918	7112	TMPO	Lamina-associated polypeptide 2, iso	11.7	0 (2)	nucleus	DNA binding	Isoform Gamma of Lamina-associated polypeptide 2, isoforms beta/gamma(IPI00181409); Lamina-associated polypeptide 2, isoforms beta/gamma variant (Fragment)(IPI00873716); 46 kDa protein(IPI00791301); Isoform Beta of Lamina-associated polypeptide 2, isoforms beta/gamma(IPI00030131); Lamina-
100	IPI00791448.1	P05388	6175	RPLP0	60S acidic ribosomal protein P0	28.4	0 (2)	cytoplasm	RNA binding	60S acidic ribosomal protein P0(IPI00008530); 60S acidic ribosomal protein P0(IPI00556485);
101	IPI00910449.1	Q14398	2804	cDNA FLJ54378	Golgin subfamily B member 1	2.9	0 (2)	ER/Golgi	protein transport	cDNA FLJ56563, highly similar to Golgin subfamily B member 1 (Fragment)(IPI00909600); Golgin subfamily B member 1(IPI00004671); Golgin B1(IPI00796891); 19 kDa
102	IPI00018248.1	A4D2P4	11014	KDELR2	ER lumen protein retaining receptor	24.1	1 (2)	ER membrane	protein binding	4 kDa protein(IPI00894313); KDEL receptor 2 isoform 2(IPI00450783);
103	IPI00414696.1	P22626	3181	HNRNPA2B1	Heterogeneous nuclear ribonucleopr	4.4	0 (2)	nucleus	DNA binding	Isoform B1 of Heterogeneous nuclear ribonucleoproteins A2/B1(IPI00396378); cDNA FLJ75945, highly similar to Homo sapiens heterogeneous nuclear ribonucleoprotein A2/B1
104	IPI00738259.2	P12532	1159	LOC731391;LOC649	Creatine kinase, ubiquitous mitochon	23.1	0 (2)	mitochondria	unknown	Creatine kinase, ubiquitous mitochondrial(IPI00658109); cDNA FLJ50967, highly similar to Creatine kinase, ubiquitous mitochondrial(IPI00877726);
105	IPI00019329.1	P63167	8655	DYNLL1	Dynein light chain 1, cytoplasmic	32.6	0 (2)	cytoplasm	protein transport	Dynein light chain 2, cytoplasmic(IPI00062037);
106	IPI00909375.1	Q15363	10959	cDNA FLJ52154	Transmembrane emp24 domain-cont	19.9	0 (2)	membrane	protein transport	cDNA FLJ52153, highly similar to Transmembrane emp24 domain-containing protein 2(IPI00797864); Transmembrane emp24 domain containing protein 2(IPI00016608);
107	IPI00816836.1	P11169	6515	SLC2A3	Solute carrier family 2, facilitated glu	22.8	0 (2)	membrane	transport	Solute carrier family 2, facilitated glucose transporter member 3(IPI00003909); 54 kDa protein(IPI00872343); Isoform 2 of Solute carrier family 2, facilitated glucose transporter member 14(IPI00607720); Isoform 1 of Solute carrier family 2, facilitated
108	IPI00029046.1	Q14165	9761	KIAA0152	Malectin	10.6	1 (2)	membrane	unknown	16 kDa protein(IPI00798088);
109	IPI00028116.1	P24390	10945	KDELR1	ER lumen protein retaining receptor	24.1	1 (2)	ER membrane	protein binding	ER lumen protein retaining receptor(IPI00074234);
110	IPI00008998.3	A0PJA1	51495	PTPLAD1	Protein tyrosine phosphatase-like pro	6.1	1 (2)	membrane	protein binding	cDNA FLJ54138, highly similar to Homo sapiens butyrate-induced transcript 1 (HSPC121), mRNA(IPI00787433);
111	IPI00385459.1	O60725	23463	ICMT	Protein-S-isoprenylcysteine O-methyl	17.2	0 (1)	ER membrane	metabolism	Protein-S-isoprenylcysteine O-methyltransferase(IPI00031458);
112	IPI00878392.1	P35268	6146	RPL22	60S ribosomal protein L22	15.8	0 (1)	cytoplasm	RNA binding	60S ribosomal protein L22(IPI00219153);
113	IPI00100656.3	O75350	9524	GPSN2	Synaptic glycoprotein SC2	12	0 (1)	ER membrane	metabolism	cDNA FLJ36768 fis, clone ADIPS1000064, highly similar to Synaptic glycoprotein SC2(IPI00644037);
114	IPI00304331.2	O94766	26229	B3GAT3	Galactosylgalactosylxylosylprotein 3-	10.7	0 (1)	ER/Golgi	metabolism	B3GAT3 protein (Fragment)(IPI00477470);
115	IPI00026167.5	P55769	4809	NHP2L1	NHP2-like protein 1	9.4	0 (1)	nucleus	RNA binding	NHP2 non-histone chromosome protein 2-like 1(IPI00893746);
116	IPI00375407.1	Q96HY6	65992	DDRGK1	Uncharacterized protein C20orf116	8.6	0 (1)	unknown	unknown	Isoform 1 of Uncharacterized protein C20orf116(IPI00028387);
117	IPI00748317.2	O95720	6510	SLC1A5 cDNA FLJ5	Neutral amino acid transporter B(0)	8.3	0 (1)	membrane	metabolism	Neutral amino acid transporter B(0)(IPI00019472);
118	IPI00641334.2	O43169	80777	CYB5B	Cytochrome b5 type B	8.2	0 (1)	mitochondria	Electron transport	cytochrome b5 outer mitochondrial membrane precursor(IPI00303954);
119	IPI00791367.1	P23284	5479	PPIB	Peptidyl-prolyl cis-trans isomerase B	7.3	0 (1)	ER/Golgi	protein folding	peptidylprolyl isomerase B precursor(IPI00646304);
120	IPI00910147.1	Q92504	7922	SLC39A7	solute carrier family 39	7	0 (1)	membrane	transport	Zinc transporter SLC39A7(IPI00021888);
121	IPI00412487.4	O94832	4642	MYO1D	Myosin-Id	6	0 (1)	cytoplasm	nucleotide binding	Isoform 1 of Myosin-Id(IPI00329719);
122	IPI00552214.1	P50402	2010	EMD	Emerin	5.5	0 (1)	nucleus	protein binding	Emerin(IPI00032003);

123	IPI00873484.1	P52907	829	CAPZA1	F-actin-capping protein subunit alph	5.4	0 (1)	cytoplasm	structure	F-actin-capping protein subunit alpha-1(IPI00005969);
124	IPI00216858.3	O14912	6641	SNTB1	Beta-1-syntrophin	4.7	0 (1)	membrane	signal transduction	Isoform 1 of Beta-1-syntrophin(IPI00026059);
125	IPI00448792.1	O75331	1522	CTSZ	Cathepsin Z	3.4	0 (1)	ER/Golgi	metabolism	Cathepsin Z(IPI00002745);
126	IPI00556260.1	Q08945	6749	SSRP1	FACT complex subunit SSRP1	2.6	0 (1)	nucleus	DNA binding	FACT complex subunit SSRP1(IPI00005154);
127	IPI00872971.1	O75787	10159	ATP6AP2	Renin receptor	11.8	0 (1)	membrane	protein binding	Protein(IPI00642797); Renin receptor(IPI00168884);
128	IPI00792159.1	P36578	6124	RPL4	60S ribosomal protein L4	10.7	0 (1)	cytoplasm	RNA binding	cDNA FLJ50996, highly similar to 60S ribosomal protein L4(IPI00795303); 60S ribosomal protein L4(IPI00003918);
129	IPI00639797.1	Q5H927	3028	HSD17B10	Hydroxysteroid (17-beta) dehydroger	10.1	0 (1)	mitochondria	metabolism	Isoform 2 of 3-hydroxyacyl-CoA dehydrogenase type-2(IPI00336094); Isoform 1 of 3-hydroxyacyl-CoA dehydrogenase type-2(IPI00017726);
130	IPI00910360.1	P14625	7184	HSP90B1	Endoplasmin	9.8	0 (1)	ER membrane	RNA binding	cDNA FLJ58626, highly similar to Endoplasmin(IPI00908897); Endoplasmin(IPI00027230);
131	IPI00643781.1	O00256	11168	PSIP1	PC4 and SFRS1-interacting protein	2.7	0 (1)	cytoplasm	DNA binding	Isoform 2 of PC4 and SFRS1-interacting protein(IPI00333317); Isoform 1 of PC4 and SFRS1-interacting protein(IPI00028122);
132	IPI00479823.1	Q05DG0	51773	RSF1	RSF1 protein	2.7	0 (1)	nucleus	RNA binding	Isoform 2 of Remodeling and spacing factor 1(IPI00514411); remodeling and spacing factor 1(IPI00290652);
133	IPI00479587.3	A2VCQ6	23005	WDR62	MAFK protein	1	0 (1)	unknown	RNA binding	WD repeat domain62 isoform 2(IPI00470483); WD repeat domain 62 isoform 1(IPI00794521);
134	IPI00016621.7	O75403	161	AP2A2	AP-2 complex subunit alpha-2	1	0 (1)	membrane	protein transport	Isoform B of AP-2 complex subunit alpha-1(IPI00256684); Isoform A of AP-2 complex subunit alpha-1(IPI00304577);
135	IPI00789405.1	P55268	3913	LAMB2	Laminin subunit beta-2	14.6	0 (1)	membrane	signal transduction	21 kDa protein(IPI00796322); Laminin subunit beta-2(IPI00296922); Similar to S-laminin(IPI00743203);
136	IPI00471928.5	P25705	498	ATP5A1 cDNA FLJ5	ATP synthase subunit alpha, mitocho	9.6	0 (1)	mitochondria	Electron transport	18 kDa protein(IPI00641249); 23 kDa protein(IPI00549805); ATP synthase subunit alpha, mitochondrial(IPI00440493);
137	IPI00376039.3	P62241	6202	RPS8	40S ribosomal protein S8	8.2	0 (1)	cytoplasm	metabolism	Ribosomal protein S8(IPI00645201); 40S ribosomal protein S8(IPI00216587); 25 kDa protein(IPI00872430);
138	IPI00796792.1	Q07157	7082	TJP1	Tight junction protein ZO-1	3.4	0 (1)	membrane	structure	Isoform Short of Tight junction protein ZO-1(IPI00335824); Putative uncharacterized protein DKFZp686A1195(IPI00795990); Isoform Long of Tight junction protein ZO-1(IPI00216219);
139	IPI00744135.2	A1A5C4	6238	RRBP1	RRBP1 protein	1.3	0 (1)	ER membrane	protein transport	Isoform 1 of Ribosome-binding protein 1(IPI00220967); Isoform 3 of Ribosome-binding protein 1(IPI00215743); p180/ribosome receptor(IPI00856098);
140	IPI00909831.1	A2I9Y7	7157	Tp53, cDNA FLJ509	Tumor protein p53	14.7	0 (1)	mitochondria	DNA binding	Cellular tumor antigen p53 (Fragment)(IPI00902894); tumor protein p53 isoform b(IPI00654847); tumor protein p53 isoform c(IPI00375319); Isoform 1 of Cellular tumor antigen
141	IPI00641244.1	P35703	5052	PRDX1	Peroxiredoxin-1	11.3	0 (1)	cytoplasm	protein binding	19 kDa protein(IPI00640741); cDNA FLJ60461, highly similar to Peroxiredoxin-2(IPI00909207); Peroxiredoxin-2(IPI00027350); Peroxiredoxin-1(IPI00000874);
142	IPI00903278.1	P07029	3184	HNRNPD	Heterogeneous nuclear ribonucleopr	4.9	0 (1)	nucleus	DNA binding	Isoform 4 of Heterogeneous nuclear ribonucleoprotein D0(IPI00220685); Isoform 3 of Heterogeneous nuclear ribonucleoprotein D0(IPI00220684); Isoform 2 of Heterogeneous nuclear ribonucleoprotein D0(IPI00220683); Isoform 1 of
143	IPI00455531.2	A6NLE7	7417	LOC729317;VDAC2	Uncharacterized protein	4.1	0 (1)	mitochondria	transport	similar to voltage-dependent anion channel(IPI00737171); Isoform 3 of Voltage-dependent anion-selective channel protein 2(IPI00216026); Isoform 1 of Voltage-dependent anion-selective channel protein 2(IPI00902560); Voltage-dependent anion-
144	IPI00514561.1	P61978	3190	HNRNPK	Heterogeneous nuclear ribonucleopr	4	0 (1)	nucleus	DNA binding	cDNA FLJ54552, highly similar to Heterogeneous nuclear ribonucleoprotein K(IPI00910458); Isoform 3 of Heterogeneous nuclear ribonucleoprotein K(IPI00807545); Isoform 1 of Heterogeneous nuclear ribonucleoprotein K(IPI00216049); Isoform
145	IPI00177716.7	P10910	3159	HMGA1	High mobility group protein HMG-I/	8.3	0 (1)	nucleus	DNA binding	Isoform HMG-I of High mobility group protein HMG-I/HMG-Y(IPI00179700); HMGA1 protein(IPI00450855); similar to high mobility group protein(IPI00889188); Isoform HMG-R of High mobility group protein HMG-I/HMG-Y(IPI00746310); cDNA FLJ54188, moderately similar to High mobility group protein

146	IPI00791315.1	Q00325	5250	SLC25A3	Phosphate carrier protein, mitochonc	6.3	0 (1)	mitochondria	transport	24 kDa protein(IPI00793177); 31 kDa protein(IPI00788624); Isoform B of Phosphate carrier protein, mitochondrial(IPI00215777); cDNA FLJ90278 fis, clone NT2RP1000325, highly similar to Phosphate carrier protein, mitochondrialprecursor(IPI00790115); Isoform A of Phosphate
147	IPI00797644.1	Q15656	10342	TFG	TRK-fused gene protein	7.8	0 (1)	cytoplasm	nucleotide binding	18 kDa protein(IPI00790186); 18 kDa protein(IPI00790804); TFG protein(IPI00796921); Putative MAPK activating protein(IPI00788849); Protein TFG(IPI00294619); Tyrosine-protein
148	IPI00902526.1	Q02543	6142	RPL18A	60S ribosomal protein L18a	5.9	0 (1)	cytoplasm	metabolism	cDNA FLJ51502, highly similar to 60S ribosomal protein L18a(IPI00909746); cDNA FLJ51501, highly similar to 60S ribosomal protein L18a(IPI00847774); similar to ribosomal protein L18a isoform 2(IPI00739109); Putative uncharacterized protein ENSP00000383883(IPI00036267); 60S ribosomal protein L18a(IPI00026202); similar to ribosomal protein L18a isoform
149	IPI00646871.3	O75032	26038	CHD5	Chromodomain-helicase-DNA-bindin	2.2	0 (1)	nucleus	DNA binding	Putative uncharacterized protein CHD5(IPI00444866); Isoform 1 of Chromodomain-helicase-DNA-binding protein 4(IPI00000846); Isoform 2 of Chromodomain-helicase-DNA-binding protein 4(IPI00455210); Chromodomain-helicase-DNA-binding protein 5(IPI00152535); Isoform 2 of Chromodomain-helicase-DNA-binding protein 3(IPI00411592); Isoform 1 of Chromodomain-helicase-DNA-binding protein 3(IPI00373870); chromodomain
150	IPI00006437.2	O15347	3149	HMG4L	High mobility group protein B3	10	0 (1)	nucleus	DNA binding	Non-histone chromosomal protein(IPI00411540); 21 kDa protein(IPI00643317); 22 kDa protein(IPI00640781); High mobility group protein B3(IPI00217477); similar to high-mobility group box 3(IPI00374293); similar to high-mobility group box 3(IPI00787656); similar to high-mobility group box 3(IPI00376756); similar to high-mobility group box 3(IPI00888596);
151	IPI00173589.2	P47914	6159	RPL29	60S ribosomal protein L29	9.7	0 (1)	cytoplasm	metabolism	hypothetical protein(IPI00454907); similar to ribosomal protein L29(IPI00888051); 60S ribosomal protein L29(IPI00419919); cDNA FLJ78093, highly similar to Homo sapiens ribosomal protein L29 (RPL29), mRNA(IPI00796934); Novel protein similar to ribosomal protein L29 RPL29(IPI00644657); similar to hCG1641491 isoform 2(IPI00052885); hypothetical protein(IPI00792336); 27 kDa
152	IPI00795725.1	P05787	3856	KRT8	Keratin, type II cytoskeletal 8	6.1	0 (1)	cytoplasm	protein binding	25 kDa protein(IPI00792642); 27 kDa protein(IPI00793917);cytokeratin [Homo sapiens](gi|1419564|gnl|PID|e251594);cytokeratin 8 (279 AA) [Homo sapiens](gi|30313);cytokeratin 8 [Homo sapiens](gi|307083);8 (version 1) - human gi|181573 (M34482) cytokeratin 8 [Homo sapiens](gi|87303|pir||JS0487);8 (version 2) - human(gi|105815|pir||A34720);cytokeratin 8 [Homo sapiens](gi|181400);8 - human gi|400416 (X74929) Keratin 8 [Homo sapiens] gi|1673575 (U76549) [org=human] human cytokeratin 8 [Homo sapiens](gi|2119212|pir||I37982);TYPE II CYTOSKELETAL 8 (CYTOKERATIN 8) (K8) (CK 8)(gi|2506774|sp|P05787|K2C8_HUMAN); Keratin, type II

Supplementary Table S1B. List of 68 proteins annotated by GO and mitochondrial proteome databases

num	IPI	EntrezID	Sym	localization	GO_CC_MITO	MitoCarta	MitoMiner	MitoProteome	MitoRes	pTarget (in-silico)	PA-SUB (in-silico)	SherLoc2 (in-silico)	Summary
1	IPI00453473	8294	HIST4H4	nucleus	X	X	X	X	X	X	X	X	
2	IPI00550239	3005	H1F0	nucleus	X	X	X	X	X	X	X	X	
3	IPI00783271	10128	LRPPRC	mitochondria	O	O	O	O	X	X	O	O	1
4	IPI00021924	8971	H1FX	nucleus	X	X	X	X	X	X	X	X	
5	IPI00008529	6181	RPLP2	cytoplasm	X	X	X	X	X	X	X	X	
6	IPI00024976	56993	TOMM22	mitochondria	O	O	O	O	O	X	O	X	1
7	IPI00221222	10923	SUB1	nucleus	X	X	X	X	X	X	X	X	
8	IPI00425902	6746	SSR2	ER membrane	X	X	X	X	X	X	X	X	
9	IPI00007188	292	SLC25A5P8	mitochondria	O	O	O	O	O	X	O	X	1
10	IPI00025974	128866	CHMP4B	cytoplasm	X	X	X	X	X	X	X	X	
11	IPI00029744	6742	SSBP1	mitochondria	O	O	O	O	O	O	O	O	1
12	IPI00396321	55379	LRRC59	ER membrane	O	X	X	X	X	X	X	X	1
13	IPI00027107	7284	TUFM	mitochondria	O	O	O	O	O	O	O	O	1
14	IPI00328170	7841	MOGS	ER membrane	X	X	X	X	X	X	X	O	1
15	IPI00297492	3703	STT3A	ER membrane	X	X	X	X	X	X	X	X	
16	IPI00026970	11198	SUPT16H	membrane	X	X	X	X	X	X	X	X	
17	IPI00166865	493856	CISD2	mitochondria	O	X	X	X	X	X	X	X	1
18	IPI00018855	527	ATP6V0C	membrane	X	X	X	X	X	O	O	X	1
19	IPI00386294	1E+08	TOMM6	mitochondria	O	X	X	X	X	X	X	X	1
20	IPI00220835	10952	SEC61B	ER membrane	X	X	X	X	X	X	X	X	
21	IPI00021785	1329	COX5B	mitochondria	O	O	O	O	O	O	O	O	1
22	IPI00739464	71	ACTG1	cytoplasm	X	X	X	X	X	X	X	O	1
23	IPI00220739	10857	PGRMC1	ER membrane	X	X	X	X	X	X	X	X	
24	IPI00220362	3336	HSPE1	mitochondria	O	O	O	O	O	O	O	O	1
25	IPI00009407	1603	DAD1	ER membrane	X	X	X	X	X	X	X	X	
26	IPI00024920	513	ATP5D	mitochondria	O	O	O	O	O	O	O	O	1
27	IPI00009368	94081	SFXN1	mitochondria	O	O	O	O	O	O	O	O	1
28	IPI00009235	6747	SSR3	ER membrane	X	X	X	X	X	X	X	X	
29	IPI00016339	5878	RAB5C	membrane	X	X	X	X	X	X	X	X	
30	IPI00006865	26984	SEC22B	ER membrane	X	X	X	X	X	X	X	O	1
31	IPI00784154	3329	HSPD1P1	mitochondria	O	O	O	O	O	O	O	O	1
32	IPI00798360	84324	CIP29	nucleus	X	X	X	X	X	X	X	X	
33	IPI00257903	79956	ERMP1	ER membrane	X	X	X	X	X	X	X	X	

34	IPI00298281	3915	LAMC1	membrane	X	X	X	X	X	O	X	X	1
35	IPI00015911	1738	DLD	mitochondria	O	O	O	O	O	O	O	O	1
36	IPI00328715	92140	MTDH	membrane	X	X	X	X	X	X	X	X	
37	IPI00017592	3954	LETM1	mitochondria	O	O	O	O	O	O	O	O	1
38	IPI00031522	3030	HADHA	mitochondria	O	O	O	O	O	O	O	O	1
39	IPI00218922	11231	SEC63	ER membrane	X	X	X	X	X	X	X	X	
40	IPI00007858	8735	MYH13	cytoplasm	X	X	X	X	X	O	X	X	1
41	IPI00024284	3339	HSPG2	membrane	X	X	X	X	X	X	X	O	1
42	IPI00019502	4627	MYH9	cytoplasm	X	X	X	X	X	O	X	X	1
43	IPI00016801	2746	GLUD1	mitochondria	O	O	O	O	O	O	O	O	1
44	IPI00217465	3006	HIST1H1C	nucleus	X	X	X	X	X	X	X	X	
45	IPI00081836	8329	HIST1H2AG	nucleus	X	X	X	X	X	O	X	X	1
46	IPI00021439	60	ACTB	cytoplasm	X	X	X	X	X	X	X	X	
47	IPI00003935	8349	HIST2H2BE	nucleus	X	X	X	X	X	X	X	X	
48	IPI00449049	142	PARP1	nucleus	X	X	X	X	X	X	X	X	
49	IPI00296337	5591	PRKDC	nucleus	X	X	X	X	X	X	X	X	
50	IPI00007765	3313	HSPA9	mitochondria	O	O	O	O	X	O	O	O	1
51	IPI00383680	6185	RPN2	ER/Golgi	X	X	X	X	X	O	X	O	1
52	IPI00303476	506	ATP5B	mitochondria	O	O	O	O	O	O	O	O	1
53	IPI00604713	10970	CKAP4	ER membrane	X	X	X	X	X	X	X	O	1
54	IPI00871391	7520	XRCC5	cytoplasm	X	X	X	X	X	O	X	X	1
55	IPI00465070	8350	HIST1H3A	nucleus	X	X	X	X	X	X	X	X	
56	IPI00220573	10627	MYL12A	cytoplasm	X	X	X	X	X	O	X	X	1
57	IPI00604476	29927	SEC61A1	ER membrane	O	X	X	X	X	X	X	O	1
58	IPI00455383	1213	CLTC	mitochondria	O	X	X	X	X	X	X	X	1
59	IPI00792677	10376	TUBA1B	cytoplasm	X	X	X	X	X	X	X	X	
60	IPI00413611	7150	TOP1	cytoplasm	X	X	X	X	X	O	X	X	1
61	IPI00299024	10409	BASP1	membrane	X	X	X	X	X	X	X	X	
62	IPI00514204	4000	LMNA	nucleus	X	X	X	X	X	X	X	X	
63	IPI00414101	7153	TOP2A	nucleus	X	X	X	X	X	X	X	X	
64	IPI00413922	4637	MYL6	cytoplasm	X	X	X	X	X	X	X	X	
65	IPI00470805	9656	MDC1	nucleus	X	X	X	X	X	X	X	O	1
66	IPI00218200	10134	BCAP31	ER membrane	X	X	X	X	X	X	X	X	
67	IPI00014230	708	C1QBP	mitochondria	O	O	O	O	O	O	O	O	1
68	IPI00790831	4001	LMNB1	nucleus	X	X	X	X	X	X	X	X	
69	IPI00893179	2547	XRCC6	cytoplasm	X	X	X	X	X	X	X	X	
70	IPI00643708	7019	TFAM	mitochondria	O	O	O	O	O	X	X	O	1

71	IPI00643414	10295	BCKDK	mitochondria	O	O	O	O	O	O	O	O	1
72	IPI00795527	7316	UBC	cytoplasm	X	X	X	X	X	O	X	X	1
73	IPI00216134	7168	TPM1	cytoplasm	X	X	X	X	X	X	X	X	
74	IPI00005614	6711	SPTBN1	cytoplasm	X	X	X	X	X	X	X	X	
75	IPI00909642	2316	FLNA	cytoplasm	X	X	X	X	X	X	X	X	
76	IPI00005996	8091	HMGA2	nucleus	X	X	X	X	X	X	X	X	
77	IPI00790304	7416	VDAC1	mitochondria	O	O	O	O	O	O	O	O	1
78	IPI00744706	6709	SPTAN1	cytoplasm	X	X	X	X	X	X	X	X	
79	IPI00020984	821	CANX	ER membrane	X	X	X	X	X	X	X	X	
80	IPI00017334	5245	PHB	mitochondria	O	O	O	O	X	X	X	X	1
81	IPI00383539	1431	CS	mitochondria	O	O	O	O	O	O	O	O	1
82	IPI00025874	6184	RPN1	ER/Golgi	X	X	X	X	X	X	X	X	
83	IPI00297084	1650	DDOST	ER membrane	X	X	X	X	X	X	X	X	
84	IPI00297211	8467	SMARCA5	nucleus	X	X	X	X	X	X	X	X	
85	IPI00027252	11331	PHB2	mitochondria	O	O	O	O	X	O	O	O	1
86	IPI00646719	84061	MAGT1	ER membrane	X	X	X	X	X	X	X	X	
87	IPI00908762	3959	LGALS3BP	unknown	X	X	X	X	X	X	X	X	
88	IPI00414005	476	ATP1A1	membrane	X	X	X	X	X	X	X	X	
89	IPI00186338	8815	BANF1	nucleus	X	X	X	X	X	X	X	X	
90	IPI00019385	6748	SSR4	ER membrane	X	X	X	X	X	X	X	O	1
91	IPI00398982	203068	TUBB	cytoplasm	X	X	X	X	X	X	X	X	
92	IPI00552772	81502	HM13	ER membrane	X	X	X	X	X	X	X	X	
93	IPI00879747	10613	ERLIN1	ER membrane	X	X	X	X	X	O	X	X	1
94	IPI00329025	84522	JAGN1	ER membrane	X	X	X	X	X	O	X	X	1
95	IPI00913922	6949	TCOF1	nucleus	X	X	X	X	X	X	X	X	
96	IPI00887976	4736	RPL10A	cytoplasm	X	O	O	X	X	O	X	X	1
97	IPI00386010	6182	MRPL12	mitochondria	O	O	O	O	O	O	O	O	1
98	IPI00329352	23420	NOMO1	membrane	X	X	X	X	X	X	X	X	
99	IPI00830089	7112	TMPO	nucleus	X	X	X	X	X	O	X	O	1
100	IPI00791448	6175	RPLP0	cytoplasm	X	X	X	X	X	X	X	O	1
101	IPI00910449	2804	GOLGB1	ER/Golgi	X	X	X	X	X	X	X	O	1
102	IPI00018248	11014	KDELR2	ER membrane	X	X	X	X	X	X	X	X	
103	IPI00414696	3181	HNRNPA2B1	nucleus	X	X	X	X	X	X	X	X	
104	IPI00738259	1159	CKMT1A	mitochondria	O	O	O	O	X	O	O	O	1
105	IPI00019329	8655	DYNLL1	cytoplasm	X	X	X	X	X	X	X	X	
106	IPI00909375	10959	TMED2	membrane	X	X	X	X	X	X	X	X	
107	IPI00816836	6515	SLC2A3	membrane	X	X	X	X	X	X	X	X	

108	IPI00029046	9761	MLEC	membrane	X	X	X	X	X	X	X	X	
109	IPI00028116	10945	KDELR1	ER membrane	X	X	X	X	X	X	X	X	
110	IPI00008998	51495	PTPLAD1	membrane	X	X	X	X	X	X	X	X	
111	IPI00385459	23463	ICMT	ER membrane	X	X	X	X	X	X	X	O	1
112	IPI00878392	6146	RPL22P11	cytoplasm	X	X	X	X	X	X	X	X	
113	IPI00100656	9524	TECR	ER membrane	X	X	X	X	X	X	X	X	
114	IPI00304331	26229	B3GAT3	ER/Golgi	X	X	X	X	X	X	X	X	
115	IPI00026167	4809	NHP2L1	nucleus	X	X	X	X	X	X	X	X	
116	IPI00375407	65992	DDRGK1	unknown	X	X	X	X	X	X	X	X	
117	IPI00748317	6510	SLC1A5	membrane	X	X	X	X	X	X	X	X	
118	IPI00641334	80777	CYB5B	mitochondria	O	O	O	O	X	O	O	O	1
119	IPI00791367	5479	PPIB	ER/Golgi	X	X	X	X	X	X	X	X	
120	IPI00910147	7922	SLC39A7	membrane	X	X	X	X	X	X	X	X	
121	IPI00412487	4642	MYO1D	cytoplasm	X	X	X	X	X	X	X	X	
122	IPI00552214	2010	EMD	nucleus	X	X	X	X	X	X	X	X	
123	IPI00873484	829	CAPZA1	cytoplasm	X	X	X	X	X	X	X	X	
124	IPI00216858	6641	SNTB1	membrane	X	X	X	X	X	X	X	X	
125	IPI00448792	1522	CTSZ	ER/Golgi	X	X	X	X	X	X	X	X	
126	IPI00556260	6749	SSRP1	nucleus	X	X	X	X	X	X	X	X	
127	IPI00872971	10159	ATP6AP2	membrane	X	X	X	X	X	X	O	O	1
128	IPI00792159	6124	RPL4	cytoplasm	X	X	X	X	X	O	X	X	1
129	IPI00639797	3028	HSD17B10	mitochondria	O	O	O	O	X	X	O	O	1
130	IPI00910360	7184	HSP90B1	ER membrane	X	X	X	X	X	X	X	X	
131	IPI00643781	11168	PSIP1	cytoplasm	X	X	X	X	X	X	X	X	
132	IPI00479823	51773	RSF1	nucleus	X	X	X	X	X	X	X	X	
133	IPI00479587	23005	MAPKBP1	unknown	X	X	X	X	X	X	X	O	1
134	IPI00016621	161	AP2A2	membrane	X	X	X	X	X	X	X	X	
135	IPI00789405	3913	LAMB2	membrane	X	X	X	X	X	X	X	O	1
136	IPI00471928	498	ATP5A1	mitochondria	O	O	O	O	O	O	O	O	1
137	IPI00376039	6202	RPS8	cytoplasm	X	X	X	X	X	X	X	O	1
138	IPI00796792	7082	TJP1	membrane	X	X	X	X	X	X	X	X	
139	IPI00744135	6238	RRBP1	ER membrane	X	X	X	X	X	X	X	X	
140	IPI00909831	7157	Tp53	mitochondria	O	X	X	X	X	X	X	X	1
141	IPI00641244	5052	PRDX1	cytoplasm	O	O	O	X	X	X	X	X	1
142	IPI00903278	3184	HNRNPD	nucleus	X	X	X	X	X	X	X	X	
143	IPI00455531	7417	VDAC2	mitochondria	O	O	O	O	O	O	O	O	1
144	IPI00514561	3190	HNRNPK	nucleus	X	X	X	X	X	X	X	X	

145	IPI00177716	3159	HMGA1	nucleus	X	X	X	X	X	X	X	X	
146	IPI00791315	5250	SLC25A3	mitochondria	O	O	O	O	O	O	O	O	1
147	IPI00797644	10342	TFG	cytoplasm	X	X	X	X	X	X	X	O	1
148	IPI00902526	6142	RPL18A	cytoplasm	X	X	X	X	X	X	X	X	
149	IPI00646871	26038	CHD5	nucleus	X	X	X	X	X	X	X	X	
150	IPI00006437	3149	HMG4L	nucleus	X	X	X	X	X	X	X	X	
151	IPI00173589	6159	RPL29	cytoplasm	X	X	X	X	X	X	X	O	1
152	IPI00795725	3856	KRT8	cytoplasm	X	X	X	X	X	X	X	X	

Supplementary Table S1C. GOBPs overrepresented by the identified proteins. Note the 7 cellular processes in different colors: the node colors are same as in Fig. 2.

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment
GOTERM_BP_FAT	GO:0018196~peptidyl-asparagine modification	6	3.947368421	2.11E-08	6184;1650;84061;3703;6185;1603	138	10	13876	60.33043478
GOTERM_BP_FAT	GO:0018279~protein amino acid N-linked glycosylation via asparagine	6	3.947368421	2.11E-08	6184;1650;84061;3703;6185;1603	138	10	13876	60.33043478
GOTERM_BP_FAT	GO:0034728~nucleosome organization	11	7.236842105	3.47E-08	8467;11198;8349;8329;8350;3005;8294;3006;51773;3159;8971	138	96	13876	11.5214372
GOTERM_BP_FAT	GO:0006333~chromatin assembly or disassembly	12	7.894736842	6.72E-08	8467;11198;8349;8329;8350;26038;3005;8294;3006;51773;3159;8971	138	131	13876	9.210753402
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	26	17.10526316	1.69E-07	10952;100188893;2316;3313;821;10959;6238;10945;23463;11014;6748;6747;6746;7184;10134;56993;11231;6711;128866;7157;161;4627;1213;5878;26984;29927	138	784	13876	3.334590358
GOTERM_BP_FAT	GO:0051276~chromosome organization	20	13.15789474	3.93E-07	8349;8329;5245;26038;3005;3006;7153;8091;3159;7157;8467;11198;8350;8294;7520;2547;51773;5591;8971;142	138	495	13876	4.062655541
GOTERM_BP_FAT	GO:0015031~protein transport	25	16.44736842	5.53E-07	10952;100188893;3313;821;10959;6238;10945;23463;11014;6748;6747;6746;7184;10134;56993;11231;6711;128866;7157;161;4627;1213;5878;26984;29927	138	777	13876	3.2352228
GOTERM_BP_FAT	GO:0030069~lysogeny	5	3.289473684	6.17E-07	8815;11168;7520;2547;3159	138	8	13876	62.8442029
GOTERM_BP_FAT	GO:0019047~provirus integration	5	3.289473684	6.17E-07	8815;11168;7520;2547;3159	138	8	13876	62.8442029
GOTERM_BP_FAT	GO:0046907~intracellular transport	23	15.13157895	6.33E-07	56993;10952;11231;6711;3313;2316;7157;513;161;10128;7168;10945;23463;4637;4627;11014;1213;6748;6747;6746;26984;29927;10134	138	670	13876	3.451741294
GOTERM_BP_FAT	GO:0008104~protein localization	27	17.76315789	6.52E-07	10952;100188893;3339;2316;3313;821;10959;6238;10945;23463;11014;6748;6747;6746;7184;10134;56993;11231;6711;128866;7157;161;4627;1213;5878;26984;29927	138	902	13876	3.009833221
GOTERM_BP_FAT	GO:0034621~cellular macromolecular complex subunit organization	17	11.18421053	7.97E-07	56993;8349;8329;2316;3005;3006;3159;10376;3329;8467;11198;8350;8294;203068;7019;51773;8971	138	372	13876	4.595059997

GOTERM_BP_FAT	GO:0006414~translational elongation	10	6.578947368	8.51E-07	6202;6181;6146;6142;6124;7284;4736;7316;6159;6175	138	104	13876	9.668338907
GOTERM_BP_FAT	GO:0006334~nucleosome assembly	9	5.921052632	2.23E-06	8467;8349;8329;8350;3005;8294;3006;51773;8971	138	87	13876	10.4017991
GOTERM_BP_FAT	GO:0006323~DNA packaging	10	6.578947368	2.83E-06	8467;8349;8329;8350;3005;8294;3006;7153;51773;8971	138	120	13876	8.379227053
GOTERM_BP_FAT	GO:0031497~chromatin assembly	9	5.921052632	2.89E-06	8467;8349;8329;8350;3005;8294;3006;51773;8971	138	90	13876	10.05507246
GOTERM_BP_FAT	GO:0034613~cellular protein localization	17	11.18421053	3.75E-06	56993;10952;11231;6711;2316;3313;7157;161;10945;23463;11014;1213;6748;6747;6746;29927;10134	138	419	13876	4.079623673
GOTERM_BP_FAT	GO:0065004~protein-DNA complex assembly	9	5.921052632	4.01E-06	8467;8349;8329;8350;3005;8294;3006;51773;8971	138	94	13876	9.62719704
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	17	11.18421053	4.11E-06	56993;10952;11231;6711;2316;3313;7157;161;10945;23463;11014;1213;6748;6747;6746;29927;10134	138	422	13876	4.050621609
GOTERM_BP_FAT	GO:0006487~protein amino acid N-linked glycosylation	7	4.605263158	4.30E-06	6184;1650;7841;84061;3703;6185;1603	138	44	13876	15.99670619
GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	15	9.868421053	5.11E-06	56993;8349;8329;2316;3005;3006;10376;3329;8467;8350;8294;203068;7019;51773;8971	138	332	13876	4.542954426
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	16	10.52631579	5.50E-06	56993;11231;10952;6711;3313;7157;161;10945;23463;11014;1213;6748;6747;6746;29927;10134	138	382	13876	4.211548676
GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	21	13.81578947	3.66E-05	56993;8349;8329;829;2316;3005;3006;3159;3028;10376;7157;3329;8467;11198;8350;3915;8294;203068;7019;51773;8971	138	738	13876	2.861199482
GOTERM_BP_FAT	GO:0015074~DNA integration	5	3.289473684	3.90E-05	8815;11168;7520;2547;3159	138	20	13876	25.13768116
GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	20	13.15789474	4.45E-05	56993;8349;8329;829;2316;3005;3006;3159;3028;10376;7157;3329;8467;8350;3915;8294;203068;7019;51773;8971	138	687	13876	2.927240892
GOTERM_BP_FAT	GO:0006259~DNA metabolic process	17	11.18421053	5.78E-05	5245;7150;7153;3159;7157;3329;8815;11198;11168;7019;7520;6749;2547;5591;6742;142;9656	138	523	13876	3.268379195
GOTERM_BP_FAT	GO:0019059~initiation of viral infection	5	3.289473684	5.79E-05	8815;11168;7520;2547;3159	138	22	13876	22.85243742

GOTERM_BP_FAT	GO:0006325~chromatin organization	14	9.210526316	1.22E-04	8349;8329;5245;26038;3005;3006;8091;3159;11198;8467;8350;8294;51773;8971	138	388	13876	3.62811893
GOTERM_BP_FAT	GO:0006605~protein targeting	10	6.578947368	2.91E-04	56993;23463;10952;11231;6711;3313;6747;6746;29927;7157	138	216	13876	4.655126141
GOTERM_BP_FAT	GO:0006310~DNA recombination	7	4.605263158	7.31E-04	8815;11168;7520;2547;3159;5591;3329	138	109	13876	6.457385986
GOTERM_BP_FAT	GO:0019058~viral infectious cycle	5	3.289473684	7.61E-04	8815;11168;7520;2547;3159	138	42	13876	11.97032436
GOTERM_BP_FAT	GO:0009180~purine ribonucleoside diphosphate biosynthetic process	3	1.973684211	9.49E-04	513;506;498	138	5	13876	60.33043478
GOTERM_BP_FAT	GO:0006172~ADP biosynthetic process	3	1.973684211	9.49E-04	513;506;498	138	5	13876	60.33043478
GOTERM_BP_FAT	GO:0009188~ribonucleoside diphosphate biosynthetic process	3	1.973684211	9.49E-04	513;506;498	138	5	13876	60.33043478
GOTERM_BP_FAT	GO:0009136~purine nucleoside diphosphate biosynthetic process	3	1.973684211	9.49E-04	513;506;498	138	5	13876	60.33043478
GOTERM_BP_FAT	GO:0006412~translation	12	7.894736842	0.001031686	6182;6238;6202;6181;6146;6142;6124;7284;4736;7316;6159;6175	138	367	13876	3.287762113
GOTERM_BP_FAT	GO:0055085~transmembrane transport	15	9.868421053	0.001321678	56993;506;5250;10952;7416;7417;6515;94081;292;498;6238;513;7922;29927;527	138	562	13876	2.683738202
GOTERM_BP_FAT	GO:0016584~nucleosome positioning	3	1.973684211	0.001414362	8467;3006;51773	138	6	13876	50.27536232
GOTERM_BP_FAT	GO:0046031~ADP metabolic process	3	1.973684211	0.001414362	513;506;498	138	6	13876	50.27536232
GOTERM_BP_FAT	GO:0043413~biopolymer glycosylation	7	4.605263158	0.001819736	6184;1650;7841;84061;3703;6185;1603	138	130	13876	5.414269788
GOTERM_BP_FAT	GO:0070085~glycosylation	7	4.605263158	0.001819736	6184;1650;7841;84061;3703;6185;1603	138	130	13876	5.414269788
GOTERM_BP_FAT	GO:0006486~protein amino acid glycosylation	7	4.605263158	0.001819736	6184;1650;7841;84061;3703;6185;1603	138	130	13876	5.414269788
GOTERM_BP_FAT	GO:0009133~nucleoside diphosphate biosynthetic process	3	1.973684211	0.001967302	513;506;498	138	7	13876	43.0931677
GOTERM_BP_FAT	GO:0030433~ER-associated protein catabolic process	4	2.631578947	0.002315361	10613;10952;7316;7184	138	27	13876	14.89640365
GOTERM_BP_FAT	GO:0006515~misfolded or incompletely synthesized protein catabolic process	4	2.631578947	0.002574617	10613;10952;7316;7184	138	28	13876	14.36438923
GOTERM_BP_FAT	GO:0000723~telomere maintenance	4	2.631578947	0.002574617	7520;2547;5591;142	138	28	13876	14.36438923
GOTERM_BP_FAT	GO:0009179~purine ribonucleoside diphosphate metabolic process	3	1.973684211	0.002606119	513;506;498	138	8	13876	37.70652174
GOTERM_BP_FAT	GO:0009135~purine nucleoside diphosphate metabolic process	3	1.973684211	0.002606119	513;506;498	138	8	13876	37.70652174

GOTERM_BP_FAT	GO:0032200~telomere organization	4	2.631578947	0.002851113	7520;2547;5591;142	138	29	13876	13.86906547
GOTERM_BP_FAT	GO:0006260~DNA replication	8	5.263157895	0.003127076	11198;5245;7150;7019;6749;7153;3159;6742	138	194	13876	4.146421635
GOTERM_BP_FAT	GO:0022415~viral reproductive process	5	3.289473684	0.003257723	8815;11168;7520;2547;3159	138	62	13876	8.108929406
GOTERM_BP_FAT	GO:0006303~double-strand break repair via nonhomologous end joining	3	1.973684211	0.00413451	7520;2547;5591	138	10	13876	30.16521739
GOTERM_BP_FAT	GO:0009185~ribonucleoside diphosphate metabolic process	3	1.973684211	0.00413451	513;506;498	138	10	13876	30.16521739
GOTERM_BP_FAT	GO:0006612~protein targeting to membrane	4	2.631578947	0.004891581	23463;11231;6747;6746	138	35	13876	11.49151139
GOTERM_BP_FAT	GO:0006461~protein complex assembly	13	8.552631579	0.005298727	56993;829;2316;3159;3028;7157;10376;3329;8467;3915;203068;7019;51773	138	519	13876	2.5186116
GOTERM_BP_FAT	GO:0070271~protein complex biogenesis	13	8.552631579	0.005298727	56993;829;2316;3159;3028;7157;10376;3329;8467;3915;203068;7019;51773	138	519	13876	2.5186116
GOTERM_BP_FAT	GO:0016032~viral reproduction	5	3.289473684	0.005300733	8815;11168;7520;2547;3159	138	71	13876	7.081036946
GOTERM_BP_FAT	GO:0009101~glycoprotein biosynthetic process	7	4.605263158	0.005403674	6184;1650;7841;84061;3703;6185;1603	138	162	13876	4.344784398
GOTERM_BP_FAT	GO:0006936~muscle contraction	7	4.605263158	0.006249595	7168;8735;4637;6641;2010;71;60	138	167	13876	4.214701033
GOTERM_BP_FAT	GO:0015986~ATP synthesis coupled proton transport	4	2.631578947	0.007124393	513;506;498;527	138	40	13876	10.05507246
GOTERM_BP_FAT	GO:0015985~energy coupled proton transport; down electrochemical gradient	4	2.631578947	0.007124393	513;506;498;527	138	40	13876	10.05507246
GOTERM_BP_FAT	GO:0033554~cellular response to stress	13	8.552631579	0.007825245	51495;7153;5052;7157;11198;7168;3913;6749;7520;2547;5591;142;9656	138	546	13876	2.394064872
GOTERM_BP_FAT	GO:0000726~non-recombinational repair	3	1.973684211	0.008147604	7520;2547;5591	138	14	13876	21.54658385
GOTERM_BP_FAT	GO:0006281~DNA repair	9	5.921052632	0.009111723	11198;7520;6749;2547;7153;5591;142;9656;7157	138	296	13876	3.057285546
GOTERM_BP_FAT	GO:0045214~sarcomere organization	3	1.973684211	0.00934066	7168;71;60	138	15	13876	20.11014493
GOTERM_BP_FAT	GO:0003012~muscle system process	7	4.605263158	0.00936528	7168;8735;4637;6641;2010;71;60	138	182	13876	3.867335563
GOTERM_BP_FAT	GO:0042110~T cell activation	6	3.947368421	0.010871792	6146;1650;4627;5591;7157;3329	138	135	13876	4.468921095
GOTERM_BP_FAT	GO:0006457~protein folding	7	4.605263158	0.011418502	11231;3313;5479;821;3336;7184;3329	138	190	13876	3.704500381
GOTERM_BP_FAT	GO:0007005~mitochondrion organization	6	3.947368421	0.011877837	6182;3954;56993;7019;6742;7157	138	138	13876	4.371770636
GOTERM_BP_FAT	GO:0006200~ATP catabolic process	3	1.973684211	0.011943546	513;506;498	138	17	13876	17.74424552
GOTERM_BP_FAT	GO:0009132~nucleoside diphosphate metabolic process	3	1.973684211	0.011943546	513;506;498	138	17	13876	17.74424552
GOTERM_BP_FAT	GO:0006754~ATP biosynthetic process	5	3.289473684	0.012542125	513;506;476;498;527	138	91	13876	5.52476509

GOTERM_BP_FAT	GO:0030029~actin filament-based process	8	5.263157895	0.013047209	7168;4637;829;4627;2316;71;60;8655	138	254	13876	3.166951957
GOTERM_BP_FAT	GO:0034220~ion transmembrane transport	4	2.631578947	0.013160119	513;506;498;527	138	50	13876	8.044057971
GOTERM_BP_FAT	GO:0007517~muscle organ development	8	5.263157895	0.014669415	7168;4637;4627;3339;2010;71;60;4000	138	260	13876	3.09386845
GOTERM_BP_FAT	GO:0044087~regulation of cellular component biogenesis	6	3.947368421	0.016093694	7168;829;6711;7316;3159;6709	138	149	13876	4.049022469
GOTERM_BP_FAT	GO:0030705~cytoskeleton-dependent intracellular transport	4	2.631578947	0.01618722	10128;7168;4637;4627	138	54	13876	7.448201825
GOTERM_BP_FAT	GO:0009207~purine ribonucleoside triphosphate catabolic process	3	1.973684211	0.016367176	513;506;498	138	20	13876	15.0826087
GOTERM_BP_FAT	GO:0009203~ribonucleoside triphosphate catabolic process	3	1.973684211	0.016367176	513;506;498	138	20	13876	15.0826087
GOTERM_BP_FAT	GO:0006119~oxidative phosphorylation	5	3.289473684	0.017200968	513;506;1738;498;527	138	100	13876	5.027536232
GOTERM_BP_FAT	GO:0009100~glycoprotein metabolic process	7	4.605263158	0.017534195	6184;1650;7841;84061;3703;6185;1603	138	209	13876	3.367727619
GOTERM_BP_FAT	GO:0009206~purine ribonucleoside triphosphate biosynthetic process	5	3.289473684	0.017776775	513;506;476;498;527	138	101	13876	4.977758645
GOTERM_BP_FAT	GO:0009201~ribonucleoside triphosphate biosynthetic process	5	3.289473684	0.01836448	513;506;476;498;527	138	102	13876	4.92895709
GOTERM_BP_FAT	GO:0009145~purine nucleoside triphosphate biosynthetic process	5	3.289473684	0.01836448	513;506;476;498;527	138	102	13876	4.92895709
GOTERM_BP_FAT	GO:0051693~actin filament capping	3	1.973684211	0.019645378	829;6711;6709	138	22	13876	13.71146245
GOTERM_BP_FAT	GO:0009146~purine nucleoside triphosphate catabolic process	3	1.973684211	0.019645378	513;506;498	138	22	13876	13.71146245
GOTERM_BP_FAT	GO:0009142~nucleoside triphosphate biosynthetic process	5	3.289473684	0.020199618	513;506;476;498;527	138	105	13876	4.788129745
GOTERM_BP_FAT	GO:0046034~ATP metabolic process	5	3.289473684	0.022144045	513;506;476;498;527	138	108	13876	4.655126141
GOTERM_BP_FAT	GO:0034984~cellular response to DNA damage stimulus	9	5.921052632	0.022458679	11198;7520;6749;2547;7153;5591;142;9656;7157	138	349	13876	2.59299863
GOTERM_BP_FAT	GO:0030835~negative regulation of actin filament depolymerization	3	1.973684211	0.023173662	829;6711;6709	138	24	13876	12.56884058
GOTERM_BP_FAT	GO:0009154~purine ribonucleotide catabolic process	3	1.973684211	0.023173662	513;506;498	138	24	13876	12.56884058
GOTERM_BP_FAT	GO:0015992~proton transport	4	2.631578947	0.023320516	513;506;498;527	138	62	13876	6.487143525
GOTERM_BP_FAT	GO:0002520~immune system development	8	5.263157895	0.0249873	6146;4627;7520;2547;5591;94081;7157;3329	138	290	13876	2.773813093
GOTERM_BP_FAT	GO:0016444~somatic cell DNA recombination	3	1.973684211	0.025028152	2547;5591;3329	138	25	13876	12.06608696

GOTERM_BP_FAT	GO:0030239~myofibril assembly	3	1.973684211	0.025028152	7168;71;60	138	25	13876	12.06608696
GOTERM_BP_FAT	GO:0009143~nucleoside triphosphate catabolic process	3	1.973684211	0.025028152	513;506;498	138	25	13876	12.06608696
GOTERM_BP_FAT	GO:0030048~actin filament-based movement	3	1.973684211	0.025028152	7168;4637;4627	138	25	13876	12.06608696
GOTERM_BP_FAT	GO:0002562~somatic diversification of immune receptors via germline recombination within a single locus	3	1.973684211	0.025028152	2547;5591;3329	138	25	13876	12.06608696
GOTERM_BP_FAT	GO:0006818~hydrogen transport	4	2.631578947	0.025329952	513;506;498;527	138	64	13876	6.28442029
GOTERM_BP_FAT	GO:0006302~double-strand break repair	4	2.631578947	0.025329952	7520;2547;5591;7157	138	64	13876	6.28442029
GOTERM_BP_FAT	GO:0014706~striated muscle tissue development	6	3.947368421	0.026102065	7168;4637;4627;3339;71;60	138	169	13876	3.569848212
GOTERM_BP_FAT	GO:0009261~ribonucleotide catabolic process	3	1.973684211	0.026941085	513;506;498	138	26	13876	11.60200669
GOTERM_BP_FAT	GO:0055002~striated muscle cell development	3	1.973684211	0.026941085	7168;71;60	138	26	13876	11.60200669
GOTERM_BP_FAT	GO:0043623~cellular protein complex assembly	6	3.947368421	0.027280134	56993;7019;2316;203068;10376;3329	138	171	13876	3.528095601
GOTERM_BP_FAT	GO:0051235~maintenance of location	4	2.631578947	0.02742978	10945;11014;2316;7184	138	66	13876	6.093983311
GOTERM_BP_FAT	GO:0006351~transcription; DNA-dependent	8	5.263157895	0.027530121	6182;8467;11198;7019;51773;6949;142;7157	138	296	13876	2.717587152
GOTERM_BP_FAT	GO:0008217~regulation of blood pressure	5	3.289473684	0.027873964	7168;10159;476;71;60	138	116	13876	4.334082959
GOTERM_BP_FAT	GO:0030834~regulation of actin filament depolymerization	3	1.973684211	0.028911143	829;6711;6709	138	27	13876	11.17230274
GOTERM_BP_FAT	GO:0032774~RNA biosynthetic process	8	5.263157895	0.029320165	6182;8467;11198;7019;51773;6949;142;7157	138	300	13876	2.681352657
GOTERM_BP_FAT	GO:0002200~somatic diversification of immune receptors	3	1.973684211	0.030937029	2547;5591;3329	138	28	13876	10.77329193
GOTERM_BP_FAT	GO:0060537~muscle tissue development	6	3.947368421	0.031015938	7168;4637;4627;3339;71;60	138	177	13876	3.40849914
GOTERM_BP_FAT	GO:0009152~purine ribonucleotide biosynthetic process	5	3.289473684	0.031040975	513;506;476;498;527	138	120	13876	4.189613527
GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	7	4.605263158	0.031798058	7168;829;4627;2316;71;60;8655	138	240	13876	2.932729469
GOTERM_BP_FAT	GO:0009205~purine ribonucleoside triphosphate metabolic process	5	3.289473684	0.031864538	513;506;476;498;527	138	121	13876	4.154988621
GOTERM_BP_FAT	GO:0009199~ribonucleoside triphosphate metabolic process	5	3.289473684	0.032700872	513;506;476;498;527	138	122	13876	4.120931338
GOTERM_BP_FAT	GO:0030837~negative regulation of actin filament polymerization	3	1.973684211	0.033017468	829;6711;6709	138	29	13876	10.4017991

GOTERM_BP_FAT	GO:0032272~negative regulation of protein polymerization	3	1.973684211	0.0351512	829;6711;6709	138	30	13876	10.05507246
GOTERM_BP_FAT	GO:0009144~purine nucleoside triphosphate metabolic process	5	3.289473684	0.036174314	513;506;476;498;527	138	126	13876	3.990108121
GOTERM_BP_FAT	GO:0009260~ribonucleotide biosynthetic process	5	3.289473684	0.037074776	513;506;476;498;527	138	127	13876	3.958689946
GOTERM_BP_FAT	GO:0055001~muscle cell development	3	1.973684211	0.037336987	7168;71;60	138	31	13876	9.730715288
GOTERM_BP_FAT	GO:0007010~cytoskeleton organization	10	6.578947368	0.039113569	7168;829;4627;2316;203068;71;60;10376;8655;3856	138	461	13876	2.181143701
GOTERM_BP_FAT	GO:0001701~in utero embryonic development	6	3.947368421	0.039414768	7168;23463;4627;7082;1603;7157	138	189	13876	3.192086496
GOTERM_BP_FAT	GO:0006974~response to DNA damage stimulus	9	5.921052632	0.039563341	11198;7520;6749;2547;7153;5591;142;9656;7157	138	390	13876	2.320401338
GOTERM_BP_FAT	GO:0007006~mitochondrial membrane organization	3	1.973684211	0.039573611	3954;56993;7157	138	32	13876	9.426630435
GOTERM_BP_FAT	GO:0031032~actomyosin structure organization	3	1.973684211	0.039573611	7168;71;60	138	32	13876	9.426630435
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	8	5.263157895	0.040014875	513;506;5250;1431;1738;498;80777;527	138	321	13876	2.505937063
GOTERM_BP_FAT	GO:0000060~protein import into nucleus; translocation	3	1.973684211	0.044194581	10952;6711;7157	138	34	13876	8.872122762
GOTERM_BP_FAT	GO:0006195~purine nucleotide catabolic process	3	1.973684211	0.044194581	513;506;498	138	34	13876	8.872122762
GOTERM_BP_FAT	GO:0012501~programmed cell death	12	7.894736842	0.045213235	7150;7316;7416;7153;5591;3336;1603;7157;10134;8655;3856;3329	138	625	13876	1.930573913
GOTERM_BP_FAT	GO:0009141~nucleoside triphosphate metabolic process	5	3.289473684	0.045745742	513;506;476;498;527	138	136	13876	3.696717818
GOTERM_BP_FAT	GO:0031333~negative regulation of protein complex assembly	3	1.973684211	0.046576581	829;6711;6709	138	35	13876	8.61863354
GOTERM_BP_FAT	GO:0002360~T cell lineage commitment	2	1.315789474	0.048407435	5591;7157	138	5	13876	40.22028986
GOTERM_BP_FAT	GO:0002326~B cell lineage commitment	2	1.315789474	0.048407435	5591;7157	138	5	13876	40.22028986

Supplementary Table S1D. GOBPs used for network analysis. Note that the proteins were represented by their EntrezID.

GO:0007010 cytoskeleton organization	GO:0006412 translation	GO:0006259 DNA metabolic process	GO:0015031 protein transport	GO:0051276 chromosome organization	GO:0018196 peptidyl-asparagine modification	GO:0006119 oxidative phosphorylation
10	12	17	25	20	6	5
7168	6182	5245	10952	8349	6184	513
829	6238	7150	100188893	8329	1650	506
4627	6202	7153	3313	5245	84061	1738
2316	6181	3159	821	26038	3703	498
203068	6146	7157	10959	3005	6185	527
71	6142	3329	6238	3006	1603	
60	6124	8815	10945	7153		
10376	7284	11198	23463	8091		
8655	4736	11168	11014	3159		
3856	7316	7019	6748	7157		
	6159	7520	6747	8467		
	6175	6749	6746	11198		
		2547	7184	8350		
		5591	10134	8294		
		6742	56993	7520		
		142	11231	2547		
		9656	6711	51773		
			128866	5591		
			7157	8971		
			161	142		
			4627			
			1213			
			5878			
			26984			
			29927			

Supplementary Table S1E. List of 68 mitochondrial proteins presented in Venn diagram.

GO only (5)	proteome only (0)	in silico only (30)	GO and proteome (2)	proteome and in silico (1)	GO and in silico (1)	all (29)
CISD2		ACTG1	PHB	RPL10A	SEC61A1	ATP5A1
CLTC		ATP6AP2	PRDX1			ATP5B
LRRC59		ATP6V0C				ATP5D
TOMM6		CKAP4				BCKDK
Tp53		ERLIN1				C1QBP
		GOLGB1				CKMT1A
		HIST1H2AG				COX5B
		HSPG2				CS
		ICMT				CYB5B
		JAGN1				DLD
		LAMB2				GLUD1
		LAMC1				HADHA
		MAPKBP1				HSD17B10
		MDC1				HSPA9
		MOGS				HSPD1P1
		MYH13				HSPE1
		MYH9				LETM1
		MYL12A				LRPPRC
		RPL29				MRPL12
		RPL4				PHB2
		RPLP0				SFXN1
		RPN2				SLC25A3
		RPS8				SLC25A5P8
		SEC22B				SSBP1
		SSR4				TFAM
		TFG				TOMM22
		TMPO				TUFM
		TOP1				VDAC1
		UBC				VDAC2
		XRCC5				

Supplementary Table S2. List of proteins identified by single-peptide-base.] and * denotes for carbamylation and the oxidation of methionine, respectively

IPI No.	Description	Peptide sequence	$[M+H]^+$	charge	Xcorr
IPI00166865.3	CDGSH iron sulfur domain-containing protein 2	LTVSEWLRLLPFLGVLALLGYLAVRPFLPK	3397.183	3	5.9006
IPI00018855.1	V-type proton ATPase 16 kDa proteolipid subunit	SGPEYASFFAVMGASAAMVFSALGAAYGTAK	3032.439	3	4.6481
IPI00386294.2	Overexpressed breast tumor protein	NLSDIDLM*APQPGV	1486.668	2	3.0205
IPI00220835.7	Protein transport protein Sec61 subunit beta	PGPTPSGTNVGSSGR	1371.438	2	3.7764
IPI00021785.2	Cytochrome c oxidase subunit 5B, mitochondrial	ASGGGVPTDEEQATGLER	1774.825	2	4.3101
IPI00739464.1	similar to beta-actin	SYKLPDGQVITIGNER	1790.998	1	2.8936
IPI00220739.3	Membrane-associated progesterone receptor compon	GDQPAASGDSDDDEPPPLPR	2037.044	2	5.0505
IPI00220362.5	10 kDa heat shock protein, mitochondrial	GGEIQPVSVK	1014.158	2	3.1067
IPI00009407.8	Dolichyl-diphosphooligosaccharide--protein glycosyltr	ADFQGISPER	1120.197	2	2.3591
IPI00024920.1	synthase subunit delta, mitochondrial	AQAELVGTADEATR	1432.519	2	4.7157
IPI00009368.4	Sideroflexin-1	TTPAVLFWQWINQSFNAVVNYTNR	2871.2	3	6.2061
IPI00009235.2	cDNA FLJ52061, highly similar to Translocon-associate	Q]QSEEDLLLQDFSR	1751.814	2	3.8693
IPI00016339.4	Ras-related protein Rab-5C	NEPQNATGAPGR	1212.255	2	2.9007
IPI00006865.3	Vesicle-trafficking protein SEC22b	DLQQYQSQAK	1209.291	2	3.3027
IPI00784154.1	60 kDa heat shock protein, mitochondrial	LVQDVANNTNEEAGDGTTTATVLAR	2561.702	3	4.2999
IPI00798360.1	cytokine induced protein 29 kDa, 18 kDa protein	STEILLR	831.9802	2	2.2644
IPI00257903.4	Endoplasmic reticulum metallopeptidase 1	AALGLALYLIALRTLVQLSLQQLVLR	2851.509	3	5.3807
IPI00298281.3	Laminin subunit gamma-1	NSVTSLLSIINDLLEQLGQLDTVDLNKLNEIEGTLNK	4069.562	3	5.9603
IPI00015911.1	Dihydrolipoyl dehydrogenase, mitochondrial	ADGGTQVIDTK	1105.181	2	3.1415
IPI00328715.4	Protein LYRIC	TVEVAEGEAVR	1160.26	2	3.4137
IPI00017592.1	LETM1 and EF-hand domain-containing protein 1, mit	VAEVEGEQVDNK	1317.384	2	3.9773
IPI00031522.2	Trifunctional enzyme subunit alpha, mitochondrial	SEVSSDEDIQFR	1412.441	2	3.0666
IPI00218922.5	Translocation protein SEC63 homolog	DQNAEQIR	974.0105	2	2.9651
IPI00007858.1	Myosin-13	QIIQANPLLEAFGNAK	1727.985	2	5.058
IPI00024284.4	Basement membrane-specific heparan sulfate proteog	AELLQVLQSLEAVLIQTVYNTK	2474.878	3	5.3097
IPI00385459.1	isoprenylcysteine carboxyl methyltransferase, ICMT pr	LSLATFLLGASVLALPLLTR	2070.547	2	4.0881
IPI00878392.1	ribosomal protein L22, 60S ribosomal protein L22, 11	YFQINQDEEEEEDED	1932.843	2	4.7881
IPI00100656.3	Isoform 1 of Synaptic glycoprotein SC2	DLGAQISWVTVFLTEYAGPLFIYLLFYFRVPFIYGHK	4387.124	3	4.8401

IPI00304331.2	Galactosylgalactosylxylosylprotein 3-beta-glucuronosyl	LHWLLVEDAEGPTPLVSGLLAASGLLFTHLVVLTPK	3809.491	3	6.4946
IPI00026167.5	NHP2-like protein 1, High mobility group-like nuclear	QQIQSIQQSIER	1458.602	2	2.8565
IPI00375407.1	Isoform 2 of Uncharacterized protein C20orf116	M*VAPVWYLVAAALLVGFILFLTRSRGR	3037.698	3	4.0888
IPI00748317.2	cDNA FLJ58403, highly similar to Neutral amino acid t	VPVGQEVEGM*NILGLVVFAIVFGVALRK	2972.576	3	6.6688
IPI00641334.2	Cytochrome b5 type B	GQEVETSVTYYR	1432.517	2	2.7351
IPI00791367.1	peptidylprolyl isomerase B (cyclophilin B), 20 kDa prot	D]TNGSQFFITTVK	1501.603	2	3.5646
IPI00910147.1	cDNA FLJ52943, highly similar to Zinc transporter SLC	VSGYLNLAADLAHNFTDGLAIGASFR	2694.983	3	5.2366
IPI00412487.4	Isoform 2 of Myosin-Id	VIGFKPEEIQTVYKILAAILHLGNLK	2909.501	3	6.9058
IPI00552214.1	Emerin	TYGEPESAGPSR	1251.284	2	3.0517
IPI00873484.1	Putative uncharacterized protein CAPZA1 (Fragment)	EASDPQPEEADGGLK	1543.571	2	3.5448
IPI00216858.3	Isoform 2 of Beta-1-syntrophin	A]VAAAAAAAGPAGAGGGR	1410.502	2	3.9215
IPI00448792.1	cathepsin Z, CTSZ protein (Fragment)	VGDYGSLSGR	1011.071	2	3.0496
IPI00556260.1	Structure specific recognition protein 1 variant (Fragm	A]ETLEFNDVYQEVK	1728.818	2	3.8234
IPI00872971.1	ATPase H(+)-transporting lysosomal accessory protein	NNEVDLLFLSELQVLHDISSLLSR	2756.104	3	4.4129
IPI00792159.1	60S ribosomal protein L4, 11 kDa protein	A]AAAAAALQAK	1000.115	2	3.5766
IPI00639797.1	Hydroxysteroid (17-beta) dehydrogenase 10	LVAGEMGQNEPDQGGQR	1786.905	2	5.2387
IPI00910360.1	cDNA FLJ58927, highly similar to Endoplasmin	DDEVDVDGTVEEDLGK	1735.739	2	5.4503
IPI00643781.1	PSIP1 protein, Transcriptional coactivator p75/p52	FSSQQAATK	968.0459	2	2.8068
IPI00479823.1	Isoform 3 of Remodeling and spacing factor 1	DNSTASASLASNGTSGGQEAGAPEEEEDELLR	3194.193	3	5.714
IPI00479587.3	WD repeat domain 62, 109 kDa protein	AGTGYASPDR	995.0282	2	2.5104
IPI00016621.7	Adaptor-related protein complex 2, alpha 2 subunit va	NADVELQQR	1073.142	2	3.5603
IPI00789405.1	Laminin, beta2, 15 kDa protein	AGNSLAASTAEETAGSAQGR	1849.895	2	5.4879
IPI00471928.5	cDNA FLJ54625, highly similar to ATP synthase subuni	TGAIVDVPVGEELLGR	1625.848	2	3.263
IPI00376039.3	Putative uncharacterized protein ENSP00000385291	IIDVVYNASNNELVR	1719.92	2	4.0179
IPI00796792.1	Tight junction protein, 42 kDa protein	GGPAEGQLQENDR	1371.395	2	3.401
IPI00744135.2	Isoform 2 of Ribosome-binding protein 1	DALNQATSQVESK	1391.466	2	3.9582
IPI00909831.1	cDNA FLJ50936, highly similar to Cellular tumor antige	VAPAPAAPTPAAPAPAPSWPLSSSVPSQK	2752.117	3	5.3437
IPI00641244.1	peroxiredoxin 1, 11 kDa protein	QITVNDLPVGR	1212.381	2	2.5712
IPI00903278.1	heterogeneous nuclear ribonucleoprotein D (AU-rich e	IFVGGLSPDTPEEK	1489.652	2	4.1255
IPI00455531.2	Uncharacterized protein ENSP00000367226	YQLDPTASISAK	1294.436	2	2.3958
IPI00514561.1	Heterogeneous nuclear ribonucleoprotein K	TDYNASVSVPDSSGPER	1781.816	2	3.566

IPI00177716.7	Isoform HMG-Y of High mobility group protein HMG-	SSQPLASK	817.9104	2	2.4454
IPI00791315.1	mitochondrial phosphate carrier protein, 21 kDa prote	IQTQPGYANTLR	1362.516	2	3.1562
IPI00797644.1	TRK-fused gene, 15 kDa protein	LLSNDEVTIK	1132.289	2	2.9292
IPI00902526.1	drebrin 1 isoform a, clone ASTRO1000165, highly simil	VEEIAASK	846.9485	2	2.9509
IPI00646871.3	Chromodomain helicase DNA binding protein 5	LLLTGTPLQNNLEELFHLLNFLTPER	3037.501	3	3.846
IPI00006437.2	High mobility group protein B3-like	STNPGISIGDVAK	1259.391	2	3.5352
IPI00173589.2	similar to ribosomal protein L29	AQAAAPASVPAQAPK	1378.559	2	4.0012
IPI00795725.1	Keratin 8, 17 kDa protein	AQYEDIANR	1080.133	2	2.8731

Supplementary Table S3. List of proteins categorized by subcellular localization and function. Proteins in red colored letters were reported as mtDNA nucleoid complex.

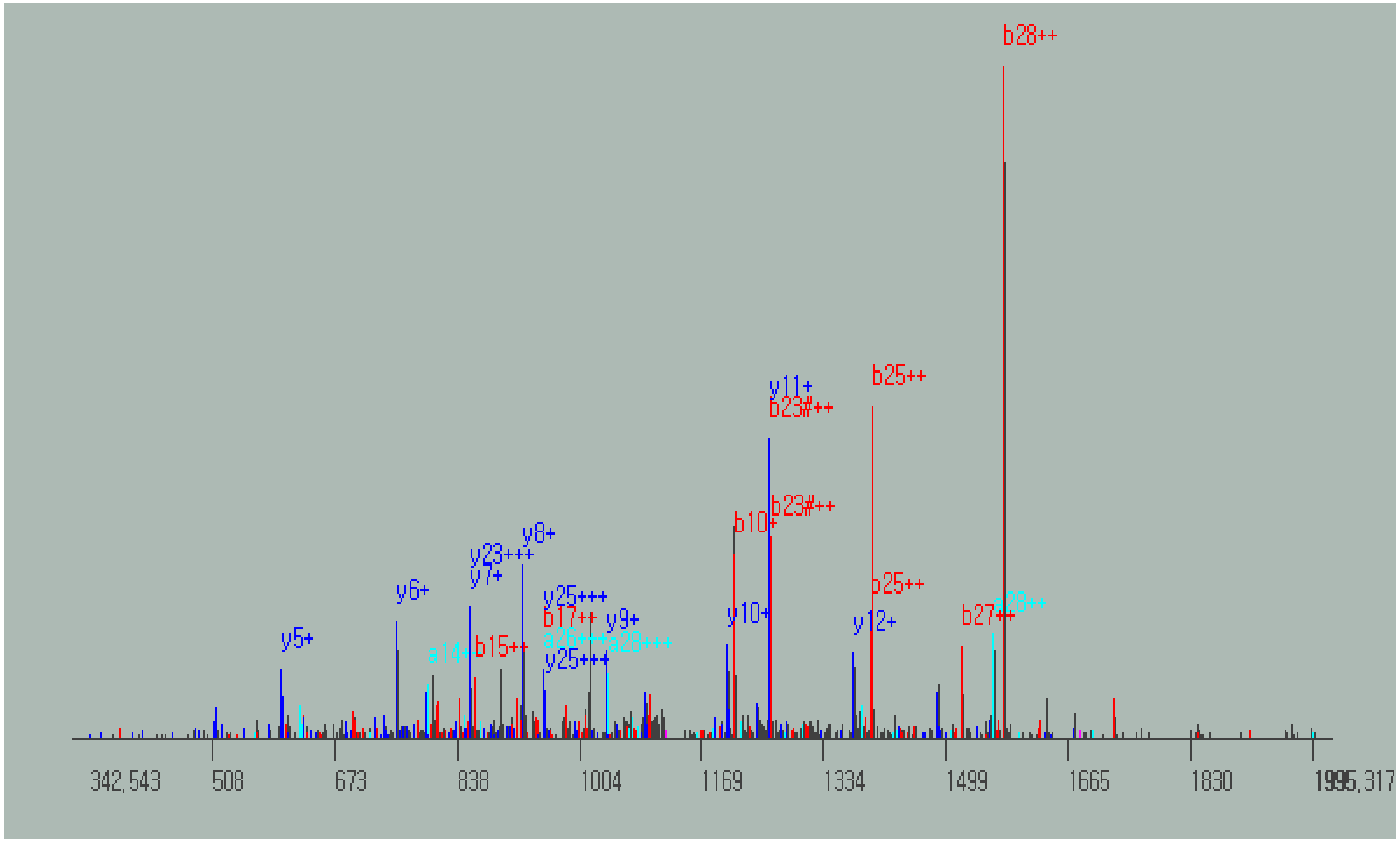
Localization	functional category	# of genes	Gene Symbols
1. Nucleus		**29**	
	DNA binding	23	TMPO, CHD5, H1F0, H1FX, HIST1H1C, HIST1H3J group, HIST1H4B group, HIST1H2AH, HIST2H2BE, MG4L, HMGA1, HMGA2, HNRNPA2B1, HNRNPD, HNRNPK, PARP1, PRKDC, SSRP1, SUB1, CIP29 , TOP2A , TCOF1, SMARCA5
	protein binding	3	EMD, MDC1, RSF1
	RNA binding	1	NHP2L1
	structure	2	LMNB1, LMNA
2. mitochondria		**34**	
	DNA binding	4	Tp53, LRPPRC, SSBP1, TFAM
	nucleotide binding	1	TUFM
	RNA binding	1	MRPL12 5C5
	protein binding	11	C1QBP, CLTC, HSD17B10, PHB, PHB2, TOMM22, BCKDK, HSPA9, HSPD1, HSPE1, TOMM6
	ion binding	2	CISD2, LETM1
	metabolism	4	DLD, CS cDNA FLJ38537 fis clone HCHON2001233, HADHA, GLUD1
	OXPHOS	5	ATP5A1 cDNA FLJ54625, ATP5B, ATP5D, COX5B, CYB5B
	transport	5	SFXN1, SLC25A3, SLC25A5, VDAC1, VDAC2
	unknown	1	LOC731391;LOC649970
3. cytoplasm		**29**	
	DNA binding	4	PSIP1, TOP1, XRCC5, XRCC6
	nucleotide binding	3	MYH9, MYO1D, TFG
	RNA binding	4	RPL22, RPL4, RPLP0, RPLP2
	protein binding	11	ACTB, CAPZA1, KRT8 , LOC646821, MRCL3, MYL6B, PRDX1, SPTAN1, SPTBN1, MYH13, RPS27A
	protein transport	1	CHMP4B
	structure	5	DYNLL1, LOC100128936, LOC647000, TPM1, TUBA1B
	unknown	1	LOC284064
4. ER/golgi/ER membrane		**32**	
	DNA binding	2	CKAP4, LRRC59
	RNA binding	8	ICMT, RRBP1, SEC22B, SEC61A1, SEC61B, SEC63, SSR2 cDNA FLJ56303, HSP90B1
	protein binding	3	CTSZ, RPN1, RPN2
	ion binding	2	ERMP1, B3GAT3
	protein folding	1	PPIB
	metabolism	3	GCS1, GPSN2, STT3A
	protein transport	10	CANX cDNA FLJ55574, DAD1, DDOST, HM13, KDELR1, KDELR2, PGRMC1, SSR3 cDNA FLJ52061, SSR4, BCAP31
	transport	2	MAGT1, JAGN1
	unknown	1	ERLIN1
5. membrane		**21**	
	DNA binding	1	SUPT16H
	nucleotide binding	1	RAB5C
	protein binding	11	ATP6V0C, LAMB2, LAMC1, MTDH, NOMO1;NOMO3, PTPLAD1, SLC1A5 cDNA FLJ58403, SNTB1, TJP1, ATP6AP2
	ion binding	1	HSPG2
	protein transport	1	AP2A2
	structure	1	BASP1
	transport	3	ATP1A1, cDNA FLJ52943, SLC2A3
	unknown	2	cDNA FLJ52154, KIAA0152
6. unknown		**7**	
	unknown	7	cDNA FLJ36806 fis, cDNA FLJ53509, cDNA FLJ54378, LOC645870, DDRGK1, WDR62, LOC388076
total number of proteins		**152**	

D loop proteins

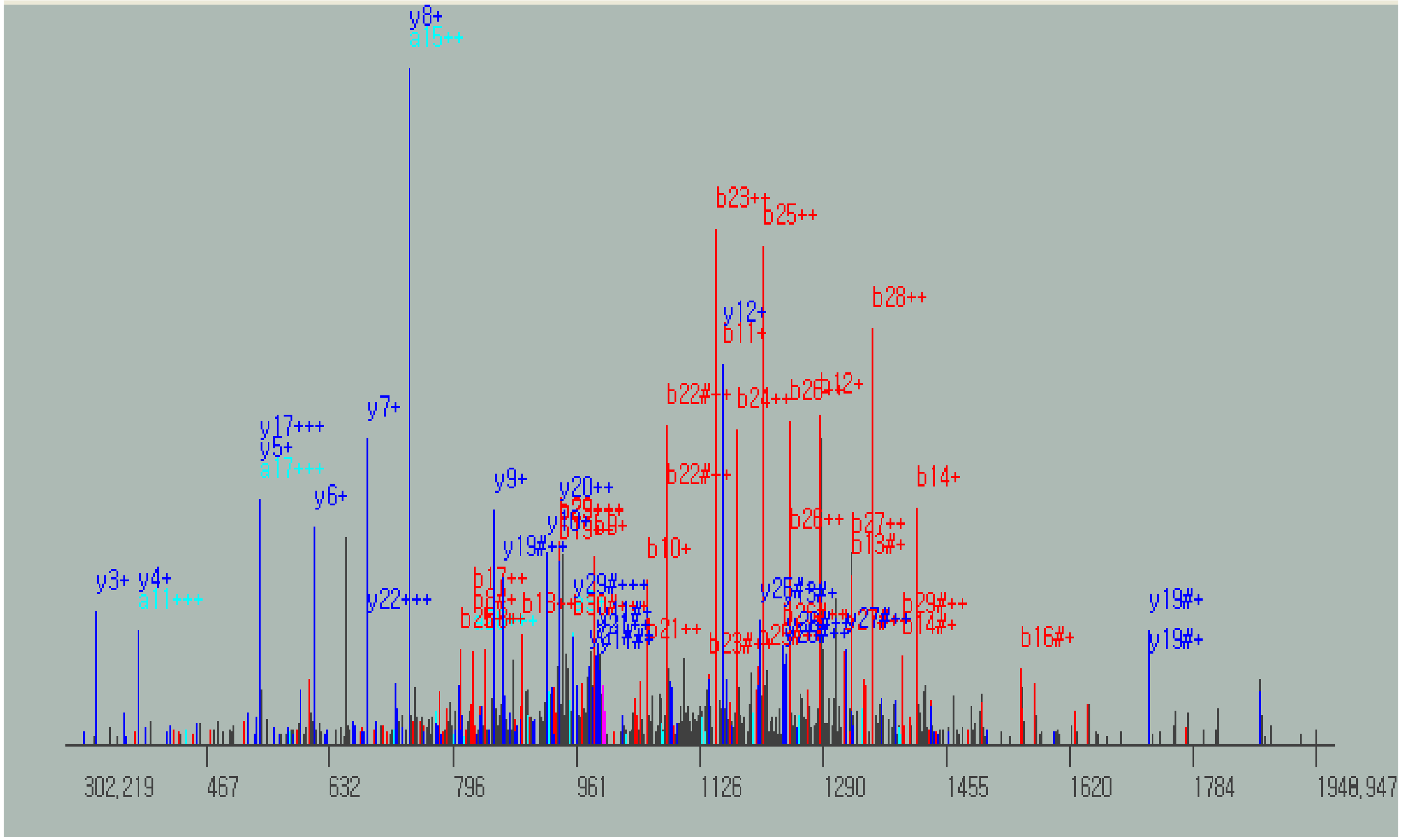
(single hit spectra)

] : carbamylation
***: Oxidation of Methionine**
Blue: y-ions
Red: b-ions
Pink: loss of water or ammonia molecules

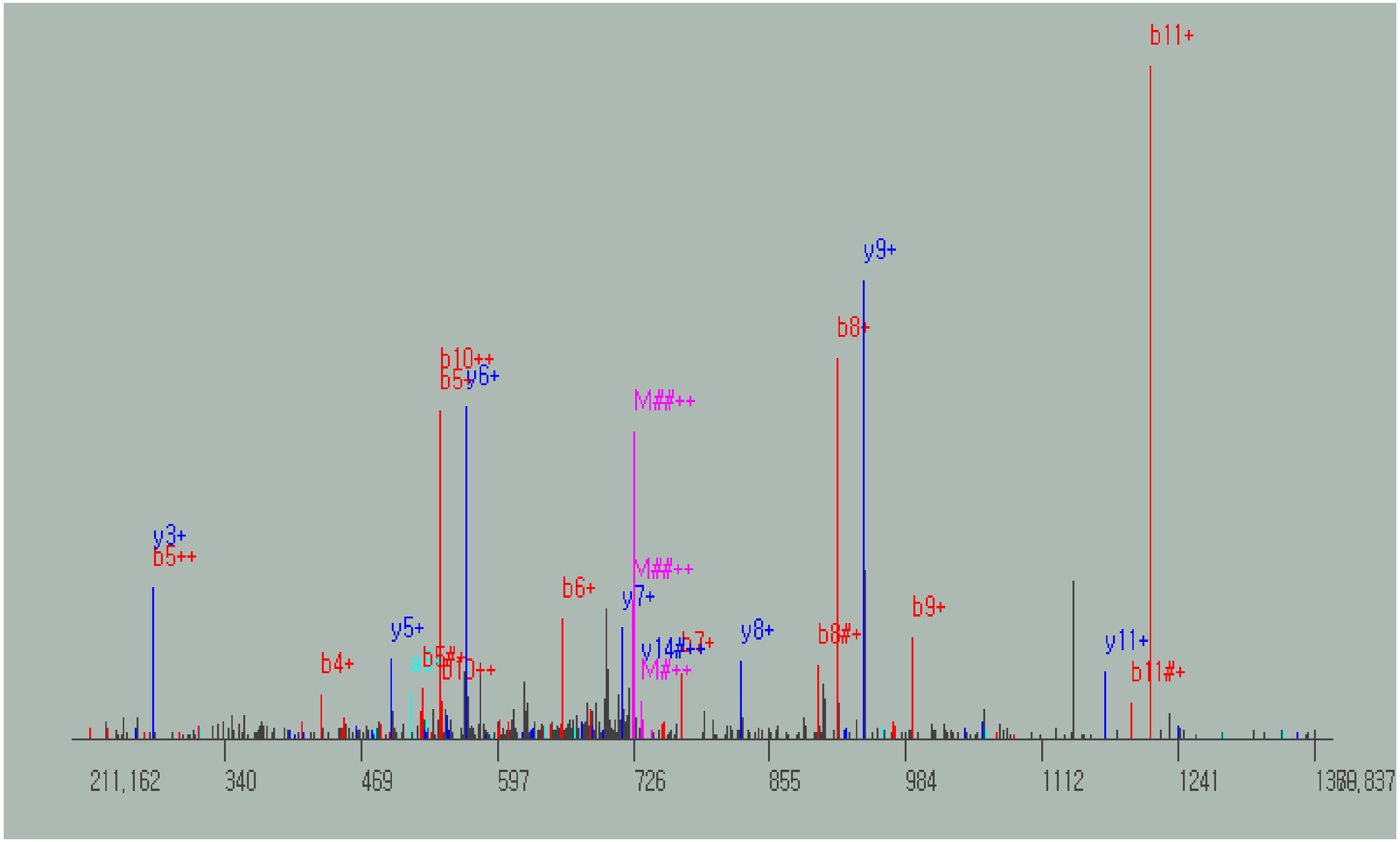
R.LTVSEWLRLLPFLGVLALLGYLAVRPFLPK.K
m/z(3397.18295), charge(+3), Xcorr(5.9006)



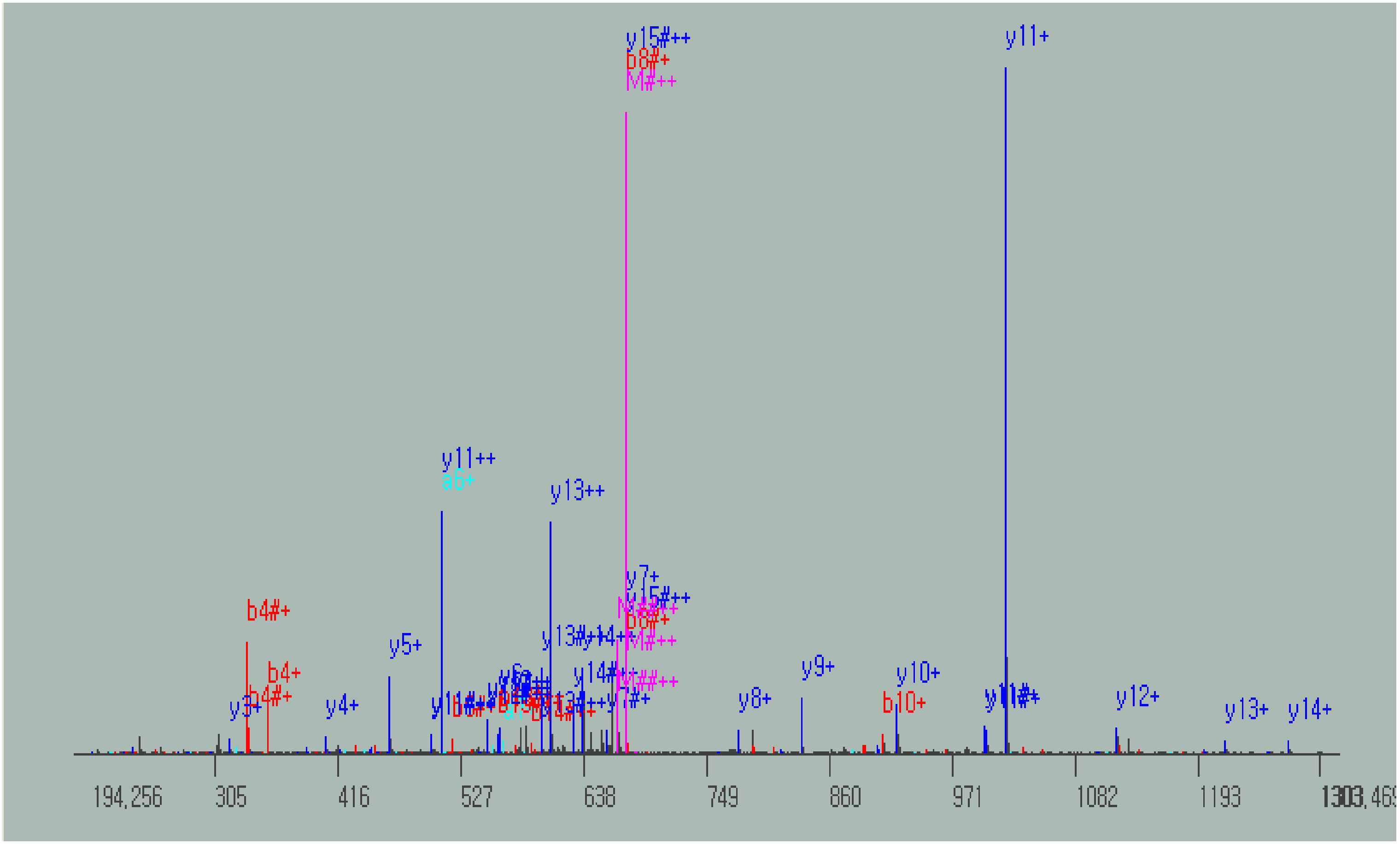
K.SGPEYASFFAVMGASAAMVFSALGAAYGTAK.S
m/z(3032.43877), charge(+3), Xcorr(4.6481)



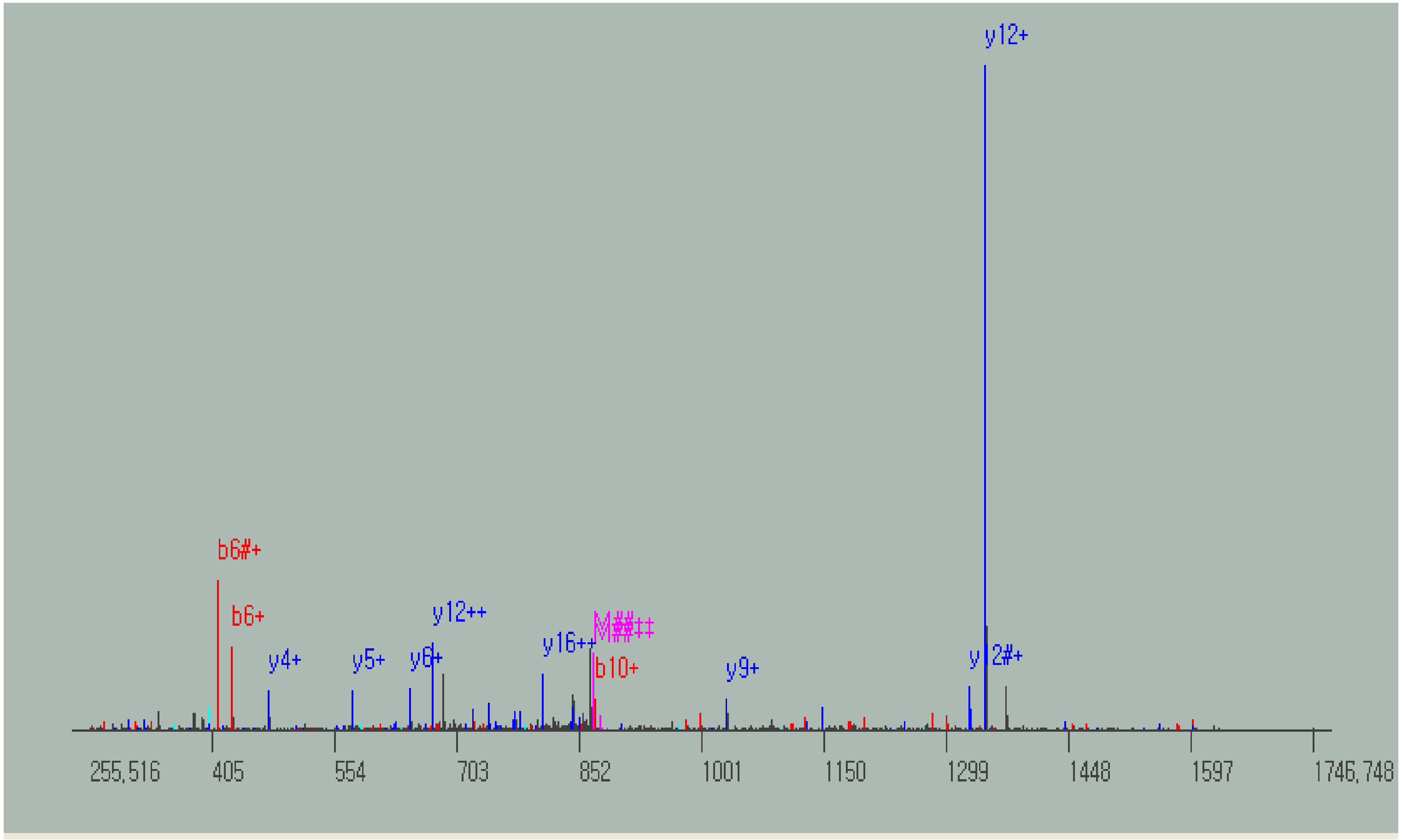
R.NLSDIDLM*APQPGV.-
m/z(1486.6683), charge(+2), Xcorr(3.0205)



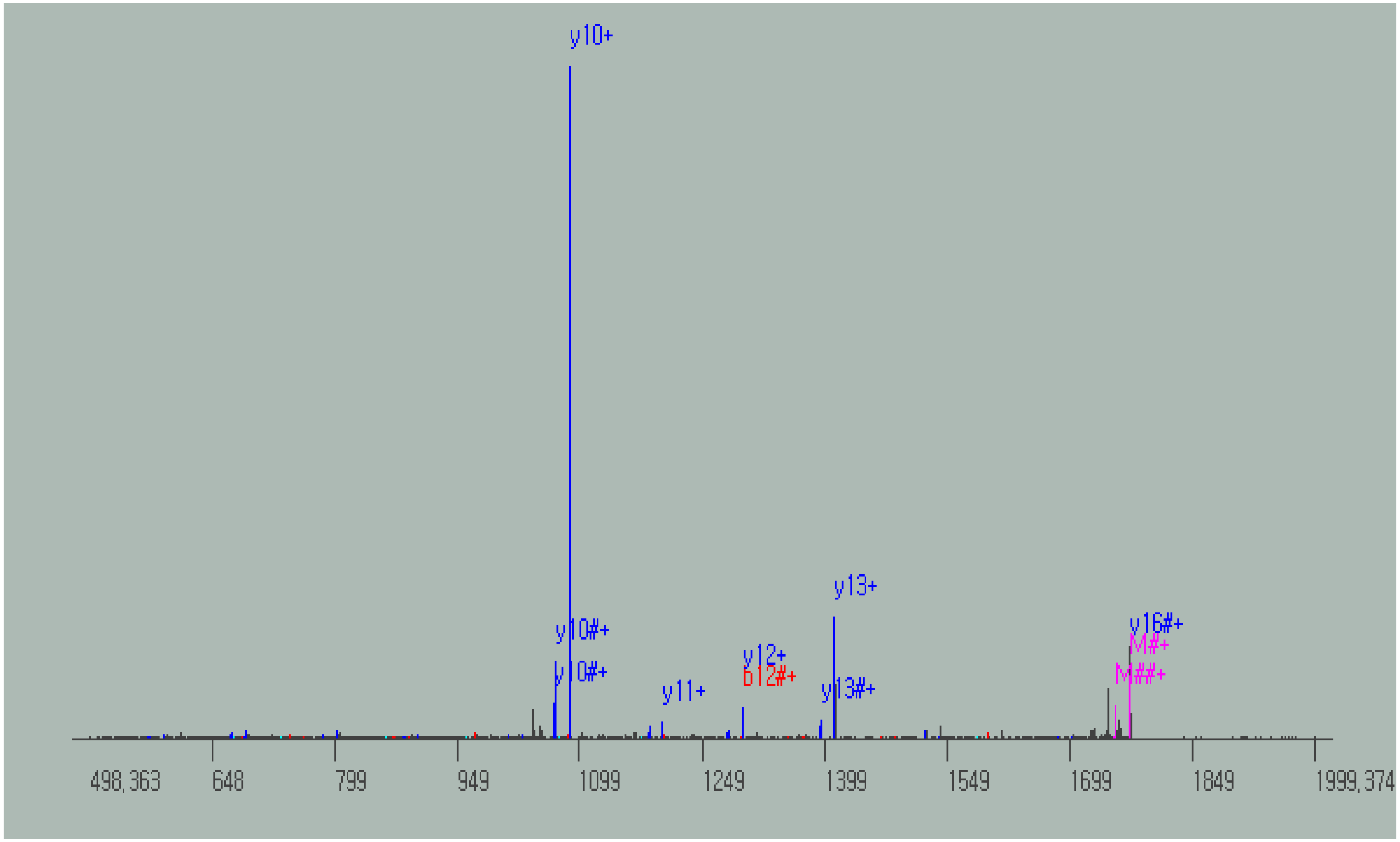
M.PGPTPSGTNVGSSGR.S
m/z(1371.43849), charge(+2), Xcorr(3.7764)



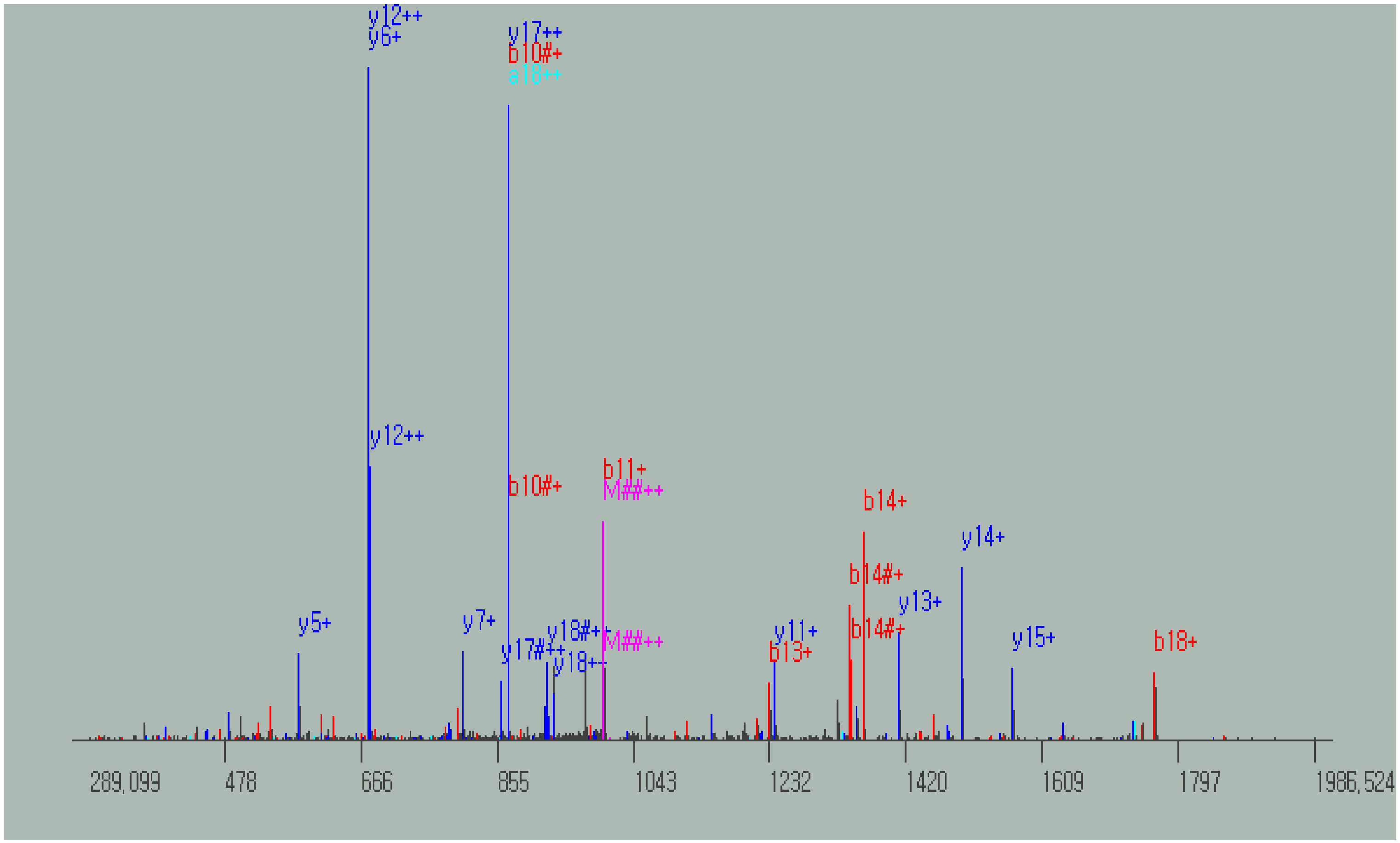
M.ASGGGVPTDEEQATGLER.E
m/z(1774.82468), charge(+2), Xcorr(4.3101)



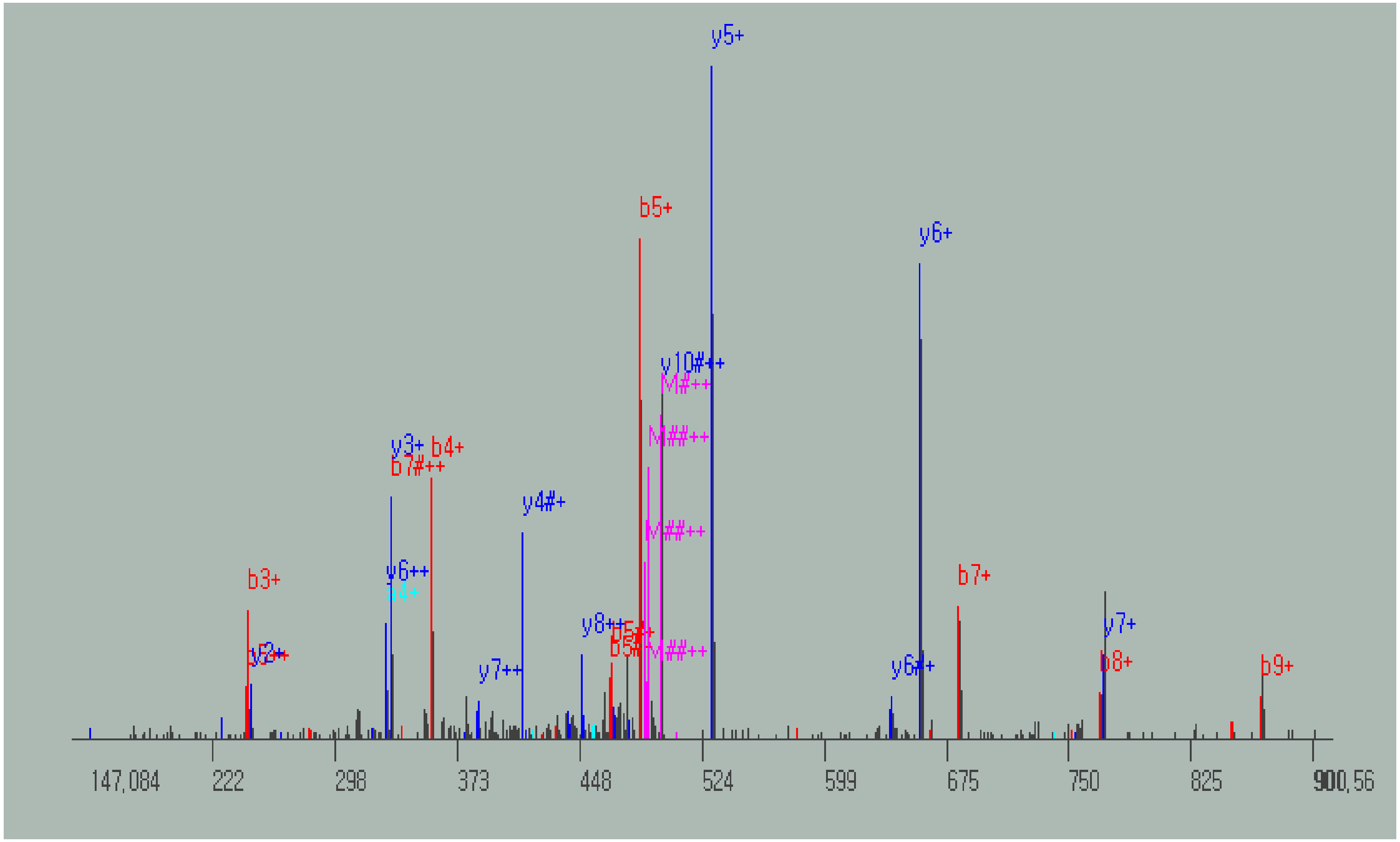
K.SYKLPDGQVITIGNER.F
m/z(1790.99835), charge(+1), Xcorr(2.8936)



R.GDQPAASGDSDDDEPPPLPR.L
m/z(2037.0441), charge(+2), Xcorr(5.0505)

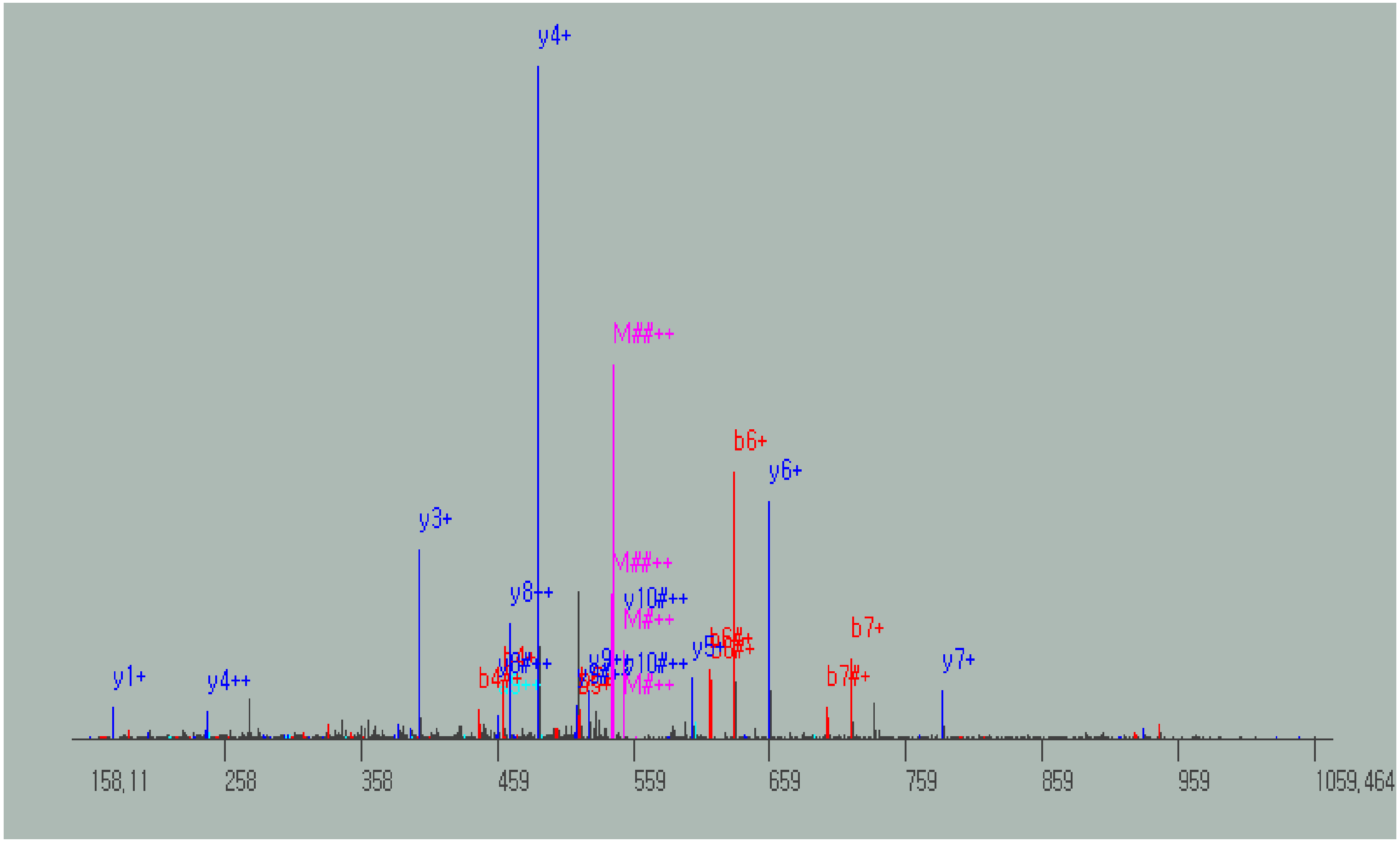


K.GGEIQPVSVK.V
m/z(1014.15766), charge(+2), Xcorr(3.1067)

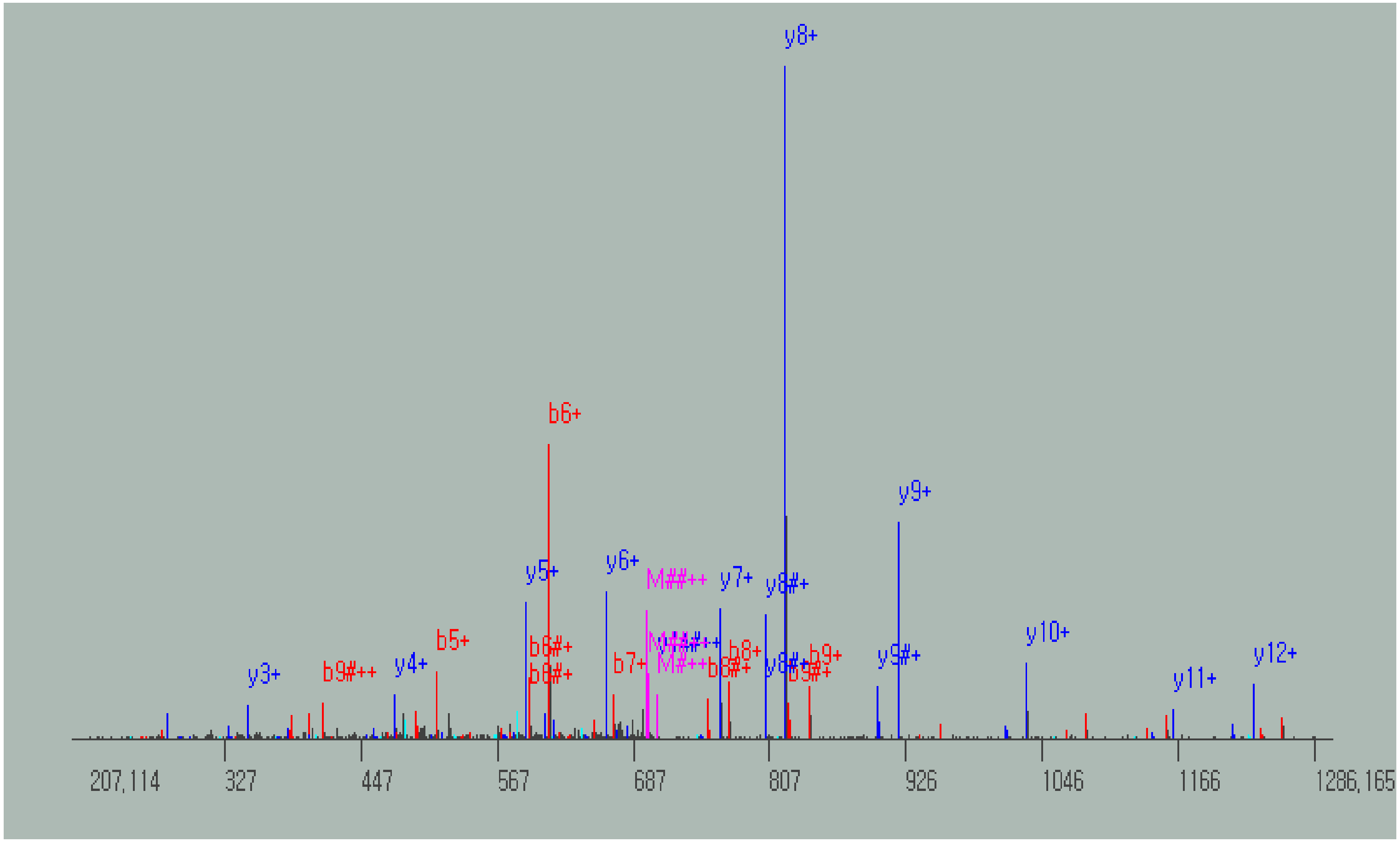


K.ADFQGISPER.A

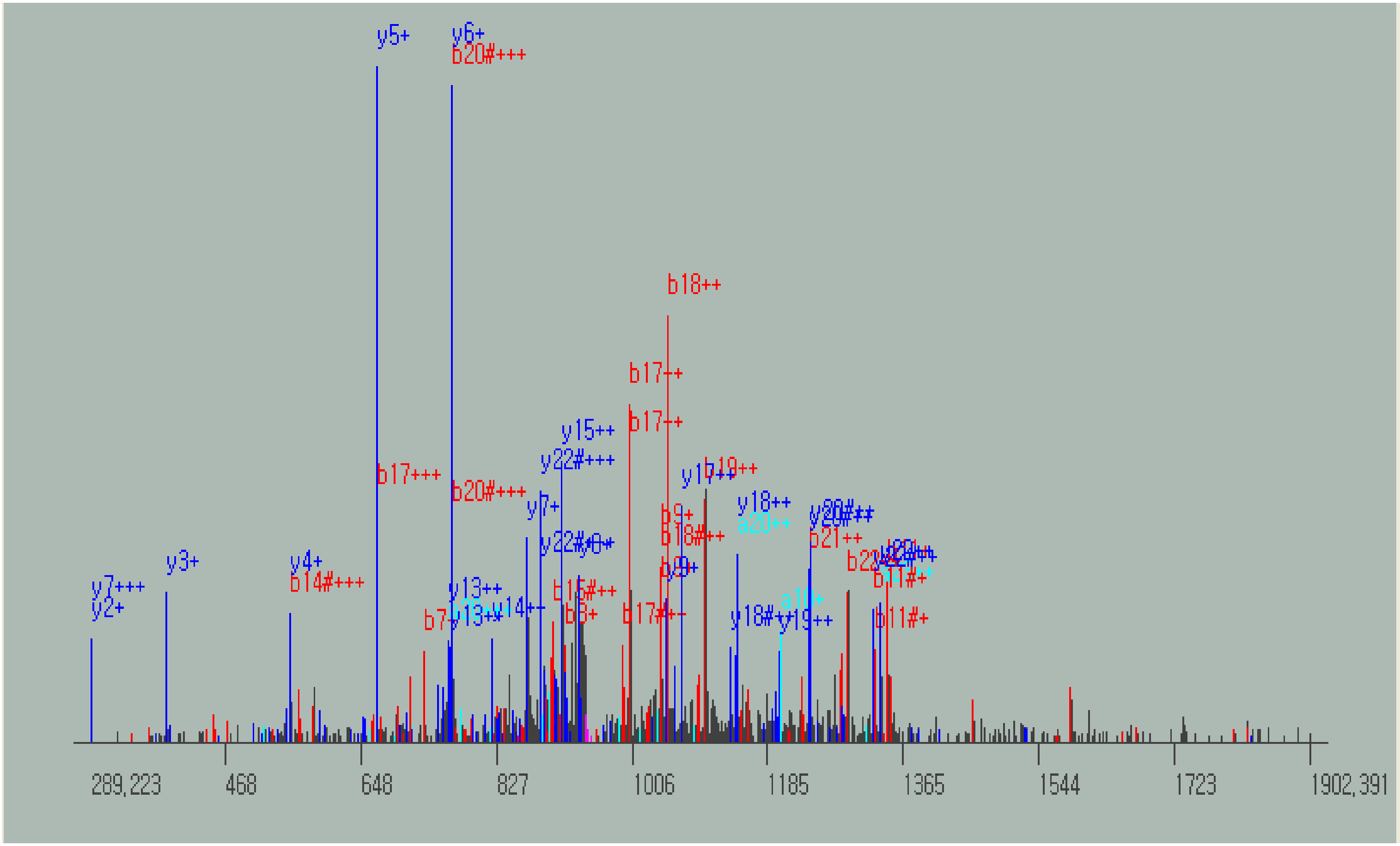
m/z(1120.19718), charge(+2), Xcorr(2.3591)



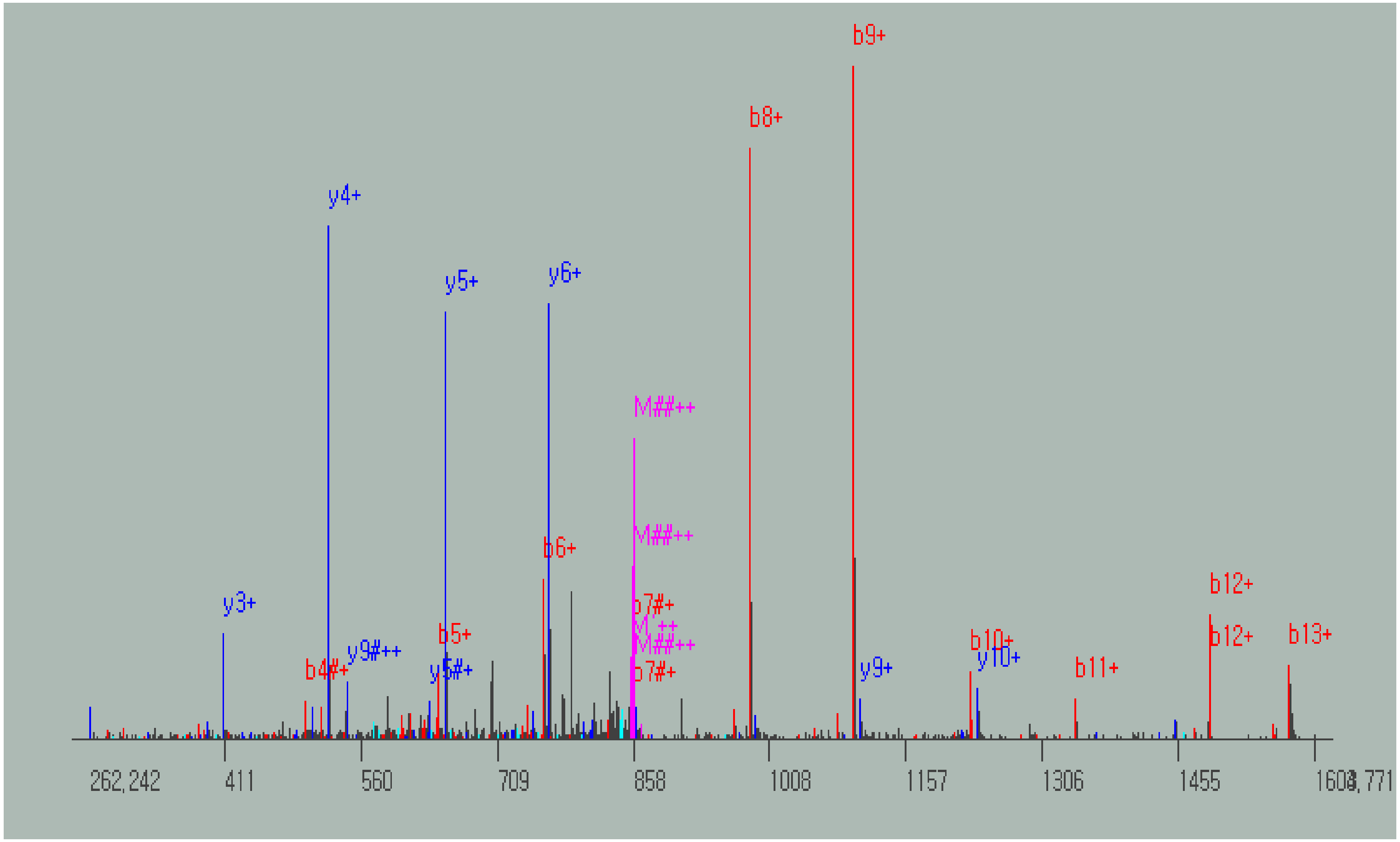
K.AQAELVGTADEATR.A
m/z(1432.5186), charge(+2), Xcorr(4.7157)



R.TTPAVLFWQWINQSFNAVVNYTNR.S
m/z(2871.20025), charge(+3), Xcorr(6.2061)

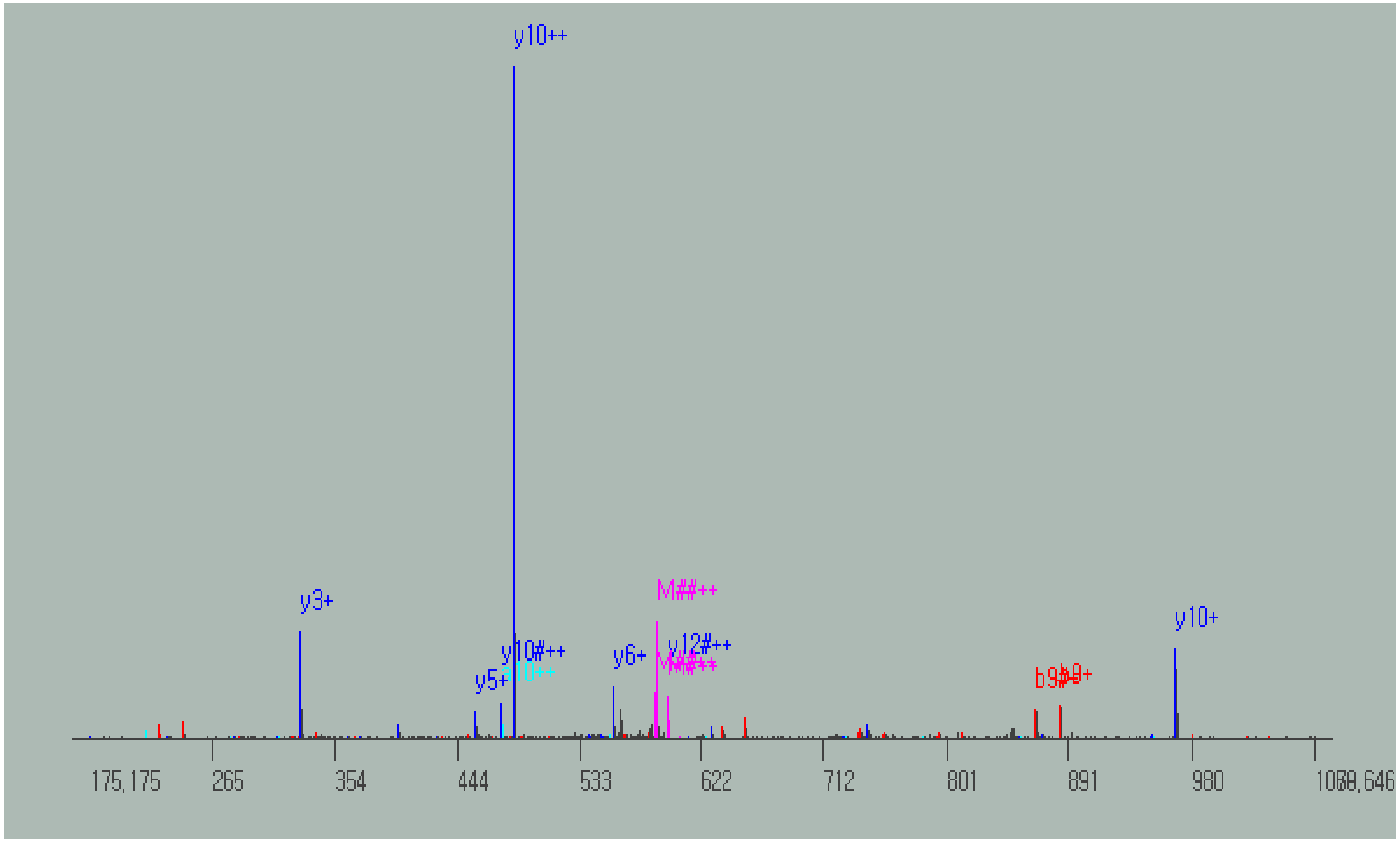


K.Q]QSEEDLLLQDFSR.N
m/z(1751.81364), charge(+2), Xcorr(3.8693)

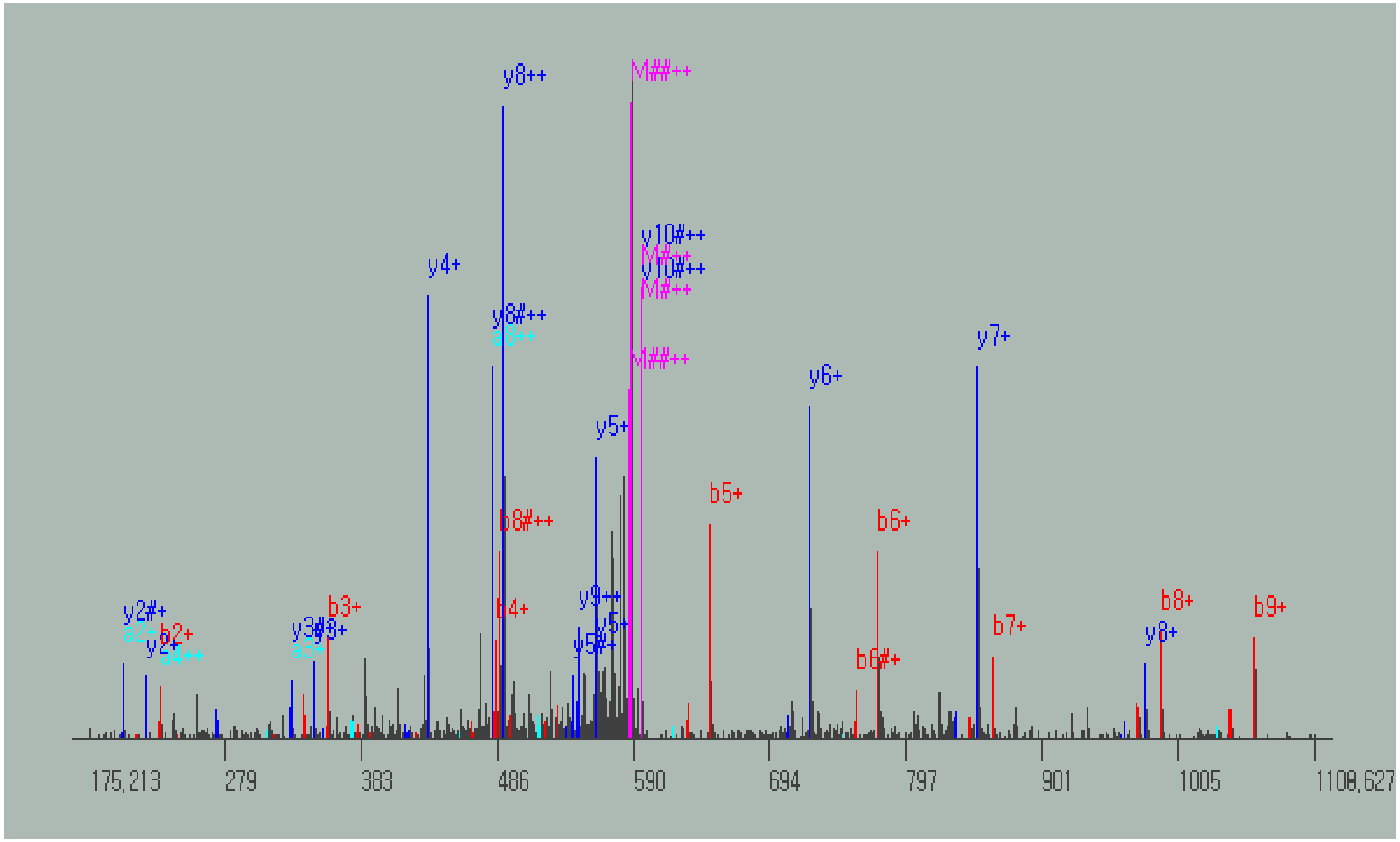


K.NEPQNATGAPGR.N

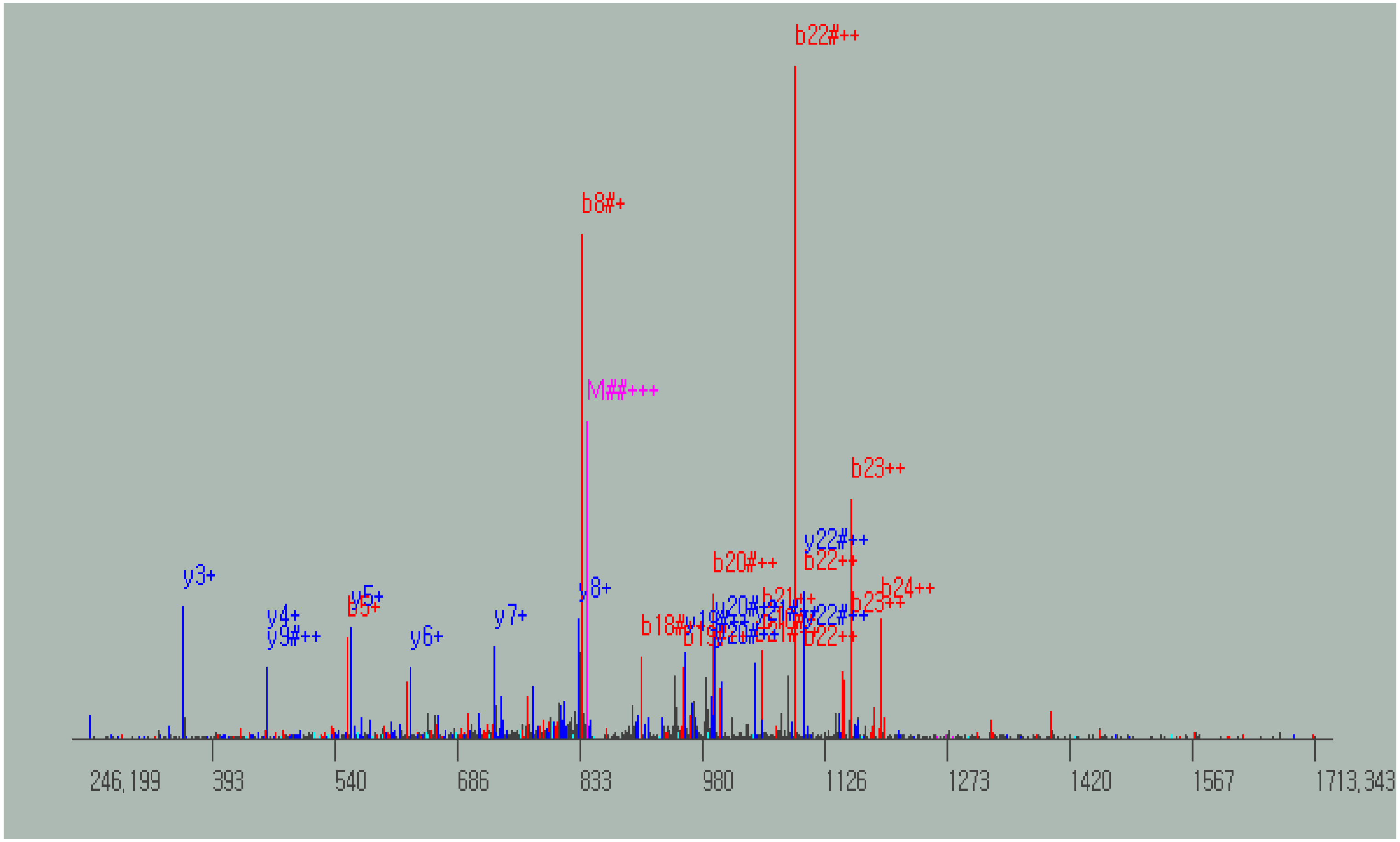
m/z(1212.25471), charge(+2), Xcorr(2.9007)



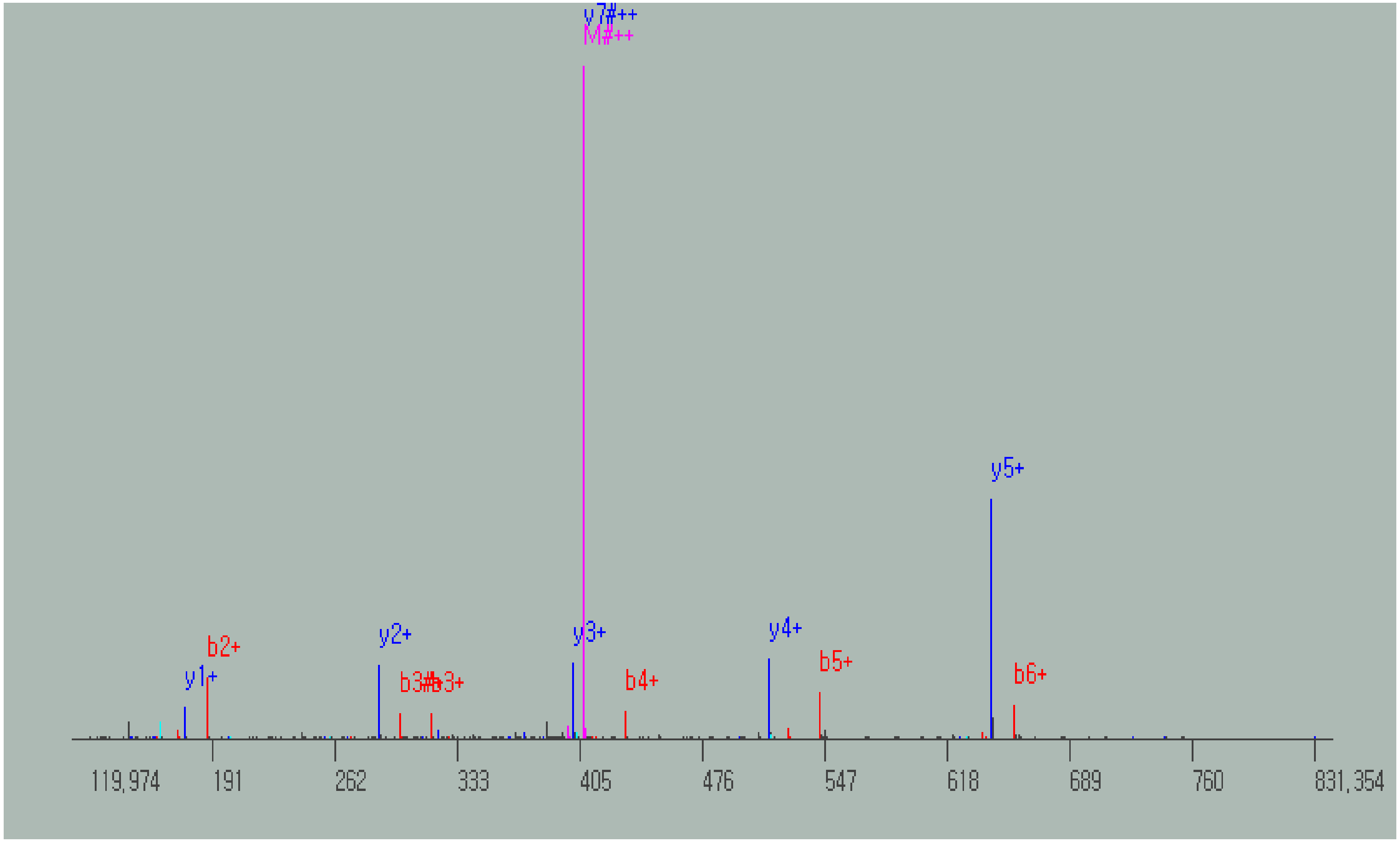
R.DLQQYQSQAK.Q
m/z(1209.29073), charge(+2), Xcorr(3.3027)



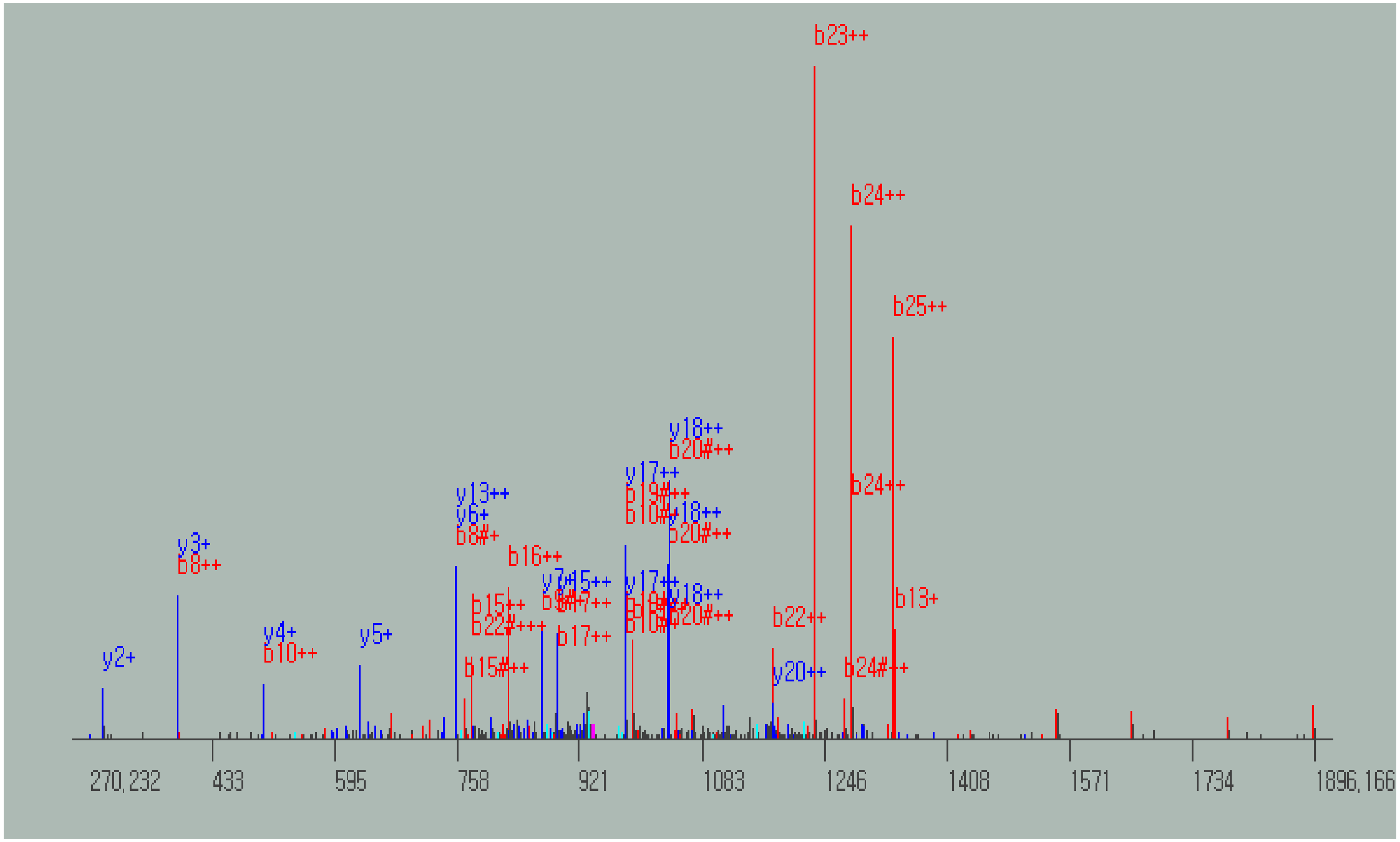
K.LVQDVANNTNEEAGDGTTTATVLAR.S
m/z(2561.7017), charge(+3), Xcorr(4.2999)



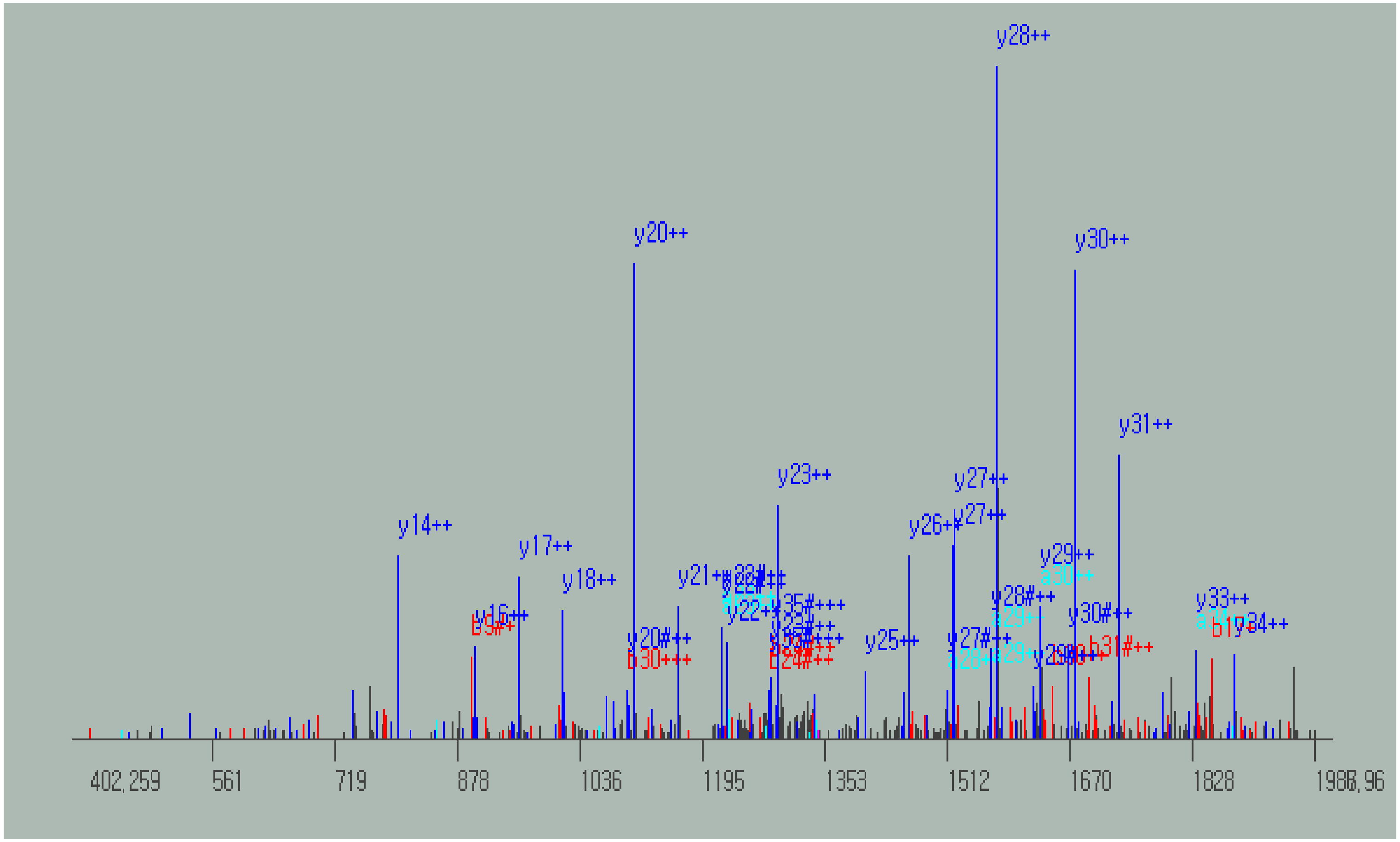
K.STEILLR.K
m/z(831.98022), charge(+2), Xcorr(2.2644)



R.AALGLALYLIALRTLVQLSLQQLVLR.G
m/z(2851.50906), charge(+3), Xcorr(5.3807)

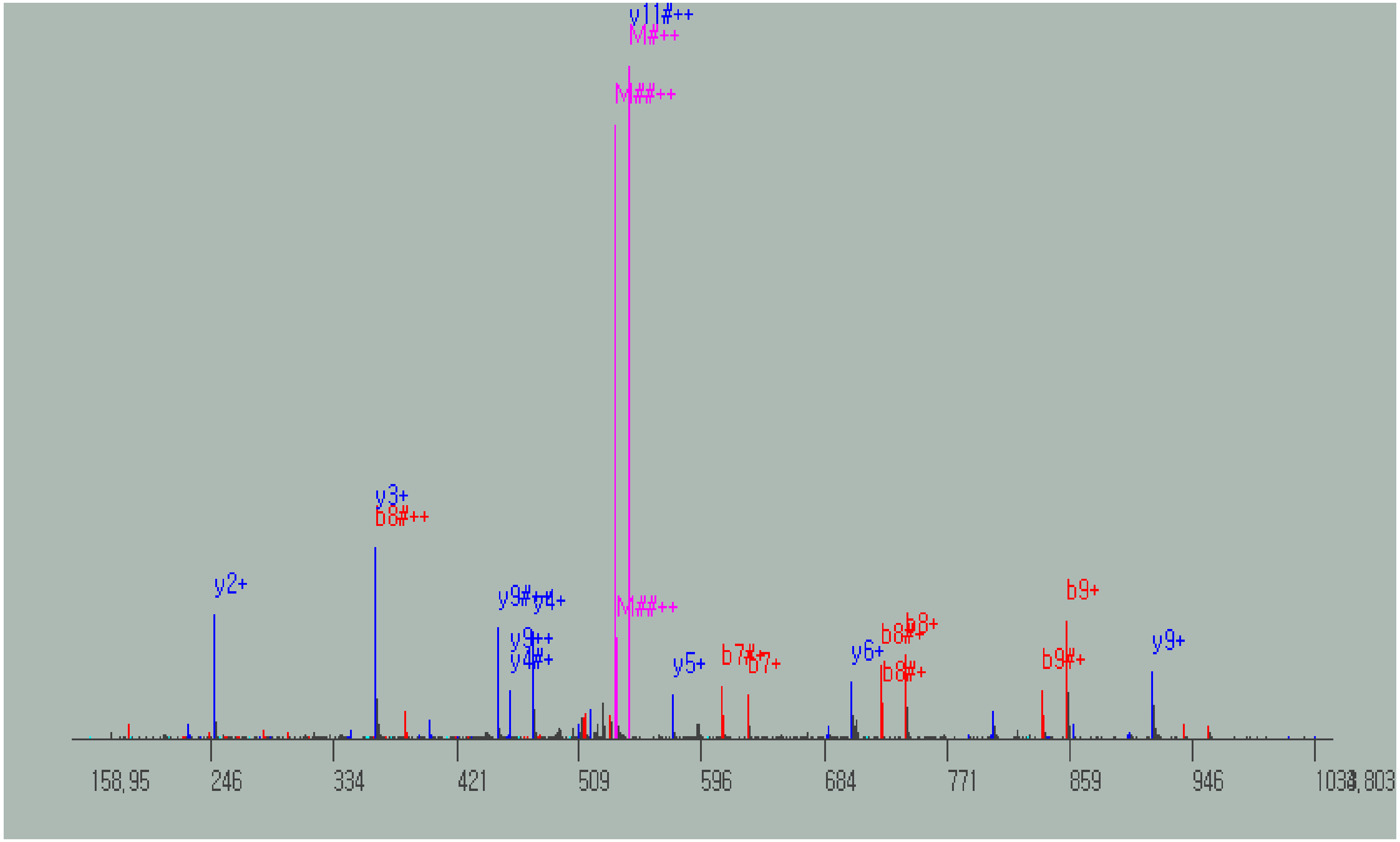


K.NSVTSLLSIINDLLEQLGQLDTVDLNKLNEIEGTLNK.A
m/z(4069.56187), charge(+3), Xcorr(5.9603)



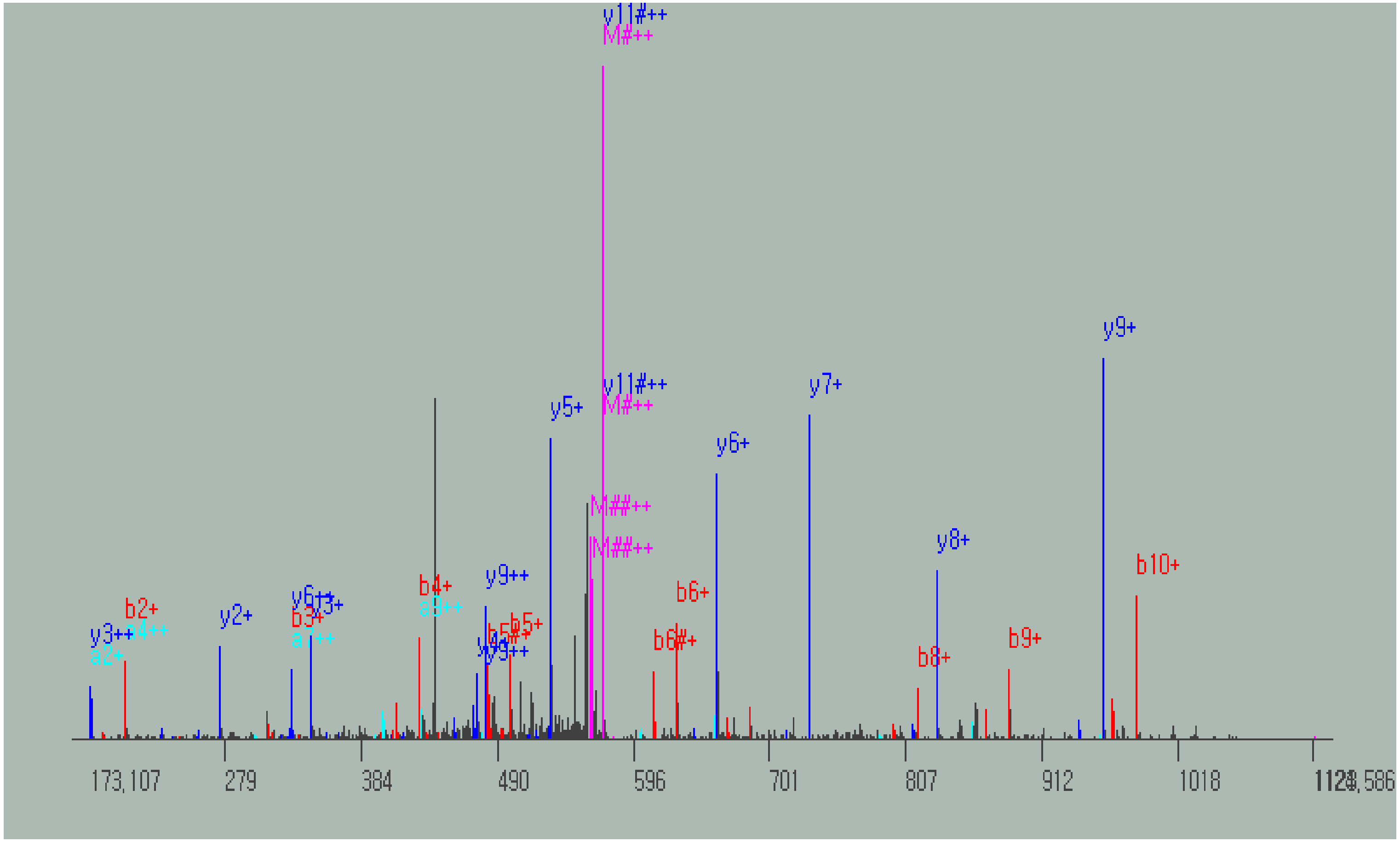
K.ADGGTQVIDTK.N

m/z(1105.18083), charge(+2), Xcorr(3.1415)



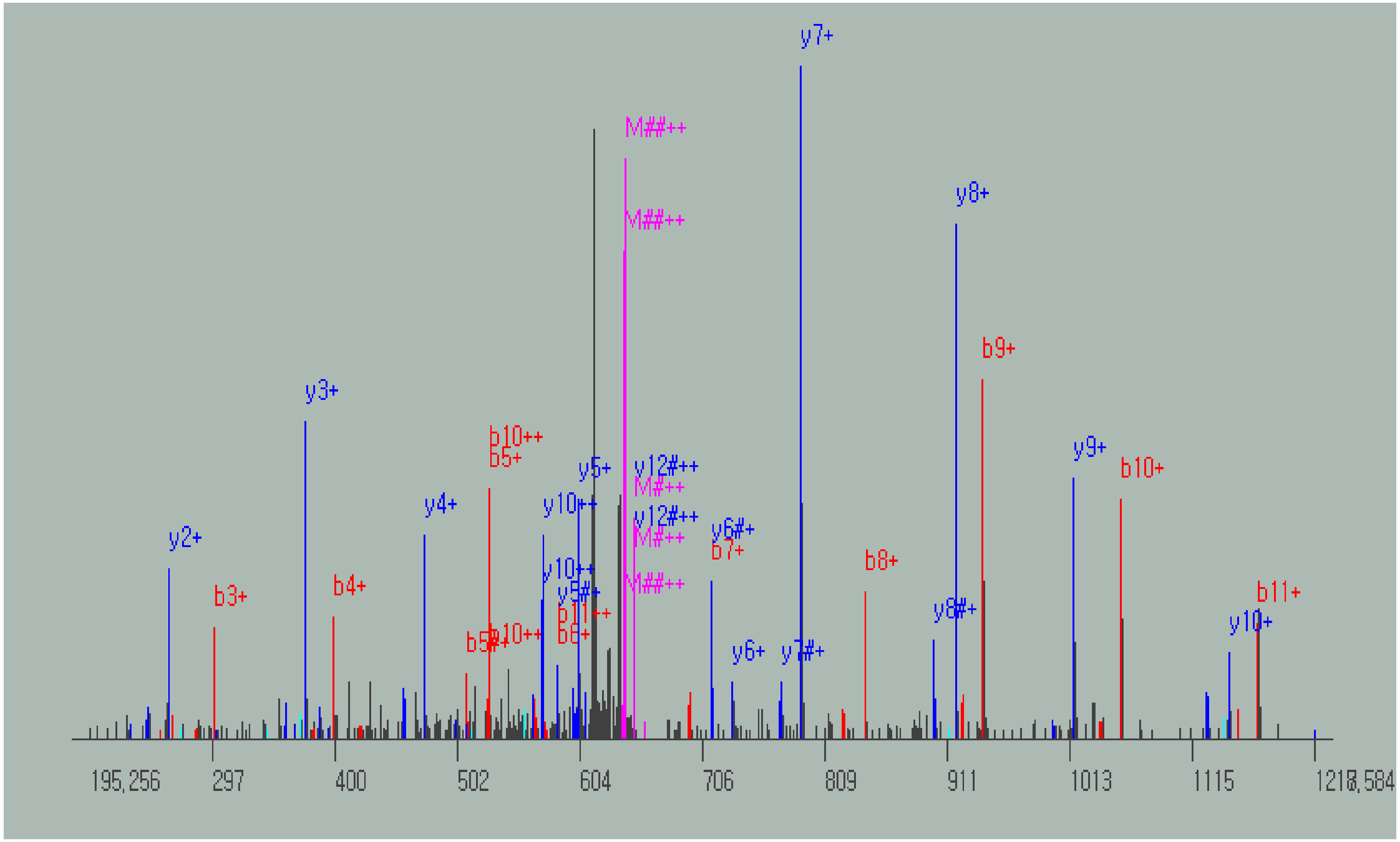
R.TVEVAEGEAVR.T

m/z(1160.25962), charge(+2), Xcorr(3.4137)

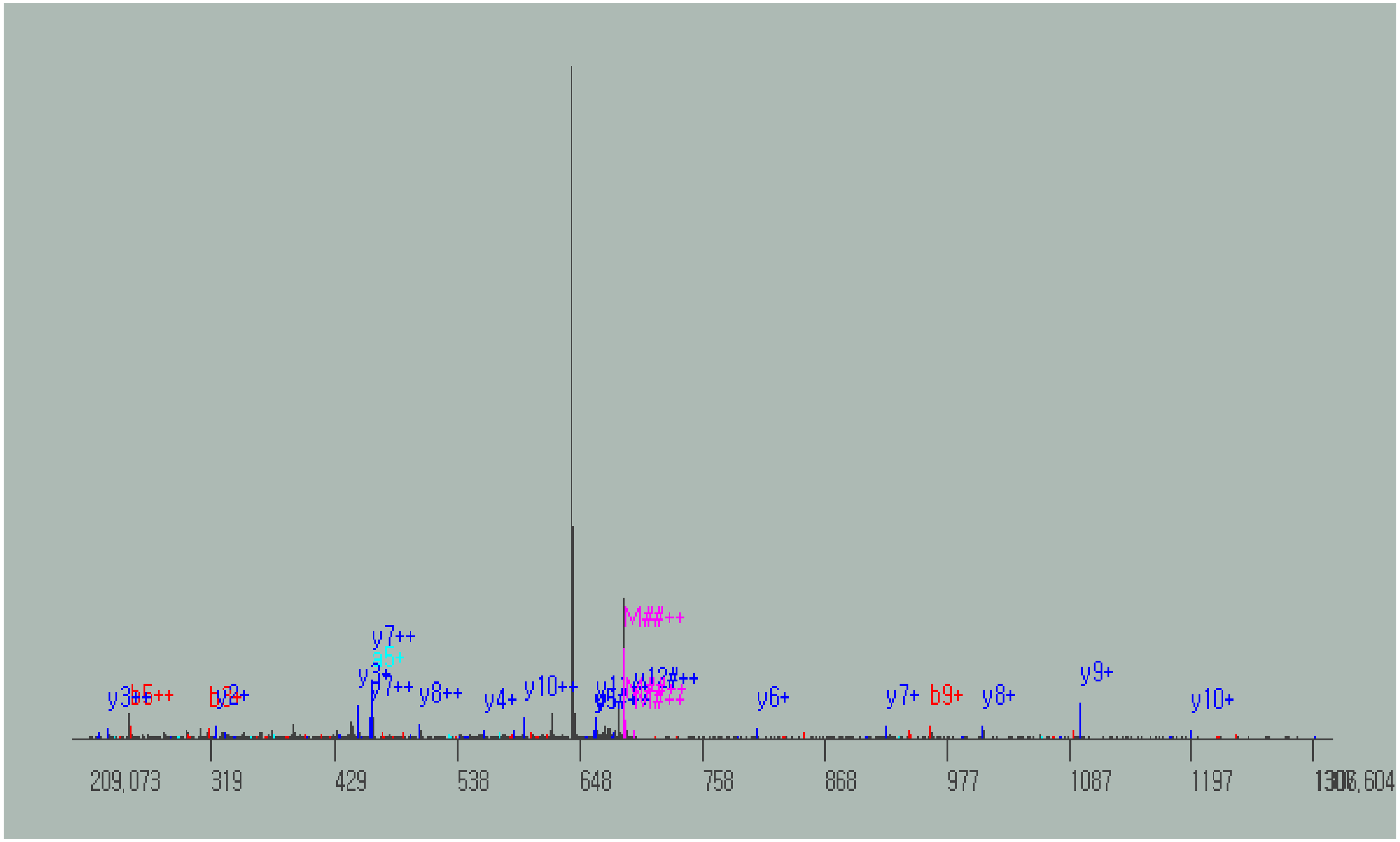


K.VAEVEGEQVDNK.A

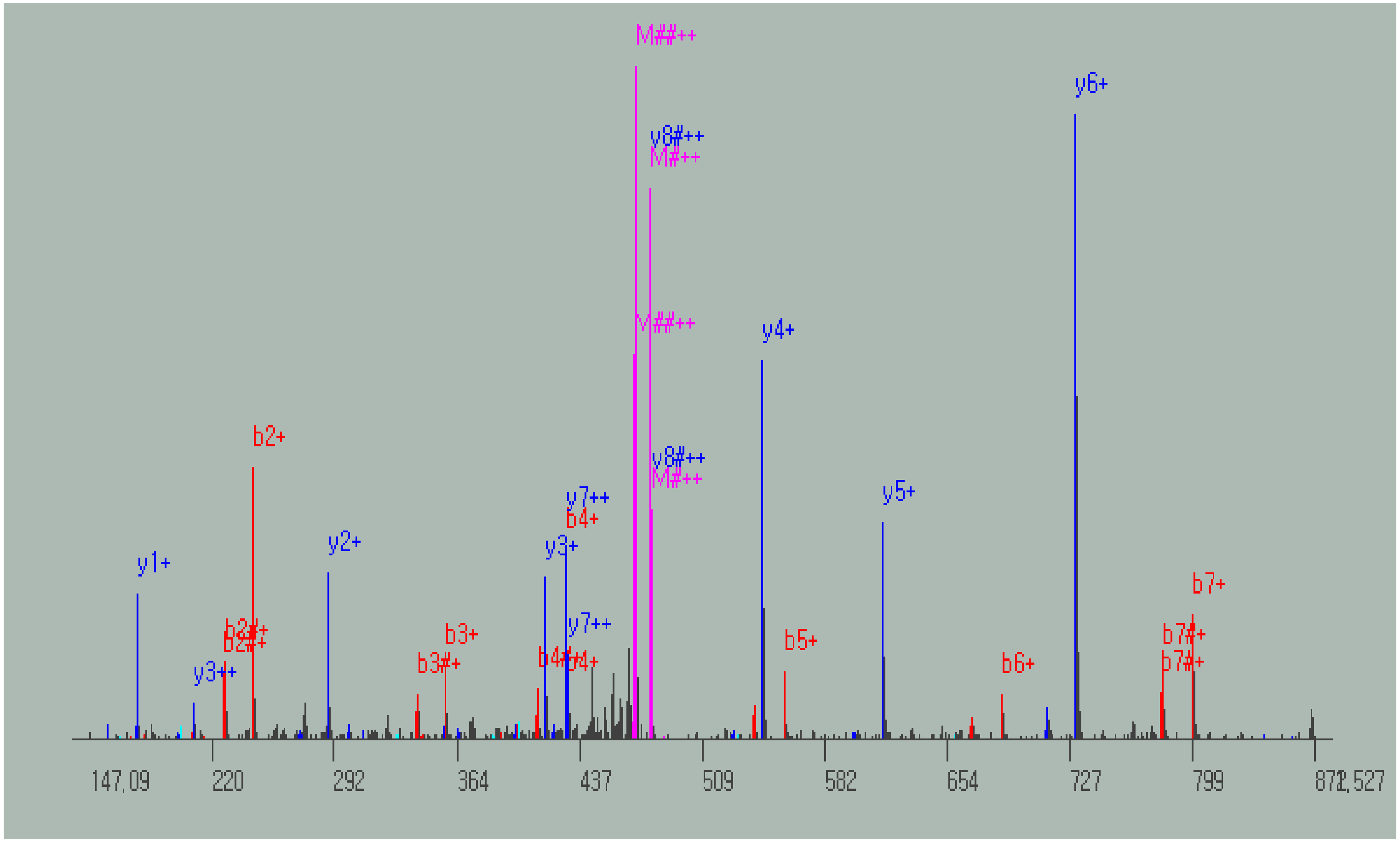
m/z(1317.38437), charge(+2), Xcorr(3.9773)



K.SEVSSDEDIQFR.L
m/z(1412.44102), charge(+2), Xcorr(3.0666)

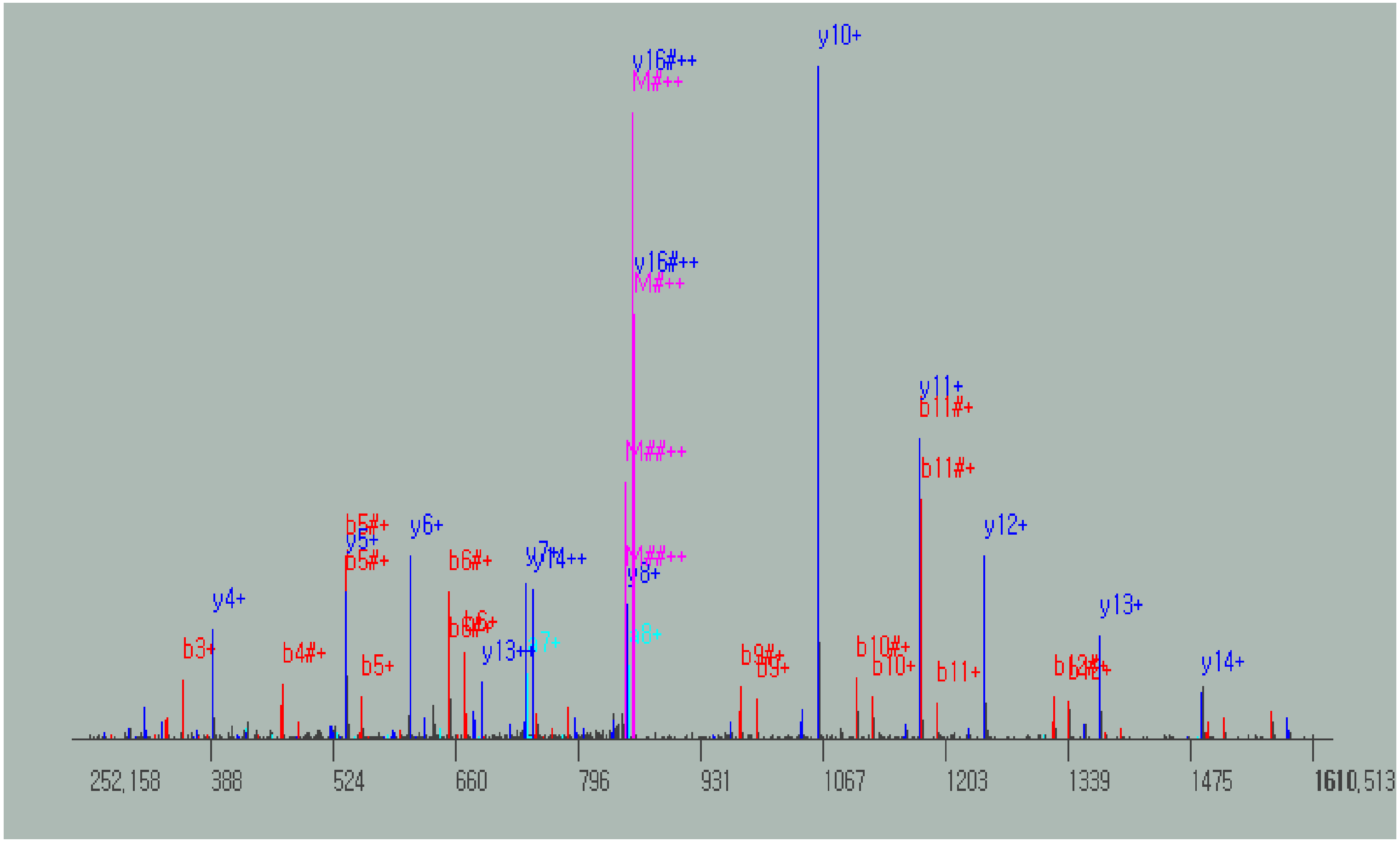


R.DQNAEQIR.L
m/z(974.01048), charge(+2), Xcorr(2.9651)

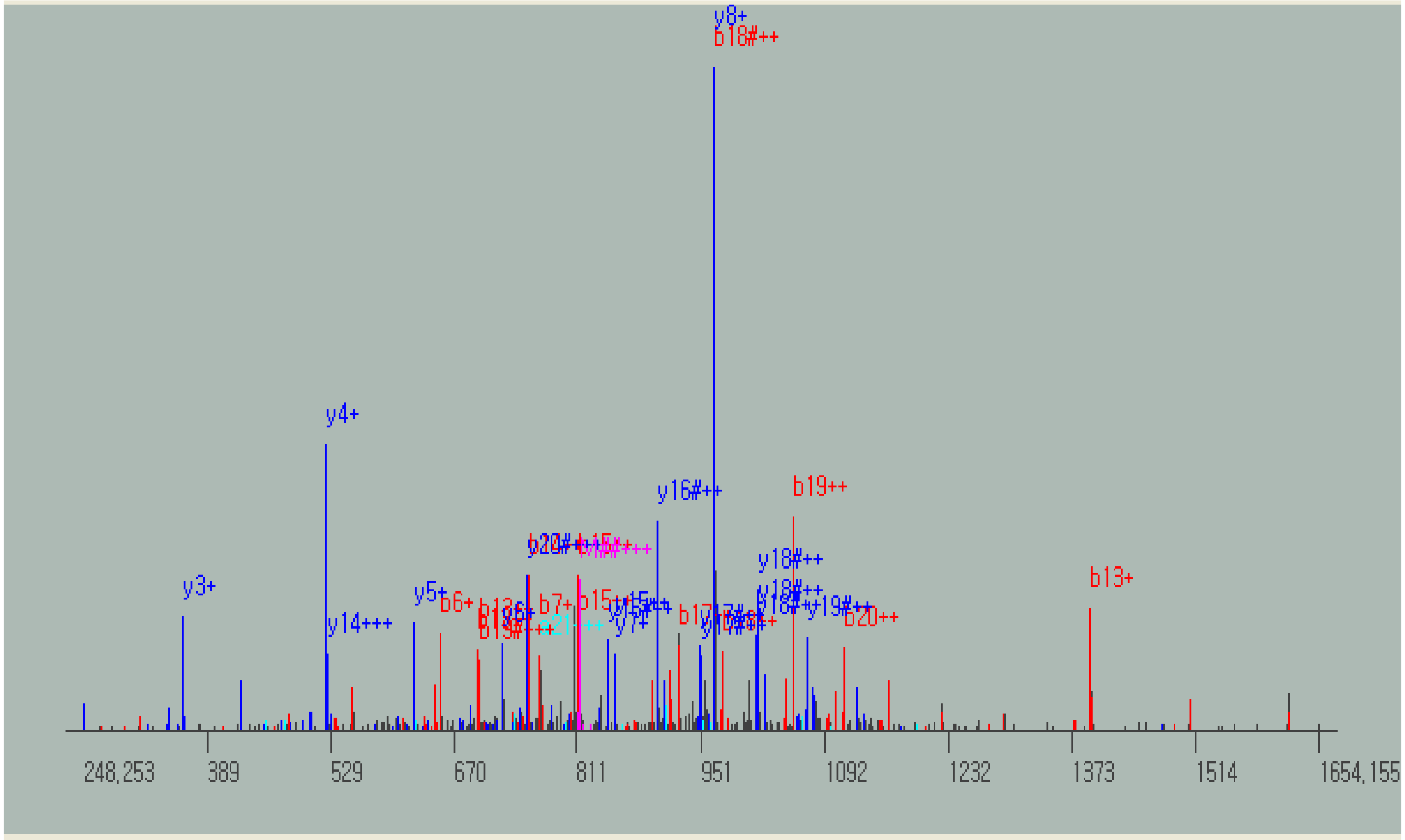


D.QIIQANPLLEAFGNAK.T

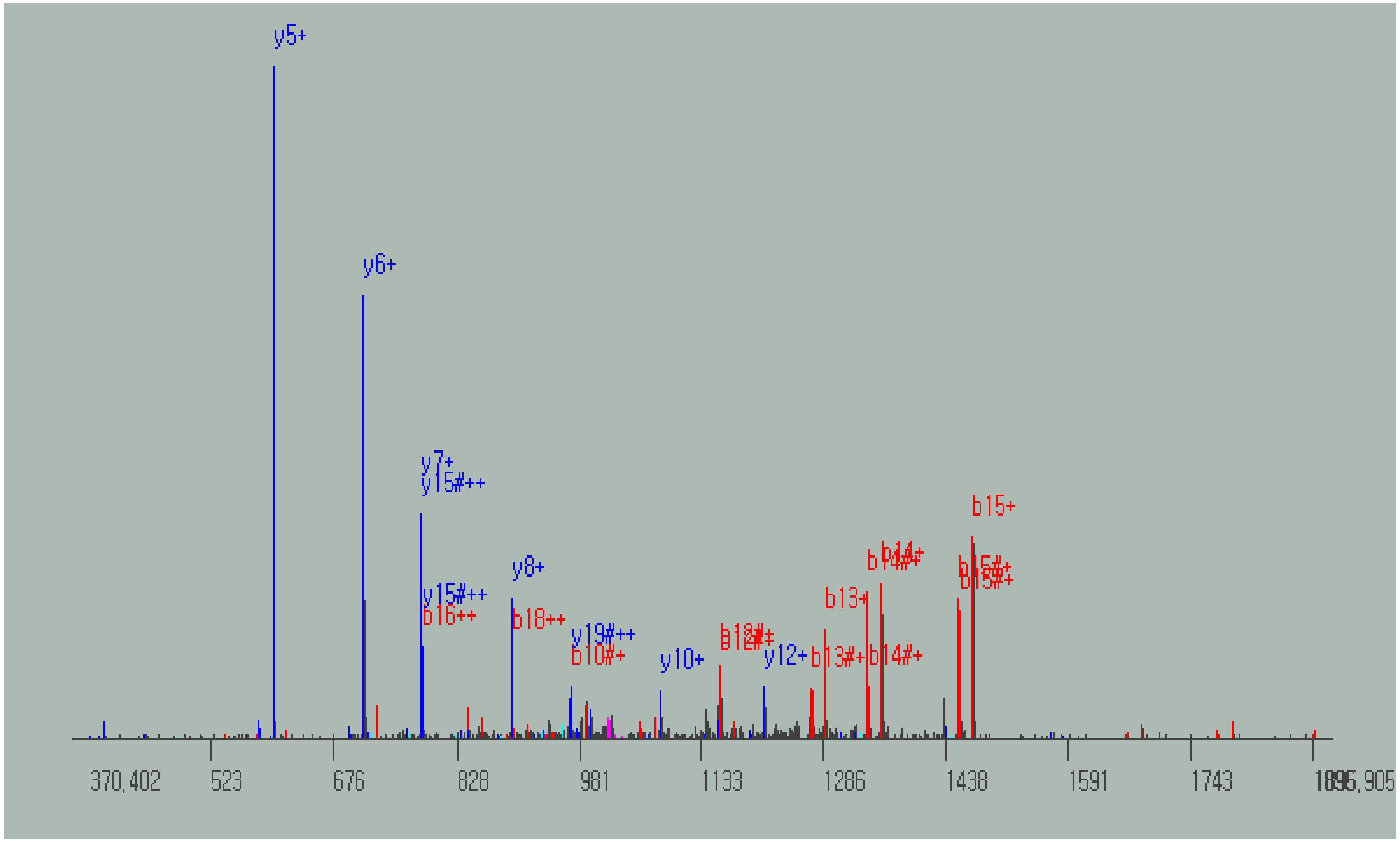
m/z(1727.9854), charge(+2), Xcorr(5.058)



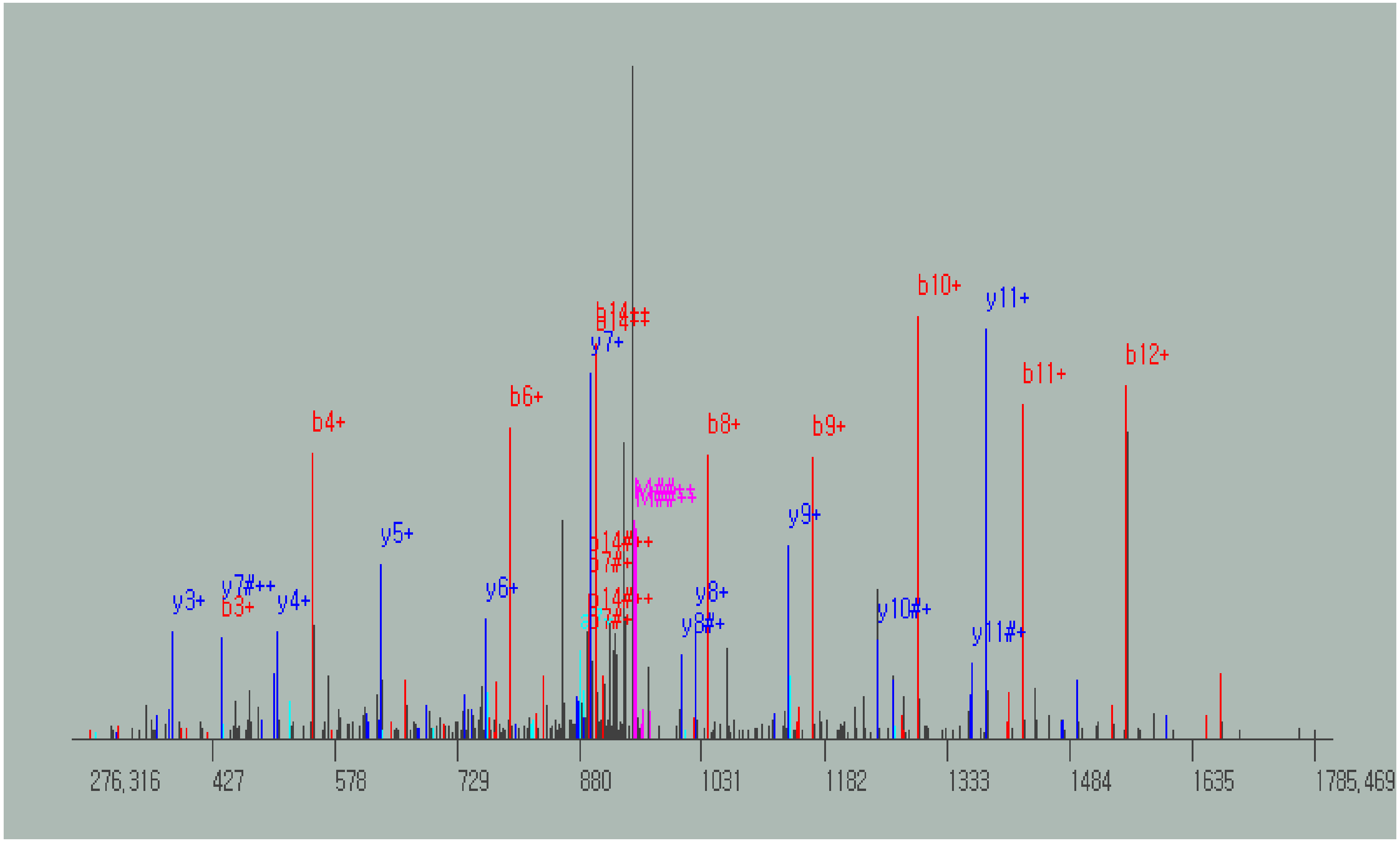
R.AELLQVLQSLEAVLIQTVYNTK.M
m/z(2474.87811), charge(+3), Xcorr(5.3097)



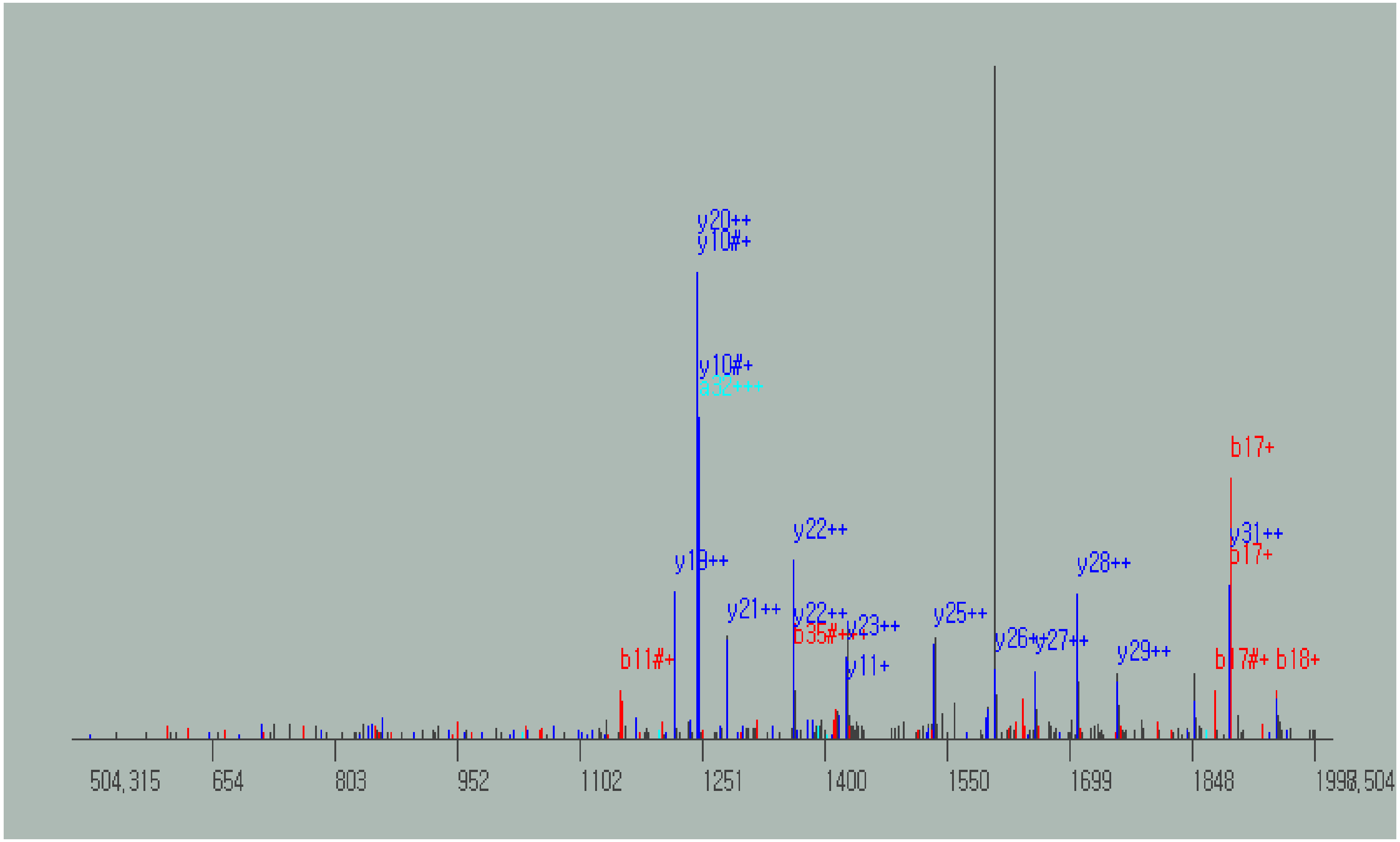
R.LSLATFLLGASVLALPLLTR.A
m/z(2070.54707), charge(+2), Xcorr(4.0881)



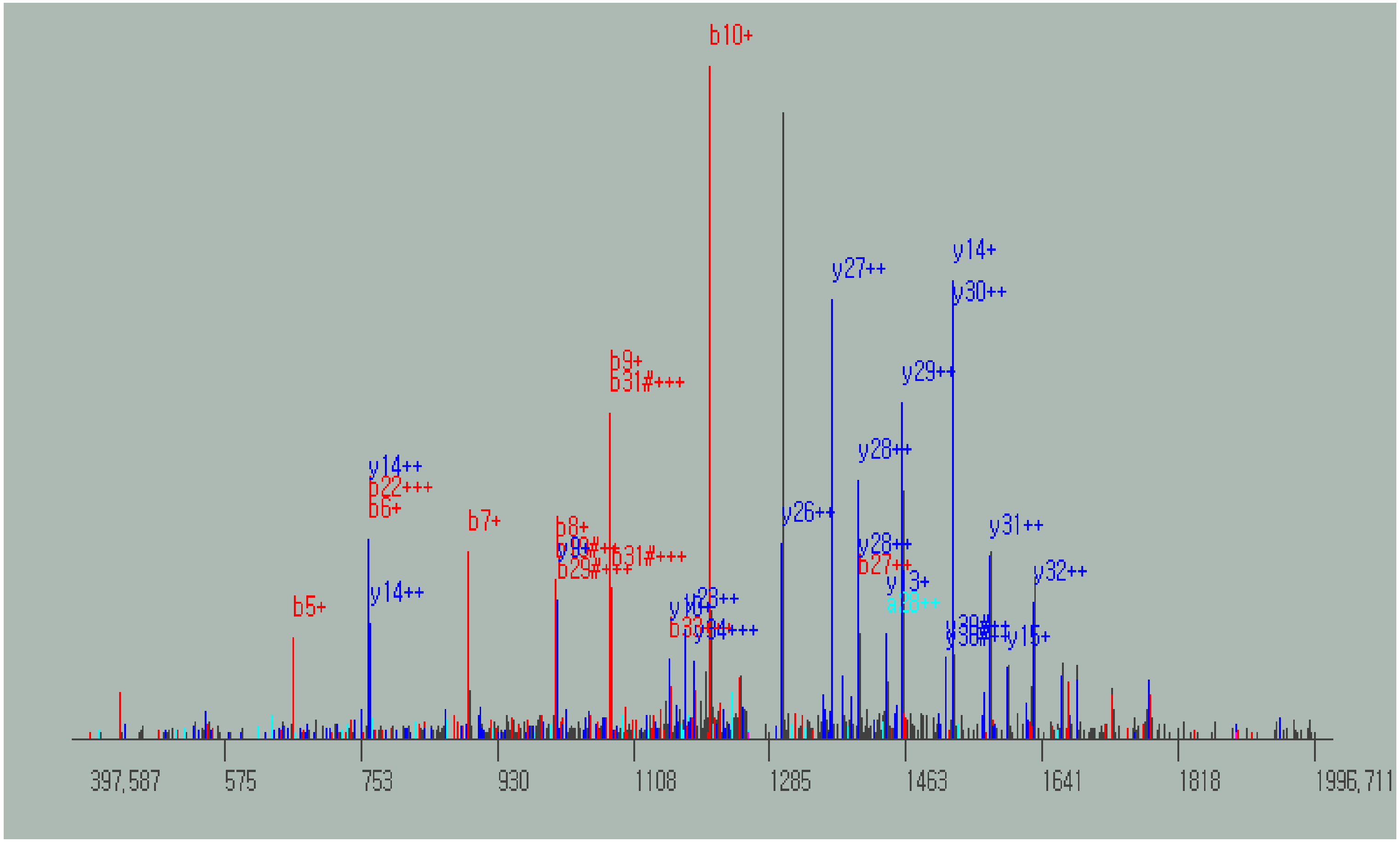
R.YFQINQDEEEEEDED.-
m/z(1932.84315), charge(+2), Xcorr(4.7881)



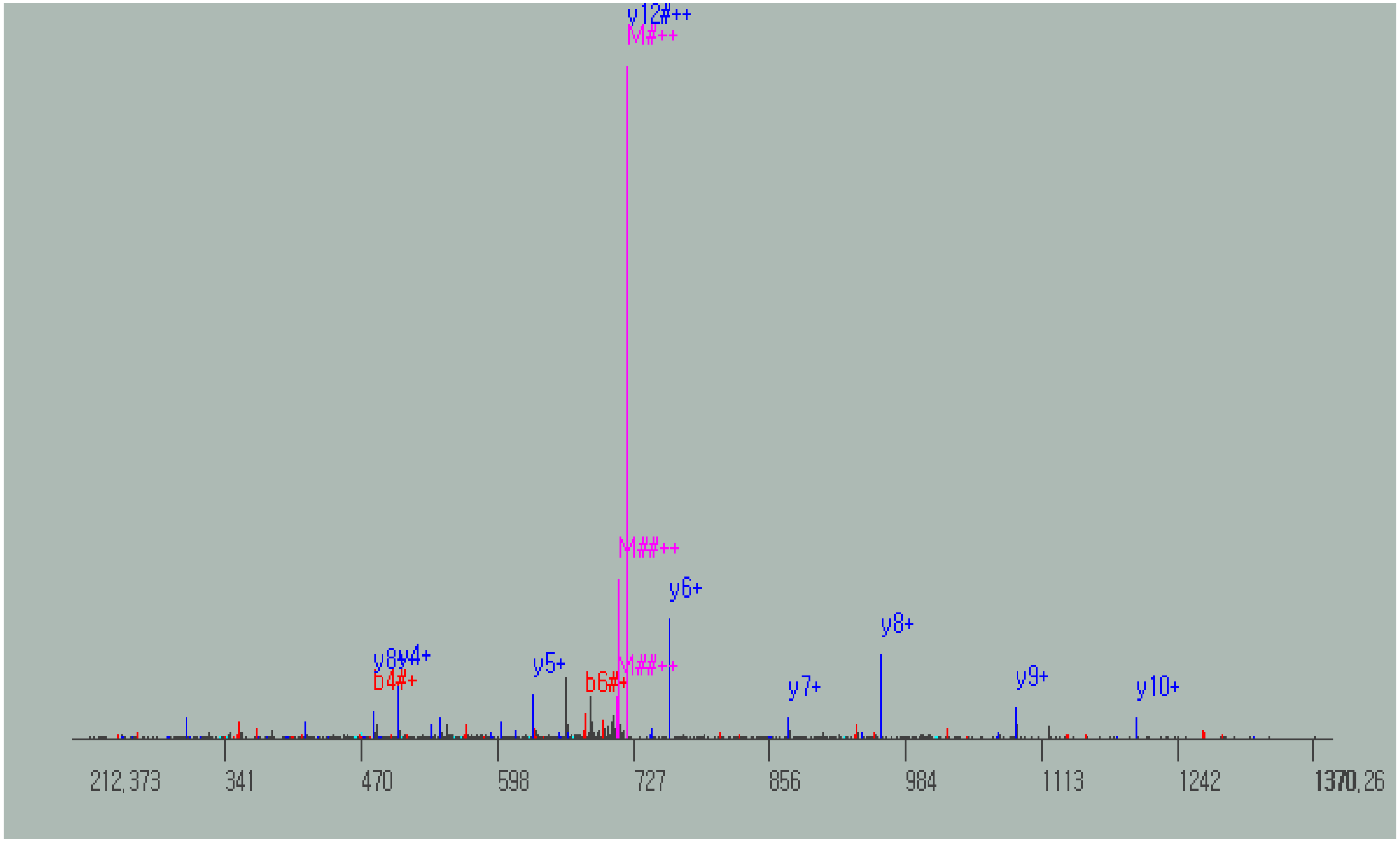
R.DLGAQISWVTVFLTEYAGPLFIYLLLFYFRVPFIYGHK.Y
m/z(4387.12429), charge(+3), Xcorr(4.8401)



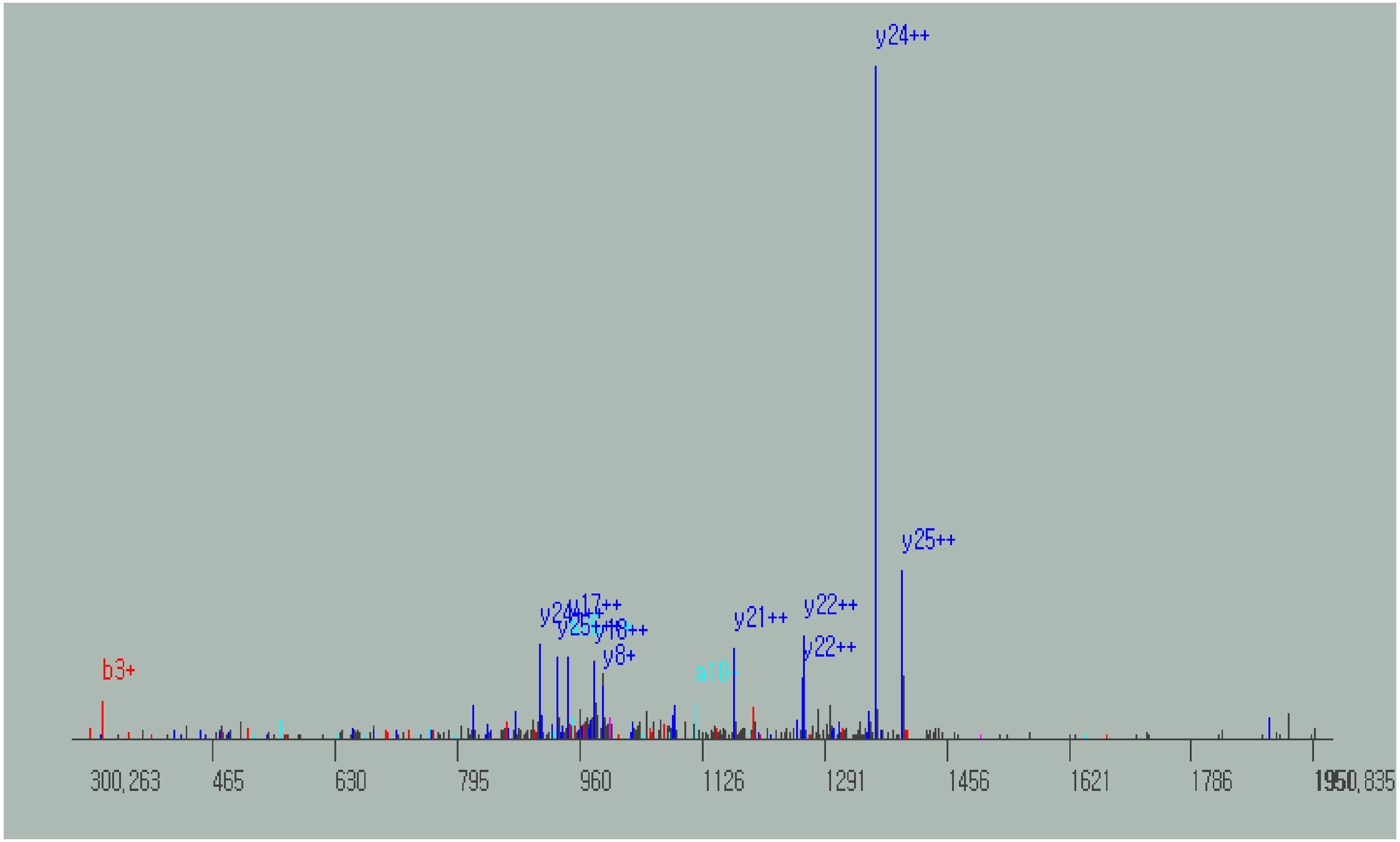
R.LHWLLVEDAEGPTPLVSGLLAASGLLFTHLVVLTPK.A
m/z(3809.49129), charge(+3), Xcorr(6.4946)



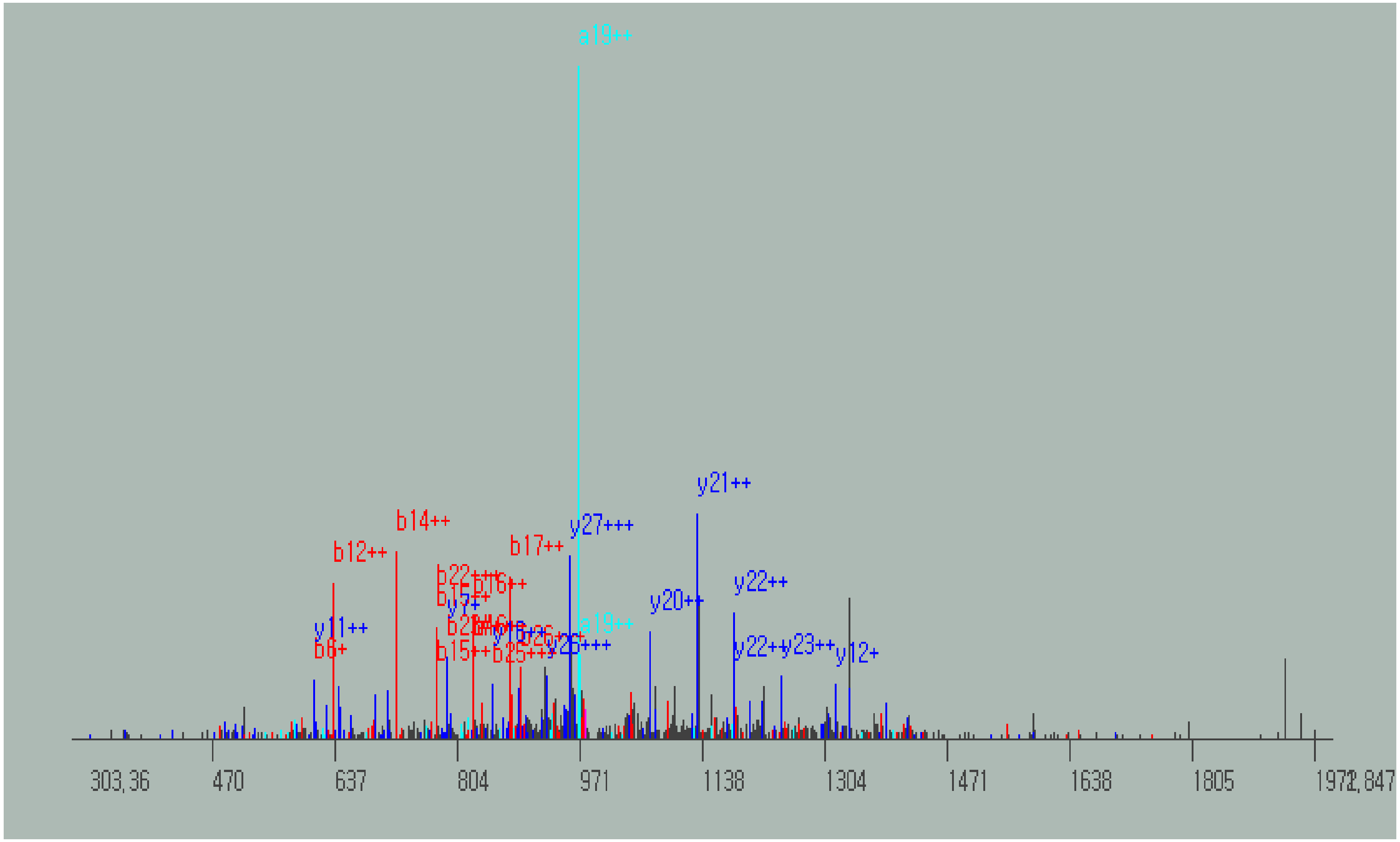
K.QQIQSIQQSIER.L
m/z(1458.60242), charge(+2), Xcorr(2.8565)



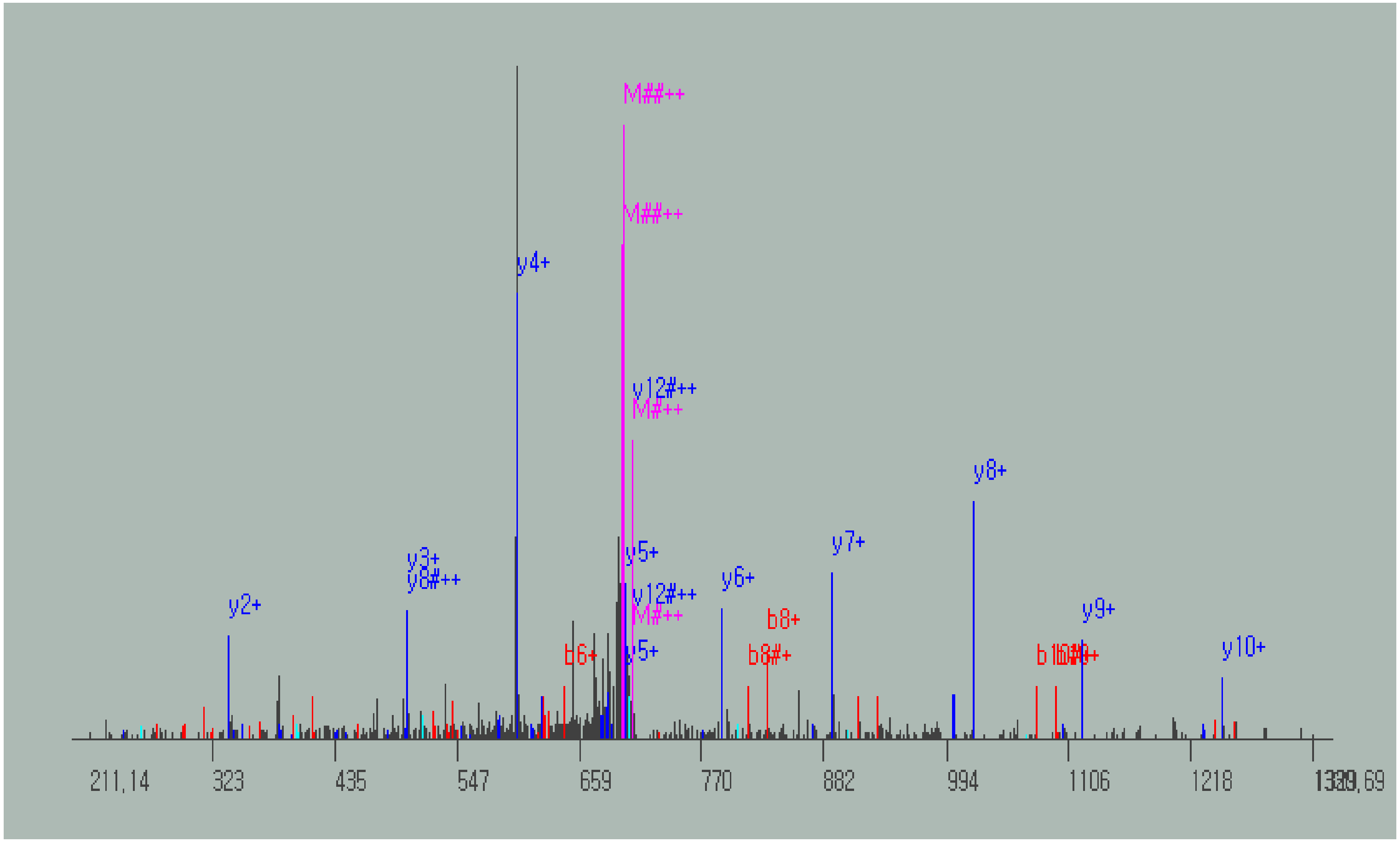
-.M*VAPVWYLVAAALLVGFILFLTRSRGR.A
m/z(3037.69752), charge(+3), Xcorr(4.0888)



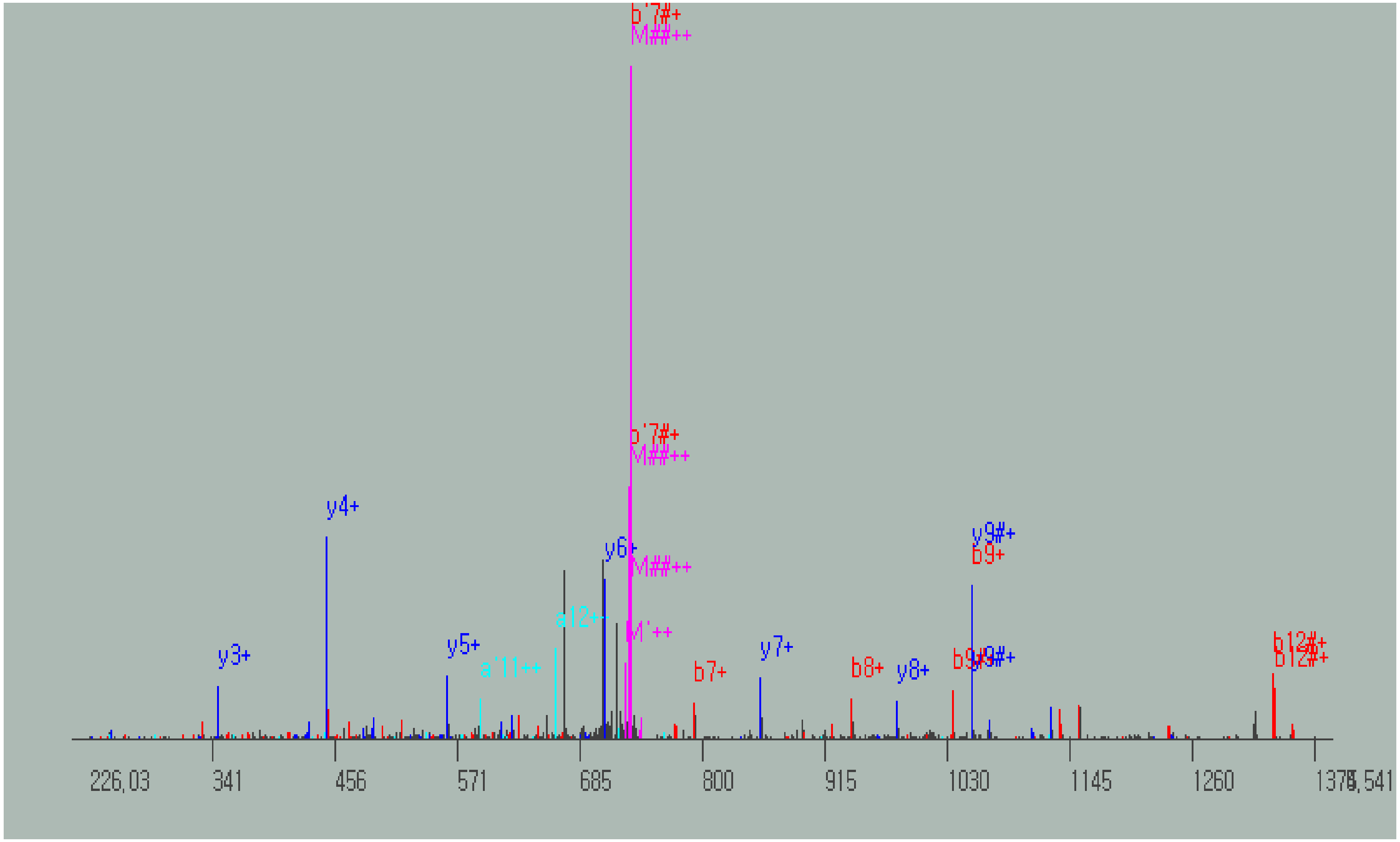
K.VPVGQEVEGM*NILGLVVFAIVFGVALRK.L
m/z(2972.57578), charge(+3), Xcorr(6.6688)



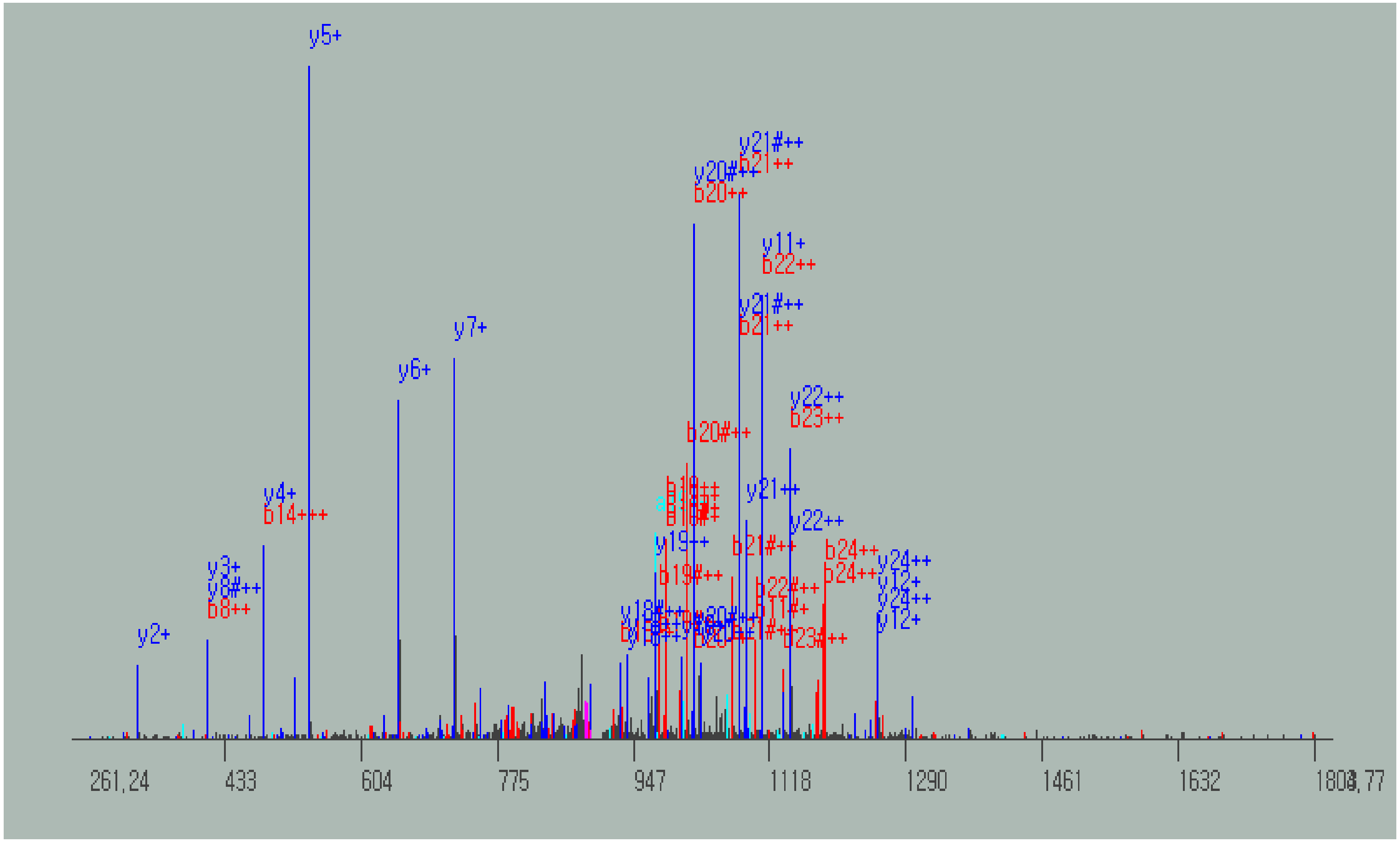
K.GQEVETSVTYYR.L
m/z(1432.51706), charge(+2), Xcorr(2.7351)



K.D]TNGSQFFITTVK.T
m/z(1501.60347), charge(+2), Xcorr(3.5646)

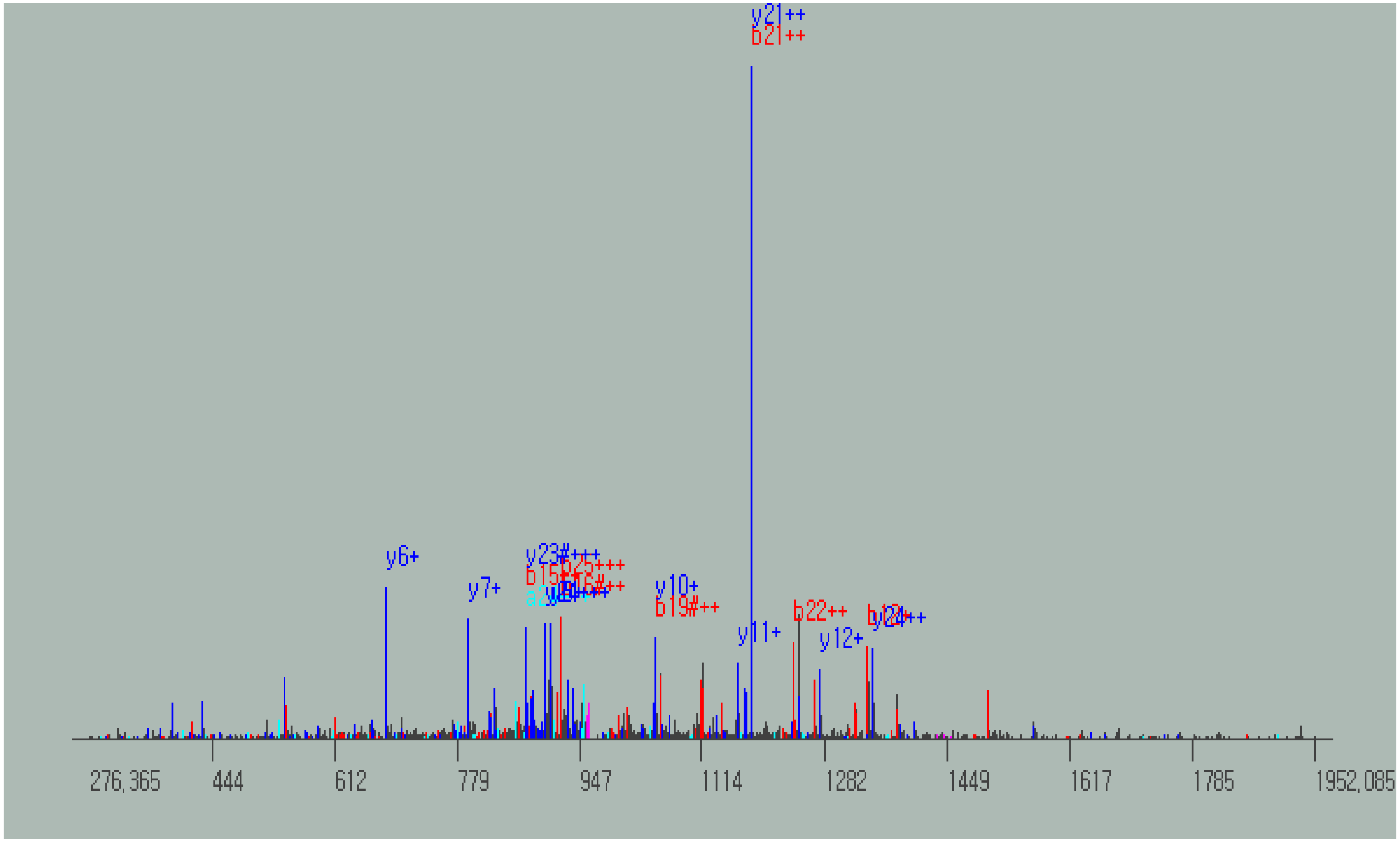


R.VSGYLNLAADLAHNFTDGLAIGASFR.G
m/z(2694.98252), charge(+3), Xcorr(5.2366)

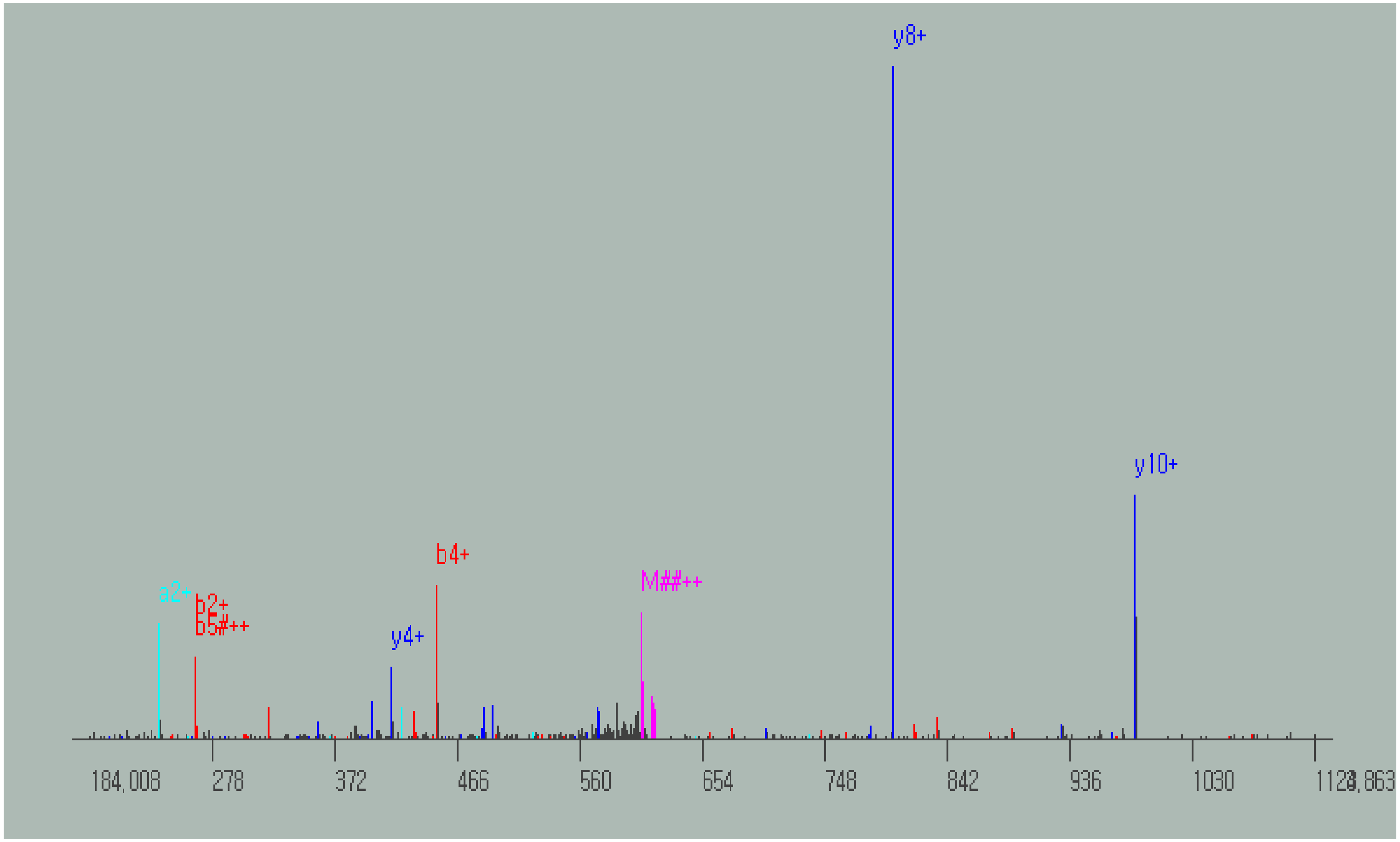


K.VIGFKPEEIQTVYKILAAILHLGNLK.F

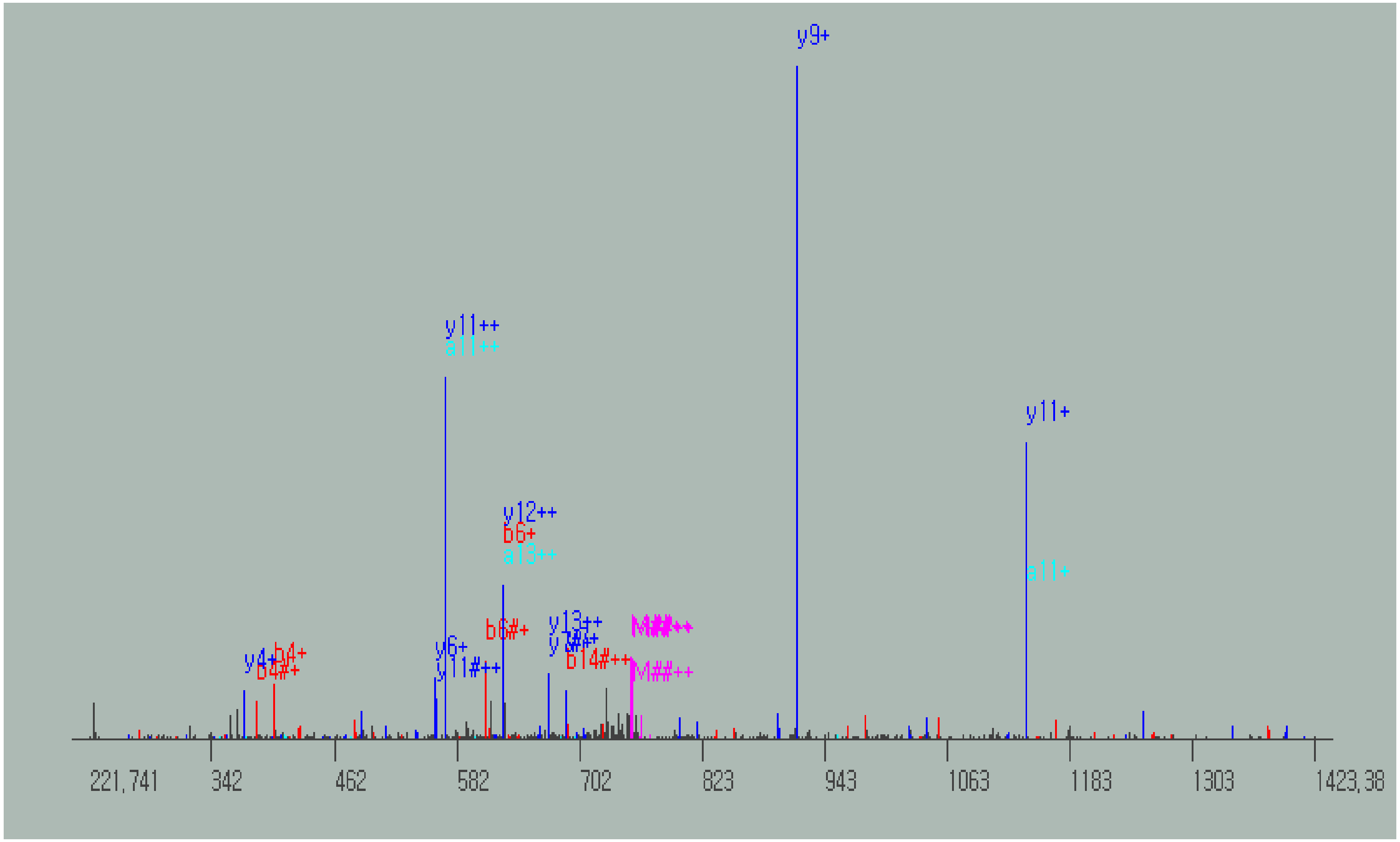
m/z(2909.5007), charge(+3), Xcorr(6.9058)



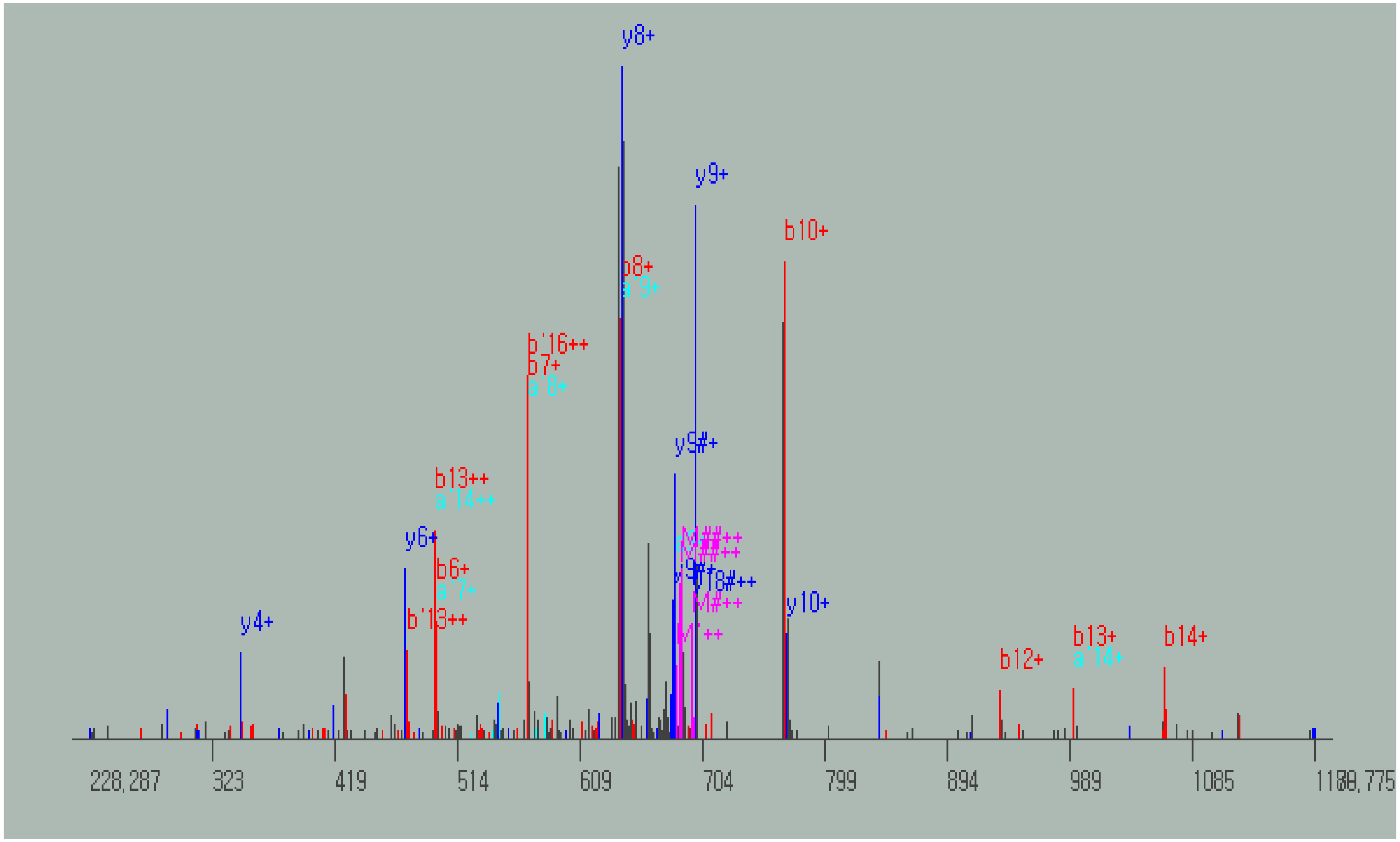
R.TYGEPESAGPSR.A
m/z(1251.28448), charge(+2), Xcorr(3.0517)



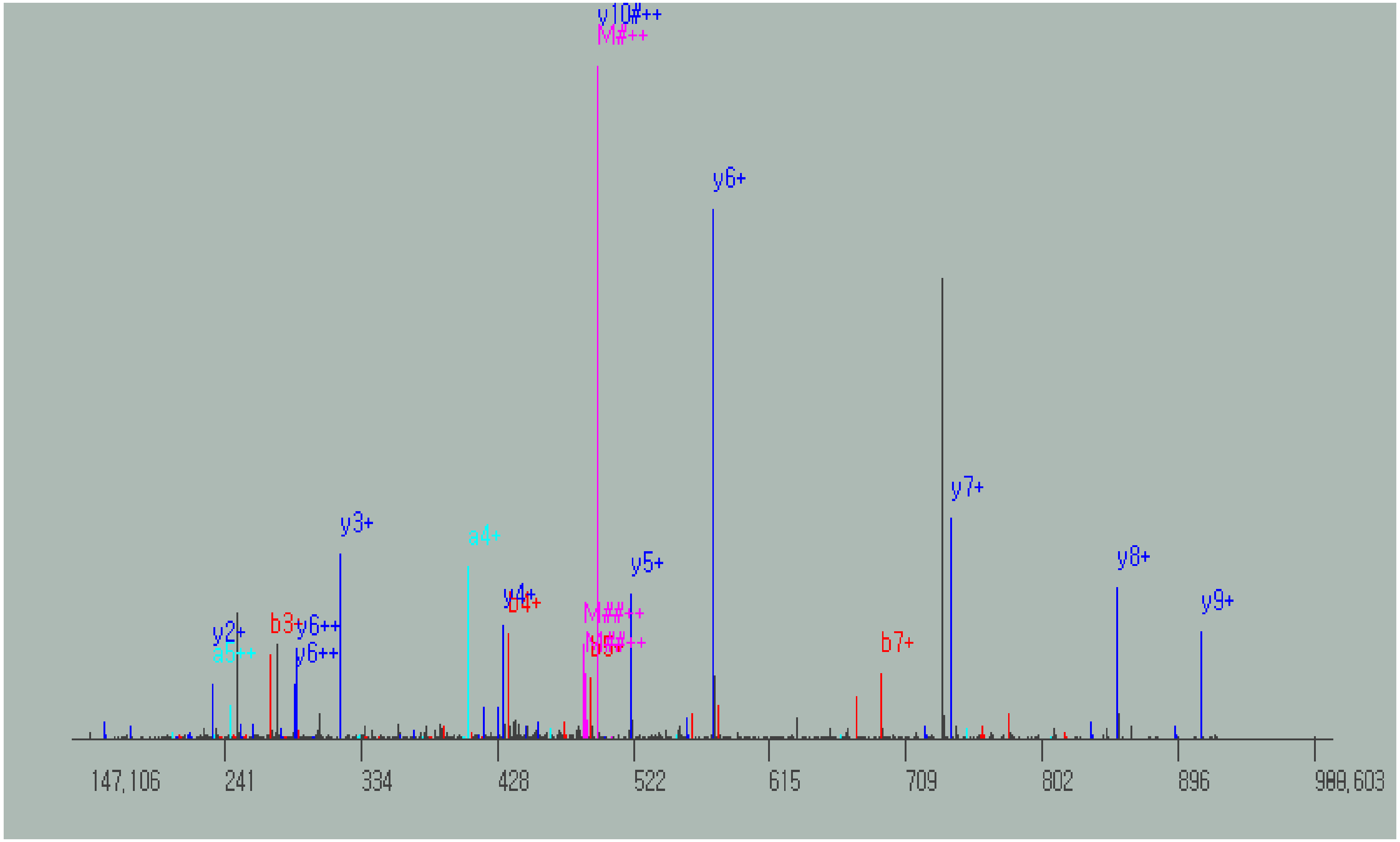
K.EASDPQPEEADGGLK.S
m/z(1543.57145), charge(+2), Xcorr(3.5448)



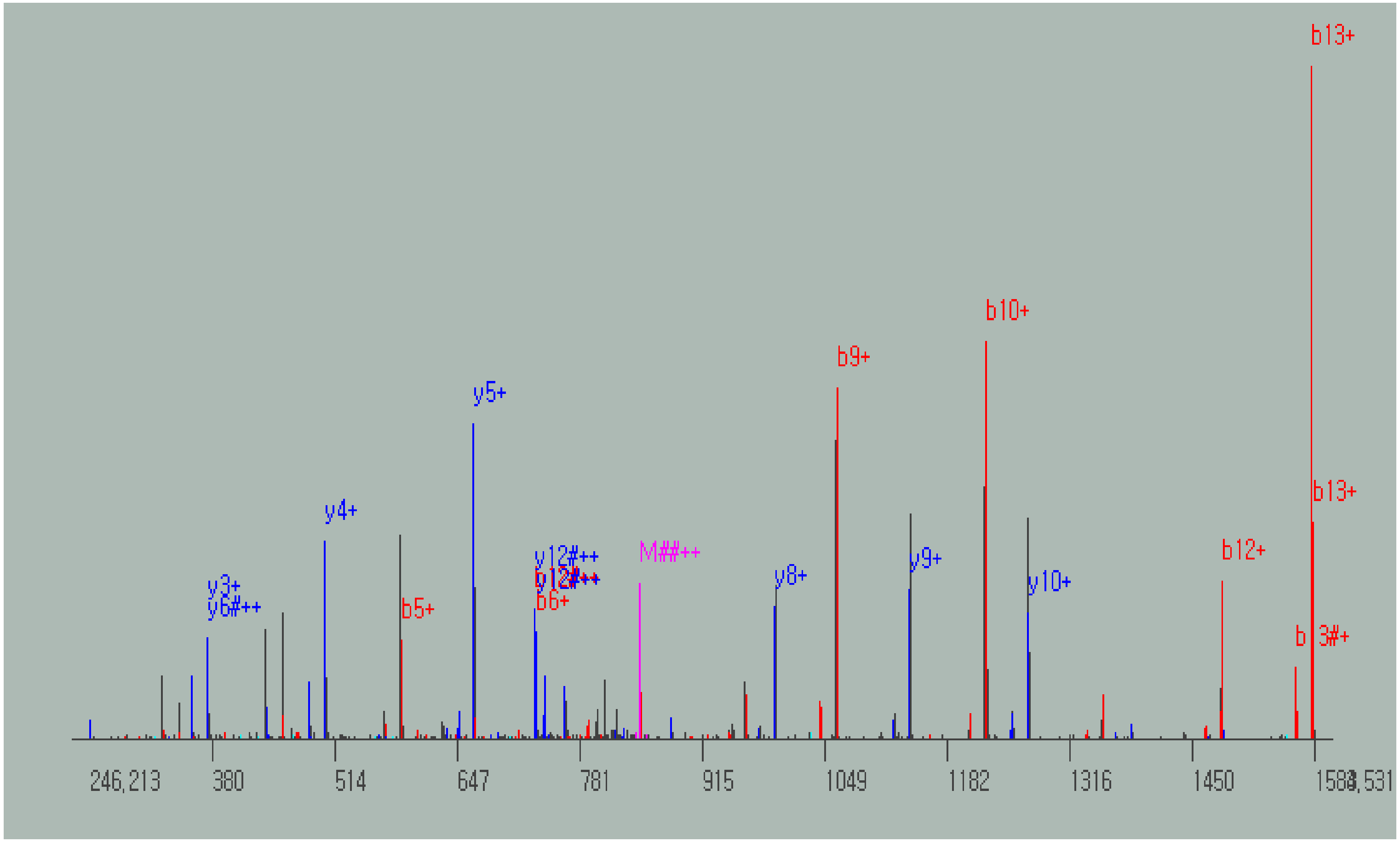
M.A]VAAAAAAAGPAGAGGGR.A
m/z(1410.50202), charge(+2), Xcorr(3.9215)



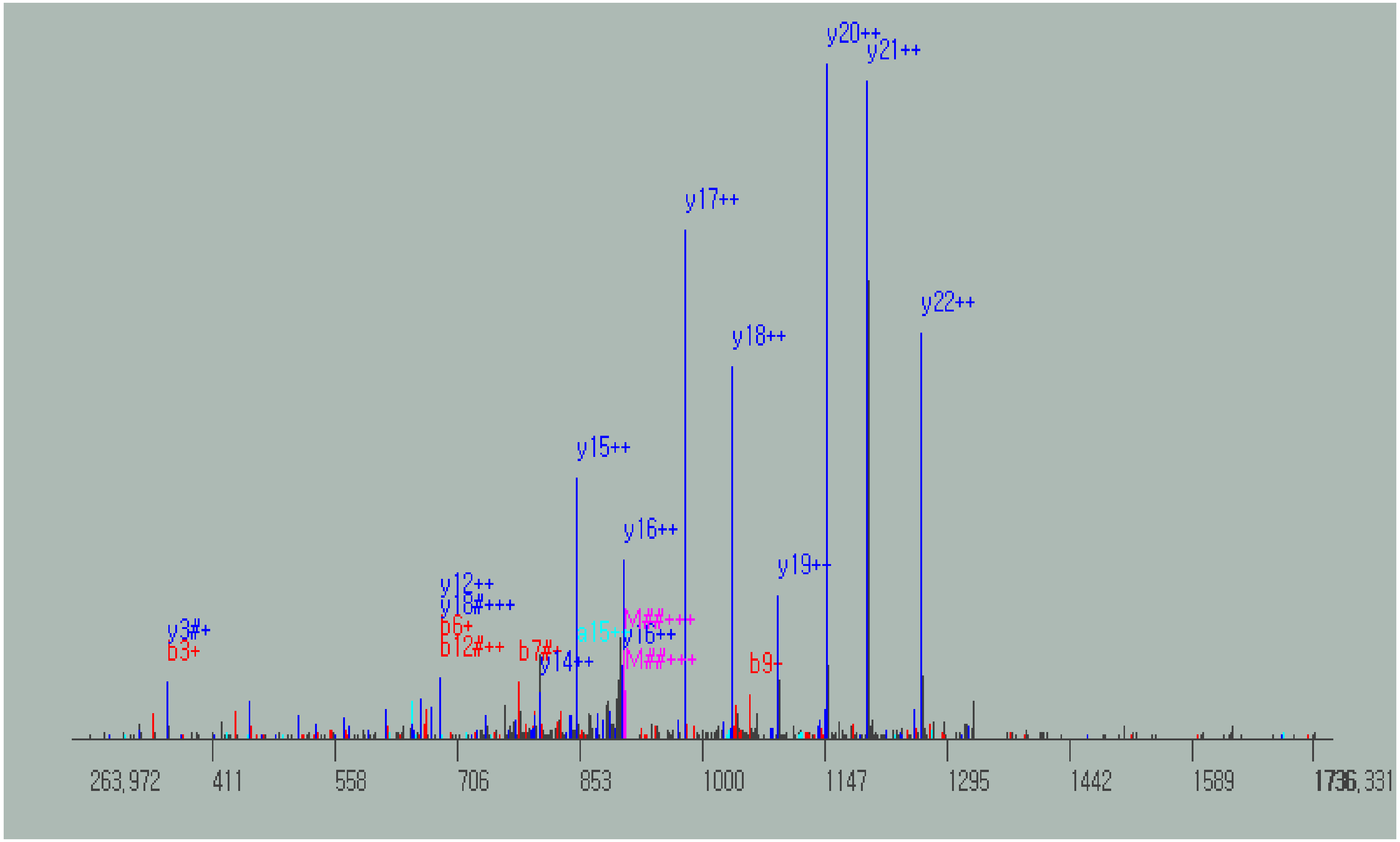
R.VGDYGSLSGR.E
m/z(1011.07073), charge(+2), Xcorr(3.0496)



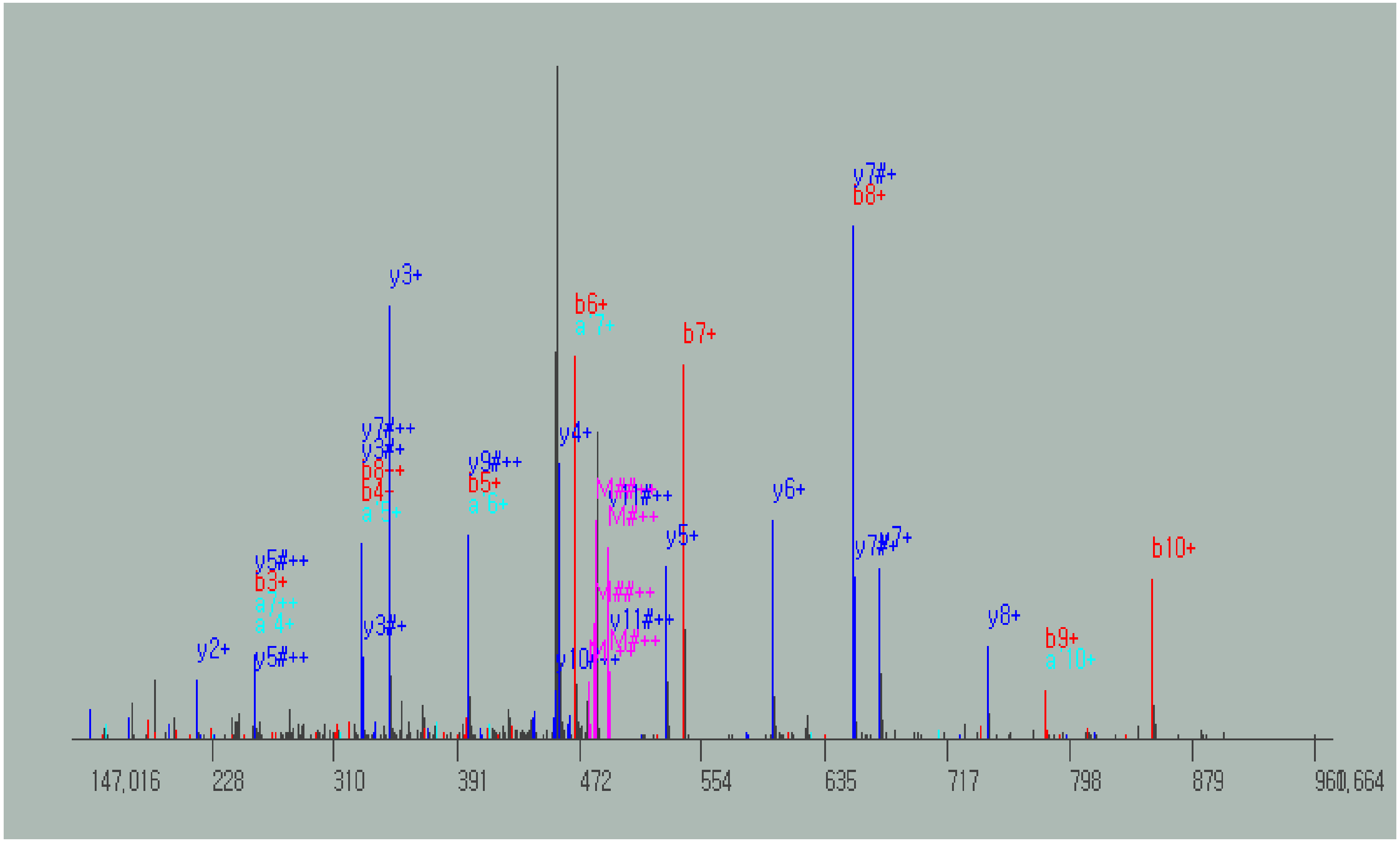
M.A]ETLEFNDVYQEVK.G
m/z(1728.81845), charge(+2), Xcorr(3.8234)



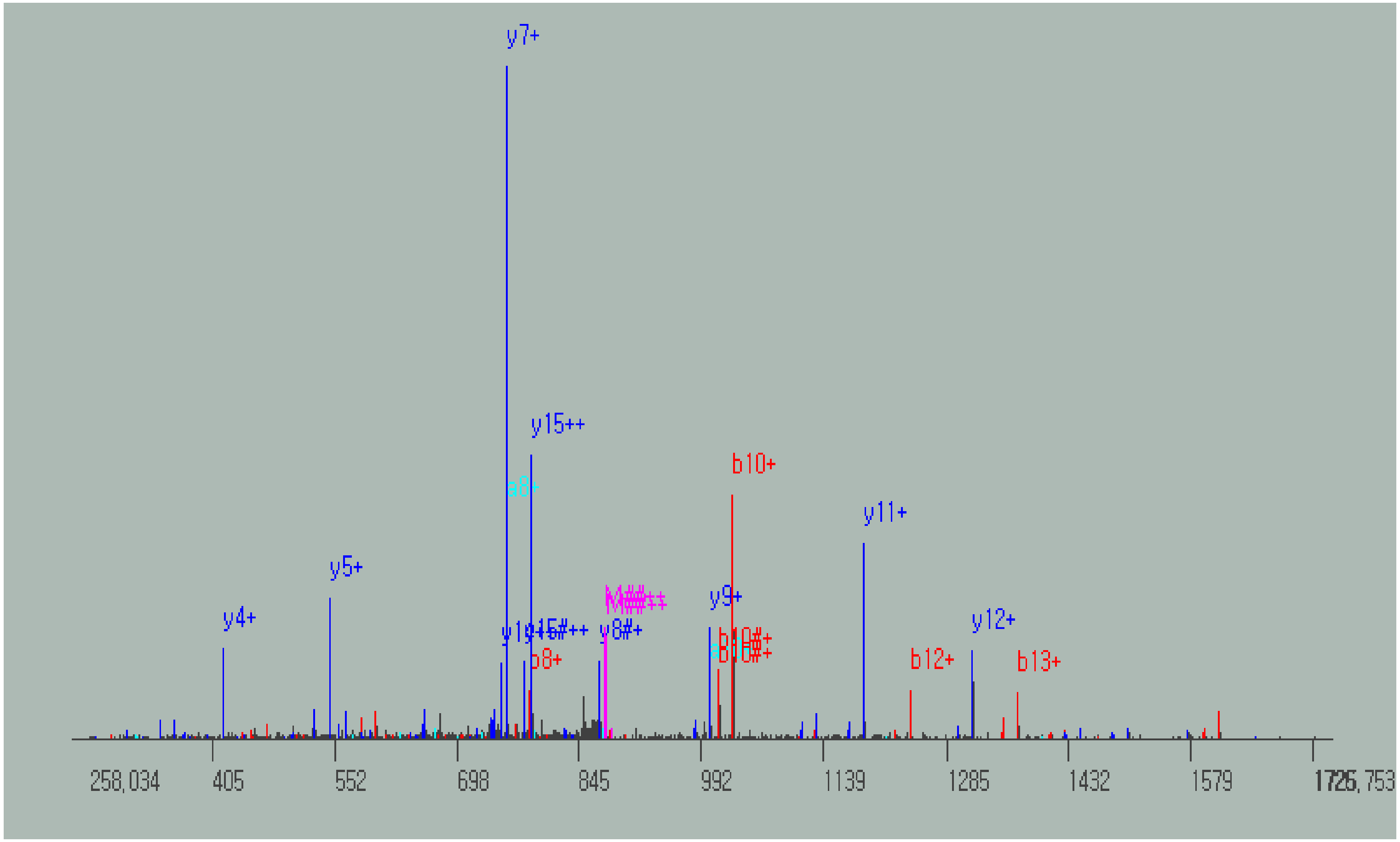
R.NNEVDLLFLSELQVLHDISSLLSR.H
m/z(2756.10408), charge(+3), Xcorr(4.4129)



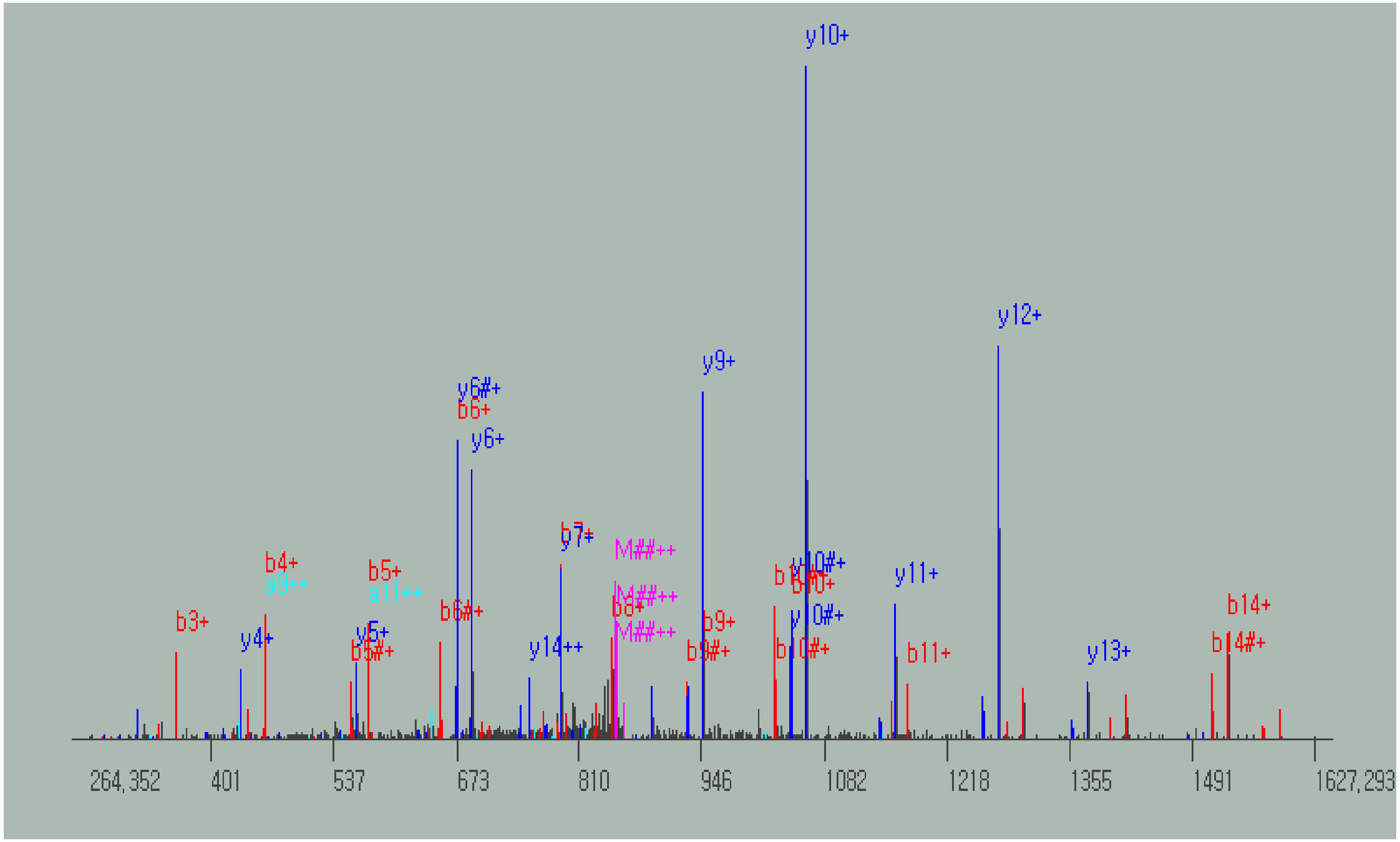
K.A]AAAAAALQAK.S
m/z(1000.11515), charge(+2), Xcorr(3.5766)



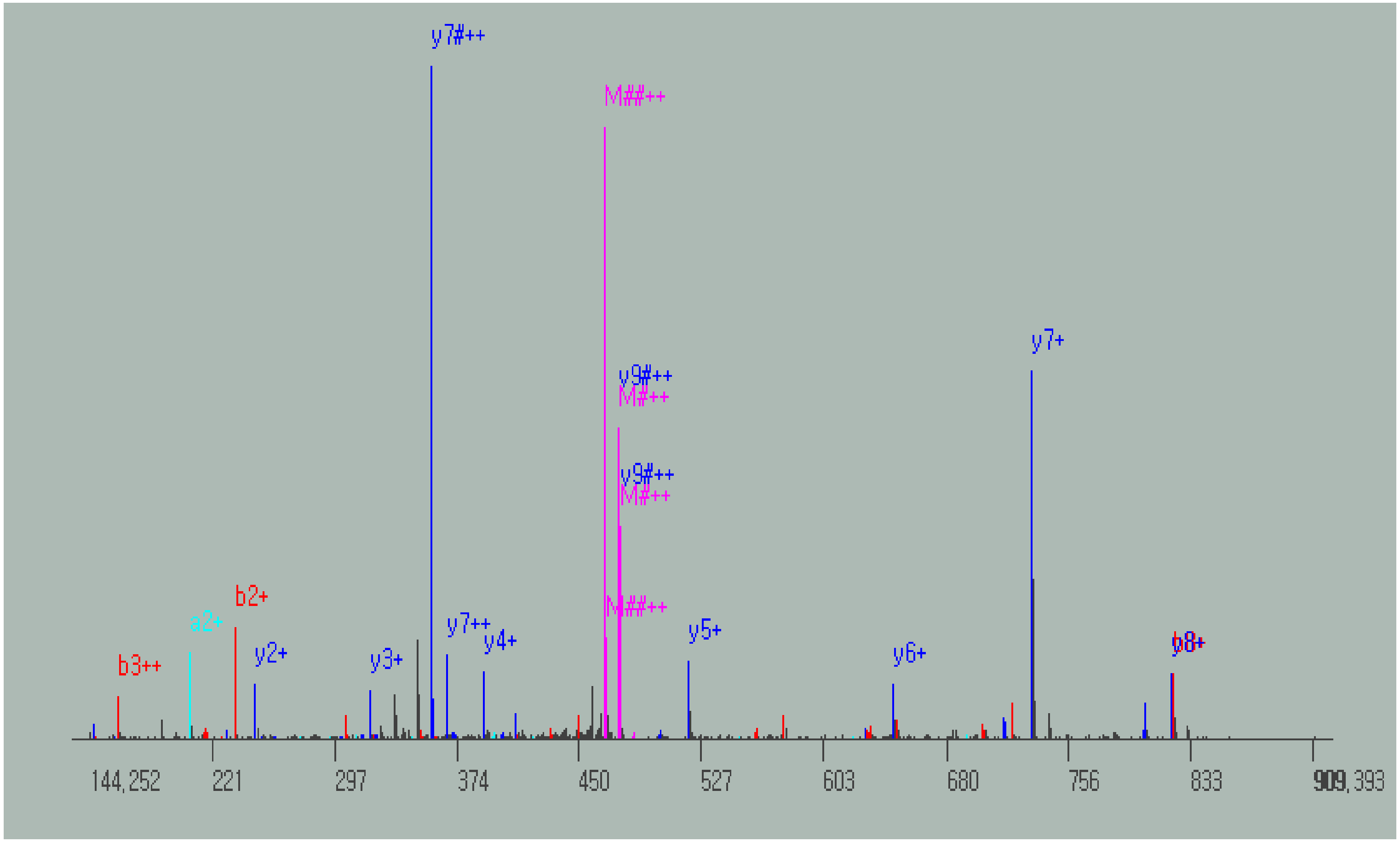
R.LVAGEMGQNEPDQGGQR.G
m/z(1786.90533), charge(+2), Xcorr(5.2387)



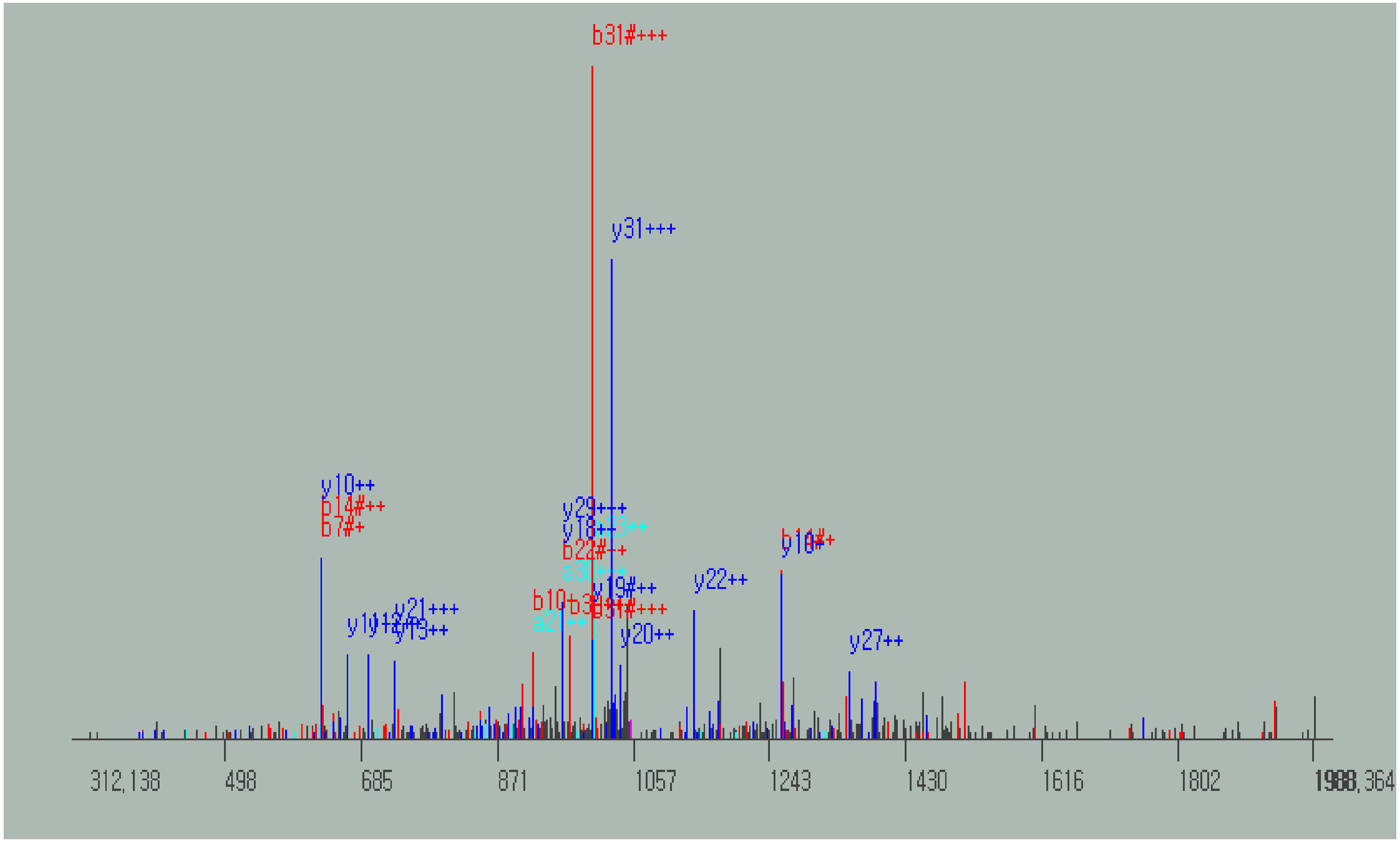
A.DDEVDVDGTVEEDLGK.S
m/z(1735.73885), charge(+2), Xcorr(5.4503)



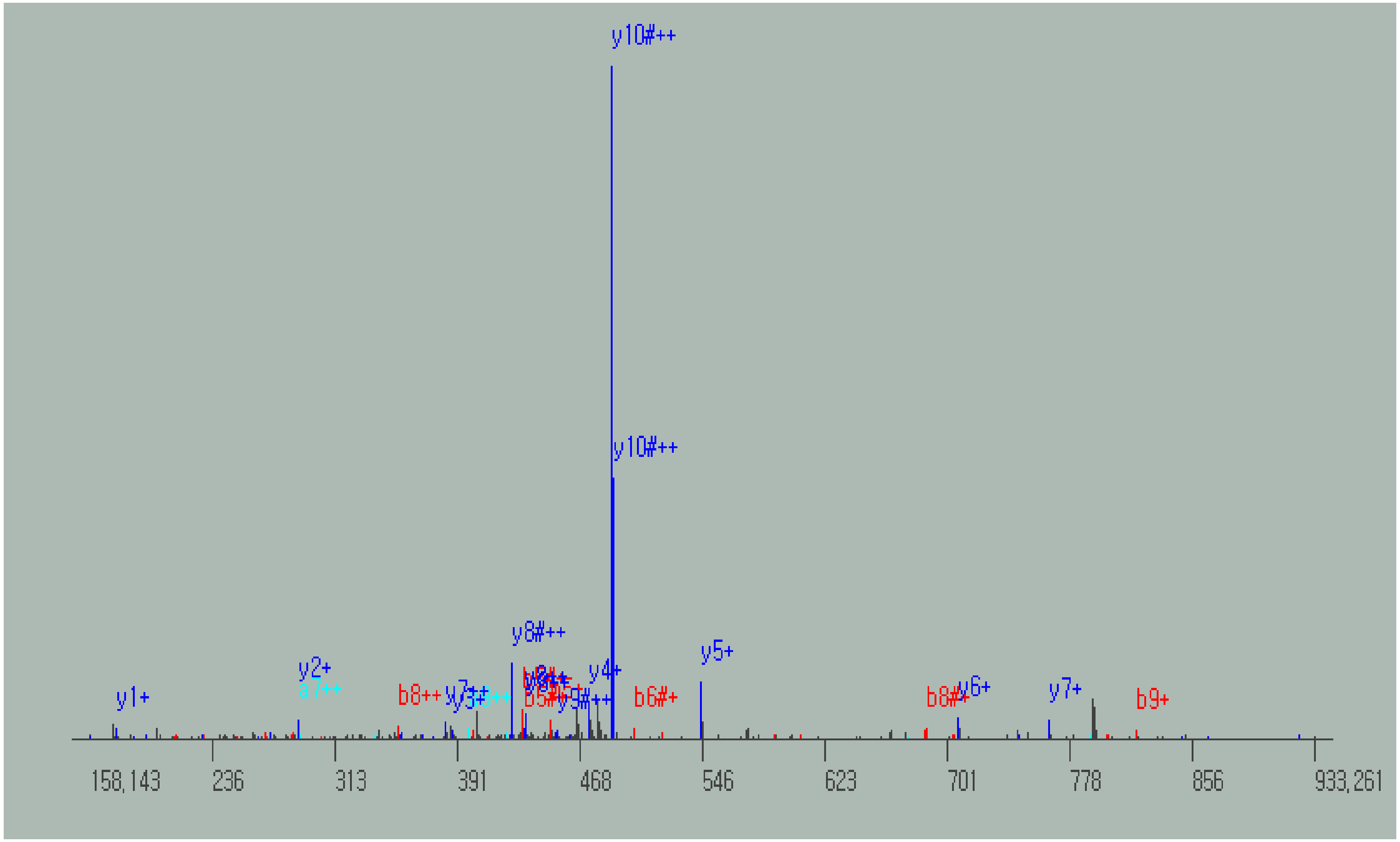
K.FSSQQAATK.Q
m/z(968.04585), charge(+2), Xcorr(2.8068)



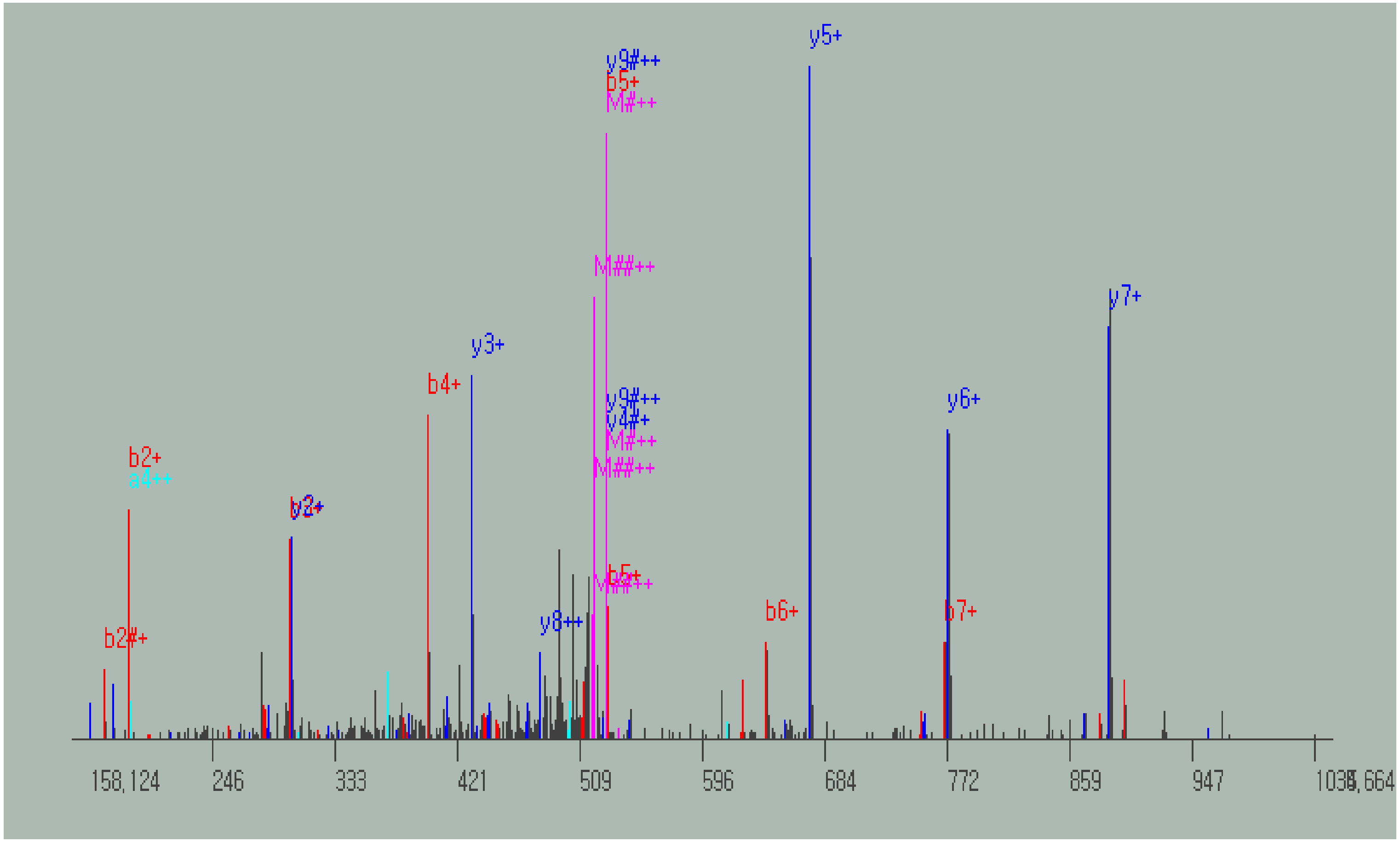
K.DNSTASASLASNGTSGGQEAGAPEEEEDELLR.V
m/z(3194.19258), charge(+3), Xcorr(5.714)



R.AGTGYASPDR.T
m/z(995.02816), charge(+2), Xcorr(2.5104)

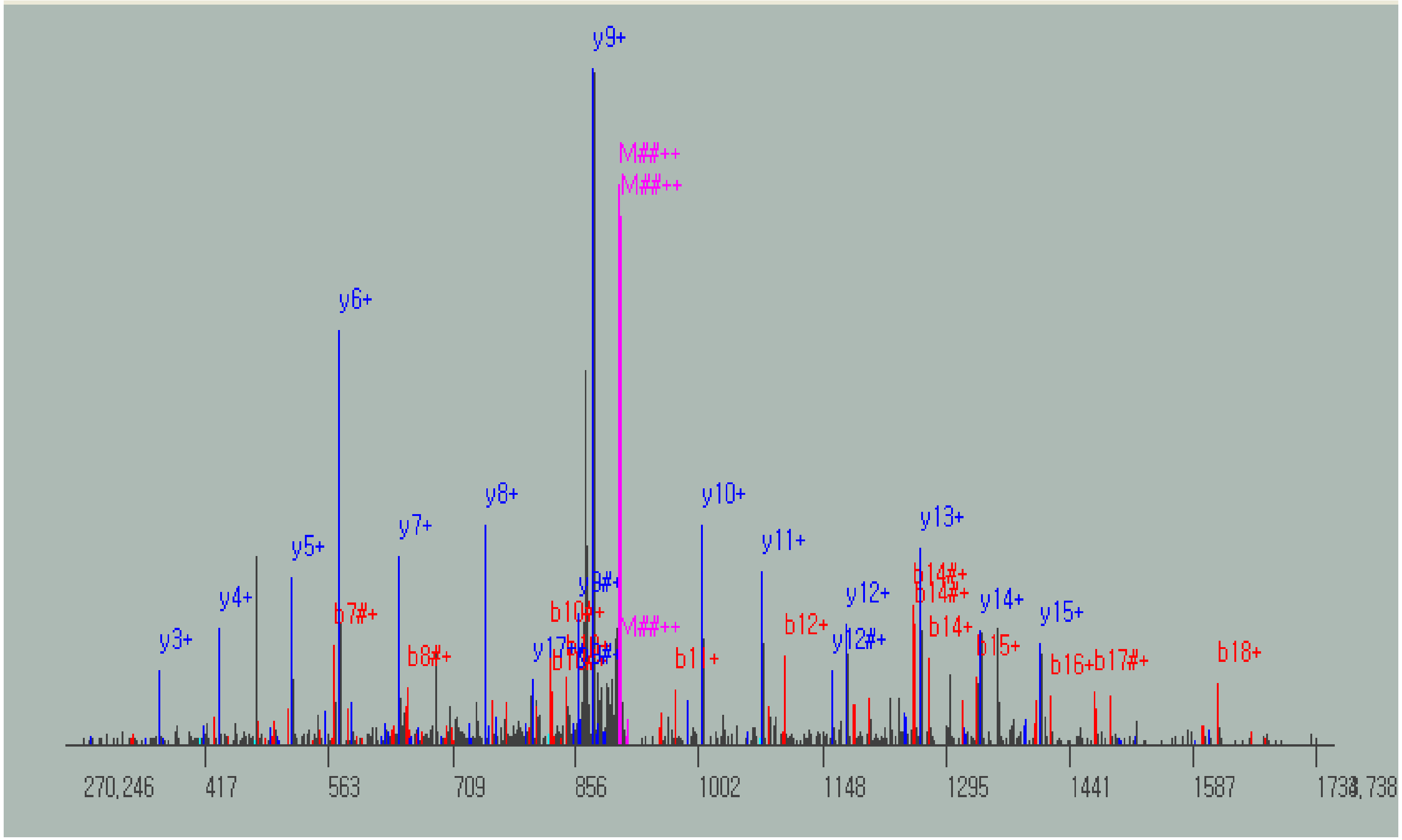


R.NADVELQQR.A
m/z(1073.14206), charge(+2), Xcorr(3.5603)

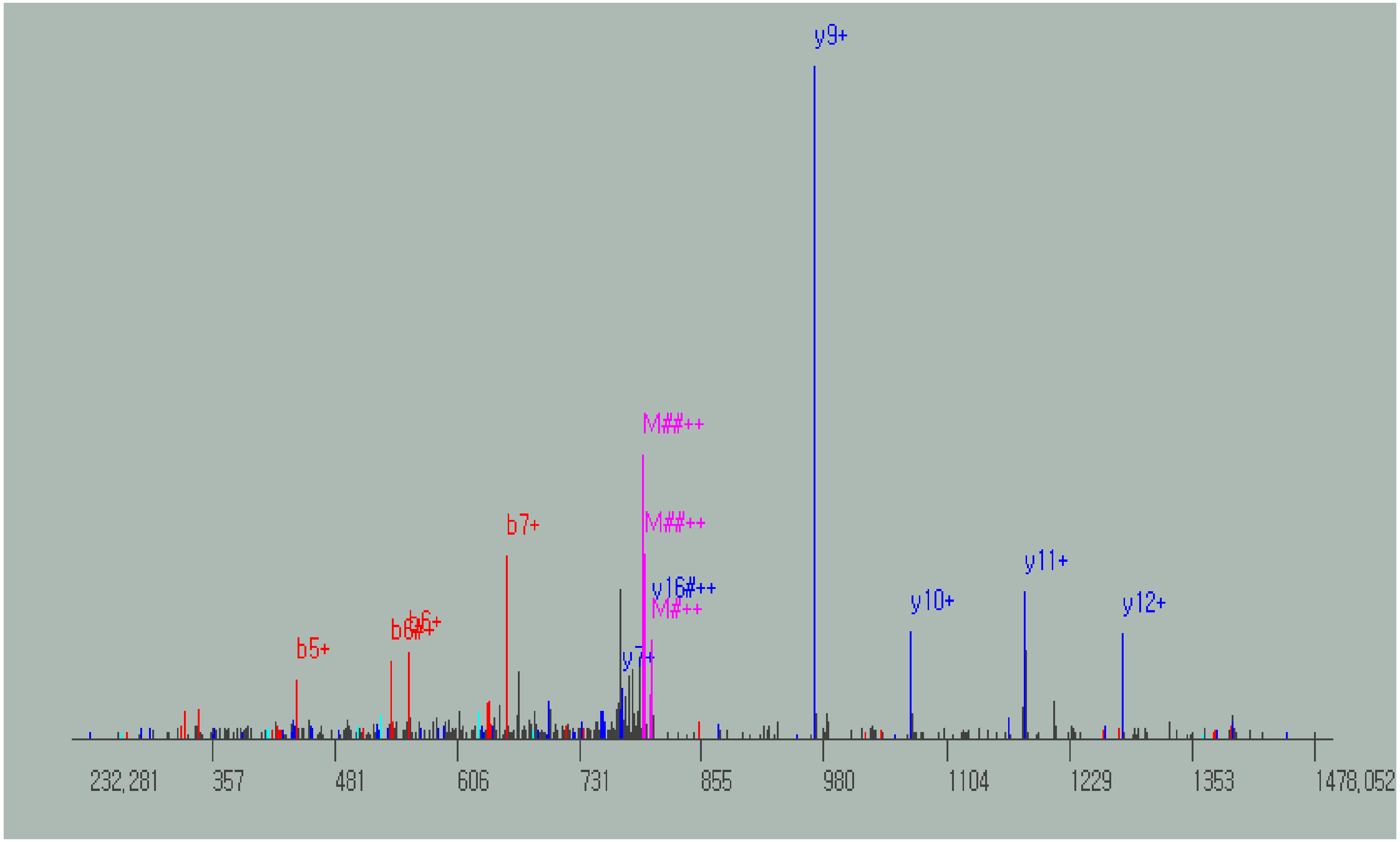


R.AGNSLAASTAEETAGSAQGR.A

m/z(1849.89478), charge(+2), Xcorr(5.4879)

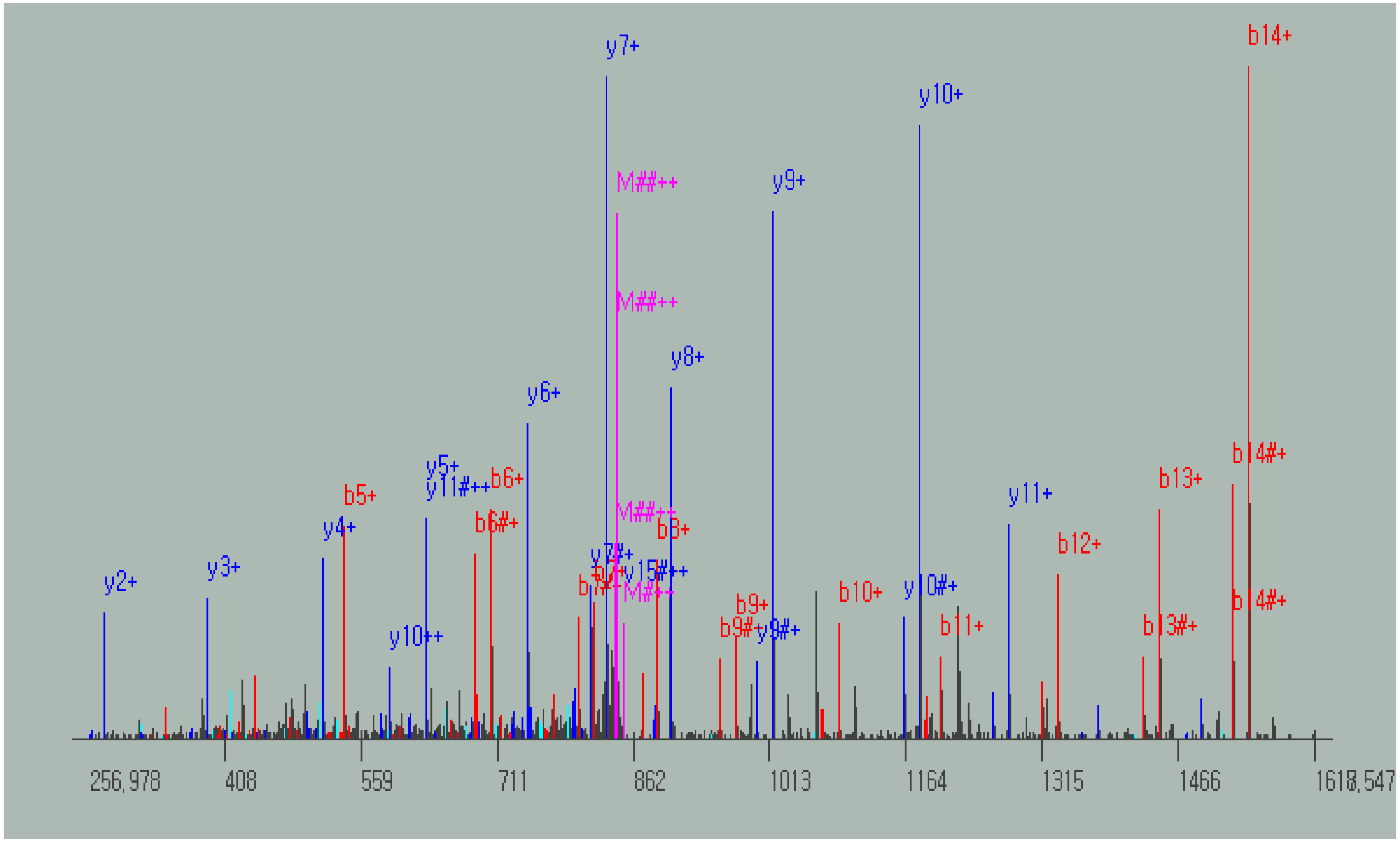


R.TGAIVDVPVGEELLGR.V
m/z(1625.84824), charge(+2), Xcorr(3.263)

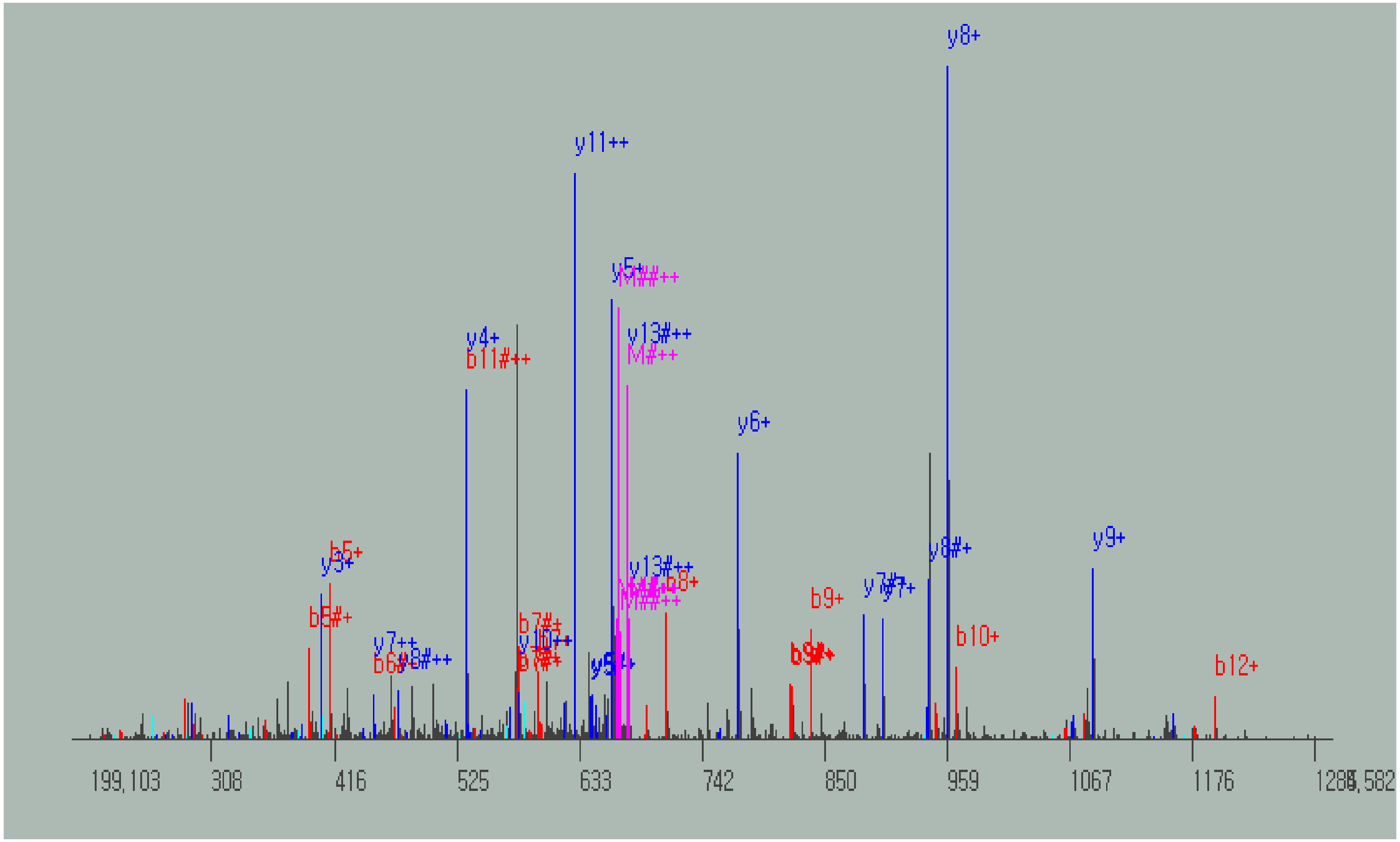


R.IIDVVYNASNNELVR.T

m/z(1719.92013), charge(+2), Xcorr(4.0179)

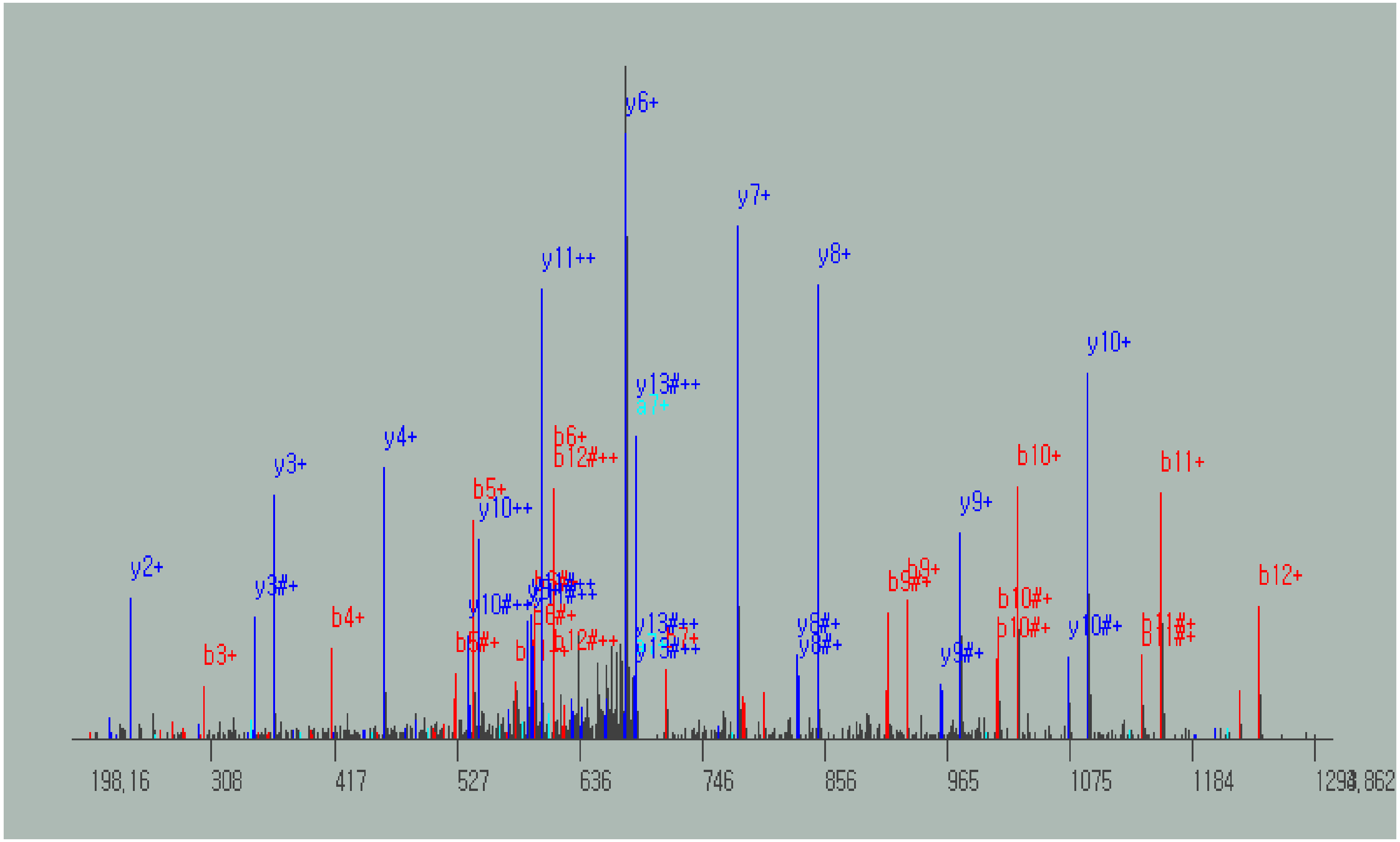


K.GGPAEGQLQENDR.V
m/z(1371.39536), charge(+2), Xcorr(3.401)

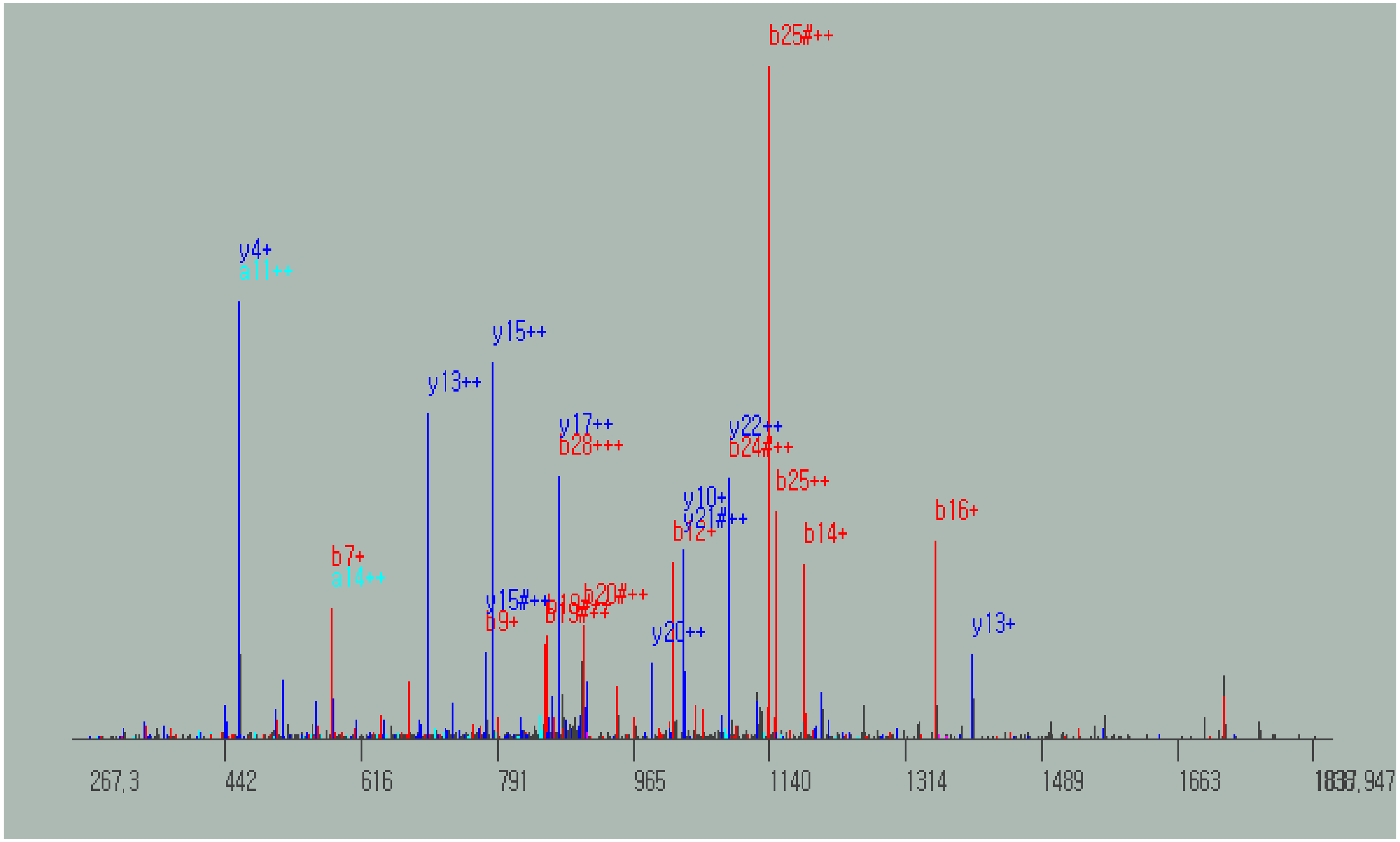


R.DALNQATSQVESK.Q

m/z(1391.46648), charge(+2), Xcorr(3.9582)



R.VAPAPAAPTPAAPAPAPSWPLSSSVPSQK.T
m/z(2752.11712), charge(+3), Xcorr(5.3437)



R.QITVNDLPVGR.S
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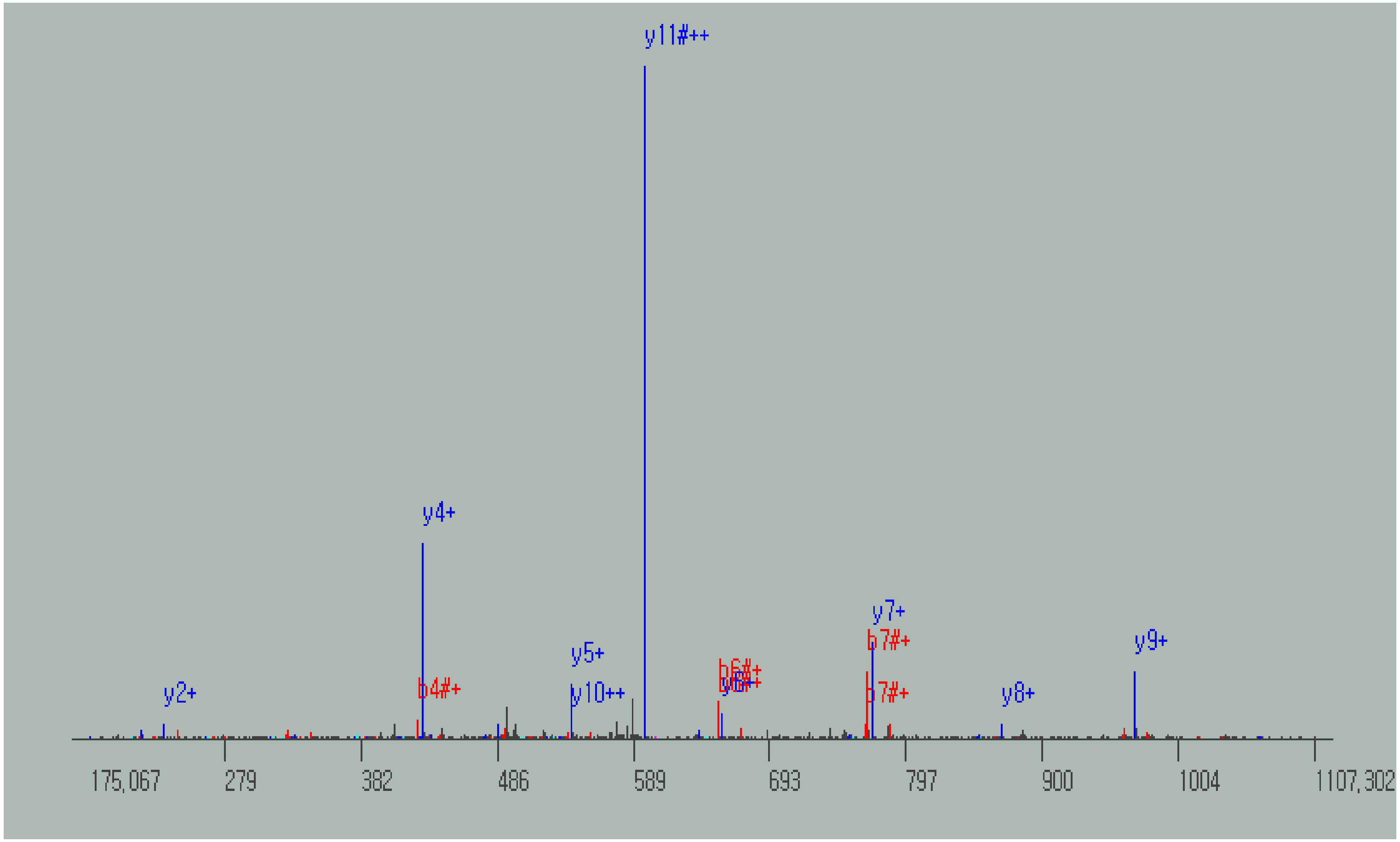
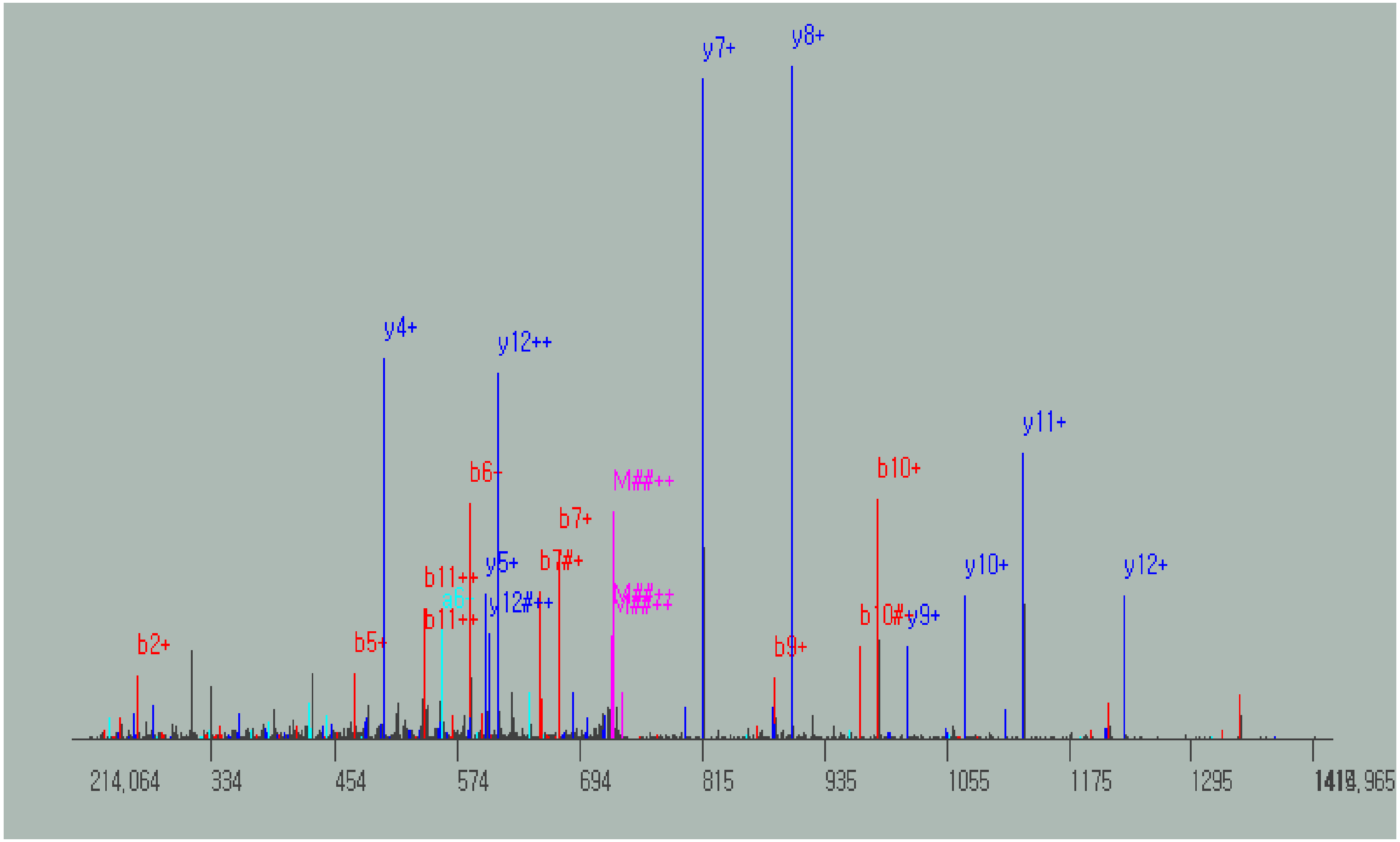


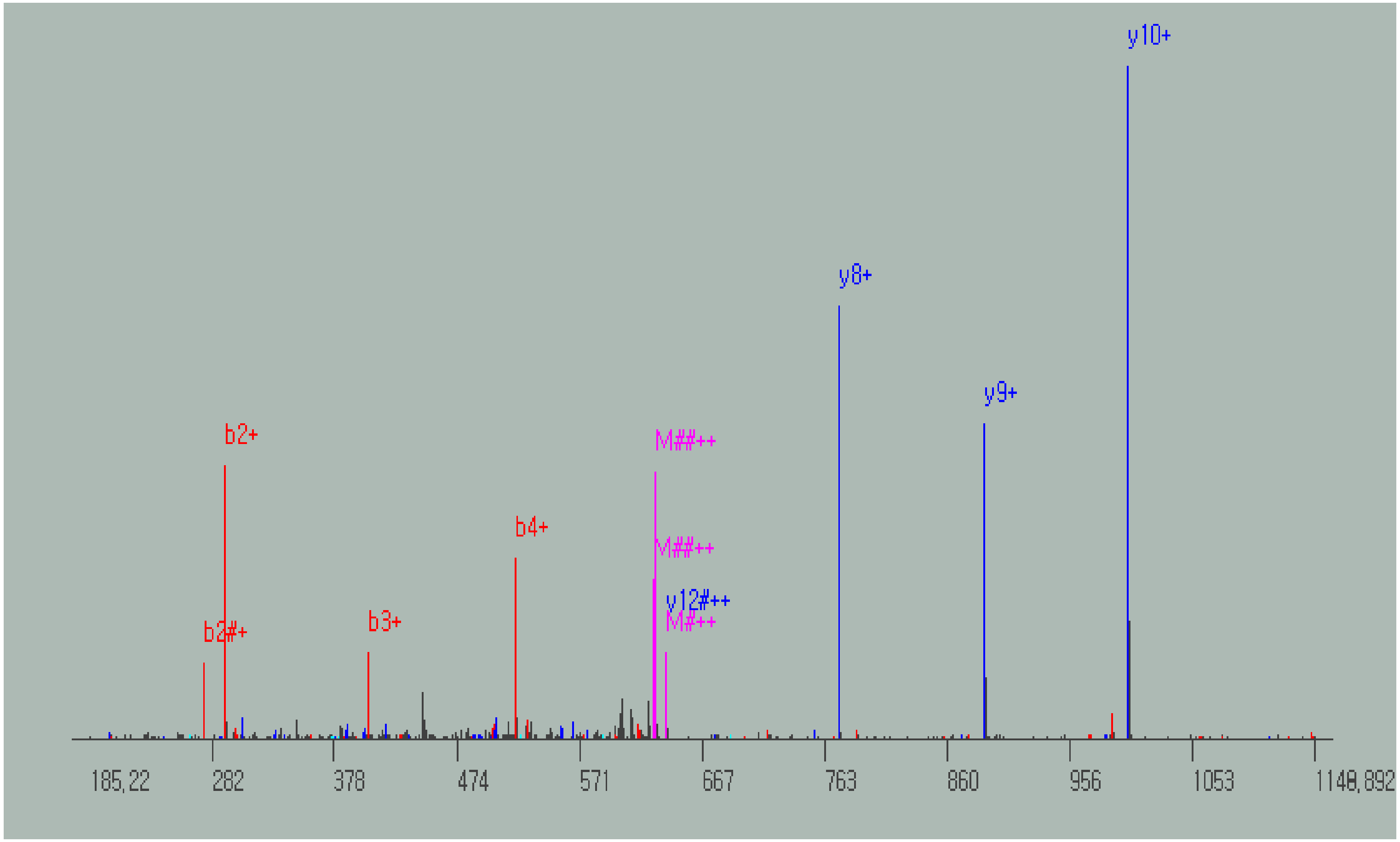
K.IFVGGLSPDTPEEK.I

m/z(1489.65166), charge(+2), Xcorr(4.1255)



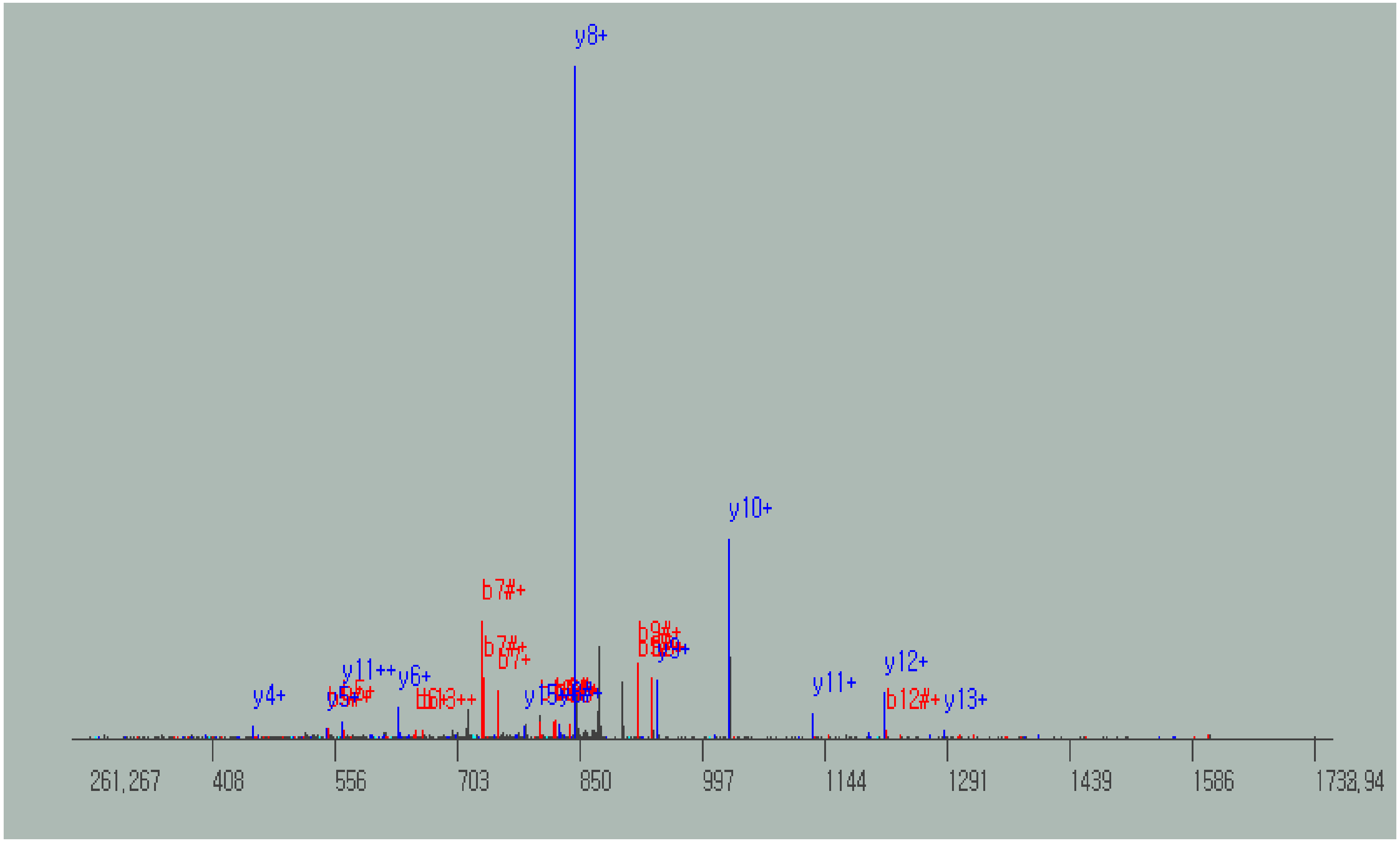
K.YQLDPTASISAK.V

m/z(1294.43554), charge(+2), Xcorr(2.3958)

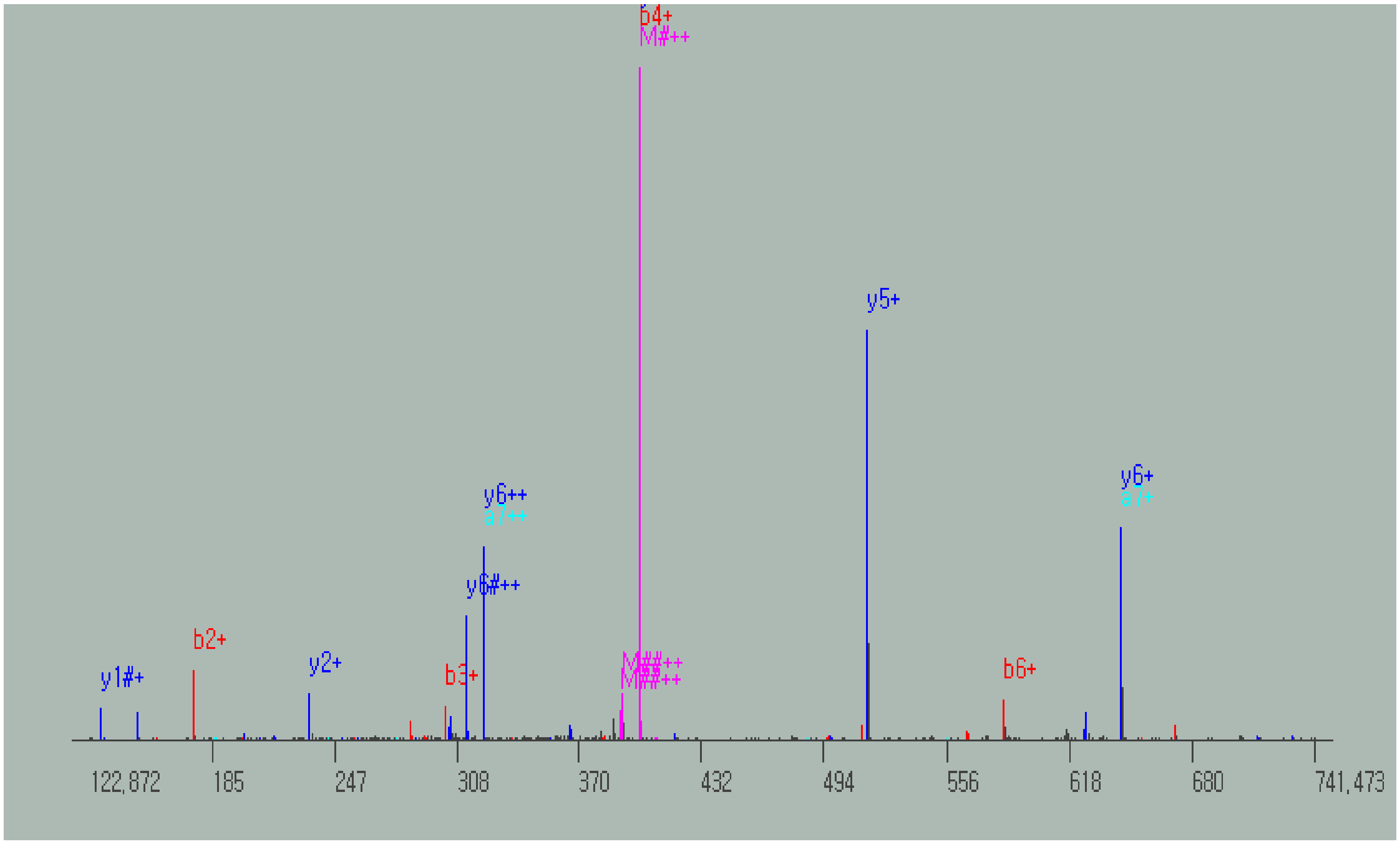


R.TDYNASVSVPDSSGPER.I

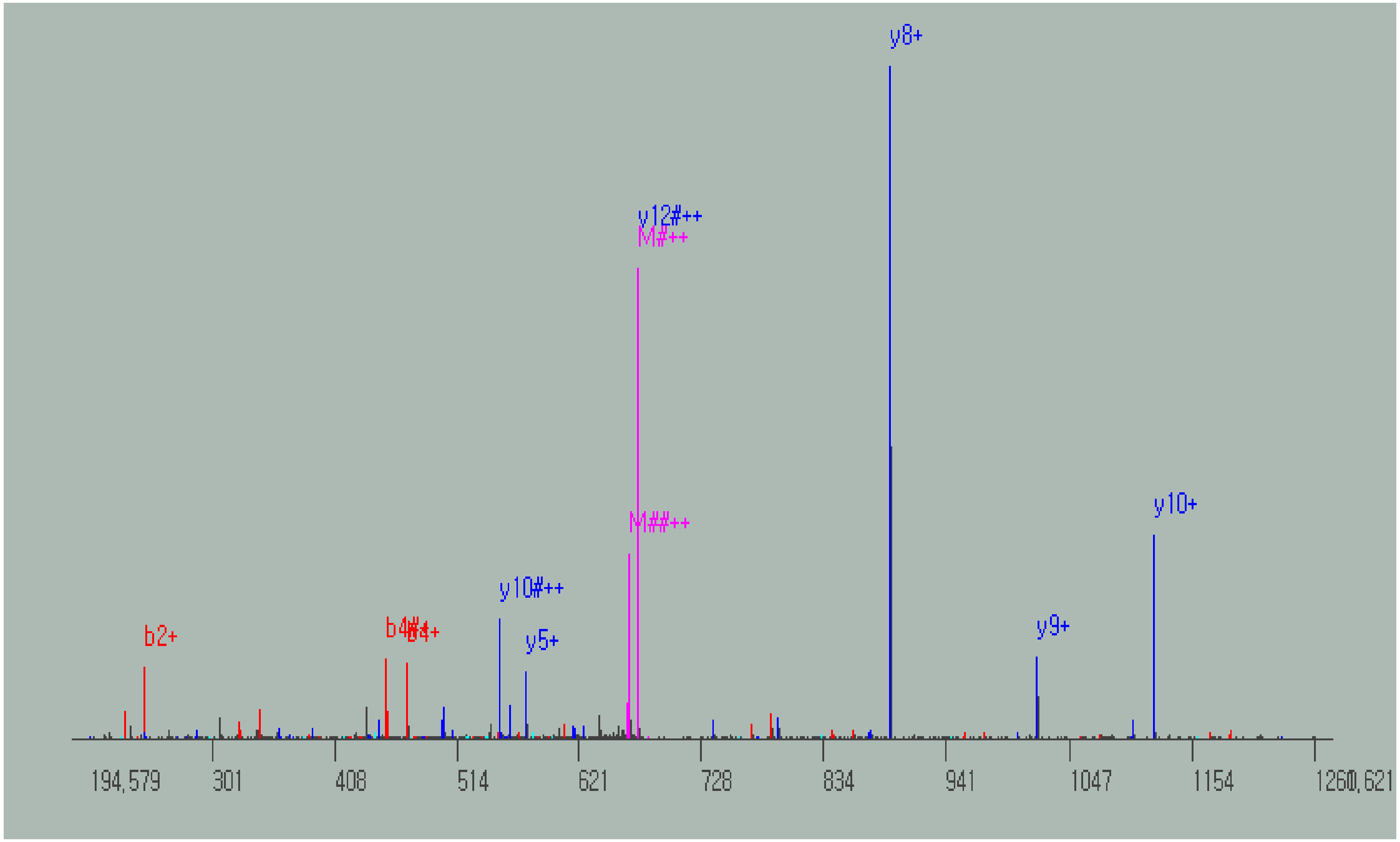
m/z(1781.81568), charge(+2), Xcorr(3.566)



K.SSQPLASK.Q
m/z(817.91041), charge(+2), Xcorr(2.4454)

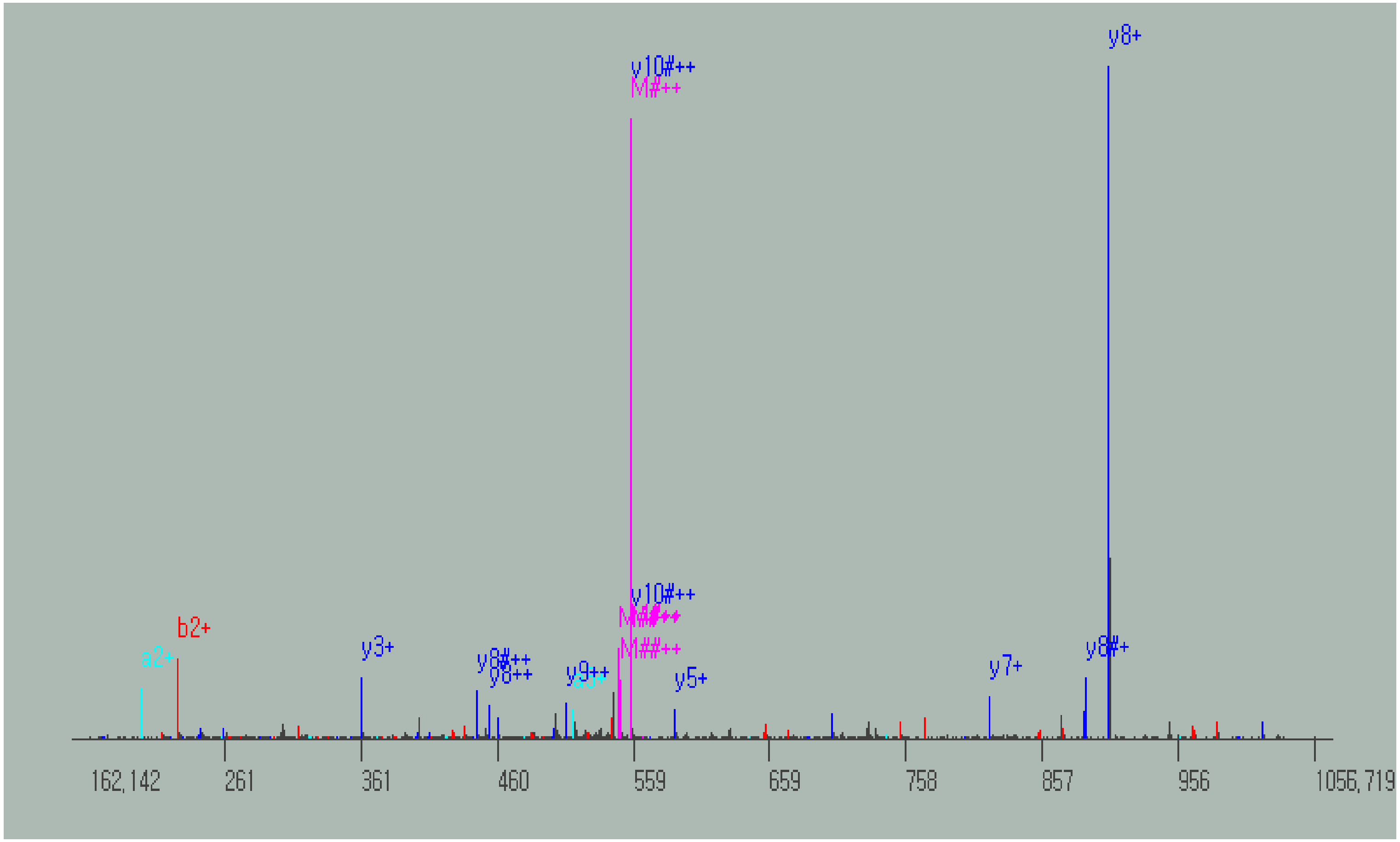


R.IQTQPGYANTLR.D
m/z(1362.51634), charge(+2), Xcorr(3.1562)

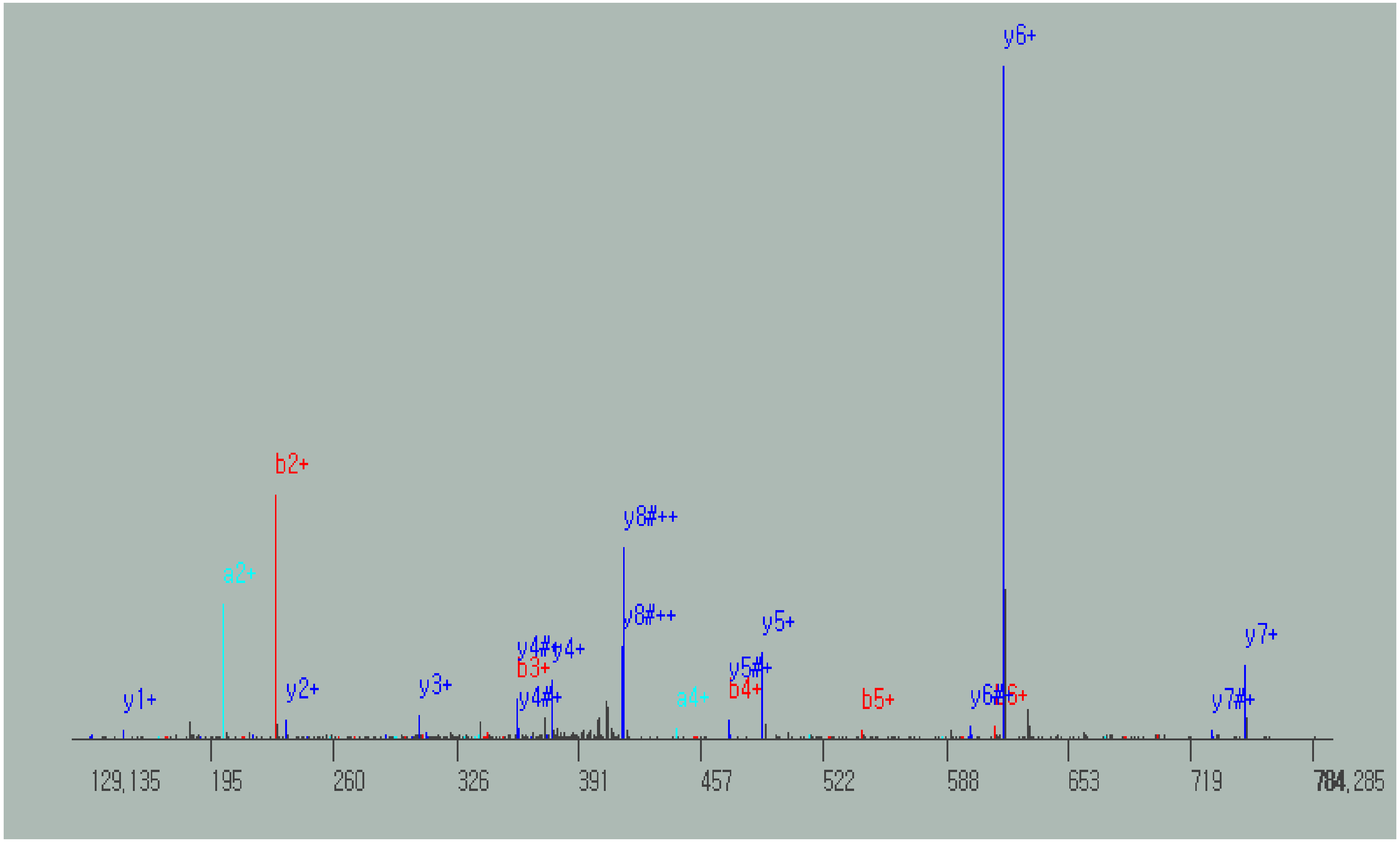


K.LLSNDEVTIK.Y

m/z(1132.28932), charge(+2), Xcorr(2.9292)

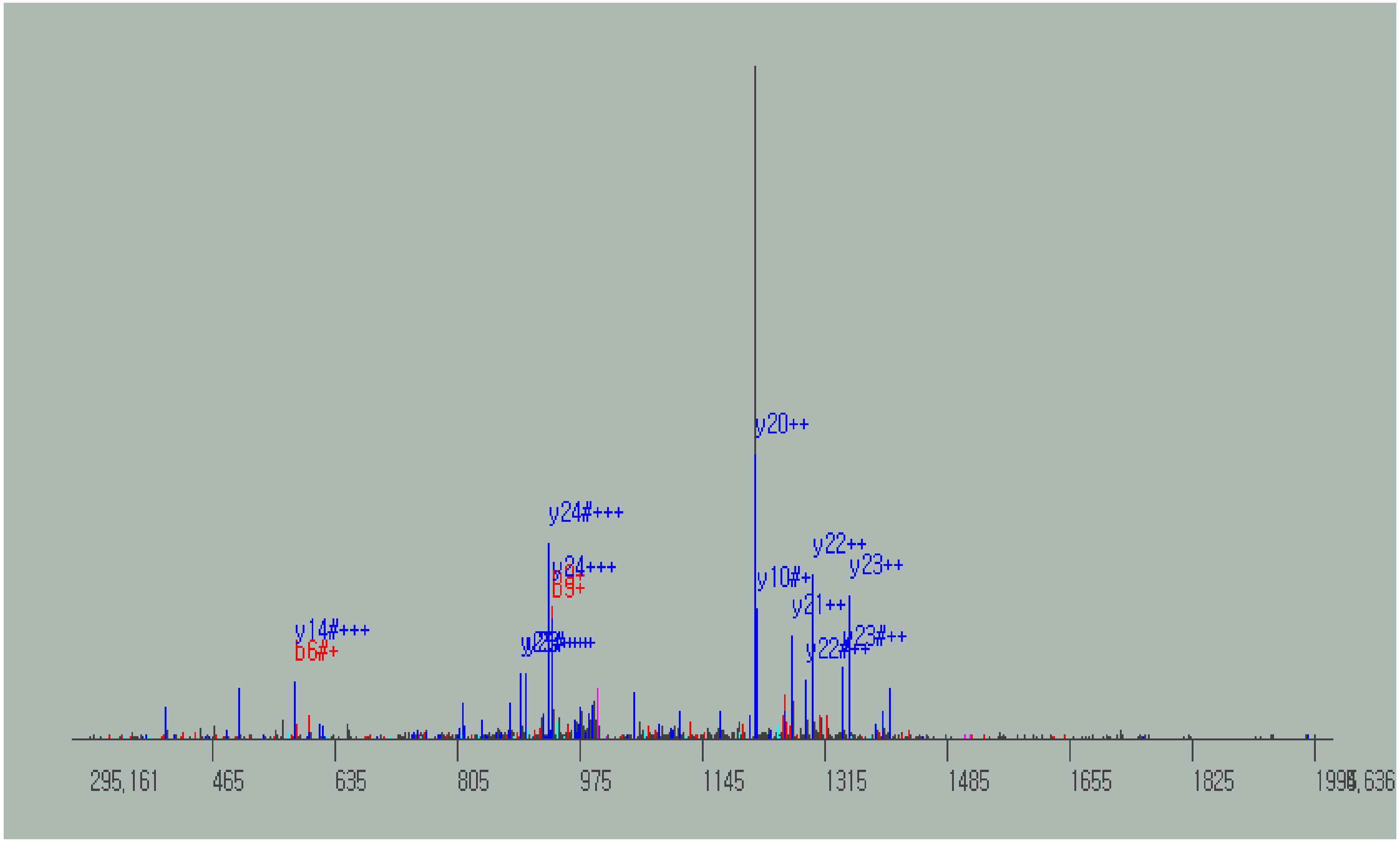


K.VEEIAASK.C
m/z(846.94852), charge(+2), Xcorr(2.9509)

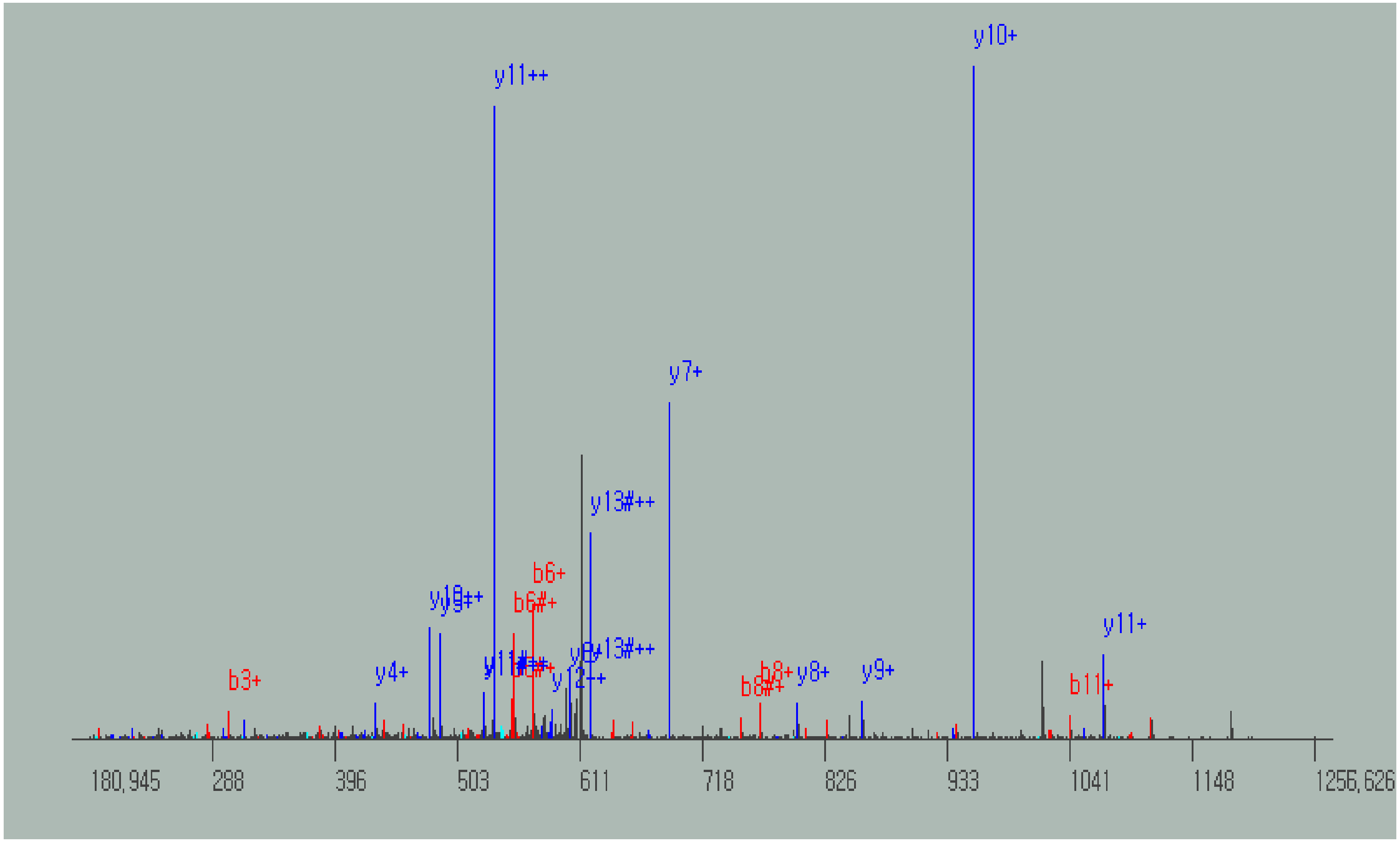


K.LLLTGTPLQNNLEELFHLLNFLTPER.F

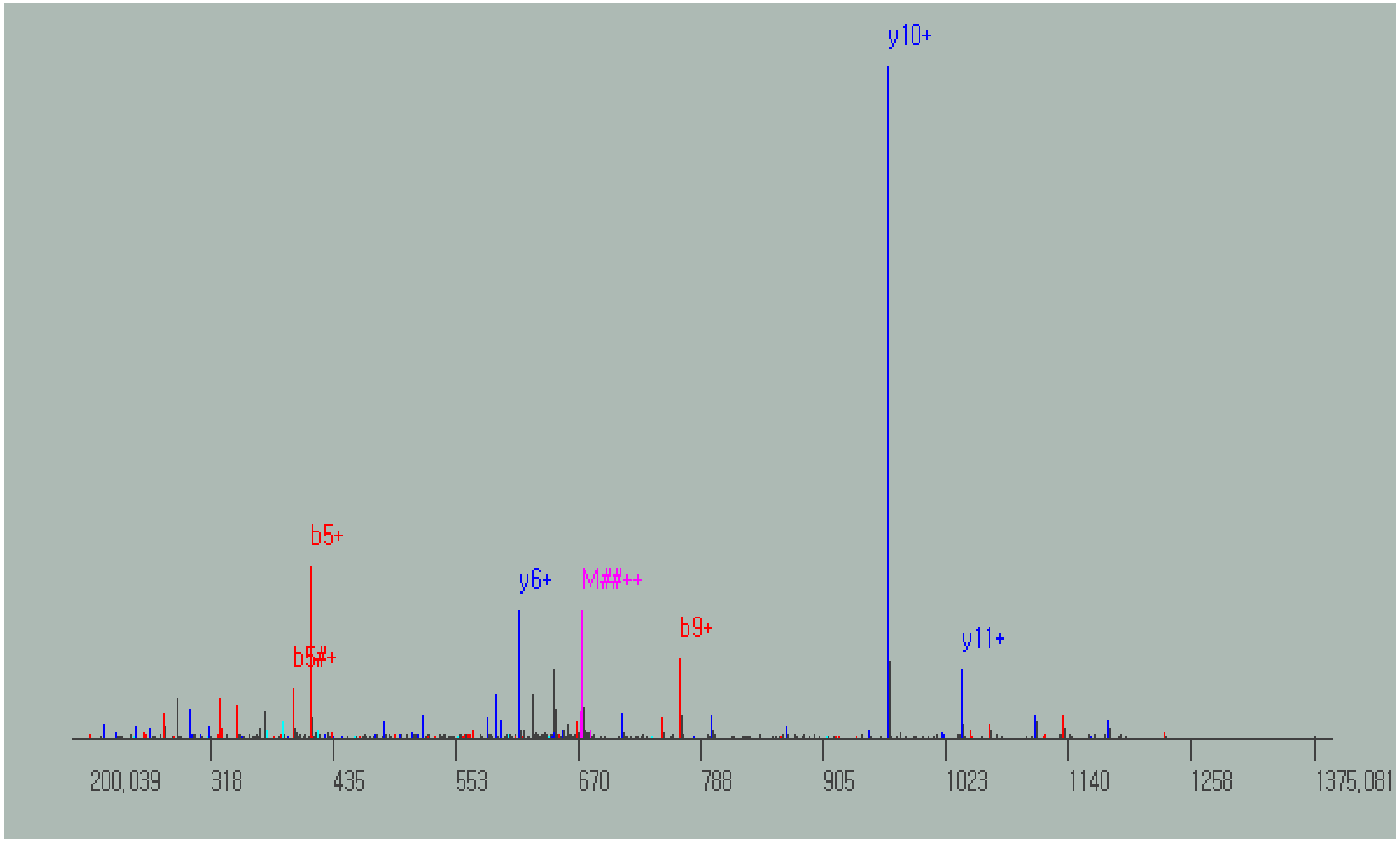
m/z(3037.50106), charge(+3), Xcorr(3.846)



K.STNPGISIGDVAK.K
m/z(1259.39119), charge(+2), Xcorr(3.5352)



K.AQAAAPASVPAQAPK.G
m/z(1378.55891), charge(+2), Xcorr(4.0012)



K.AQYEDIANR.S
m/z(1080.13306), charge(+2), Xcorr(2.8731)