

Fig. 1-1

sp	P15692	VEGFA	MNFLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRS
sp	P15692-2	VEGFA189	MNFLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRS
sp	P15692-3	VEGFA183	MNFLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRS
sp	P15692-4	VEGFA165	MNFLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRS
sp	P15692-5	VEGFA148	MNFLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRS
sp	P15692-6	VEGFA145	MNFLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRS
sp	P15692-7	VEGFA121	MNFLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRS
sp	P15692-8	VEGFA165B	MNFLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRS
sp	P15692-9	VEGFA121B	MNFLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRS
sp	P15692-10	VEGFA111	MNFLLSWVHWSLALLLYLHHAKWSQAAPMAEGGGQNHHEVVKFMDVYQRS

sp	P15692	VEGFA	YCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTES
sp	P15692-2	VEGFA189	YCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTES
sp	P15692-3	VEGFA183	YCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTES
sp	P15692-4	VEGFA165	YCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTES
sp	P15692-5	VEGFA148	YCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTES
sp	P15692-6	VEGFA145	YCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTES
sp	P15692-7	VEGFA121	YCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTES
sp	P15692-8	VEGFA165B	YCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTES
sp	P15692-9	VEGFA121B	YCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTES
sp	P15692-10	VEGFA111	YCHPIETLVDIFQEYPDEIEYIFKPSCVPLMRCGGCCNDEGLECVPTES

sp	P15692	VEGFA	NITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRARQEKKSVRGKKG
sp	P15692-2	VEGFA189	NITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRARQEKKSVRGKKG
sp	P15692-3	VEGFA183	NITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRARQEKKSVRGKKG
sp	P15692-4	VEGFA165	NITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRARQEN-----
sp	P15692-5	VEGFA148	NITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRARQEN-----
sp	P15692-6	VEGFA145	NITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRARQEK-----
sp	P15692-7	VEGFA121	NITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRARQEN-----
sp	P15692-8	VEGFA165B	NITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRARQEN-----
sp	P15692-9	VEGFA121B	NITMQIMRIKPHQGQHIGEMSFLQHNKCECRPKKDRARQEK-----
sp	P15692-10	VEGFA111	NITMQIMRIKPHQGQHIGEMSFLQHNKCECRCDKPRR-----
***** . * *			

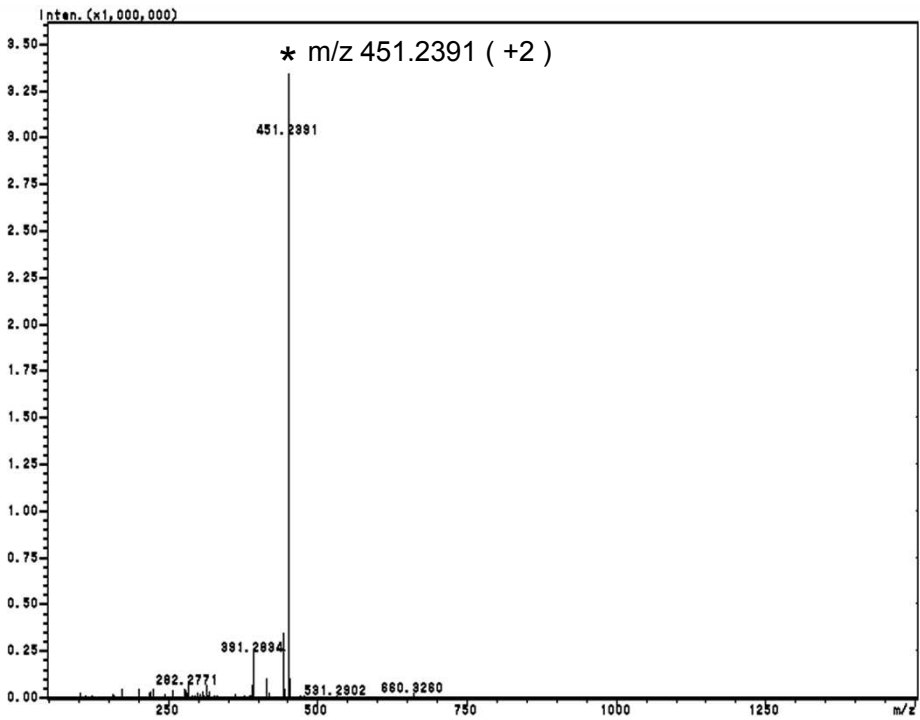
Fig. 1-2

sp	P15692	VEGFA	QKRKRKKSRYKSWSVYVGARCCLMPWSLPGPHPCGPCSEERRKHLFVQDPQ
sp	P15692-2	VEGFA189	QKRKRKKSRYKSW-----SVPCGPCSEERRKHLFVQDPQ
sp	P15692-3	VEGFA183	QKRKRKKS-----RPCGPCSEERRKHLFVQDPQ
sp	P15692-4	VEGFA165	-----PCGPCSEERRKHLFVQDPQ
sp	P15692-5	VEGFA148	-----PCGPCSEERRKHLFVQDPQ
sp	P15692-6	VEGFA145	-----KSVRGKGKGQKRK
sp	P15692-7	VEGFA121	-----CDKPRR-----
sp	P15692-8	VEGFA165B	-----PCGPCSEERRKHLFVQDPQ
sp	P15692-9	VEGFA121B	-----CDKPRR-----
sp	P15692-10	VEGFA111	-----

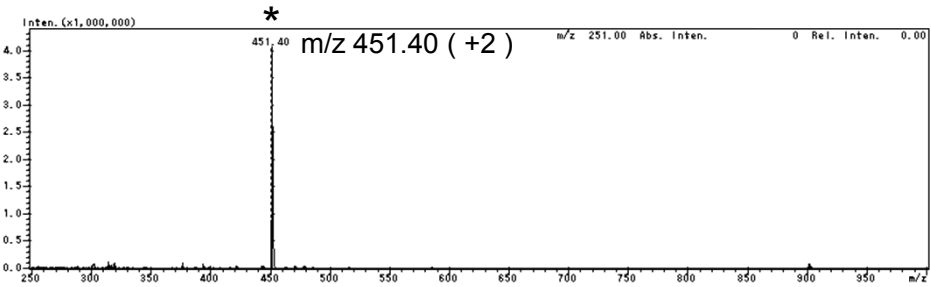
sp	P15692	VEGFA	TCKCSCKNTDSRCKARQLELNERTCRCDKPRR (SEQ ID NO.1)
sp	P15692-2	VEGFA189	TCKCSCKNTDSRCKARQLELNERTCRCDKPRR (SEQ ID NO.2)
sp	P15692-3	VEGFA183	TCKCSCKNTDSRCKARQLELNERTCRCDKPRR (SEQ ID NO.3)
sp	P15692-4	VEGFA165	TCKCSCKNTDSRCKARQLELNERTCRCDKPRR (SEQ ID NO.4)
sp	P15692-5	VEGFA148	TCKCSCKNTDSRCKM----- (SEQ ID NO.5)
sp	P15692-6	VEGFA145	RKKSRYKSWSVCDKPRR----- (SEQ ID NO.6)
sp	P15692-7	VEGFA121	----- (SEQ ID NO.7)
sp	P15692-8	VEGFA165B	TCKCSCKNTDSRCKARQLELNERTCRSLTRKD (SEQ ID NO.8)
sp	P15692-9	VEGFA121B	----- (SEQ ID NO.9)
sp	P15692-10	VEGFA111	----- (SEQ ID NO.10)

Fig. 2-1

LCMS-IT-TOF



LCMS-8040



LCMS-8050

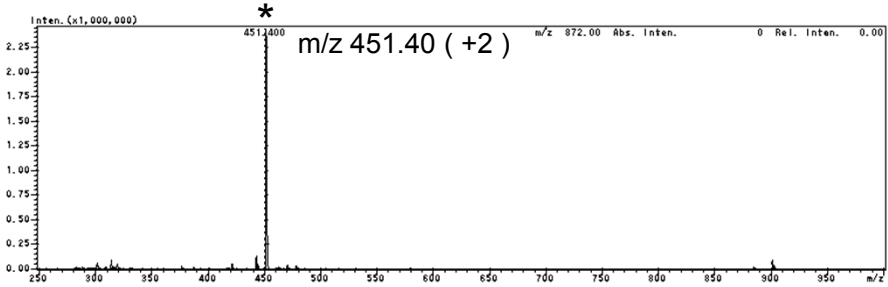
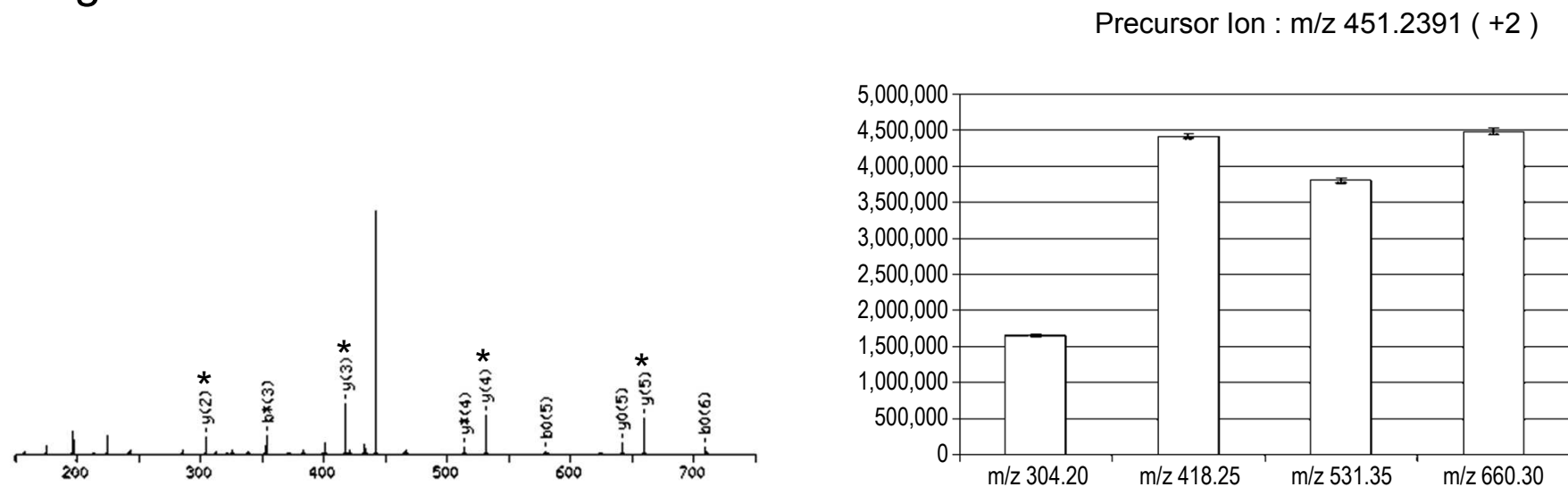


Fig. 2-2



Monoisotopic mass of neutral peptide Mr(calc): 900.4665
Ions Score: 26 Expect: 0.0025
Matches : 9/66 fragment ions using 12 most intense peaks (help)

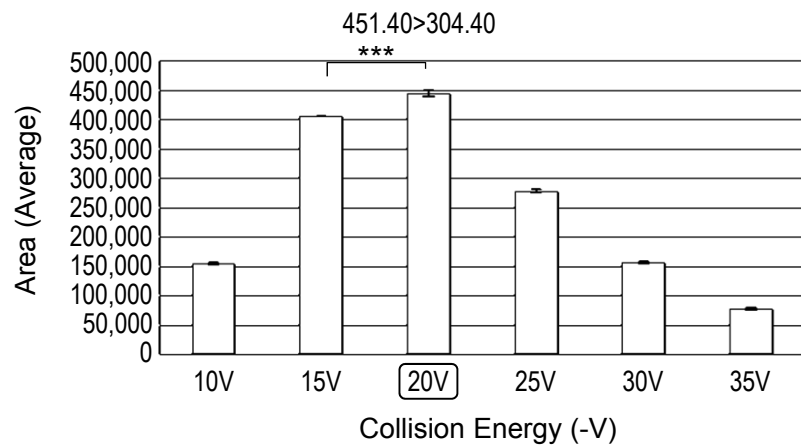
#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							7
2	242.1499	121.5786	225.1234	113.0653			L	773.4152	387.2112	756.3886	378.6980	755.4046	378.2060	6
3	371.1925	186.0999	354.1660	177.5866	353.1819	177.0946	E	660.3311	330.6692	643.3046	322.1559	642.3206	321.6639	5
4	484.2766	242.6419	467.2500	234.1287	466.2660	233.6366	L	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
5	598.3195	299.6634	581.2930	291.1501	580.3089	290.6581	N	418.2045	209.6059	401.1779	201.0926	400.1939	200.6006	3
6	727.3621	364.1847	710.3355	355.6714	709.3515	355.1794	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
7							R	175.1190	88.0631	158.0924	79.5498			1

*  Ion confirmed by both MS2 and product ion scan

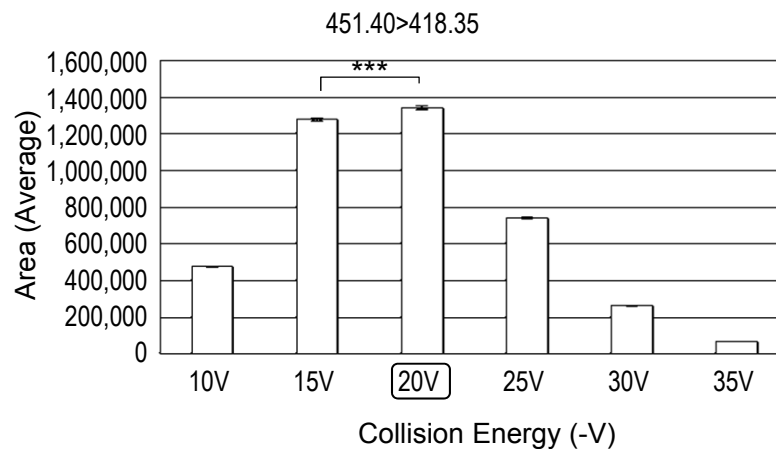
Fig. 2-3

LCMS-8040

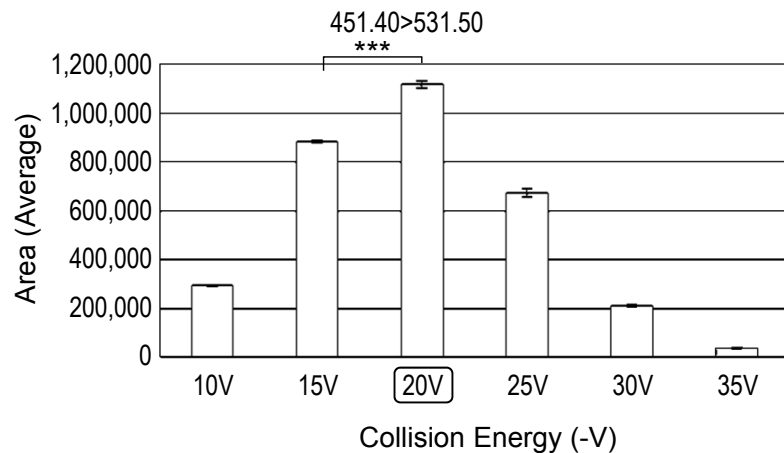
m/z 304.40 y (2)



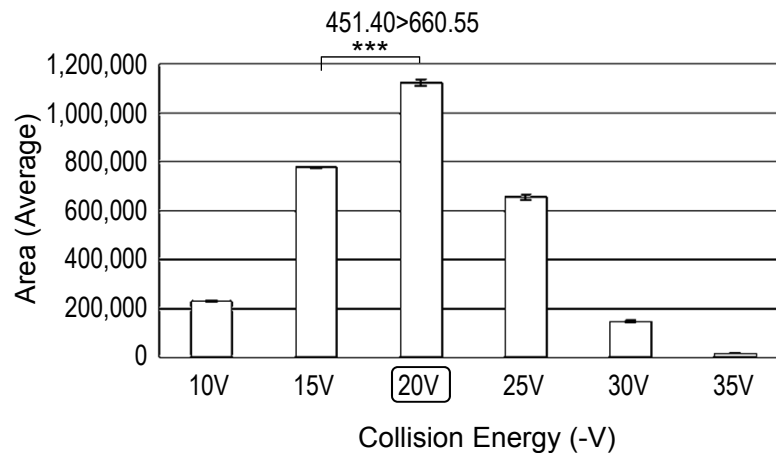
m/z 418.35 y (3)



m/z 531.50 y (4)



m/z 660.55 y (5)



P<0.001 ***

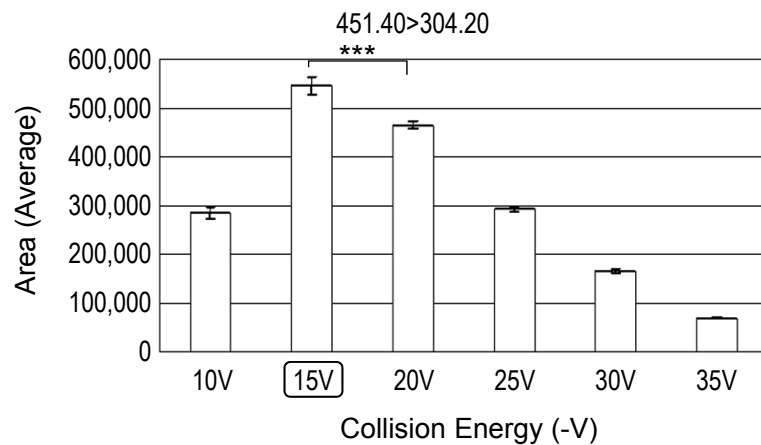
P<0.01 **

P<0.05 *

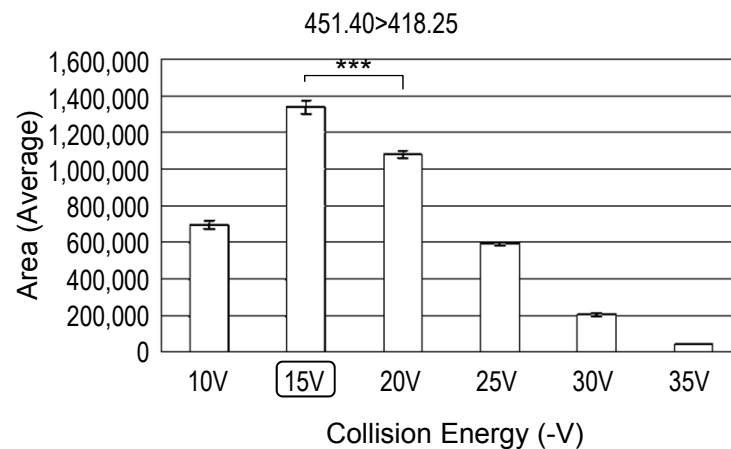
Fig. 2-4

LCMS-8050

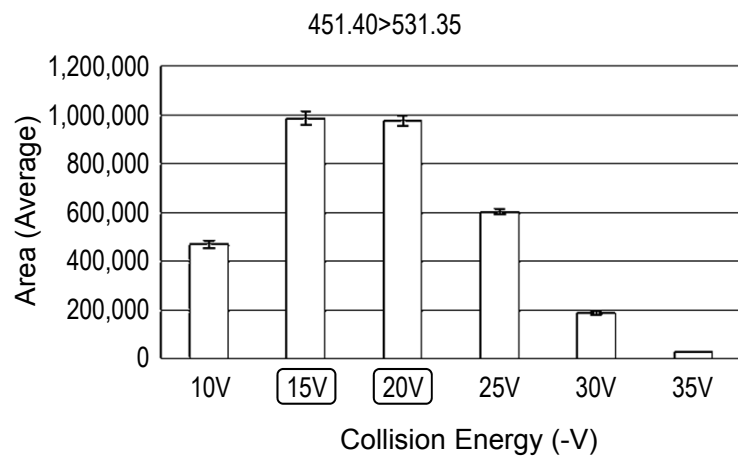
m/z 304.20 y (2)



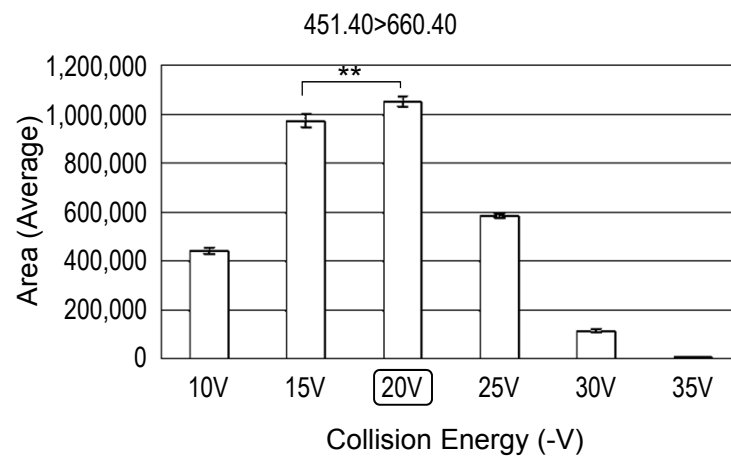
m/z 418.25 y (3)



m/z 531.35 y (4)



m/z 660.40 y (5)



P<0.001 ***

P<0.01 **

P<0.05 *

Fig. 2-5

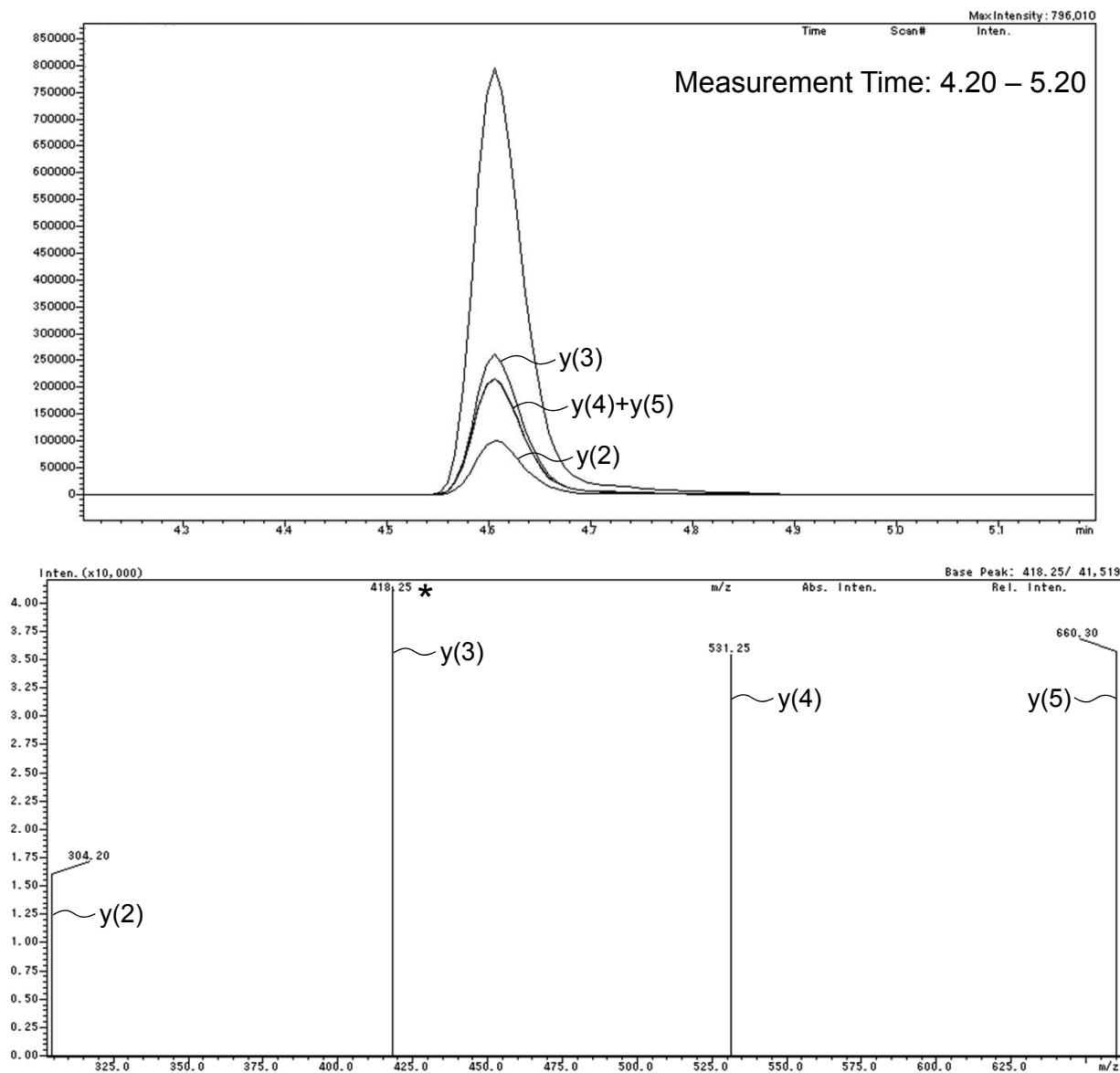
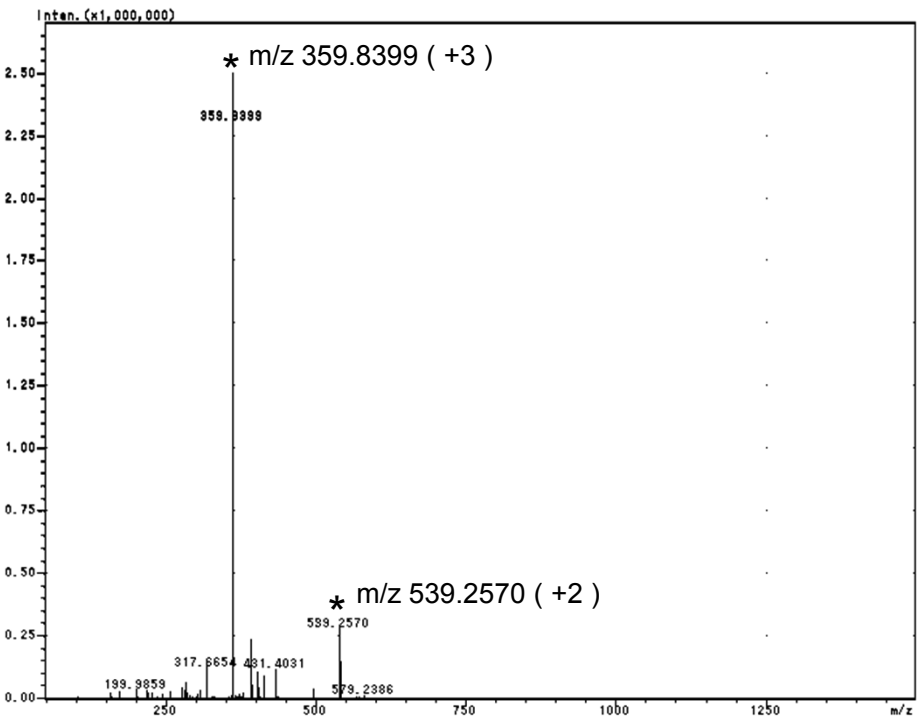
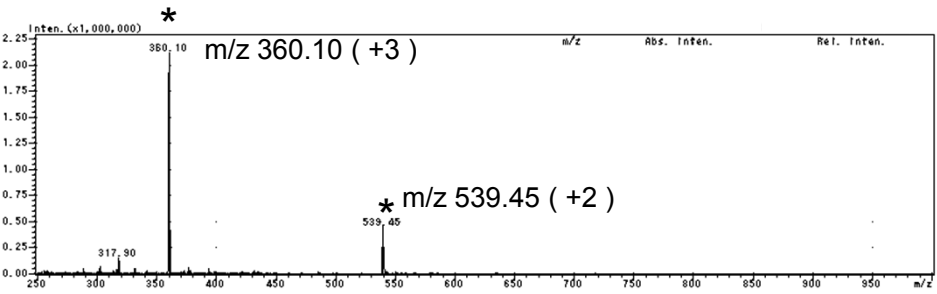


Fig. 3-1

LCMS-IT-TOF



LCMS-8040



LCMS-8050

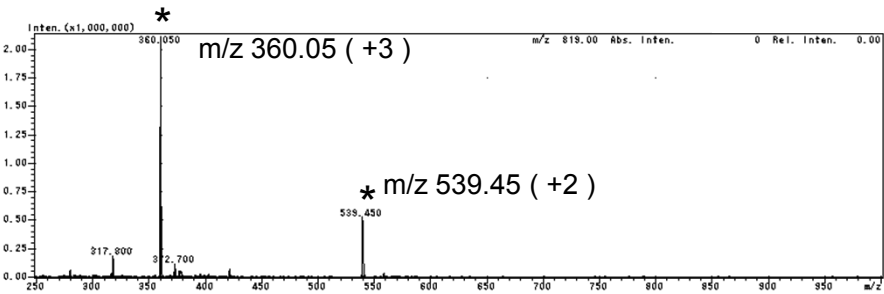
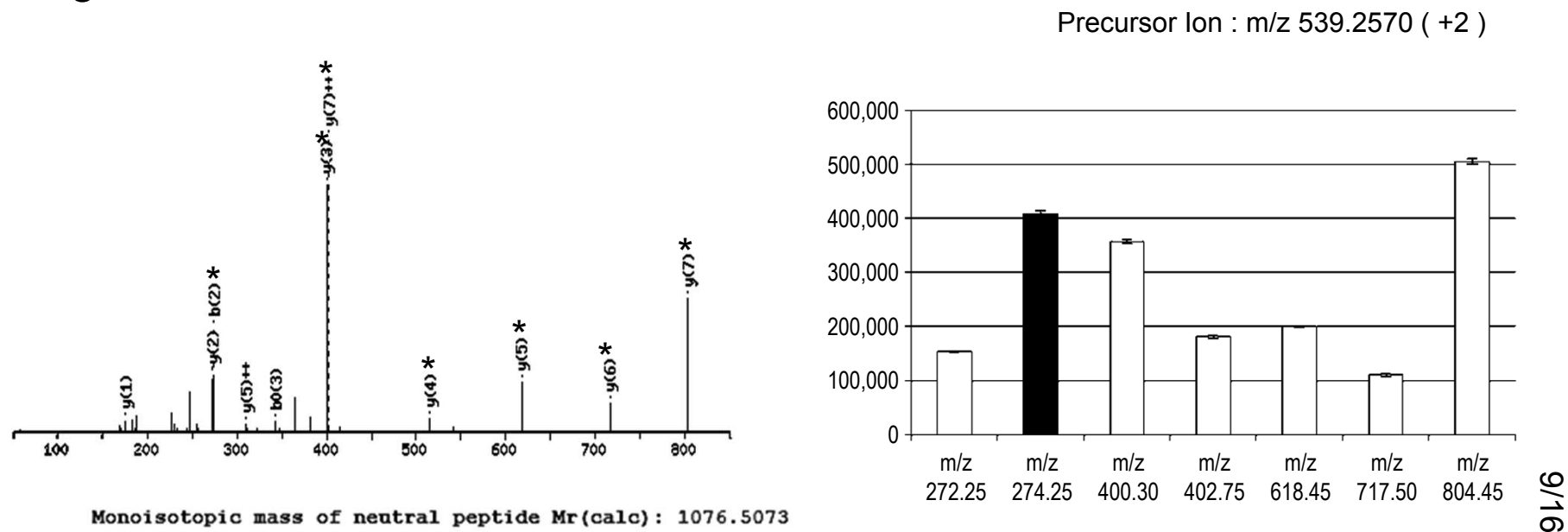


Fig. 3-2



Monoisotopic mass of neutral peptide Mr(calc): 1076.5073
 Ions Score: 45 Expect: 3e-005
 Matches : 11/78 fragment ions using 21 most intense peaks (help)

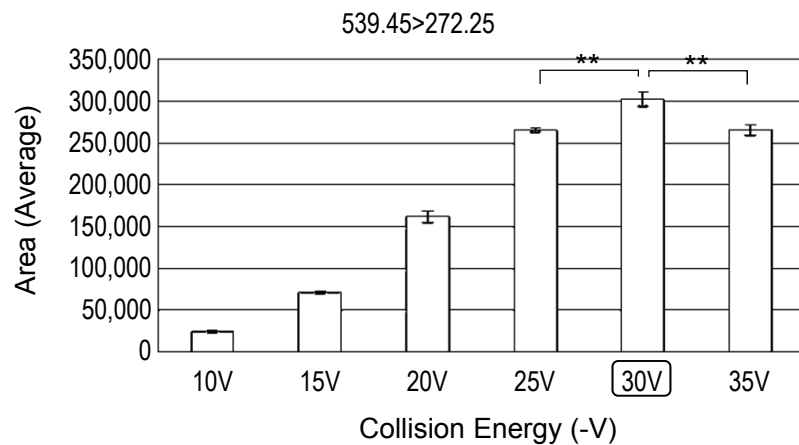
#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							9
2	274.1186	137.5629			256.1081	128.5577	W	990.4826	495.7449	973.4560	487.2316	972.4720	486.7396	8
3	361.1506	181.0790			343.1401	172.0737	S	804.4032	402.7053	787.3767	394.1920	786.3927	393.7000	7
4	460.2191	230.6132			442.2085	221.6079	V	717.3712	359.1892	700.3447	350.6760	699.3607	350.1840	6
5	563.2282	282.1178			545.2177	273.1125	C	618.3028	309.6550	601.2763	301.1418	600.2922	300.6498	5
6	678.2552	339.6312			660.2446	330.6259	D	515.2936	258.1504	498.2671	249.6372	497.2831	249.1452	4
7	806.3502	403.6787	789.3236	395.1654	788.3396	394.6734	K	400.2667	200.6370	383.2401	192.1237			3
8	903.4029	452.2051	886.3764	443.6918	885.3923	443.1998	P	272.1717	136.5895	255.1452	128.0762			2
9							R	175.1190	88.0631	158.0924	79.5498			1

* Ion confirmed by both MS2 and product ion scan

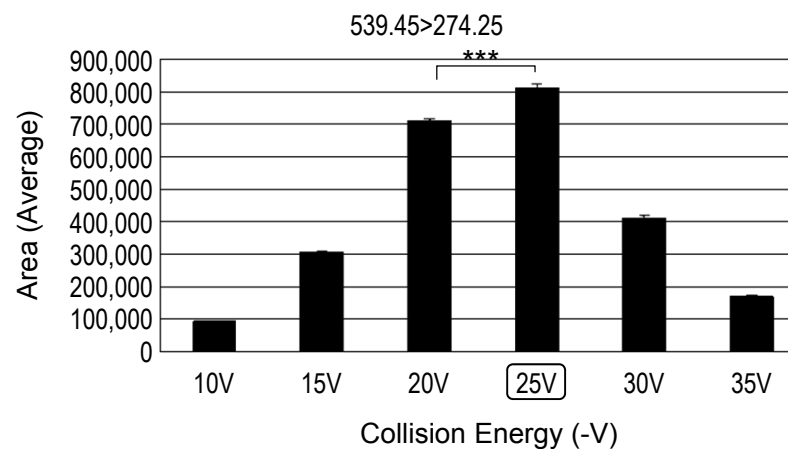
Fig. 3-3

LCMS-8050

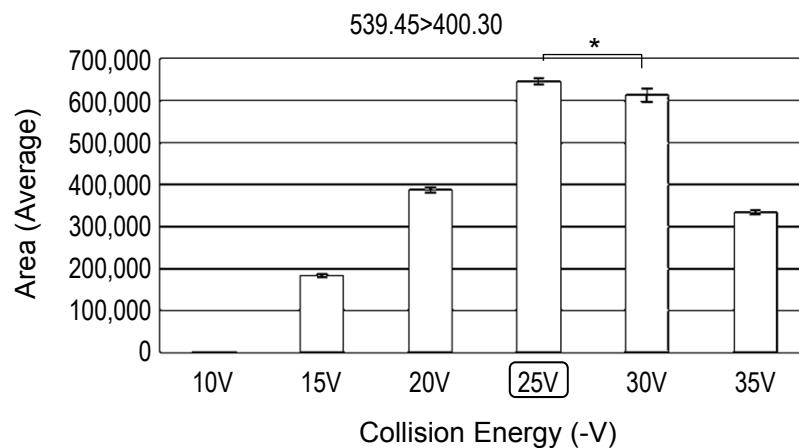
m/z 272.25 y (2)



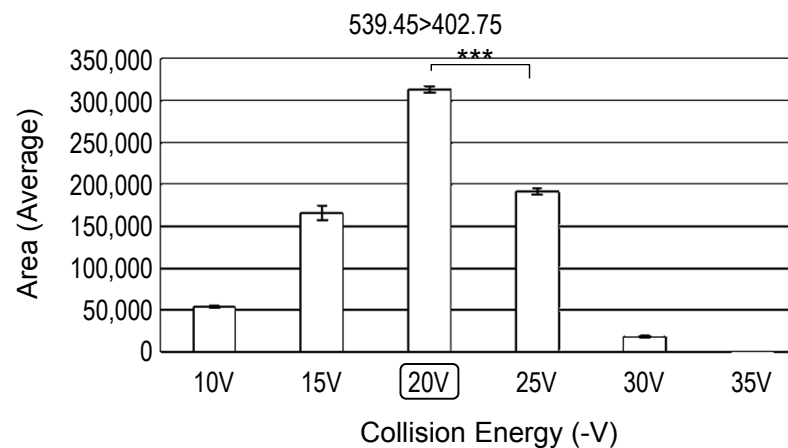
m/z 274.25 b(2)



m/z 400.30 y (3)



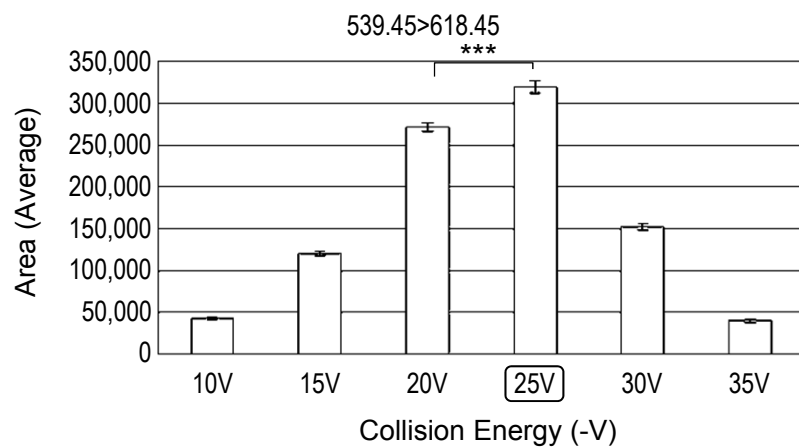
m/z 402.75 y (7)++



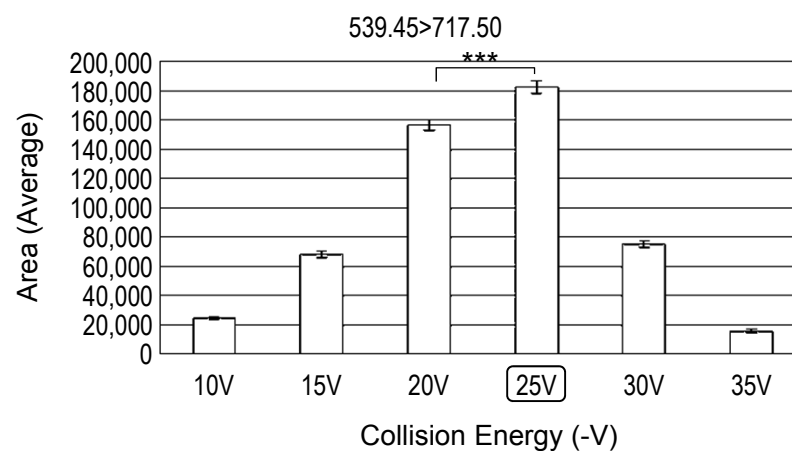
P<0.001 ***
P<0.01 **
P<0.05 *

Fig. 3-4

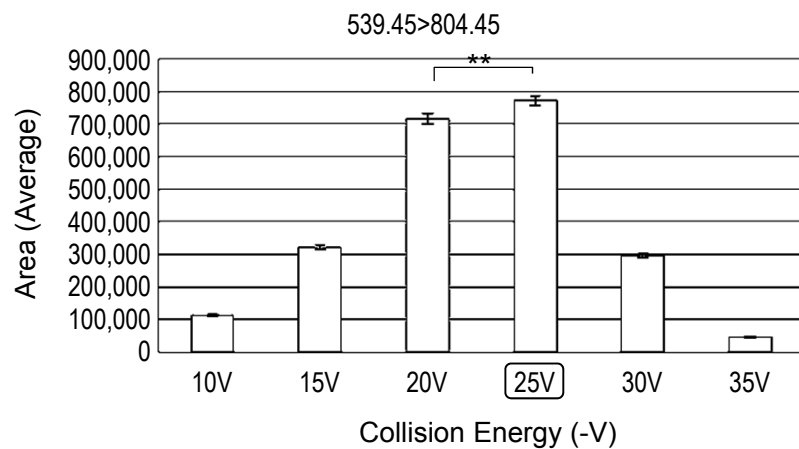
m/z 618.45 y (5)



m/z 717.50 y (6)

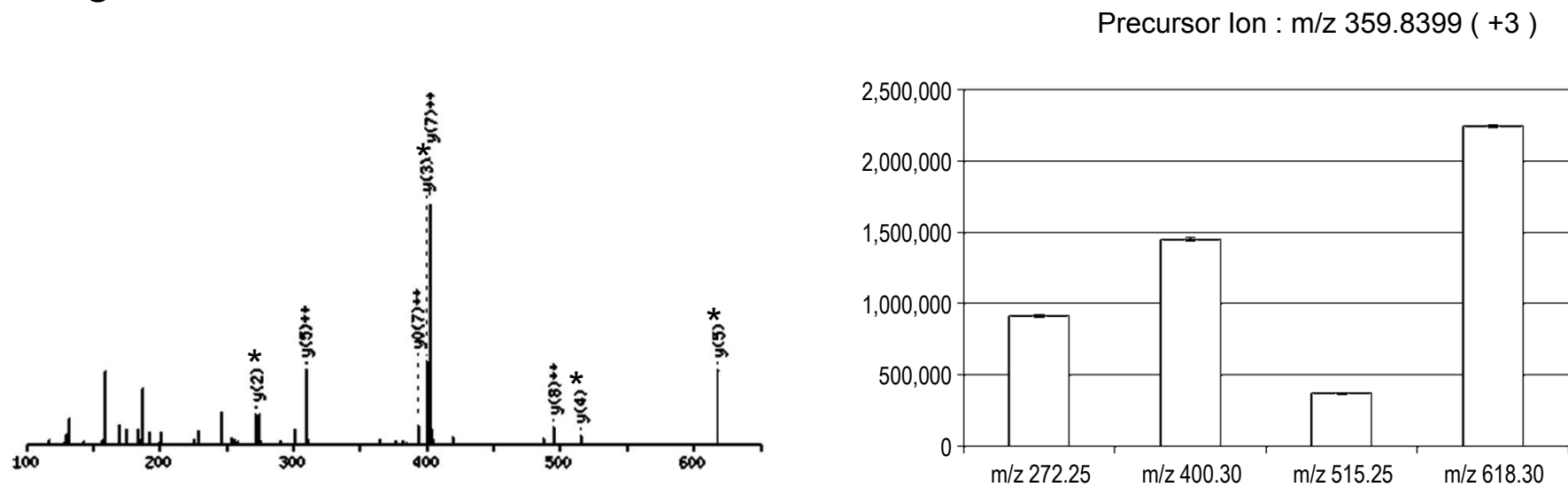


m/z 804.45 y (7)



P<0.001 ***
P<0.01 **
P<0.05 *

Fig. 3-5



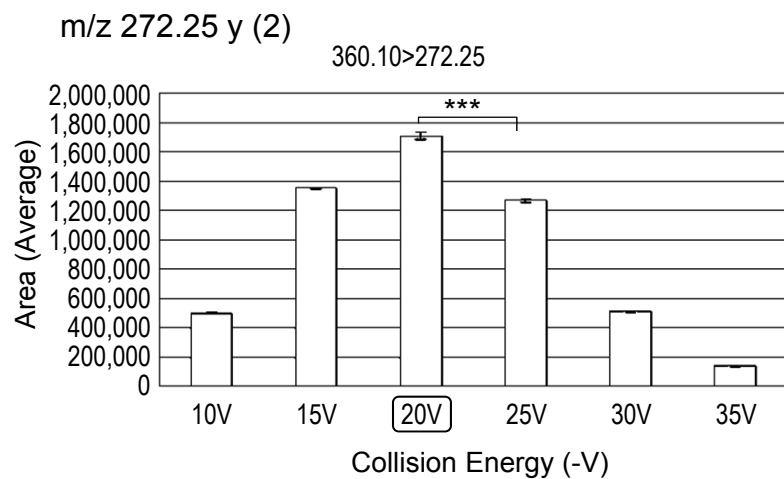
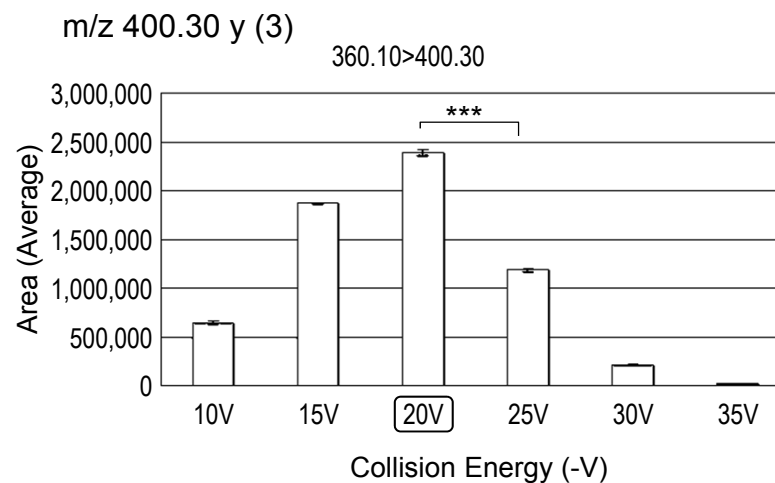
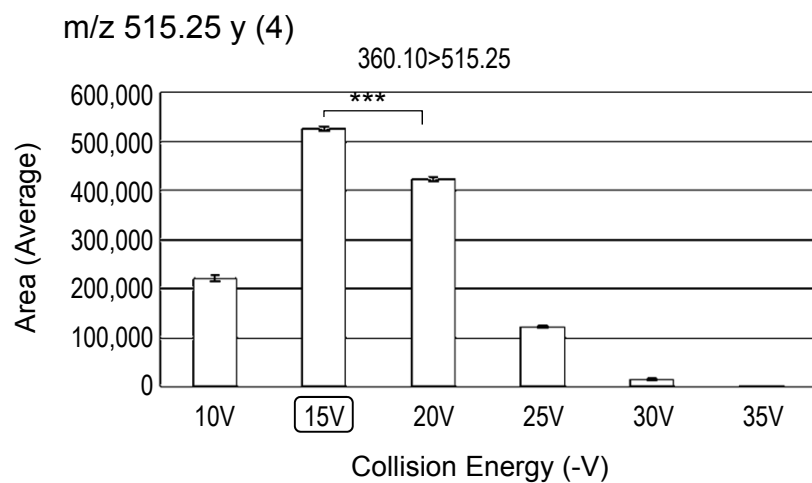
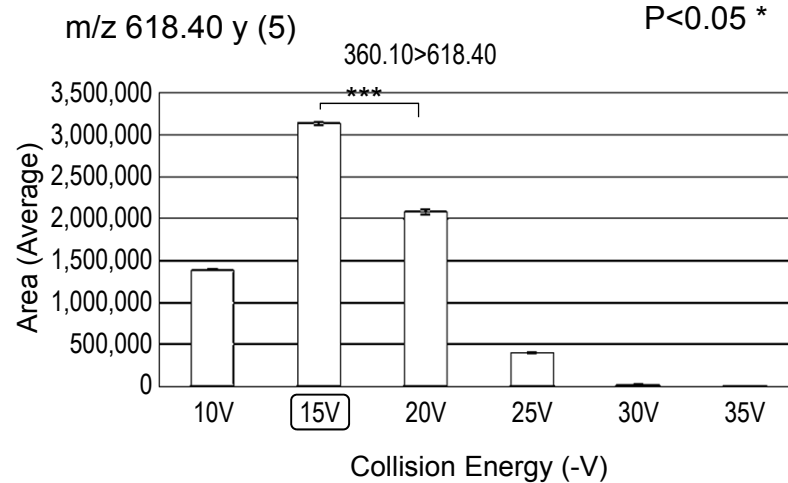
Monoisotopic mass of neutral peptide Mr(calc): 1076.5073
Ions Score: 30 Expect: 0.00091
Matches : 8/78 fragment ions using 13 most intense peaks (help)

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							9
2	274.1186	137.5629			256.1081	128.5577	W	990.4826	495.7449	973.4560	487.2316	972.4720	486.7396	8
3	361.1506	181.0790			343.1401	172.0737	S	804.4032	402.7053	787.3767	394.1920	786.3927	393.7000	7
4	460.2191	230.6132			442.2085	221.6079	V	717.3712	359.1892	700.3447	350.6760	699.3607	350.1840	6
5	563.2282	282.1178			545.2177	273.1125	C	618.3028	309.6550	601.2763	301.1418	600.2922	300.6498	5
6	678.2552	339.6312			660.2446	330.6259	D	515.2936	258.1504	498.2671	249.6372	497.2831	249.1452	4
7	806.3502	403.6787	789.3236	395.1654	788.3396	394.6734	K	400.2667	200.6370	383.2401	192.1237			3
8	903.4029	452.2051	886.3764	443.6918	885.3923	443.1998	P	272.1717	136.5895	255.1452	128.0762			2
9							R	175.1190	88.0631	158.0924	79.5498			1

*  Ion confirmed by both MS2 and product ion scan

Fig. 3-6

LCMS-8050



P<0.001 ***
P<0.01 **
P<0.05 *

Fig. 3-7

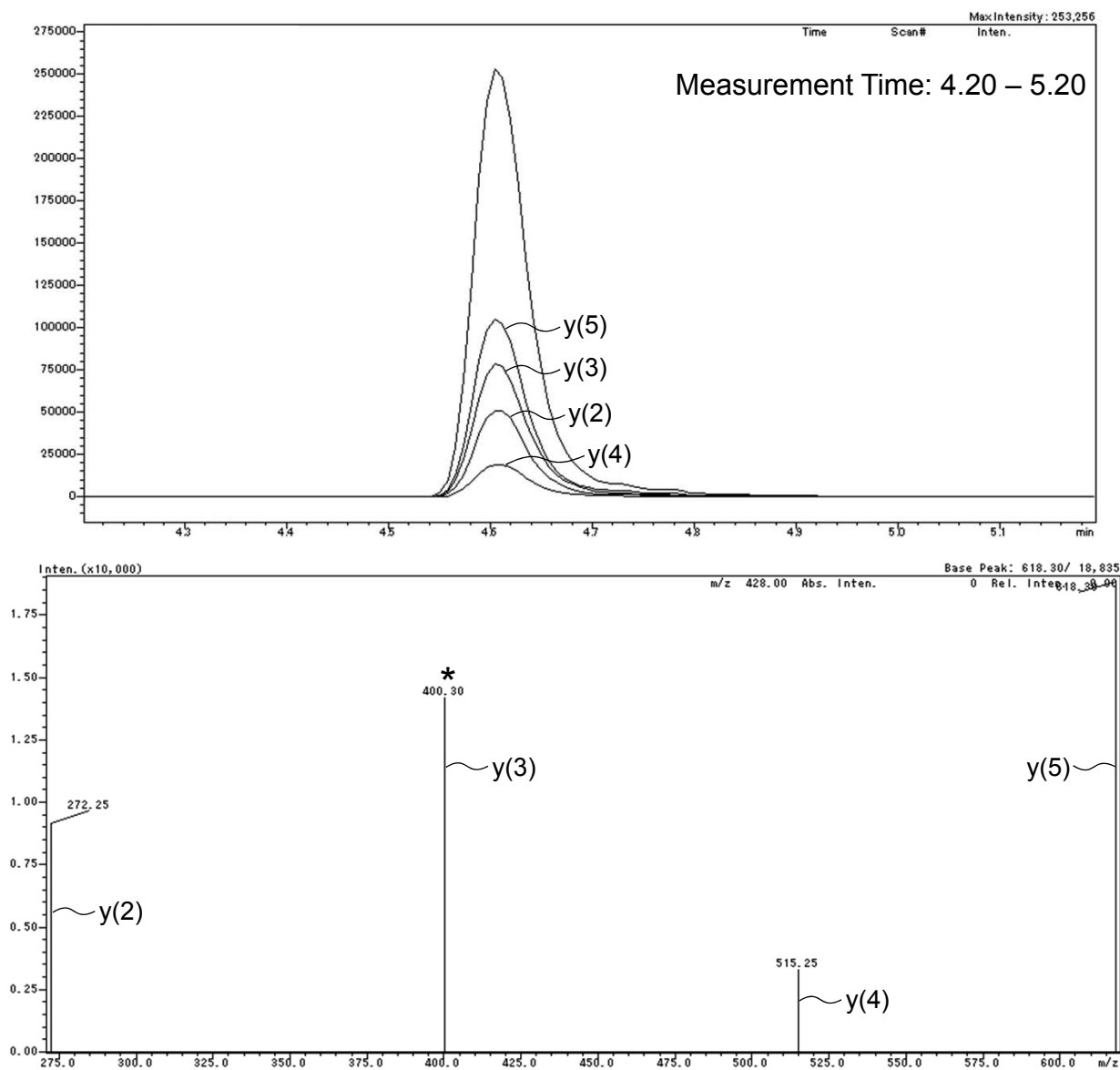
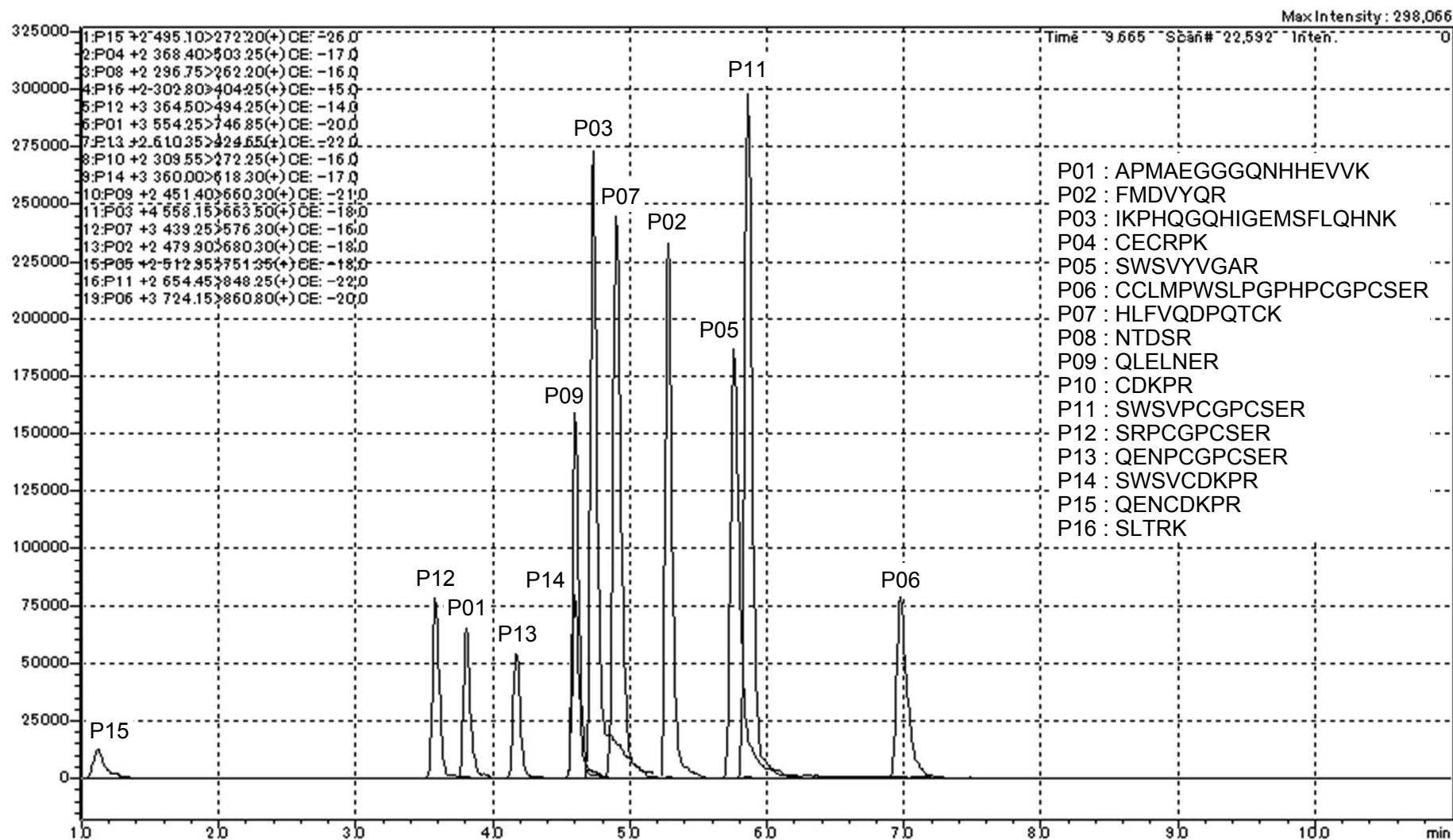


Fig. 4

Precursor Ion m/z		Product Ion m/z		Q1 Pre Bias	CE	Q3 Pre Bias	Retention Time (Minute)
P01 +3	554.25	746.85	MAEGGGQNHHEVVK	-22.0	-20.0	-28.0	3.40 – 4.40
P02 +2	479.90	680.30	DVYQR	-18.0	-18.0	-36.0	4.90 – 5.90
P03 +4	558.15	663.50	PHQGQHIGEMSFLQHNK	-22.0	-18.0	-24.0	4.40 – 5.40
P04 +2	368.40	503.25	CRPK	-14.0	-17.0	-38.0	-
P05 +2	512.95	751.35	SVYVGAR	-38.0	-18.0	-28.0	5.30 – 6.30
P06 +3	724.15	860.80	PWSLPGPHPCGPCSE	-28.0	-20.0	-32.0	6.60 – 7.60
P07 +3	439.25	576.30	PQTCK	-16.0	-15.0	-30.0	4.50 – 5.50
P08 +2	296.75	262.20	SR	-11.0	-16.0	-29.0	-
P09 +2	451.40	660.30	ELNER	-17.0	-21.0	-34.0	4.20 – 5.20
P10 +2	309.55	272.25	PR	-12.0	-16.0	-30.0	-
P11 +2	654.45	848.25	PCGPCSER	-26.0	-22.0	-32.0	5.50 – 6.50
P12 +3	364.50	494.25	CSER	-26.0	-14.0	-25.0	3.10 – 4.40
P13 +2	610.35	424.65	PCGPCSER	-24.0	-22.0	-30.0	3.80 – 4.80
P14 +3	360.00	618.30	CDKPR	-26.0	-17.0	-32.0	4.20 – 5.20
P15 +2	495.10	272.20	PR	-18.0	-26.0	-19.0	-
P16 +2	302.80	404.25	TRK	-24.0	-15.0	-29.0	-

Fig. 5



*Measurement Time: 1.0 – 11.0 minutes, Event Time: 0.023 seconds, Event Number: 19, Dwell Time : 20.0 milliseconds, Loop Time: 0.437seconds, Resolution: High