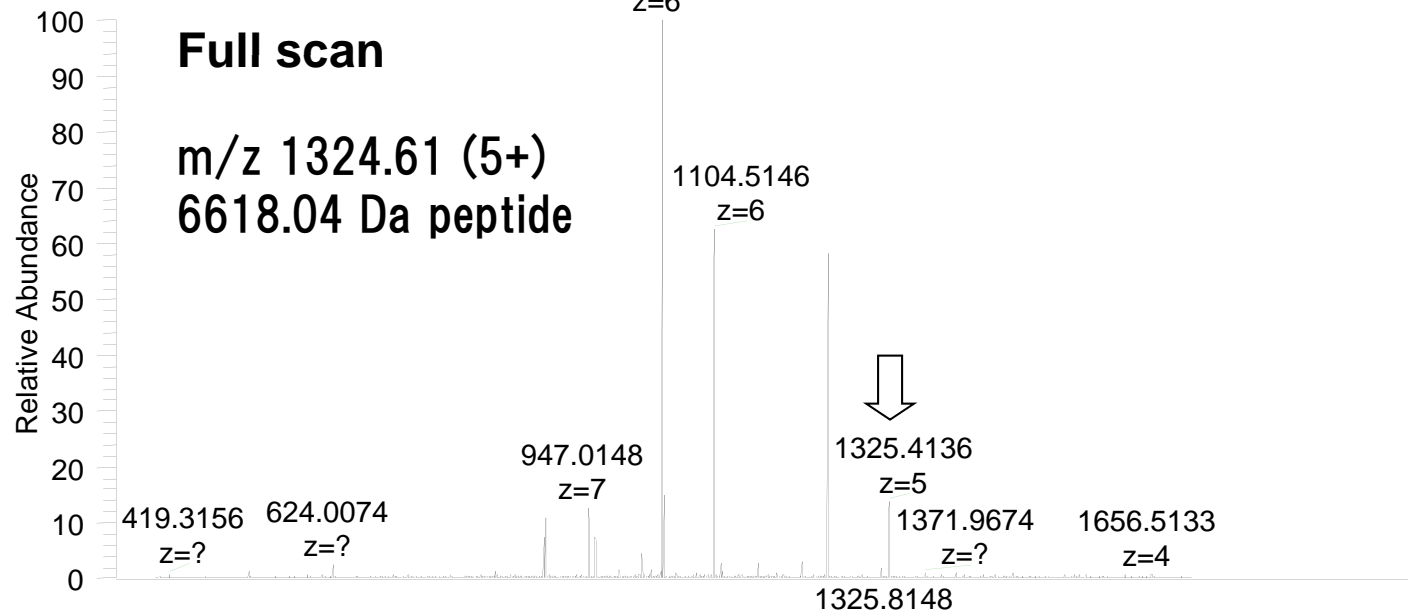


Supplemental Figure S3

a)

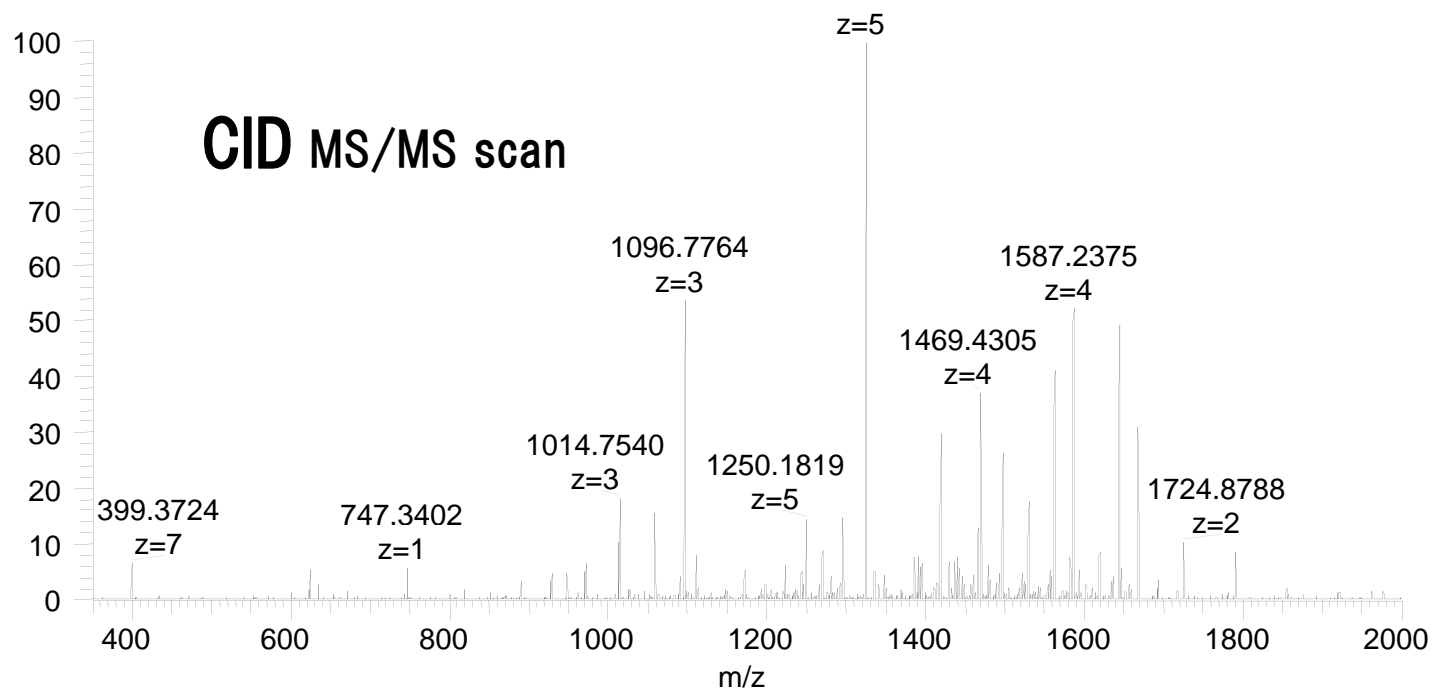
NL: 5.23E7

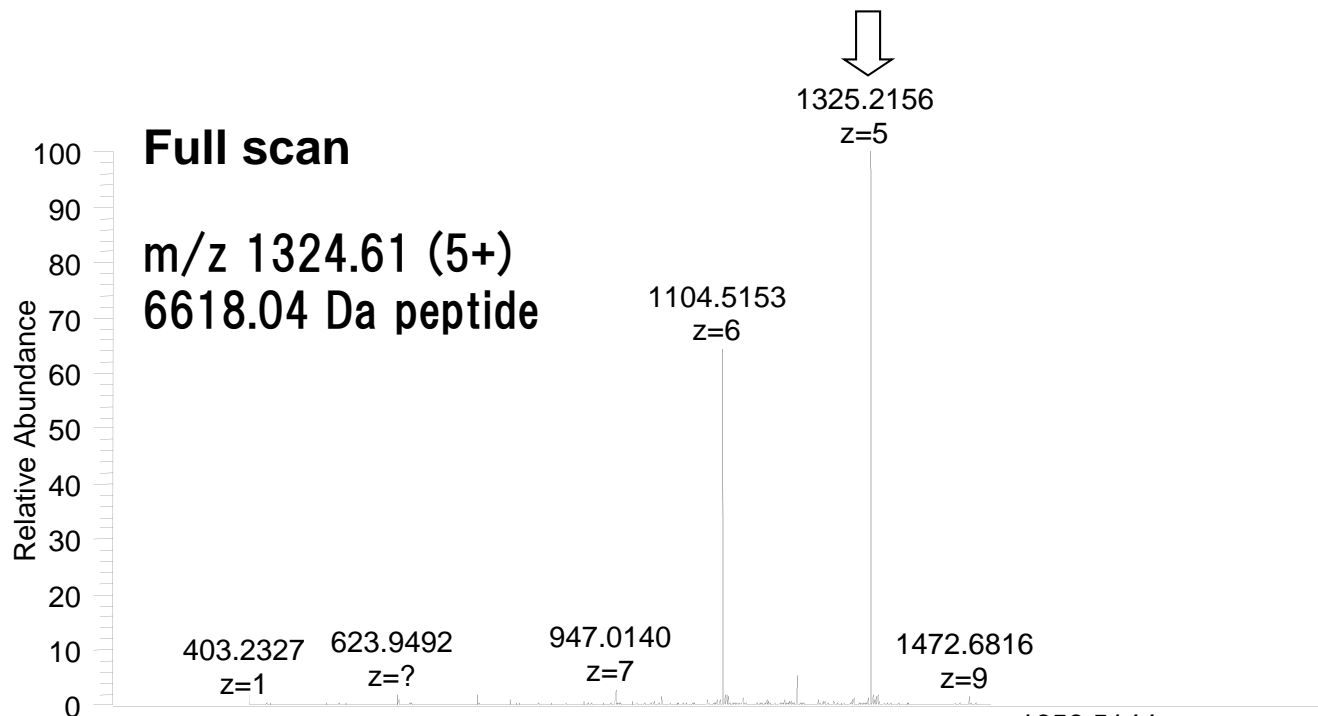
CID_test#2001 RT: 45.54 AV:
1 T: FTMS + p NSI Full ms
[400.00-1700.00]



NL: 3.20E5

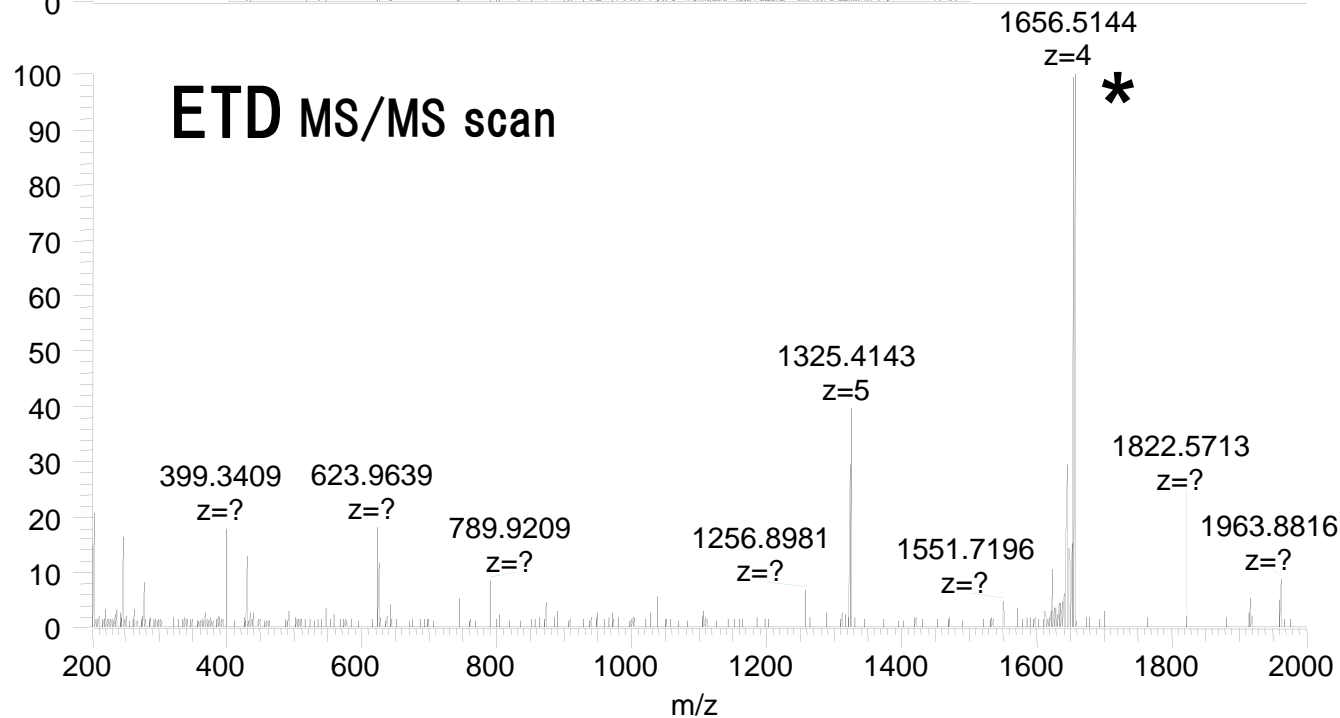
CID_test#2002 RT: 45.56 AV:
1 T: FTMS + p NSI d Full ms2
1325.41 @cid35.00
[350.00-2000.00]





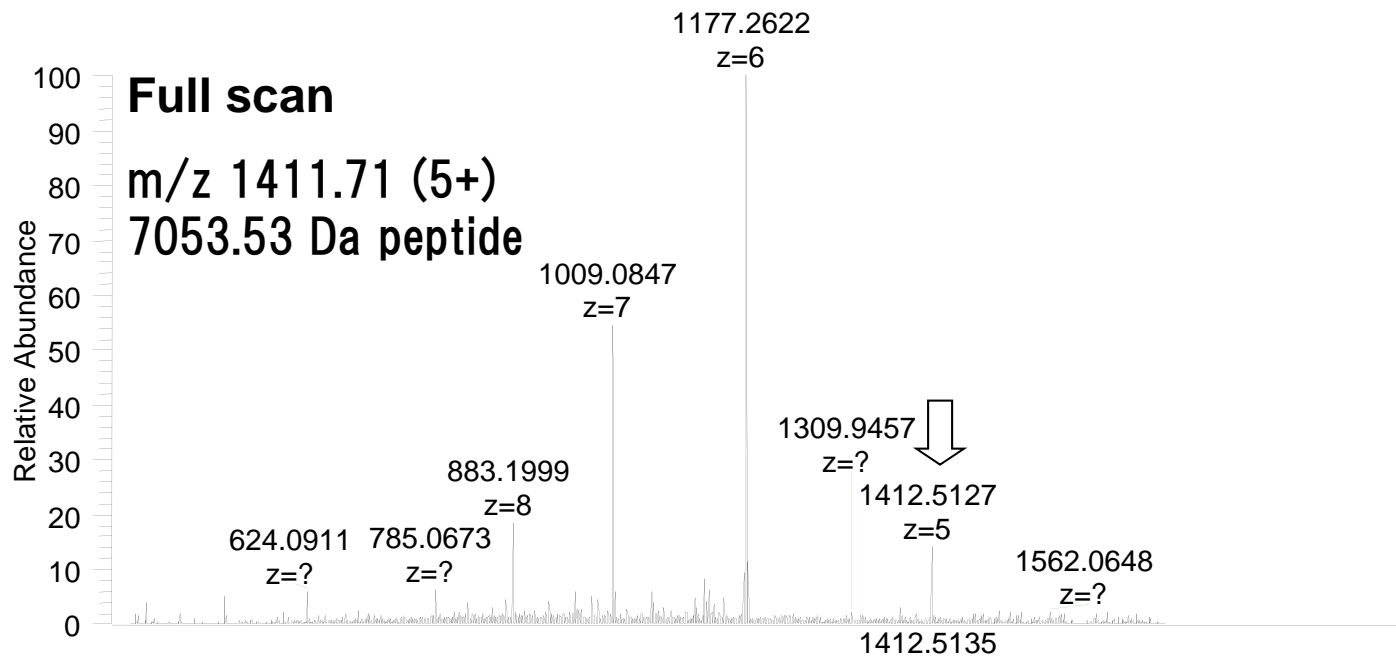
NL: 1.86E7

2000msec_uS2#1249 RT: 50.52
AV: 1 T: FTMS + p NSI Full ms
[403.00-1500.00]



NL: 1.10E5

2000msec_uS2#1250 RT: 50.57
AV: 1 T: FTMS + p NSI d sa Full
ms2 1325.22@etd36.00
[200.00-2000.00]

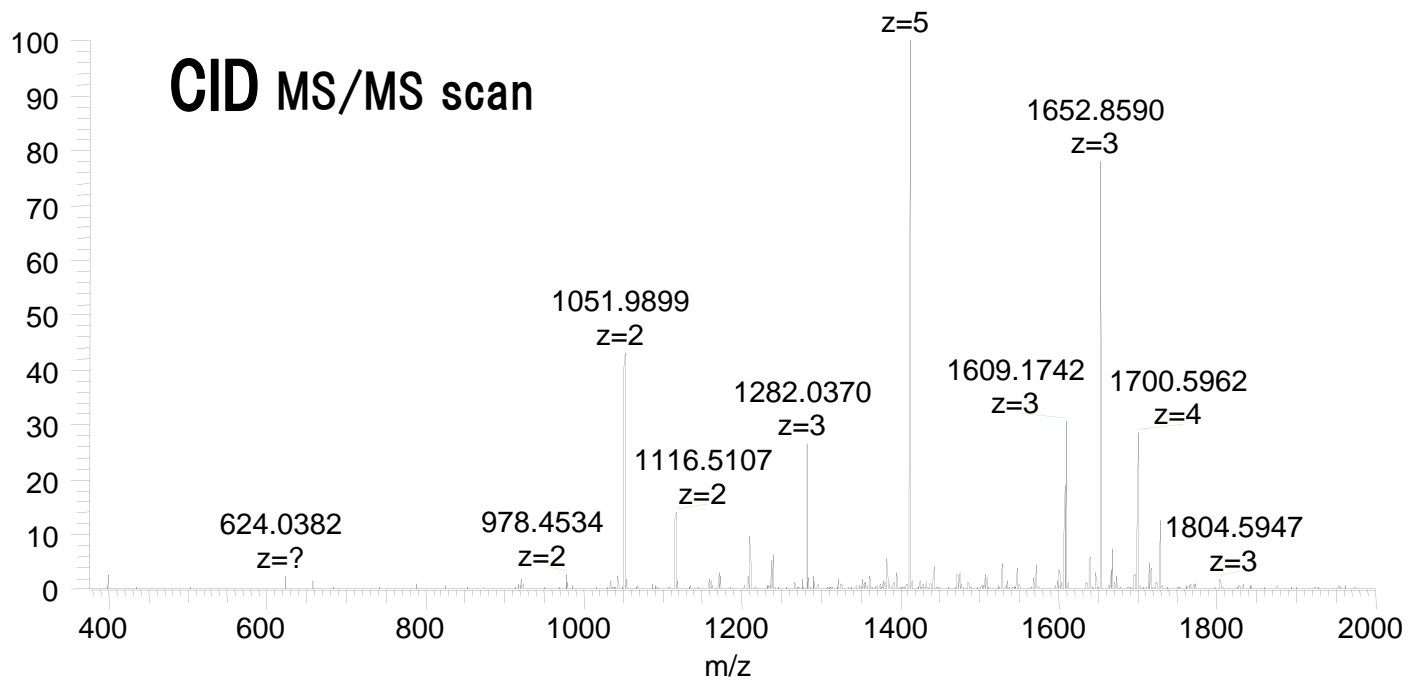


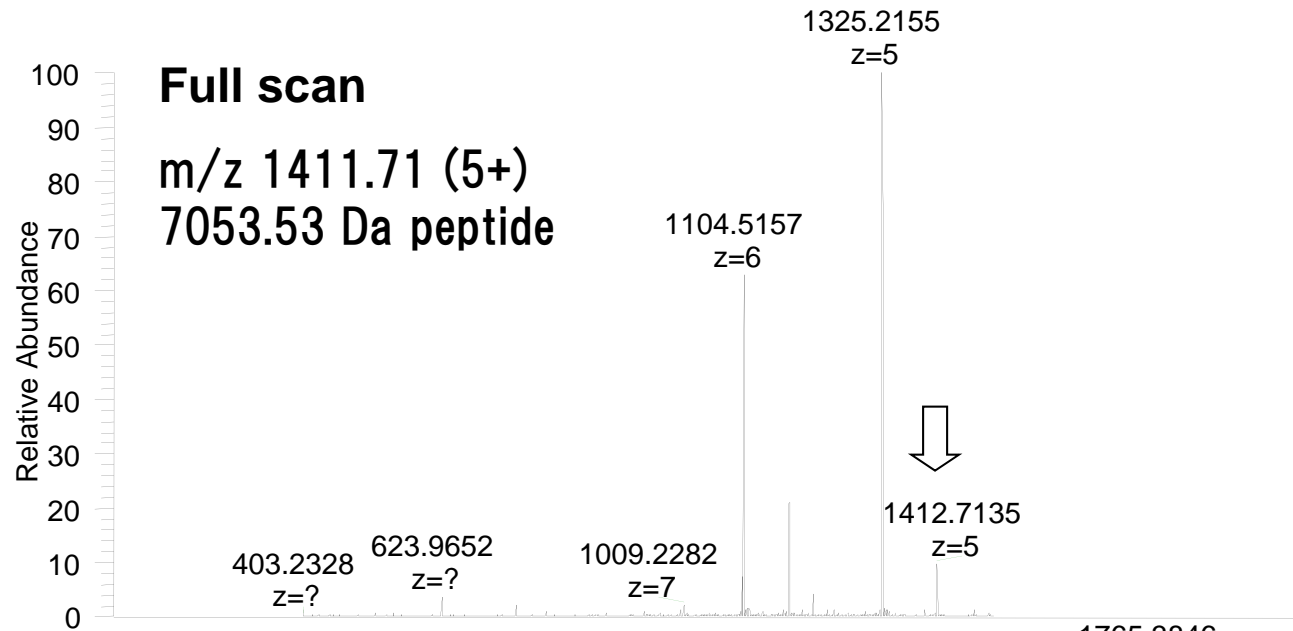
NL: 1.10E7

CID_test#1953 RT: 44.49 AV:
 1 T: FTMS + p NSI Full ms
 [400.00-1700.00]

NL: 3.06E5

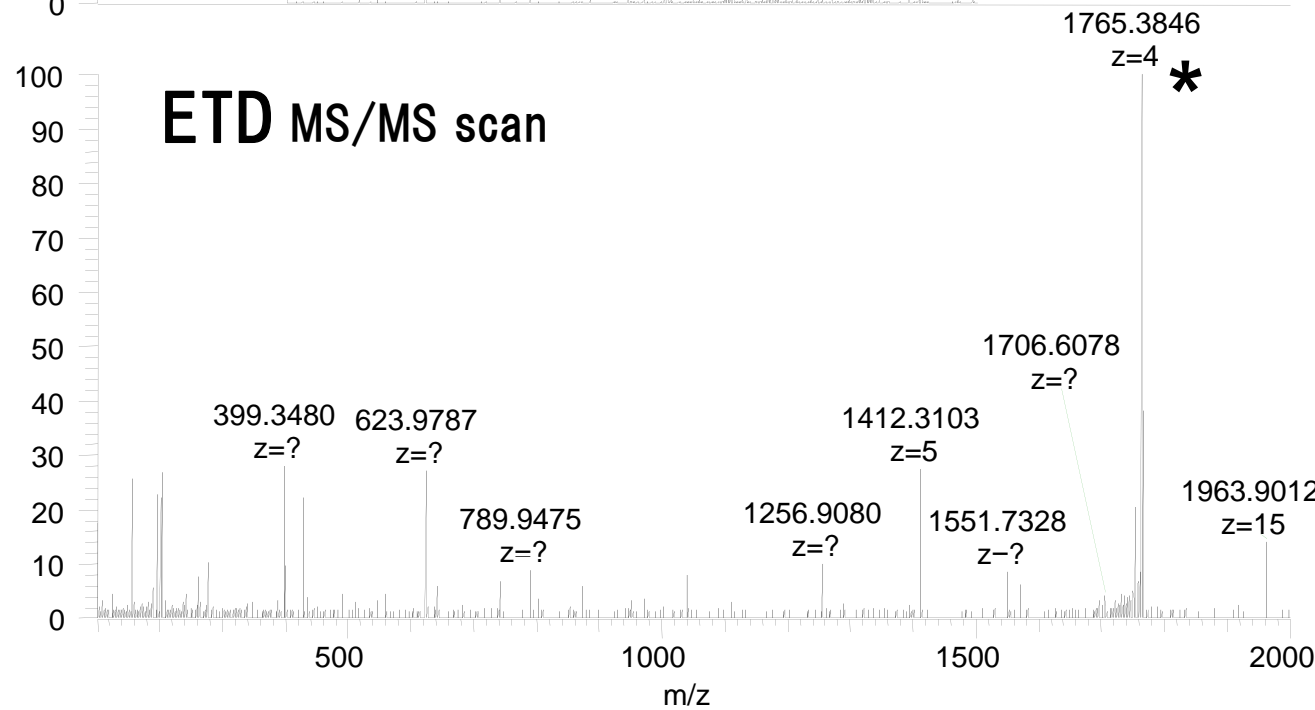
CID_test#1955 RT: 44.52 AV:
 1 T: FTMS + p NSI d Full ms2
 1412.51 @cid35.00
 [375.00-2000.00]





NL: 1.23E7

2000msec_uS2#1267 RT: 51.25
AV: 1 T: FTMS + p NSI Full ms
[403.00-1500.00]



NL: 9.56E3

2000msec_uS2#1268 RT: 51.29
AV: 1 T: FTMS + p NSI d sa Full
ms2 1412.71@etd36.00
[100.00-2000.00]

Supplemental Figure S3

b) Mascot Search Results

Peptide View

MS/MS Fragmentation of **SQEETPGHRRKEAEGTEEGGEEEDDEEMDPQTIDSLIELSTKLHLPADDVVSIIIEVEE**
 Found in **gj17136078** in **NCBI nr**, neurosecretory protein VGF precursor [Homo sapiens]

Match to Query 372: 6618.020620 from(1324.611400,5+) intensity(12476334.0000) scans(2002) rtinseconds(2733.7388)

Title: 540: Scan 2002 (rt=2733.74)

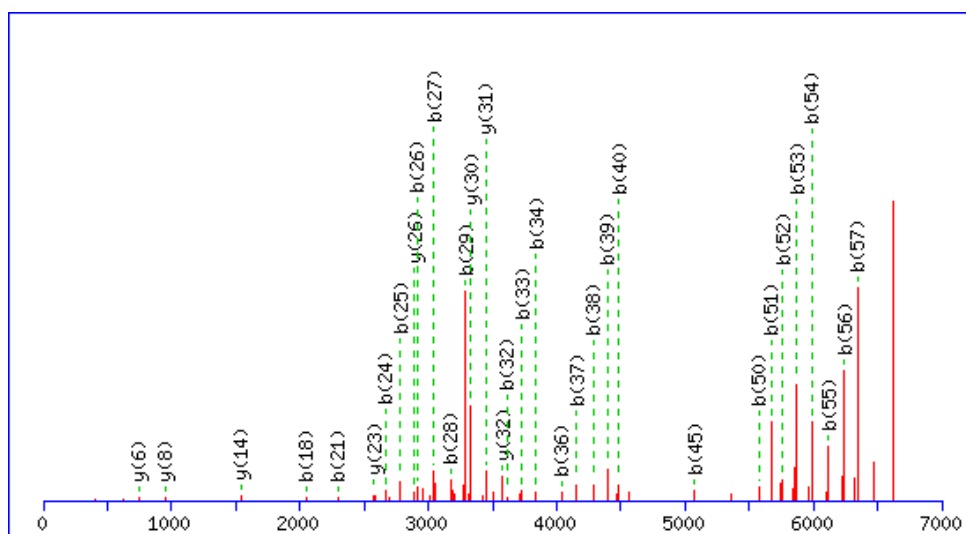
Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, 0 to Da

Label all possible matches Label matches used for scoring

Show Y-axis



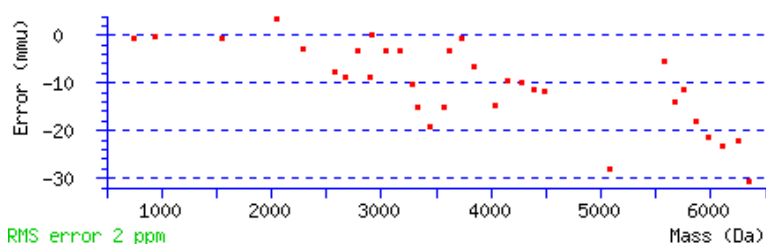
Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 6618.0362

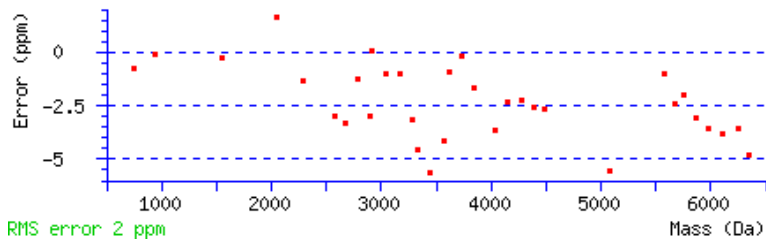
Ions Score: 203 Expect: 4.8e-017

Matches : 33/329 fragment ions using 40 most intense peaks ([help](#))

#	a	a*	b	b*	Seq.	y	y*	#
1	60.0444		88.0393		S			59
2	188.1030	171.0764	216.0979	199.0713	Q	6532.0115	6514.9850	58
3	317.1456	300.1190	345.1405	328.1139	E	6403.9530	6386.9264	57
4	446.1882	429.1616	474.1831	457.1565	E	6274.9104	6257.8838	56
5	547.2358	530.2093	575.2307	558.2042	T	6145.8678	6128.8412	55
6	644.2886	627.2620	672.2835	655.2570	P	6044.8201	6027.7935	54
7	701.3101	684.2835	729.3050	712.2784	G	5947.7673	5930.7408	53
8	838.3690	821.3424	866.3639	849.3373	H	5890.7459	5873.7193	52
9	994.4701	977.4435	1022.4650	1005.4384	R	5753.6869	5736.6604	51
10	1150.5712	1133.5446	1178.5661	1161.5396	R	5597.5858	5580.5593	50
11	1278.6662	1261.6396	1306.6611	1289.6345	K	5441.4847	5424.4582	49
12	1407.7088	1390.6822	1435.7037	1418.6771	E	5313.3898	5296.3632	48
13	1478.7459	1461.7193	1506.7408	1489.7142	A	5184.3472	5167.3206	47
14	1607.7885	1590.7619	1635.7834	1618.7568	E	5113.3101	5096.2835	46
15	1664.8099	1647.7834	1692.8048	1675.7783	G	4984.2675	4967.2409	45
16	1765.8576	1748.8311	1793.8525	1776.8260	T	4927.2460	4910.2194	44
17	1894.9002	1877.8736	1922.8951	1905.8686	E	4826.1983	4809.1718	43
18	2023.9428	2006.9162	2051.9377	2034.9112	E	4697.1557	4680.1292	42
19	2080.9642	2063.9377	2108.9592	2091.9326	G	4568.1131	4551.0866	41

20	2137.9857	2120.9592	2165.9806	2148.9541	G	4511.0917	4494.0651	40
21	2267.0283	2250.0018	2295.0232	2277.9967	E	4454.0702	4437.0437	39
22	2396.0709	2379.0444	2424.0658	2407.0393	E	4325.0276	4308.0011	38
23	2525.1135	2508.0869	2553.1084	2536.0819	E	4195.9850	4178.9585	37
24	2640.1404	2623.1139	2668.1354	2651.1088	D	4066.9424	4049.9159	36
25	2755.1674	2738.1408	2783.1623	2766.1357	D	3951.9155	3934.8889	35
26	2884.2100	2867.1834	2912.2049	2895.1783	E	3836.8885	3819.8620	34
27	3013.2526	2996.2260	3041.2475	3024.2209	E	3707.8459	3690.8194	33
28	3144.2930	3127.2665	3172.2880	3155.2614	M	3578.8034	3561.7768	32
29	3259.3200	3242.2934	3287.3149	3270.2884	D	3447.7629	3430.7363	31
30	3356.3728	3339.3462	3384.3677	3367.3411	P	3332.7359	3315.7094	30
31	3484.4313	3467.4048	3512.4263	3495.3997	Q	3235.6832	3218.6566	29
32	3585.4790	3568.4525	3613.4739	3596.4474	T	3107.6246	3090.5980	28
33	3698.5631	3681.5365	3726.5580	3709.5314	I	3006.5769	2989.5504	27
34	3813.5900	3796.5635	3841.5849	3824.5584	D	2893.4928	2876.4663	26
35	3900.6220	3883.5955	3928.6170	3911.5904	S	2778.4659	2761.4393	25
36	4013.7061	3996.6796	4041.7010	4024.6745	L	2691.4339	2674.4073	24
37	4126.7902	4109.7636	4154.7851	4137.7585	I	2578.3498	2561.3233	23
38	4255.8328	4238.8062	4283.8277	4266.8011	E	2465.2657	2448.2392	22
39	4368.9168	4351.8903	4396.9117	4379.8852	L	2336.2231	2319.1966	21
40	4455.9489	4438.9223	4483.9438	4466.9172	S	2223.1391	2206.1125	20
41	4556.9965	4539.9700	4584.9915	4567.9649	T	2136.1071	2119.0805	19
42	4685.0915	4668.0650	4713.0864	4696.0599	K	2035.0594	2018.0328	18
43	4798.1756	4781.1490	4826.1705	4809.1439	L	1906.9644		17
44	4935.2345	4918.2079	4963.2294	4946.2028	H	1793.8804		16
45	5048.3185	5031.2920	5076.3135	5059.2869	L	1656.8214		15
46	5145.3713	5128.3448	5173.3662	5156.3397	P	1543.7374		14
47	5216.4084	5199.3819	5244.4033	5227.3768	A	1446.6846		13
48	5331.4354	5314.4088	5359.4303	5342.4037	D	1375.6475		12
49	5446.4623	5429.4358	5474.4572	5457.4307	D	1260.6206		11
50	5545.5307	5528.5042	5573.5256	5556.4991	V	1145.5936		10
51	5644.5991	5627.5726	5672.5941	5655.5675	V	1046.5252		9
52	5731.6312	5714.6046	5759.6261	5742.5995	S	947.4568		8
53	5844.7152	5827.6887	5872.7101	5855.6836	I	860.4248		7
54	5957.7993	5940.7727	5985.7942	5968.7677	I	747.3407		6
55	6086.8419	6069.8153	6114.8368	6097.8103	E	634.2566		5
56	6215.8845	6198.8579	6243.8794	6226.8528	E	505.2140		4
57	6314.9529	6297.9263	6342.9478	6325.9213	V	376.1714		3
58	6443.9955	6426.9689	6471.9904	6454.9639	E	277.1030		2
59					E	148.0604		1





NCBI **BLAST** search of [SQEETPGHRRKEAEGTEEGGEEEDDEEMDPQTIDSLIELSTKLHLPADDVVSIIIEVEE](#)
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
202.9	6618.0362	-0.0156	SQEETPGHRRKEAEGTEEGGEEEDDEEMDPQTIDSLIELSTKLHLPADDVVSIIIEVEE
2.5	6617.9977	0.0229	LFKRISQFTAMFRRKAFLHWYTGEGMDEMFEAEASNNDLVSEYQQYQDATAE
0.9	6618.0067	0.0140	EDMEEIRTEMNKRKENCSENILDSMPDIRSALQRDAAAAYAHPEQYEERFLQEET
0.9	6617.9940	0.0266	SDIGTGCLSSLENLRLPTLREESSPRELEDSSGDQGRCPHQGSEDPSMLSQAQSATEVEE
0.7	6618.0525	-0.0319	FAFPRATLITVMLAFIMYMLRNATQQKDMVENPEPPSGVRCCQMCCGPFLLETPSE
0.7	6618.0525	-0.0319	FAFPRATLITVMLAFIMYMLRNATQQKDMVENPEPPSGVRCCQMCCGPFLLETPSE
0.7	6618.0525	-0.0319	FAFPRATLITVMLAFIMYMLRNATQQKDMVENPEPPSGVRCCQMCCGPFLLETPSE

Mascot: <http://www.matrixscience.com/>

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of

APSDPRLRQFLQKSLAAAGKQELAKYFLAELLSEPNQTENDALEPEDLSQAAEQDEMRLLEQ

Found in **gi|4507243** in **NCBIInr**, somatostatin preproprotein [Homo sapiens]

Match to Query 429: 7053.512120 from(1411.709700,5+) intensity(7144084.0000) scans(1955) rtinseconds(2671.3214)

Title: 505: Scan 1955 (rt=2671.32)

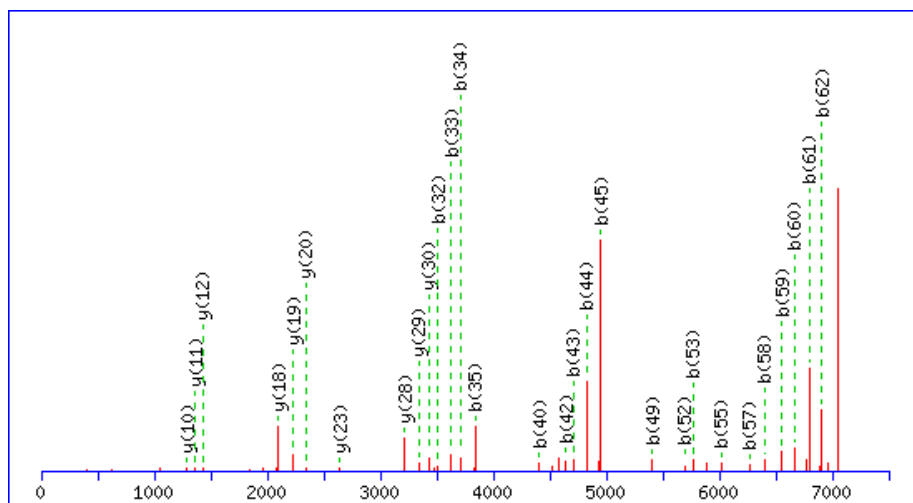
Data file tempfile

Click mouse within plot area to zoom in by factor of two about that point

Or, 0 to Da

Label all possible matches Label matches used for scoring

Show Y-axis



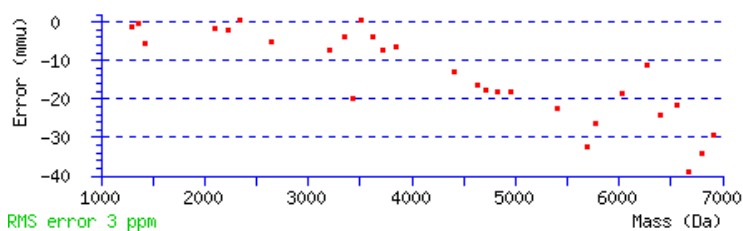
Monoisotopic mass of neutral peptide $M_r(\text{calc})$: 7053.5304

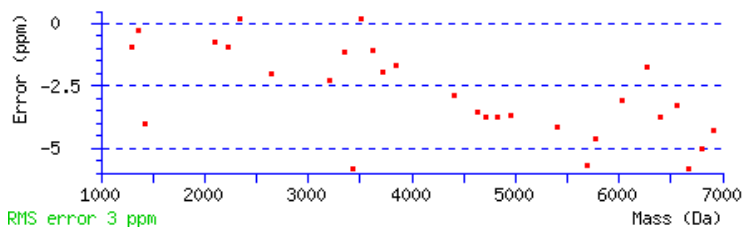
Ions Score: 129 Expect: 5.1e-009

Matches : 29/362 fragment ions using 38 most intense peaks ([help](#))

#	a	a*	b	b*	Seq.	y	y*	#
1	44.0495		72.0444		A			63
2	141.1022		169.0972		P	6983.5008	6966.4742	62
3	228.1343		256.1292		S	6886.4480	6869.4214	61
4	343.1612		371.1561		D	6799.4160	6782.3894	60
5	440.2140		468.2089		P	6684.3890	6667.3625	59
6	596.3151	579.2885	624.3100	607.2835	R	6587.3363	6570.3097	58
7	709.3991	692.3726	737.3941	720.3675	L	6431.2351	6414.2086	57
8	865.5003	848.4737	893.4952	876.4686	R	6318.1511	6301.1245	56
9	993.5588	976.5323	1021.5538	1004.5272	Q	6162.0500	6145.0234	55
10	1140.6273	1123.6007	1168.6222	1151.5956	F	6033.9914	6016.9648	54
11	1253.7113	1236.6848	1281.7062	1264.6797	L	5886.9230	5869.8964	53
12	1381.7699	1364.7433	1409.7648	1392.7383	Q	5773.8389	5756.8124	52
13	1509.8649	1492.8383	1537.8598	1520.8332	K	5645.7803	5628.7538	51
14	1596.8969	1579.8703	1624.8918	1607.8653	S	5517.6854	5500.6588	50
15	1709.9809	1692.9544	1737.9759	1720.9493	L	5430.6533	5413.6268	49
16	1781.0181	1763.9915	1809.0130	1791.9864	A	5317.5693	5300.5427	48
17	1852.0552	1835.0286	1880.0501	1863.0235	A	5246.5322	5229.5056	47
18	1923.0923	1906.0657	1951.0872	1934.0607	A	5175.4951	5158.4685	46
19	1994.1294	1977.1029	2022.1243	2005.0978	A	5104.4579	5087.4314	45
20	2051.1509	2034.1243	2079.1458	2062.1192	G	5033.4208	5016.3943	44
21	2179.2458	2162.2193	2207.2407	2190.2142	K	4976.3994	4959.3728	43

22	2307.3044	2290.2779	2335.2993	2318.2728	Q	4848.3044	4831.2778	42
23	2436.3470	2419.3205	2464.3419	2447.3154	E	4720.2458	4703.2193	41
24	2549.4311	2532.4045	2577.4260	2560.3994	L	4591.2032	4574.1767	40
25	2620.4682	2603.4416	2648.4631	2631.4365	A	4478.1192	4461.0926	39
26	2748.5631	2731.5366	2776.5581	2759.5315	K	4407.0820	4390.0555	38
27	2911.6265	2894.5999	2939.6214	2922.5948	Y	4278.9871	4261.9605	37
28	3058.6949	3041.6683	3086.6898	3069.6633	F	4115.9238	4098.8972	36
29	3171.7790	3154.7524	3199.7739	3182.7473	L	3968.8553	3951.8288	35
30	3242.8161	3225.7895	3270.8110	3253.7844	A	3855.7713	3838.7447	34
31	3371.8587	3354.8321	3399.8536	3382.8270	E	3784.7342	3767.7076	33
32	3484.9427	3467.9162	3512.9376	3495.9111	L	3655.6916	3638.6650	32
33	3598.0268	3581.0002	3626.0217	3608.9952	L	3542.6075	3525.5810	31
34	3685.0588	3668.0323	3713.0537	3696.0272	S	3429.5234	3412.4969	30
35	3814.1014	3797.0749	3842.0963	3825.0698	E	3342.4914	3325.4649	29
36	3911.1542	3894.1276	3939.1491	3922.1225	P	3213.4488	3196.4223	28
37	4025.1971	4008.1705	4053.1920	4036.1655	N	3116.3961	3099.3695	27
38	4153.2557	4136.2291	4181.2506	4164.2240	Q	3002.3531	2985.3266	26
39	4254.3034	4237.2768	4282.2983	4265.2717	T	2874.2946	2857.2680	25
40	4383.3459	4366.3194	4411.3409	4394.3143	E	2773.2469	2756.2203	24
41	4497.3889	4480.3623	4525.3838	4508.3572	N	2644.2043	2627.1777	23
42	4612.4158	4595.3893	4640.4107	4623.3842	D	2530.1614	2513.1348	22
43	4683.4529	4666.4264	4711.4478	4694.4213	A	2415.1344	2398.1079	21
44	4796.5370	4779.5104	4824.5319	4807.5054	L	2344.0973	2327.0707	20
45	4925.5796	4908.5530	4953.5745	4936.5480	E	2231.0132	2213.9867	19
46	5022.6324	5005.6058	5050.6273	5033.6007	P	2101.9706	2084.9441	18
47	5151.6749	5134.6484	5179.6699	5162.6433	E	2004.9179	1987.8913	17
48	5266.7019	5249.6753	5294.6968	5277.6703	D	1875.8753	1858.8487	16
49	5379.7860	5362.7594	5407.7809	5390.7543	L	1760.8483	1743.8218	15
50	5466.8180	5449.7914	5494.8129	5477.7863	S	1647.7643	1630.7377	14
51	5594.8766	5577.8500	5622.8715	5605.8449	Q	1560.7322	1543.7057	13
52	5665.9137	5648.8871	5693.9086	5676.8820	A	1432.6737	1415.6471	12
53	5736.9508	5719.9242	5764.9457	5747.9192	A	1361.6366	1344.6100	11
54	5865.9934	5848.9668	5893.9883	5876.9617	E	1290.5994	1273.5729	10
55	5994.0520	5977.0254	6022.0469	6005.0203	Q	1161.5569	1144.5303	9
56	6109.0789	6092.0524	6137.0738	6120.0473	D	1033.4983	1016.4717	8
57	6238.1215	6221.0949	6266.1164	6249.0899	E	918.4713	901.4448	7
58	6369.1620	6352.1354	6397.1569	6380.1303	M	789.4287	772.4022	6
59	6525.2631	6508.2365	6553.2580	6536.2315	R	658.3883	641.3617	5
60	6638.3472	6621.3206	6666.3421	6649.3155	L	502.2871	485.2606	4
61	6767.3897	6750.3632	6795.3847	6778.3581	E	389.2031	372.1765	3
62	6880.4738	6863.4473	6908.4687	6891.4422	L	260.1605	243.1339	2
63					Q	147.0764	130.0499	1





NCBI BLAST search of [APSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPNQTENDALEPEDLSQAAEQDEMRLLEQ](#)
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc)	Delta	Sequence
129.4	7053.5304	-0.0183	APSDPRLRQFLQKSLAAAAGKQELAKYFLAELLSEPNQTENDALEPEDLSQAAEQDEMRLLEQ
6.7	7053.5147	-0.0026	IGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYVAGIELLHQKLELPDENVSGEFWSFCLACVS
6.7	7053.5147	-0.0026	IGLCACICRSLYPTIATGILHLLAGLCTLGSVSCYVAGIELLHQKLELPDENVSGEFGWSFCLACVSA
5.3	7053.5433	-0.0312	QRSGEESYNLDSVAKNGLGLELGPQPQGVLRADIFSRMRTLVA TVLDFIELFNQGTAFPAFEME
5.1	7053.5309	-0.0188	HPETIVLDTLPAIRTLDRSKSYELIRKIEAYMEDDRICSPFMELTS LCGDDTMRLEK
4.0	7053.5451	-0.0330	NFVVDQMCEIGKPEPLNEEEARGVVENYNDEEV SIRVGGNTQPSKVLNKKNVEAIGLLGGQSK
3.9	7053.5083	0.0038	MEEIEGSVTVRDYIQSTMETEKTPQGLSNLAKTIGQVLARMHDEDLIHGDLTTSNMLLKPPLE
3.8	7053.5129	-0.0008	TLSSPAESCRSKVRGTSKPIFSLFADNVDLKELGRKEKEMQMELREKMSEYQMEKLASDNK
3.8	7053.5129	-0.0008	TLSSPAESCRSKVRGTSKPIFSLFADNVDLKELGRKEKEMQMELREKMSEYQMEKLASDNK
3.7	7053.4975	0.0146	PFMLFDPSNPLLASQLLSGAIPQIPASSATSPSTPTSTMNTLKRKLEEKASASPGENDSGTGGEEPQR

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