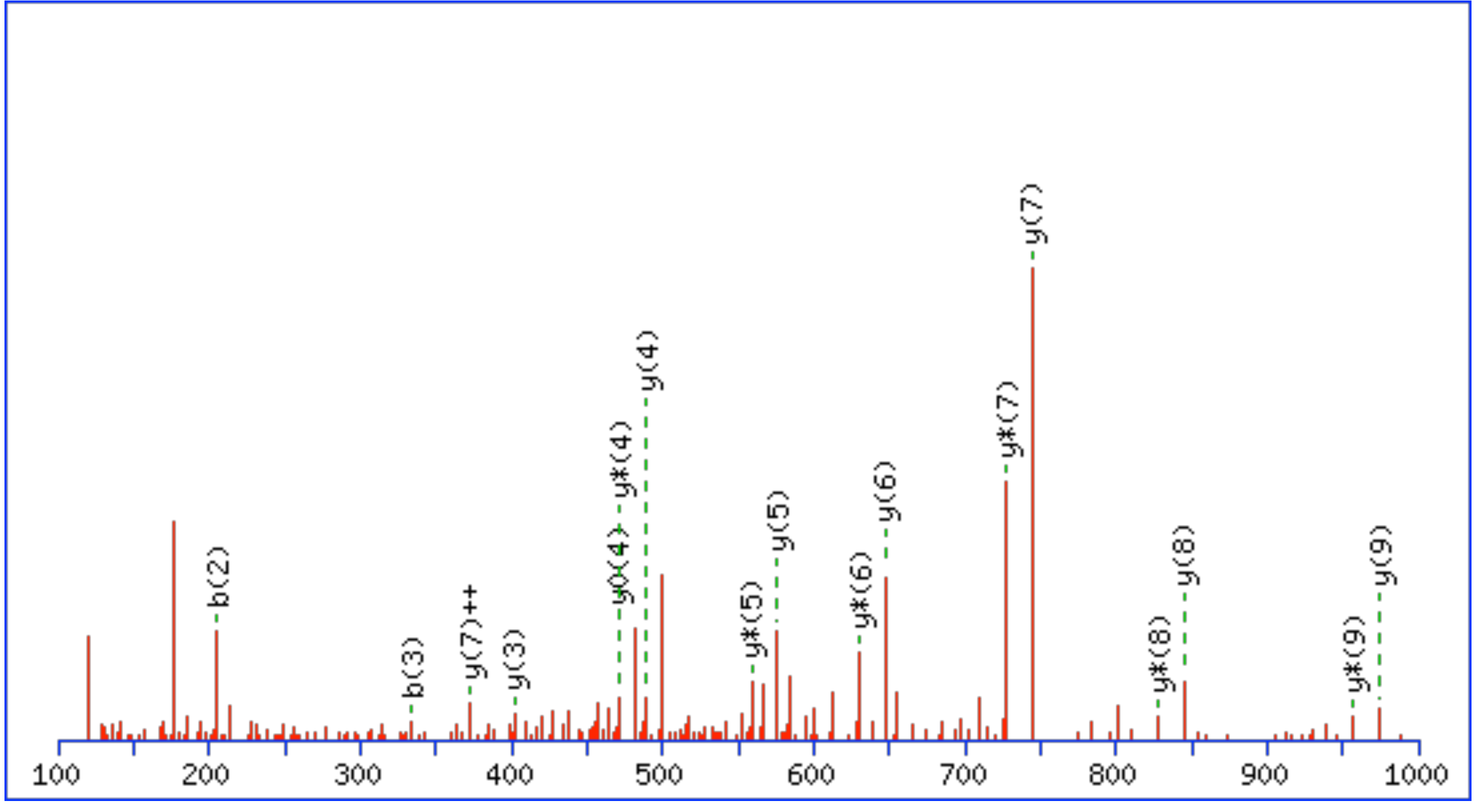
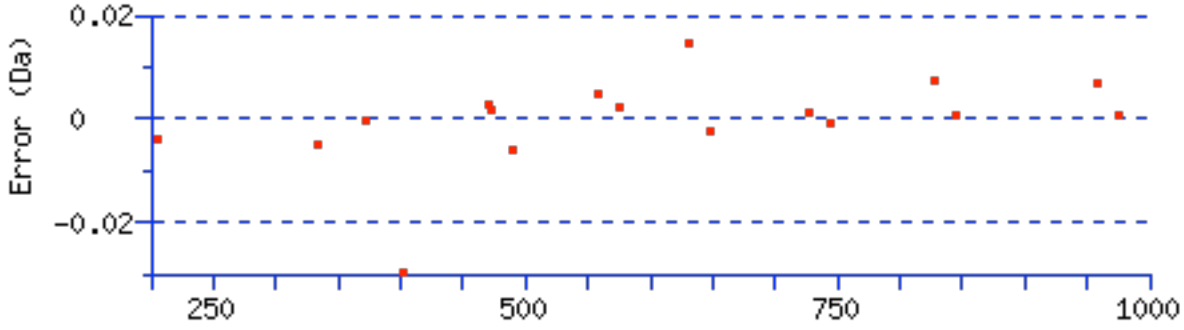
MS/MS Fragmentation of **GFETPASSRIN**
Found in **XP_001176287**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
Match to Query 415: 1177.587888 from(589.801220,2+) intensity(394140.0000)
Title: Cmpd 101, +MSn(589.7772), 24.4 min
Data file Qtof_all.mgf



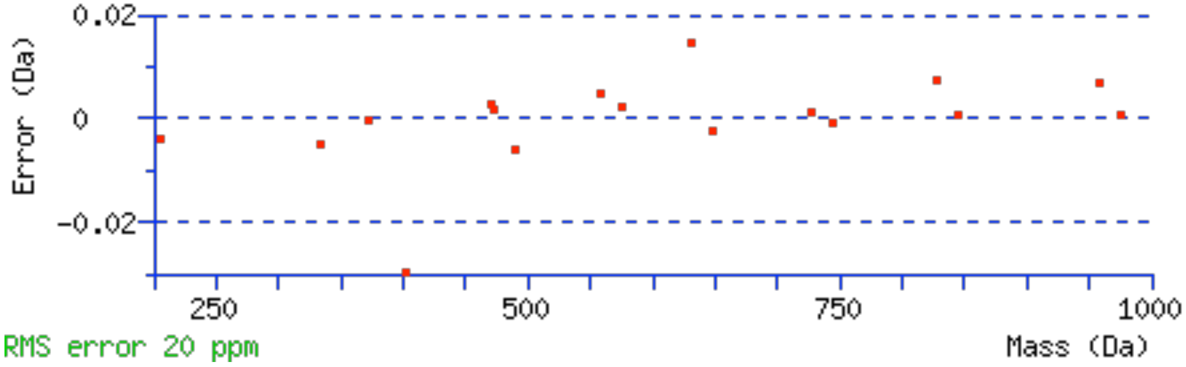
Monoisotopic mass of neutral peptide Mr(calc): 1177.5727 **Ions Score:** 43 **Expect:** 0.76 **Matches (Bold Red):** 17/94 fragment ions using 38 most intense peaks

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#

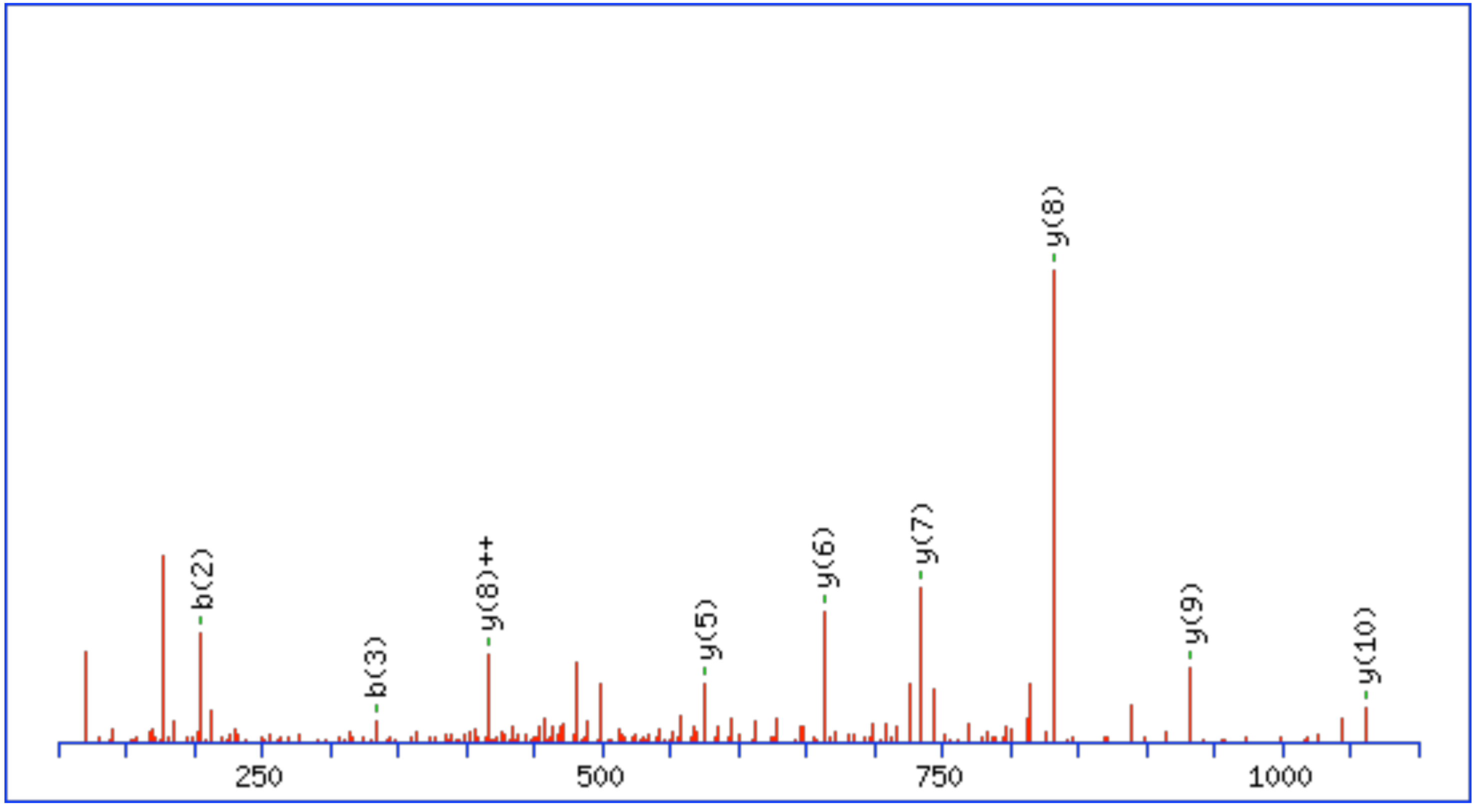
1	58.0287	29.5180					G							11
2	**205.0972**	103.0522					F	1121.5586	561.2829	1104.5320	552.7696	1103.5480	552.2776	10
3	**334.1397**	167.5735			316.1292	158.5682	E	**974.4901**	487.7487	**957.4636**	479.2354	956.4796	478.7434	9
4	435.1874	218.0974			417.1769	209.0921	T	**845.4476**	423.2274	**828.4210**	414.7141	827.4370	414.2221	8
5	532.2402	266.6237			514.2296	257.6185	P	**744.3999**	**372.7036**	**727.3733**	364.1903	726.3893	363.6983	7
6	603.2773	302.1423			585.2667	293.1370	A	**647.3471**	324.1772	**630.3206**	315.6639	629.3365	315.1719	6
7	690.3093	345.6583			672.2988	336.6530	S	**576.3100**	288.6586	**559.2834**	280.1454	558.2994	279.6534	5
8	777.3414	389.1743			759.3308	380.1690	S	**489.2780**	245.1426	**472.2514**	236.6293	**471.2674**	236.1373	4
9	933.4425	467.2249	916.4159	458.7116	915.4319	458.2196	R	**402.2459**	201.6266	385.2194	193.1133			3
10	1046.5265	523.7669	1029.5000	515.2536	1028.5160	514.7616	I	246.1448	123.5761	229.1183	115.0628			2
11							N	133.0608	67.0340	116.0342	58.5207			1



RMS error 20 ppm



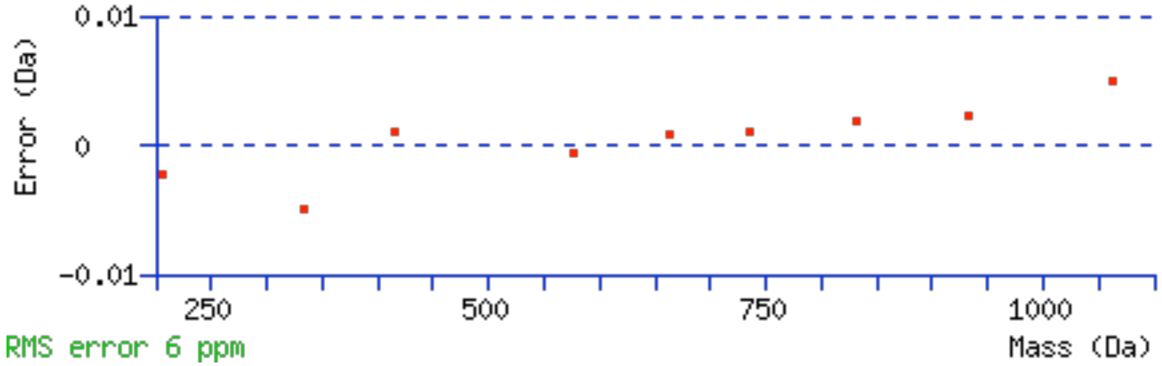
MS/MS Fragmentation of **GFETPASSRINS**
Found in **XP_001176287**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
Match to Query 466: 1264.636128 from(633.325340,2+) intensity(1458960.0000)
Title: Cmpd 104, +MSn(633.7875), 24.7 min
Data file Qtof_all.mgf

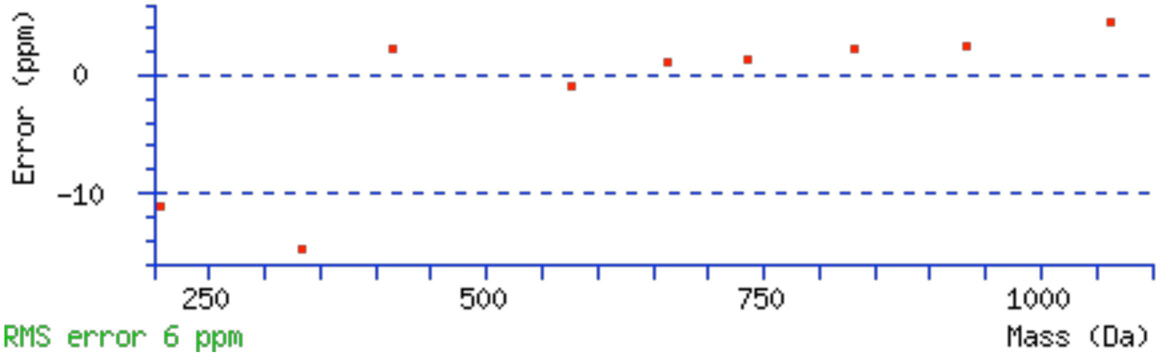


Monoisotopic mass of neutral peptide Mr(calc): 1264.6048 **Ions Score:** 46 **Expect:** 0.33 **Matches (Bold Red):** 9/110 fragment ions using 15 most intense peaks

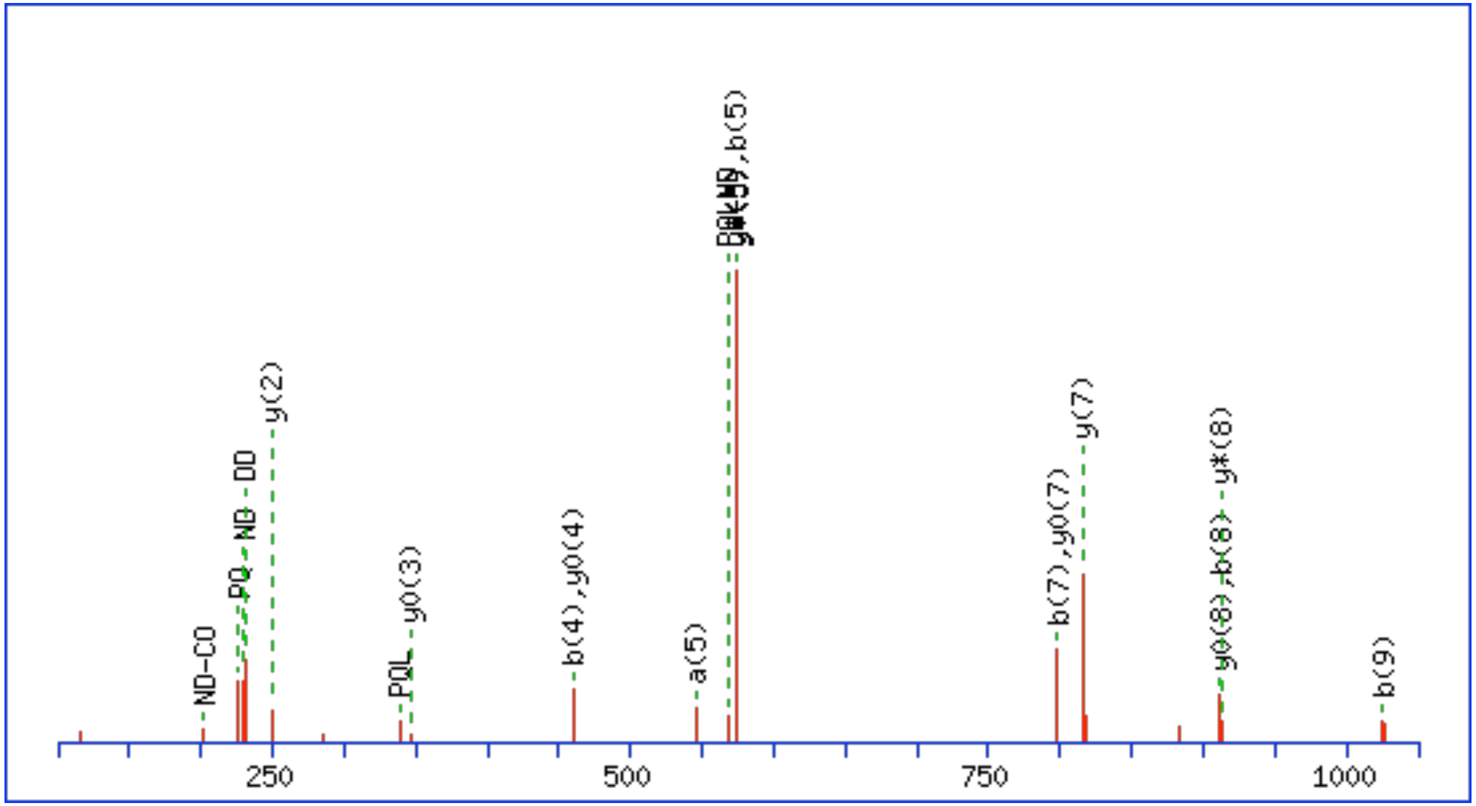
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							12
2	**205.0972**	103.0522					F	1208.5906	604.7989	1191.5640	596.2857	1190.5800	595.7937	11
3	**334.1397**	167.5735			316.1292	158.5682	E	**1061.5222**	531.2647	1044.4956	522.7515	1043.5116	522.2594	10
4	435.1874	218.0974			417.1769	209.0921	T	**932.4796**	466.7434	915.4530	458.2302	914.4690	457.7381	9

5	532.2402	266.6237			514.2296	257.6185	P	**831.4319**	**416.2196**	814.4054	407.7063	813.4213	407.2143	8
6	603.2773	302.1423			585.2667	293.1370	A	**734.3791**	367.6932	717.3526	359.1799	716.3686	358.6879	7
7	690.3093	345.6583			672.2988	336.6530	S	**663.3420**	332.1747	646.3155	323.6614	645.3315	323.1694	6
8	777.3414	389.1743			759.3308	380.1690	S	**576.3100**	288.6586	559.2835	280.1454	558.2994	279.6534	5
9	933.4425	467.2249	916.4159	458.7116	915.4319	458.2196	R	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	4
10	1046.5265	523.7669	1029.5000	515.2536	1028.5160	514.7616	I	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
11	1160.5695	580.7884	1143.5429	572.2751	1142.5589	571.7831	N	220.0928	110.5500	203.0662	102.0368	202.0822	101.5448	2
12							S	106.0499	53.5286			88.0393	44.5233	1





MS/MS Fragmentation of **GFRVLPQLNDDD**
Found in **XP_001176287**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
Match to Query 154: 1387.407848 from(694.711200,2+) intensity(1157.2195)
Data file Maldi_All.mgf

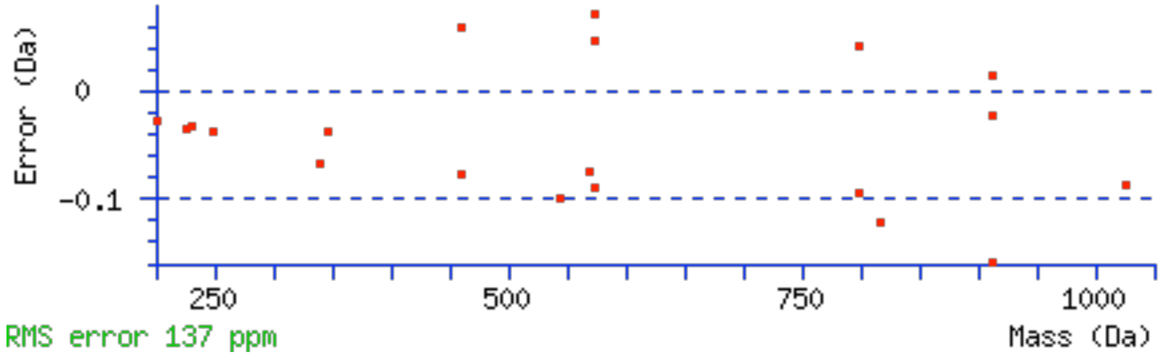


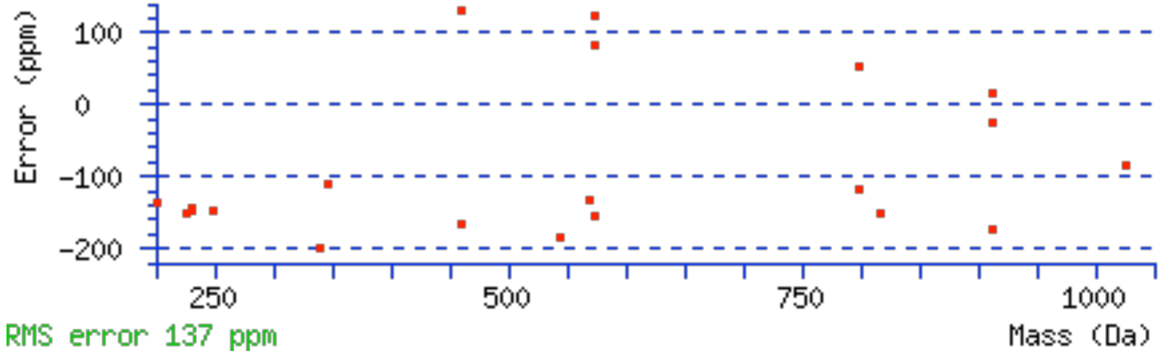
Monoisotopic mass of neutral peptide Mr(calc): 1387.6732 **Ions Score:** 40 **Expect:** 1.9 **Matches (Bold Red):** 23/165 fragment ions using 20 most intense peaks

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	30.0338	30.0338			58.0287				**G**						**12**
2	120.0808	177.1022			205.0972				**F**	1239.5964		1331.6590	1314.6325	1313.6484	**11**
3	129.1135	333.2034	316.1768		361.1983	344.1717		248.1394	**R**	1083.4953	1082.5000	1184.5906	1167.5640	1166.5800	**10**
4	72.0808	432.2718	415.2452		**460.2667**	443.2401		418.2561	**V**			1028.4895	1011.4629	1010.4789	**9**

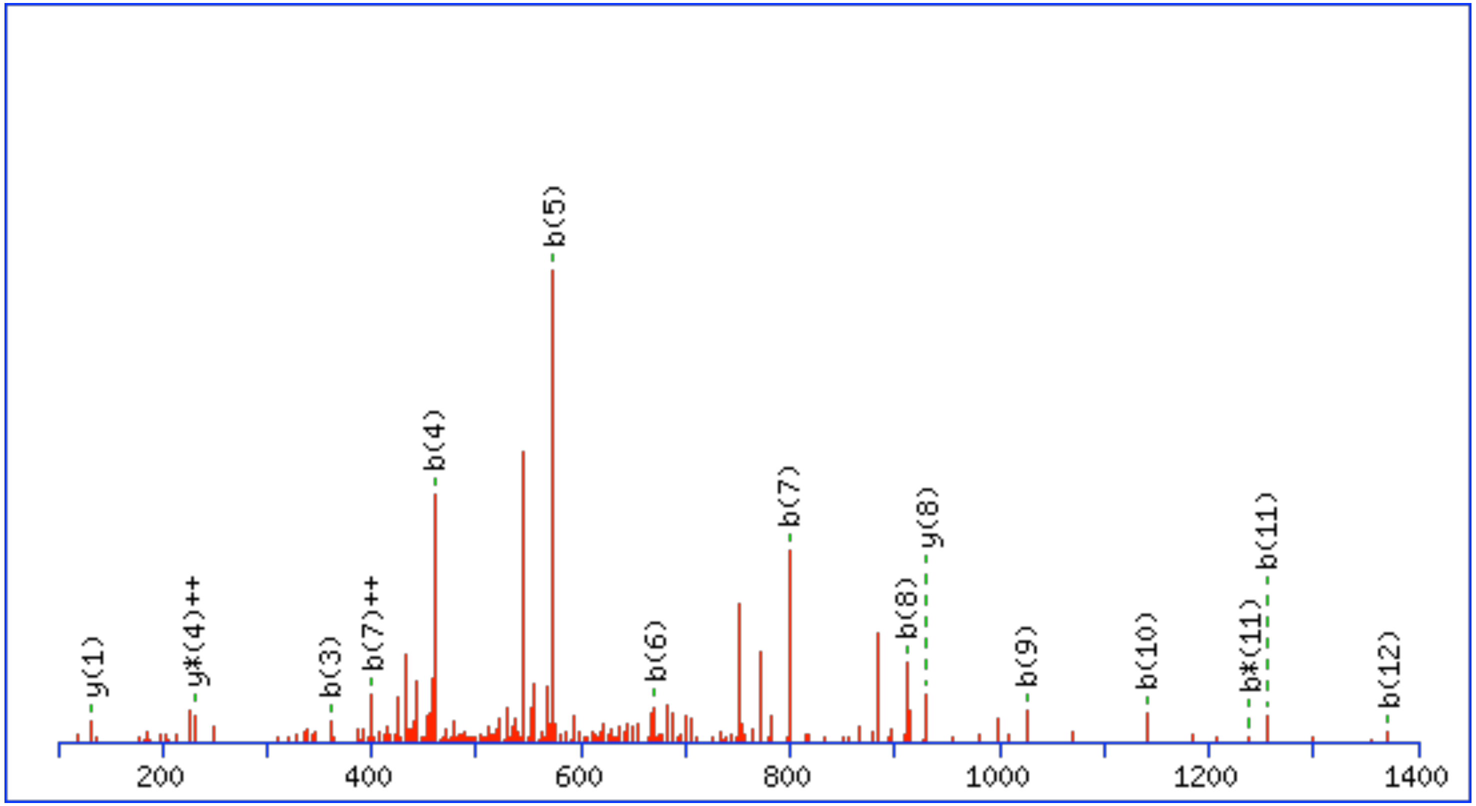
5	86.0964	**545.3558**	528.3293		**573.3507**	556.3242		503.3089	**L**			929.4211	**912.3945**	**911.4105**	**8**
6	70.0651	642.4086	625.3820		670.4035	653.3770		616.3929	**P**			**816.3370**	799.3105	**798.3264**	**7**
7	101.0709	770.4672	753.4406		**798.4621**	781.4355		713.4457	**Q**			719.2842	702.2577	701.2737	**6**
8	86.0964	883.5512	866.5247		**911.5461**	894.5196		841.5043	**L**			591.2257	**574.1991**	**573.2151**	**5**
9	87.0553	997.5942	980.5676		**1025.5891**	1008.5625		954.5883	**N**			478.1416	461.1150	**460.1310**	**4**
10	88.0393	1112.6211	1095.5946	1094.6105	1140.6160	1123.5895	1122.6055	1068.6313	**D**			364.0987		**346.0881**	**3**
11	88.0393	1227.6480	1210.6215	1209.6375	1255.6430	1238.6164	1237.6324	1183.6582	**D**			**249.0717**		**231.0612**	**2**
12	88.0393								**D**			134.0448		116.0342	**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FR	276.1819	304.1768	**FRV**	375.2503	403.2452	**FRVL**	488.3344	516.3293
FRVLP	585.3871	613.3820	**RV**	228.1819	256.1768	**RVL**	341.2660	369.2609
RVLP	438.3187	466.3136	**RVLPQ**	566.3773	594.3722	**RVLPQL**	679.4614	707.4563
VL	185.1648	213.1598	**VLP**	282.2176	310.2125	**VLPQ**	410.2762	438.2711
VLPQL	523.3602	551.3552	**VLPQLN**	637.4032	665.3981	**LP**	183.1492	211.1441
LPQ	311.2078	**339.2027**	**LPQL**	424.2918	452.2867	**LPQLN**	538.3348	566.3297
LPQLND	653.3617	681.3566	**PQ**	198.1237	**226.1186**	**PQL**	311.2078	**339.2027**
PQLN	425.2507	453.2456	**PQLND**	540.2776	**568.2726**	**PQLNDD**	655.3046	683.2995
QL	214.1550	242.1499	**QLN**	328.1979	356.1928	**QLND**	443.2249	471.2198
QLNDD	558.2518	586.2467	**LN**	200.1394	228.1343	**LND**	315.1663	343.1612
LNDD	430.1932	458.1882	**ND**	**202.0822**	**230.0771**	**NDD**	317.1092	345.1041
DD	203.0662	**231.0612**						





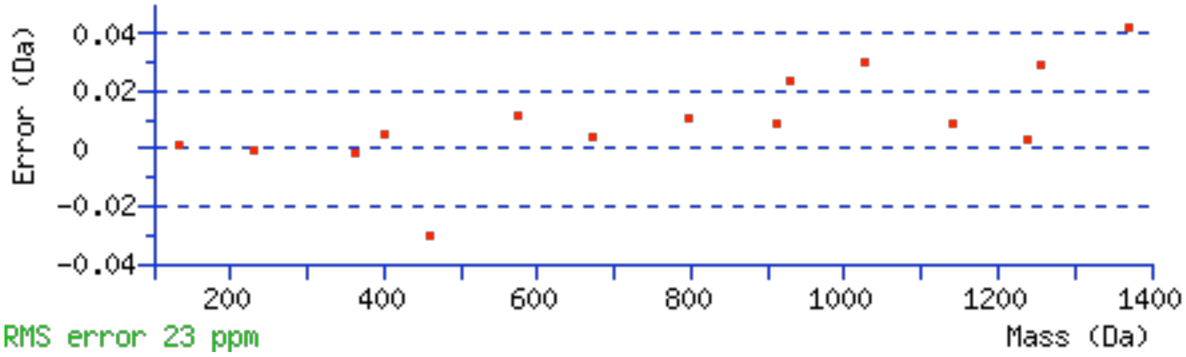
MS/MS Fragmentation of **GFRVLPQLNDDDN**
Found in **XP_001176287**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
Match to Query 631: 1501.741188 from(751.877870,2+) intensity(810152.0000)
Title: Cmpd 169, +MSn(752.2778), 29.6 min
Data file Qtof_all.mgf

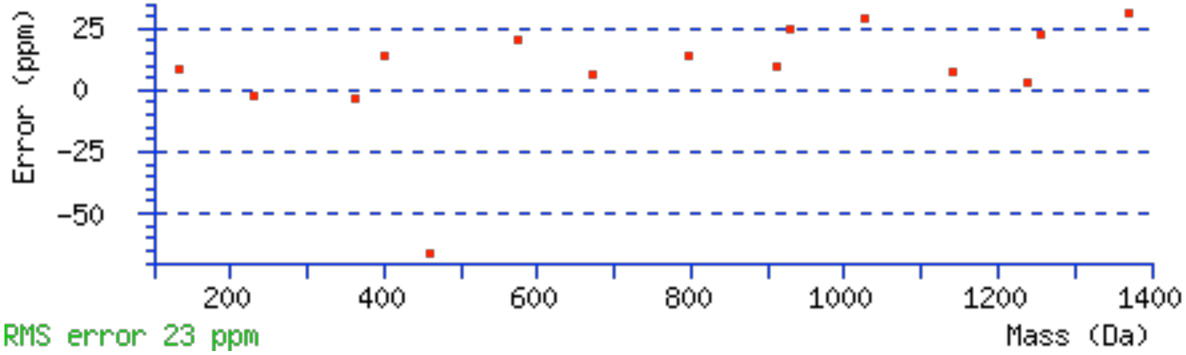


Monoisotopic mass of neutral peptide Mr(calc): 1501.7161 **Ions Score:** 73 **Expect:** 0.00065 **Matches (Bold Red):** 16/120 fragment ions using 26 most intense peaks

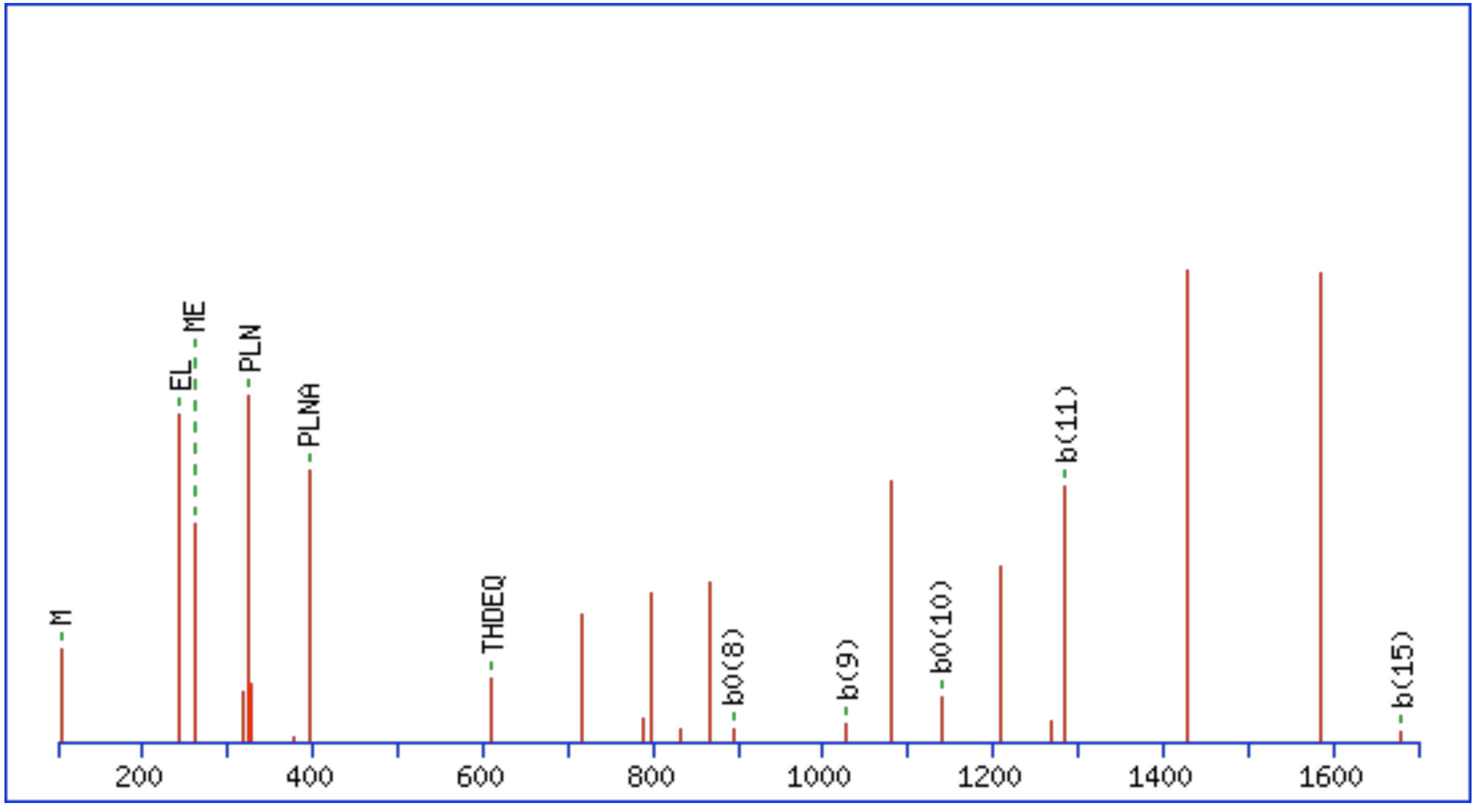
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					**G**							**13**
2	205.0972	103.0522					**F**	1445.7019	723.3546	1428.6754	714.8413	1427.6914	714.3493	**12**
3	**361.1983**	181.1028	344.1717	172.5895			**R**	1298.6335	649.8204	1281.6070	641.3071	1280.6230	640.8151	**11**
4	**460.2667**	230.6370	443.2401	222.1237			**V**	1142.5324	571.7698	1125.5059	563.2566	1124.5218	562.7646	**10**

5	**573.3507**	287.1790	556.3242	278.6657			**L**	1043.4640	522.2356	1026.4374	513.7224	1025.4534	513.2304	**9**
6	**670.4035**	335.7054	653.3770	327.1921			**P**	**930.3799**	465.6936	913.3534	457.1803	912.3694	456.6883	**8**
7	**798.4621**	**399.7347**	781.4355	391.2214			**Q**	833.3272	417.1672	816.3006	408.6539	815.3166	408.1619	**7**
8	**911.5461**	456.2767	894.5196	447.7634			**L**	705.2686	353.1379	688.2420	344.6247	687.2580	344.1326	**6**
9	**1025.5891**	513.2982	1008.5625	504.7849			**N**	592.1845	296.5959	575.1580	288.0826	574.1740	287.5906	**5**
10	**1140.6160**	570.8116	1123.5895	562.2984	1122.6055	561.8064	**D**	478.1416	239.5744	461.1150	**231.0612**	460.1310	230.5692	**4**
11	**1255.6430**	628.3251	**1238.6164**	619.8118	1237.6324	619.3198	**D**	363.1147	182.0610	346.0881	173.5477	345.1041	173.0557	**3**
12	**1370.6699**	685.8386	1353.6434	677.3253	1352.6593	676.8333	**D**	248.0877	124.5475	**231.0612**	116.0342	230.0771	115.5422	**2**
13							**N**	**133.0608**	67.0340	116.0342	58.5207			**1**





MS/MS Fragmentation of **EDGMELTHDEQPLNAMEI**
Found in **XP_001176287**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
Match to Query 355: 2070.465648 from(1036.240100,2+) intensity(7861.3037)
Data file Maldi_All.mgf



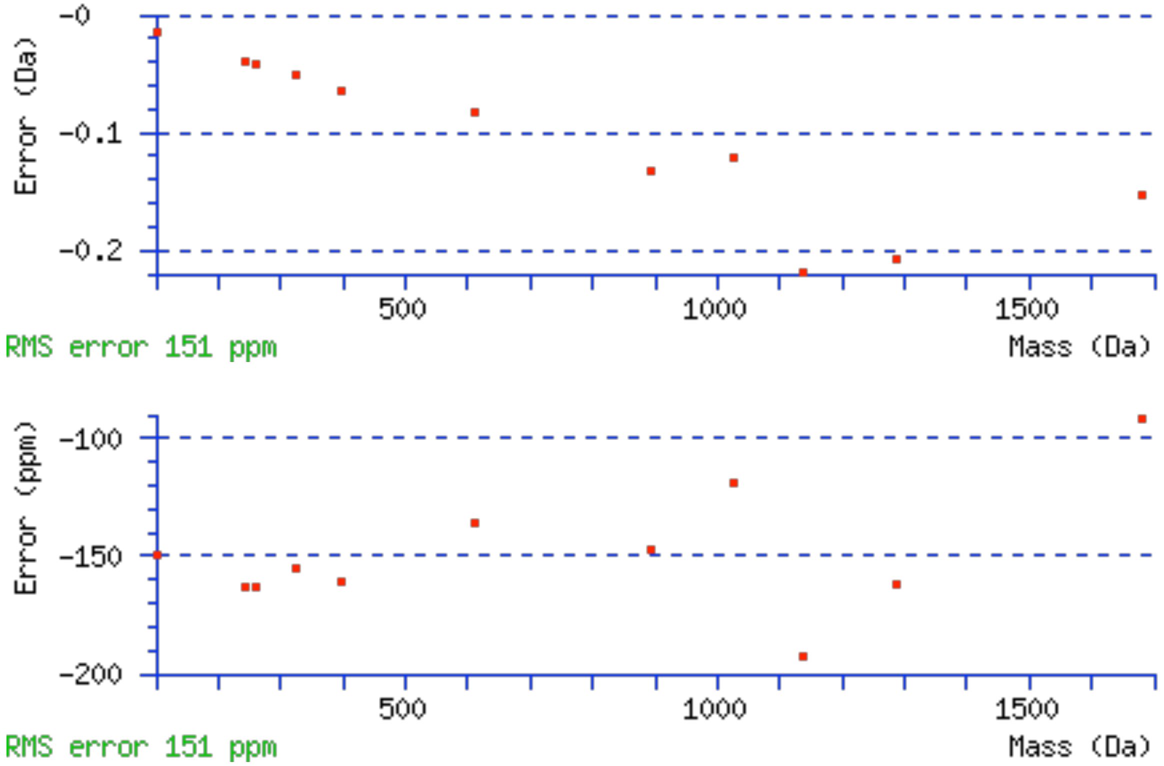
Monoisotopic mass of neutral peptide Mr(calc): 2069.9034 **Variable modifications: C-term :** Amidated (C-term) **Ions Score:** 11 **Expect:** 2.2e+03 **Matches (Bold Red):** 13/271 fragment ions using 18 most intense peaks

#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	y	y*	y^0	#
1	102.0550	102.0550		84.0444	130.0499		112.0393	**E**				**18**
2	88.0393	217.0819		199.0713	245.0768		227.0662	**D**	1941.8681	1924.8415	1923.8575	**17**
3	30.0338	274.1034		256.0928	302.0983		284.0877	**G**	1826.8411	1809.8146	1808.8306	**16**
4	**104.0528**	405.1438		387.1333	433.1388		415.1282	**M**	1769.8197	1752.7931	1751.8091	**15**

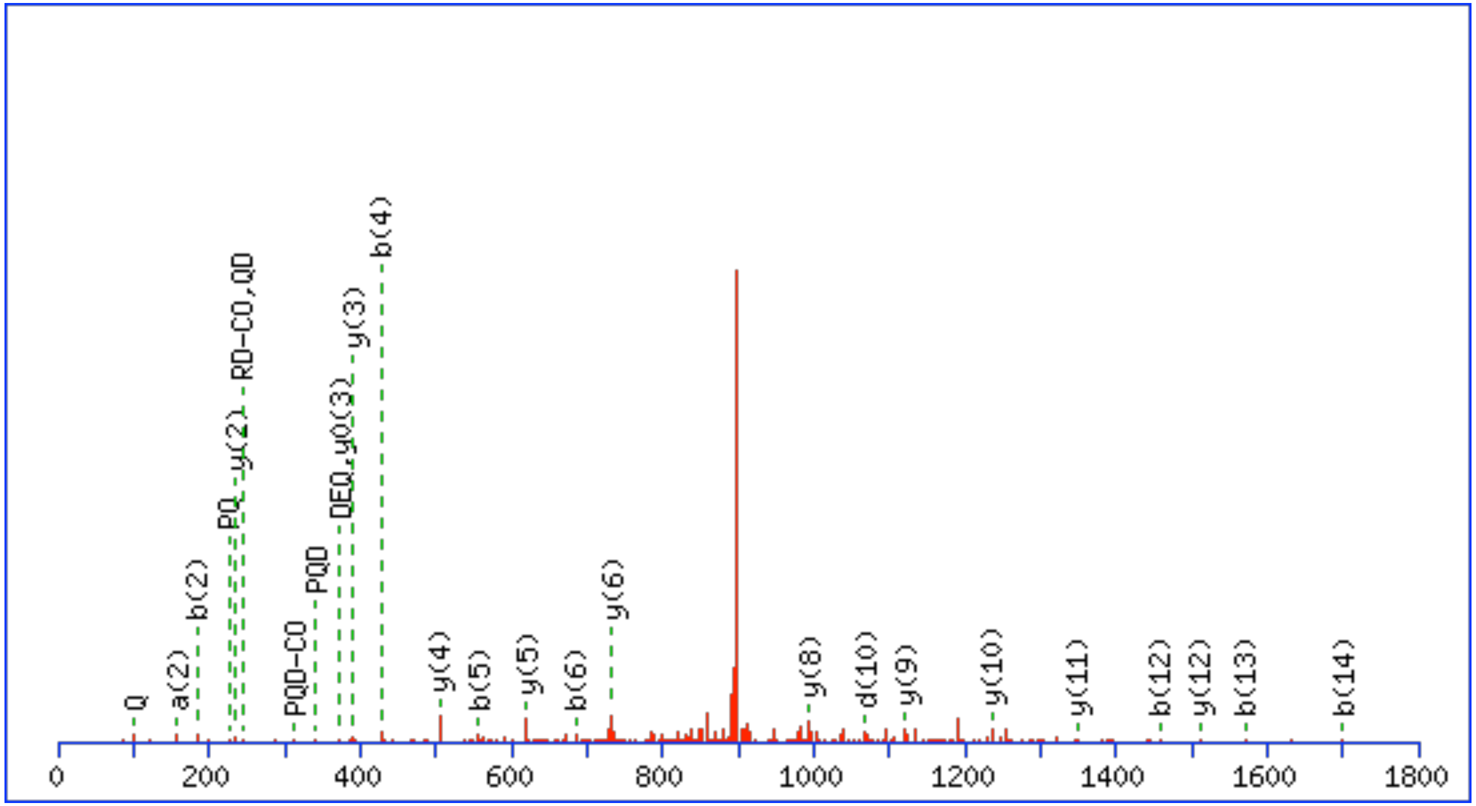
5	102.0550	534.1864		516.1759	562.1814		544.1708	**E**	1638.7792	1621.7526	1620.7686	**14**
6	86.0964	647.2705		629.2599	675.2654		657.2549	**L**	1509.7366	1492.7100	1491.7260	**13**
7	74.0600	748.3182		730.3076	776.3131		758.3025	**T**	1396.6525	1379.6260	1378.6420	**12**
8	110.0713	885.3771		867.3665	913.3720		**895.3614**	**H**	1295.6049	1278.5783	1277.5943	**11**
9	88.0393	1000.4040		982.3935	**1028.3990**		1010.3884	**D**	1158.5459	1141.5194	1140.5354	**10**
10	102.0550	1129.4466		1111.4361	1157.4415		**1139.4310**	**E**	1043.5190	1026.4925	1025.5084	**9**
11	101.0709	1257.5052	1240.4787	1239.4946	**1285.5001**	1268.4736	1267.4896	**Q**	914.4764	897.4499	896.4658	**8**
12	70.0651	1354.5580	1337.5314	1336.5474	1382.5529	1365.5263	1364.5423	**P**	786.4178	769.3913	768.4073	**7**
13	86.0964	1467.6420	1450.6155	1449.6315	1495.6370	1478.6104	1477.6264	**L**	689.3651	672.3385	671.3545	**6**
14	87.0553	1581.6850	1564.6584	1563.6744	1609.6799	1592.6533	1591.6693	**N**	576.2810	559.2545	558.2704	**5**
15	44.0495	1652.7221	1635.6955	1634.7115	**1680.7170**	1663.6904	1662.7064	**A**	462.2381		444.2275	**4**
16	**104.0528**	1783.7626	1766.7360	1765.7520	1811.7575	1794.7309	1793.7469	**M**	391.2010		373.1904	**3**
17	102.0550	1912.8052	1895.7786	1894.7946	1940.8001	1923.7735	1922.7895	**E**	260.1605		242.1499	**2**
18	86.0964							**I**	131.1179			**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
DG	145.0608	173.0557	**DGM**	276.1013	304.0962	**DGME**	405.1438	433.1388
DGMEL	518.2279	546.2228	**DGMELT**	619.2756	647.2705	**GM**	161.0743	189.0692
GME	290.1169	318.1118	**GMEL**	403.2010	431.1959	**GMELT**	504.2486	532.2436
GMELTH	641.3076	669.3025	**ME**	233.0954	**261.0904**	**MEL**	346.1795	374.1744
MELT	447.2272	475.2221	**MELTH**	584.2861	612.2810	**MELTHD**	699.3130	727.3080
EL	215.1390	**243.1339**	**ELT**	316.1867	344.1816	**ELTH**	453.2456	481.2405
ELTHD	568.2726	596.2675	**ELTHDE**	697.3151	725.3101	**LT**	187.1441	215.1390
LTH	324.2030	352.1979	**LTHD**	439.2300	467.2249	**LTHDE**	568.2726	596.2675
LTHDEQ	696.3311	724.3260	**TH**	211.1190	239.1139	**THD**	326.1459	354.1408

THDE	455.1885	483.1834	**THDEQ**	583.2471	**611.2420**	**THDEQP**	680.2998	708.2947
HD	225.0982	253.0931	**HDE**	354.1408	382.1357	**HDEQ**	482.1994	510.1943
HDEQP	579.2522	607.2471	**HDEQPL**	692.3362	720.3311	**DE**	217.0819	245.0768
DEQ	345.1405	373.1354	**DEQP**	442.1932	470.1882	**DEQPL**	555.2773	583.2722
DEQPLN	669.3202	697.3151	**EQ**	230.1135	258.1084	**EQP**	327.1663	355.1612
EQPL	440.2504	468.2453	**EQPLN**	554.2933	582.2882	**EQPLNA**	625.3304	653.3253
QP	198.1237	226.1186	**QPL**	311.2078	339.2027	**QPLN**	425.2507	453.2456
QPLNA	496.2878	524.2827	**QPLNAM**	627.3283	655.3232	**PL**	183.1492	211.1441
PLN	297.1921	**325.1870**	**PLNA**	368.2292	**396.2241**	**PLNAM**	499.2697	527.2646
PLNAME	628.3123	656.3072	**LN**	200.1394	228.1343	**LNA**	271.1765	299.1714
LNAM	402.2170	430.2119	**LNAME**	531.2595	559.2545	**NA**	158.0924	186.0873
NAM	289.1329	317.1278	**NAME**	418.1755	446.1704	**AM**	175.0900	203.0849
AME	304.1326	332.1275	**ME**	233.0954	**261.0904**			



MS/MS Fragmentation of **SPQDEQIDLRYLLQNFLDNRDT**
Found in **XP_001176287**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
Match to Query 470: 2692.793772 from(898.605200,3+) intensity(21701.3164)
Data file Maldi_All.mgf



Monoisotopic mass of neutral peptide Mr(calc): 2692.3092 **Ions Score:** 48 **Expect:** 0.42 **Matches (Bold Red):** 31/394 fragment ions using 69 most intense peaks

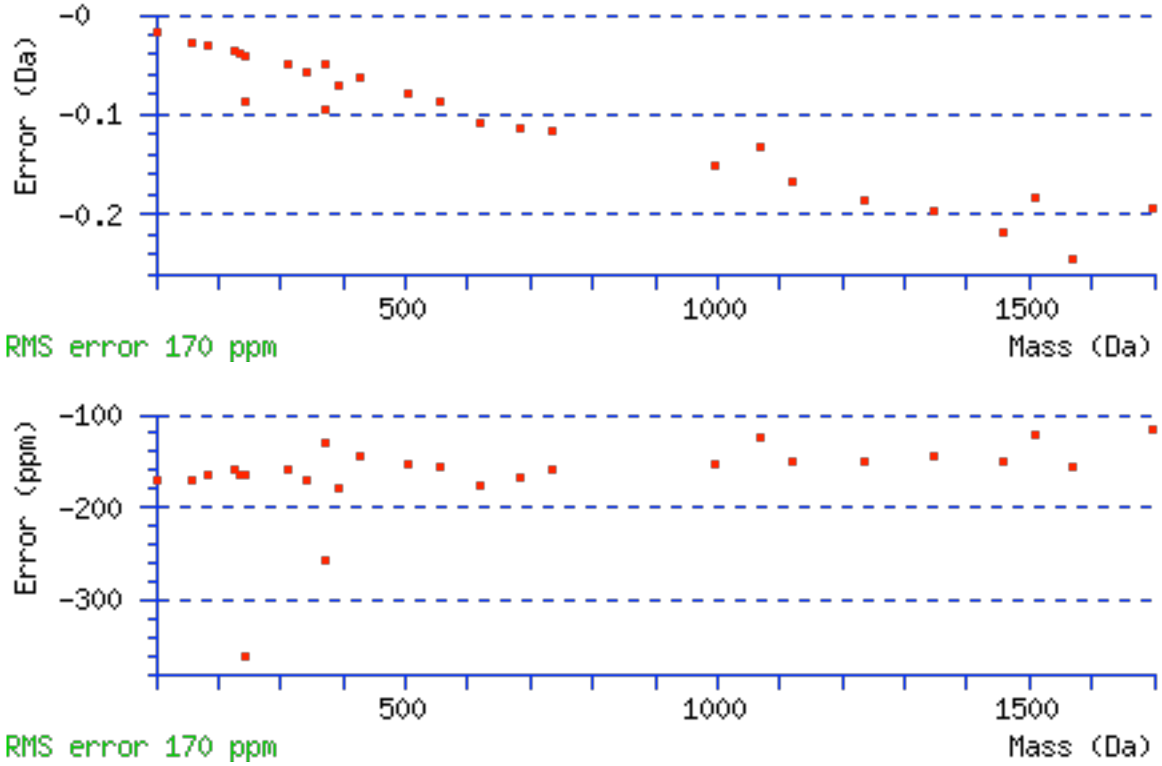
#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	w'	y	y*	y^0	#
1	60.0444	60.0444		42.0338	88.0393		70.0287		S							22
2	70.0651	**157.0972**		139.0866	**185.0921**		167.0815		P	2564.2376	2563.2423		2606.2845	2589.2580	2588.2740	21

3	**101.0709**	285.1557	268.1292	267.1452	**313.1506**	296.1241	295.1401		**Q**	2436.1790	2435.1837		2509.2318	2492.2052	2491.2212	**20**
4	88.0393	400.1827	383.1561	382.1721	**428.1776**	411.1510	410.1670		**D**	2321.1521	2320.1568		2381.1732	2364.1466	2363.1626	**19**
5	102.0550	529.2253	512.1987	511.2147	**557.2202**	540.1936	539.2096		**E**	2192.1095	2191.1142		2266.1462	2249.1197	2248.1357	**18**
6	**101.0709**	657.2838	640.2573	639.2733	**685.2788**	668.2522	667.2682		**Q**	2064.0509	2063.0556		2137.1036	2120.0771	2119.0931	**17**
7	86.0964	770.3679	753.3414	752.3573	798.3628	781.3363	780.3523		**I**	1950.9668	1963.9872	1978.0029	2009.0451	1992.0185	1991.0345	**16**
8	88.0393	885.3949	868.3683	867.3843	913.3898	896.3632	895.3792		**D**	1835.9399	1834.9446		1895.9610	1878.9345	1877.9504	**15**
9	86.0964	998.4789	981.4524	980.4684	1026.4738	1009.4473	1008.4633		**L**	1722.8558	1721.8606		1780.9341	1763.9075	1762.9235	**14**
10	129.1135	1154.5800	1137.5535	1136.5695	1182.5749	1165.5484	1164.5644	**1069.5160**	**R**	1566.7547	1565.7594		1667.8500	1650.8234	1649.8394	**13**
11	136.0757	1317.6434	1300.6168	1299.6328	1345.6383	1328.6117	1327.6277		**Y**	1403.6914			**1511.7489**	1494.7223	1493.7383	**12**
12	86.0964	1430.7274	1413.7009	1412.7169	**1458.7223**	1441.6958	1440.7118	1388.6805	**L**	1290.6073	1289.6121		**1348.6856**	1331.6590	1330.6750	**11**
13	86.0964	1543.8115	1526.7849	1525.8009	**1571.8064**	1554.7798	1553.7958	1501.7645	**L**	1177.5232	1176.5280		**1235.6015**	1218.5749	1217.5909	**10**
14	**101.0709**	1671.8701	1654.8435	1653.8595	**1699.8650**	1682.8384	1681.8544	1614.8486	**Q**	1049.4647	1048.4694		**1122.5174**	1105.4909	1104.5069	**9**
15	87.0553	1785.9130	1768.8864	1767.9024	1813.9079	1796.8814	1795.8973	1742.9072	**N**	935.4217	934.4265		**994.4588**	977.4323	976.4483	**8**
16	120.0808	1932.9814	1915.9549	1914.9708	1960.9763	1943.9498	1942.9658		**F**	788.3533			880.4159	863.3894	862.4054	**7**

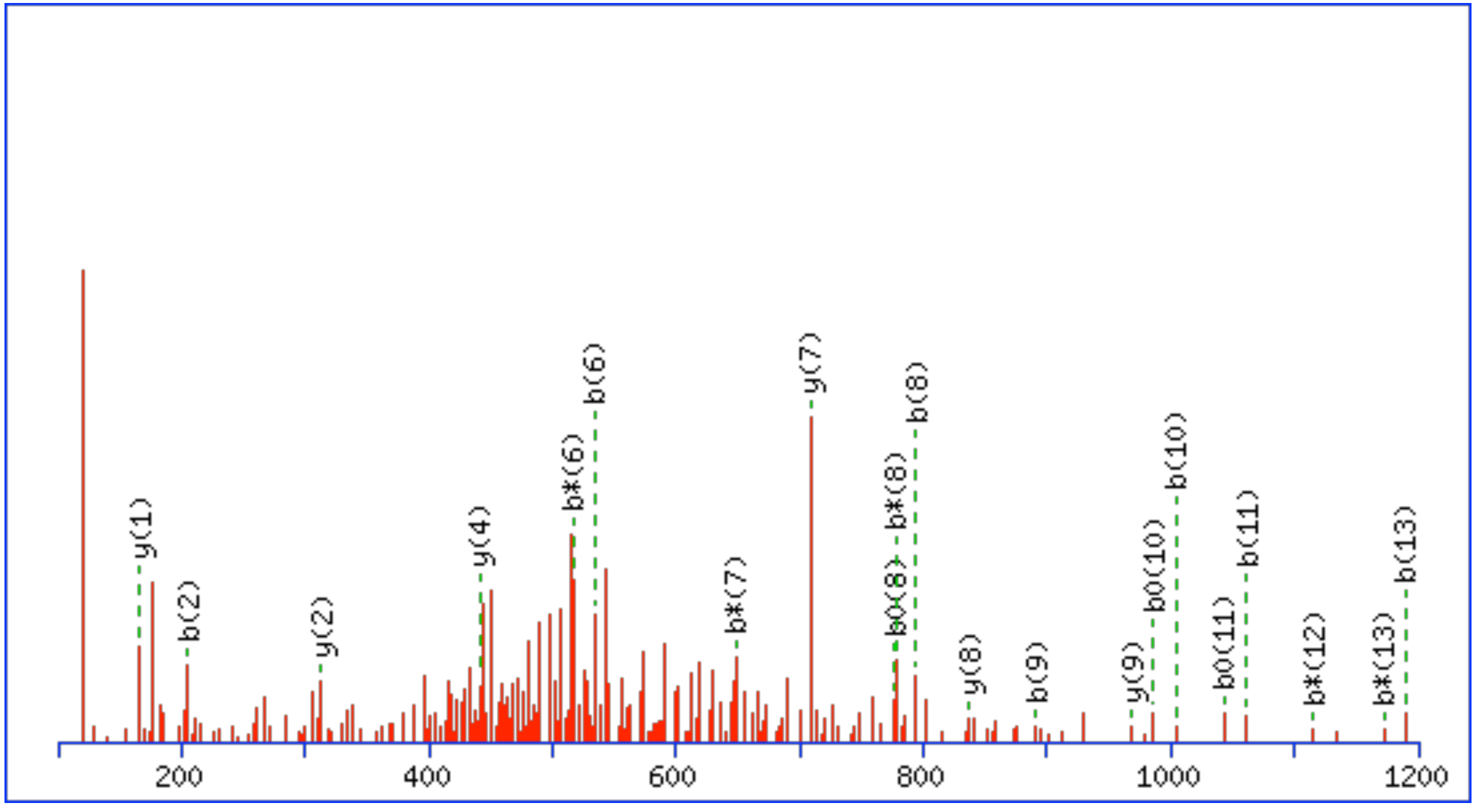
17	86.0964	2046.0655	2029.0389	2028.0549	2074.0604	2057.0338	2056.0498	2004.0185	**L**	675.2693	674.2740		**733.3475**	716.3210	715.3369	**6**
18	88.0393	2161.0924	2144.0659	2143.0818	2189.0873	2172.0608	2171.0768	2117.1026	**D**	560.2423	559.2471		**620.2634**	603.2369	602.2529	**5**
19	87.0553	2275.1353	2258.1088	2257.1248	2303.1303	2286.1037	2285.1197	2232.1295	**N**	446.1994	445.2041		**505.2365**	488.2100	487.2259	**4**
20	129.1135	2431.2364	2414.2099	2413.2259	2459.2314	2442.2048	2441.2208	2346.1725	**R**	290.0983	289.1030		**391.1936**	374.1670	**373.1830**	**3**
21	88.0393	2546.2634	2529.2368	2528.2528	2574.2583	2557.2318	2556.2477	2502.2736	**D**				**235.0925**		217.0819	**2**
22	74.0600								**T**				120.0655		102.0550	**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PQ	198.1237	**226.1186**	**PQD**	**313.1506**	**341.1456**	**PQDE**	442.1932	470.1882
PQDEQ	570.2518	598.2467	**PQDEQI**	683.3359	711.3308	**QD**	216.0979	**244.0928**
QDE	345.1405	**373.1354**	**QDEQ**	473.1991	501.1940	**QDEQI**	586.2831	614.2780
DE	217.0819	245.0768	**DEQ**	345.1405	**373.1354**	**DEQI**	458.2245	486.2195
DEQID	573.2515	601.2464	**DEQIDL**	686.3355	714.3305	**EQ**	230.1135	258.1084
EQI	343.1976	371.1925	**EQID**	458.2245	486.2195	**EQIDL**	571.3086	599.3035
QI	214.1550	242.1499	**QID**	329.1819	357.1769	**QIDL**	442.2660	470.2609
QIDLR	598.3671	626.3620	**ID**	201.1234	229.1183	**IDL**	314.2074	342.2023
IDLR	470.3085	498.3035	**IDLRY**	633.3719	661.3668	**DL**	201.1234	229.1183
DLR	357.2245	385.2194	**DLRY**	520.2878	548.2827	**DLRYL**	633.3719	661.3668
LR	242.1975	270.1925	**LRY**	405.2609	433.2558	**LRYL**	518.3449	546.3398
LRYLL	631.4290	659.4239	**RY**	292.1768	320.1717	**RYL**	405.2609	433.2558
RYLL	518.3449	546.3398	**RYLLQ**	646.4035	674.3984	**YL**	249.1598	277.1547

YLL	362.2438	390.2387	**YLLQ**	490.3024	518.2973	**YLLQN**	604.3453	632.3402
LL	199.1805	227.1754	**LLQ**	327.2391	355.2340	**LLQN**	441.2820	469.2769
LLQNF	588.3504	616.3453	**LQ**	214.1550	242.1499	**LQN**	328.1979	356.1928
LQNF	475.2663	503.2613	**LQNFL**	588.3504	616.3453	**QN**	215.1139	243.1088
QNF	362.1823	390.1772	**QNFL**	475.2663	503.2613	**QNFLD**	590.2933	618.2882
NF	234.1237	262.1186	**NFL**	347.2078	375.2027	**NFLD**	462.2347	490.2296
NFLDN	576.2776	604.2726	**FL**	233.1648	261.1598	**FLD**	348.1918	376.1867
FLDN	462.2347	490.2296	**FLDNR**	618.3358	646.3307	**LD**	201.1234	229.1183
LDN	315.1663	343.1612	**LDNR**	471.2674	499.2623	**LDNRD**	586.2943	614.2893
DN	202.0822	230.0771	**DNR**	358.1833	386.1783	**DNRD**	473.2103	501.2052
NR	243.1564	271.1513	**NRD**	358.1833	386.1783	**RD**	**244.1404**	272.1353



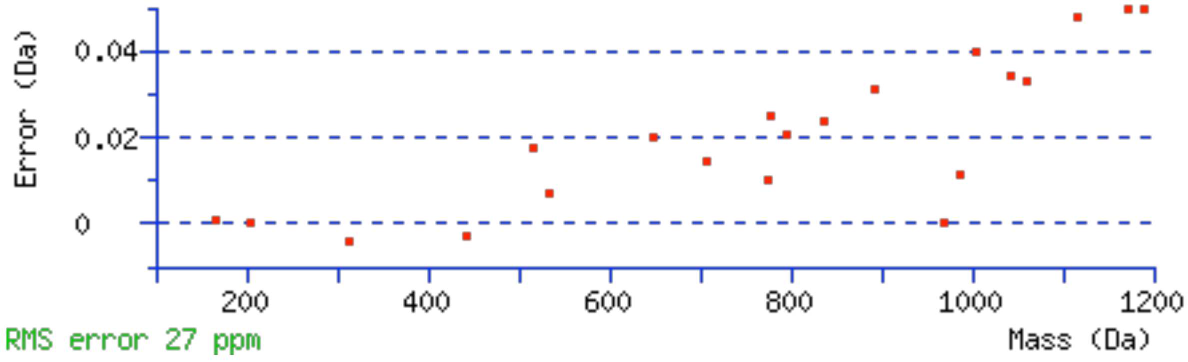
MS/MS Fragmentation of **GFNSGAMEPLGAGFF**
Found in **XP_785647**, PREDICTED: similar to pedal peptide precursor protein [Strongylocentrotus purpuratus].
Match to Query 628: 1500.706768 from(751.360660,2+) intensity(701012.0000)
Title: Cmpd 248, +MSn(751.6144), 36.7 min
Data file Qtof_all.mgf

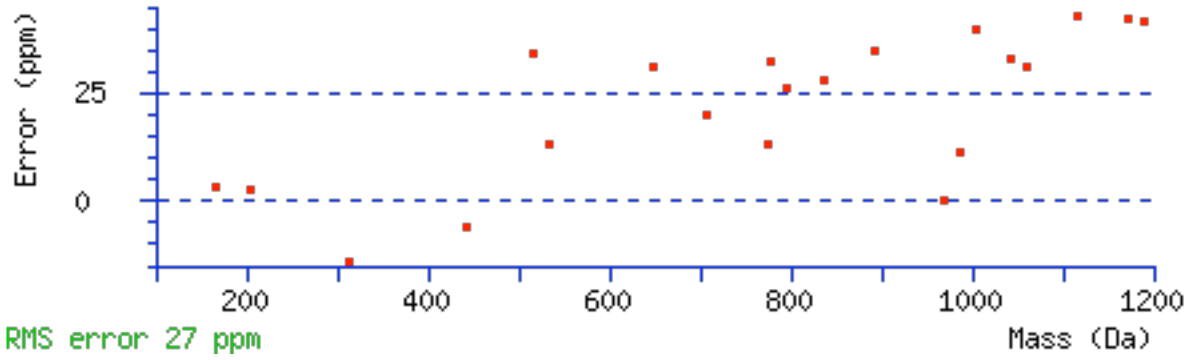


Monoisotopic mass of neutral peptide Mr(calc): 1500.6708 **Ions Score:** 30 **Expect:** 12 **Matches (Bold Red):** 21/120 fragment ions using 47 most intense peaks

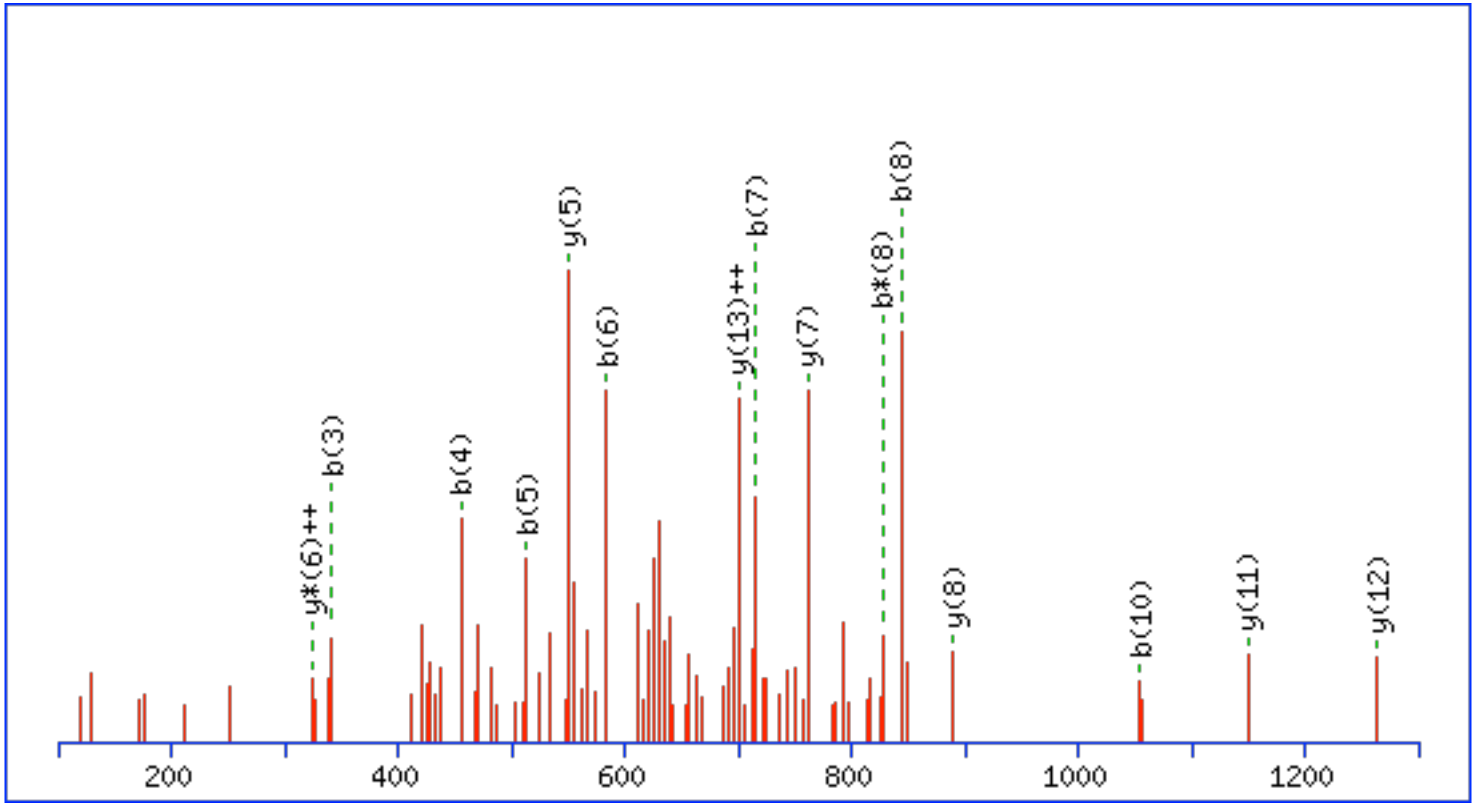
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							15
2	**205.0972**	103.0522					F	1444.6566	722.8319	1427.6300	714.3186	1426.6460	713.8266	14
3	319.1401	160.0737	302.1135	151.5604			N	1297.5882	649.2977	1280.5616	640.7844	1279.5776	640.2924	13
4	406.1721	203.5897	389.1456	195.0764	388.1615	194.5844	S	1183.5452	592.2762			1165.5347	583.2710	12

5	463.1936	232.1004	446.1670	223.5872	445.1830	223.0951	**G**	1096.5132	548.7602			1078.5026	539.7550	**11**
6	**534.2307**	267.6190	**517.2041**	259.1057	516.2201	258.6137	**A**	1039.4917	520.2495			1021.4812	511.2442	**10**
7	665.2712	333.1392	**648.2446**	324.6259	647.2606	324.1339	**M**	**968.4546**	484.7309			950.4441	475.7257	**9**
8	**794.3138**	397.6605	**777.2872**	389.1472	**776.3032**	388.6552	**E**	**837.4141**	419.2107			819.4036	410.2054	**8**
9	**891.3665**	446.1869	874.3400	437.6736	873.3560	437.1816	**P**	**708.3715**	354.6894					**7**
10	**1004.4506**	502.7289	987.4240	494.2157	**986.4400**	493.7237	**L**	611.3188	306.1630					**6**
11	**1061.4721**	531.2397	1044.4455	522.7264	**1043.4615**	522.2344	**G**	498.2347	249.6210					**5**
12	1132.5092	566.7582	**1115.4826**	558.2449	1114.4986	557.7529	**A**	**441.2132**	221.1103					**4**
13	**1189.5306**	595.2690	**1172.5041**	586.7557	1171.5201	586.2637	**G**	370.1761	185.5917					**3**
14	1336.5990	668.8032	1319.5725	660.2899	1318.5885	659.7979	**F**	**313.1547**	157.0810					**2**
15							**F**	**166.0863**	83.5468					**1**





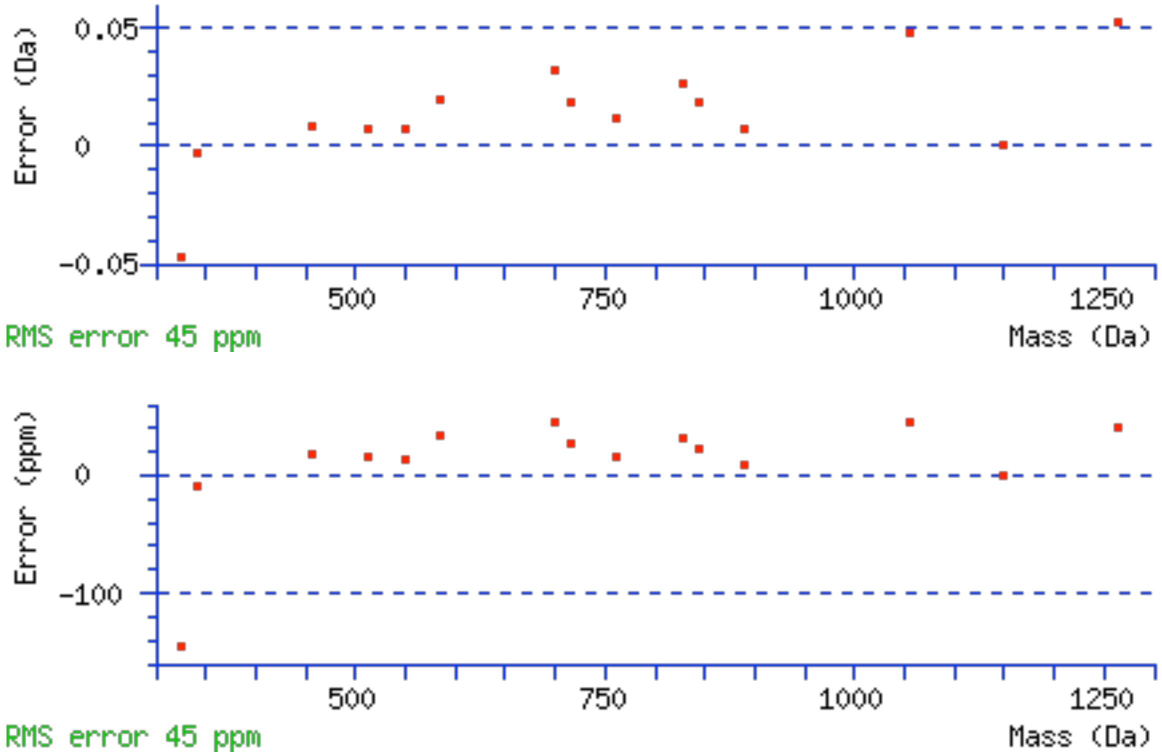
MS/MS Fragmentation of **GFHNGAMEPLKSGFL**
Found in **XP_785647**, PREDICTED: similar to pedal peptide precursor protein [Strongylocentrotus purpuratus].
Match to Query 682: 1603.811368 from(802.912960,2+) intensity(624924.0000)
Title: Cmpd 170, +MSn(803.4391), 29.6 min
Data file Qtof_all.mgf



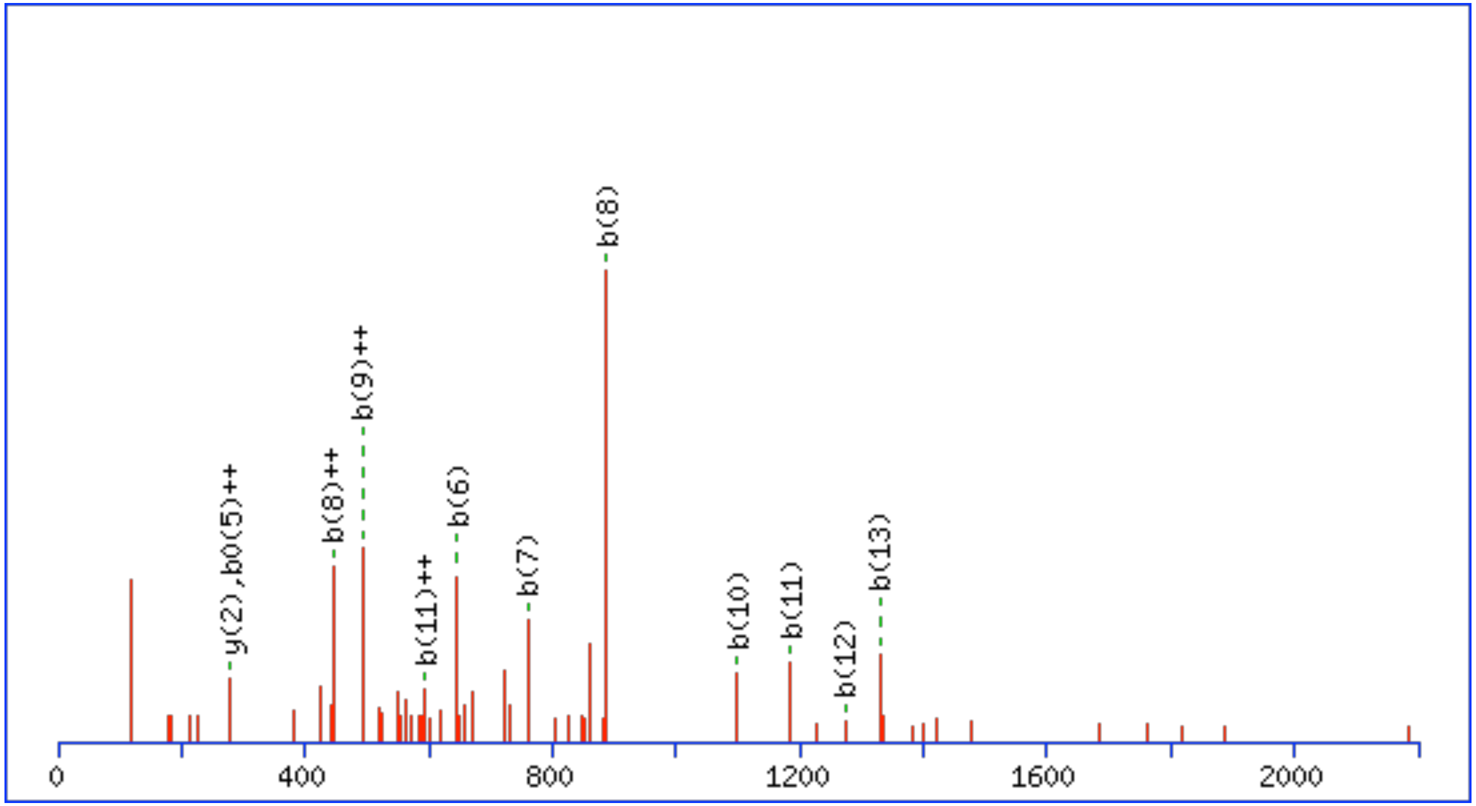
Monoisotopic mass of neutral peptide Mr(calc): 1603.7817 **Ions Score:** 51 **Expect:** 0.099 **Matches (Bold Red):** 15/134 fragment ions using 23 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	58.0287	29.5180					**G**							**15**
2	205.0972	103.0522					**F**	1547.7675	774.3874	1530.7410	765.8741	1529.7569	765.3821	**14**
3	**342.1561**	171.5817					**H**	1400.6991	**700.8532**	1383.6725	692.3399	1382.6885	691.8479	**13**
4	**456.1990**	228.6031	439.1724	220.0899			**N**	**1263.6402**	632.3237	1246.6136	623.8105	1245.6296	623.3184	**12**

5	**513.2205**	257.1139	496.1939	248.6006			**G**	**1149.5973**	575.3023	1132.5707	566.7890	1131.5867	566.2970	**11**
6	**584.2576**	292.6324	567.2310	284.1191			**A**	1092.5758	546.7915	1075.5492	538.2783	1074.5652	537.7863	**10**
7	**715.2981**	358.1527	698.2715	349.6394			**M**	1021.5387	511.2730	1004.5121	502.7597	1003.5281	502.2677	**9**
8	**844.3406**	422.6740	**827.3141**	414.1607	826.3301	413.6687	**E**	**890.4982**	445.7527	873.4716	437.2395	872.4876	436.7475	**8**
9	941.3934	471.2003	924.3669	462.6871	923.3828	462.1951	**P**	**761.4556**	381.2314	744.4291	372.7182	743.4450	372.2262	**7**
10	**1054.4775**	527.7424	1037.4509	519.2291	1036.4669	518.7371	**L**	664.4028	332.7051	647.3763	**324.1918**	646.3923	323.6998	**6**
11	1182.5724	591.7899	1165.5459	583.2766	1164.5619	582.7846	**K**	**551.3188**	276.1630	534.2922	267.6498	533.3082	267.1577	**5**
12	1269.6045	635.3059	1252.5779	626.7926	1251.5939	626.3006	**S**	423.2238	212.1155			405.2132	203.1103	**4**
13	1326.6259	663.8166	1309.5994	655.3033	1308.6154	654.8113	**G**	336.1918	168.5995					**3**
14	1473.6943	737.3508	1456.6678	728.8375	1455.6838	728.3455	**F**	279.1703	140.0888					**2**
15							**L**	132.1019	66.5546					**1**



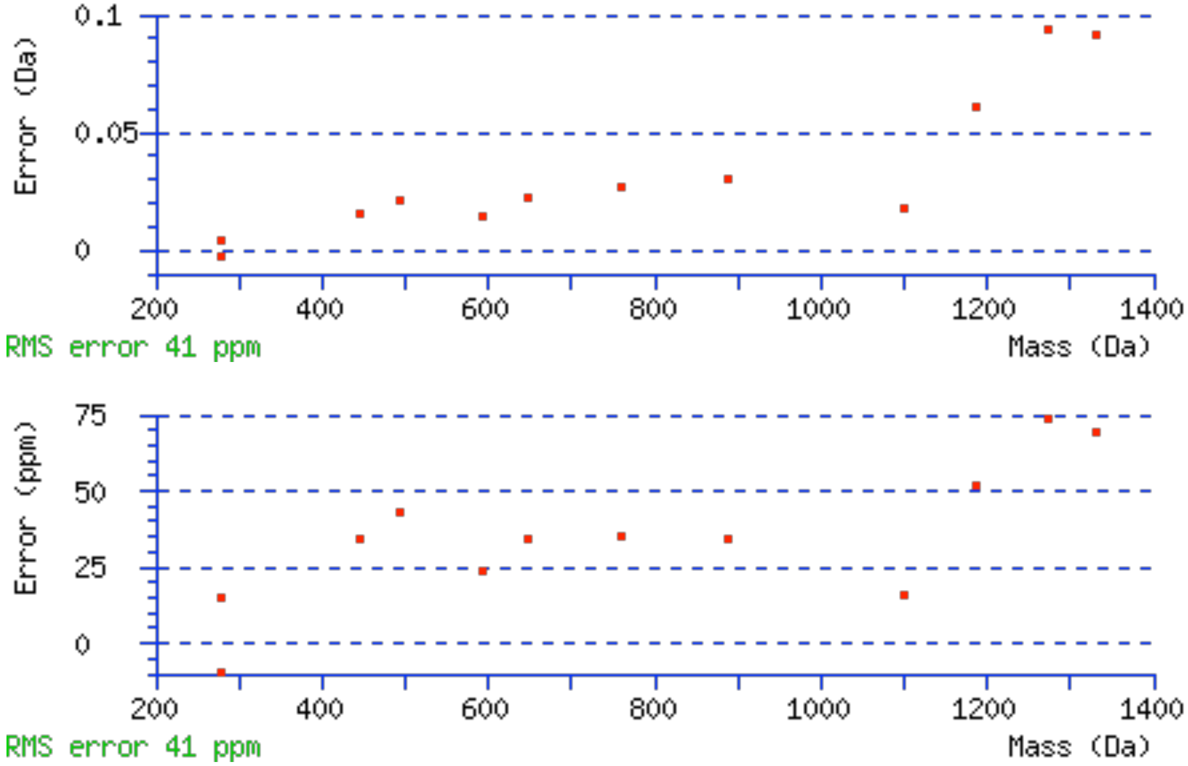
MS/MS Fragmentation of **RFLTGALEPLSSGFI**
Found in **XP_785647**, PREDICTED: similar to pedal peptide precursor protein [Strongylocentrotus purpuratus].
Match to Query 685: 1606.898788 from(804.456670,2+) intensity(121516.0000)
Title: Cmpd 225, +MSn(804.9464), 34.7 min
Data file Qtof_all.mgf



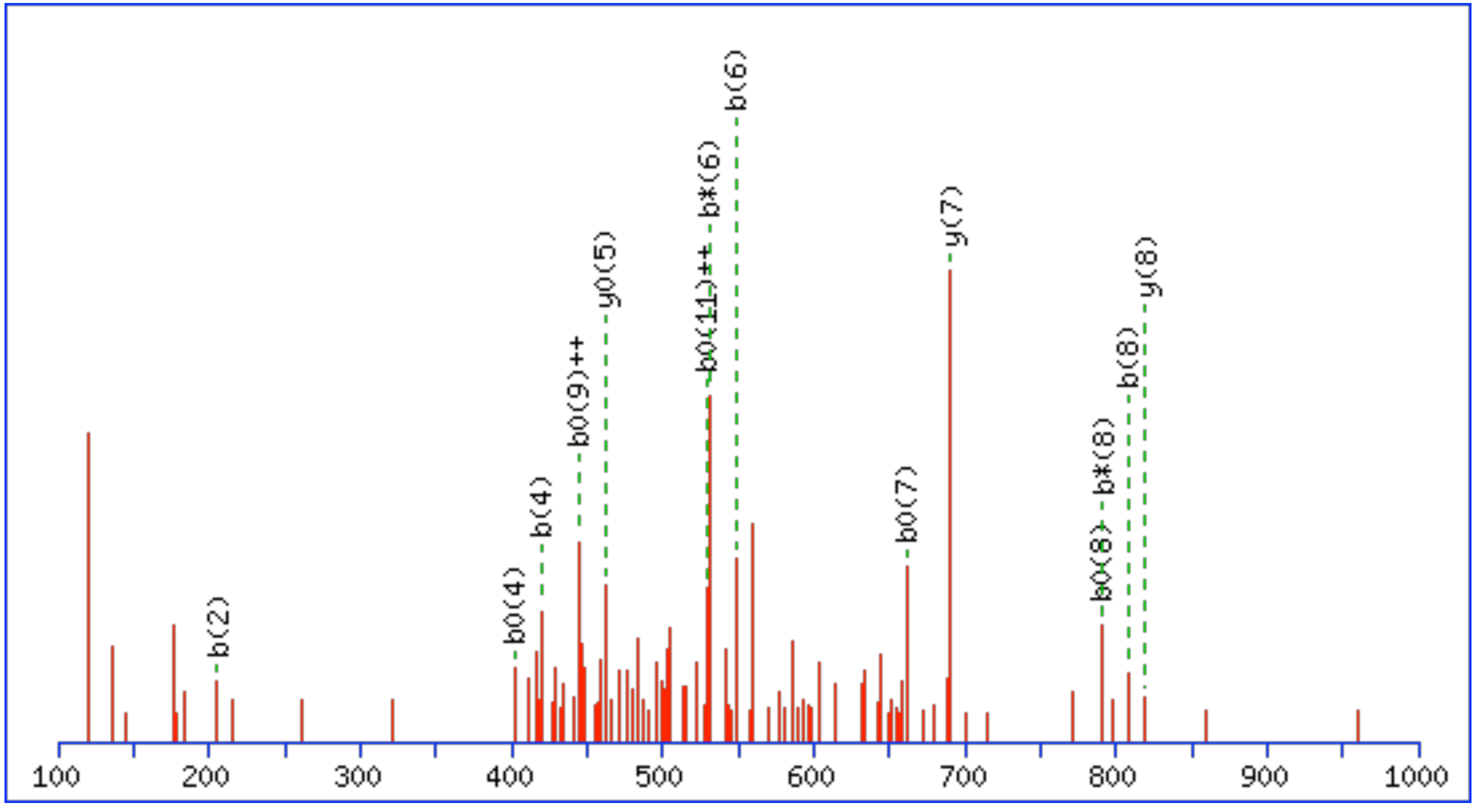
Monoisotopic mass of neutral peptide Mr(calc): 1606.8719 **Ions Score:** 56 **Expect:** 0.024 **Matches (Bold Red):** 12/128 fragment ions using 17 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	157.1084	79.0578	140.0818	70.5446			**R**					**15**
2	304.1768	152.5920	287.1503	144.0788			**F**	1451.7781	726.3927	1433.7675	717.3874	**14**
3	417.2609	209.1341	400.2343	200.6208			**L**	1304.7096	652.8585	1286.6991	643.8532	**13**
4	518.3085	259.6579	501.2820	251.1446	500.2980	250.6526	**T**	1191.6256	596.3164	1173.6150	587.3111	**12**

5	575.3300	288.1686	558.3035	279.6554	557.3194	**279.1634**	**G**	1090.5779	545.7926	1072.5673	536.7873	**11**
6	**646.3671**	323.6872	629.3406	315.1739	628.3566	314.6819	**A**	1033.5564	517.2819	1015.5459	508.2766	**10**
7	**759.4512**	380.2292	742.4246	371.7160	741.4406	371.2239	**L**	962.5193	481.7633	944.5088	472.7580	**9**
8	**888.4938**	**444.7505**	871.4672	436.2373	870.4832	435.7452	**E**	849.4353	425.2213	831.4247	416.2160	**8**
9	985.5465	**493.2769**	968.5200	484.7636	967.5360	484.2716	**P**	720.3927	360.7000	702.3821	351.6947	**7**
10	**1098.6306**	549.8189	1081.6041	541.3057	1080.6200	540.8137	**L**	623.3399	312.1736	605.3293	303.1683	**6**
11	**1185.6626**	**593.3350**	1168.6361	584.8217	1167.6521	584.3297	**S**	510.2558	255.6316	492.2453	246.6263	**5**
12	**1272.6947**	636.8510	1255.6681	628.3377	1254.6841	627.8457	**S**	423.2238	212.1155	405.2132	203.1103	**4**
13	**1329.7161**	665.3617	1312.6896	656.8484	1311.7056	656.3564	**G**	336.1918	168.5995			**3**
14	1476.7845	738.8959	1459.7580	730.3826	1458.7740	729.8906	**F**	**279.1703**	140.0888			**2**
15							**I**	132.1019	66.5546			**1**



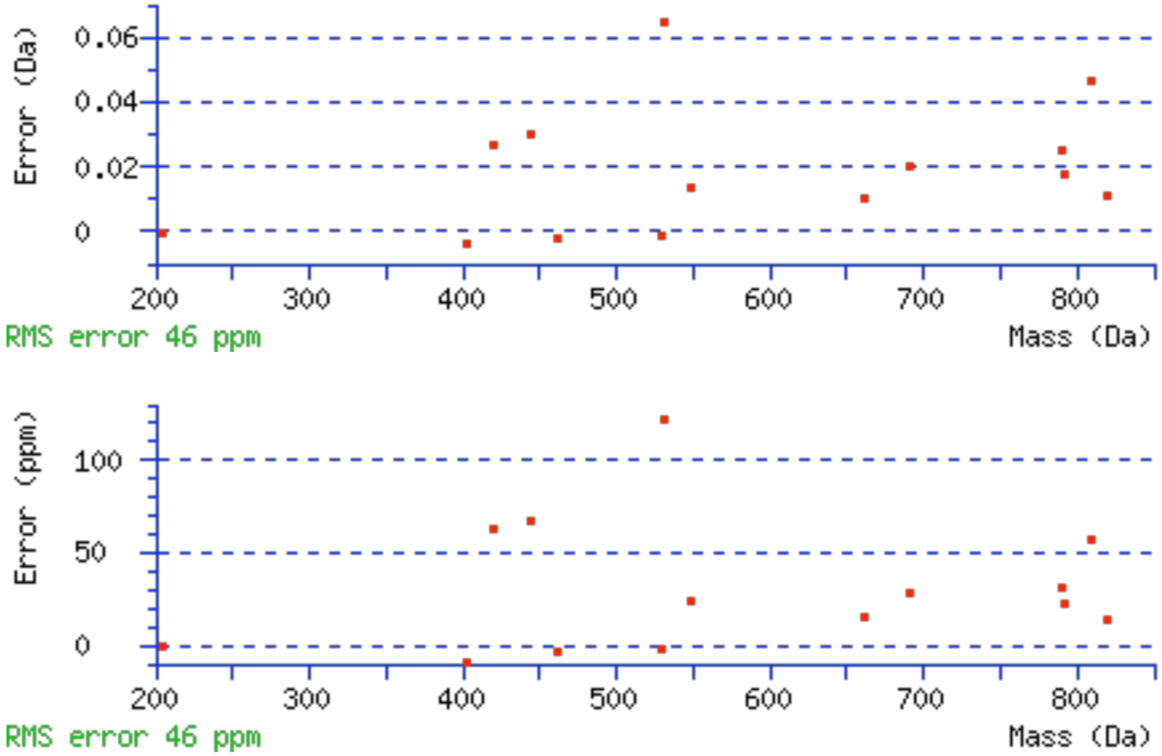
MS/MS Fragmentation of **GFNTGAMEPLGSGFI**
Found in **XP_785647**, PREDICTED: similar to pedal peptide precursor protein [Strongylocentrotus purpuratus].
Match to Query 622: 1496.712628 from(749.363590,2+) intensity(132832.0000)
Title: Cmpd 235, +MSn(749.8255), 35.5 min
Data file Qtof_all.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1496.6970 **Ions Score:** 11 **Expect:** 1.2e+03 **Matches (Bold Red):** 14/128 fragment ions using 30 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							15
2	**205.0972**	103.0522					F	1440.6828	720.8450	1423.6562	712.3318	1422.6722	711.8397	14
3	319.1401	160.0737	302.1135	151.5604			N	1293.6144	647.3108	1276.5878	638.7975	1275.6038	638.3055	13
4	**420.1878**	210.5975	403.1612	202.0842	**402.1772**	201.5922	T	1179.5714	590.2894			1161.5609	581.2841	12

5	477.2092	239.1082	460.1827	230.5950	459.1987	230.1030	**G**	1078.5238	539.7655			1060.5132	530.7602	**11**
6	**548.2463**	274.6268	**531.2198**	266.1135	530.2358	265.6215	**A**	1021.5023	511.2548			1003.4917	502.2495	**10**
7	679.2868	340.1470	662.2603	331.6338	**661.2763**	331.1418	**M**	950.4652	475.7362			932.4546	466.7309	**9**
8	**808.3294**	404.6683	**791.3029**	396.1551	**790.3189**	395.6631	**E**	**819.4247**	410.2160			801.4141	401.2107	**8**
9	905.3822	453.1947	888.3556	444.6815	887.3716	**444.1894**	**P**	**690.3821**	345.6947			672.3715	336.6894	**7**
10	1018.4662	509.7368	1001.4397	501.2235	1000.4557	500.7315	**L**	593.3293	297.1683			575.3188	288.1630	**6**
11	1075.4877	538.2475	1058.4612	529.7342	1057.4771	**529.2422**	**G**	480.2453	240.6263			**462.2347**	231.6210	**5**
12	1162.5197	581.7635	1145.4932	573.2502	1144.5092	572.7582	**S**	423.2238	212.1155			405.2132	203.1103	**4**
13	1219.5412	610.2742	1202.5147	601.7610	1201.5306	601.2690	**G**	336.1918	168.5995					**3**
14	1366.6096	683.8084	1349.5831	675.2952	1348.5990	674.8032	**F**	279.1703	140.0888					**2**
15							**I**	132.1019	66.5546					**1**



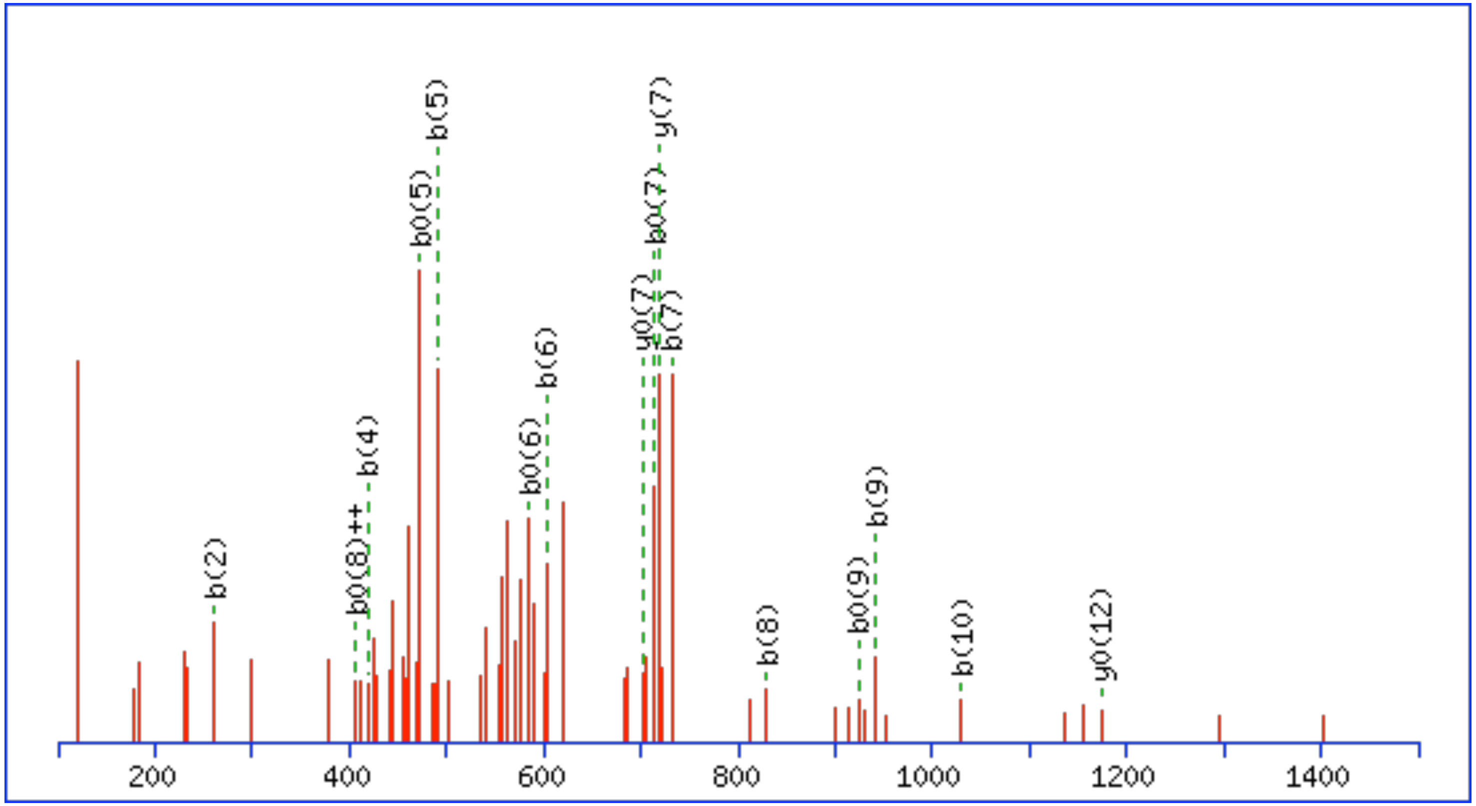
MS/MS Fragmentation of **FLTGALEPLSSGFI**

Found in **XP_785647**, PREDICTED: similar to pedal peptide precursor protein [Strongylocentrotus purpuratus].

Match to Query 585: 1450.689648 from(726.352100,2+) intensity(170280.0000)

Title: Cmpd 298, +MSn(726.8289), 41.5 min

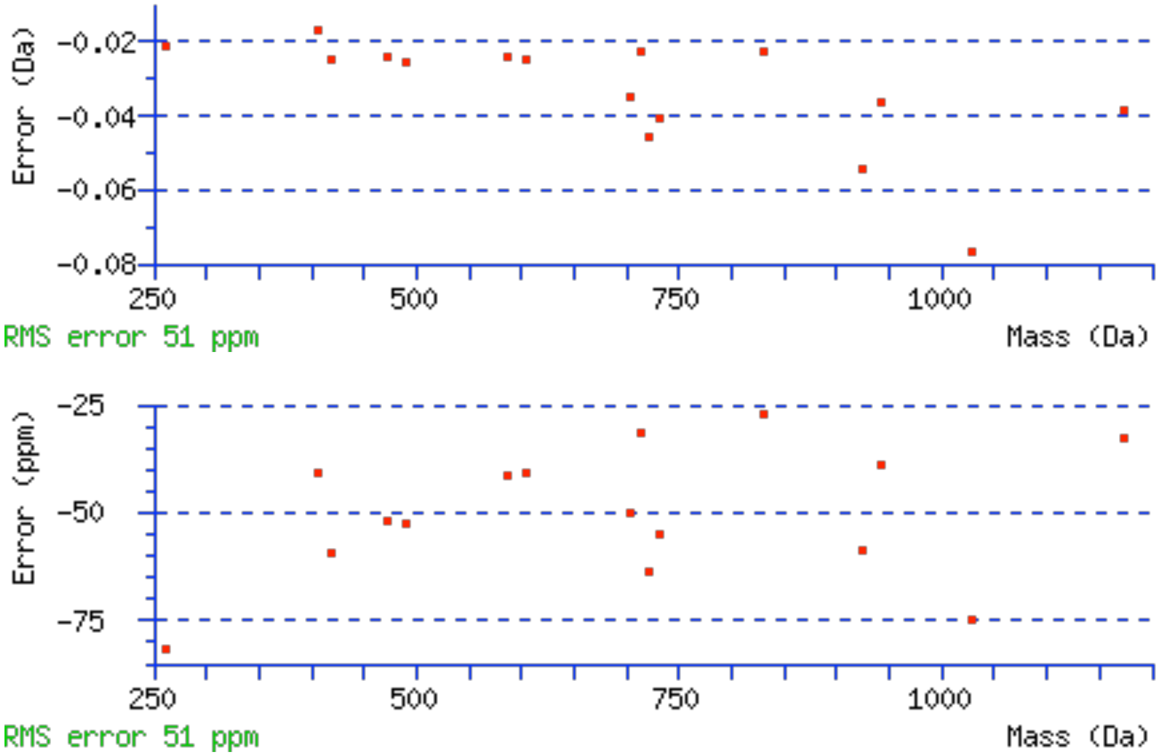
Data file Qtof_all.mgf



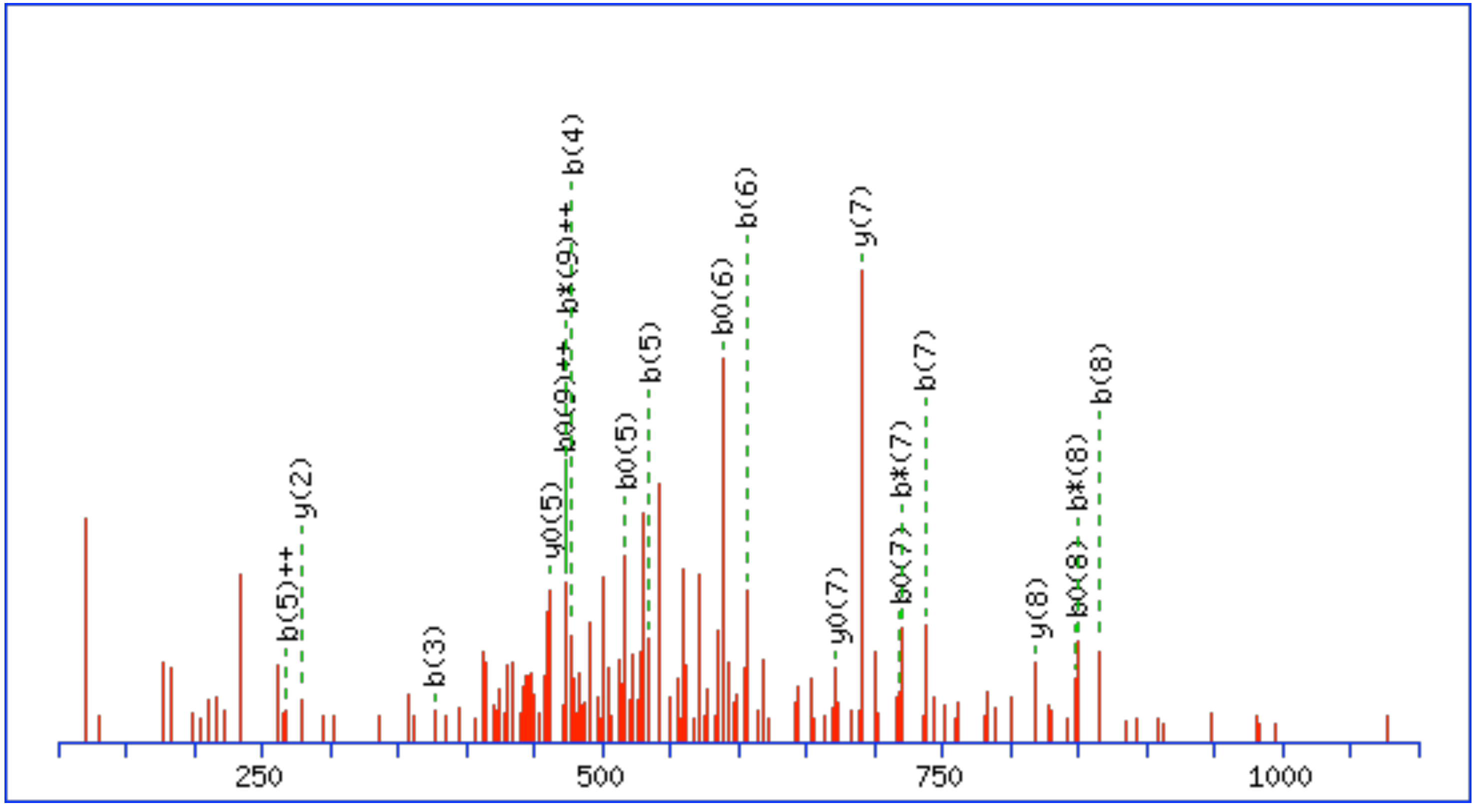
Monoisotopic mass of neutral peptide Mr(calc): 1450.7708 **Ions Score:** 42 **Expect:** 0.82 **Matches (Bold Red):** 17/94 fragment ions using 44 most intense peaks

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	148.0757	74.5415			F					14
2	**261.1598**	131.0835			L	1304.7096	652.8585	1286.6991	643.8532	13
3	362.2074	181.6074	344.1969	172.6021	T	1191.6256	596.3164	**1173.6150**	587.3111	12
4	**419.2289**	210.1181	401.2183	201.1128	G	1090.5779	545.7926	1072.5673	536.7873	11

5	**490.2660**	245.6366	**472.2554**	236.6314	**A**	1033.5564	517.2819	1015.5459	508.2766	**10**
6	**603.3501**	302.1787	**585.3395**	293.1734	**L**	962.5193	481.7633	944.5088	472.7580	**9**
7	**732.3927**	366.7000	**714.3821**	357.6947	**E**	849.4353	425.2213	831.4247	416.2160	**8**
8	**829.4454**	415.2264	811.4349	**406.2211**	**P**	**720.3927**	360.7000	**702.3821**	351.6947	**7**
9	**942.5295**	471.7684	**924.5189**	462.7631	**L**	623.3399	312.1736	605.3293	303.1683	**6**
10	**1029.5615**	515.2844	1011.5510	506.2791	**S**	510.2558	255.6316	492.2453	246.6263	**5**
11	1116.5936	558.8004	1098.5830	549.7951	**S**	423.2238	212.1155	405.2132	203.1103	**4**
12	**1173.6150**	587.3111	1155.6045	578.3059	**G**	336.1918	168.5995			**3**
13	1320.6834	660.8454	1302.6729	651.8401	**F**	279.1703	140.0888			**2**
14					**I**	132.1019	66.5546			**1**



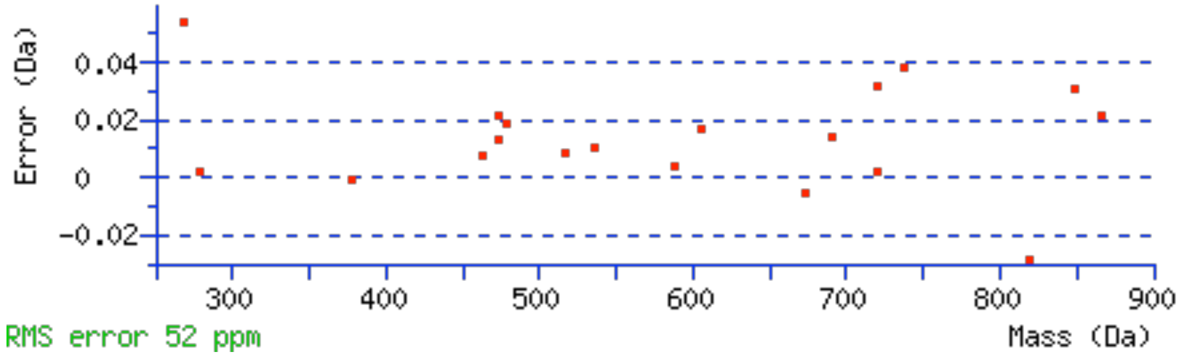
MS/MS Fragmentation of **DFNTGAMEPLGSGFI**
Found in **XP_785647**, PREDICTED: similar to pedal peptide precursor protein [Strongylocentrotus purpuratus].
Match to Query 664: 1554.726348 from(778.370450,2+) intensity(109704.0000)
Title: Cmpd 244, +MSn(778.8585), 36.3 min
Data file Qtof_all.mgf

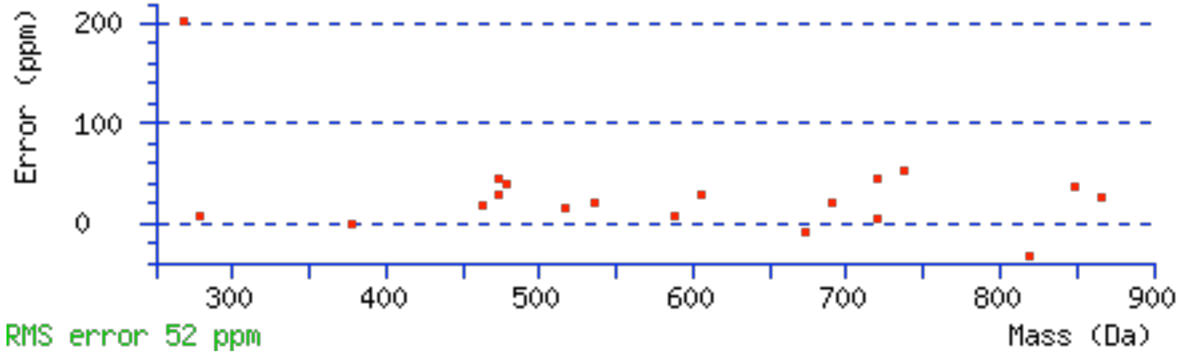


Monoisotopic mass of neutral peptide Mr(calc): 1554.7025 **Ions Score:** 11 **Expect:** 9.3e+02 **Matches (Bold Red):** 20/134 fragment ions using 70 most intense peaks

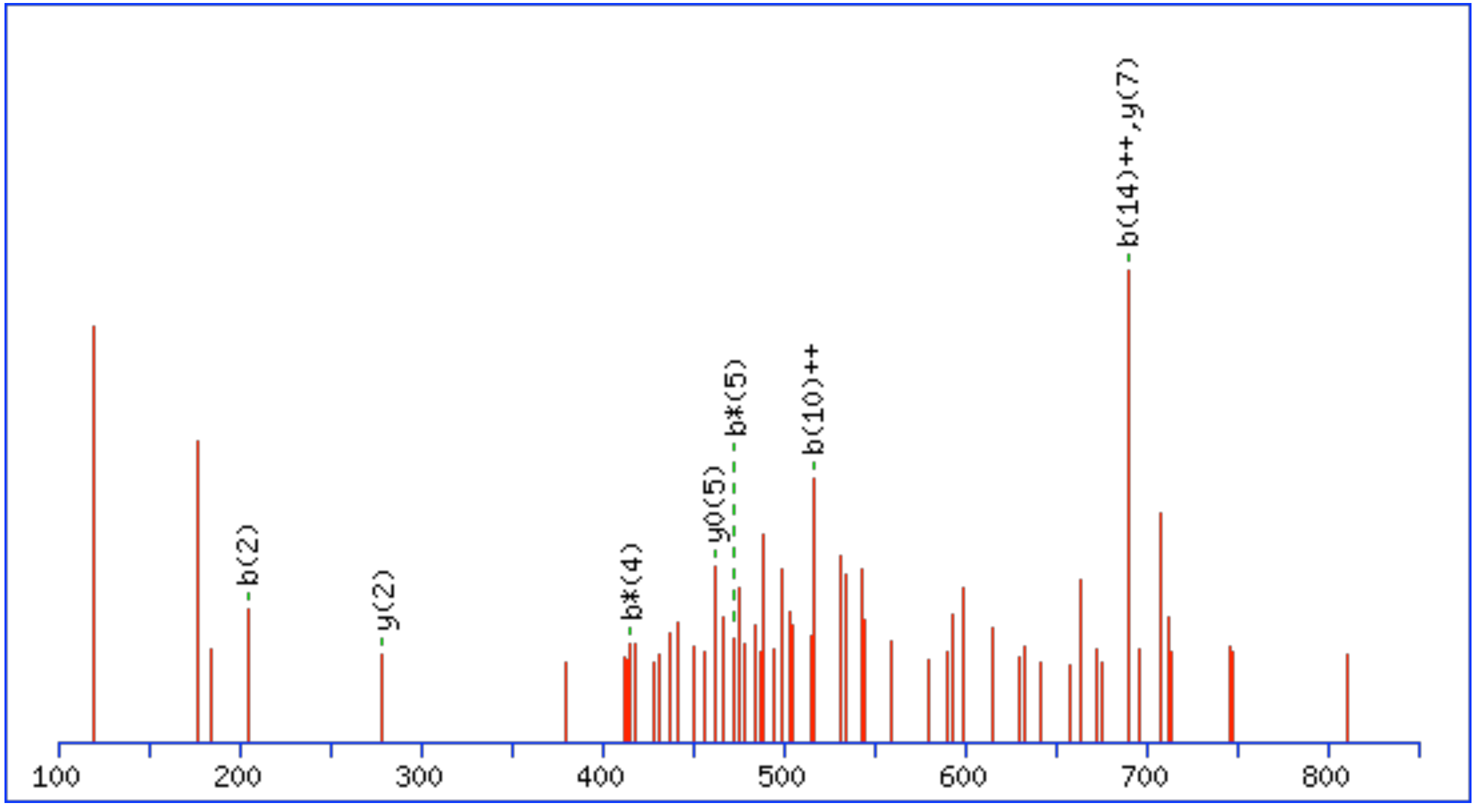
#	b	b^{++}	b^*	b^{*++}	b^0	b^{0++}	Seq.	y	y^{++}	y^*	y^{*++}	y^0	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	**D**							**15**
2	263.1026	132.0550			245.0921	123.0497	**F**	1440.6828	720.8450	1423.6562	712.3318	1422.6722	711.8397	**14**
3	**377.1456**	189.0764	360.1190	180.5631	359.1350	180.0711	**N**	1293.6144	647.3108	1276.5878	638.7975	1275.6038	638.3055	**13**
4	**478.1932**	239.6003	461.1667	231.0870	460.1827	230.5950	**T**	1179.5714	590.2894			1161.5609	581.2841	**12**

5	**535.2147**	**268.1110**	518.1882	259.5977	**517.2041**	259.1057	**G**	1078.5238	539.7655			1060.5132	530.7602	**11**
6	**606.2518**	303.6295	589.2253	295.1163	**588.2413**	294.6243	**A**	1021.5023	511.2548			1003.4917	502.2495	**10**
7	**737.2923**	369.1498	**720.2658**	360.6365	**719.2817**	360.1445	**M**	950.4652	475.7362			932.4546	466.7309	**9**
8	**866.3349**	433.6711	**849.3083**	425.1578	**848.3243**	424.6658	**E**	**819.4247**	410.2160			801.4141	401.2107	**8**
9	963.3877	482.1975	946.3611	**473.6842**	945.3771	**473.1922**	**P**	**690.3821**	345.6947			**672.3715**	336.6894	**7**
10	1076.4717	538.7395	1059.4452	530.2262	1058.4612	529.7342	**L**	593.3293	297.1683			575.3188	288.1630	**6**
11	1133.4932	567.2502	1116.4666	558.7370	1115.4826	558.2449	**G**	480.2453	240.6263			**462.2347**	231.6210	**5**
12	1220.5252	610.7662	1203.4987	602.2530	1202.5147	601.7610	**S**	423.2238	212.1155			405.2132	203.1103	**4**
13	1277.5467	639.2770	1260.5201	630.7637	1259.5361	630.2717	**G**	336.1918	168.5995					**3**
14	1424.6151	712.8112	1407.5885	704.2979	1406.6045	703.8059	**F**	**279.1703**	140.0888					**2**
15							**I**	132.1019	66.5546					**1**





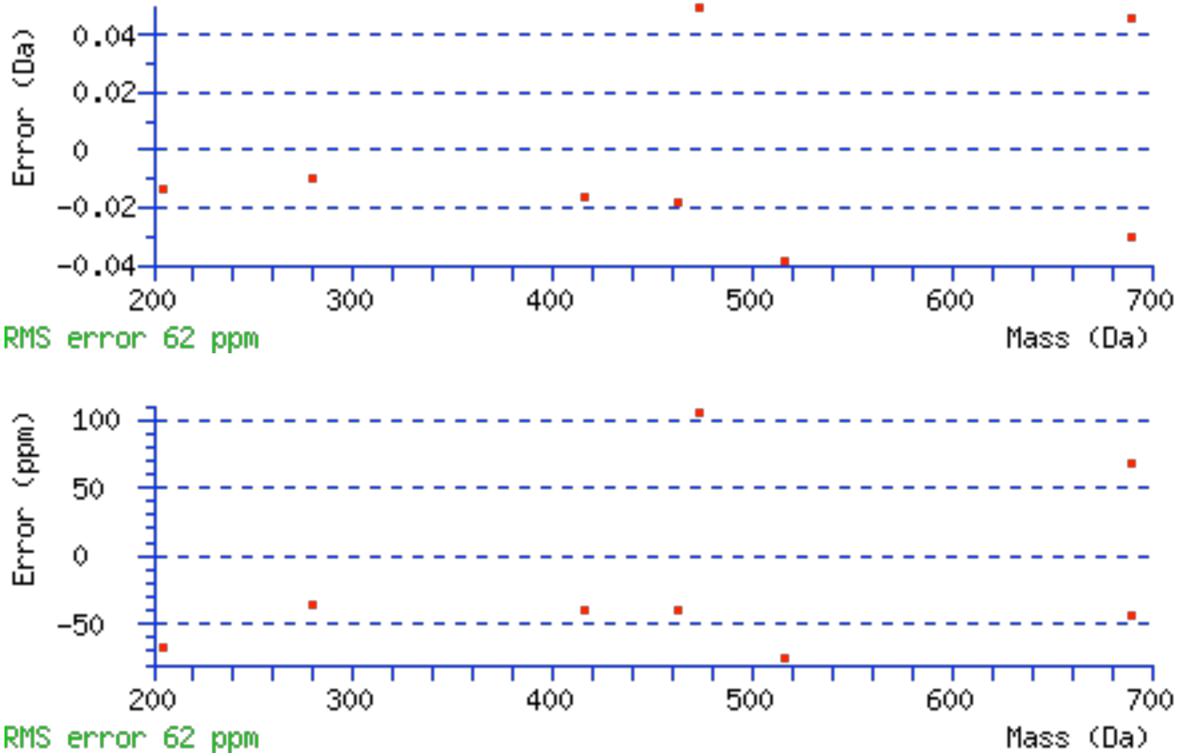
MS/MS Fragmentation of **GFNNGAMEPLGSGFI**
Found in **gi|115974537**, ref|XP_00118|PREDICTED:similartopedalpeptideprecursorprotein[Strongylocentrotuspurpuratus]
Match to Query 634: 1509.603008 from(755.808780,2+) intensity(175652.0000)
Title: Cmpd 268, +MSn(755.6070), 38.6 min
Data file Qtof_all.mgf



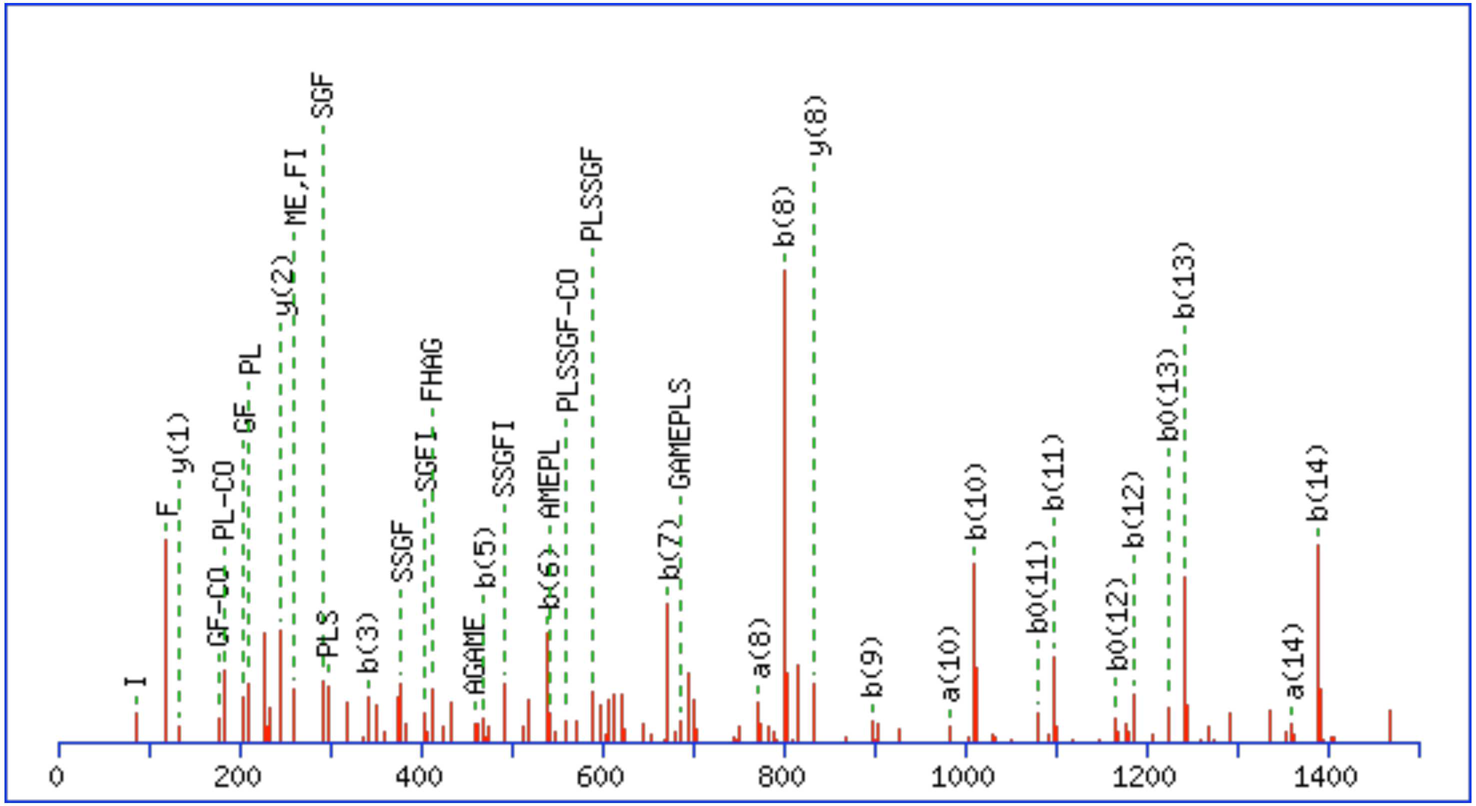
Monoisotopic mass of neutral peptide Mr(calc): 1509.6922 **Ions Score:** 4 **Expect:** 9.7 **Matches (Bold Red):** 8/122 fragment ions using 24 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					**G**							**15**
2	**205.0972**	103.0522					**F**	1453.6780	727.3427	1436.6515	718.8294	1435.6675	718.3374	**14**
3	319.1401	160.0737	302.1135	151.5604			**N**	1306.6096	653.8084	1289.5831	645.2952	1288.5990	644.8032	**13**
4	433.1830	217.0951	**416.1565**	208.5819			**N**	1192.5667	596.7870	1175.5401	588.2737	1174.5561	587.7817	**12**

5	490.2045	245.6059	**473.1779**	237.0926			**G**	1078.5238	539.7655			1060.5132	530.7602	**11**
6	561.2416	281.1244	544.2150	272.6112			**A**	1021.5023	511.2548			1003.4917	502.2495	**10**
7	692.2821	346.6447	675.2555	338.1314			**M**	950.4652	475.7362			932.4546	466.7309	**9**
8	821.3247	411.1660	804.2981	402.6527	803.3141	402.1607	**E**	819.4247	410.2160			801.4141	401.2107	**8**
9	918.3774	459.6924	901.3509	451.1791	900.3669	450.6871	**P**	**690.3821**	345.6947			672.3715	336.6894	**7**
10	1031.4615	**516.2344**	1014.4349	507.7211	1013.4509	507.2291	**L**	593.3293	297.1683			575.3188	288.1630	**6**
11	1088.4830	544.7451	1071.4564	536.2318	1070.4724	535.7398	**G**	480.2453	240.6263			**462.2347**	231.6210	**5**
12	1175.5150	588.2611	1158.4884	579.7479	1157.5044	579.2558	**S**	423.2238	212.1155			405.2132	203.1103	**4**
13	1232.5364	616.7719	1215.5099	608.2586	1214.5259	607.7666	**G**	336.1918	168.5995					**3**
14	1379.6049	**690.3061**	1362.5783	681.7928	1361.5943	681.3008	**F**	**279.1703**	140.0888					**2**
15							**I**	132.1019	66.5546					**1**



MS/MS Fragmentation of **GFHAGAMEPLSSGFID**
Found in **XP_785647**, PREDICTED: similar to pedal peptide precursor protein [Strongylocentrotus purpuratus].
Match to Query 294: 1633.430048 from(817.722300,2+) intensity(2903.1006)
Data file Maldi_All.mgf



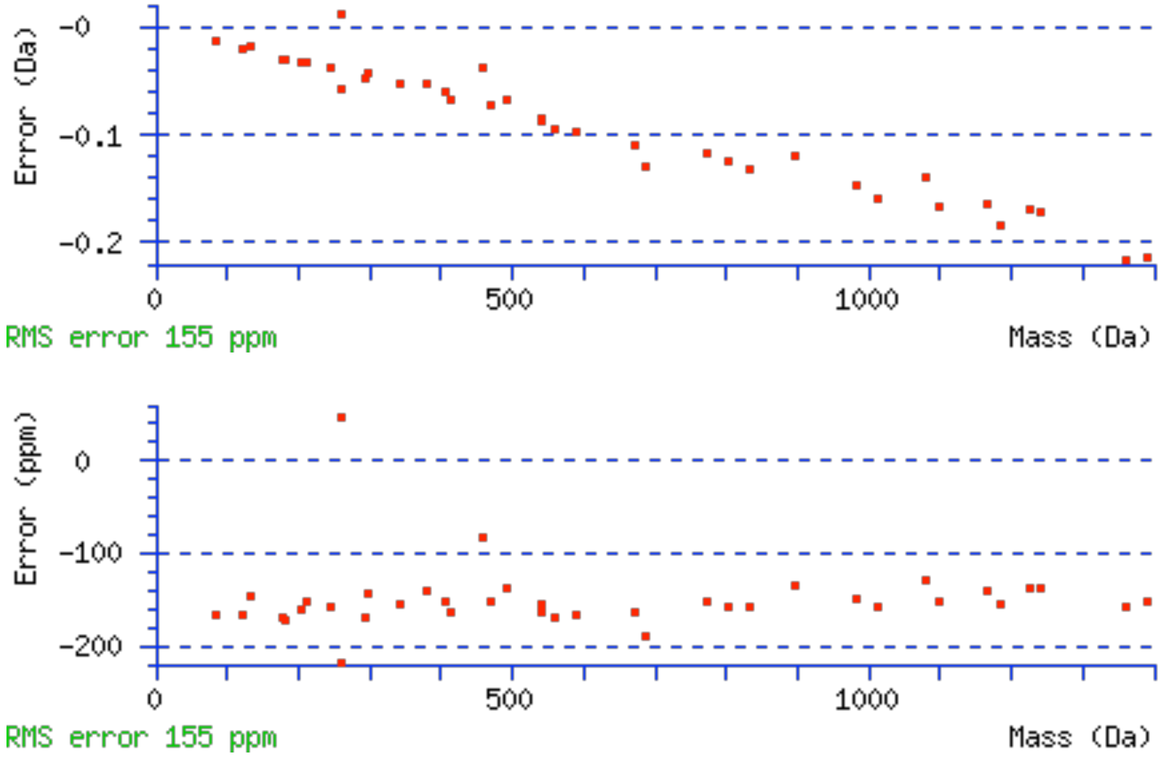
Monoisotopic mass of neutral peptide Mr(calc): 1633.7559 **Variable modifications: C-term :** Amidated (C-term) **Ions Score:** 85 **Expect:** 7.6e-05 **Matches (Bold Red):** 45/212 fragment ions using 70 most intense peaks

#	Immon.	a	a^0	b	b^0	Seq.	y	y^0	#
1	30.0338	30.0338		58.0287		**G**			**16**
2	**120.0808**	**177.1022**		**205.0972**		**F**	1577.7417	1559.7311	**15**
3	110.0713	314.1612		**342.1561**		**H**	1430.6733	1412.6627	**14**
4	44.0495	385.1983		**413.1932**		**A**	1293.6144	1275.6038	**13**

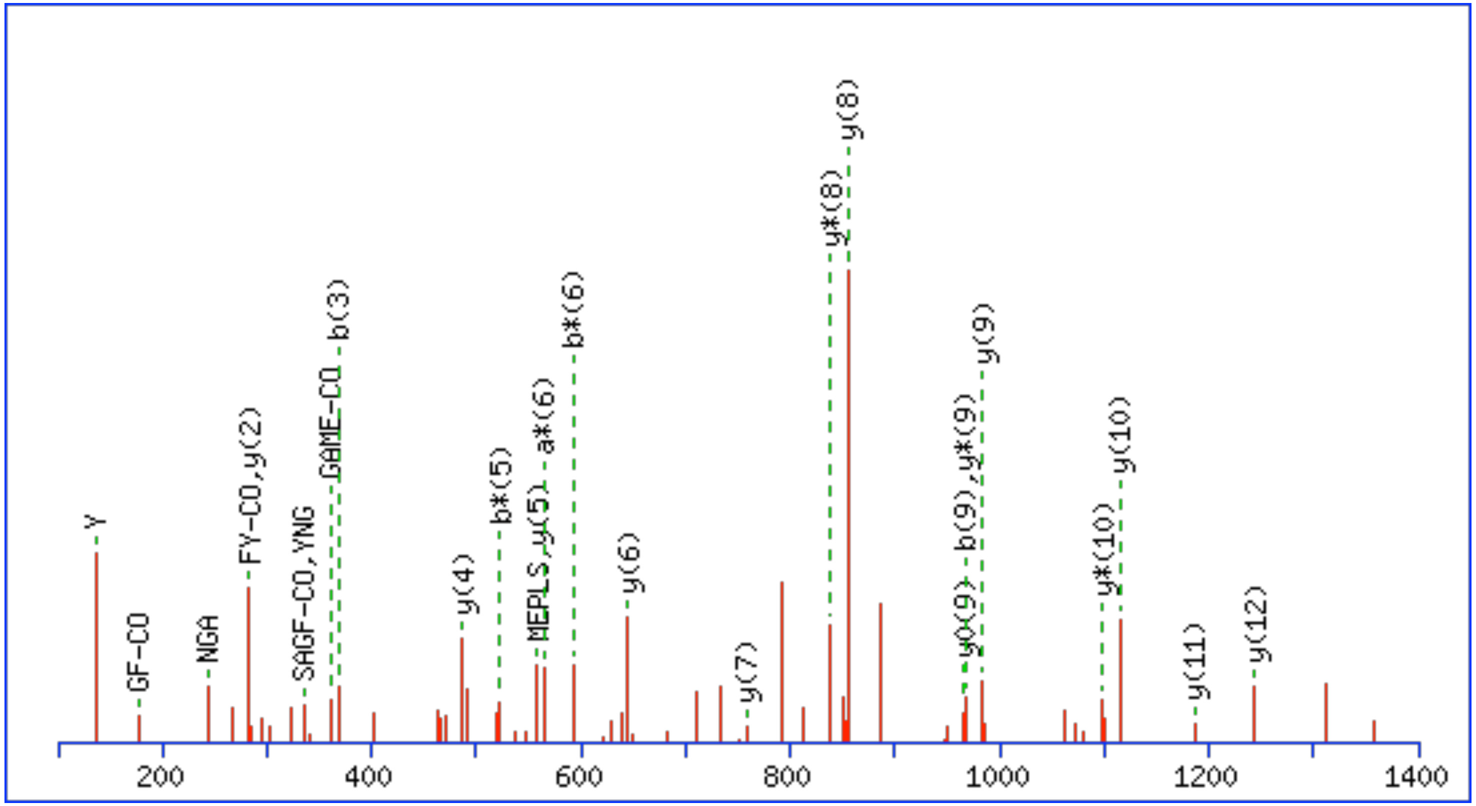
5	30.0338	442.2197		**470.2146**		**G**	1222.5772	1204.5667	**12**
6	44.0495	513.2568		**541.2518**		**A**	1165.5558	1147.5452	**11**
7	104.0528	644.2973		**672.2922**		**M**	1094.5187	1076.5081	**10**
8	102.0550	**773.3399**	755.3294	**801.3348**	783.3243	**E**	963.4782	945.4676	**9**
9	70.0651	870.3927	852.3821	**898.3876**	880.3770	**P**	**834.4356**	816.4250	**8**
10	**86.0964**	**983.4767**	965.4662	**1011.4717**	993.4611	**L**	737.3828	719.3723	**7**
11	60.0444	1070.5088	1052.4982	**1098.5037**	**1080.4931**	**S**	624.2988	606.2882	**6**
12	60.0444	1157.5408	1139.5302	**1185.5357**	**1167.5252**	**S**	537.2667	519.2562	**5**
13	30.0338	1214.5623	1196.5517	**1242.5572**	**1224.5466**	**G**	450.2347	432.2241	**4**
14	**120.0808**	**1361.6307**	1343.6201	**1389.6256**	1371.6150	**F**	393.2132	375.2027	**3**
15	**86.0964**	1474.7147	1456.7042	1502.7097	1484.6991	**I**	**246.1448**	228.1343	**2**
16	88.0393					**D**	**133.0608**	115.0502	**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FH	257.1397	285.1346	**FHA**	328.1768	356.1717	**FHAG**	385.1983	**413.1932**
FHAGA	456.2354	484.2303	**FHAGAM**	587.2759	615.2708	**HA**	181.1084	209.1033
HAG	238.1299	266.1248	**HAGA**	309.1670	337.1619	**HAGAM**	440.2074	468.2024
HAGAME	569.2500	597.2450	**HAGAMEP**	666.3028	694.2977	**AG**	101.0709	129.0659
AGA	172.1081	200.1030	**AGAM**	303.1485	331.1435	**AGAME**	432.1911	**460.1860**
AGAMEP	529.2439	557.2388	**AGAMEPL**	642.3280	670.3229	**GA**	101.0709	129.0659
GAM	232.1114	260.1063	**GAME**	361.1540	389.1489	**GAMEP**	458.2068	486.2017
GAMEPL	571.2908	599.2858	**GAMEPLS**	658.3229	**686.3178**	**AM**	175.0900	203.0849
AME	304.1326	332.1275	**AMEP**	401.1853	429.1802	**AMEPL**	514.2694	**542.2643**
AMEPLS	601.3014	629.2963	**AMEPLSS**	688.3334	716.3284	**ME**	233.0954	**261.0904**
MEP	330.1482	358.1431	**MEPL**	443.2323	471.2272	**MEPLS**	530.2643	558.2592

MEPLSS	617.2963	645.2912	**MEPLSSG**	674.3178	702.3127	**EP**	199.1077	227.1026
EPL	312.1918	340.1867	**EPLS**	399.2238	427.2187	**EPLSS**	486.2558	514.2508
EPLSSG	543.2773	571.2722	**EPLSSGF**	690.3457	718.3406	**PL**	**183.1492**	**211.1441**
PLS	270.1812	**298.1761**	**PLSS**	357.2132	385.2082	**PLSSG**	414.2347	442.2296
PLSSGF	**561.3031**	**589.2980**	**PLSSGFI**	674.3872	702.3821	**LS**	173.1285	201.1234
LSS	260.1605	288.1554	**LSSG**	317.1819	345.1769	**LSSGF**	464.2504	**492.2453**
LSSGFI	577.3344	605.3293	**SS**	147.0764	175.0713	**SSG**	204.0979	232.0928
SSGF	351.1663	**379.1612**	**SSGFI**	464.2504	**492.2453**	**SG**	117.0659	145.0608
SGF	264.1343	**292.1292**	**SGFI**	377.2183	**405.2132**	**GF**	**177.1022**	**205.0972**
GFI	290.1863	318.1812	**FI**	233.1648	**261.1598**			



MS/MS Fragmentation of **GFYNGAMEPLSAGFHQ**
Found in **XP_785647**, PREDICTED: similar to pedal peptide precursor protein [Strongylocentrotus purpuratus].
Match to Query 317: 1723.435048 from(862.724800,2+) intensity(5856.6147)
Data file Maldi_All.mgf



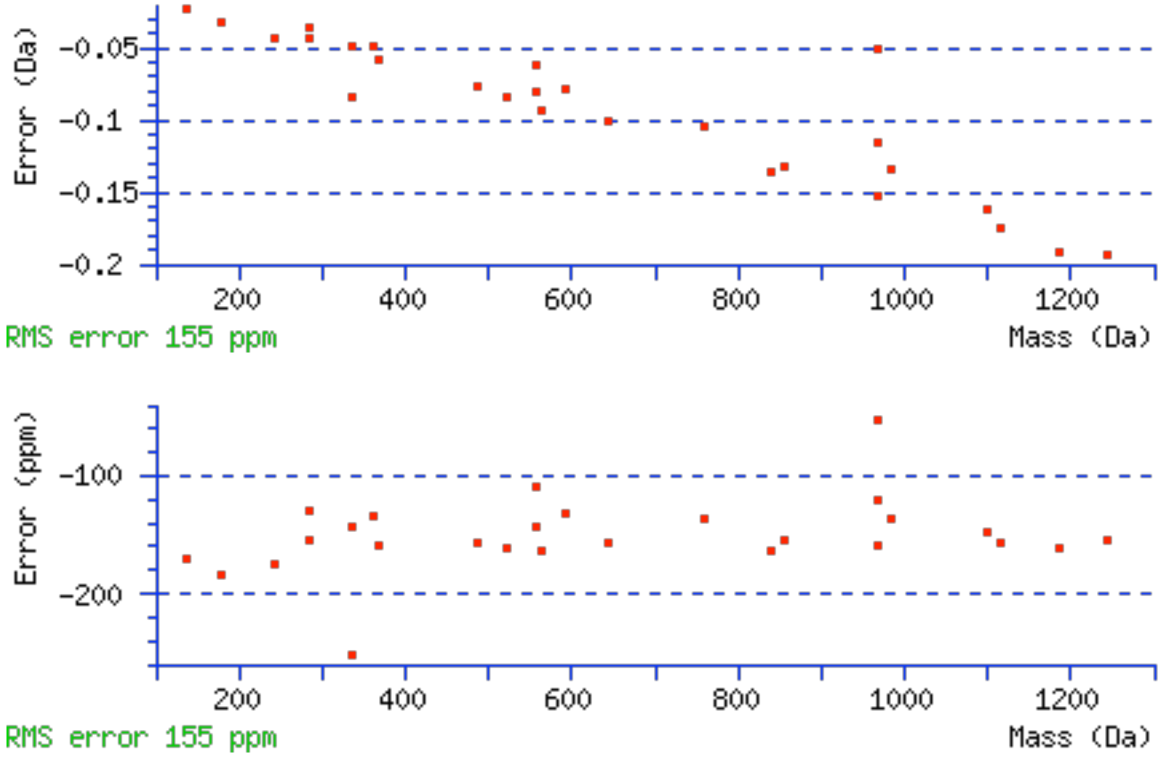
Monoisotopic mass of neutral peptide Mr(calc): 1723.7777 **Variable modifications: C-term :** Amidated (C-term) **Ions Score:** 69 **Expect:** 0.0031 **Matches (Bold Red):** 28/244 fragment ions using 37 most intense peaks

#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	y	y*	y^0	#
1	30.0338	30.0338			58.0287			G				16
2	120.0808	**177.1022**			205.0972			F	1667.7635	1650.7369	1649.7529	15
3	**136.0757**	340.1656			**368.1605**			Y	1520.6951	1503.6685	1502.6845	14
4	87.0553	454.2085	437.1819		482.2034	465.1769		N	1357.6317	1340.6052	1339.6212	13

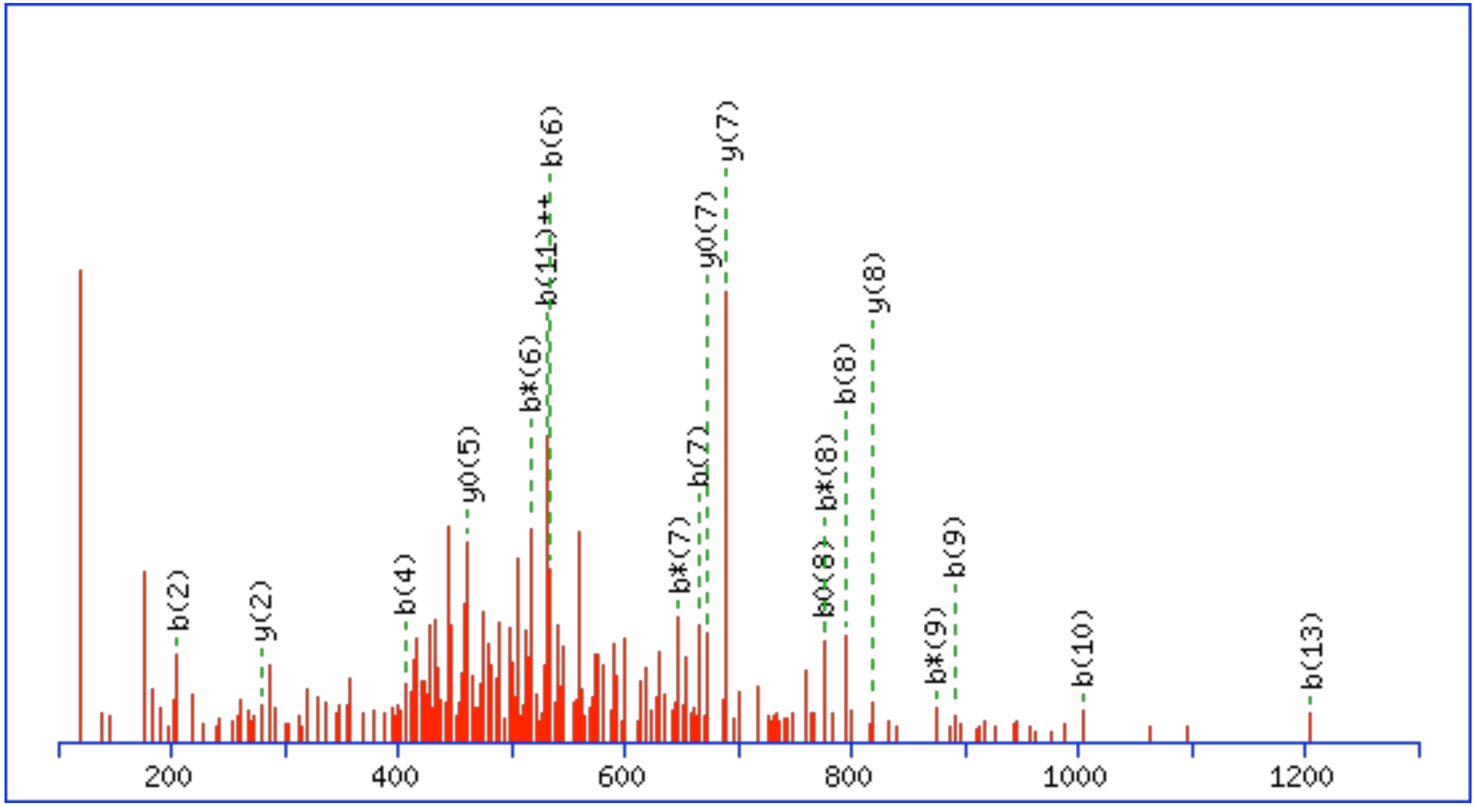
5	30.0338	511.2300	494.2034		539.2249	**522.1983**		**G**	**1243.5888**	1226.5623	1225.5782	**12**
6	44.0495	582.2671	**565.2405**		610.2620	**593.2354**		**A**	**1186.5673**	1169.5408	1168.5568	**11**
7	104.0528	713.3076	696.2810		741.3025	724.2759		**M**	**1115.5302**	**1098.5037**	1097.5197	**10**
8	102.0550	842.3502	825.3236	824.3396	870.3451	853.3185	852.3345	**E**	**984.4897**	**967.4632**	**966.4792**	**9**
9	70.0651	939.4029	922.3764	921.3924	**967.3978**	950.3713	949.3873	**P**	**855.4472**	**838.4206**	837.4366	**8**
10	86.0964	1052.4870	1035.4604	1034.4764	1080.4819	1063.4553	1062.4713	**L**	**758.3944**	741.3678	740.3838	**7**
11	60.0444	1139.5190	1122.4925	1121.5084	1167.5139	1150.4874	1149.5034	**S**	**645.3103**	628.2838	627.2998	**6**
12	44.0495	1210.5561	1193.5296	1192.5456	1238.5510	1221.5245	1220.5405	**A**	**558.2783**	541.2517		**5**
13	30.0338	1267.5776	1250.5510	1249.5670	1295.5725	1278.5460	1277.5619	**G**	**487.2412**	470.2146		**4**
14	120.0808	1414.6460	1397.6195	1396.6354	1442.6409	1425.6144	1424.6303	**F**	430.2197	413.1932		**3**
15	110.0713	1551.7049	1534.6784	1533.6943	1579.6998	1562.6733	1561.6893	**H**	**283.1513**	266.1248		**2**
16	101.0709							**Q**	146.0924	129.0658		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FY	**283.1441**	311.1390	**FYN**	397.1870	425.1819	**FYNG**	454.2085	482.2034
FYNGA	525.2456	553.2405	**FYNGAM**	656.2861	684.2810	**YN**	250.1186	278.1135
YNG	307.1401	**335.1350**	**YNGA**	378.1772	406.1721	**YNGAM**	509.2177	537.2126
YNGAME	638.2603	666.2552	**NG**	144.0768	172.0717	**NGA**	215.1139	**243.1088**
NGAM	346.1544	374.1493	**NGAME**	475.1969	503.1919	**NGAMEP**	572.2497	600.2446
NGAMEPL	685.3338	713.3287	**GA**	101.0709	129.0659	**GAM**	232.1114	260.1063
GAME	**361.1540**	389.1489	**GAMEP**	458.2068	486.2017	**GAMEPL**	571.2908	599.2858
GAMEPLS	658.3229	686.3178	**AM**	175.0900	203.0849	**AME**	304.1326	332.1275
AMEP	401.1853	429.1802	**AMEPL**	514.2694	542.2643	**AMEPLS**	601.3014	629.2963
AMEPLSA	672.3385	700.3334	**ME**	233.0954	261.0904	**MEP**	330.1482	358.1431
MEPL	443.2323	471.2272	**MEPLS**	530.2643	**558.2592**	**MEPLSA**	601.3014	629.2963

MEPLSAG	658.3229	686.3178	**EP**	199.1077	227.1026	**EPL**	312.1918	340.1867
EPLS	399.2238	427.2187	**EPLSA**	470.2609	498.2558	**EPLSAG**	527.2824	555.2773
EPLSAGF	674.3508	702.3457	**PL**	183.1492	211.1441	**PLS**	270.1812	298.1761
PLSA	341.2183	369.2132	**PLSAG**	398.2398	426.2347	**PLSAGF**	545.3082	573.3031
PLSAGFH	682.3671	710.3620	**LS**	173.1285	201.1234	**LSA**	244.1656	272.1605
LSAG	301.1870	329.1819	**LSAGF**	448.2554	476.2504	**LSAGFH**	585.3144	613.3093
SA	131.0815	159.0764	**SAG**	188.1030	216.0979	**SAGF**	**335.1714**	363.1663
SAGFH	472.2303	500.2252	**AG**	101.0709	129.0659	**AGF**	248.1394	276.1343
AGFH	385.1983	413.1932	**GF**	**177.1022**	205.0972	**GFH**	314.1612	342.1561
FH	257.1397	285.1346						



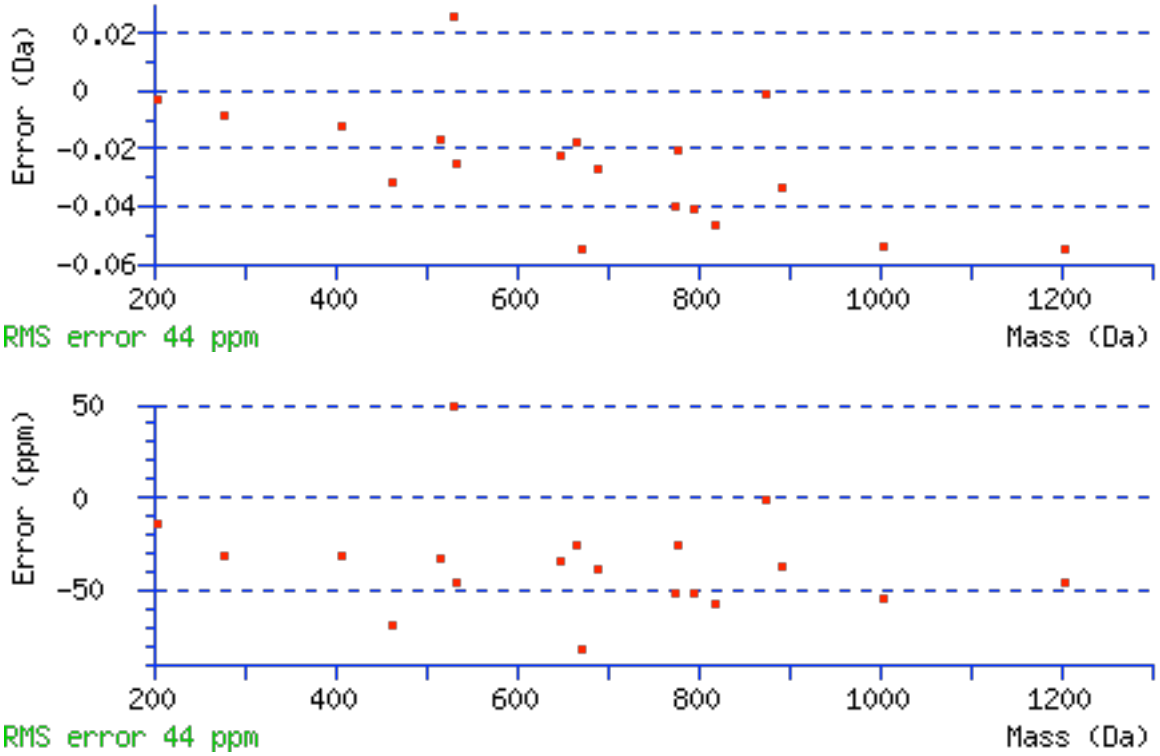
MS/MS Fragmentation of **GFNSGAMEPLGSGFI**
Found in **XP_785647**, PREDICTED: similar to pedal peptide precursor protein [Strongylocentrotus purpuratus].
Match to Query 607: 1482.594188 from(742.304370,2+) intensity(403812.0000)
Title: Cmpd 272, +MSn(742.3936), 38.8 min
Data file Qtof_all.mgf



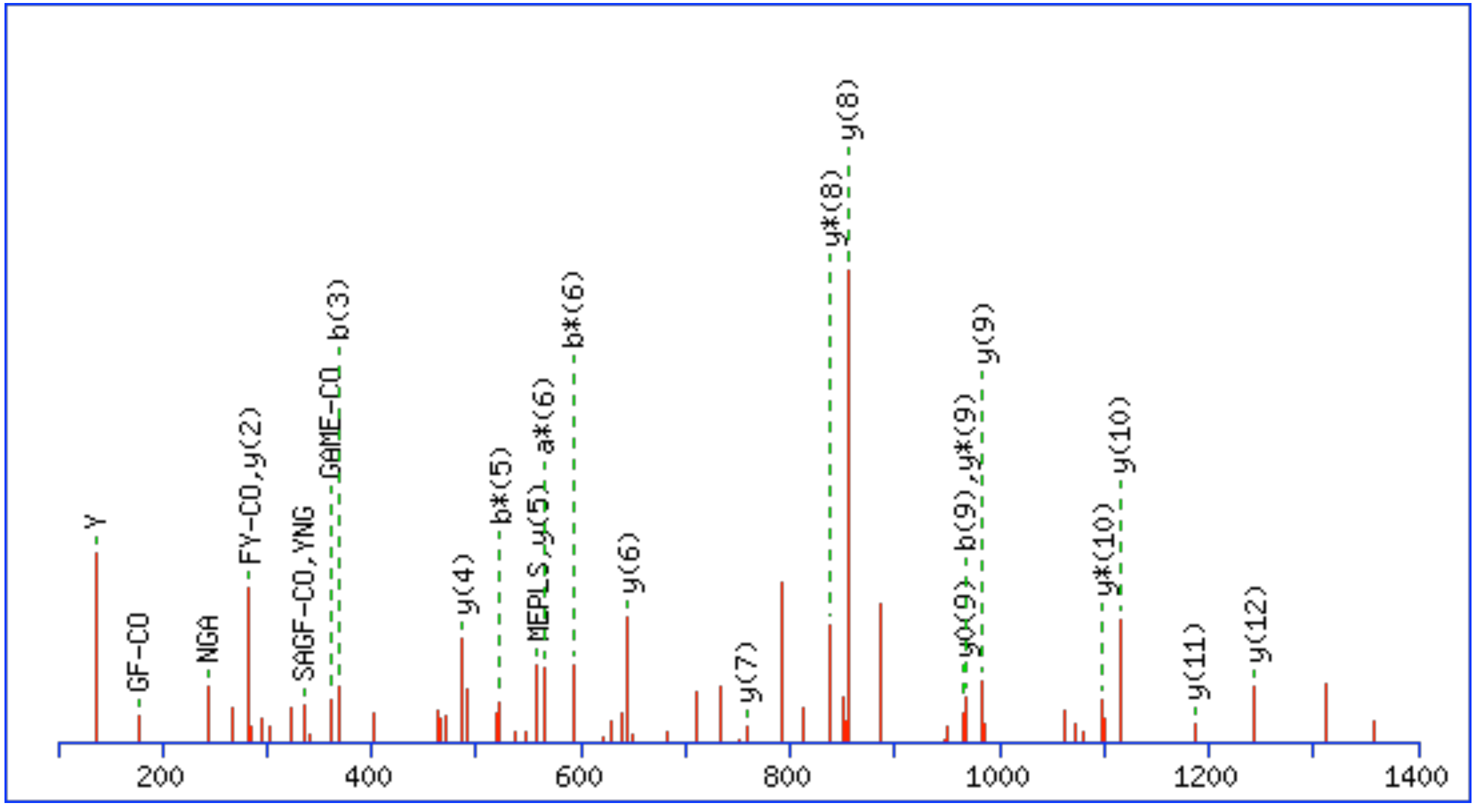
Monoisotopic mass of neutral peptide Mr(calc): 1482.6813 **Ions Score:** 36 **Expect:** 0.97 **Matches (Bold Red):** 19/128 fragment ions using 49 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							15
2	**205.0972**	103.0522					F	1426.6671	713.8372	1409.6406	705.3239	1408.6566	704.8319	14
3	319.1401	160.0737	302.1135	151.5604			N	1279.5987	640.3030	1262.5722	631.7897	1261.5881	631.2977	13
4	**406.1721**	203.5897	389.1456	195.0764	388.1615	194.5844	S	1165.5558	583.2815			1147.5452	574.2762	12

5	463.1936	232.1004	446.1670	223.5872	445.1830	223.0951	**G**	1078.5238	539.7655			1060.5132	530.7602	**11**
6	**534.2307**	267.6190	**517.2041**	259.1057	516.2201	258.6137	**A**	1021.5023	511.2548			1003.4917	502.2495	**10**
7	**665.2712**	333.1392	**648.2446**	324.6259	647.2606	324.1339	**M**	950.4652	475.7362			932.4546	466.7309	**9**
8	**794.3138**	397.6605	**777.2872**	389.1472	**776.3032**	388.6552	**E**	**819.4247**	410.2160			801.4141	401.2107	**8**
9	**891.3665**	446.1869	**874.3400**	437.6736	873.3560	437.1816	**P**	**690.3821**	345.6947			**672.3715**	336.6894	**7**
10	**1004.4506**	502.7289	987.4240	494.2157	986.4400	493.7237	**L**	593.3293	297.1683			575.3188	288.1630	**6**
11	1061.4721	**531.2397**	1044.4455	522.7264	1043.4615	522.2344	**G**	480.2453	240.6263			**462.2347**	231.6210	**5**
12	1148.5041	574.7557	1131.4775	566.2424	1130.4935	565.7504	**S**	423.2238	212.1155			405.2132	203.1103	**4**
13	**1205.5255**	603.2664	1188.4990	594.7531	1187.5150	594.2611	**G**	336.1918	168.5995					**3**
14	1352.5940	676.8006	1335.5674	668.2873	1334.5834	667.7953	**F**	**279.1703**	140.0888					**2**
15							**I**	132.1019	66.5546					**1**



MS/MS Fragmentation of **GFYNGAMEPLSAGFHQ**
Found in **XP_785647**, PREDICTED: similar to pedal peptide precursor protein [Strongylocentrotus purpuratus].
Match to Query 317: 1723.435048 from(862.724800,2+) intensity(5856.6147)
Data file Maldi_All.mgf



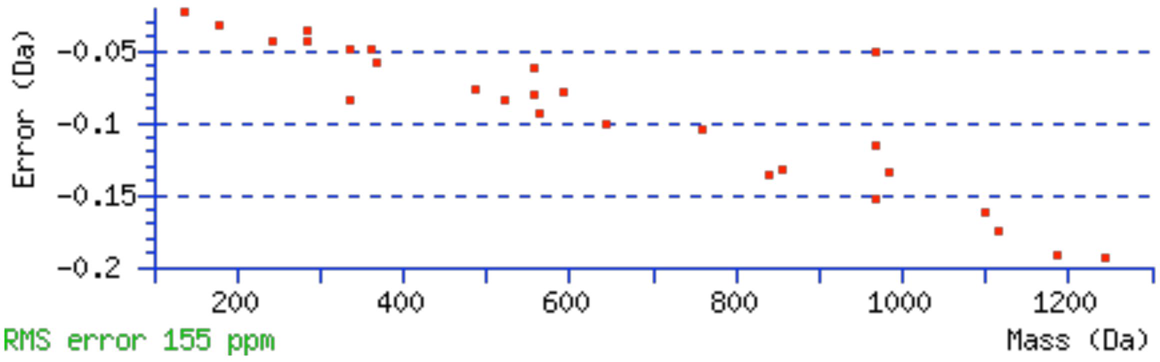
Monoisotopic mass of neutral peptide Mr(calc): 1723.7777 **Variable modifications: C-term :** Amidated (C-term) **Ions**
Score: 69 **Expect:** 0.0031 **Matches (Bold Red):** 28/244 fragment ions using 37 most intense peaks

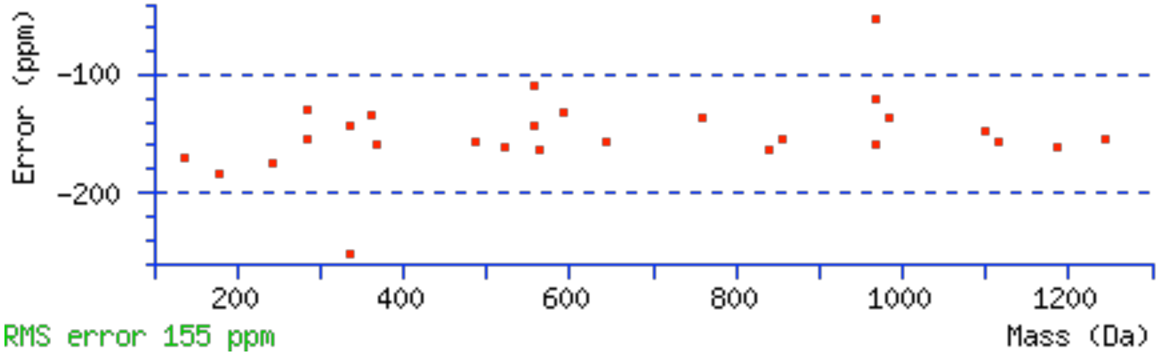
#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	y	y*	y^0	#
1	30.0338	30.0338			58.0287			**G**				**16**
2	120.0808	**177.1022**			205.0972			**F**	1667.7635	1650.7369	1649.7529	**15**
3	**136.0757**	340.1656			**368.1605**			**Y**	1520.6951	1503.6685	1502.6845	**14**
4	87.0553	454.2085	437.1819		482.2034	465.1769		**N**	1357.6317	1340.6052	1339.6212	**13**

5	30.0338	511.2300	494.2034		539.2249	**522.1983**		**G**	**1243.5888**	1226.5623	1225.5782	**12**
6	44.0495	582.2671	**565.2405**		610.2620	**593.2354**		**A**	**1186.5673**	1169.5408	1168.5568	**11**
7	104.0528	713.3076	696.2810		741.3025	724.2759		**M**	**1115.5302**	**1098.5037**	1097.5197	**10**
8	102.0550	842.3502	825.3236	824.3396	870.3451	853.3185	852.3345	**E**	**984.4897**	**967.4632**	**966.4792**	**9**
9	70.0651	939.4029	922.3764	921.3924	**967.3978**	950.3713	949.3873	**P**	**855.4472**	**838.4206**	837.4366	**8**
10	86.0964	1052.4870	1035.4604	1034.4764	1080.4819	1063.4553	1062.4713	**L**	**758.3944**	741.3678	740.3838	**7**
11	60.0444	1139.5190	1122.4925	1121.5084	1167.5139	1150.4874	1149.5034	**S**	**645.3103**	628.2838	627.2998	**6**
12	44.0495	1210.5561	1193.5296	1192.5456	1238.5510	1221.5245	1220.5405	**A**	**558.2783**	541.2517		**5**
13	30.0338	1267.5776	1250.5510	1249.5670	1295.5725	1278.5460	1277.5619	**G**	**487.2412**	470.2146		**4**
14	120.0808	1414.6460	1397.6195	1396.6354	1442.6409	1425.6144	1424.6303	**F**	430.2197	413.1932		**3**
15	110.0713	1551.7049	1534.6784	1533.6943	1579.6998	1562.6733	1561.6893	**H**	**283.1513**	266.1248		**2**
16	101.0709							**Q**	146.0924	129.0658		**1**

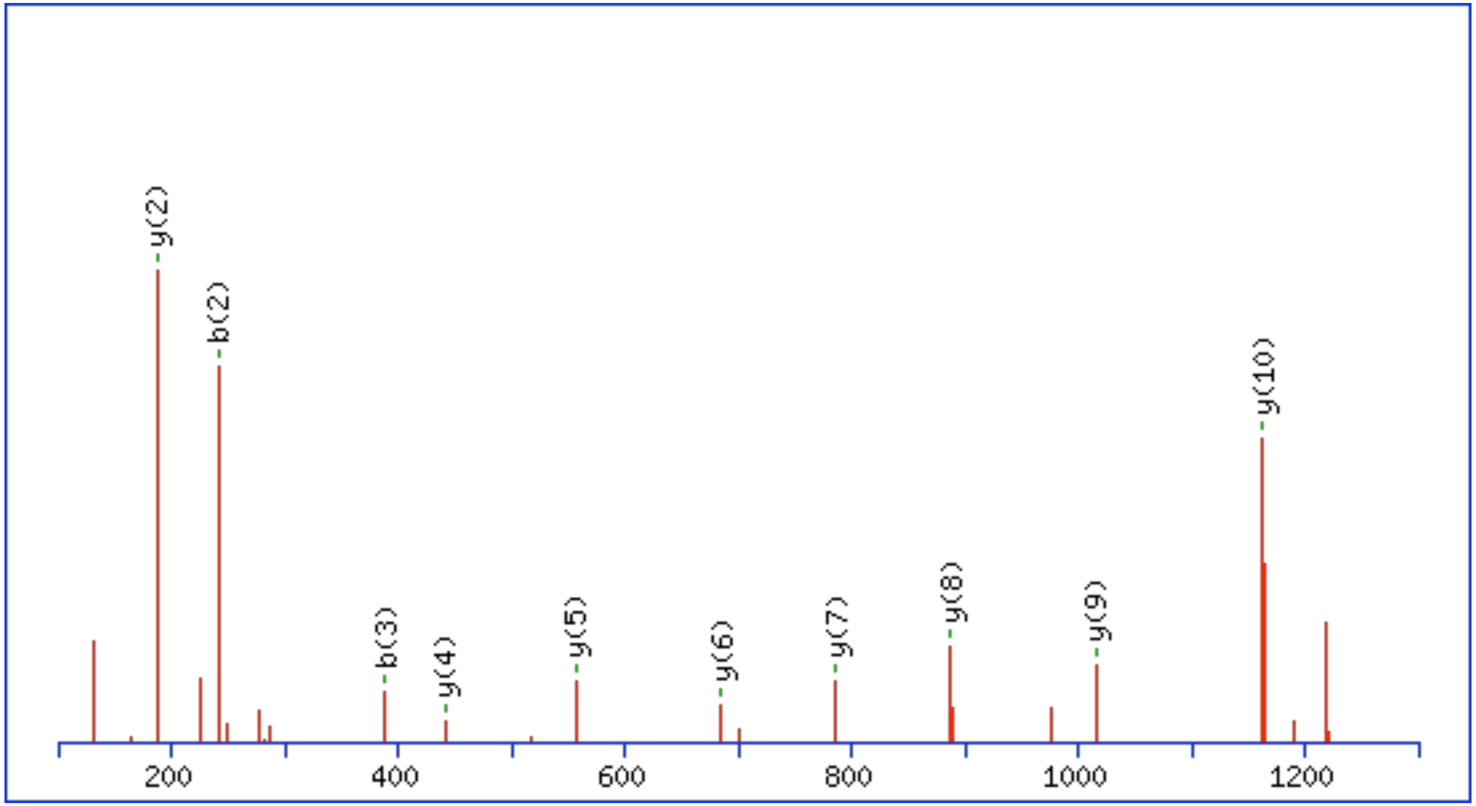
Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FY	**283.1441**	311.1390	**FYN**	397.1870	425.1819	**FYNG**	454.2085	482.2034
FYNGA	525.2456	553.2405	**FYNGAM**	656.2861	684.2810	**YN**	250.1186	278.1135
YNG	307.1401	**335.1350**	**YNGA**	378.1772	406.1721	**YNGAM**	509.2177	537.2126
YNGAME	638.2603	666.2552	**NG**	144.0768	172.0717	**NGA**	215.1139	**243.1088**
NGAM	346.1544	374.1493	**NGAME**	475.1969	503.1919	**NGAMEP**	572.2497	600.2446
NGAMEPL	685.3338	713.3287	**GA**	101.0709	129.0659	**GAM**	232.1114	260.1063
GAME	**361.1540**	389.1489	**GAMEP**	458.2068	486.2017	**GAMEPL**	571.2908	599.2858
GAMEPLS	658.3229	686.3178	**AM**	175.0900	203.0849	**AME**	304.1326	332.1275
AMEP	401.1853	429.1802	**AMEPL**	514.2694	542.2643	**AMEPLS**	601.3014	629.2963
AMEPLSA	672.3385	700.3334	**ME**	233.0954	261.0904	**MEP**	330.1482	358.1431
MEPL	443.2323	471.2272	**MEPLS**	530.2643	**558.2592**	**MEPLSA**	601.3014	629.2963

MEPLSAG	658.3229	686.3178	**EP**	199.1077	227.1026	**EPL**	312.1918	340.1867
EPLS	399.2238	427.2187	**EPLSA**	470.2609	498.2558	**EPLSAG**	527.2824	555.2773
EPLSAGF	674.3508	702.3457	**PL**	183.1492	211.1441	**PLS**	270.1812	298.1761
PLSA	341.2183	369.2132	**PLSAG**	398.2398	426.2347	**PLSAGF**	545.3082	573.3031
PLSAGFH	682.3671	710.3620	**LS**	173.1285	201.1234	**LSA**	244.1656	272.1605
LSAG	301.1870	329.1819	**LSAGF**	448.2554	476.2504	**LSAGFH**	585.3144	613.3093
SA	131.0815	159.0764	**SAG**	188.1030	216.0979	**SAGF**	**335.1714**	363.1663
SAGFH	472.2303	500.2252	**AG**	101.0709	129.0659	**AGF**	248.1394	276.1343
AGFH	385.1983	413.1932	**GF**	**177.1022**	205.0972	**GFH**	314.1612	342.1561
FH	257.1397	285.1346						





MS/MS Fragmentation of **LQFETTQDRVPA**
Found in **XP_001175944**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
Match to Query 160: 1403.477448 from(702.746000,2+) intensity(1298.1272)
Data file Maldi_All.mgf



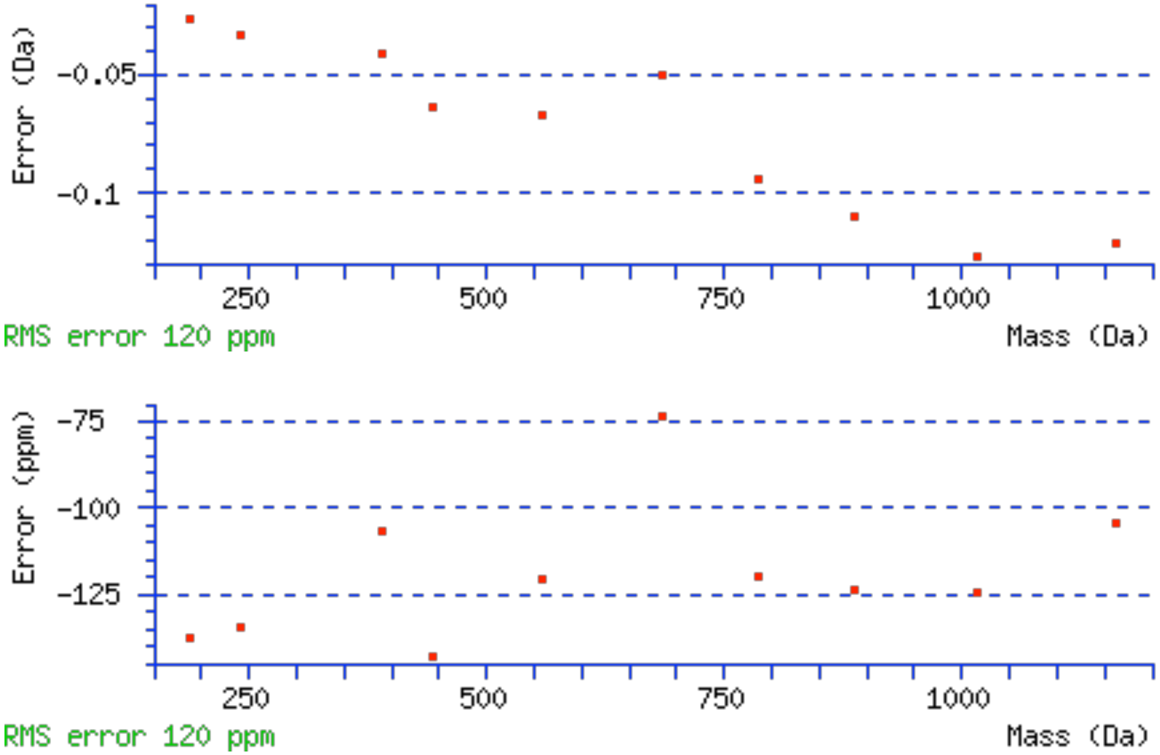
Monoisotopic mass of neutral peptide Mr(calc): 1403.7045 **Ions Score:** 87 **Expect:** 3.6e-05 **Matches (Bold Red):** 10/180 fragment ions using 10 most intense peaks

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	w'	y	y*	y^0	#
1	86.0964	86.0964			114.0913				L							12
2	101.0709	214.1550	197.1285		**242.1499**	225.1234			Q	1218.5749	1217.5797		1291.6277	1274.6012	1273.6171	11

3	120.0808	361.2234	344.1969		**389.2183**	372.1918			**F**	1071.5065			**1163.5691**	1146.5426	1145.5586	**10**
4	102.0550	490.2660	473.2395	472.2554	518.2609	501.2344	500.2504		**E**	942.4639	941.4687		**1016.5007**	999.4742	998.4902	**9**
5	74.0600	591.3137	574.2871	573.3031	619.3086	602.2821	601.2980		**T**	841.4163	854.4367	856.4159	**887.4581**	870.4316	869.4476	**8**
6	74.0600	692.3614	675.3348	674.3508	720.3563	703.3297	702.3457		**T**	740.3686	753.3890	755.3682	**786.4104**	769.3839	768.3999	**7**
7	101.0709	820.4199	803.3934	802.4094	848.4149	831.3883	830.4043		**Q**	612.3100	611.3148		**685.3628**	668.3362	667.3522	**6**
8	88.0393	935.4469	918.4203	917.4363	963.4418	946.4153	945.4312		**D**	497.2831	496.2878		**557.3042**	540.2776	539.2936	**5**
9	129.1135	1091.5480	1074.5215	1073.5374	1119.5429	1102.5164	1101.5323	1006.4840	**R**	341.1819	340.1867		**442.2772**	425.2507		**4**
10	72.0808	1190.6164	1173.5899	1172.6058	1218.6113	1201.5848	1200.6008	1176.6008	**V**				286.1761			**3**
11	70.0651	1287.6692	1270.6426	1269.6586	1315.6641	1298.6375	1297.6535	1261.6535	**P**				**187.1077**			**2**
12	44.0495								**A**				90.0550			**1**

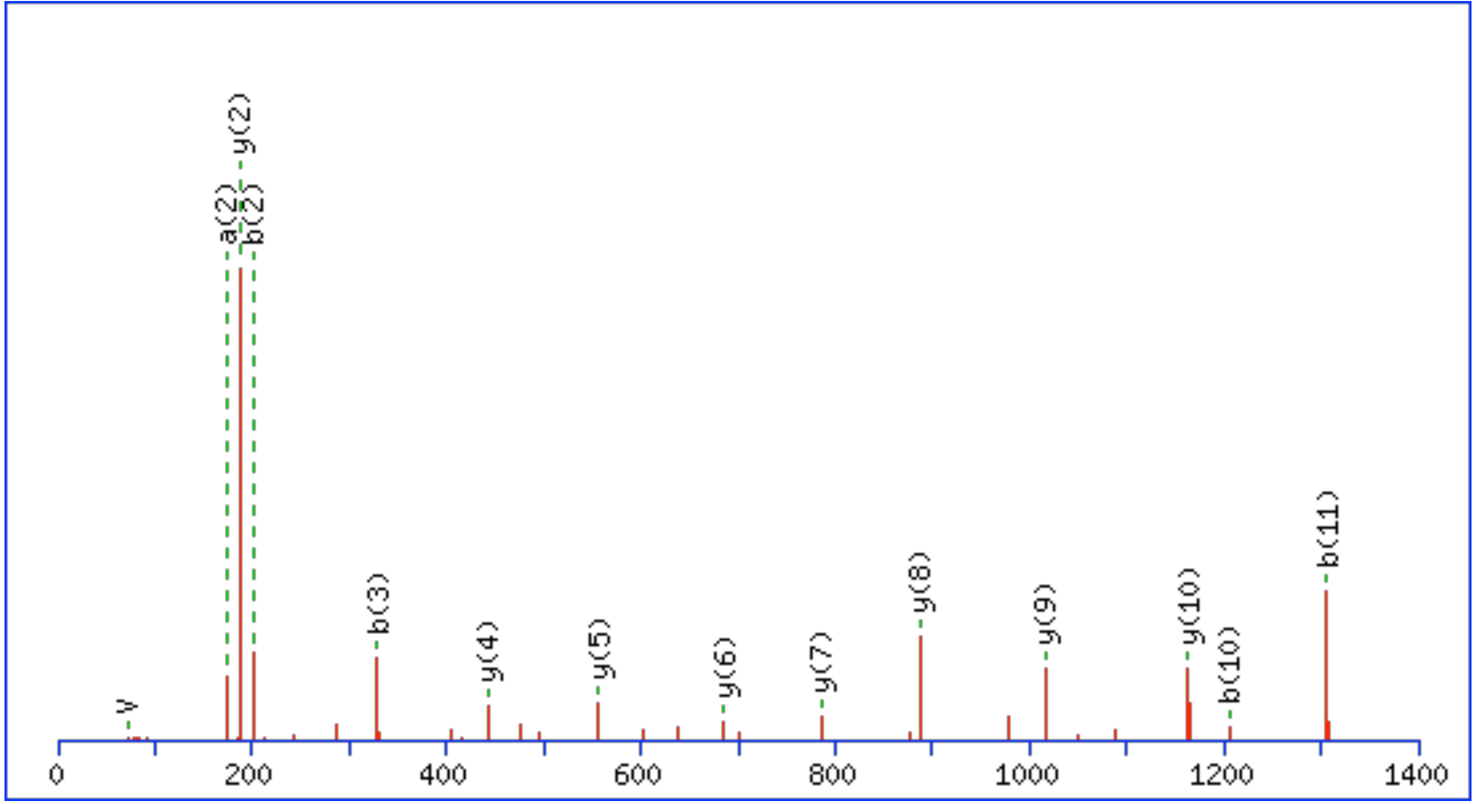
Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
QF	248.1394	276.1343	**QFE**	377.1819	405.1769	**QFET**	478.2296	506.2245
QFETT	579.2773	607.2722	**FE**	249.1234	277.1183	**FET**	350.1710	378.1660
FETT	451.2187	479.2136	**FETTQ**	579.2773	607.2722	**FETTQD**	694.3042	722.2992
ET	203.1026	231.0975	**ETT**	304.1503	332.1452	**ETTQ**	432.2089	460.2038
ETTQD	547.2358	575.2307	**TT**	175.1077	203.1026	**TTQ**	303.1663	331.1612
TTQD	418.1932	446.1882	**TTQDR**	574.2944	602.2893	**TTQDRV**	673.3628	701.3577
TQ	202.1186	230.1135	**TQD**	317.1456	345.1405	**TQDR**	473.2467	501.2416

TQDRV	572.3151	600.3100	**TQDRVP**	669.3679	697.3628	**QD**	216.0979	244.0928
QDR	372.1990	400.1939	**QDRV**	471.2674	499.2623	**QDRVP**	568.3202	596.3151
DR	244.1404	272.1353	**DRV**	343.2088	371.2037	**DRVP**	440.2616	468.2565
RV	228.1819	256.1768	**RVP**	325.2347	353.2296	**VP**	169.1335	197.1285



MS/MS Fragmentation of **SLQFETTQDRVPA**
Found in **XP_001175944**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].

Match to Query 225: 1490.442448 from(746.228500,2+) intensity(1765.4166)
Data file Maldi_All.mgf



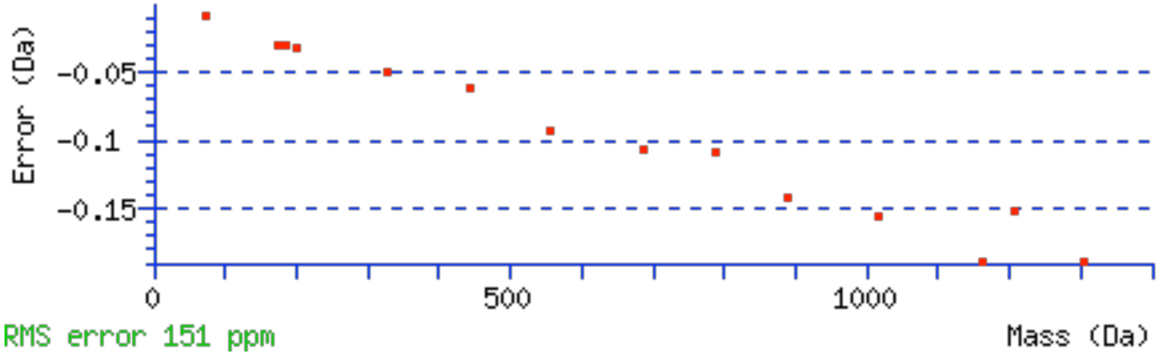
Monoisotopic mass of neutral peptide Mr(calc): 1490.7365 **Ions Score:** 80 **Expect:** 0.0002 **Matches (Bold Red):** 14/205 fragment ions using 17 most intense peaks

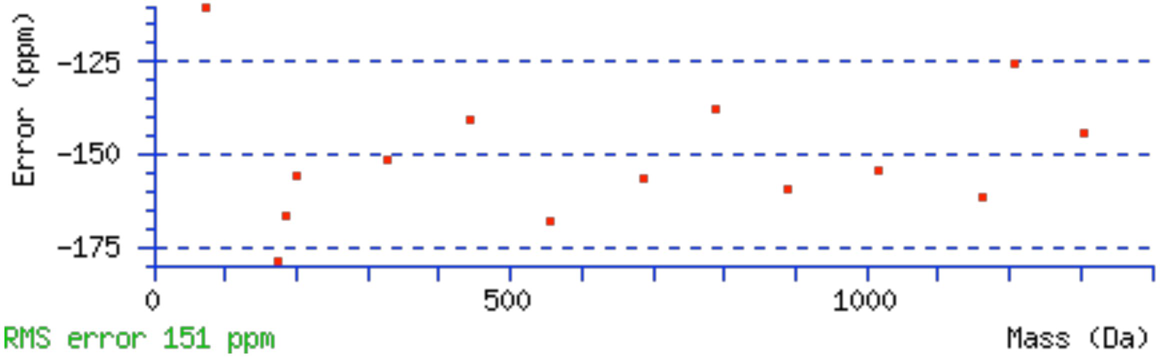
#	Immon.	a	a*	a^{0}	b	b*	b^{0}	d	Seq.	v	w	w'	y	y*	y^{0}	#
1	60.0444	60.0444		42.0338	88.0393		70.0287		S							13

2	86.0964	**173.1285**		155.1179	**201.1234**		183.1128		**L**	1346.6335	1345.6383		1404.7118	1387.6852	1386.7012	**12**
3	101.0709	301.1870	284.1605	283.1765	**329.1819**	312.1554	311.1714		**Q**	1218.5749	1217.5797		1291.6277	1274.6012	1273.6171	**11**
4	120.0808	448.2554	431.2289	430.2449	476.2504	459.2238	458.2398		**F**	1071.5065			**1163.5691**	1146.5426	1145.5586	**10**
5	102.0550	577.2980	560.2715	559.2875	605.2930	588.2664	587.2824		**E**	942.4639	941.4687		**1016.5007**	999.4742	998.4902	**9**
6	74.0600	678.3457	661.3192	660.3352	706.3406	689.3141	688.3301		**T**	841.4163	854.4367	856.4159	**887.4581**	870.4316	869.4476	**8**
7	74.0600	779.3934	762.3668	761.3828	807.3883	790.3618	789.3777		**T**	740.3686	753.3890	755.3682	**786.4104**	769.3839	768.3999	**7**
8	101.0709	907.4520	890.4254	889.4414	935.4469	918.4203	917.4363		**Q**	612.3100	611.3148		**685.3628**	668.3362	667.3522	**6**
9	88.0393	1022.4789	1005.4524	1004.4684	1050.4738	1033.4473	1032.4633		**D**	497.2831	496.2878		**557.3042**	540.2776	539.2936	**5**
10	129.1135	1178.5800	1161.5535	1160.5695	**1206.5749**	1189.5484	1188.5644	1093.5160	**R**	341.1819	340.1867		**442.2772**	425.2507		**4**
11	**72.0808**	1277.6484	1260.6219	1259.6379	**1305.6434**	1288.6168	1287.6328	1263.6328	**V**				286.1761			**3**
12	70.0651	1374.7012	1357.6747	1356.6906	1402.6961	1385.6696	1384.6856	1348.6856	**P**				**187.1077**			**2**
13	44.0495								**A**				90.0550			**1**

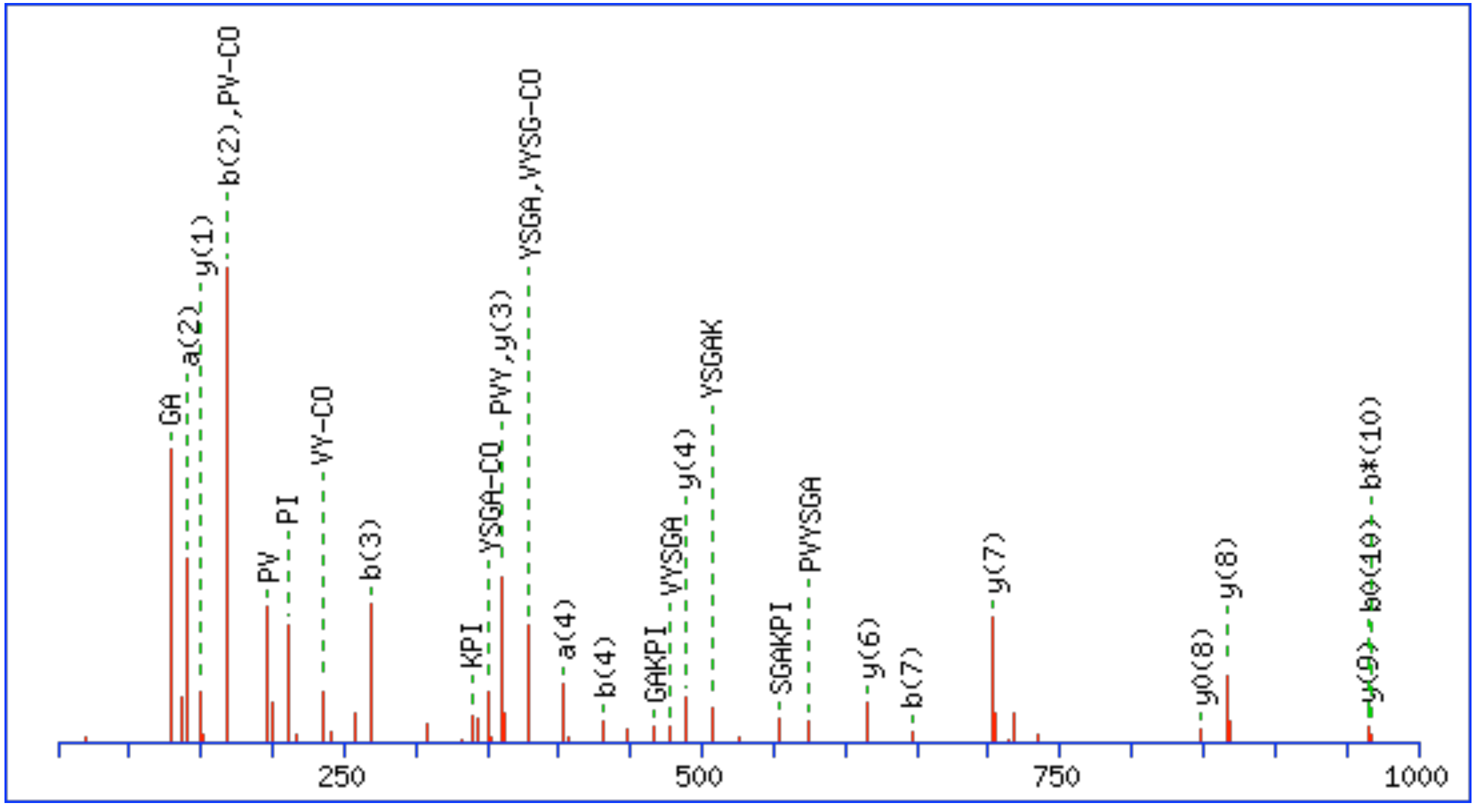
Seq	**ya**	**yb**	**Seq**	**ya**	**yb**	**Seq**	**ya**	**yb**
LQ	214.1550	242.1499	**LQF**	361.2234	389.2183	**LQFE**	490.2660	518.2609
LQFET	591.3137	619.3086	**LQFETT**	692.3614	720.3563	**QF**	248.1394	276.1343
QFE	377.1819	405.1769	**QFET**	478.2296	506.2245	**QFETT**	579.2773	607.2722

FE	249.1234	277.1183	**FET**	350.1710	378.1660	**FETT**	451.2187	479.2136
FETTQ	579.2773	607.2722	**FETTQD**	694.3042	722.2992	**ET**	203.1026	231.0975
ETT	304.1503	332.1452	**ETTQ**	432.2089	460.2038	**ETTQD**	547.2358	575.2307
TT	175.1077	203.1026	**TTQ**	303.1663	331.1612	**TTQD**	418.1932	446.1882
TTQDR	574.2944	602.2893	**TTQDRV**	673.3628	701.3577	**TQ**	202.1186	230.1135
TQD	317.1456	345.1405	**TQDR**	473.2467	501.2416	**TQDRV**	572.3151	600.3100
TQDRVP	669.3679	697.3628	**QD**	216.0979	244.0928	**QDR**	372.1990	400.1939
QDRV	471.2674	499.2623	**QDRVP**	568.3202	596.3151	**DR**	244.1404	272.1353
DRV	343.2088	371.2037	**DRVP**	440.2616	468.2565	**RV**	228.1819	256.1768
RVP	325.2347	353.2296	**VP**	169.1335	197.1285			





MS/MS Fragmentation of **APVYSGAKPIM**
Found in **XP_799858**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
Match to Query 105: 1132.374248 from(567.194400,2+) intensity(766.4834)
Data file Maldi_All.mgf

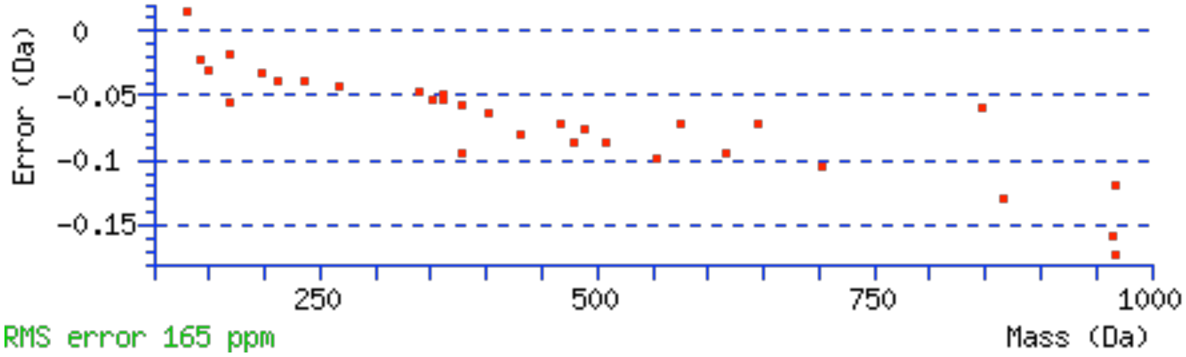


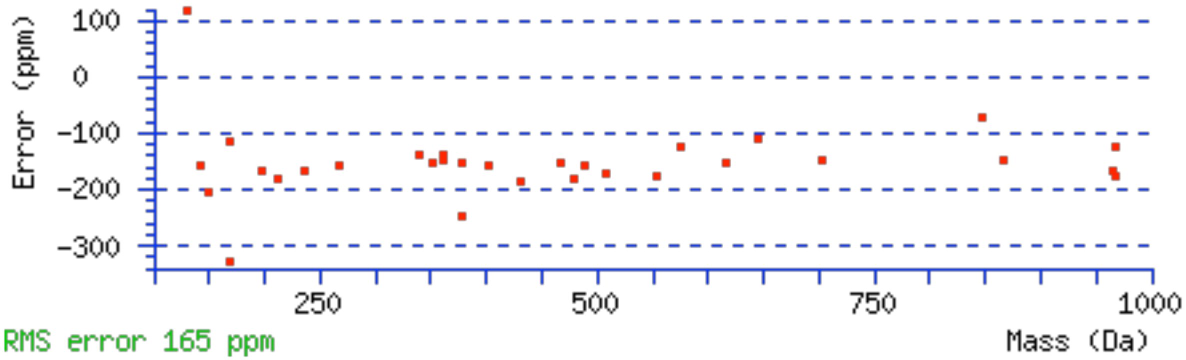
Monoisotopic mass of neutral peptide Mr(calc): 1132.5950 **Ions Score:** 62 **Expect:** 0.012 **Matches (Bold Red):** 32/133 fragment ions using 33 most intense peaks

#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	y	y*	y^0	#
1	44.0495	44.0495			72.0444			A				11
2	70.0651	**141.1022**			**169.0972**			P	1062.5652	1045.5387	1044.5547	10
3	72.0808	240.1707			**268.1656**			V	**965.5125**	948.4859	947.5019	9
4	136.0757	**403.2340**			**431.2289**			Y	**866.4441**	849.4175	**848.4335**	8

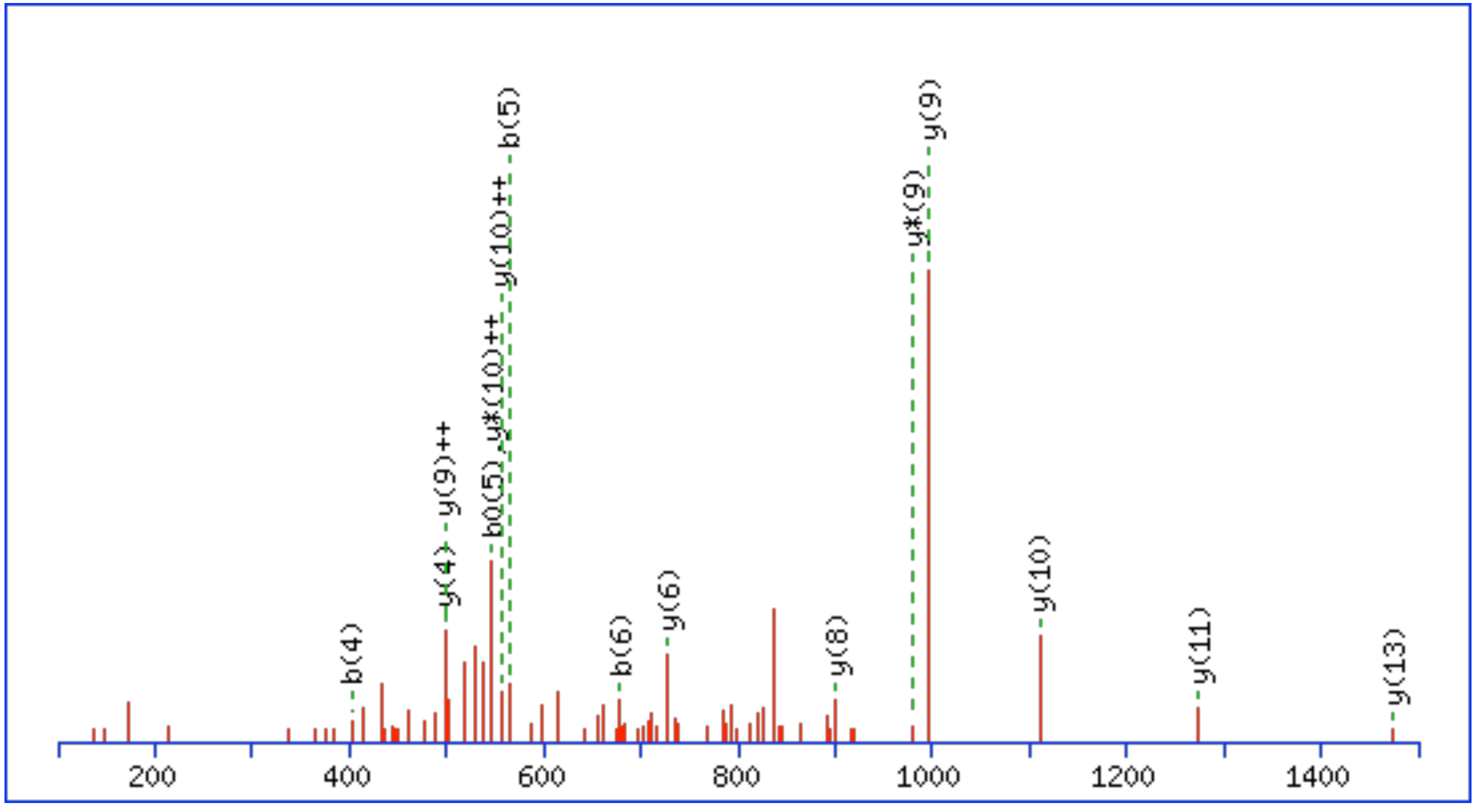
5	60.0444	490.2660		472.2554	518.2609		500.2504	**S**	**703.3807**	686.3542	685.3702	**7**
6	30.0338	547.2875		529.2769	**575.2824**		557.2718	**G**	**616.3487**	599.3221		**6**
7	44.0495	618.3246		600.3140	**646.3195**		628.3089	**A**	559.3272	542.3007		**5**
8	101.1073	746.4196	729.3930	728.4090	774.4145	757.3879	756.4039	**K**	**488.2901**	471.2636		**4**
9	70.0651	843.4723	826.4458	825.4618	871.4672	854.4407	853.4567	**P**	**360.1952**			**3**
10	86.0964	956.5564	939.5298	938.5458	984.5513	**967.5247**	**966.5407**	**I**	263.1424			**2**
11	104.0528							**M**	**150.0583**			**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PV	**169.1335**	**197.1285**	**PVY**	332.1969	**360.1918**	**PVYS**	419.2289	447.2238
PVYSG	476.2504	504.2453	**PVYSGA**	547.2875	**575.2824**	**PVYSGAK**	675.3824	703.3774
VY	**235.1441**	263.1390	**VYS**	322.1761	350.1710	**VYSG**	**379.1976**	407.1925
VYSGA	450.2347	**478.2296**	**VYSGAK**	578.3297	606.3246	**VYSGAKP**	675.3824	703.3774
YS	223.1077	251.1026	**YSG**	280.1292	308.1241	**YSGA**	**351.1663**	**379.1612**
YSGAK	479.2613	**507.2562**	**YSGAKP**	576.3140	604.3089	**YSGAKPI**	689.3981	717.3930
SG	117.0659	145.0608	**SGA**	188.1030	216.0979	**SGAK**	316.1979	344.1928
SGAKP	413.2507	441.2456	**SGAKPI**	526.3348	**554.3297**	**GA**	101.0709	**129.0659**
GAK	229.1659	257.1608	**GAKP**	326.2187	354.2136	**GAKPI**	439.3027	**467.2976**
AK	172.1444	200.1394	**AKP**	269.1972	297.1921	**AKPI**	382.2813	410.2762
KP	198.1601	226.1550	**KPI**	311.2442	**339.2391**	**PI**	183.1492	**211.1441**





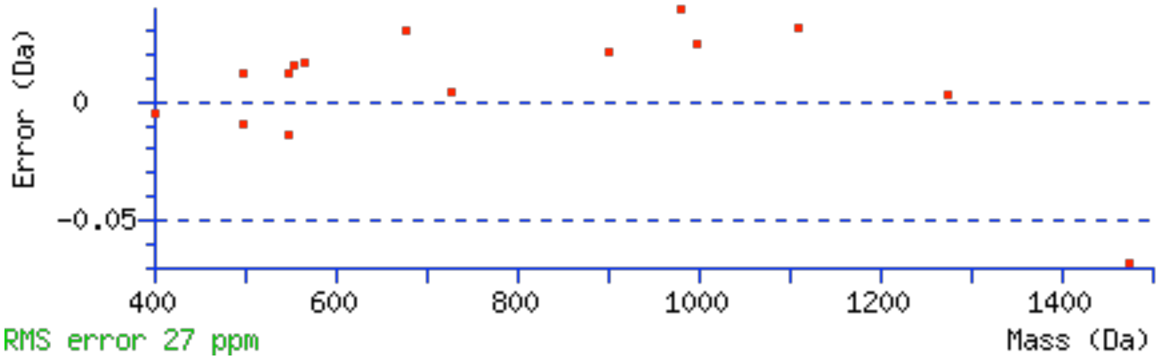
MS/MS Fragmentation of **SINSYLPGDMVRHVS**
Found in **XP_799858**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
Match to Query 695: 1673.826648 from(837.920600,2+) intensity(119524.0000)
Title: Cmpd 155, +MSn(838.4670), 28.2 min
Data file Qtof_all.mgf

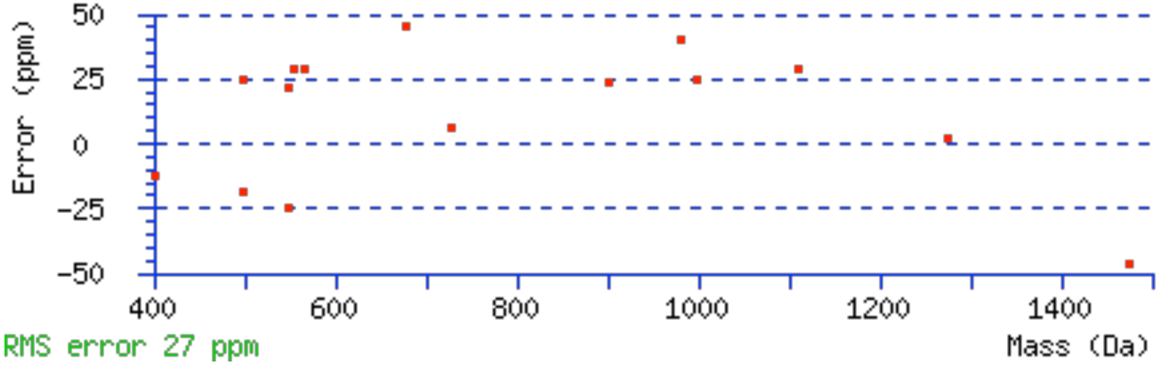


Monoisotopic mass of neutral peptide Mr(calc): 1673.8195 **Ions Score:** 42 **Expect:** 0.76 **Matches (Bold Red):** 15/158 fragment ions using 24 most intense peaks

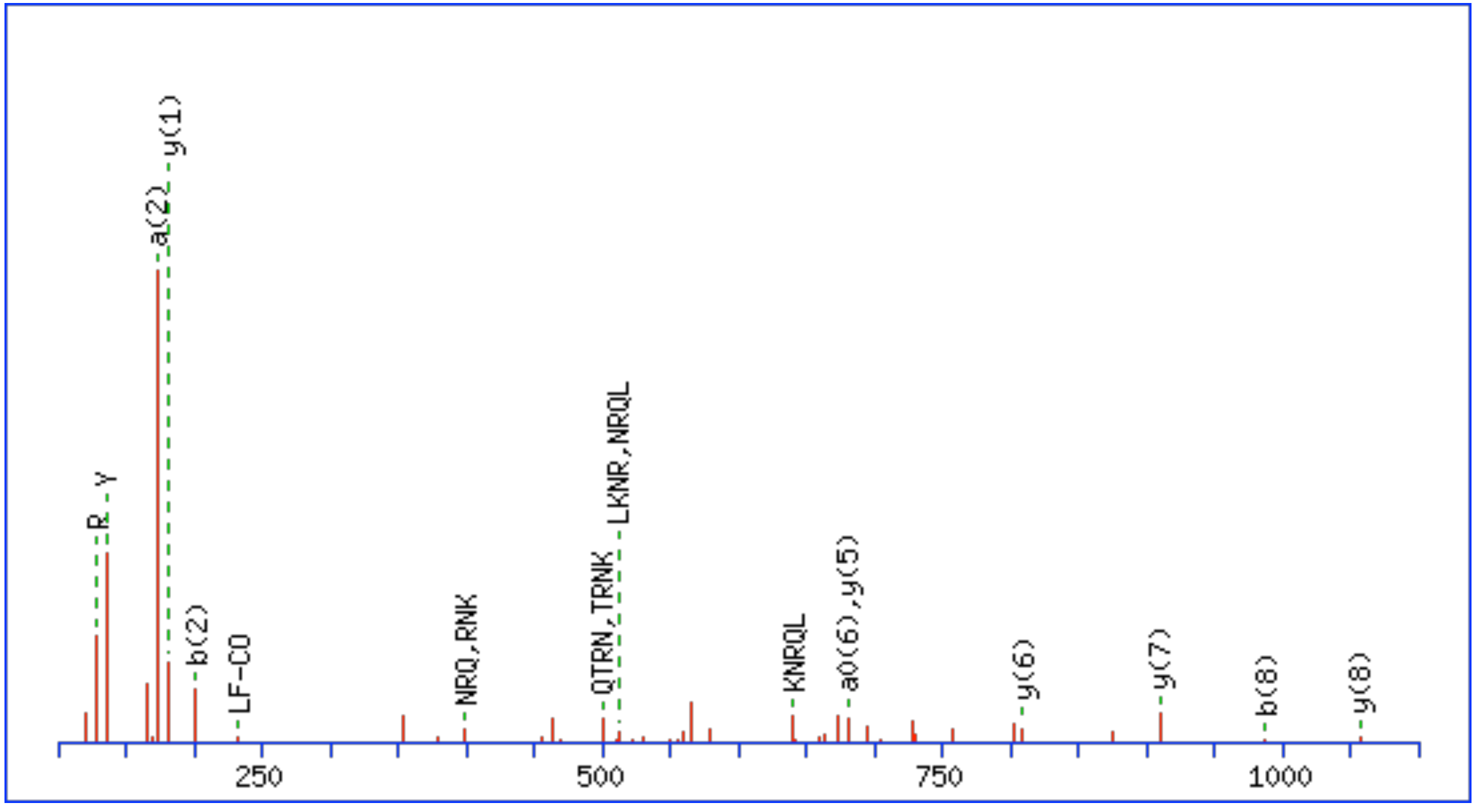
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	**S**							**15**
2	201.1234	101.0653			183.1128	92.0600	**I**	1587.7948	794.4010	1570.7682	785.8878	1569.7842	785.3957	**14**
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	**N**	**1474.7107**	737.8590	1457.6842	729.3457	1456.7002	728.8537	**13**
4	**402.1983**	201.6028	385.1718	193.0895	384.1878	192.5975	**S**	1360.6678	680.8375	1343.6412	672.3243	1342.6572	671.8323	**12**

5	**565.2617**	283.1345	548.2351	274.6212	**547.2511**	274.1292	**Y**	**1273.6358**	637.3215	1256.6092	628.8082	1255.6252	628.3162	**11**
6	**678.3457**	339.6765	661.3192	331.1632	660.3352	330.6712	**L**	**1110.5724**	**555.7899**	1093.5459	**547.2766**	1092.5619	546.7846	**10**
7	775.3985	388.2029	758.3719	379.6896	757.3879	379.1976	**P**	**997.4884**	**499.2478**	**980.4618**	490.7346	979.4778	490.2425	**9**
8	832.4199	416.7136	815.3934	408.2003	814.4094	407.7083	**G**	**900.4356**	450.7214	883.4091	442.2082	882.4250	441.7162	**8**
9	947.4469	474.2271	930.4203	465.7138	929.4363	465.2218	**D**	843.4141	422.2107	826.3876	413.6974	825.4036	413.2054	**7**
10	1078.4874	539.7473	1061.4608	531.2340	1060.4768	530.7420	**M**	**728.3872**	364.6972	711.3607	356.1840	710.3766	355.6920	**6**
11	1177.5558	589.2815	1160.5292	580.7683	1159.5452	580.2762	**V**	597.3467	299.1770	580.3202	290.6637	579.3362	290.1717	**5**
12	1333.6569	667.3321	1316.6303	658.8188	1315.6463	658.3268	**R**	**498.2783**	249.6428	481.2518	241.1295	480.2677	240.6375	**4**
13	1470.7158	735.8615	1453.6893	727.3483	1452.7052	726.8563	**H**	342.1772	171.5922			324.1666	162.5870	**3**
14	1569.7842	785.3957	1552.7577	776.8825	1551.7737	776.3905	**V**	205.1183	103.0628			187.1077	94.0575	**2**
15							**S**	106.0499	53.5286			88.0393	44.5233	**1**





MS/MS Fragmentation of **SLKNRQLFTQTRNKY**
Found in **XP_799858**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
Match to Query 332: 1895.491696 from(474.880200,4+) intensity(558.8305)
Data file Maldi_All.mgf



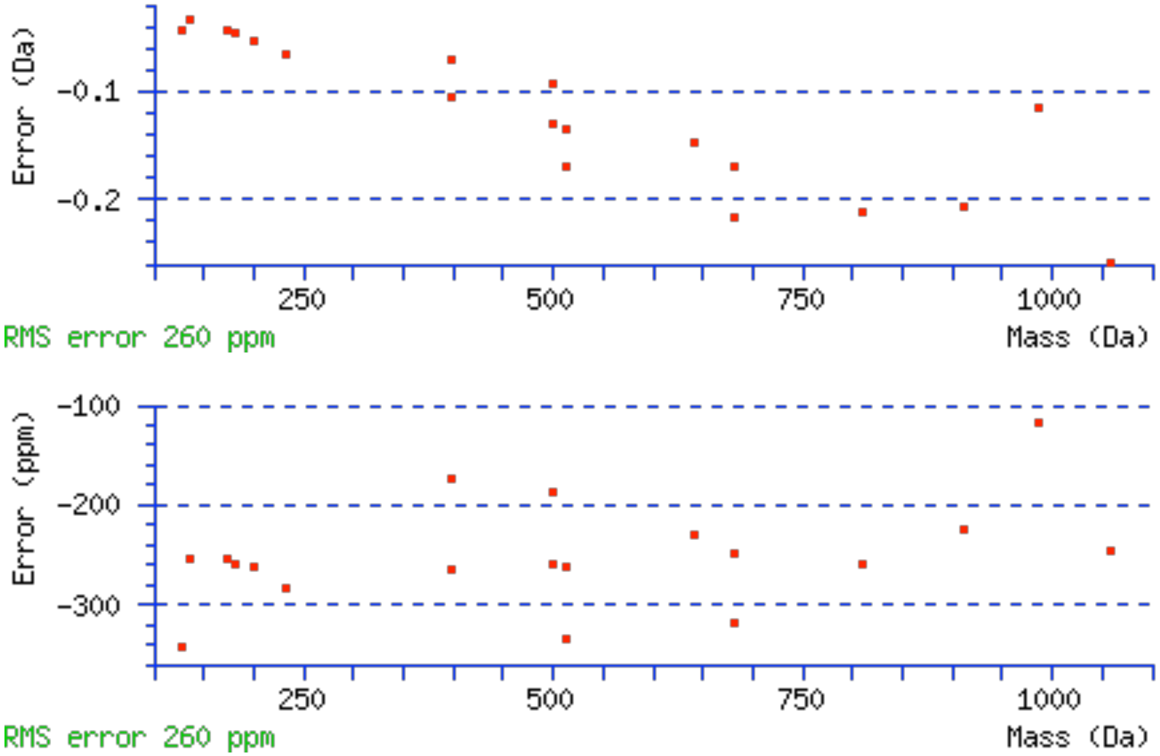
Monoisotopic mass of neutral peptide Mr(calc): 1896.0329 **Ions Score:** 18 **Expect:** 4.1e+02 **Matches (Bold Red):** 22/251 fragment ions using 29 most intense peaks

#	Immon.	a	a*	a^0	b	b*	b^0	d	d'	Seq.	v	w	w'	y	y*	y^0	#
1	60.0444	60.0444		42.0338	88.0393		70.0287			S							15
2	86.0964	**173.1285**		155.1179	**201.1234**		183.1128			L	1751.9300	1750.9347		1810.0082	1792.9817	1791.9977	14

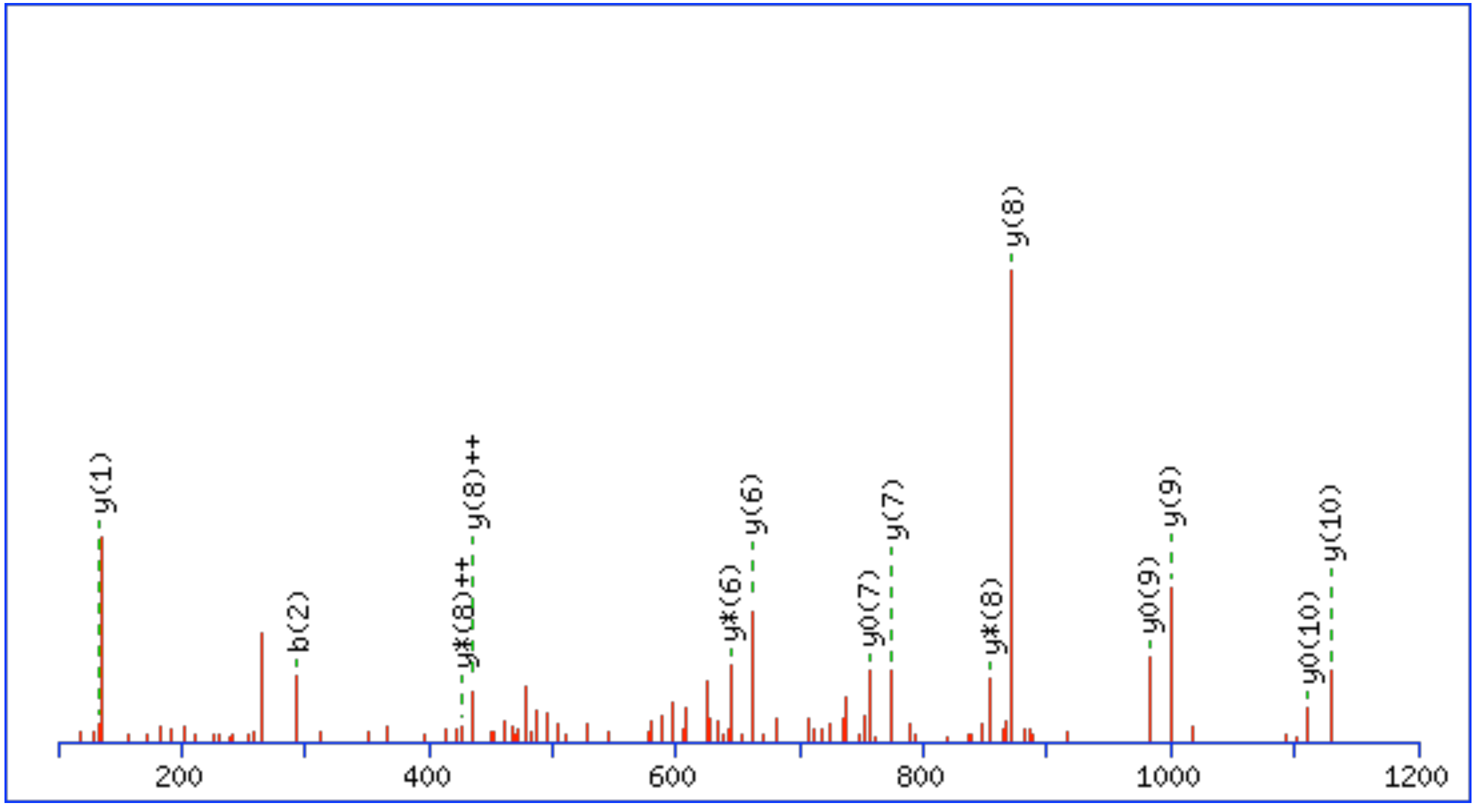
3	101.1073	301.2234	284.1969	283.2129	329.2183	312.1918	311.2078			**K**	1623.8350	1622.8398		1696.9242	1679.8976	1678.9136	**13**
4	87.0553	415.2663	398.2398	397.2558	443.2613	426.2347	425.2507			**N**	1509.7921	1508.7968		1568.8292	1551.8027	1550.8186	**12**
5	**129.1135**	571.3675	554.3409	553.3569	599.3624	582.3358	581.3518	486.3035		**R**	1353.6910	1352.6957		1454.7863	1437.7597	1436.7757	**11**
6	101.0709	699.4260	682.3995	**681.4155**	727.4209	710.3944	709.4104	642.4046		**Q**	1225.6324	1224.6372		1298.6852	1281.6586	1280.6746	**10**
7	86.0964	812.5101	795.4835	794.4995	840.5050	823.4785	822.4944	770.4631		**L**	1112.5483	1111.5531		1170.6266	1153.6000	1152.6160	**9**
8	120.0808	959.5785	942.5520	941.5679	**987.5734**	970.5469	969.5629			**F**	965.4799			**1057.5425**	1040.5160	1039.5320	**8**
9	74.0600	1060.6262	1043.5996	1042.6156	1088.6211	1071.5946	1070.6105	1044.6313	1046.6105	**T**	864.4322	877.4526	879.4319	**910.4741**	893.4476	892.4635	**7**
10	101.0709	1188.6848	1171.6582	1170.6742	1216.6797	1199.6531	1198.6691	1131.6633		**Q**	736.3737	735.3784		**809.4264**	792.3999	791.4159	**6**
11	74.0600	1289.7324	1272.7059	1271.7219	1317.7274	1300.7008	1299.7168	1273.7375	1275.7168	**T**	635.3260	648.3464	650.3257	**681.3679**	664.3413	663.3573	**5**
12	**129.1135**	1445.8336	1428.8070	1427.8230	1473.8285	1456.8019	1455.8179	1360.7696		**R**	479.2249	478.2296		580.3202	563.2936		**4**
13	87.0553	1559.8765	1542.8499	1541.8659	1587.8714	1570.8449	1569.8608	1516.8707		**N**				424.2191	407.1925		**3**
14	101.1073	1687.9714	1670.9449	1669.9609	1715.9664	1698.9398	1697.9558	1630.9136		**K**				310.1761	293.1496		**2**
15	**136.0757**									**Y**				**182.0812**			**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
LK	214.1914	242.1863	**LKN**	328.2343	356.2292	**LKNR**	484.3354	**512.3303**

LKNRQ	612.3940	**640.3889**	**KN**	215.1503	243.1452	**KNR**	371.2514	**399.2463**
KNRQ	499.3099	527.3049	**KNRQL**	612.3940	**640.3889**	**NR**	243.1564	271.1513
NRQ	371.2150	**399.2099**	**NRQL**	484.2990	**512.2940**	**NRQLF**	631.3675	659.3624
RQ	257.1721	285.1670	**RQL**	370.2561	398.2510	**RQLF**	517.3245	545.3194
RQLFT	618.3722	646.3671	**QL**	214.1550	242.1499	**QLF**	361.2234	389.2183
QLFT	462.2711	490.2660	**QLFTQ**	590.3297	618.3246	**QLFTQT**	691.3774	719.3723
LF	**233.1648**	261.1598	**LFT**	334.2125	362.2074	**LFTQ**	462.2711	490.2660
LFTQT	563.3188	591.3137	**FT**	221.1285	249.1234	**FTQ**	349.1870	377.1819
FTQT	450.2347	478.2296	**FTQTR**	606.3358	634.3307	**TQ**	202.1186	230.1135
TQT	303.1663	331.1612	**TQTR**	459.2674	487.2623	**TQTRN**	573.3103	601.3053
QT	202.1186	230.1135	**QTR**	358.2197	386.2146	**QTRN**	472.2627	**500.2576**
QTRNK	600.3576	628.3525	**TR**	230.1612	258.1561	**TRN**	344.2041	372.1990
TRNK	472.2990	**500.2940**	**RN**	243.1564	271.1513	**RNK**	371.2514	**399.2463**
NK	215.1503	243.1452						



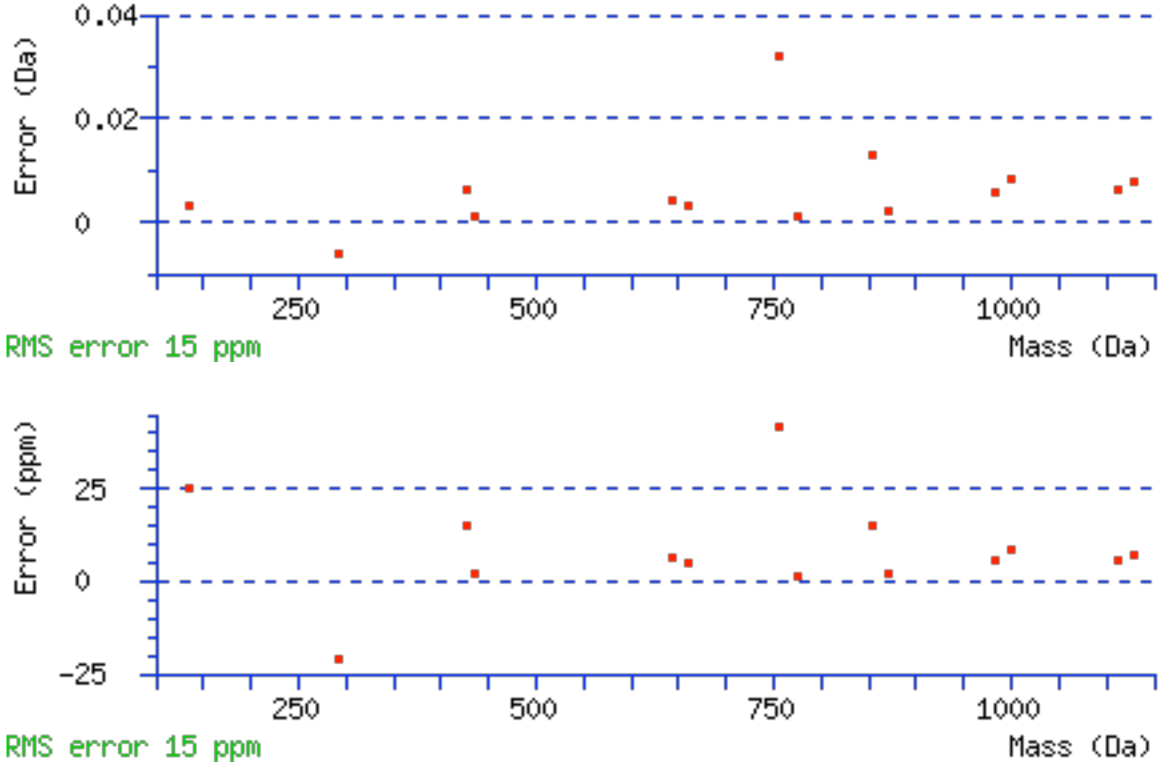
MS/MS Fragmentation of **YEEPIRQEGGD**
Found in **XP_001175555**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
Match to Query 475: 1291.590148 from(646.802350,2+) intensity(613940.0000)
Title: Cmpd 86, +MSn(647.1935), 23.1 min
Data file Qtof_all.mgf



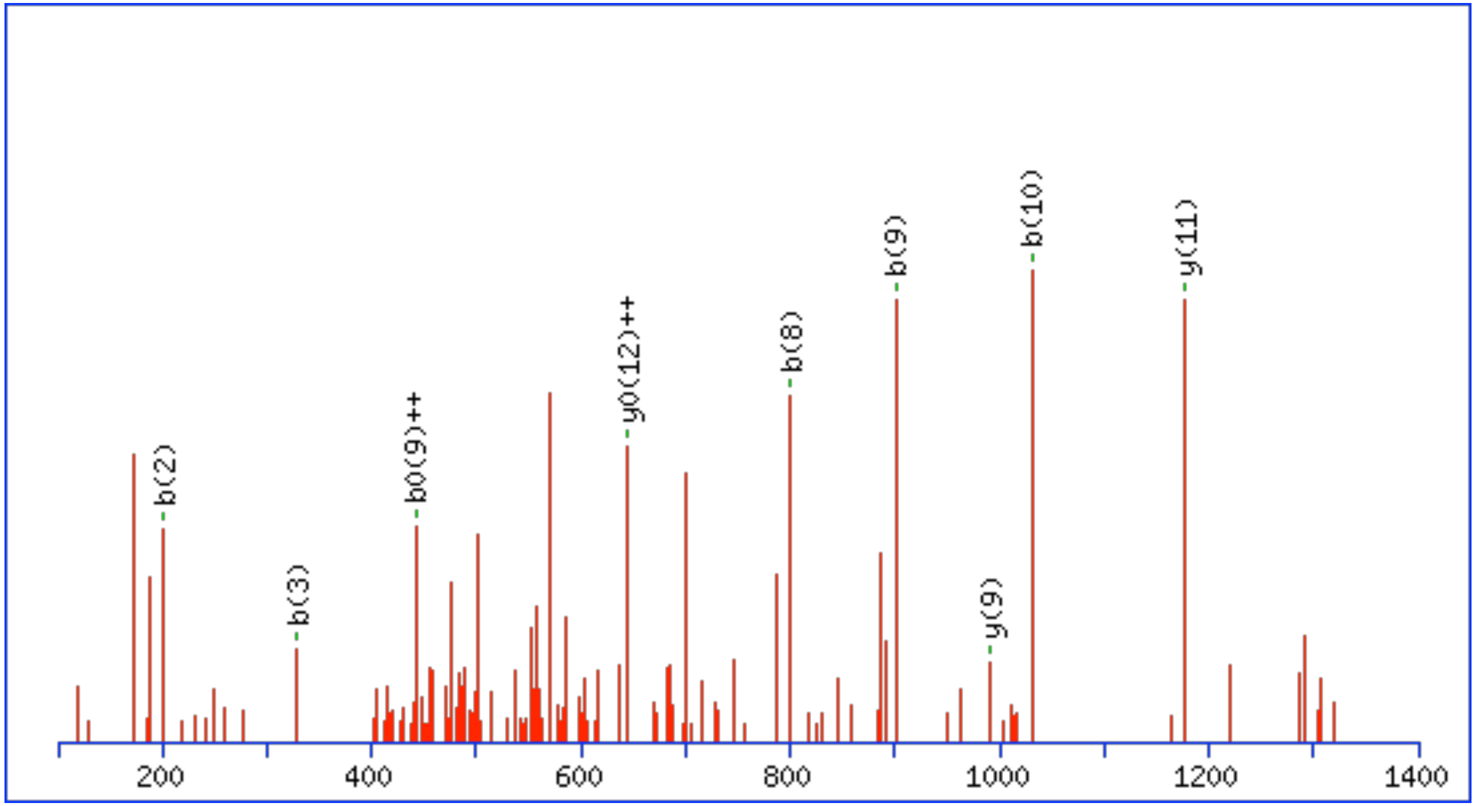
Monoisotopic mass of neutral peptide Mr(calc): 1291.5680 **Ions Score:** 39 **Expect:** 1.7 **Matches (Bold Red):** 14/100 fragment ions using 25 most intense peaks

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	164.0706	82.5389					Y							11
2	**293.1132**	147.0602			275.1026	138.0550	E	**1129.5120**	565.2596	1112.4855	556.7464	**1111.5014**	556.2544	10
3	422.1558	211.5815			404.1452	202.5763	E	**1000.4694**	500.7383	983.4429	492.2251	**982.4588**	491.7331	9
4	519.2086	260.1079			501.1980	251.1026	P	**871.4268**	**436.2170**	**854.4003**	**427.7038**	853.4163	427.2118	8

5	632.2926	316.6499			614.2821	307.6447	**I**	**774.3741**	387.6907	757.3475	379.1774	**756.3635**	378.6854	**7**
6	788.3937	394.7005	771.3672	386.1872	770.3832	385.6952	**R**	**661.2900**	331.1486	**644.2634**	322.6354	643.2794	322.1434	**6**
7	916.4523	458.7298	899.4258	450.2165	898.4417	449.7245	**Q**	505.1889	253.0981	488.1623	244.5848	487.1783	244.0928	**5**
8	1045.4949	523.2511	1028.4684	514.7378	1027.4843	514.2458	**E**	377.1303	189.0688			359.1197	180.0635	**4**
9	1102.5164	551.7618	1085.4898	543.2485	1084.5058	542.7565	**G**	248.0877	124.5475			230.0771	115.5422	**3**
10	1159.5378	580.2726	1142.5113	571.7593	1141.5273	571.2673	**G**	191.0662	96.0368			173.0557	87.0315	**2**
11							**D**	**134.0448**	67.5260			116.0342	58.5207	**1**



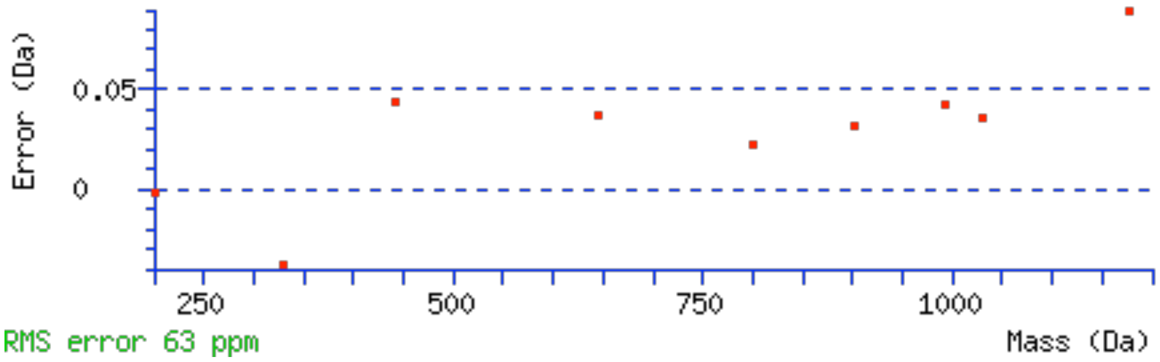
MS/MS Fragmentation of **SIKADGEVTEDVDK**
Found in **XP_001188391**, PREDICTED: similar to arginine/serine-rich splicing factor 4 [Strongylocentrotus purpuratus].
Match to Query 633: 1504.763968 from(753.389260,2+) intensity(556664.0000)
Title: Cmpd 152, +MSn(753.7278), 28.1 min
Data file Qtof_all.mgf

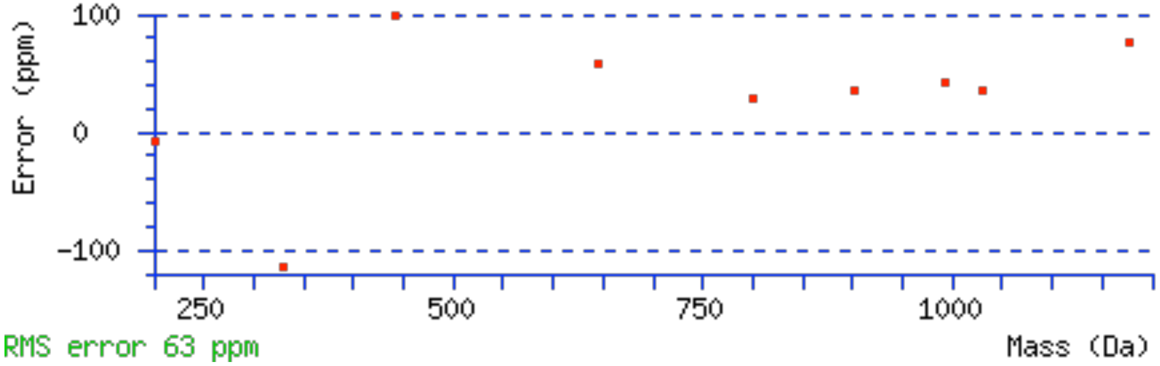


Monoisotopic mass of neutral peptide Mr(calc): 1504.7257 **Ions Score:** 21 **Expect:** 1e+02 **Matches (Bold Red):** 9/150 fragment ions using 14 most intense peaks

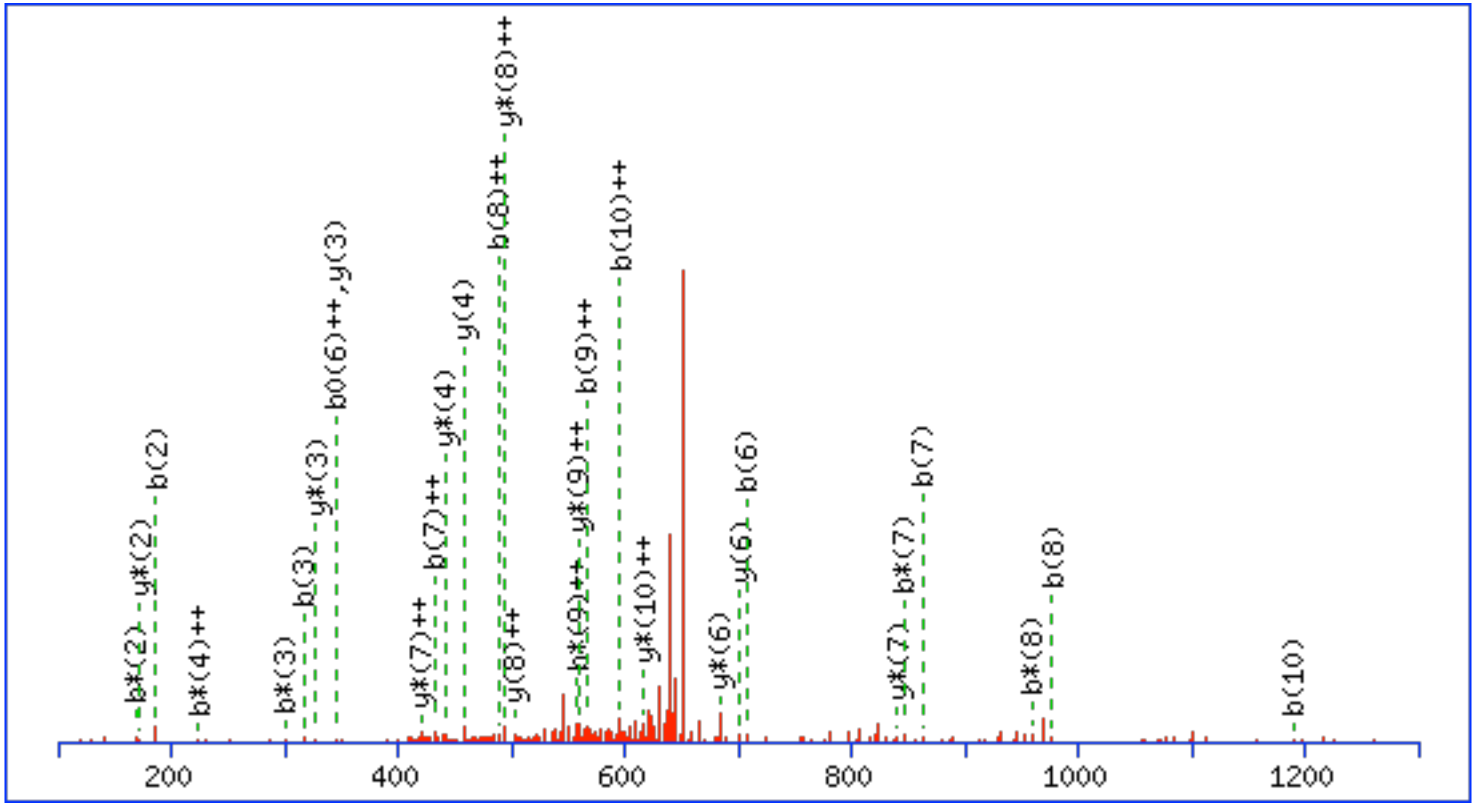
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							14
2	**201.1234**	101.0653			183.1128	92.0600	I	1418.7009	709.8541	1401.6744	701.3408	1400.6904	700.8488	13
3	**329.2183**	165.1128	312.1918	156.5995	311.2078	156.1075	K	1305.6169	653.3121	1288.5903	644.7988	1287.6063	**644.3068**	12
4	400.2554	200.6314	383.2289	192.1181	382.2449	191.6261	A	**1177.5219**	589.2646	1160.4954	580.7513	1159.5113	580.2593	11

5	515.2824	258.1448	498.2558	249.6316	497.2718	249.1395	**D**	1106.4848	553.7460	1089.4582	545.2328	1088.4742	544.7408	**10**
6	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	**G**	**991.4578**	496.2326	974.4313	487.7193	973.4473	487.2273	**9**
7	701.3464	351.1769	684.3199	342.6636	683.3359	342.1716	**E**	934.4364	467.7218	917.4098	459.2086	916.4258	458.7165	**8**
8	**800.4149**	400.7111	783.3883	392.1978	782.4043	391.7058	**V**	805.3938	403.2005	788.3672	394.6873	787.3832	394.1953	**7**
9	**901.4625**	451.2349	884.4360	442.7216	883.4520	**442.2296**	**T**	706.3254	353.6663	689.2988	345.1531	688.3148	344.6610	**6**
10	**1030.5051**	515.7562	1013.4786	507.2429	1012.4946	506.7509	**E**	605.2777	303.1425	588.2511	294.6292	587.2671	294.1372	**5**
11	1145.5321	573.2697	1128.5055	564.7564	1127.5215	564.2644	**D**	476.2351	238.6212	459.2086	230.1079	458.2245	229.6159	**4**
12	1244.6005	622.8039	1227.5739	614.2906	1226.5899	613.7986	**V**	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	**3**
13	1359.6274	680.3174	1342.6009	671.8041	1341.6169	671.3121	**D**	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	**2**
14							**K**	147.1128	74.0600	130.0863	65.5468			**1**





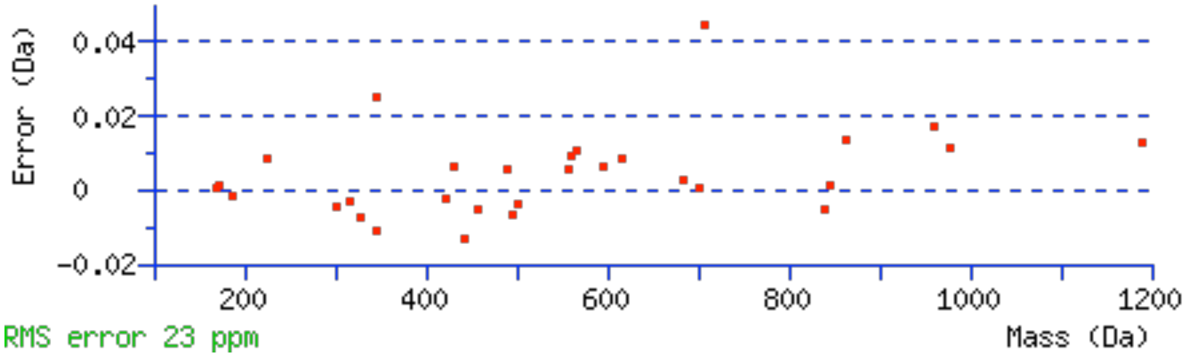
MS/MS Fragmentation of **ANMFRSRLRGN**
Found in **XP_001188391**, PREDICTED: similar to arginine/serine-rich splicing factor 4 [Strongylocentrotus purpuratus].
Match to Query 489: 1319.743788 from(660.879170,2+) intensity(841204.0000)
Title: Cmpd 76, +MSn(661.3308), 22.3 min
Data file Qtof_all.mgf

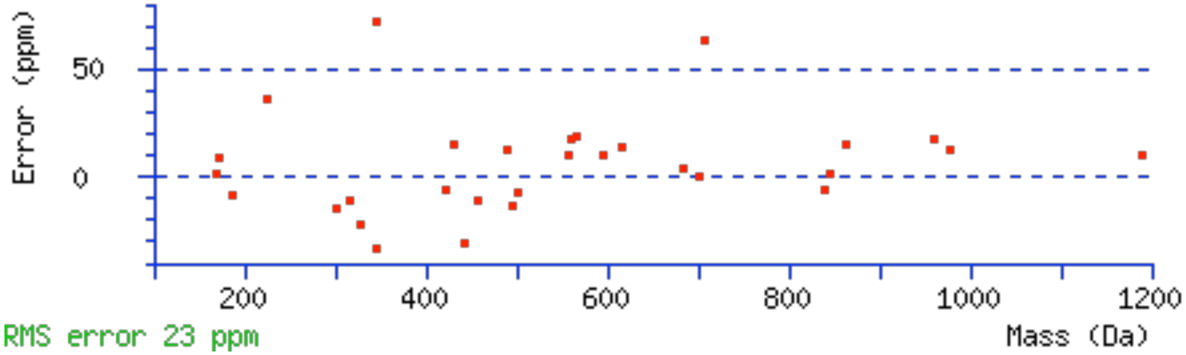


Monoisotopic mass of neutral peptide Mr(calc): 1319.6993 **Variable modifications: C-term :** Amidated (C-term) **Ions Score:** 9 **Expect:** 1.2e+03 **Matches (Bold Red):** 30/98 fragment ions using 104 most intense peaks

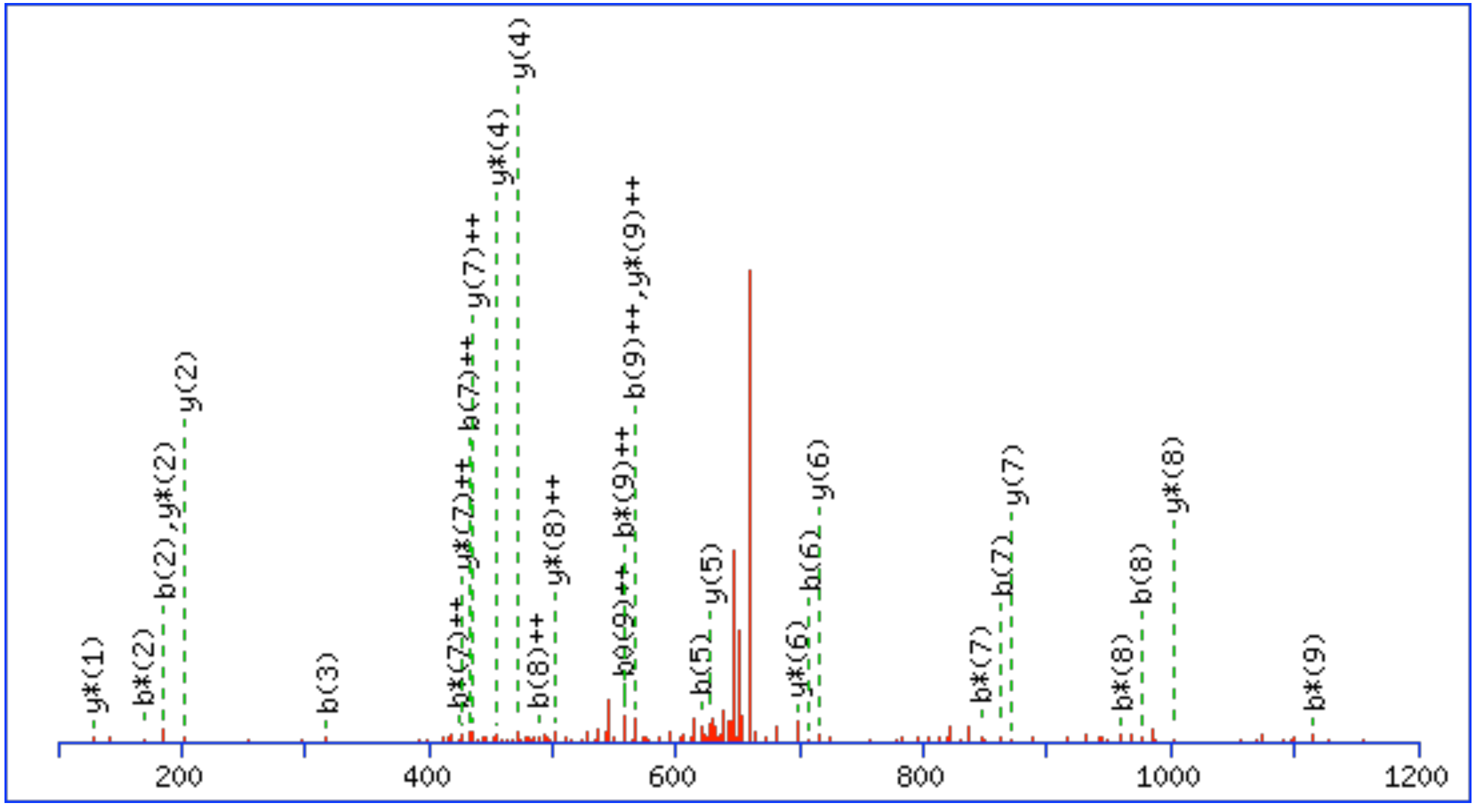
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					**A**							**11**
2	**186.0873**	93.5473	**169.0608**	85.0340			**N**	1249.6695	625.3384	1232.6429	**616.8251**	1231.6589	616.3331	**10**
3	**317.1278**	159.0675	**300.1013**	150.5543			**M**	1135.6265	568.3169	1118.6000	**559.8036**	1117.6160	559.3116	**9**
4	464.1962	232.6017	447.1697	**224.0885**			**F**	1004.5860	**502.7967**	987.5595	**494.2834**	986.5755	493.7914	**8**

5	620.2973	310.6523	603.2708	302.1390			**R**	857.5176	429.2625	**840.4911**	**420.7492**	839.5071	420.2572	**7**
6	**707.3294**	354.1683	690.3028	345.6550	689.3188	**345.1630**	**S**	**701.4165**	351.2119	**684.3900**	342.6986	683.4060	342.2066	**6**
7	**863.4305**	**432.2189**	**846.4039**	423.7056	845.4199	423.2136	**R**	614.3845	307.6959	597.3579	299.1826			**5**
8	**976.5145**	**488.7609**	**959.4880**	480.2476	958.5040	479.7556	**L**	**458.2834**	229.6453	**441.2568**	221.1321			**4**
9	1132.6156	**566.8115**	1115.5891	**558.2982**	1114.6051	557.8062	**R**	**345.1993**	173.1033	**328.1728**	164.5900			**3**
10	**1189.6371**	**595.3222**	1172.6106	586.8089	1171.6265	586.3169	**G**	189.0982	95.0527	**172.0717**	86.5395			**2**
11							**N**	132.0767	66.5420	115.0502	58.0287			**1**





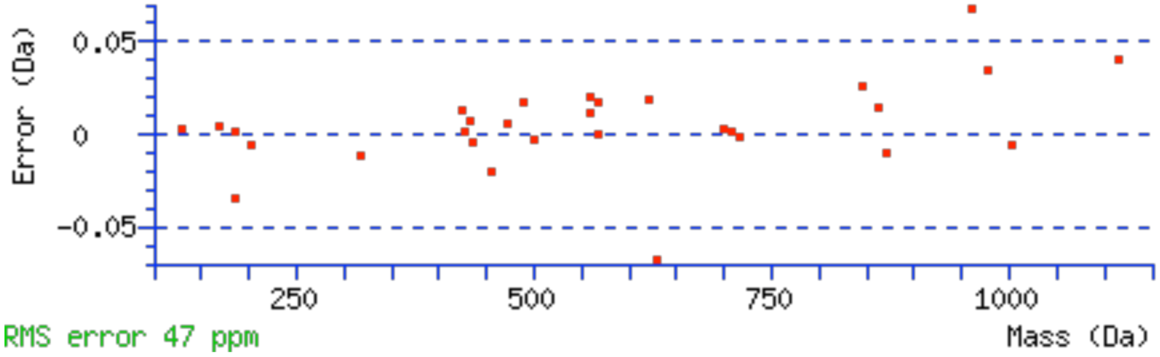
MS/MS Fragmentation of **ANMFRSRLRGK**
Found in **XP_001188391**, PREDICTED: similar to arginine/serine-rich splicing factor 4 [Strongylocentrotus purpuratus].
Match to Query 501: 1333.796708 from(667.905630,2+) intensity(664260.0000)
Title: Cmpd 64, +MSn(668.3428), 21.0 min
Data file Qtof_all.mgf

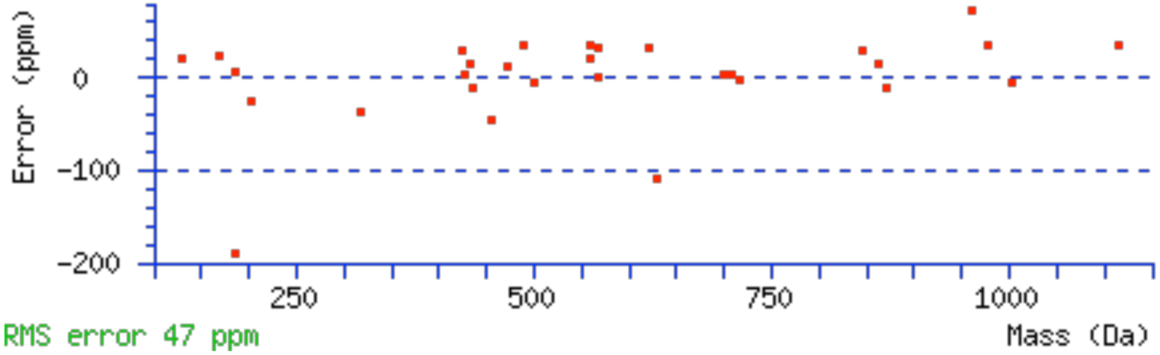


Monoisotopic mass of neutral peptide Mr(calc): 1333.7513 **Variable modifications: C-term :** Amidated (C-term) **Ions Score:** 18 **Expect:** 1e+02 **Matches (Bold Red):** 30/98 fragment ions using 84 most intense peaks

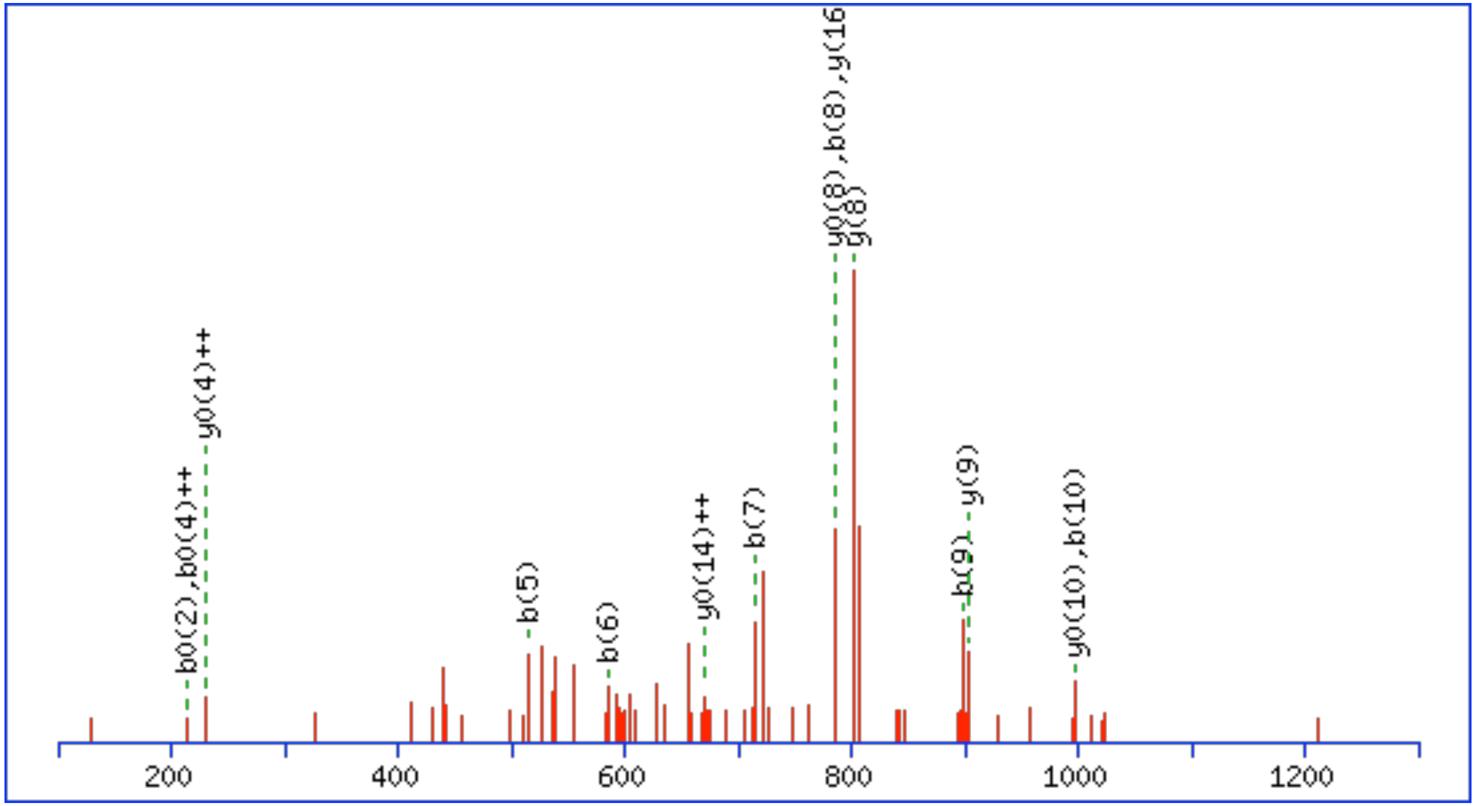
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							11
2	**186.0873**	93.5473	**169.0608**	85.0340			N	1263.7215	632.3644	1246.6949	623.8511	1245.7109	623.3591	10
3	**317.1278**	159.0675	300.1013	150.5543			M	1149.6786	575.3429	1132.6520	**566.8296**	1131.6680	566.3376	9
4	464.1962	232.6017	447.1697	224.0885			F	1018.6381	509.8227	**1001.6115**	**501.3094**	1000.6275	500.8174	8

5	**620.2973**	310.6523	603.2708	302.1390			**R**	**871.5697**	**436.2885**	854.5431	**427.7752**	853.5591	427.2832	**7**
6	**707.3294**	354.1683	690.3028	345.6550	689.3188	345.1630	**S**	**715.4686**	358.2379	**698.4420**	349.7246	697.4580	349.2326	**6**
7	**863.4305**	**432.2189**	**846.4039**	**423.7056**	845.4199	423.2136	**R**	**628.4365**	314.7219	611.4100	306.2086			**5**
8	**976.5145**	**488.7609**	**959.4880**	480.2476	958.5040	479.7556	**L**	**472.3354**	236.6713	**455.3089**	228.1581			**4**
9	1132.6156	**566.8115**	**1115.5891**	**558.2982**	1114.6051	**557.8062**	**R**	359.2514	180.1293	342.2248	171.6160			**3**
10	1189.6371	595.3222	1172.6106	586.8089	1171.6265	586.3169	**G**	**203.1502**	102.0788	**186.1237**	93.5655			**2**
11							**K**	146.1288	73.5680	**129.1022**	65.0548			**1**





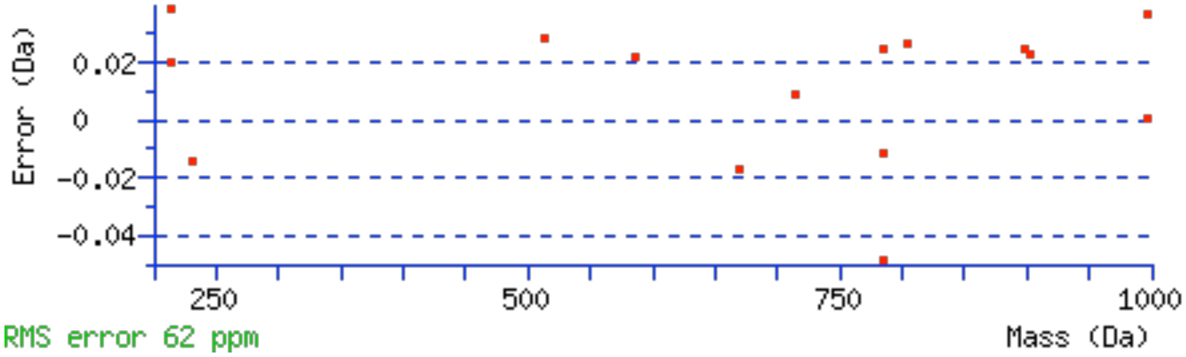
MS/MS Fragmentation of **DDPDAAEALVPGGDLSEE**
Found in **XP_001188391**, PREDICTED: similar to arginine/serine-rich splicing factor 4 [Strongylocentrotus purpuratus].
Match to Query 726: 1798.805548 from(900.410050,2+) intensity(150588.0000)
Title: Cmpd 191, +MSn(900.8790), 31.4 min
Data file Qtof_all.mgf

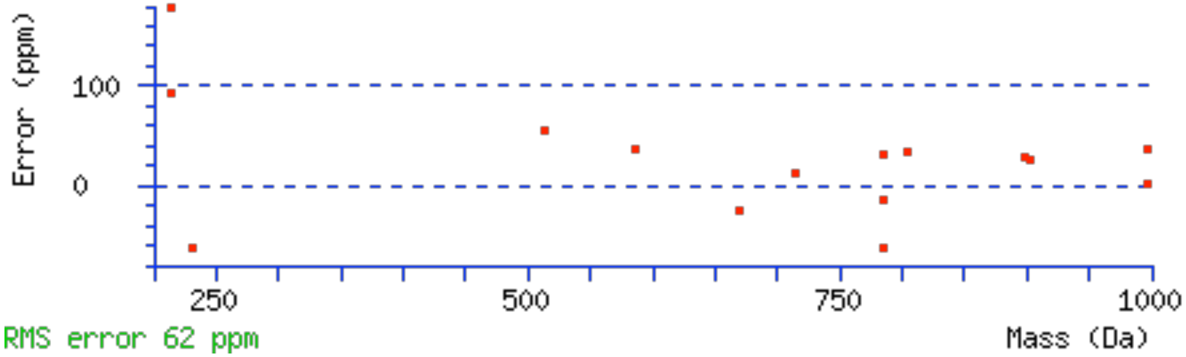


Monoisotopic mass of neutral peptide Mr(calc): 1798.7745 **Ions Score:** 19 **Expect:** 92 **Matches (Bold Red):** 15/136 fragment ions using 30 most intense peaks

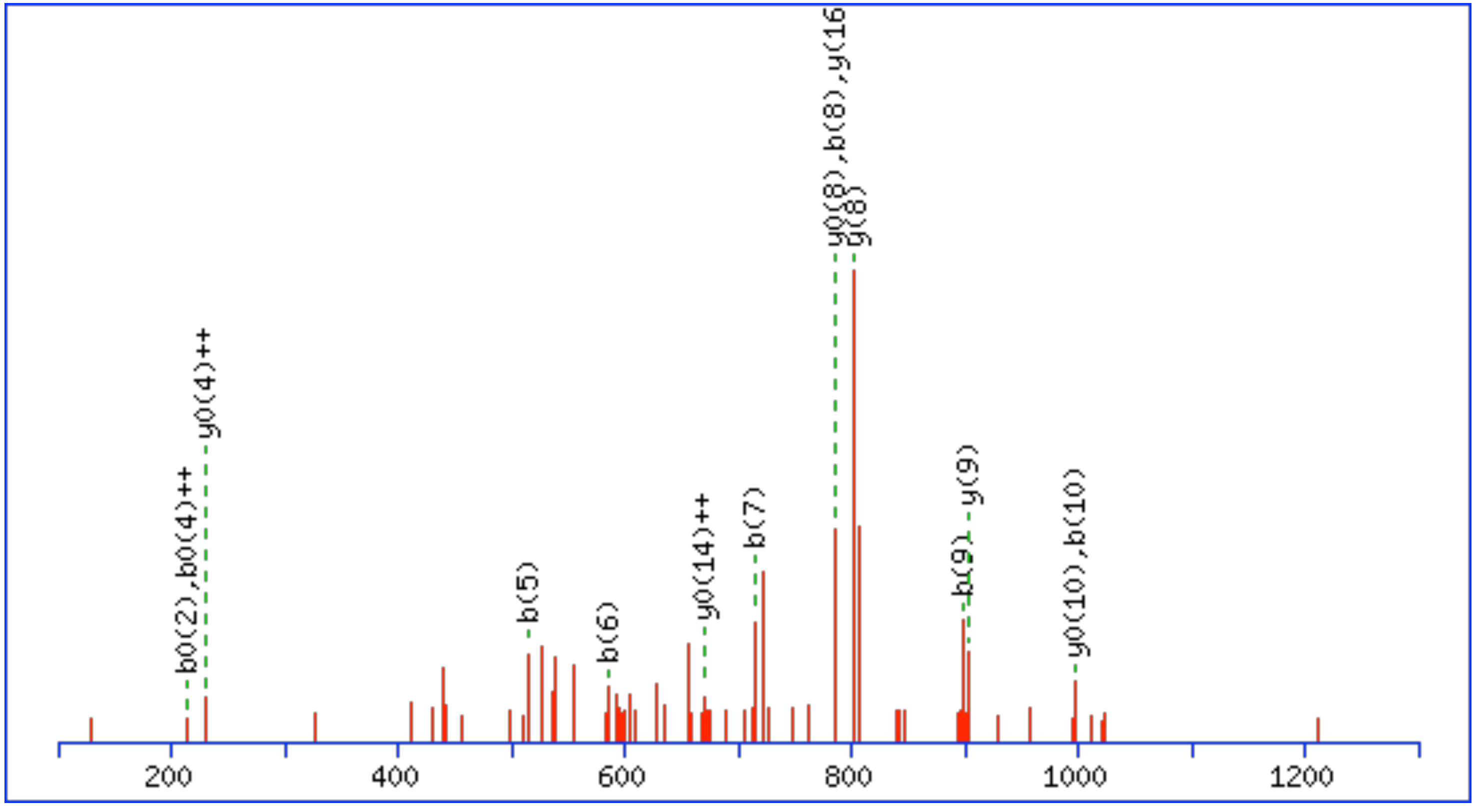
#	b	b⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y⁰	y⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	**D**					**18**
2	231.0612	116.0342	**213.0506**	107.0289	**D**	1684.7548	842.8810	1666.7443	833.8758	**17**
3	328.1139	164.5606	310.1034	155.5553	**P**	1569.7279	**785.3676**	1551.7173	776.3623	**16**
4	443.1409	222.0741	425.1303	**213.0688**	**D**	1472.6751	736.8412	1454.6645	727.8359	**15**

5	**514.1780**	257.5926	496.1674	248.5873	**A**	1357.6482	679.3277	1339.6376	**670.3224**	**14**
6	**585.2151**	293.1112	567.2045	284.1059	**A**	1286.6111	643.8092	1268.6005	634.8039	**13**
7	**714.2577**	357.6325	696.2471	348.6272	**E**	1215.5739	608.2906	1197.5634	599.2853	**12**
8	**785.2948**	393.1510	767.2842	384.1458	**A**	1086.5313	543.7693	1068.5208	534.7640	**11**
9	**898.3789**	449.6931	880.3683	440.6878	**L**	1015.4942	508.2508	**997.4837**	499.2455	**10**
10	**997.4473**	499.2273	979.4367	490.2220	**V**	**902.4102**	451.7087	884.3996	442.7034	**9**
11	1094.5000	547.7537	1076.4895	538.7484	**P**	**803.3418**	402.1745	**785.3312**	393.1692	**8**
12	1151.5215	576.2644	1133.5109	567.2591	**G**	706.2890	353.6481	688.2784	344.6429	**7**
13	1208.5430	604.7751	1190.5324	595.7698	**G**	649.2675	325.1374	631.2570	316.1321	**6**
14	1323.5699	662.2886	1305.5594	653.2833	**D**	592.2461	296.6267	574.2355	287.6214	**5**
15	1436.6540	718.8306	1418.6434	709.8253	**L**	477.2191	239.1132	459.2086	**230.1079**	**4**
16	1523.6860	762.3466	1505.6754	753.3414	**S**	364.1351	182.5712	346.1245	173.5659	**3**
17	1652.7286	826.8679	1634.7180	817.8627	**E**	277.1030	139.0552	259.0925	130.0499	**2**
18					**E**	148.0604	74.5339	130.0499	65.5286	**1**





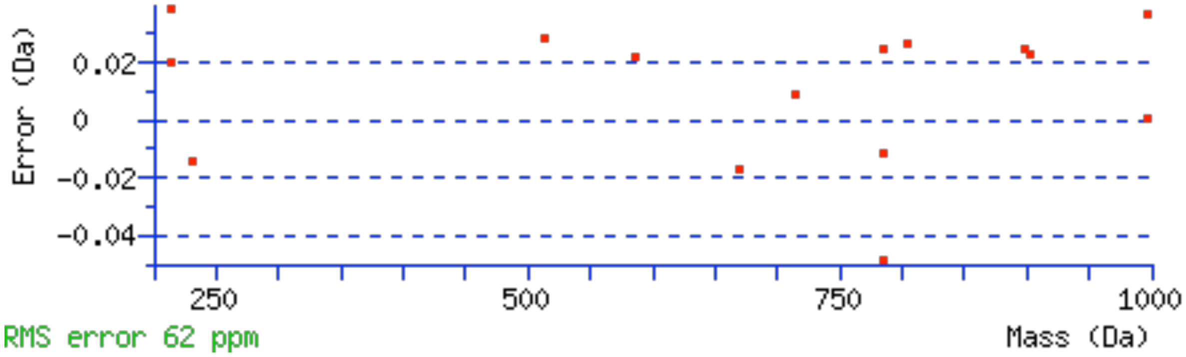
MS/MS Fragmentation of **DDPDAAEALVPGGDLSEE**
Found in **XP_001188391**, PREDICTED: similar to arginine/serine-rich splicing factor 4 [Strongylocentrotus purpuratus].
Match to Query 726: 1798.805548 from(900.410050,2+) intensity(150588.0000)
Title: Cmpd 191, +MSn(900.8790), 31.4 min
Data file Qtof_all.mgf

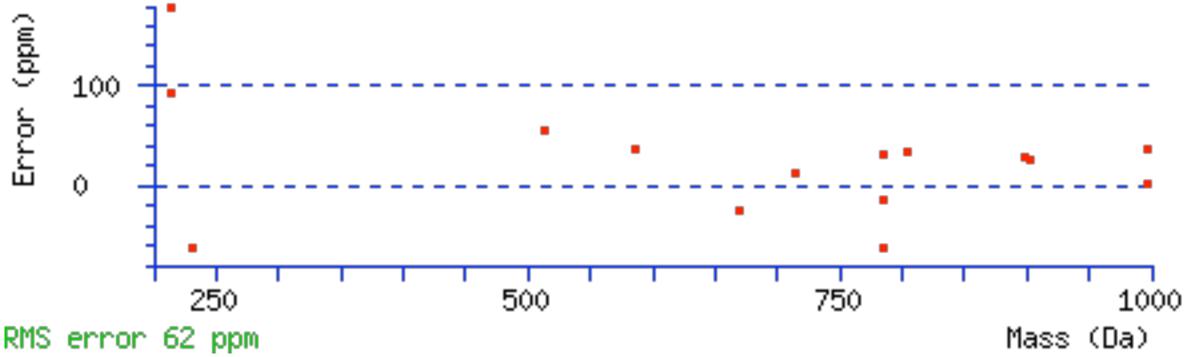


Monoisotopic mass of neutral peptide Mr(calc): 1798.7745 **Ions Score:** 19 **Expect:** 92 **Matches (Bold Red):** 15/136 fragment ions using 30 most intense peaks

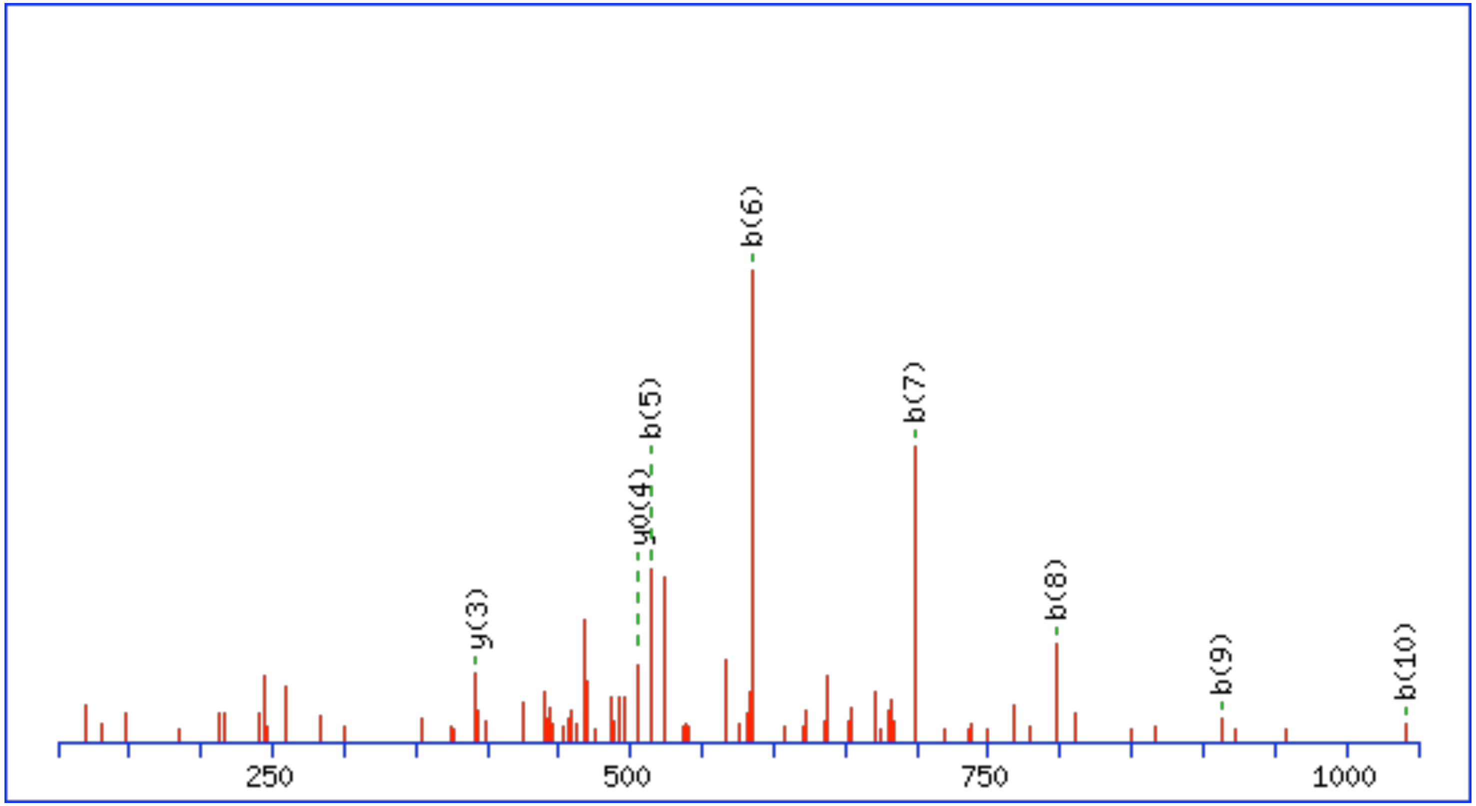
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	116.0342	58.5207	98.0237	49.5155	D					18
2	231.0612	116.0342	**213.0506**	107.0289	D	1684.7548	842.8810	1666.7443	833.8758	17
3	328.1139	164.5606	310.1034	155.5553	P	1569.7279	**785.3676**	1551.7173	776.3623	16
4	443.1409	222.0741	425.1303	**213.0688**	D	1472.6751	736.8412	1454.6645	727.8359	15

5	**514.1780**	257.5926	496.1674	248.5873	**A**	1357.6482	679.3277	1339.6376	**670.3224**	**14**
6	**585.2151**	293.1112	567.2045	284.1059	**A**	1286.6111	643.8092	1268.6005	634.8039	**13**
7	**714.2577**	357.6325	696.2471	348.6272	**E**	1215.5739	608.2906	1197.5634	599.2853	**12**
8	**785.2948**	393.1510	767.2842	384.1458	**A**	1086.5313	543.7693	1068.5208	534.7640	**11**
9	**898.3789**	449.6931	880.3683	440.6878	**L**	1015.4942	508.2508	**997.4837**	499.2455	**10**
10	**997.4473**	499.2273	979.4367	490.2220	**V**	**902.4102**	451.7087	884.3996	442.7034	**9**
11	1094.5000	547.7537	1076.4895	538.7484	**P**	**803.3418**	402.1745	**785.3312**	393.1692	**8**
12	1151.5215	576.2644	1133.5109	567.2591	**G**	706.2890	353.6481	688.2784	344.6429	**7**
13	1208.5430	604.7751	1190.5324	595.7698	**G**	649.2675	325.1374	631.2570	316.1321	**6**
14	1323.5699	662.2886	1305.5594	653.2833	**D**	592.2461	296.6267	574.2355	287.6214	**5**
15	1436.6540	718.8306	1418.6434	709.8253	**L**	477.2191	239.1132	459.2086	**230.1079**	**4**
16	1523.6860	762.3466	1505.6754	753.3414	**S**	364.1351	182.5712	346.1245	173.5659	**3**
17	1652.7286	826.8679	1634.7180	817.8627	**E**	277.1030	139.0552	259.0925	130.0499	**2**
18					**E**	148.0604	74.5339	130.0499	65.5286	**1**





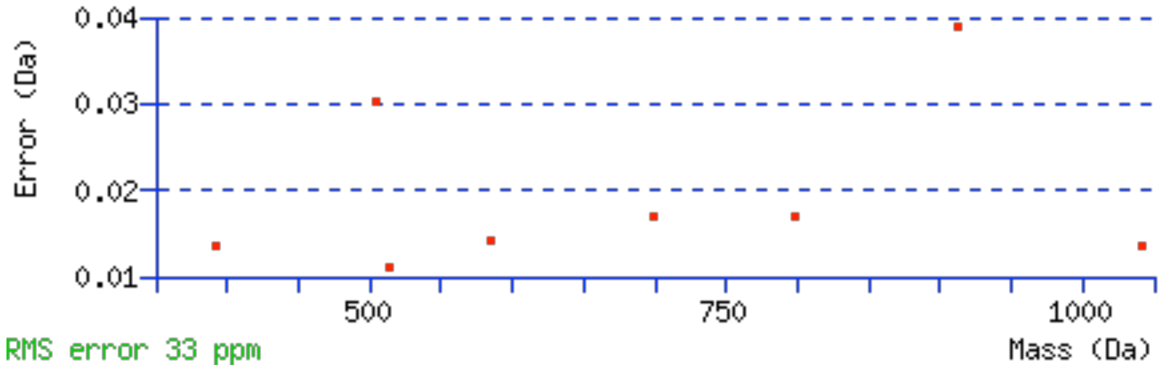
MS/MS Fragmentation of **DDPDAALVDEFMDEE**
Found in **XP_001188391**, PREDICTED: similar to arginine/serine-rich splicing factor 4 [Strongylocentrotus purpuratus].
Match to Query 697: 1709.693008 from(855.853780,2+) intensity(235080.0000)
Title: Cmpd 242, +MSn(856.4203), 36.1 min
Data file Qtof_all.mgf



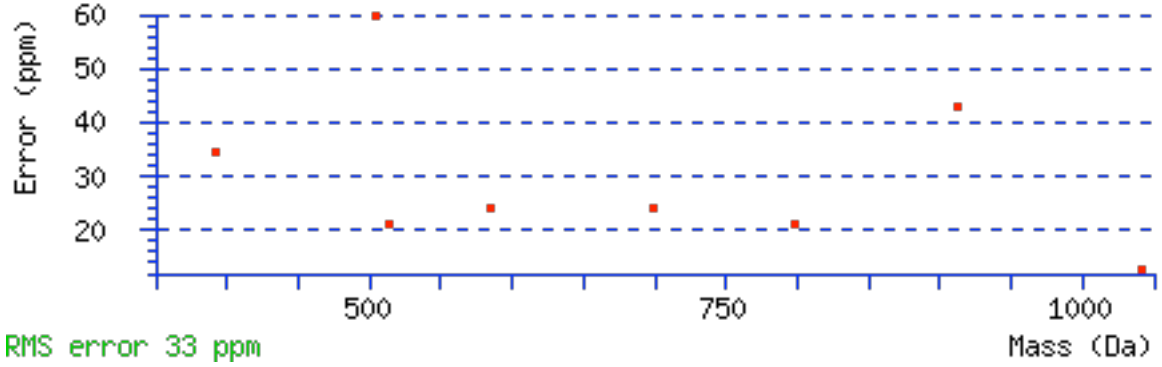
Monoisotopic mass of neutral peptide Mr(calc): 1709.6614 **Ions Score:** 42 **Expect:** 0.23 **Matches (Bold Red):** 8/112
fragment ions using 13 most intense peaks

#	b	b++	b0	b0++	Seq.	y	y++	y0	y0++	#
1	116.0342	58.5207	98.0237	49.5155	D					15
2	231.0612	116.0342	213.0506	107.0289	D	1595.6418	798.3245	1577.6312	789.3192	14
3	328.1139	164.5606	310.1034	155.5553	P	1480.6148	740.8110	1462.6043	731.8058	13
4	443.1409	222.0741	425.1303	213.0688	D	1383.5621	692.2847	1365.5515	683.2794	12

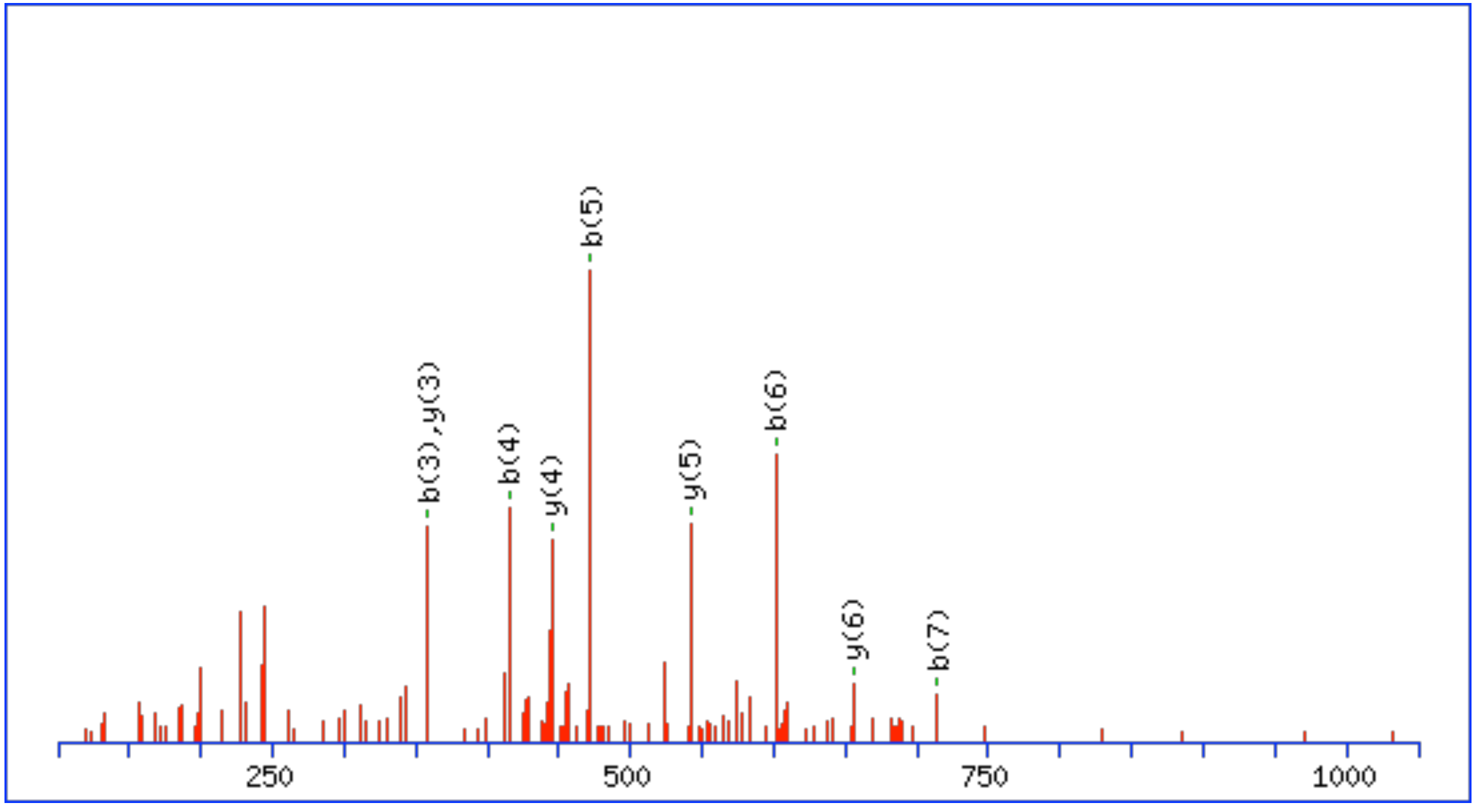
5	**514.1780**	257.5926	496.1674	248.5873	**A**	1268.5351	634.7712	1250.5245	625.7659	**11**
6	**585.2151**	293.1112	567.2045	284.1059	**A**	1197.4980	599.2526	1179.4874	590.2474	**10**
7	**698.2992**	349.6532	680.2886	340.6479	**L**	1126.4609	563.7341	1108.4503	554.7288	**9**
8	**797.3676**	399.1874	779.3570	390.1821	**V**	1013.3768	507.1920	995.3663	498.1868	**8**
9	**912.3945**	456.7009	894.3840	447.6956	**D**	914.3084	457.6578	896.2978	448.6526	**7**
10	**1041.4371**	521.2222	1023.4265	512.2169	**E**	799.2815	400.1444	781.2709	391.1391	**6**
11	1188.5055	594.7564	1170.4950	585.7511	**F**	670.2389	335.6231	652.2283	326.6178	**5**
12	1319.5460	660.2766	1301.5354	651.2714	**M**	523.1705	262.0889	**505.1599**	253.0836	**4**
13	1434.5730	717.7901	1416.5624	708.7848	**D**	**392.1300**	196.5686	374.1194	187.5633	**3**
14	1563.6155	782.3114	1545.6050	773.3061	**E**	277.1030	139.0552	259.0925	130.0499	**2**
15					**E**	148.0604	74.5339	130.0499	65.5286	**1**



RMS error 33 ppm



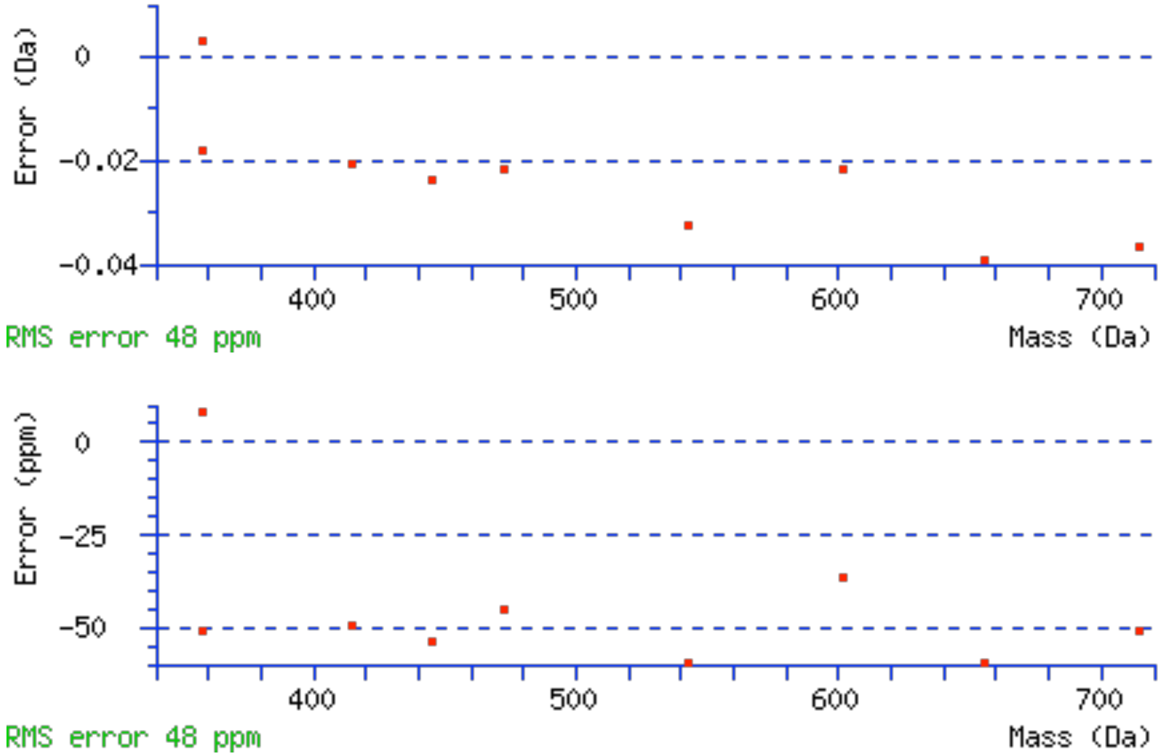
MS/MS Fragmentation of **QFVGGELIPSPEL**
Found in **ABU55286**, GnRH-like tetrapeptide [Strongylocentrotus purpuratus].
Match to Query 521: 1367.616628 from(684.815590,2+) intensity(135132.0000)
Title: Cmpd 314, +MSn(685.2786), 42.8 min
Data file Qtof_all.mgf



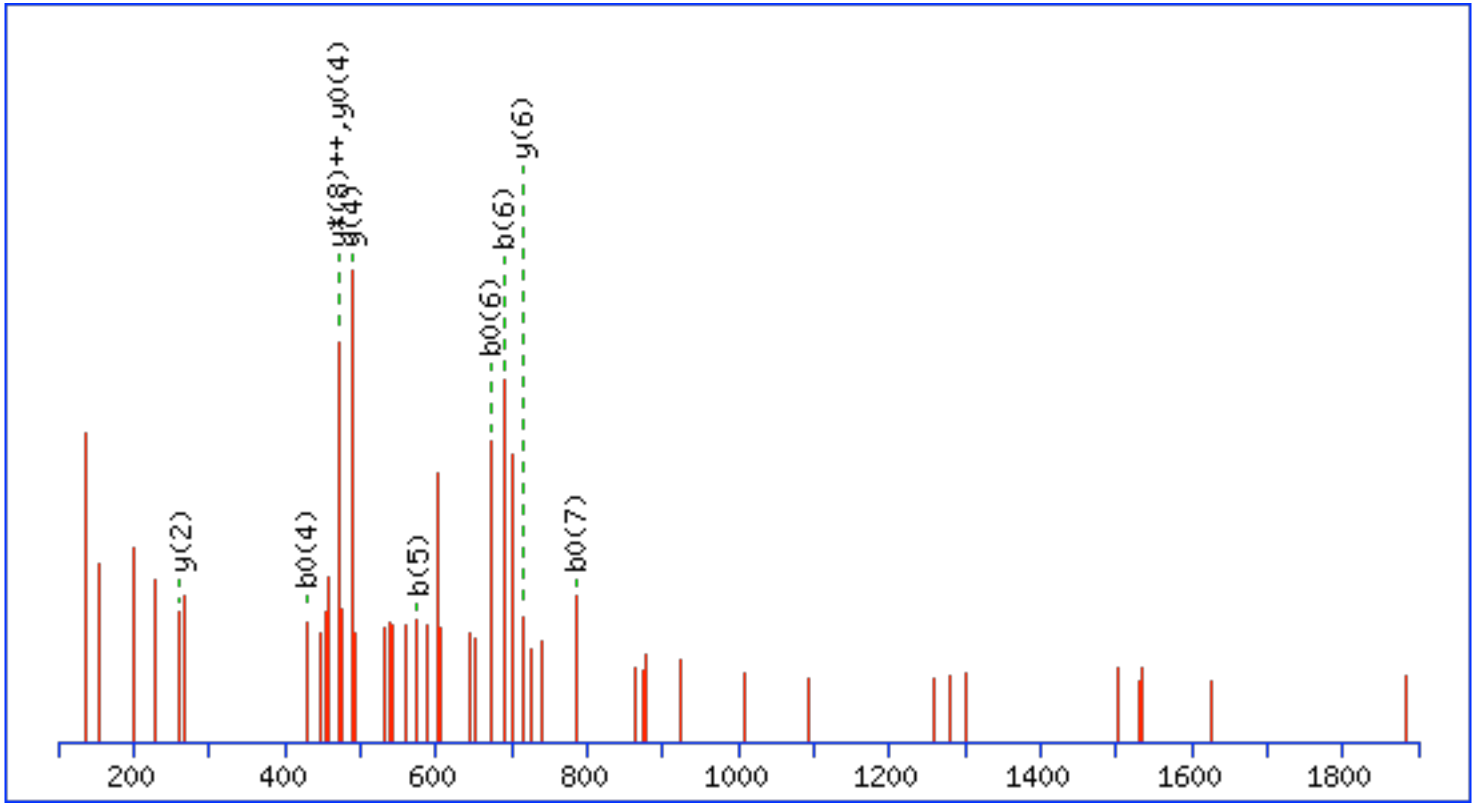
Monoisotopic mass of neutral peptide Mr(calc): 1367.6973 **Variable modifications:** **N-term :** Gln->pyro-Glu (N-term Q)
Ions Score: 29 **Expect:** 12 **Matches (Bold Red):** 9/108 fragment ions using 17 most intense peaks

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{0}	y^{0++}	#
1	112.0393	56.5233	95.0128	48.0100			**Q**					**13**
2	259.1077	130.0575	242.0812	121.5442			**F**	1257.6725	629.3399	1239.6620	620.3346	**12**
3	**358.1761**	179.5917	341.1496	171.0784			**V**	1110.6041	555.8057	1092.5936	546.8004	**11**
4	**415.1976**	208.1024	398.1711	199.5892			**G**	1011.5357	506.2715	993.5251	497.2662	**10**

5	**472.2191**	236.6132	455.1925	228.0999			**G**	954.5142	477.7608	936.5037	468.7555	**9**
6	**601.2617**	301.1345	584.2351	292.6212	583.2511	292.1292	**E**	897.4928	449.2500	879.4822	440.2447	**8**
7	**714.3457**	357.6765	697.3192	349.1632	696.3352	348.6712	**L**	768.4502	384.7287	750.4396	375.7234	**7**
8	827.4298	414.2185	810.4032	405.7053	809.4192	405.2133	**I**	**655.3661**	328.1867	637.3556	319.1814	**6**
9	924.4826	462.7449	907.4560	454.2316	906.4720	453.7396	**P**	**542.2821**	271.6447	524.2715	262.6394	**5**
10	1011.5146	506.2609	994.4880	497.7477	993.5040	497.2556	**S**	**445.2293**	223.1183	427.2187	214.1130	**4**
11	1108.5674	554.7873	1091.5408	546.2740	1090.5568	545.7820	**P**	**358.1973**	179.6023	340.1867	170.5970	**3**
12	1237.6099	619.3086	1220.5834	610.7953	1219.5994	610.3033	**E**	261.1445	131.0759	243.1339	122.0706	**2**
13							**L**	132.1019	66.5546			**1**



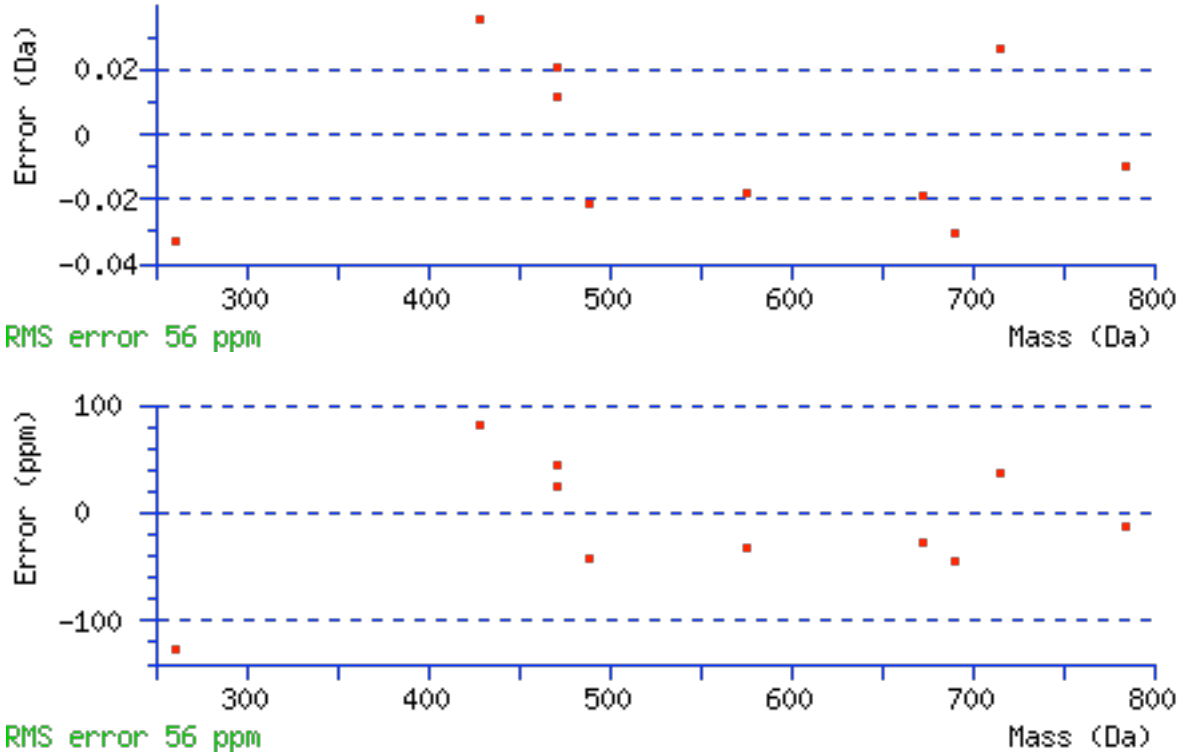
MS/MS Fragmentation of **SEDDQDLLPMEI**
Found in **ABU55286**, GnRH-like tetrapeptide [Strongylocentrotus purpuratus].
Match to Query 556: 1403.534888 from(702.774720,2+) intensity(44696.0000)
Title: Cmpd 262, +MSn(703.2881), 37.9 min
Data file Qtof_all.mgf



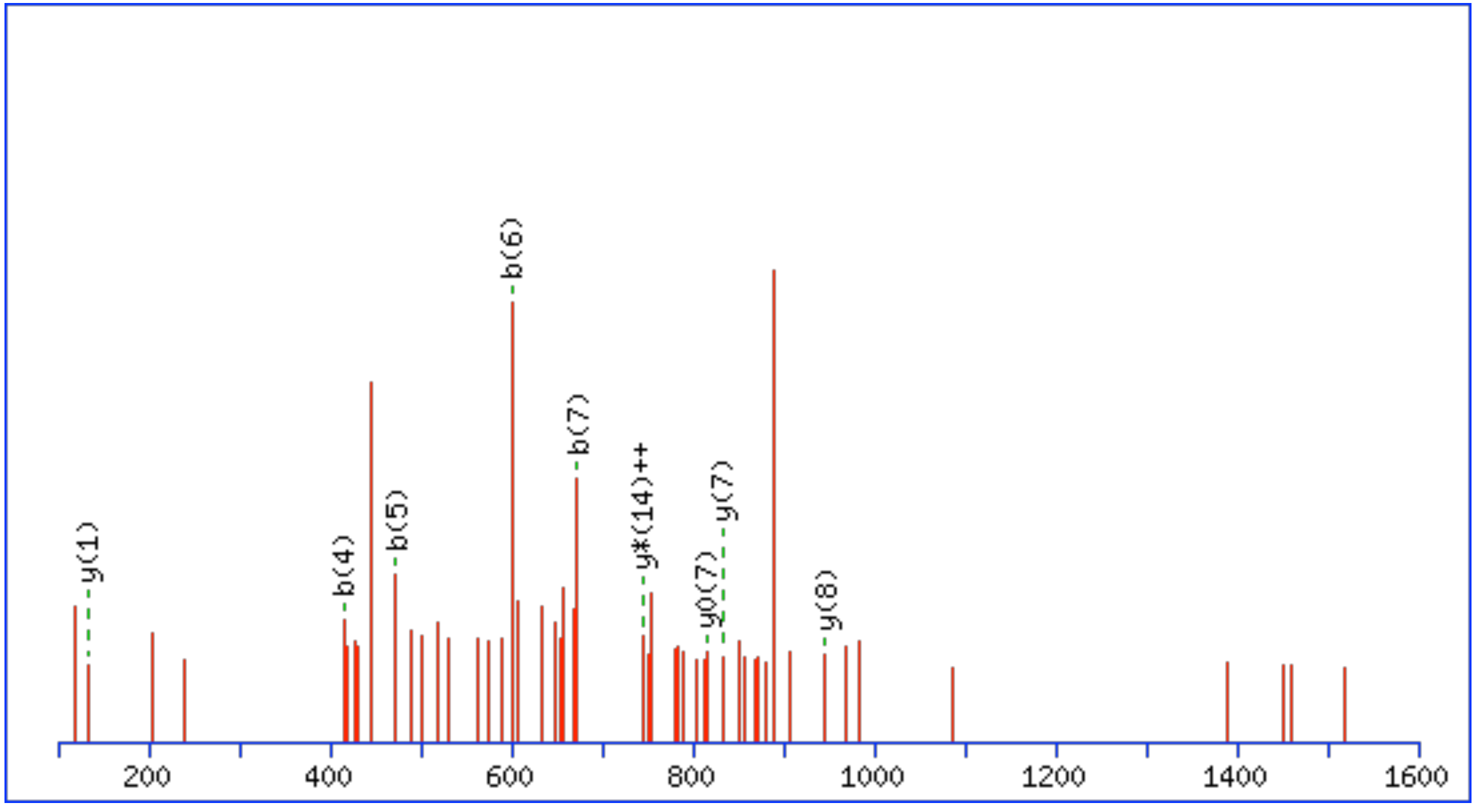
Monoisotopic mass of neutral peptide Mr(calc): 1403.6126 **Ions Score:** 4 **Expect:** 1.1e+03 **Matches (Bold Red):** 10/108 fragment ions using 28 most intense peaks

#	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							12
2	217.0819	109.0446			199.0713	100.0393	E	1317.5879	659.2976	1300.5613	650.7843	1299.5773	650.2923	11
3	332.1088	166.5581			314.0983	157.5528	D	1188.5453	594.7763	1171.5187	586.2630	1170.5347	585.7710	10
4	447.1358	224.0715			**429.1252**	215.0662	D	1073.5183	537.2628	1056.4918	528.7495	1055.5078	528.2575	9

5	**575.1944**	288.1008	558.1678	279.5875	557.1838	279.0955	**Q**	958.4914	479.7493	941.4648	**471.2361**	940.4808	470.7441	**8**
6	**690.2213**	345.6143	673.1948	337.1010	**672.2107**	336.6090	**D**	830.4328	415.7200			812.4223	406.7148	**7**
7	803.3054	402.1563	786.2788	393.6430	**785.2948**	393.1510	**L**	**715.4059**	358.2066			697.3953	349.2013	**6**
8	916.3894	458.6984	899.3629	450.1851	898.3789	449.6931	**L**	602.3218	301.6645			584.3112	292.6593	**5**
9	1013.4422	507.2247	996.4156	498.7115	995.4316	498.2195	**P**	**489.2377**	245.1225			**471.2272**	236.1172	**4**
10	1144.4827	572.7450	1127.4561	564.2317	1126.4721	563.7397	**M**	392.1850	196.5961			374.1744	187.5908	**3**
11	1273.5253	637.2663	1256.4987	628.7530	1255.5147	628.2610	**E**	**261.1445**	131.0759			243.1339	122.0706	**2**
12							**I**	132.1019	66.5546					**1**



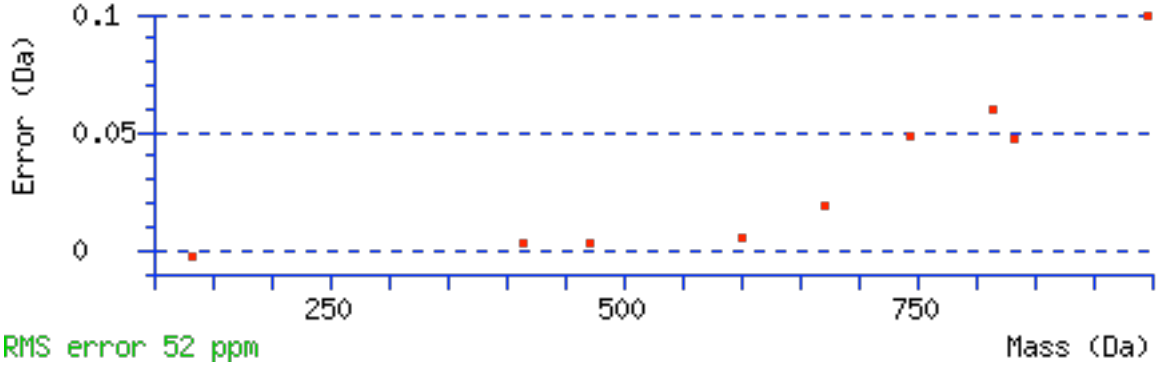
MS/MS Fragmentation of **QFVGGEALEQESNIN**
Found in **ABU55286**, GnRH-like tetrapeptide [Strongylocentrotus purpuratus].
Match to Query 686: 1616.764868 from(809.389710,2+) intensity(50776.0000)
Title: Cmpd 223, +MSn(809.8710), 34.4 min
Data file Qtof_all.mgf

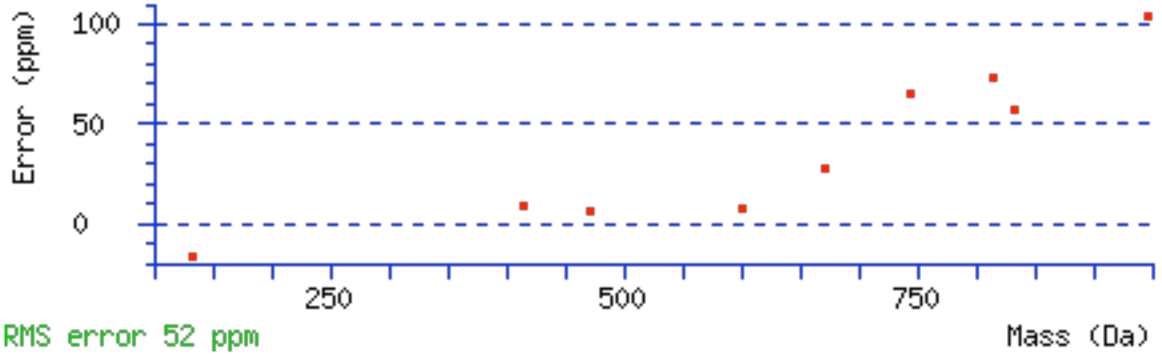


Monoisotopic mass of neutral peptide Mr(calc): 1616.7318 **Variable modifications: N-term :** Gln->pyro-Glu (N-term Q)
Ions Score: 3 **Expect:** 5.5e+03 **Matches (Bold Red):** 9/152 fragment ions using 42 most intense peaks

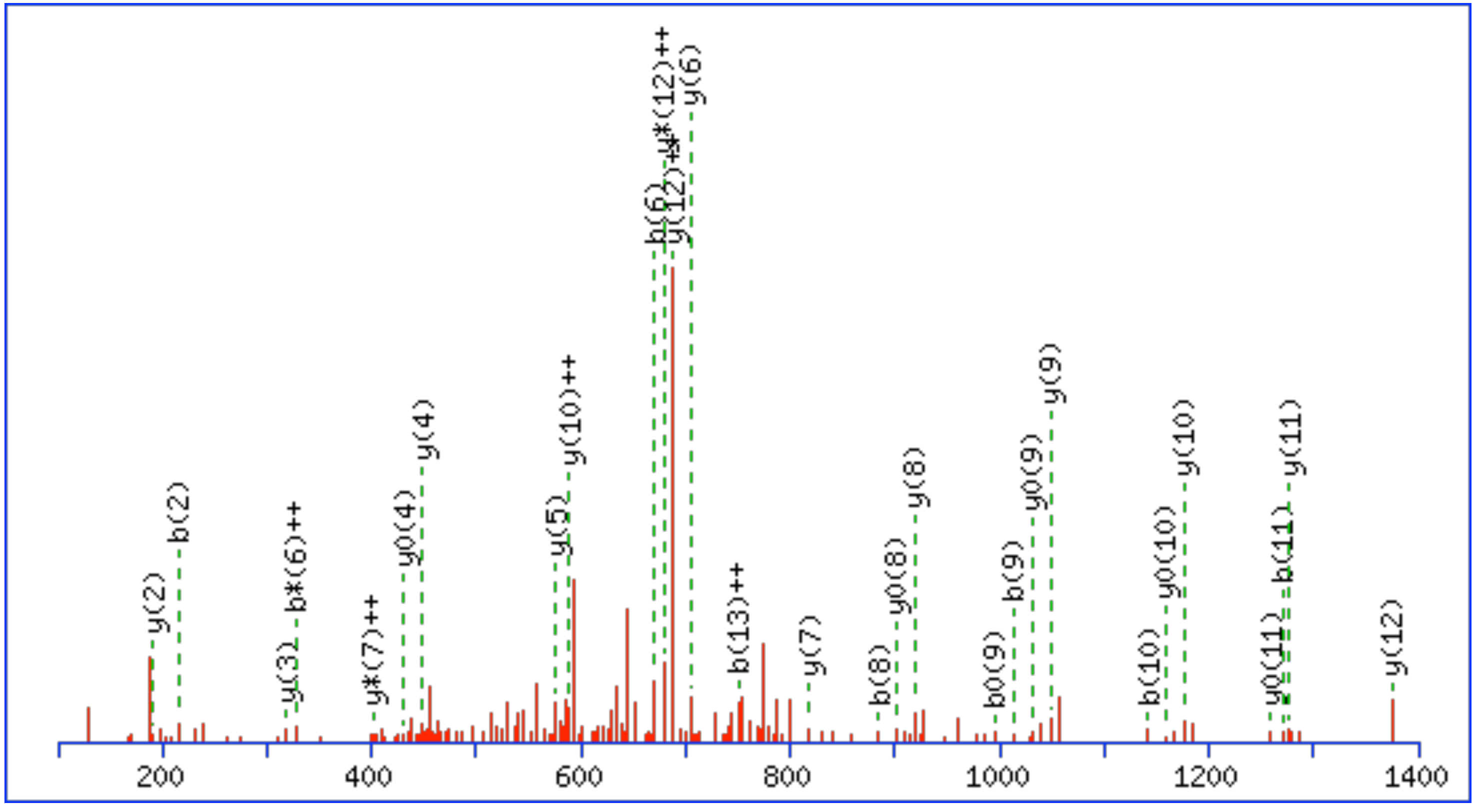
#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	112.0393	56.5233	95.0128	48.0100			Q							15
2	259.1077	130.0575	242.0812	121.5442			F	1506.7071	753.8572	1489.6805	**745.3439**	1488.6965	744.8519	14
3	358.1761	179.5917	341.1496	171.0784			V	1359.6387	680.3230	1342.6121	671.8097	1341.6281	671.3177	13
4	**415.1976**	208.1024	398.1711	199.5892			G	1260.5702	630.7888	1243.5437	622.2755	1242.5597	621.7835	12

5	**472.2191**	236.6132	455.1925	228.0999			**G**	1203.5488	602.2780	1186.5222	593.7648	1185.5382	593.2727	**11**
6	**601.2617**	301.1345	584.2351	292.6212	583.2511	292.1292	**E**	1146.5273	573.7673	1129.5008	565.2540	1128.5168	564.7620	**10**
7	**672.2988**	336.6530	655.2722	328.1398	654.2882	327.6477	**A**	1017.4847	509.2460	1000.4582	500.7327	999.4742	500.2407	**9**
8	785.3828	393.1951	768.3563	384.6818	767.3723	384.1898	**L**	**946.4476**	473.7274	929.4211	465.2142	928.4370	464.7222	**8**
9	914.4254	457.7164	897.3989	449.2031	896.4149	448.7111	**E**	**833.3636**	417.1854	816.3370	408.6721	**815.3530**	408.1801	**7**
10	1042.4840	521.7456	1025.4575	513.2324	1024.4735	512.7404	**Q**	704.3210	352.6641	687.2944	344.1508	686.3104	343.6588	**6**
11	1171.5266	586.2669	1154.5001	577.7537	1153.5160	577.2617	**E**	576.2624	288.6348	559.2358	280.1216	558.2518	279.6295	**5**
12	1258.5586	629.7830	1241.5321	621.2697	1240.5481	620.7777	**S**	447.2198	224.1135	430.1932	215.6003	429.2092	215.1082	**4**
13	1372.6016	686.8044	1355.5750	678.2911	1354.5910	677.7991	**N**	360.1878	180.5975	343.1612	172.0842			**3**
14	1485.6856	743.3465	1468.6591	734.8332	1467.6751	734.3412	**I**	246.1448	123.5761	229.1183	115.0628			**2**
15							**N**	**133.0608**	67.0340	116.0342	58.5207			**1**





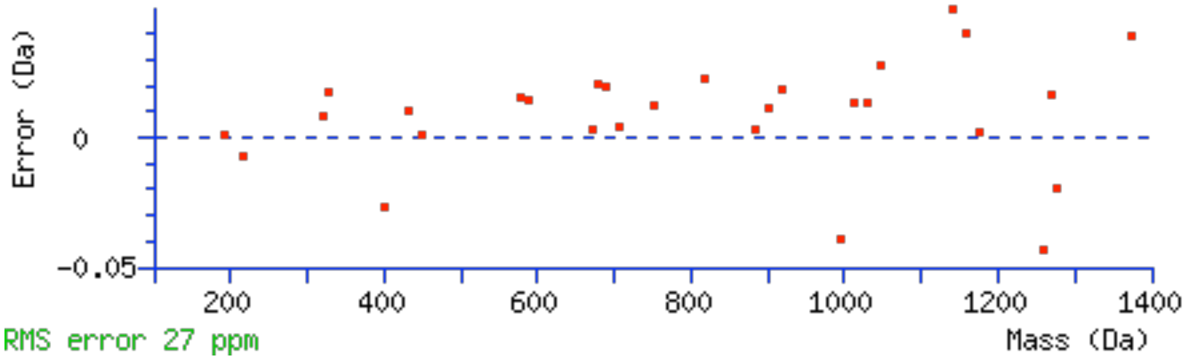
MS/MS Fragmentation of **TLPTKETIEQEKTA**
Found in **AAC26833**, thymosin beta [Strongylocentrotus purpuratus].
Match to Query 676: 1587.846888 from(794.930720,2+) intensity(228024.0000)
Title: Cmpd 102, +MSn(795.4395), 23.5 min
Data file Qtof_all.mgf

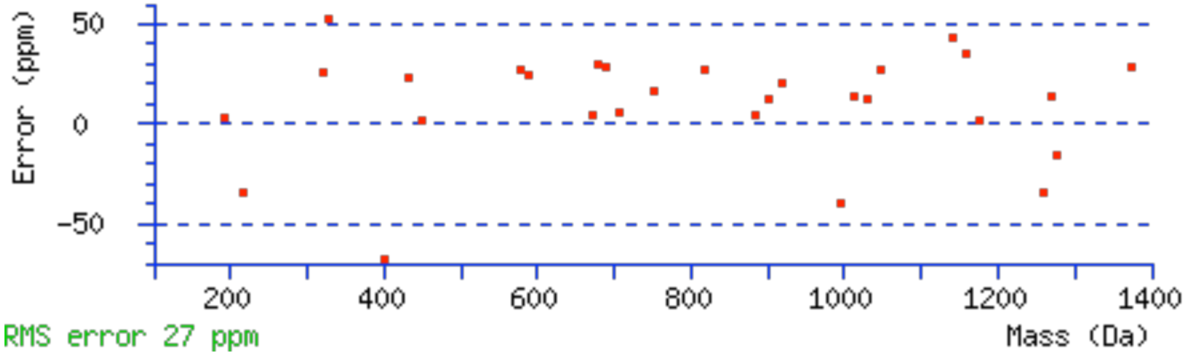


Monoisotopic mass of neutral peptide Mr(calc): 1587.8355 **Ions Score:** 43 **Expect:** 0.68 **Matches (Bold Red):** 29/142 fragment ions using 73 most intense peaks

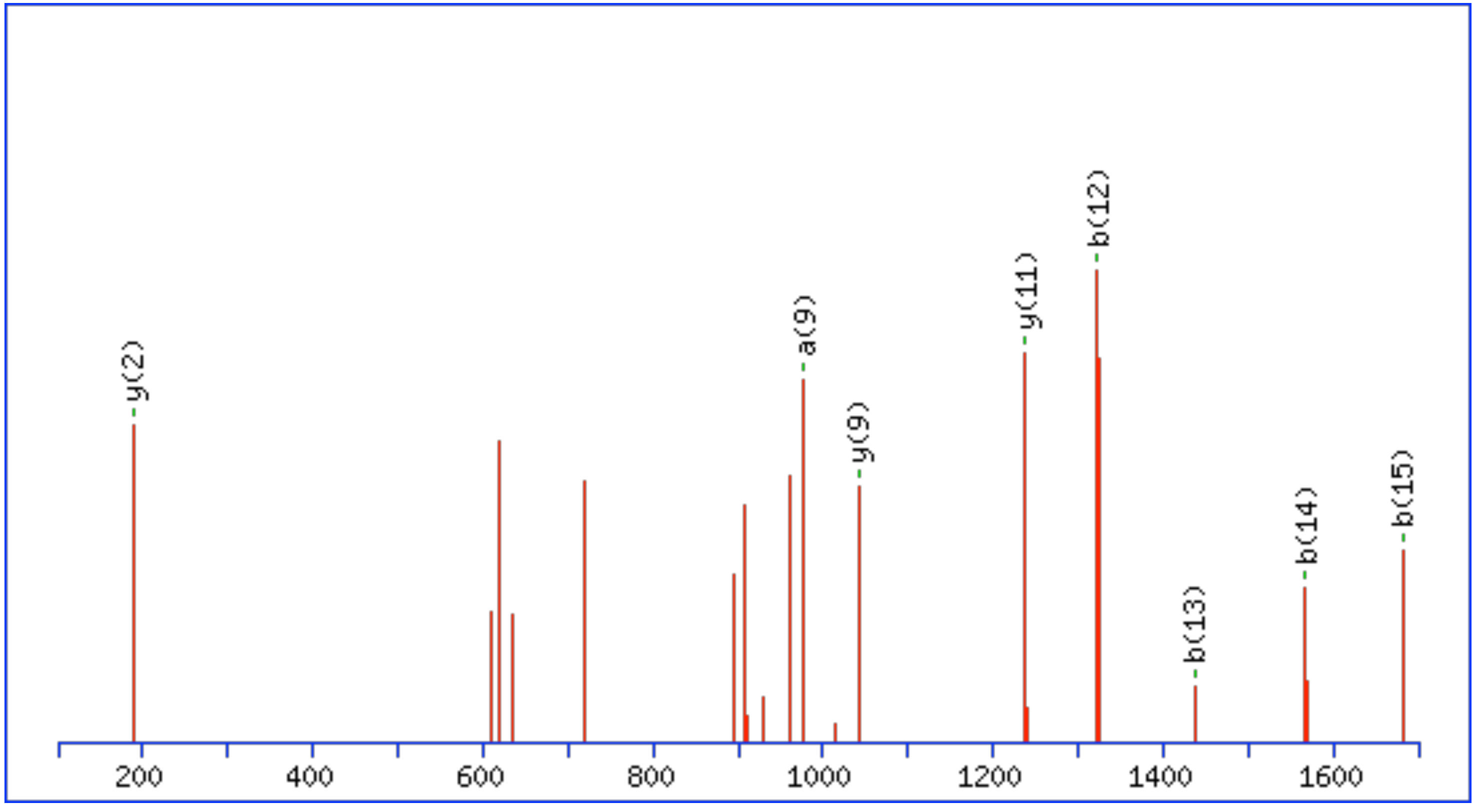
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311			84.0444	42.5258	**T**							**14**
2	**215.1390**	108.0731			197.1285	99.0679	**L**	1487.7952	744.4012	1470.7686	735.8879	1469.7846	735.3959	**13**
3	312.1918	156.5995			294.1812	147.5942	**P**	**1374.7111**	**687.8592**	1357.6846	**679.3459**	1356.7005	678.8539	**12**
4	413.2395	207.1234			395.2289	198.1181	**T**	**1277.6583**	639.3328	1260.6318	630.8195	**1259.6478**	630.3275	**11**

5	541.3344	271.1709	524.3079	262.6576	523.3239	262.1656	**K**	**1176.6107**	**588.8090**	1159.5841	580.2957	**1158.6001**	579.8037	**10**
6	**670.3770**	335.6921	653.3505	**327.1789**	652.3665	326.6869	**E**	**1048.5157**	524.7615	1031.4891	516.2482	**1030.5051**	515.7562	**9**
7	771.4247	386.2160	754.3981	377.7027	753.4141	377.2107	**T**	**919.4731**	460.2402	902.4466	451.7269	**901.4625**	451.2349	**8**
8	**884.5088**	442.7580	867.4822	434.2447	866.4982	433.7527	**I**	**818.4254**	409.7164	801.3989	**401.2031**	800.4149	400.7111	**7**
9	**1013.5514**	507.2793	996.5248	498.7660	**995.5408**	498.2740	**E**	**705.3414**	353.1743	688.3148	344.6610	687.3308	344.1690	**6**
10	**1141.6099**	571.3086	1124.5834	562.7953	1123.5994	562.3033	**Q**	**576.2988**	288.6530	559.2722	280.1397	558.2882	279.6477	**5**
11	**1270.6525**	635.8299	1253.6260	627.3166	1252.6420	626.8246	**E**	**448.2402**	224.6237	431.2136	216.1105	**430.2296**	215.6185	**4**
12	1398.7475	699.8774	1381.7209	691.3641	1380.7369	690.8721	**K**	**319.1976**	160.1024	302.1710	151.5892	301.1870	151.0972	**3**
13	1499.7952	**750.4012**	1482.7686	741.8879	1481.7846	741.3959	**T**	**191.1026**	96.0550			173.0921	87.0497	**2**
14							**A**	90.0550	45.5311					**1**





MS/MS Fragmentation of **APAPYFDEDAMDLMDPVFNFKDDSAV**
Found in **XP_001175484**, PREDICTED: hypothetical protein [Strongylocentrotus purpuratus].
Match to Query 482: 2919.784872 from(974.268900,3+) intensity(255.5370)
Data file Maldi_All.mgf



Monoisotopic mass of neutral peptide Mr(calc): 2919.2619 **Ions Score:** 25 **Expect:** 62 **Matches (Bold Red):** 8/389 fragment ions using 12 most intense peaks

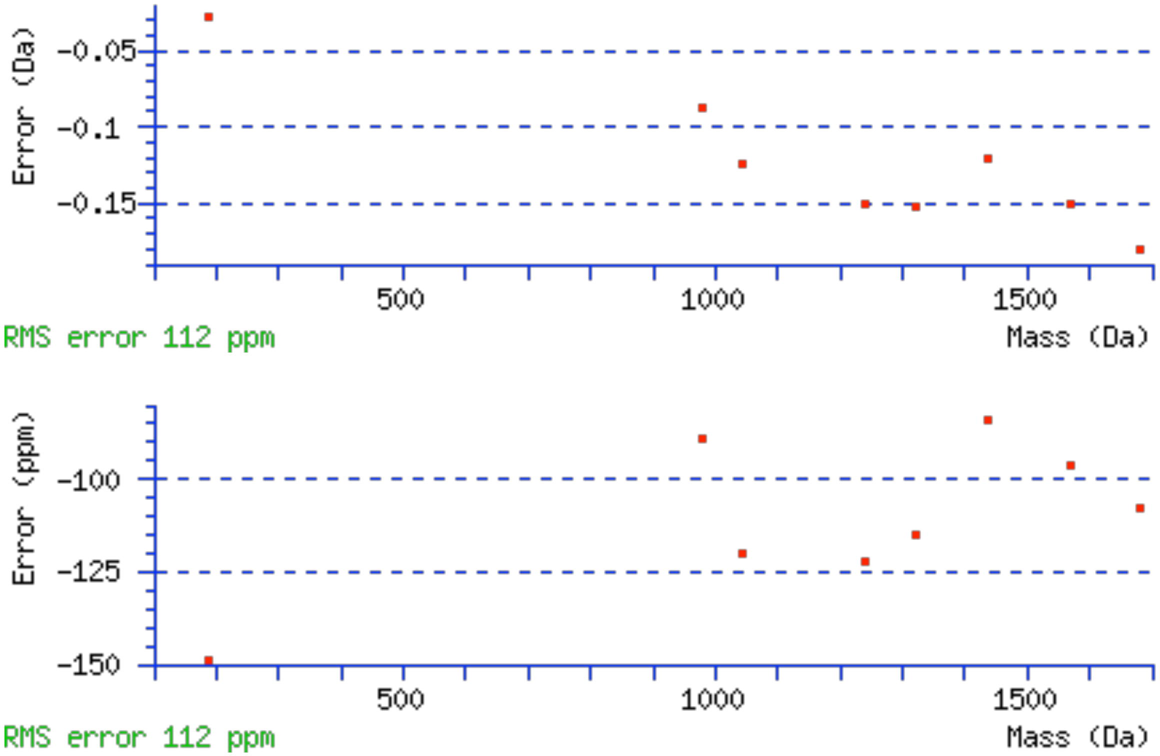
#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	y	y*	y^0	#
1	44.0495	44.0495			72.0444			**A**				**26**
2	70.0651	141.1022			169.0972			**P**	2849.2321	2832.2055	2831.2215	**25**
3	44.0495	212.1394			240.1343			**A**	2752.1793	2735.1528	2734.1687	**24**
4	70.0651	309.1921			337.1870			**P**	2681.1422	2664.1156	2663.1316	**23**

5	136.0757	472.2554			500.2504			**Y**	2584.0894	2567.0629	2566.0789	**22**
6	120.0808	619.3239			647.3188			**F**	2421.0261	2403.9996	2403.0155	**21**
7	88.0393	734.3508		716.3402	762.3457		744.3352	**D**	2273.9577	2256.9311	2255.9471	**20**
8	102.0550	863.3934		845.3828	891.3883		873.3777	**E**	2158.9307	2141.9042	2140.9202	**19**
9	88.0393	**978.4203**		960.4098	1006.4153		988.4047	**D**	2029.8882	2012.8616	2011.8776	**18**
10	44.0495	1049.4575		1031.4469	1077.4524		1059.4418	**A**	1914.8612	1897.8347	1896.8506	**17**
11	104.0528	1180.4979		1162.4874	1208.4929		1190.4823	**M**	1843.8241	1826.7976	1825.8135	**16**
12	88.0393	1295.5249		1277.5143	**1323.5198**		1305.5092	**D**	1712.7836	1695.7571	1694.7730	**15**
13	86.0964	1408.6089		1390.5984	**1436.6039**		1418.5933	**L**	1597.7567	1580.7301	1579.7461	**14**
14	104.0528	1539.6494		1521.6389	**1567.6443**		1549.6338	**M**	1484.6726	1467.6461	1466.6620	**13**
15	88.0393	1654.6764		1636.6658	**1682.6713**		1664.6607	**D**	1353.6321	1336.6056	1335.6216	**12**
16	70.0651	1751.7291		1733.7186	1779.7241		1761.7135	**P**	**1238.6052**	1221.5786	1220.5946	**11**
17	72.0808	1850.7976		1832.7870	1878.7925		1860.7819	**V**	1141.5524	1124.5259	1123.5419	**10**
18	120.0808	1997.8660		1979.8554	2025.8609		2007.8503	**F**	**1042.4840**	1025.4575	1024.4734	**9**
19	87.0553	2111.9089	2094.8823	2093.8983	2139.9038	2122.8773	2121.8932	**N**	895.4156	878.3890	877.4050	**8**
20	120.0808	2258.9773	2241.9508	2240.9667	2286.9722	2269.9457	2268.9617	**F**	781.3727	764.3461	763.3621	**7**
21	101.1073	2387.0723	2370.0457	2369.0617	2415.0672	2398.0406	2397.0566	**K**	634.3042	617.2777	616.2937	**6**
22	88.0393	2502.0992	2485.0727	2484.0886	2530.0941	2513.0676	2512.0836	**D**	506.2093		488.1987	**5**
23	88.0393	2617.1262	2600.0996	2599.1156	2645.1211	2628.0945	2627.1105	**D**	391.1823		373.1718	**4**
24	60.0444	2704.1582	2687.1316	2686.1476	2732.1531	2715.1265	2714.1425	**S**	276.1554		258.1448	**3**
25	44.0495	2775.1953	2758.1687	2757.1847	2803.1902	2786.1637	2785.1796	**A**	**189.1234**			**2**
26	72.0808							**V**	118.0863			**1**

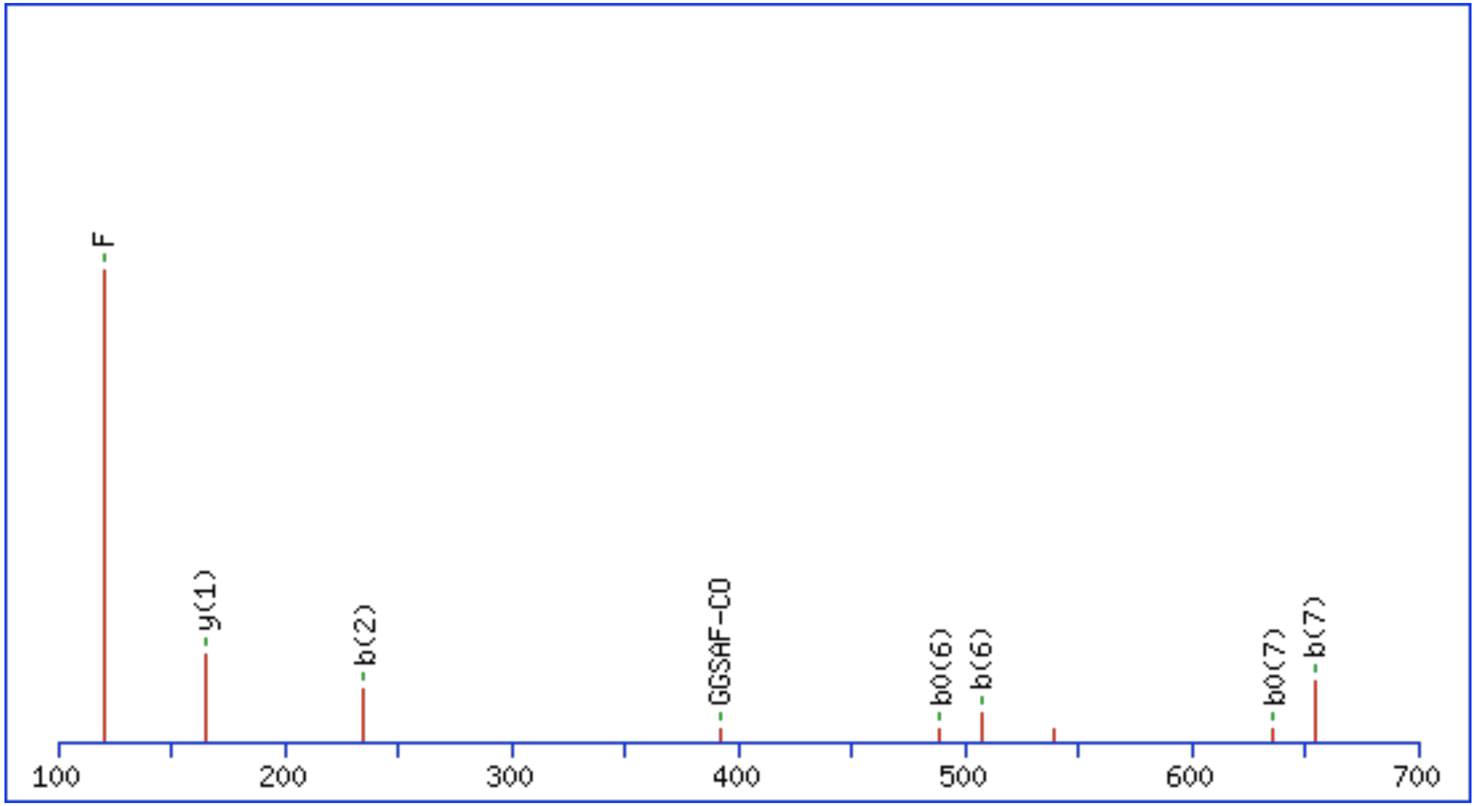
Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
PA	141.1022	169.0972	**PAP**	238.1550	266.1499	**PAPY**	401.2183	429.2132

PAPYF	548.2867	576.2817	**PAPYFD**	663.3137	691.3086	**AP**	141.1022	169.0972
APY	304.1656	332.1605	**APYF**	451.2340	479.2289	**APYFD**	566.2609	594.2558
APYFDE	695.3035	723.2984	**PY**	233.1285	261.1234	**PYF**	380.1969	408.1918
PYFD	495.2238	523.2187	**PYFDE**	624.2664	652.2613	**YF**	283.1441	311.1390
YFD	398.1710	426.1660	**YFDE**	527.2136	555.2086	**YFDED**	642.2406	670.2355
FD	235.1077	263.1026	**FDE**	364.1503	392.1452	**FDED**	479.1773	507.1722
FDEDA	550.2144	578.2093	**FDEDAM**	681.2549	709.2498	**DE**	217.0819	245.0768
DED	332.1088	360.1038	**DEDA**	403.1460	431.1409	**DEDAM**	534.1864	562.1814
DEDAMD	649.2134	677.2083	**ED**	217.0819	245.0768	**EDA**	288.1190	316.1139
EDAM	419.1595	447.1544	**EDAMD**	534.1864	562.1814	**EDAMDL**	647.2705	675.2654
DA	159.0764	187.0713	**DAM**	290.1169	318.1118	**DAMD**	405.1438	433.1388
DAMDL	518.2279	546.2228	**DAMDLM**	649.2684	677.2633	**AM**	175.0900	203.0849
AMD	290.1169	318.1118	**AMDL**	403.2010	431.1959	**AMDLM**	534.2415	562.2364
AMDLMD	649.2684	677.2633	**MD**	219.0798	247.0747	**MDL**	332.1639	360.1588
MDLM	463.2043	491.1993	**MDLMD**	578.2313	606.2262	**MDLMDP**	675.2840	703.2790
DL	201.1234	229.1183	**DLM**	332.1639	360.1588	**DLMD**	447.1908	475.1857
DLMDP	544.2436	572.2385	**DLMDPV**	643.3120	671.3069	**LM**	217.1369	245.1318
LMD	332.1639	360.1588	**LMDP**	429.2166	457.2115	**LMDPV**	528.2850	556.2799
LMDPVF	675.3534	703.3484	**MD**	219.0798	247.0747	**MDP**	316.1326	344.1275
MDPV	415.2010	443.1959	**MDPVF**	562.2694	590.2643	**MDPVFN**	676.3123	704.3072
DP	185.0921	213.0870	**DPV**	284.1605	312.1554	**DPVF**	431.2289	459.2238
DPVFN	545.2718	573.2667	**DPVFNF**	692.3402	720.3352	**PV**	169.1335	197.1285
PVF	316.2020	344.1969	**PVFN**	430.2449	458.2398	**PVFNF**	577.3133	605.3082
VF	219.1492	247.1441	**VFN**	333.1921	361.1870	**VFNF**	480.2605	508.2554

VFNFK	608.3555	636.3504	**FN**	234.1237	262.1186	**FNF**	381.1921	409.1870
FNFK	509.2871	537.2820	**FNFKD**	624.3140	652.3089	**NF**	234.1237	262.1186
NFK	362.2187	390.2136	**NFKD**	477.2456	505.2405	**NFKDD**	592.2726	620.2675
NFKDDS	679.3046	707.2995	**FK**	248.1757	276.1707	**FKD**	363.2027	391.1976
FKDD	478.2296	506.2245	**FKDDS**	565.2617	593.2566	**FKDDSA**	636.2988	664.2937
KD	216.1343	244.1292	**KDD**	331.1612	359.1561	**KDDS**	418.1932	446.1882
KDDSA	489.2304	517.2253	**DD**	203.0662	231.0612	**DDS**	290.0983	318.0932
DDSA	361.1354	389.1303	**DS**	175.0713	203.0662	**DSA**	246.1084	274.1034
SA	131.0815	159.0764						



MS/MS Fragmentation of **PHGGSAFVF**
Found in **XP_001186882**, PREDICTED: similar to LFRFa precursor [Strongylocentrotus purpuratus].
Match to Query 91: 916.281248 from(459.147900,2+) intensity(67.4726)
Data file Maldi_All.mgf

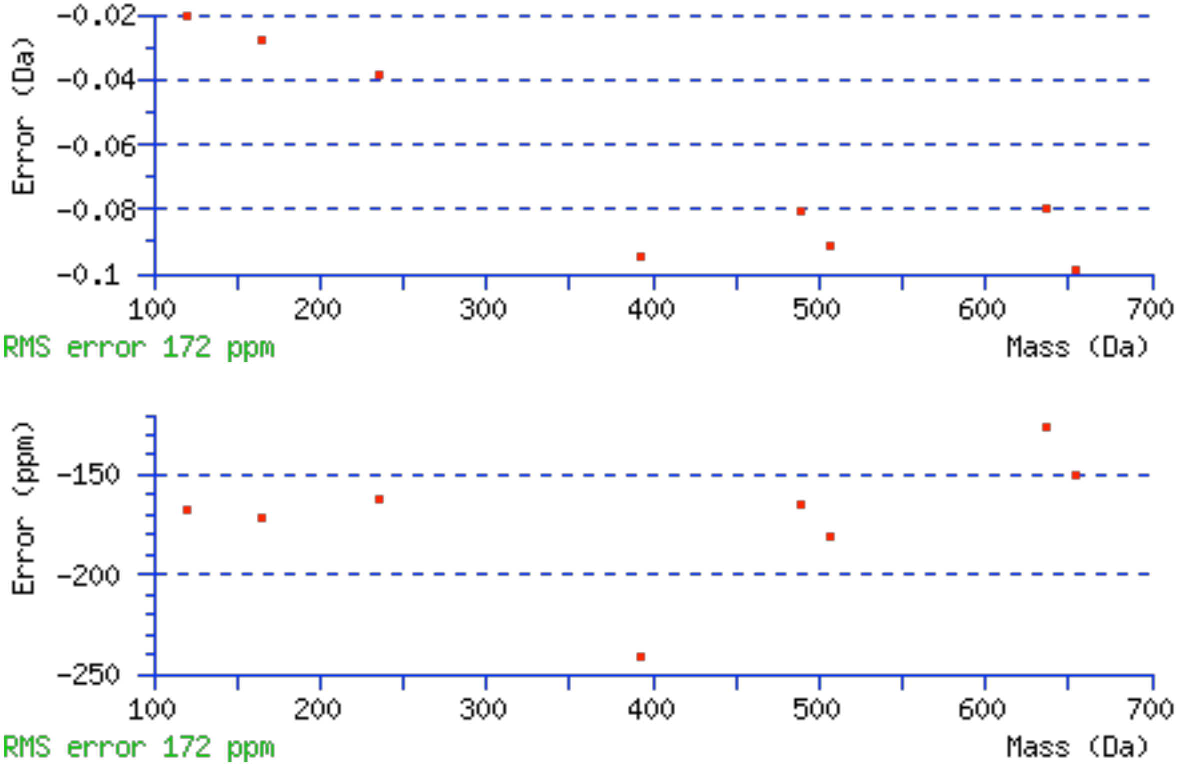


Monoisotopic mass of neutral peptide Mr(calc): 916.4556 **Variable modifications:** **C-term :** Amidated (C-term) **Ions Score:** 25 **Expect:** 59 **Matches (Bold Red):** 9/87 fragment ions using 9 most intense peaks

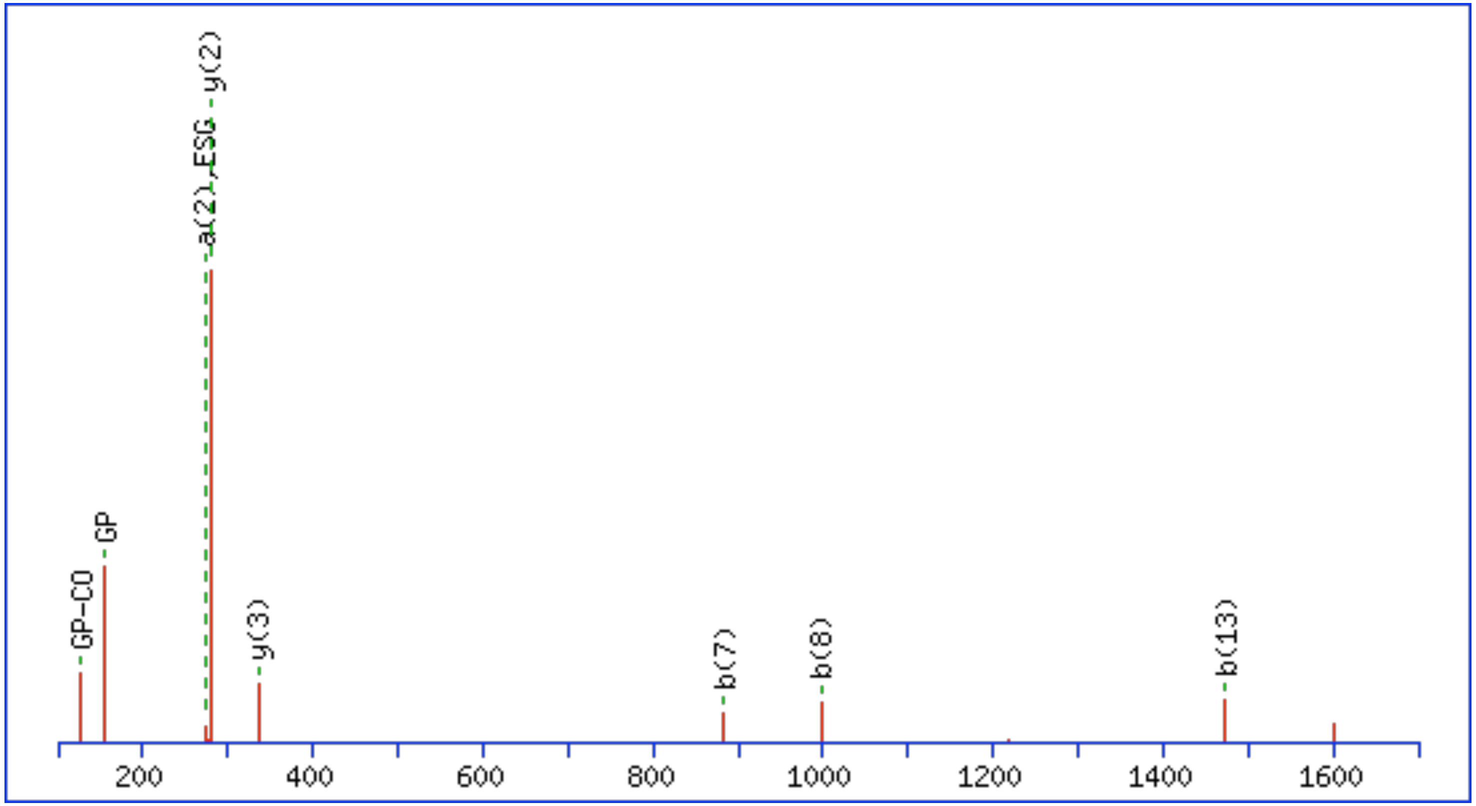
#	Immon.	a	a^0	b	b^0	Seq.	y	y^0	#
1	70.0651	70.0651		98.0600		**P**			**9**
2	110.0713	207.1240		**235.1190**		**H**	820.4100	802.3995	**8**
3	30.0338	264.1455		292.1404		**G**	683.3511	665.3406	**7**
4	30.0338	321.1670		349.1619		**G**	626.3297	608.3191	**6**

5	60.0444	408.1990	390.1884	436.1939	418.1833	**S**	569.3082	551.2976	**5**
6	44.0495	479.2361	461.2255	**507.2310**	**489.2205**	**A**	482.2762		**4**
7	**120.0808**	626.3045	608.2940	**654.2994**	**636.2889**	**F**	411.2391		**3**
8	72.0808	725.3729	707.3624	753.3678	735.3573	**V**	264.1706		**2**
9	**120.0808**					**F**	**165.1022**		**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
HG	167.0927	195.0877	**HGG**	224.1142	252.1091	**HGGS**	311.1462	339.1411
HGGSA	382.1833	410.1783	**HGGSAF**	529.2518	557.2467	**HGGSAFV**	628.3202	656.3151
GG	87.0553	115.0502	**GGS**	174.0873	202.0822	**GGSA**	245.1244	273.1193
GGSAF	392.1928	420.1878	**GGSAFV**	491.2613	519.2562	**GS**	117.0659	145.0608
GSA	188.1030	216.0979	**GSAF**	335.1714	363.1663	**GSAFV**	434.2398	462.2347
SA	131.0815	159.0764	**SAF**	278.1499	306.1448	**SAFV**	377.2183	405.2132
AF	191.1179	219.1128	**AFV**	290.1863	318.1812	**FV**	219.1492	247.1441



MS/MS Fragmentation of **DWAPREQDFANAAEESGPY**
Found in **XP_001186882**, PREDICTED: similar to LFRFa precursor [Strongylocentrotus purpuratus].
Match to Query 374: 2151.598248 from(1076.806400,2+) intensity(1839.8896)
Data file Maldi_All.mgf



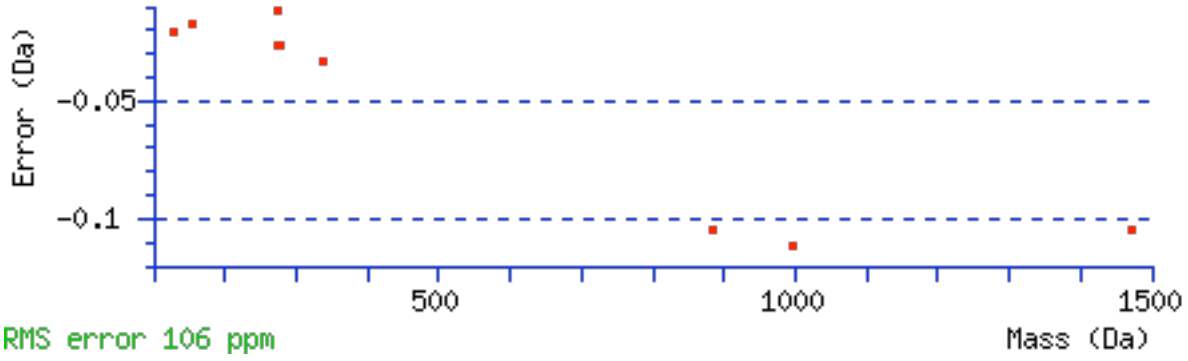
Monoisotopic mass of neutral peptide Mr(calc): 2151.9133 **Ions Score:** 23 **Expect:** 1.3e+02 **Matches (Bold Red):** 9/318 fragment ions using 10 most intense peaks

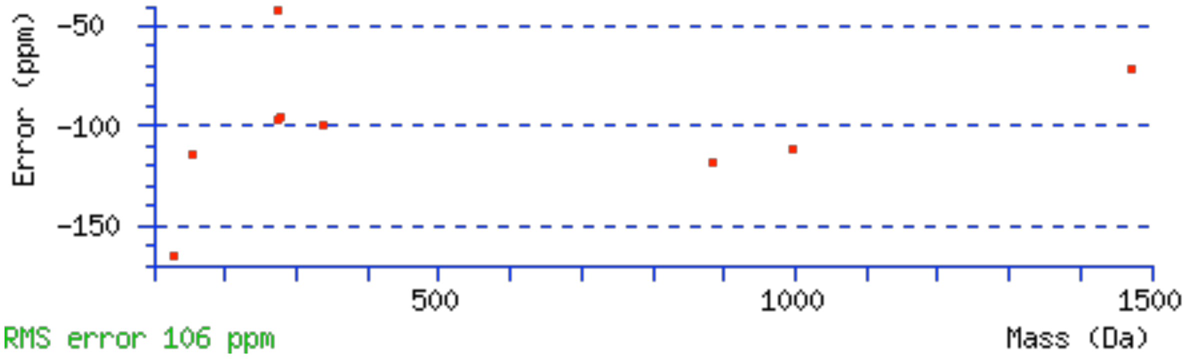
#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	88.0393	88.0393		70.0287	116.0342		98.0237		**D**						**19**
2	159.0917	**274.1186**		256.1081	302.1135		284.1030		**W**	1906.8202		2037.8937	2020.8672	2019.8831	**18**
3	44.0495	345.1557		327.1452	373.1506		355.1401		**A**	1835.7831		1851.8144	1834.7878	1833.8038	**17**
4	70.0651	442.2085		424.1979	470.2034		452.1928		**P**	1738.7303	1737.7351	1780.7773	1763.7507	1762.7667	**16**

5	129.1135	598.3096	581.2831	580.2990	626.3045	609.2780	608.2940	513.2456	**R**	1582.6292	1581.6340	1683.7245	1666.6980	1665.7140	**15**
6	102.0550	727.3522	710.3256	709.3416	755.3471	738.3206	737.3365	669.3467	**E**			1527.6234	1510.5969	1509.6128	**14**
7	101.0709	855.4108	838.3842	837.4002	**883.4057**	866.3791	865.3951	798.3893	**Q**			1398.5808	1381.5543	1380.5703	**13**
8	88.0393	970.4377	953.4112	952.4272	**998.4326**	981.4061	980.4221	926.4479	**D**			1270.5222	1253.4957	1252.5117	**12**
9	120.0808	1117.5061	1100.4796	1099.4956	1145.5010	1128.4745	1127.4905		**F**			1155.4953	1138.4687	1137.4847	**11**
10	44.0495	1188.5432	1171.5167	1170.5327	1216.5382	1199.5116	1198.5276		**A**			1008.4269	991.4003	990.4163	**10**
11	87.0553	1302.5862	1285.5596	1284.5756	1330.5811	1313.5545	1312.5705	1259.5804	**N**			937.3898	920.3632	919.3792	**9**
12	44.0495	1373.6233	1356.5967	1355.6127	1401.6182	1384.5917	1383.6076		**A**			823.3468		805.3363	**8**
13	44.0495	1444.6604	1427.6339	1426.6498	**1472.6553**	1455.6288	1454.6448		**A**			752.3097		734.2992	**7**
14	102.0550	1573.7030	1556.6764	1555.6924	1601.6979	1584.6714	1583.6873	1515.6975	**E**			681.2726		663.2620	**6**
15	102.0550	1702.7456	1685.7190	1684.7350	1730.7405	1713.7140	1712.7299	1644.7401	**E**			552.2300		534.2195	**5**
16	60.0444	1789.7776	1772.7511	1771.7671	1817.7725	1800.7460	1799.7620	1773.7827	**S**			423.1874		405.1769	**4**
17	30.0338	1846.7991	1829.7725	1828.7885	1874.7940	1857.7674	1856.7834		**G**			**336.1554**			**3**
18	70.0651	1943.8518	1926.8253	1925.8413	1971.8468	1954.8202	1953.8362	1917.8362	**P**			**279.1339**			**2**
19	136.0757								**Y**			182.0812			**1**

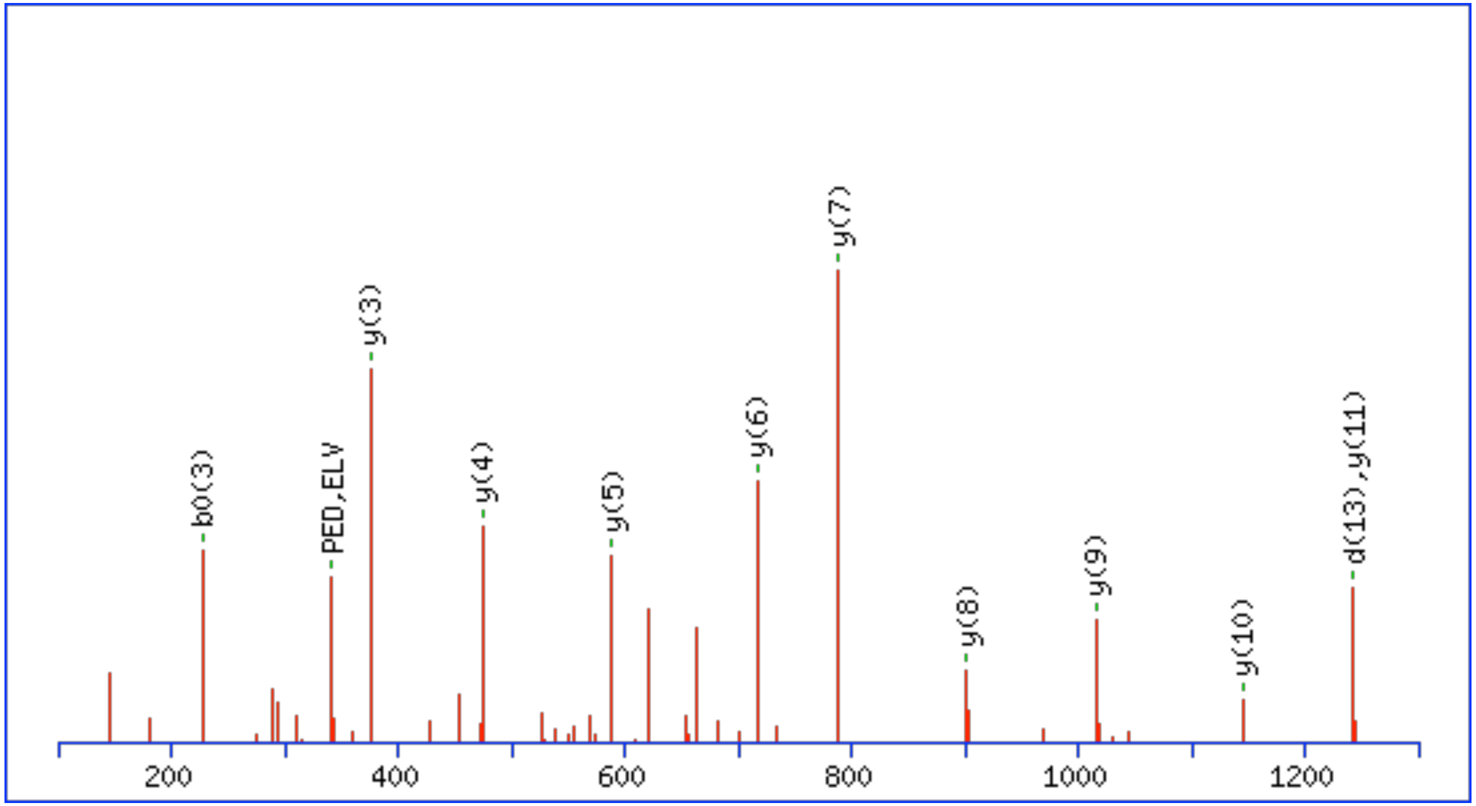
Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
WA	230.1288	258.1237	**WAP**	327.1816	355.1765	**WAPR**	483.2827	511.2776
WAPRE	612.3253	640.3202	**AP**	141.1022	169.0972	**APR**	297.2033	325.1983
APRE	426.2459	454.2409	**APREQ**	554.3045	582.2994	**APREQD**	669.3315	697.3264
PR	226.1662	254.1612	**PRE**	355.2088	383.2037	**PREQ**	483.2674	511.2623
PREQD	598.2944	626.2893	**RE**	258.1561	286.1510	**REQ**	386.2146	414.2096
REQD	501.2416	529.2365	**REQDF**	648.3100	676.3049	**EQ**	230.1135	258.1084
EQD	345.1405	373.1354	**EQDF**	492.2089	520.2038	**EQDFA**	563.2460	591.2409
EQDFAN	677.2889	705.2838	**QD**	216.0979	244.0928	**QDF**	363.1663	391.1612

QDFA	434.2034	462.1983	**QDFAN**	548.2463	576.2413	**QDFANA**	619.2835	647.2784
QDFANAA	690.3206	718.3155	**DF**	235.1077	263.1026	**DFA**	306.1448	334.1397
DFAN	420.1878	448.1827	**DFANA**	491.2249	519.2198	**DFANAA**	562.2620	590.2569
DFANAAE	691.3046	719.2995	**FA**	191.1179	219.1128	**FAN**	305.1608	333.1557
FANA	376.1979	404.1928	**FANAA**	447.2350	475.2300	**FANAAE**	576.2776	604.2726
AN	158.0924	186.0873	**ANA**	229.1295	257.1244	**ANAA**	300.1666	328.1615
ANAAE	429.2092	457.2041	**ANAAEE**	558.2518	586.2467	**ANAAEES**	645.2838	673.2788
NA	158.0924	186.0873	**NAA**	229.1295	257.1244	**NAAE**	358.1721	386.1670
NAAEE	487.2147	515.2096	**NAAEES**	574.2467	602.2416	**NAAEESG**	631.2682	659.2631
AA	115.0866	143.0815	**AAE**	244.1292	272.1241	**AAEE**	373.1718	401.1667
AAEES	460.2038	488.1987	**AAEESG**	517.2253	545.2202	**AAEESGP**	614.2780	642.2729
AE	173.0921	201.0870	**AEE**	302.1347	330.1296	**AEES**	389.1667	417.1616
AEESG	446.1882	474.1831	**AEESGP**	543.2409	571.2358	**EE**	231.0975	259.0925
EES	318.1296	346.1245	**EESG**	375.1510	403.1460	**EESGP**	472.2038	500.1987
ES	189.0870	217.0819	**ESG**	246.1084	**274.1034**	**ESGP**	343.1612	371.1561
SG	117.0659	145.0608	**SGP**	214.1186	242.1135	**GP**	**127.0866**	**155.0815**





MS/MS Fragmentation of **GSTPEDIAELVSRN**
Found in **New_Precursor_GSTPEDIA**, (3 exons, 112 aa), EST(BM322032)
Match to Query 207: 1486.434448 from(744.224500,2+) intensity(183.7582)
Data file Maldi_All.mgf



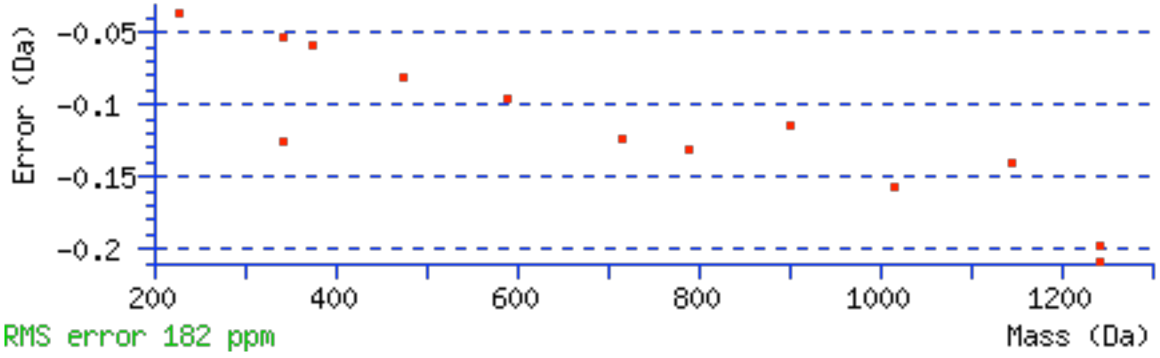
Monoisotopic mass of neutral peptide Mr(calc): 1486.7263 **Ions Score:** 92 **Expect:** 1.2e-05 **Matches (Bold Red):** 13/220 fragment ions using 11 most intense peaks

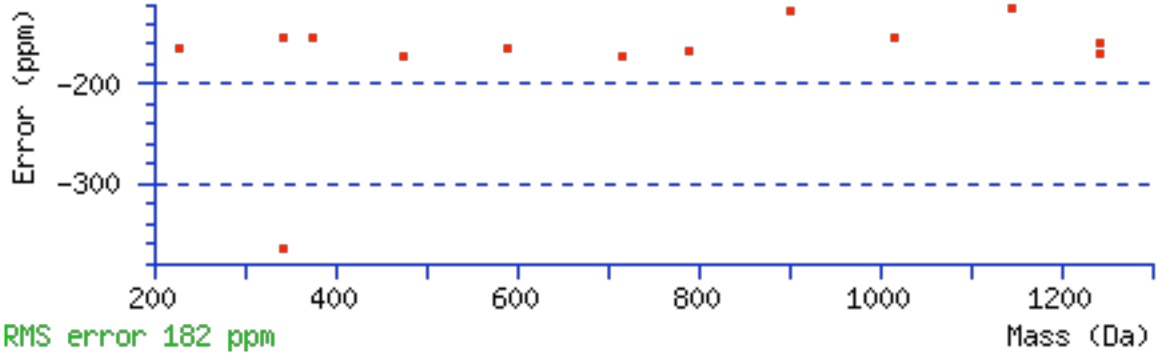
#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	w'	y	y*	y^0	#
1	30.0338	30.0338			58.0287				G							14
2	60.0444	117.0659		99.0553	145.0608		127.0502		S	1398.6859	1397.6907		1430.7122	1413.6856	1412.7016	13

3	74.0600	218.1135		200.1030	246.1084		**228.0979**		**T**	1297.6383	1310.6587	1312.6379	1343.6801	1326.6536	1325.6696	**12**
4	70.0651	315.1663		297.1557	343.1612		325.1506		**P**	1200.5855	1199.5903		**1242.6325**	1225.6059	1224.6219	**11**
5	102.0550	444.2089		426.1983	472.2038		454.1932		**E**	1071.5429	1070.5477		**1145.5797**	1128.5531	1127.5691	**10**
6	88.0393	559.2358		541.2253	587.2307		569.2202		**D**	956.5160	955.5207		**1016.5371**	999.5105	998.5265	**9**
7	86.0964	672.3199		654.3093	700.3148		682.3042		**I**	843.4319	856.4523	870.4680	**901.5102**	884.4836	883.4996	**8**
8	44.0495	743.3570		725.3464	771.3519		753.3414		**A**	772.3948			**788.4261**	771.3995	770.4155	**7**
9	102.0550	872.3996		854.3890	900.3945		882.3840		**E**	643.3522	642.3570		**717.3890**	700.3624	699.3784	**6**
10	86.0964	985.4837		967.4731	1013.4786		995.4680		**L**	530.2681	529.2729		**588.3464**	571.3198	570.3358	**5**
11	72.0808	1084.5521		1066.5415	1112.5470		1094.5364		**V**	431.1997	444.2201		**475.2623**	458.2358	457.2518	**4**
12	60.0444	1171.5841		1153.5735	1199.5790		1181.5685		**S**	344.1677	343.1724		**376.1939**	359.1674	358.1833	**3**
13	129.1135	1327.6852	1310.6587	1309.6747	1355.6801	1338.6536	1337.6696	**1242.6212**	**R**	188.0666	187.0713		289.1619	272.1353		**2**
14	87.0553								**N**				133.0608	116.0342		**1**

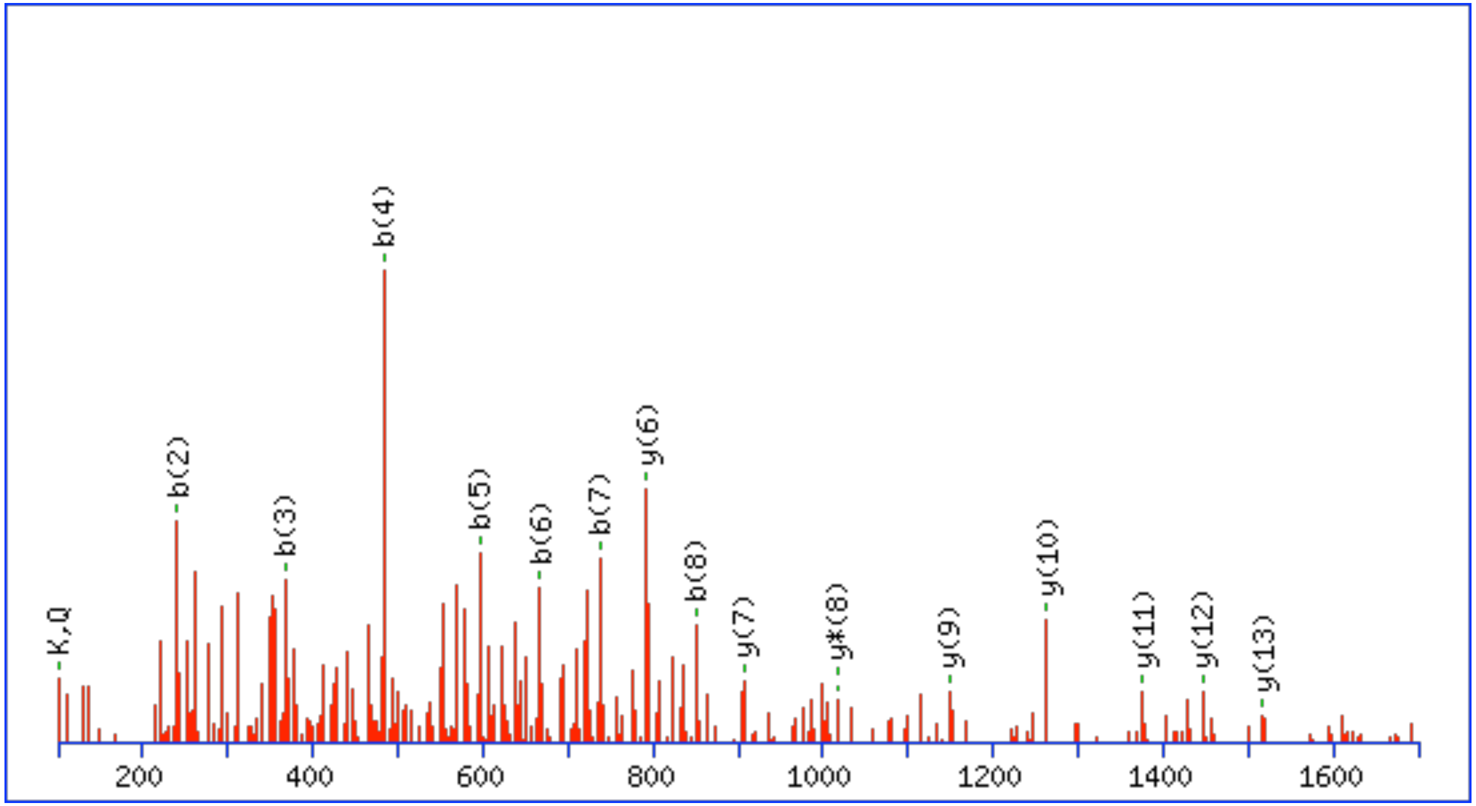
Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
ST	161.0921	189.0870	**STP**	258.1448	286.1397	**STPE**	387.1874	415.1823
STPED	502.2144	530.2093	**STPEDI**	615.2984	643.2933	**STPEDIA**	686.3355	714.3305
TP	171.1128	199.1077	**TPE**	300.1554	328.1503	**TPED**	415.1823	443.1773
TPEDI	528.2664	556.2613	**TPEDIA**	599.3035	627.2984	**PE**	199.1077	227.1026

PED	314.1347	**342.1296**	**PEDI**	427.2187	455.2136	**PEDIA**	498.2558	526.2508
PEDIAE	627.2984	655.2933	**ED**	217.0819	245.0768	**EDI**	330.1660	358.1609
EDIA	401.2031	429.1980	**EDIAE**	530.2457	558.2406	**EDIAEL**	643.3297	671.3246
DI	201.1234	229.1183	**DIA**	272.1605	300.1554	**DIAE**	401.2031	429.1980
DIAEL	514.2871	542.2821	**DIAELV**	613.3556	641.3505	**IA**	157.1335	185.1285
IAE	286.1761	314.1710	**IAEL**	399.2602	427.2551	**IAELV**	498.3286	526.3235
IAELVS	585.3606	613.3556	**AE**	173.0921	201.0870	**AEL**	286.1761	314.1710
AELV	385.2445	413.2395	**AELVS**	472.2766	500.2715	**AELVSR**	628.3777	656.3726
EL	215.1390	243.1339	**ELV**	314.2074	**342.2023**	**ELVS**	401.2395	429.2344
ELVSR	557.3406	585.3355	**LV**	185.1648	213.1598	**LVS**	272.1969	300.1918
LVSR	428.2980	456.2929	**VS**	159.1128	187.1077	**VSR**	315.2139	343.2088
SR	216.1455	244.1404						





MS/MS Fragmentation of **QKQDLAAILDQLHNTYQM**
Found in **New_Precursor_GSTPEDIA**, (3 exons, 112 aa), EST(BM322032)
Match to Query 359: 2111.592648 from(1056.803600,2+) intensity(15571.3008)
Data file Maldi_All.mgf



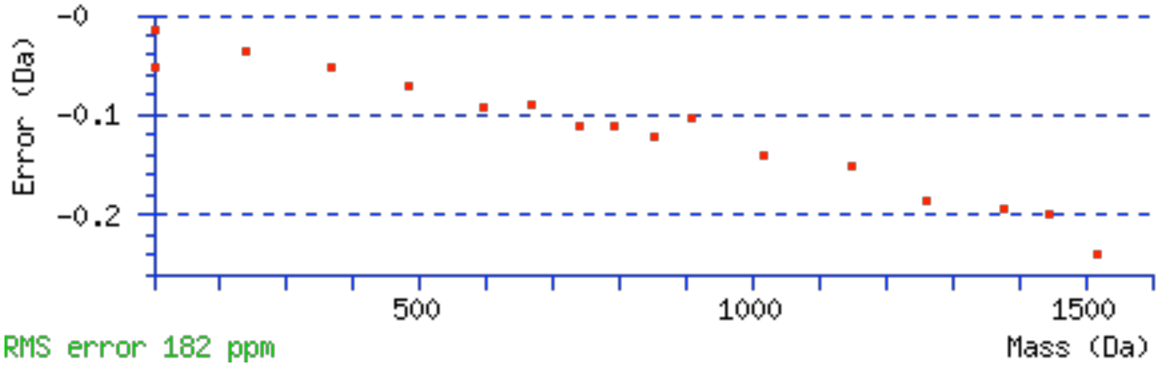
Monoisotopic mass of neutral peptide Mr(calc): 2112.0310 **Variable modifications: N-term :** Gln->pyro-Glu (N-term Q)
Ions Score: 70 **Expect:** 0.003 **Matches (Bold Red):** 20/288 fragment ions using 25 most intense peaks

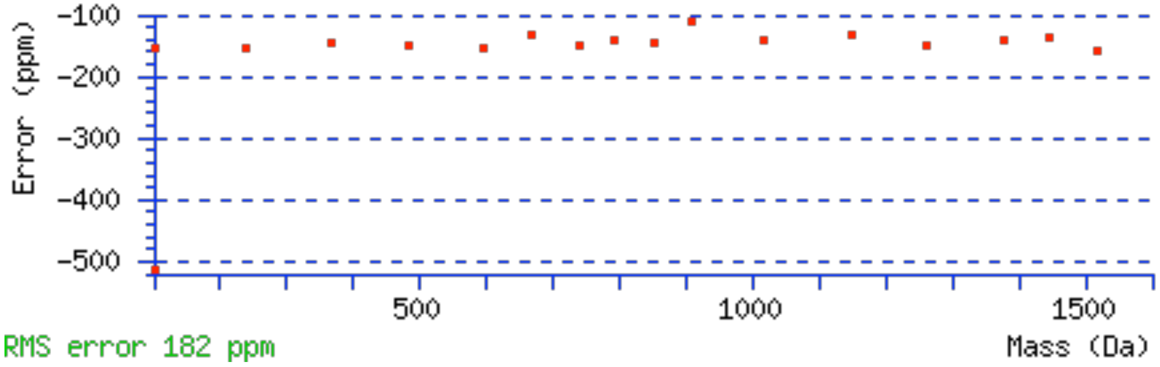
#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	y	y*	y^0	#
1	**101.0709**	84.0444	67.0179		112.0393	95.0128		**Q**				**18**
2	**101.1073**	212.1394	195.1128		**240.1343**	223.1077		**K**	2002.0062	1984.9797	1983.9957	**17**
3	**101.0709**	340.1979	323.1714		**368.1929**	351.1663		**Q**	1873.9113	1856.8847	1855.9007	**16**
4	88.0393	455.2249	438.1983	437.2143	**483.2198**	466.1933	465.2092	**D**	1745.8527	1728.8262	1727.8421	**15**

5	86.0964	568.3090	551.2824	550.2984	**596.3039**	579.2773	578.2933	**L**	1630.8258	1613.7992	1612.8152	**14**
6	44.0495	639.3461	622.3195	621.3355	**667.3410**	650.3144	649.3304	**A**	**1517.7417**	1500.7151	1499.7311	**13**
7	44.0495	710.3832	693.3566	692.3726	**738.3781**	721.3515	720.3675	**A**	**1446.7046**	1429.6780	1428.6940	**12**
8	86.0964	823.4672	806.4407	805.4567	**851.4622**	834.4356	833.4516	**I**	**1375.6675**	1358.6409	1357.6569	**11**
9	86.0964	936.5513	919.5248	918.5407	964.5462	947.5197	946.5357	**L**	**1262.5834**	1245.5569	1244.5728	**10**
10	88.0393	1051.5783	1034.5517	1033.5677	1079.5732	1062.5466	1061.5626	**D**	**1149.4993**	1132.4728	1131.4888	**9**
11	**101.0709**	1179.6368	1162.6103	1161.6263	1207.6317	1190.6052	1189.6212	**Q**	1034.4724	**1017.4458**	1016.4618	**8**
12	86.0964	1292.7209	1275.6943	1274.7103	1320.7158	1303.6893	1302.7052	**L**	**906.4138**	889.3873	888.4033	**7**
13	110.0713	1429.7798	1412.7533	1411.7692	1457.7747	1440.7482	1439.7642	**H**	**793.3298**	776.3032	775.3192	**6**
14	87.0553	1543.8227	1526.7962	1525.8122	1571.8176	1554.7911	1553.8071	**N**	656.2708	639.2443	638.2603	**5**
15	74.0600	1644.8704	1627.8439	1626.8598	1672.8653	1655.8388	1654.8548	**T**	542.2279	525.2014	524.2173	**4**
16	136.0757	1807.9337	1790.9072	1789.9232	1835.9287	1818.9021	1817.9181	**Y**	441.1802	424.1537		**3**
17	**101.0709**	1935.9923	1918.9658	1917.9818	1963.9872	1946.9607	1945.9767	**Q**	278.1169	261.0904		**2**
18	104.0528							**M**	150.0583			**1**

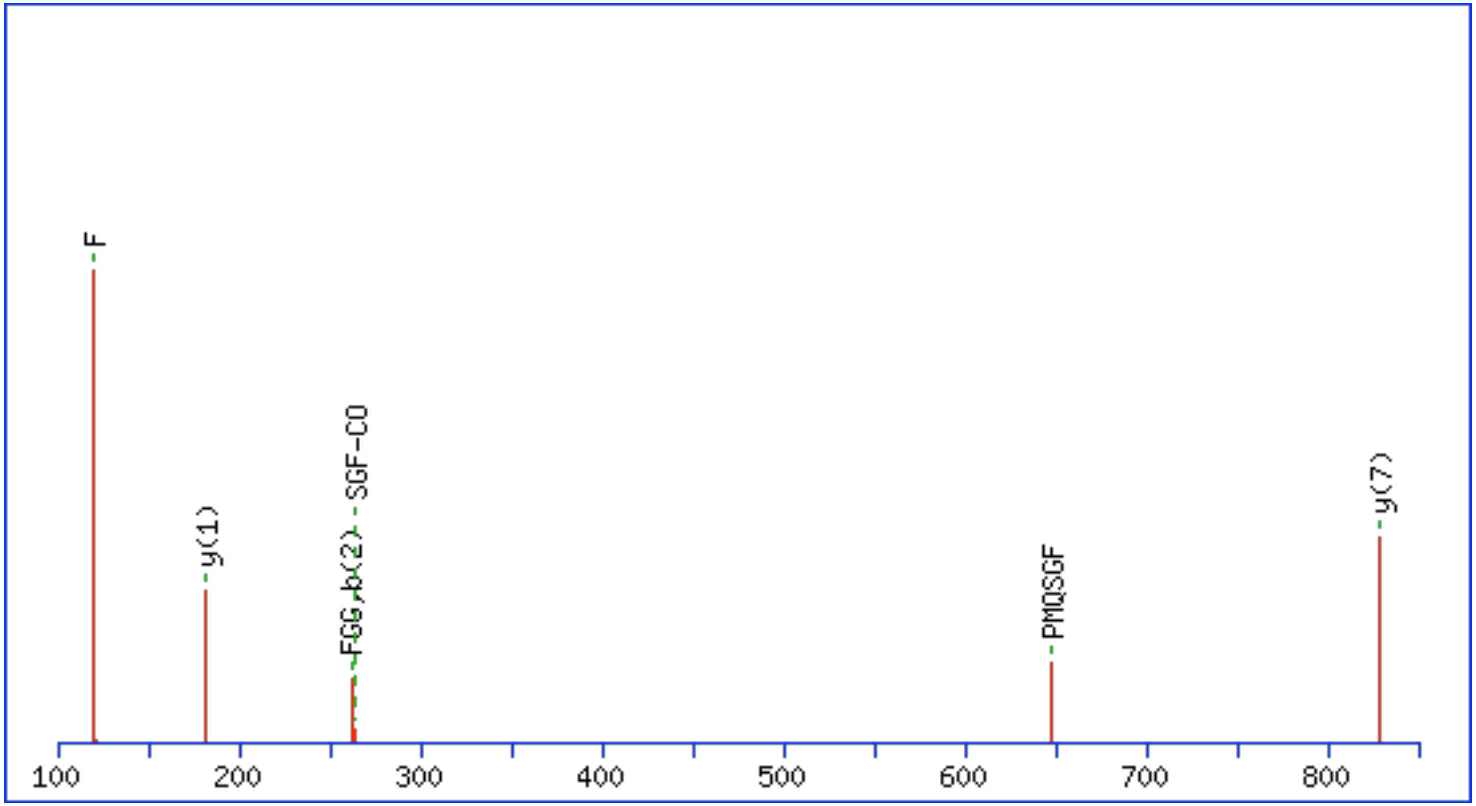
Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
KQ	229.1659	257.1608	**KQD**	344.1928	372.1878	**KQDL**	457.2769	485.2718
KQDLA	528.3140	556.3089	**KQDLAA**	599.3511	627.3461	**QD**	216.0979	244.0928
QDL	329.1819	357.1769	**QDLA**	400.2191	428.2140	**QDLAA**	471.2562	499.2511
QDLAAI	584.3402	612.3352	**QDLAAIL**	697.4243	725.4192	**DL**	201.1234	229.1183
DLA	272.1605	300.1554	**DLAA**	343.1976	371.1925	**DLAAI**	456.2817	484.2766
DLAAIL	569.3657	597.3606	**DLAAILD**	684.3927	712.3876	**LA**	157.1335	185.1285
LAA	228.1707	256.1656	**LAAI**	341.2547	369.2496	**LAAIL**	454.3388	482.3337
LAAILD	569.3657	597.3606	**LAAILDQ**	697.4243	725.4192	**AA**	115.0866	143.0815
AAI	228.1707	256.1656	**AAIL**	341.2547	369.2496	**AAILD**	456.2817	484.2766

AAILDQ	584.3402	612.3352	**AAILDQL**	697.4243	725.4192	**AI**	157.1335	185.1285
AIL	270.2176	298.2125	**AILD**	385.2445	413.2395	**AILDQ**	513.3031	541.2980
AILDQL	626.3872	654.3821	**IL**	199.1805	227.1754	**ILD**	314.2074	342.2023
ILDQ	442.2660	470.2609	**ILDQL**	555.3501	583.3450	**ILDQLH**	692.4090	720.4039
LD	201.1234	229.1183	**LDQ**	329.1819	357.1769	**LDQL**	442.2660	470.2609
LDQLH	579.3249	607.3198	**LDQLHN**	693.3678	721.3628	**DQ**	216.0979	244.0928
DQL	329.1819	357.1769	**DQLH**	466.2409	494.2358	**DQLHN**	580.2838	608.2787
DQLHNT	681.3315	709.3264	**QL**	214.1550	242.1499	**QLH**	351.2139	379.2088
QLHN	465.2568	493.2518	**QLHNT**	566.3045	594.2994	**LH**	223.1553	251.1503
LHN	337.1983	365.1932	**LHNT**	438.2459	466.2409	**LHNTY**	601.3093	629.3042
HN	224.1142	252.1091	**HNT**	325.1619	353.1568	**HNTY**	488.2252	516.2201
HNTYQ	616.2838	644.2787	**NT**	188.1030	216.0979	**NTY**	351.1663	379.1612
NTYQ	479.2249	507.2198	**TY**	237.1234	265.1183	**TYQ**	365.1819	393.1769
YQ	264.1343	292.1292						





MS/MS Fragmentation of **NFGGSMEPMQSGFY**
Found in **New_Precursor_FGGANEPM**, (2 exons, 184 aa), EST(CD294941)
Match to Query 277: 1550.310648 from(776.162600,2+) intensity(718.3754)
Data file Maldi_All.mgf



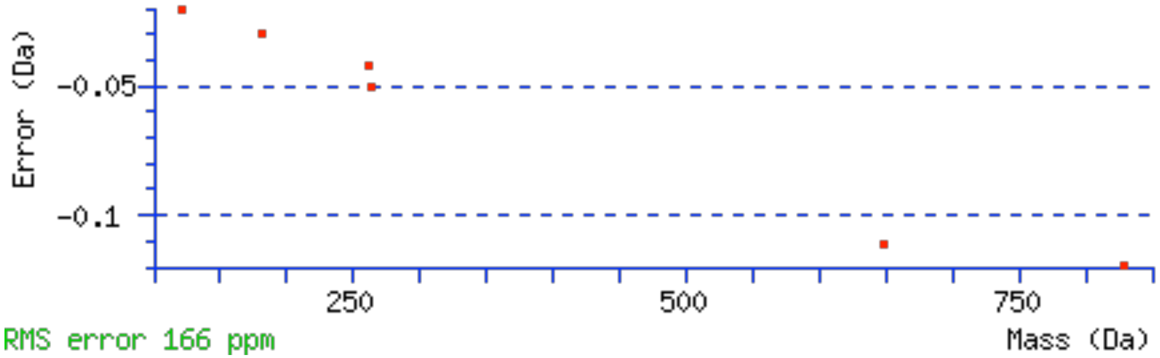
Monoisotopic mass of neutral peptide Mr(calc): 1550.6170 **Ions Score:** 18 **Expect:** 5.2e+02 **Matches (Bold Red):** 8/207 fragment ions using 6 most intense peaks

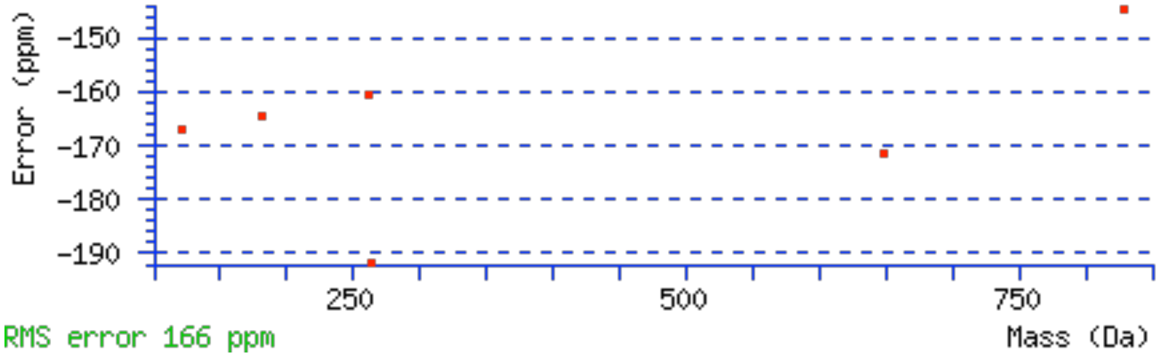
#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	y	y*	y^0	#
1	87.0553	87.0553	70.0287		115.0502	98.0237		**N**				**14**
2	**120.0808**	234.1237	217.0972		**262.1186**	245.0921		**F**	1437.5814	1420.5548	1419.5708	**13**
3	30.0338	291.1452	274.1186		319.1401	302.1135		**G**	1290.5129	1273.4864	1272.5024	**12**
4	30.0338	348.1666	331.1401		376.1615	359.1350		**G**	1233.4915	1216.4649	1215.4809	**11**

5	60.0444	435.1987	418.1721	417.1881	463.1936	446.1670	445.1830	S	1176.4700	1159.4435	1158.4594	10
6	104.0528	566.2391	549.2126	548.2286	594.2341	577.2075	576.2235	M	1089.4380	1072.4114	1071.4274	9
7	102.0550	695.2817	678.2552	677.2712	723.2767	706.2501	705.2661	E	958.3975	941.3709	940.3869	8
8	70.0651	792.3345	775.3080	774.3239	820.3294	803.3029	802.3188	P	**829.3549**	812.3284	811.3443	7
9	104.0528	923.3750	906.3484	905.3644	951.3699	934.3434	933.3593	M	732.3021	715.2756	714.2916	6
10	101.0709	1051.4336	1034.4070	1033.4230	1079.4285	1062.4019	1061.4179	Q	601.2617	584.2351	583.2511	5
11	60.0444	1138.4656	1121.4390	1120.4550	1166.4605	1149.4340	1148.4499	S	473.2031		455.1925	4
12	30.0338	1195.4871	1178.4605	1177.4765	1223.4820	1206.4554	1205.4714	G	386.1710			3
13	**120.0808**	1342.5555	1325.5289	1324.5449	1370.5504	1353.5238	1352.5398	F	329.1496			2
14	136.0757							Y	**182.0812**			1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
FG	177.1022	205.0972	FGG	234.1237	**262.1186**	FGGS	321.1557	349.1506
FGGSM	452.1962	480.1911	FGGSME	581.2388	609.2337	FGGSMEP	678.2916	706.2865
GG	87.0553	115.0502	GGS	174.0873	202.0822	GGSM	305.1278	333.1227
GGSME	434.1704	462.1653	GGSMEP	531.2232	559.2181	GGSMEPM	662.2636	690.2586
GS	117.0659	145.0608	GSM	248.1063	276.1013	GSME	377.1489	405.1438
GSMEP	474.2017	502.1966	GSMEPM	605.2422	633.2371	SM	191.0849	219.0798
SME	320.1275	348.1224	SMEP	417.1802	445.1751	SMEPM	548.2207	576.2156
SMEPMQ	676.2793	704.2742	ME	233.0954	261.0904	MEP	330.1482	358.1431
MEPM	461.1887	489.1836	MEPMQ	589.2473	617.2422	MEPMQS	676.2793	704.2742
EP	199.1077	227.1026	EPM	330.1482	358.1431	EPMQ	458.2068	486.2017
EPMQS	545.2388	573.2337	EPMQSG	602.2603	630.2552	PM	201.1056	229.1005
PMQ	329.1642	357.1591	PMQS	416.1962	444.1911	PMQSG	473.2177	501.2126
PMQSGF	620.2861	**648.2810**	MQ	232.1114	260.1063	MQS	319.1435	347.1384

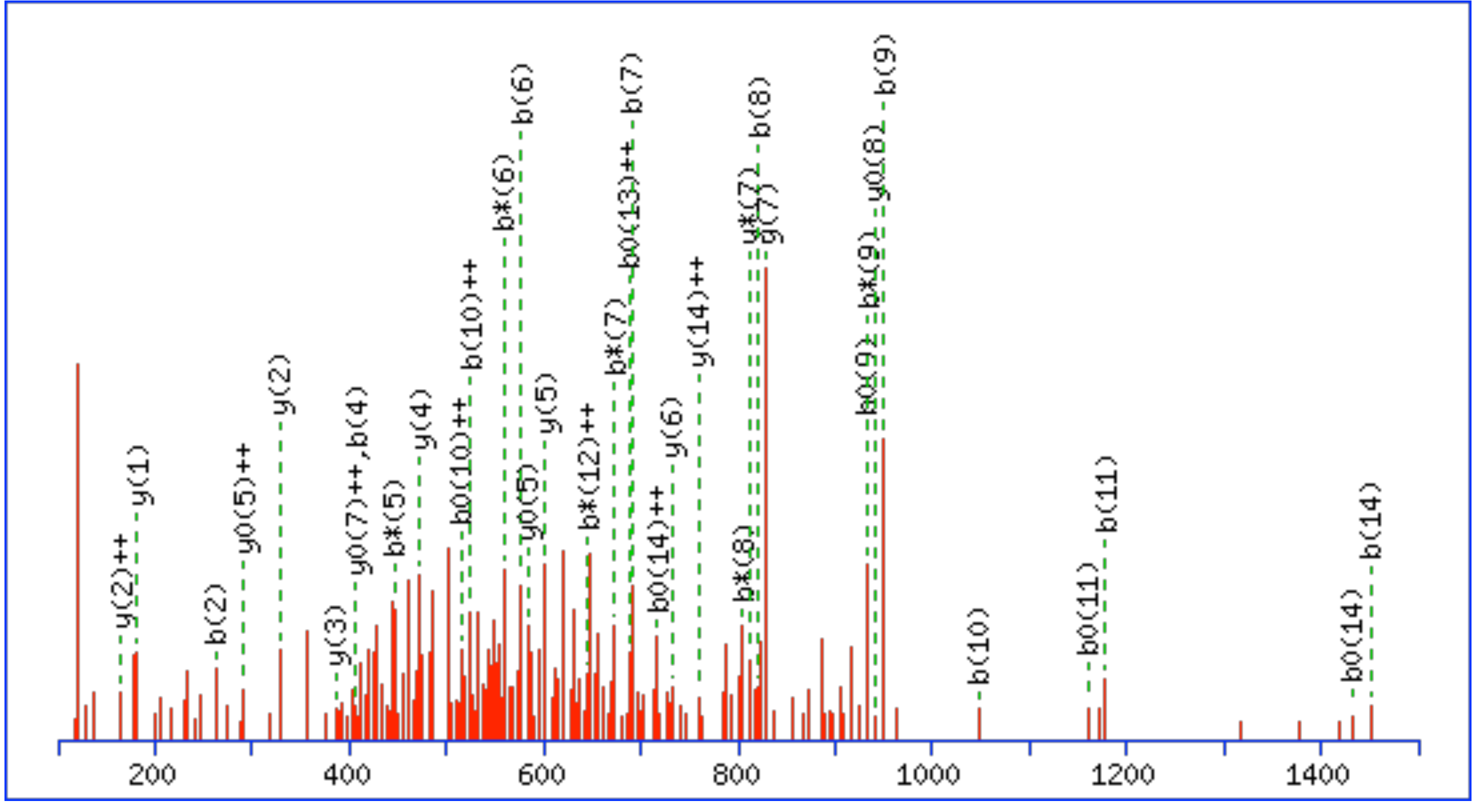
MQSG	376.1649	404.1598	**MQSGF**	523.2333	551.2282	**QS**	188.1030	216.0979
QSG	245.1244	273.1193	**QSGF**	392.1928	420.1878	**SG**	117.0659	145.0608
SGF	**264.1343**	292.1292	**GF**	177.1022	205.0972			





MS/MS Fragmentation of **NFGSGLNMEPMQSGFY**
Found in **New_Precursor_FGGANEPM**, (2 exons, 184 aa), EST(CD294941)

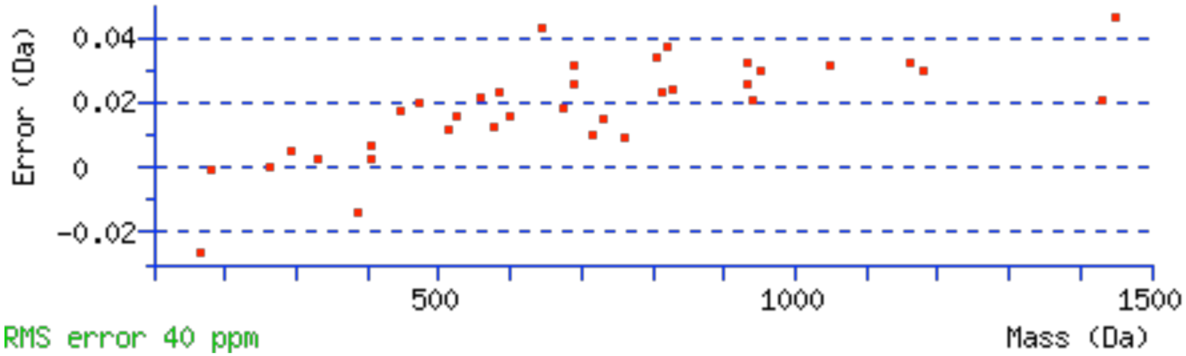
Match to Query 725: 1777.760968 from(889.887760,2+) intensity(173056.0000)
Title: Cmpd 228, +MSn(890.4839), 34.8 min
Data file Qtof_all.mgf

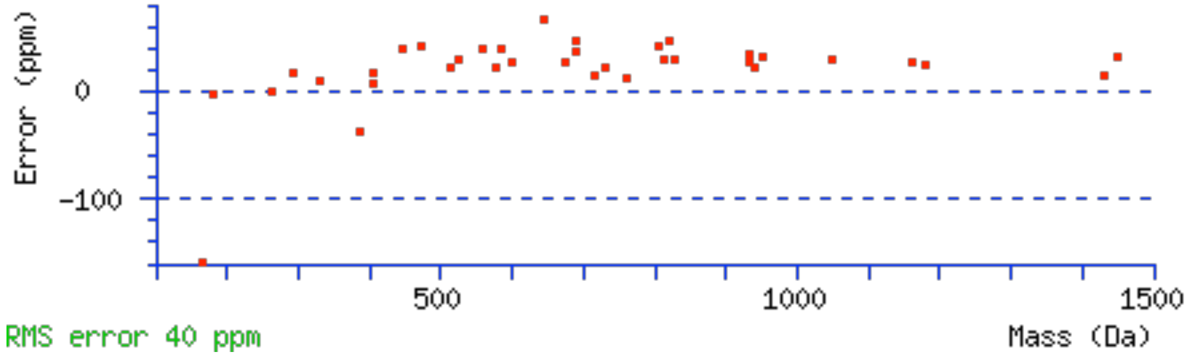


Monoisotopic mass of neutral peptide Mr(calc): 1777.7440 **Ions Score:** 35 **Expect:** 1.7 **Matches (Bold Red):** 36/160 fragment ions using 86 most intense peaks

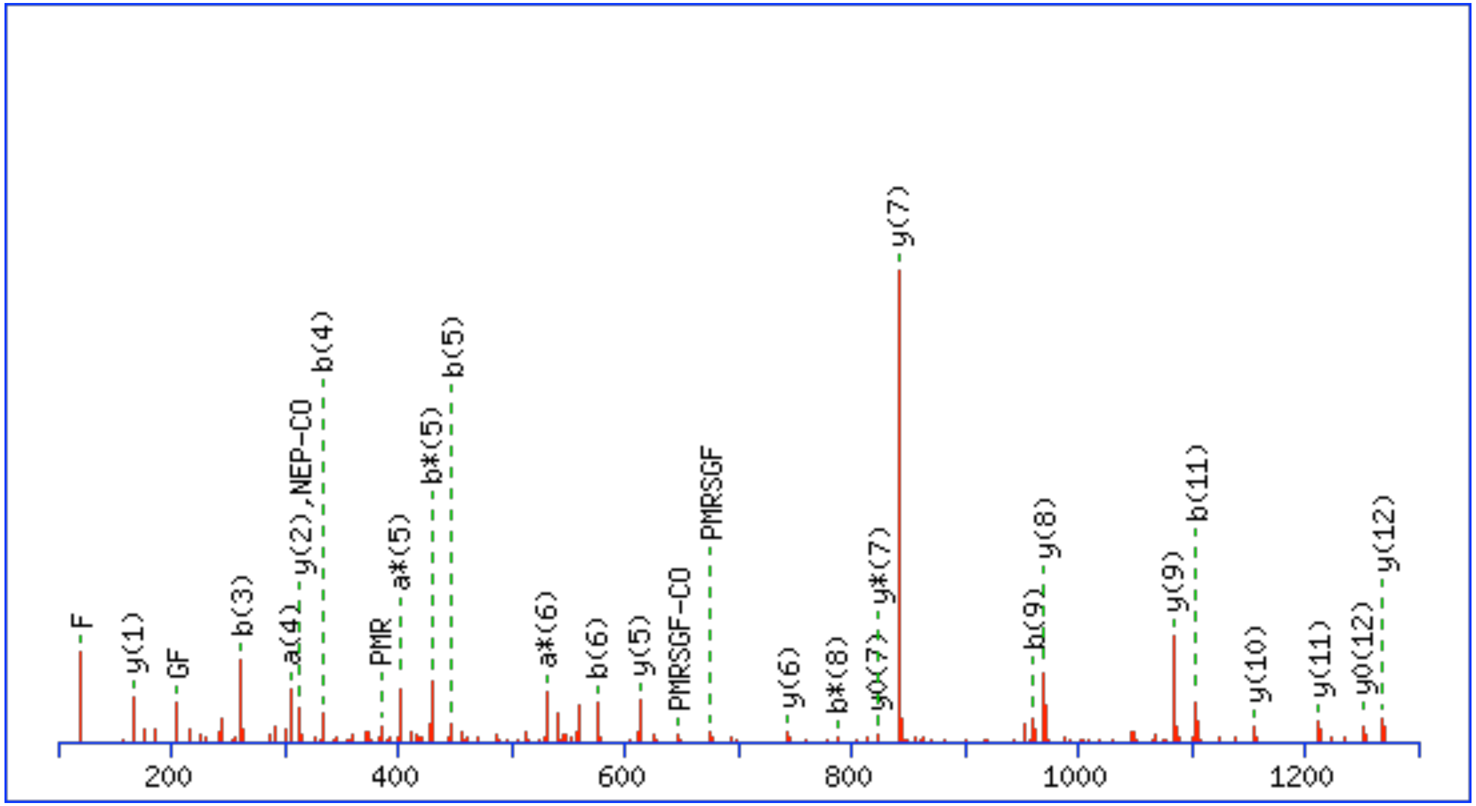
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			**N**							**16**
2	**262.1186**	131.5629	245.0921	123.0497			**F**	1664.7083	832.8578	1647.6818	824.3445	1646.6978	823.8525	**15**

3	319.1401	160.0737	302.1135	151.5604			**G**	1517.6399	**759.3236**	1500.6134	750.8103	1499.6294	750.3183	**14**
4	**406.1721**	203.5897	389.1456	195.0764	388.1615	194.5844	**S**	1460.6185	730.8129	1443.5919	722.2996	1442.6079	721.8076	**13**
5	463.1936	232.1004	**446.1670**	223.5871	445.1830	223.0951	**G**	1373.5864	687.2969	1356.5599	678.7836	1355.5759	678.2916	**12**
6	**576.2776**	288.6425	**559.2511**	280.1292	558.2671	279.6372	**L**	1316.5650	658.7861	1299.5384	650.2728	1298.5544	649.7808	**11**
7	**690.3206**	345.6639	**673.2940**	337.1506	672.3100	336.6586	**N**	1203.4809	602.2441	1186.4544	593.7308	1185.4703	593.2388	**10**
8	**821.3610**	411.1842	**804.3345**	402.6709	803.3505	402.1789	**M**	1089.4380	545.2226	1072.4114	536.7094	1071.4274	536.2173	**9**
9	**950.4036**	475.7055	**933.3771**	467.1922	**932.3931**	466.7002	**E**	958.3975	479.7024	941.3709	471.1891	**940.3869**	470.6971	**8**
10	**1047.4564**	**524.2318**	1030.4299	515.7186	1029.4458	**515.2266**	**P**	**829.3549**	415.1811	**812.3284**	406.6678	811.3443	**406.1758**	**7**
11	**1178.4969**	589.7521	1161.4703	581.2388	**1160.4863**	580.7468	**M**	**732.3021**	366.6547	715.2756	358.1414	714.2916	357.6494	**6**
12	1306.5555	653.7814	1289.5289	**645.2681**	1288.5449	644.7761	**Q**	**601.2617**	301.1345	584.2351	292.6212	**583.2511**	**292.1292**	**5**
13	1393.5875	697.2974	1376.5609	688.7841	1375.5769	**688.2921**	**S**	**473.2031**	237.1052			455.1925	228.0999	**4**
14	**1450.6090**	725.8081	1433.5824	717.2948	**1432.5984**	**716.8028**	**G**	**386.1710**	193.5892					**3**
15	1597.6774	799.3423	1580.6508	790.8291	1579.6668	790.3370	**F**	**329.1496**	**165.0784**					**2**
16							**Y**	**182.0812**	91.5442					**1**





MS/MS Fragmentation of **FGGANEPMRSGFF**
Found in **New_Precursor_FGGANEPM**, (2 exons, 184 aa), EST(CD294941)
Match to Query 170: 1415.331248 from(708.672900,2+) intensity(12263.6895)
Data file Maldi_All.mgf

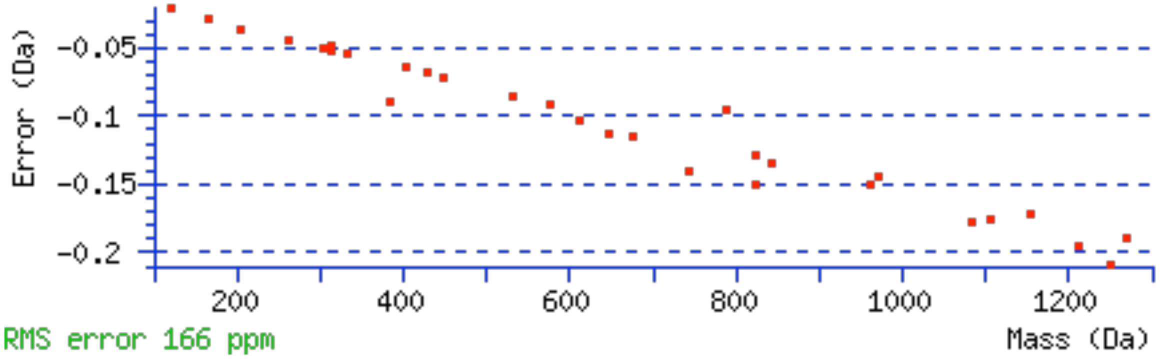


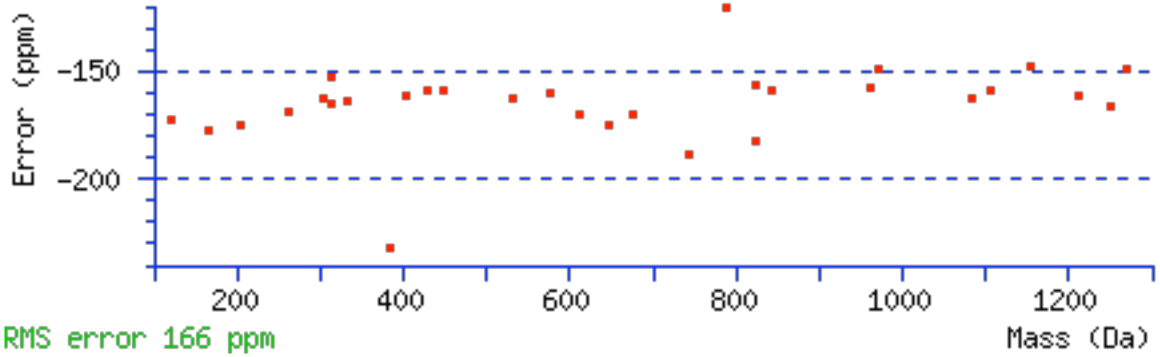
Monoisotopic mass of neutral peptide Mr(calc): 1415.6292 **Ions Score:** 86 **Expect:** 7.1e-05 **Matches (Bold Red):** 35/190 fragment ions using 40 most intense peaks

#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	**120.0808**	**120.0808**			148.0757				F						13
2	30.0338	177.1022			**205.0972**				G			**1269.5681**	1252.5415	**1251.5575**	12
3	30.0338	234.1237			**262.1186**				G			**1212.5466**	1195.5201	1194.5361	11
4	44.0495	**305.1608**			**333.1557**				A	1139.4939		**1155.5252**	1138.4986	1137.5146	10

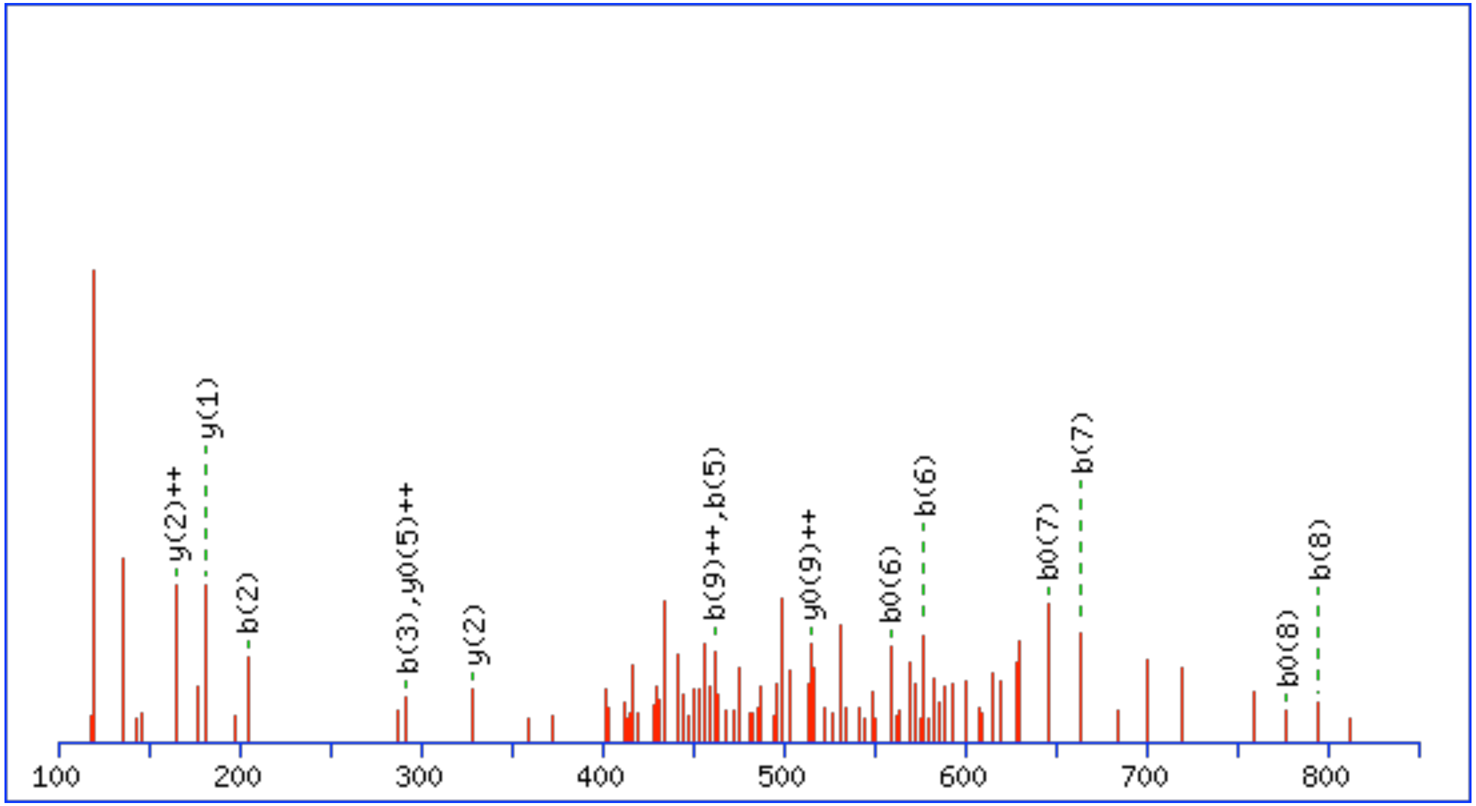
5	87.0553	419.2037	**402.1772**		**447.1987**	**430.1721**			**N**	1025.4509	1024.4557	**1084.4880**	1067.4615	1066.4775	**9**
6	102.0550	548.2463	**531.2198**	530.2358	**576.2413**	559.2147	558.2307		**E**	896.4083	895.4131	**970.4451**	953.4186	952.4345	**8**
7	70.0651	645.2991	628.2726	627.2885	673.2940	656.2675	655.2835		**P**	799.3556	798.3603	**841.4025**	**824.3760**	**823.3920**	**7**
8	104.0528	776.3396	759.3130	758.3290	804.3345	**787.3080**	786.3239		**M**	668.3151	667.3198	**744.3498**	727.3232	726.3392	**6**
9	129.1135	932.4407	915.4141	914.4301	**960.4356**	943.4091	942.4250	847.3767	**R**	512.2140	511.2187	**613.3093**	596.2827	595.2987	**5**
10	60.0444	1019.4727	1002.4462	1001.4622	1047.4676	1030.4411	1029.4571	1003.4778	**S**			457.2082		439.1976	**4**
11	30.0338	1076.4942	1059.4676	1058.4836	**1104.4891**	1087.4626	1086.4785		**G**			370.1761			**3**
12	**120.0808**	1223.5626	1206.5361	1205.5520	**1251.5575**	1234.5310	1233.5470		**F**			**313.1547**			**2**
13	**120.0808**								**F**			**166.0863**			**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GG	87.0553	115.0502	**GGA**	158.0924	186.0873	**GGAN**	272.1353	300.1302
GGANE	401.1779	429.1728	**GGANEP**	498.2307	526.2256	**GGANEPM**	629.2712	657.2661
GA	101.0709	129.0659	**GAN**	215.1139	243.1088	**GANE**	344.1565	372.1514
GANEP	441.2092	469.2041	**GANEPM**	572.2497	600.2446	**AN**	158.0924	186.0873
ANE	287.1350	315.1299	**ANEP**	384.1878	412.1827	**ANEPM**	515.2282	543.2232
ANEPMR	671.3294	699.3243	**NE**	216.0979	244.0928	**NEP**	**313.1506**	341.1456
NEPM	444.1911	472.1860	**NEPMR**	600.2922	628.2872	**NEPMRS**	687.3243	715.3192
EP	199.1077	227.1026	**EPM**	330.1482	358.1431	**EPMR**	486.2493	514.2442
EPMRS	573.2813	601.2763	**EPMRSG**	630.3028	658.2977	**PM**	201.1056	229.1005
PMR	357.2067	**385.2016**	**PMRS**	444.2387	472.2337	**PMRSG**	501.2602	529.2551
PMRSGF	**648.3286**	**676.3235**	**MR**	260.1540	288.1489	**MRS**	347.1860	375.1809
MRSG	404.2074	432.2024	**MRSGF**	551.2759	579.2708	**RS**	216.1455	244.1404
RSG	273.1670	301.1619	**RSGF**	420.2354	448.2303	**SG**	117.0659	145.0608
SGF	264.1343	292.1292	**GF**	177.1022	**205.0972**			





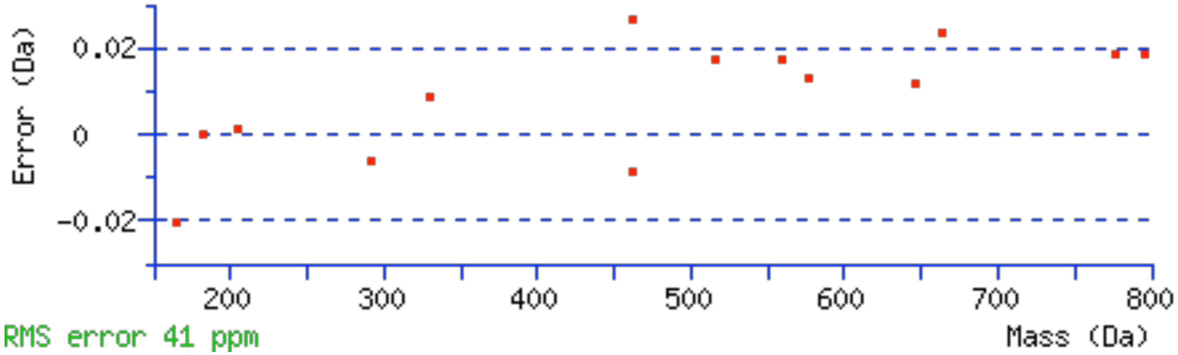
MS/MS Fragmentation of **FGSGLDSMQSGFY**
Found in **New_Precursor_FGGANEPM**, (2 exons, 184 aa), EST(CD294941)
Match to Query 548: 1394.613908 from(698.314230,2+) intensity(339896.0000)
Title: Cmpd 208, +MSn(698.8380), 33.2 min
Data file Qtof_all.mgf

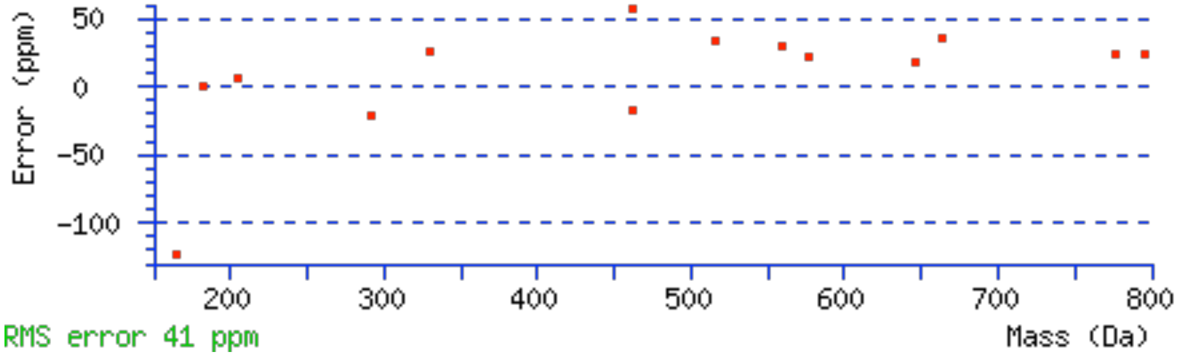


Monoisotopic mass of neutral peptide Mr(calc): 1394.5813 **Ions Score:** 21 **Expect:** 68 **Matches (Bold Red):** 15/110 fragment ions using 32 most intense peaks

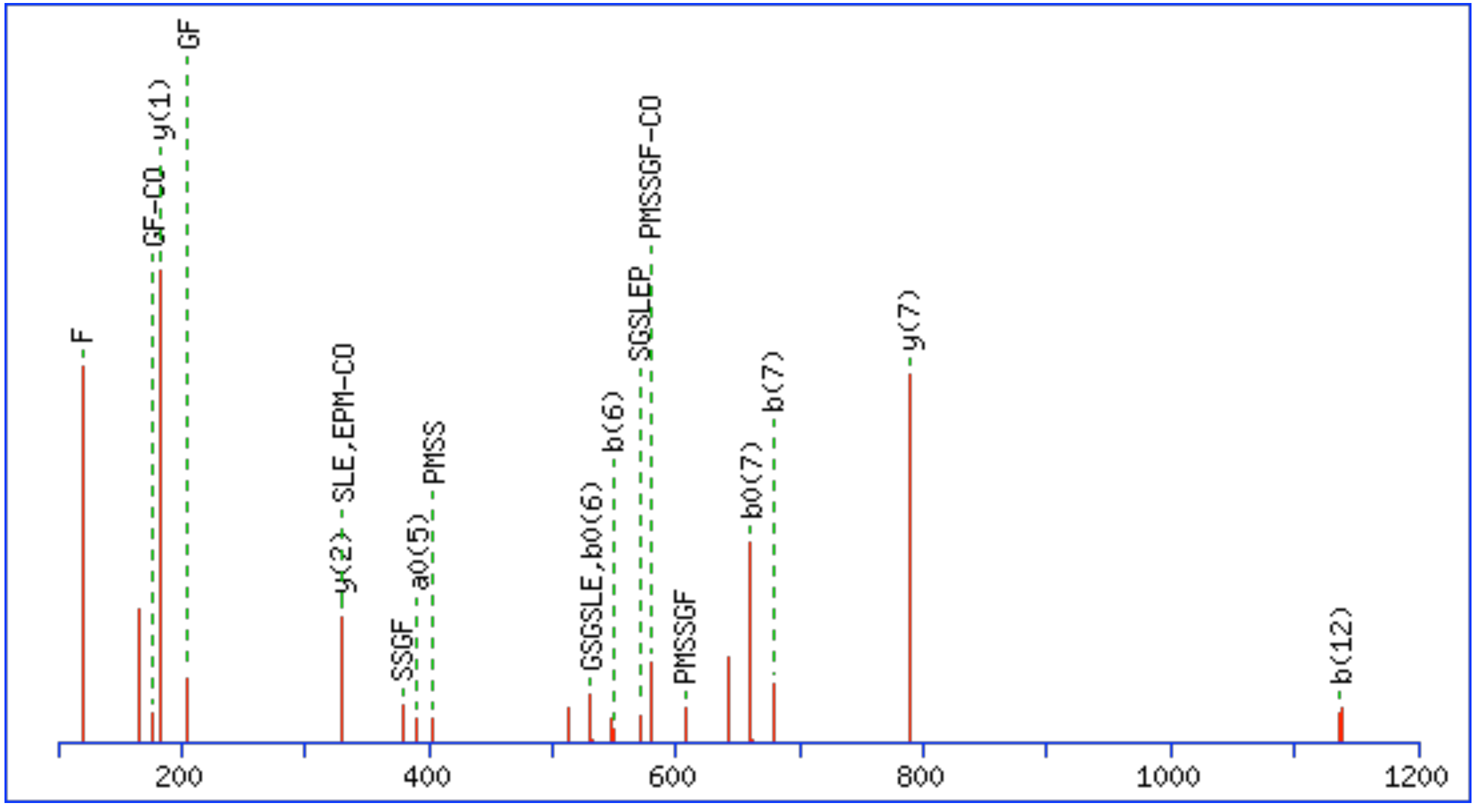
#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							13
2	**205.0972**	103.0522					G	1248.5201	624.7637	1231.4936	616.2504	1230.5096	615.7584	12
3	**292.1292**	146.5682			274.1186	137.5629	S	1191.4987	596.2530	1174.4721	587.7397	1173.4881	587.2477	11
4	349.1506	175.0790			331.1401	166.0737	G	1104.4666	552.7370	1087.4401	544.2237	1086.4561	543.7317	10

5	**462.2347**	231.6210			444.2241	222.6157	**L**	1047.4452	524.2262	1030.4186	515.7130	1029.4346	**515.2209**	**9**
6	**577.2617**	289.1345			**559.2511**	280.1292	**D**	934.3611	467.6842	917.3346	459.1709	916.3505	458.6789	**8**
7	**664.2937**	332.6505			**646.2831**	323.6452	**S**	819.3342	410.1707	802.3076	401.6574	801.3236	401.1654	**7**
8	**795.3342**	398.1707			**777.3236**	389.1654	**M**	732.3021	366.6547	715.2756	358.1414	714.2916	357.6494	**6**
9	923.3927	**462.2000**	906.3662	453.6867	905.3822	453.1947	**Q**	601.2617	301.1345	584.2351	292.6212	583.2511	**292.1292**	**5**
10	1010.4248	505.7160	993.3982	497.2027	992.4142	496.7107	**S**	473.2031	237.1052			455.1925	228.0999	**4**
11	1067.4462	534.2268	1050.4197	525.7135	1049.4357	525.2215	**G**	386.1710	193.5892					**3**
12	1214.5147	607.7610	1197.4881	599.2477	1196.5041	598.7557	**F**	**329.1496**	**165.0784**					**2**
13							**Y**	**182.0812**	91.5442					**1**





MS/MS Fragmentation of **FGSGSLEPMSSGFY**
Found in **New_Precursor_FGGANEPM**, (2 exons, 184 aa), EST(CD294941)
Match to Query 193: 1464.394048 from(733.204300,2+) intensity(465.4211)
Data file Maldi_All.mgf



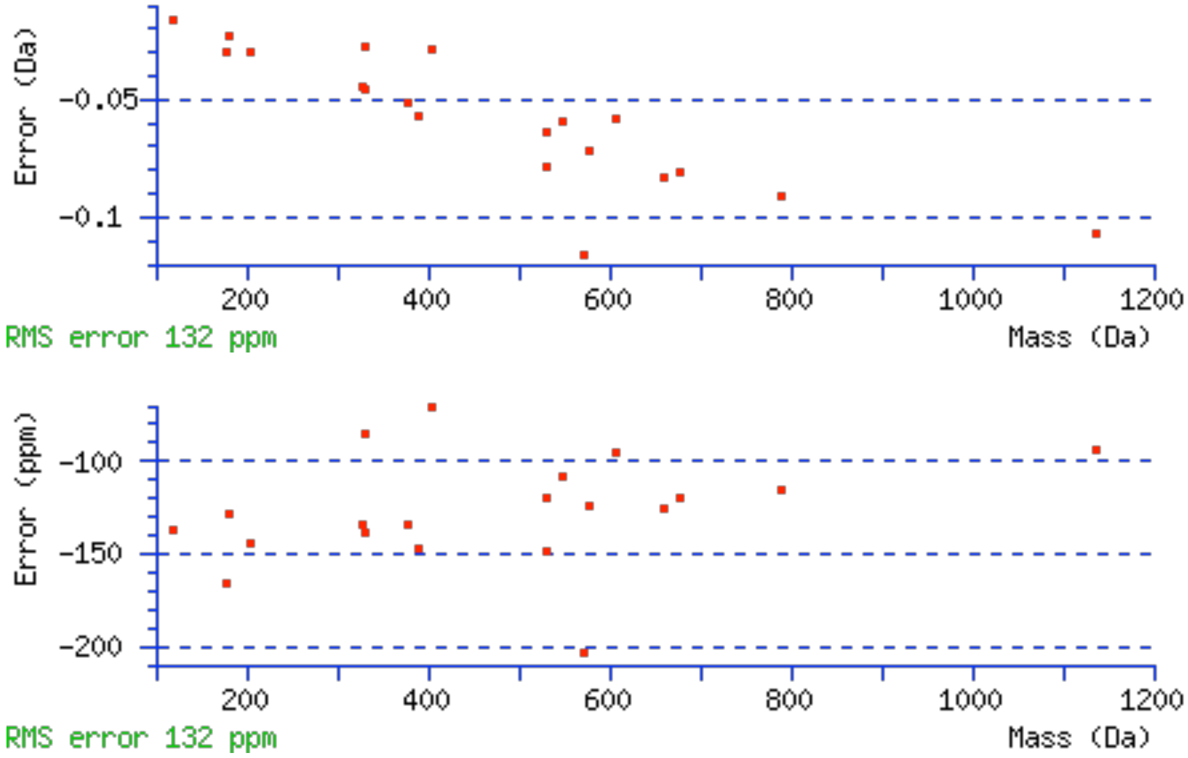
Monoisotopic mass of neutral peptide Mr(calc): 1464.6231 **Ions Score:** 24 **Expect:** 89 **Matches (Bold Red):** 24/180 fragment ions using 29 most intense peaks

#	Immon.	a	a^0	b	b^0	Seq.	y	y^0	#
1	**120.0808**	**120.0808**		148.0757		**F**			**14**
2	30.0338	**177.1022**		**205.0972**		**G**	1318.5620	1300.5514	**13**
3	60.0444	264.1343	246.1237	292.1292	274.1186	**S**	1261.5405	1243.5300	**12**
4	30.0338	321.1557	303.1452	349.1506	331.1401	**G**	1174.5085	1156.4979	**11**

5	60.0444	408.1878	**390.1772**	436.1827	418.1721	**S**	1117.4870	1099.4765	**10**
6	86.0964	521.2718	503.2613	**549.2667**	**531.2562**	**L**	1030.4550	1012.4444	**9**
7	102.0550	650.3144	632.3039	**678.3093**	**660.2988**	**E**	917.3709	899.3604	**8**
8	70.0651	747.3672	729.3566	775.3621	757.3515	**P**	**788.3284**	770.3178	**7**
9	104.0528	878.4077	860.3971	906.4026	888.3920	**M**	691.2756	673.2650	**6**
10	60.0444	965.4397	947.4291	993.4346	975.4240	**S**	560.2351	542.2245	**5**
11	60.0444	1052.4717	1034.4612	1080.4666	1062.4561	**S**	473.2031	455.1925	**4**
12	30.0338	1109.4932	1091.4826	**1137.4881**	1119.4775	**G**	386.1710		**3**
13	**120.0808**	1256.5616	1238.5510	1284.5565	1266.5459	**F**	**329.1496**		**2**
14	136.0757					**Y**	**182.0812**		**1**

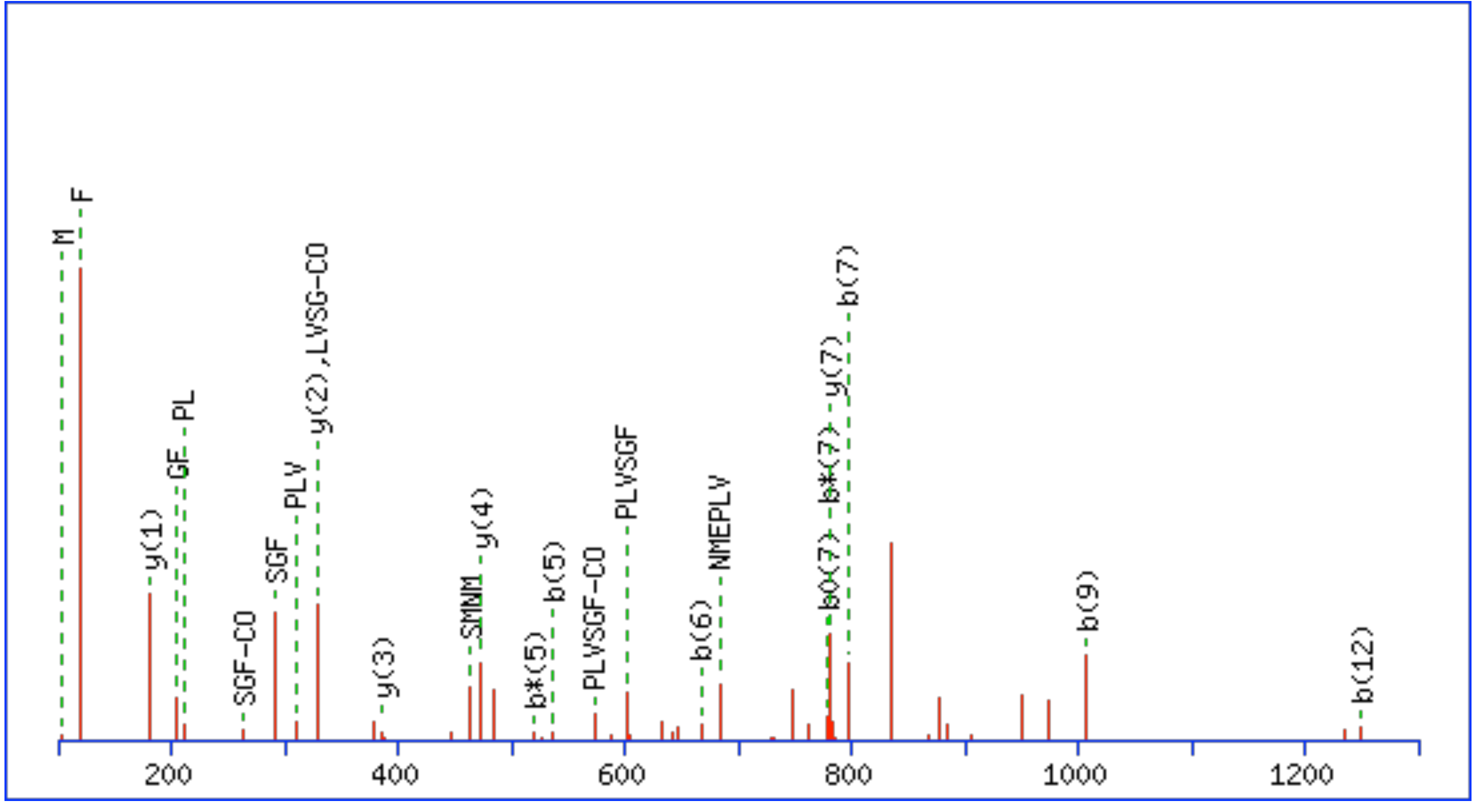
Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GS	117.0659	145.0608	**GSG**	174.0873	202.0822	**GSGS**	261.1193	289.1143
GSGSL	374.2034	402.1983	**GSGSLE**	503.2460	**531.2409**	**GSGSLEP**	600.2988	628.2937
SG	117.0659	145.0608	**SGS**	204.0979	232.0928	**SGSL**	317.1819	345.1769
SGSLE	446.2245	474.2195	**SGSLEP**	543.2773	**571.2722**	**SGSLEPM**	674.3178	702.3127
GS	117.0659	145.0608	**GSL**	230.1499	258.1448	**GSLE**	359.1925	387.1874
GSLEP	456.2453	484.2402	**GSLEPM**	587.2858	615.2807	**GSLEPMS**	674.3178	702.3127
SL	173.1285	201.1234	**SLE**	302.1710	**330.1660**	**SLEP**	399.2238	427.2187
SLEPM	530.2643	558.2592	**SLEPMS**	617.2963	645.2912	**LE**	215.1390	243.1339
LEP	312.1918	340.1867	**LEPM**	443.2323	471.2272	**LEPMS**	530.2643	558.2592
LEPMSS	617.2963	645.2912	**LEPMSSG**	674.3178	702.3127	**EP**	199.1077	227.1026
EPM	**330.1482**	358.1431	**EPMS**	417.1802	445.1751	**EPMSS**	504.2123	532.2072
EPMSSG	561.2337	589.2286	**PM**	201.1056	229.1005	**PMS**	288.1376	316.1326
PMSS	375.1697	**403.1646**	**PMSSG**	432.1911	460.1860	**PMSSGF**	**579.2595**	**607.2545**

MS	191.0849	219.0798	**MSS**	278.1169	306.1118	**MSSG**	335.1384	363.1333
MSSGF	482.2068	510.2017	**SS**	147.0764	175.0713	**SSG**	204.0979	232.0928
SSGF	351.1663	**379.1612**	**SG**	117.0659	145.0608	**SGF**	264.1343	292.1292
GF	**177.1022**	**205.0972**						



MS/MS Fragmentation of **FGSMNMEPLVSGFY**
Found in **New_Precursor_FGGANEPM**, (2 exons, 184 aa), EST(CD294941)

Match to Query 284: 1577.417048 from(789.715800,2+) intensity(526.1715)
Data file Maldi_All.mgf



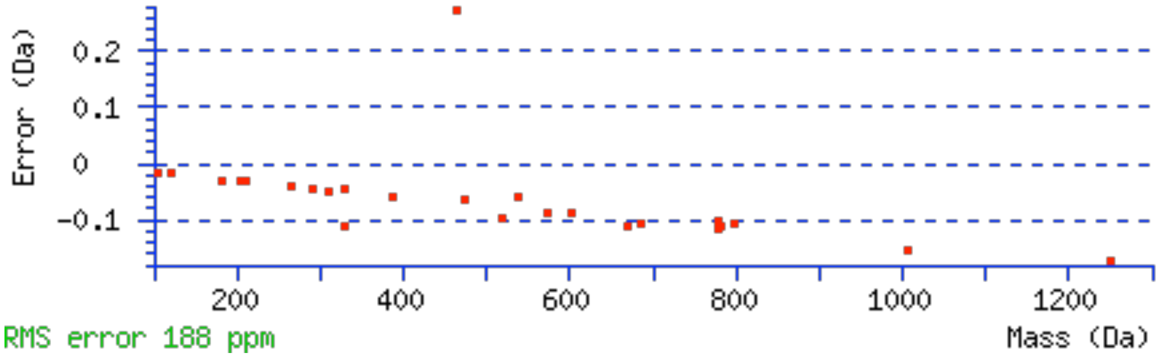
Monoisotopic mass of neutral peptide Mr(calc): 1577.6894 **Ions Score:** 45 **Expect:** 0.82 **Matches (Bold Red):** 31/197 fragment ions using 41 most intense peaks

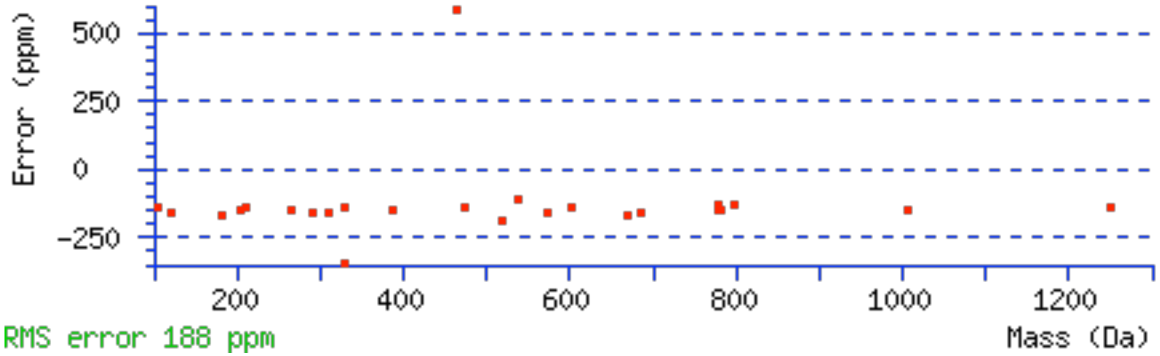
#	Immon.	a	a*	a^0	b	b*	b^0	Seq.	y	y*	y^0	#
1	**120.0808**	**120.0808**			148.0757			**F**				**14**
2	30.0338	177.1022			**205.0972**			**G**	1431.6283	1414.6018	1413.6177	**13**

3	60.0444	**264.1343**		246.1237	**292.1292**		274.1186	**S**	1374.6068	1357.5803	1356.5963	**12**
4	**104.0528**	395.1748		377.1642	423.1697		405.1591	**M**	1287.5748	1270.5483	1269.5642	**11**
5	87.0553	509.2177	492.1911	491.2071	**537.2126**	**520.1860**	519.2020	**N**	1156.5343	1139.5078	1138.5238	**10**
6	**104.0528**	640.2582	623.2316	622.2476	**668.2531**	651.2265	650.2425	**M**	1042.4914		1024.4808	**9**
7	102.0550	769.3008	752.2742	751.2902	**797.2957**	**780.2691**	**779.2851**	**E**	911.4509		893.4403	**8**
8	70.0651	866.3535	849.3270	848.3430	894.3484	877.3219	876.3379	**P**	**782.4083**		764.3978	**7**
9	86.0964	979.4376	962.4110	961.4270	**1007.4325**	990.4060	989.4219	**L**	685.3556		667.3450	**6**
10	72.0808	1078.5060	1061.4795	1060.4954	1106.5009	1089.4744	1088.4903	**V**	572.2715		554.2609	**5**
11	60.0444	1165.5380	1148.5115	1147.5275	1193.5329	1176.5064	1175.5224	**S**	**473.2031**		455.1925	**4**
12	30.0338	1222.5595	1205.5329	1204.5489	**1250.5544**	1233.5279	1232.5438	**G**	**386.1710**			**3**
13	**120.0808**	1369.6279	1352.6014	1351.6173	1397.6228	1380.5963	1379.6123	**F**	**329.1496**			**2**
14	136.0757							**Y**	**182.0812**			**1**

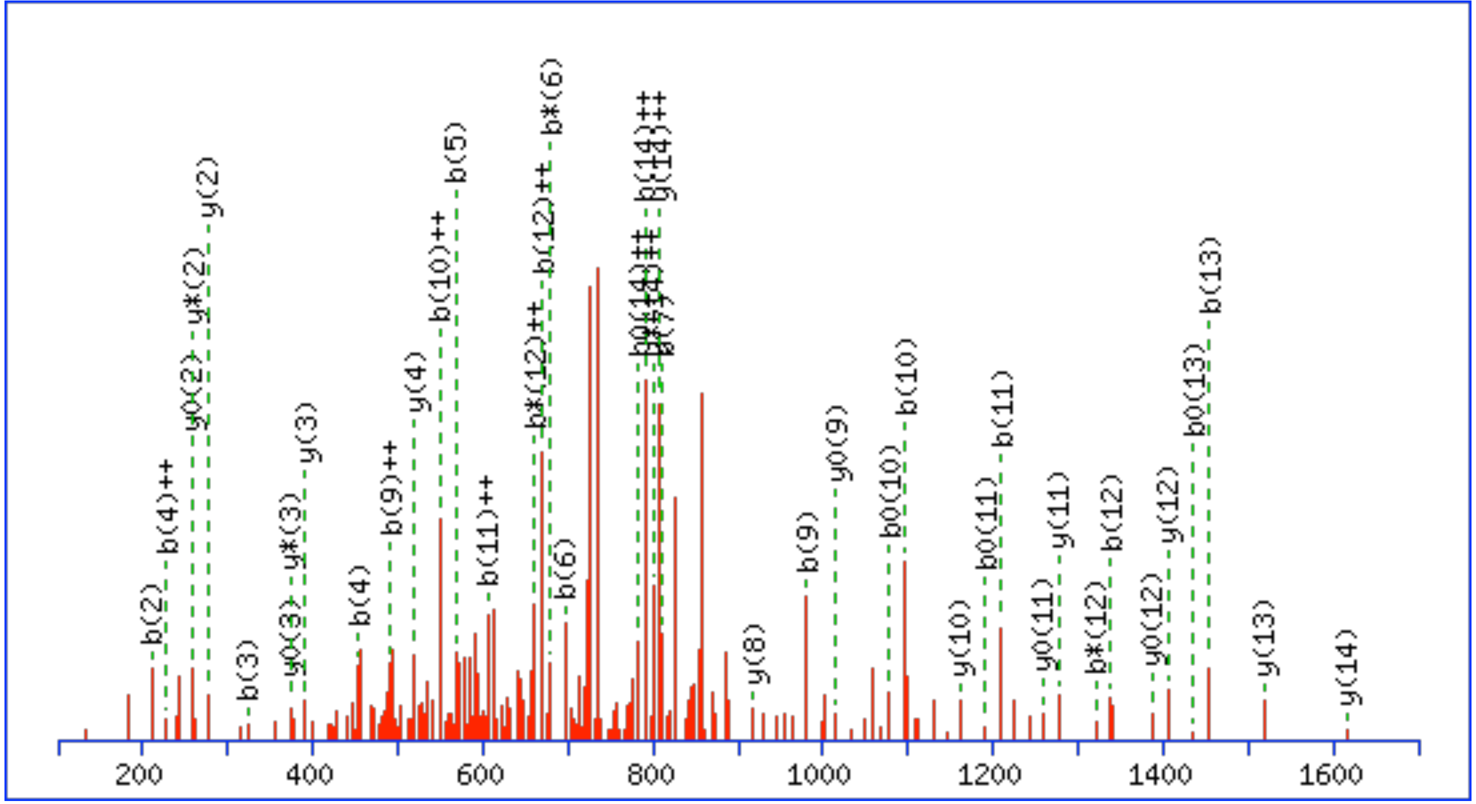
Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
GS	117.0659	145.0608	**GSM**	248.1063	276.1013	**GSMN**	362.1493	390.1442
GSMNM	493.1898	521.1847	**GSMNME**	622.2323	650.2273	**SM**	191.0849	219.0798
SMN	305.1278	333.1227	**SMNM**	436.1683	**464.1632**	**SMNME**	565.2109	593.2058
SMNMEP	662.2636	690.2586	**MN**	218.0958	246.0907	**MNM**	349.1363	377.1312
MNME	478.1789	506.1738	**MNMEP**	575.2316	603.2265	**MNMEPL**	688.3157	716.3106
NM	218.0958	246.0907	**NME**	347.1384	375.1333	**NMEP**	444.1911	472.1860
NMEPL	557.2752	585.2701	**NMEPLV**	656.3436	**684.3385**	**ME**	233.0954	261.0904
MEP	330.1482	358.1431	**MEPL**	443.2323	471.2272	**MEPLV**	542.3007	570.2956
MEPLVS	629.3327	657.3276	**MEPLVSG**	686.3542	714.3491	**EP**	199.1077	227.1026
EPL	312.1918	340.1867	**EPLV**	411.2602	439.2551	**EPLVS**	498.2922	526.2871
EPLVSG	555.3137	583.3086	**PL**	183.1492	**211.1441**	**PLV**	282.2176	**310.2125**

PLVS	369.2496	397.2445	**PLVSG**	426.2711	454.2660	**PLVSGF**	**573.3395**	**601.3344**
LV	185.1648	213.1598	**LVS**	272.1969	300.1918	**LVSG**	**329.2183**	357.2132
LVSGF	476.2867	504.2817	**VS**	159.1128	187.1077	**VSG**	216.1343	244.1292
VSGF	363.2027	391.1976	**SG**	117.0659	145.0608	**SGF**	**264.1343**	**292.1292**
GF	177.1022	**205.0972**						





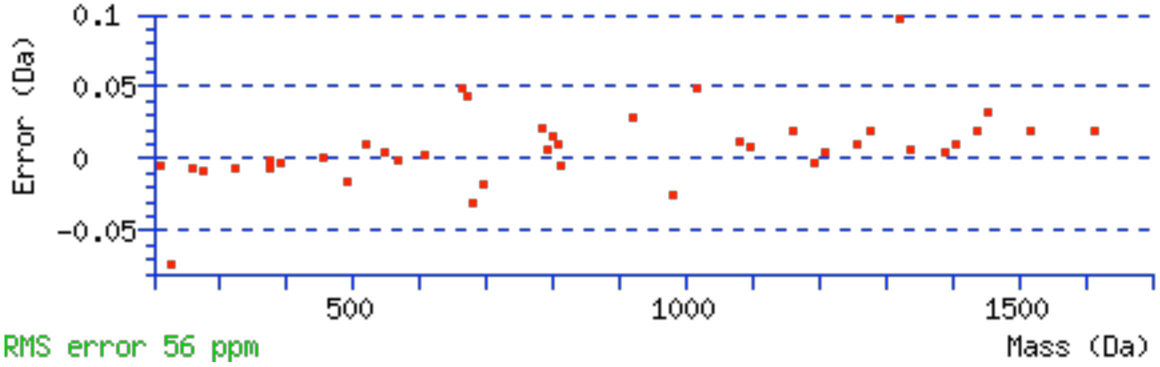
MS/MS Fragmentation of **LPIEDKDGLDIEDQE**
Found in **New_Precursor_FGGANEPM**, (2 exons, 184 aa), EST(CD294941)
Match to Query 707: 1727.858188 from(864.936370,2+) intensity(439580.0000)
Title: Cmpd 148, +MSn(865.4518), 28.4 min
Data file Qtof_all.mgf

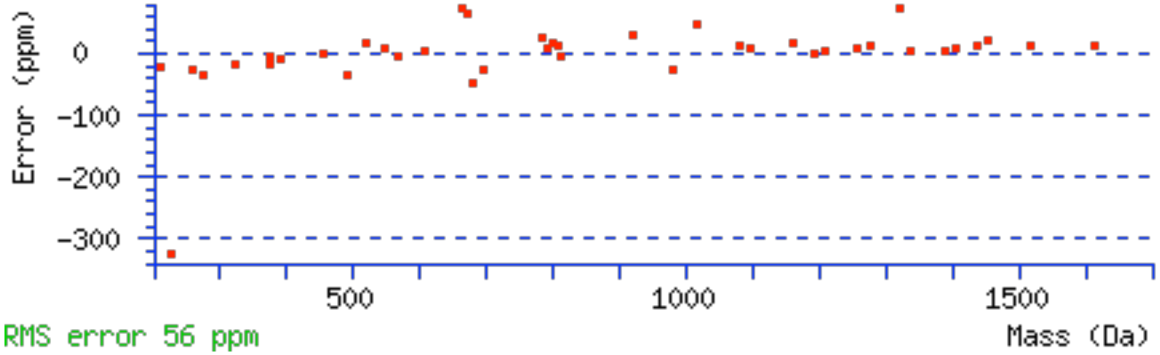


Monoisotopic mass of neutral peptide Mr(calc): 1727.8101 **Ions Score:** 54 **Expect:** 0.046 **Matches (Bold Red):** 42/150 fragment ions using 89 most intense peaks

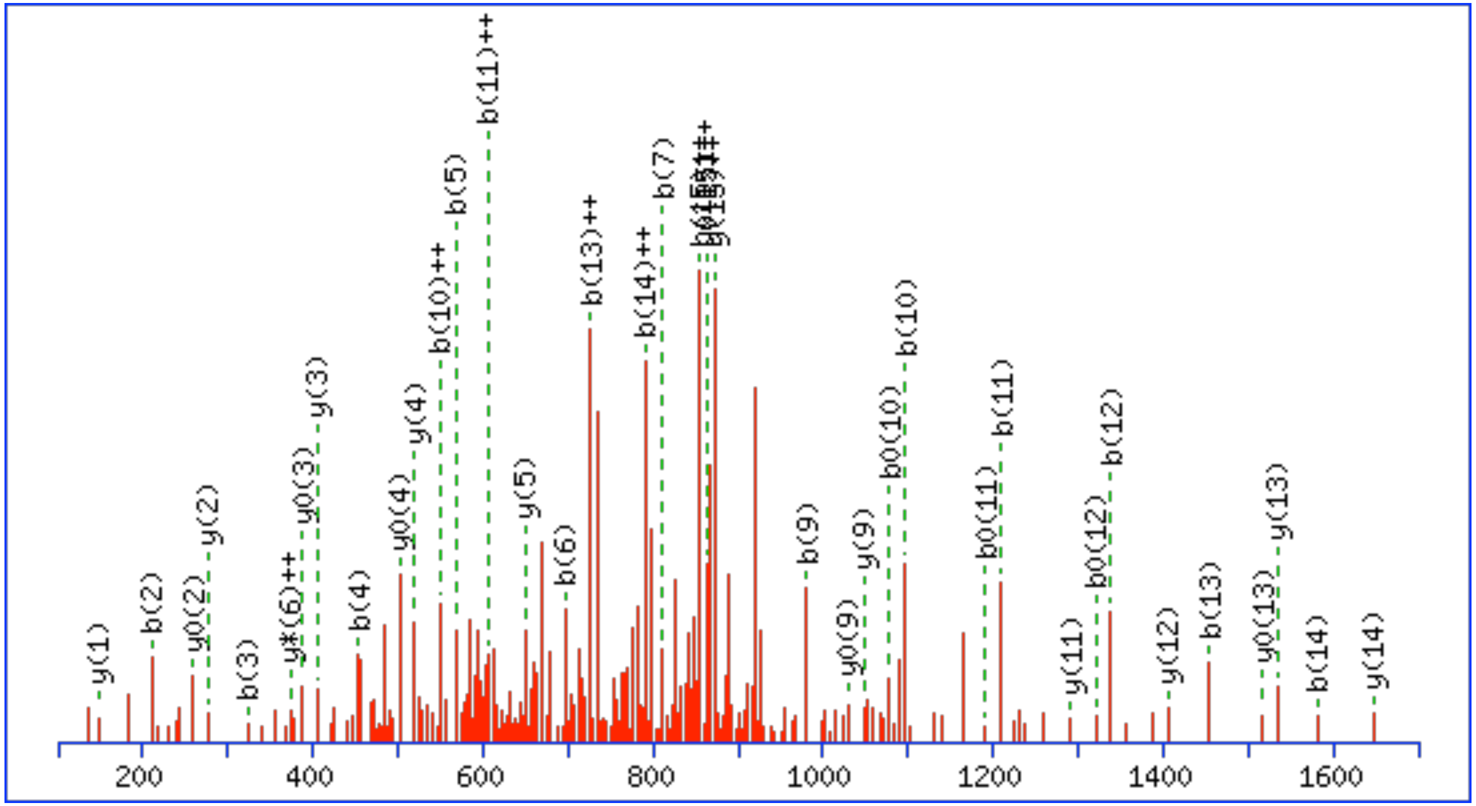
#	b	b⁺⁺	b*	b*⁺⁺	b⁰	b⁰⁺⁺	Seq.	y	y⁺⁺	y*	y*⁺⁺	y⁰	y⁰⁺⁺	#

1	114.0913	57.5493					**L**							**15**
2	**211.1441**	106.0757					**P**	**1615.7334**	**808.3703**	1598.7068	**799.8570**	1597.7228	799.3650	**14**
3	**324.2282**	162.6177					**I**	**1518.6806**	759.8439	1501.6540	751.3307	1500.6700	750.8387	**13**
4	**453.2708**	**227.1390**			435.2602	218.1337	**E**	**1405.5965**	703.3019	1388.5700	694.7886	**1387.5860**	694.2966	**12**
5	**568.2977**	284.6525			550.2871	275.6472	**D**	**1276.5539**	638.7806	1259.5274	630.2673	**1258.5434**	629.7753	**11**
6	**696.3927**	348.7000	**679.3661**	340.1867	678.3821	339.6947	**K**	**1161.5270**	581.2671	1144.5004	572.7539	1143.5164	572.2618	**10**
7	**811.4196**	406.2134	794.3931	397.7002	793.4090	397.2082	**D**	1033.4320	517.2197	1016.4055	508.7064	**1015.4215**	508.2144	**9**
8	868.4411	434.7242	851.4145	426.2109	850.4305	425.7189	**G**	**918.4051**	459.7062	901.3785	451.1929	900.3945	450.7009	**8**
9	**981.5251**	**491.2662**	964.4986	482.7529	963.5146	482.2609	**L**	861.3836	431.1954	844.3571	422.6822	843.3731	422.1902	**7**
10	**1096.5521**	**548.7797**	1079.5255	540.2664	**1078.5415**	539.7744	**D**	748.2996	374.6534	731.2730	366.1401	730.2890	365.6481	**6**
11	**1209.6361**	**605.3217**	1192.6096	596.8084	**1191.6256**	596.3164	**I**	633.2726	317.1399	616.2461	308.6267	615.2620	308.1347	**5**
12	**1338.6787**	**669.8430**	**1321.6522**	**661.3297**	1320.6682	660.8377	**E**	**520.1885**	260.5979	503.1620	252.0846	502.1780	251.5926	**4**
13	**1453.7057**	727.3565	1436.6791	718.8432	**1435.6951**	718.3512	**D**	**391.1460**	196.0766	**374.1194**	187.5633	**373.1354**	187.0713	**3**
14	1581.7643	**791.3858**	1564.7377	782.8725	1563.7537	**782.3805**	**Q**	**276.1190**	138.5631	**259.0925**	130.0499	**258.1084**	129.5579	**2**
15							**E**	148.0604	74.5339			130.0499	65.5286	**1**





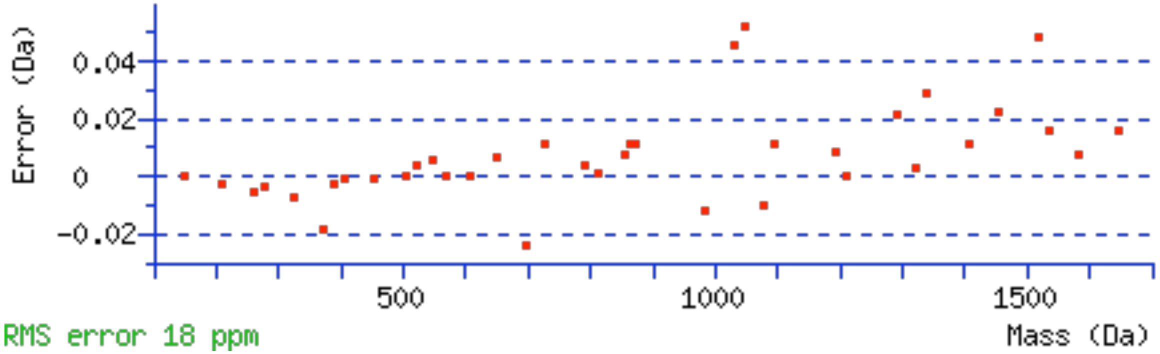
MS/MS Fragmentation of **LPIEDKDGLDIEDQEE**
Found in **New_Precursor_FGGANEPM**, (2 exons, 184 aa), EST(CD294941)
Match to Query 732: 1856.876468 from(929.445510,2+) intensity(325208.0000)
Title: Cmpd 149, +MSn(929.8602), 28.5 min
Data file Qtof_all.mgf

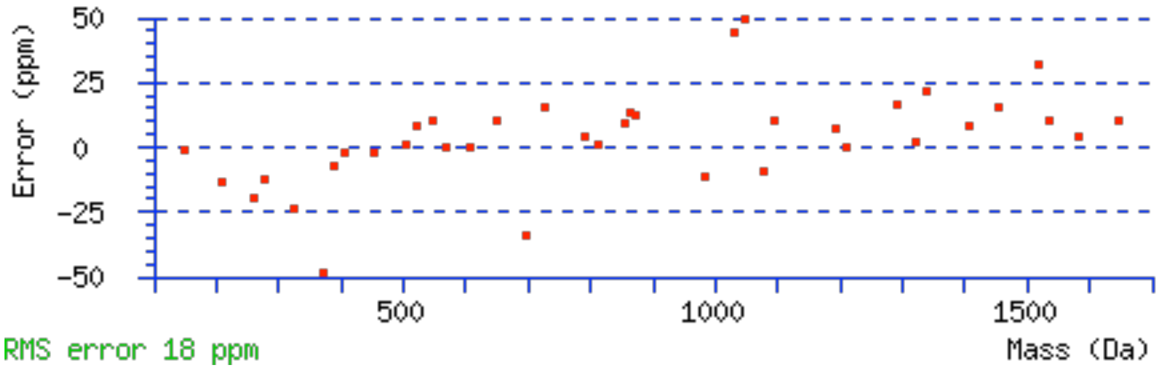


Monoisotopic mass of neutral peptide Mr(calc): 1856.8527 **Ions Score:** 64 **Expect:** 0.0045 **Matches (Bold Red):** 38/160 fragment ions using 81 most intense peaks

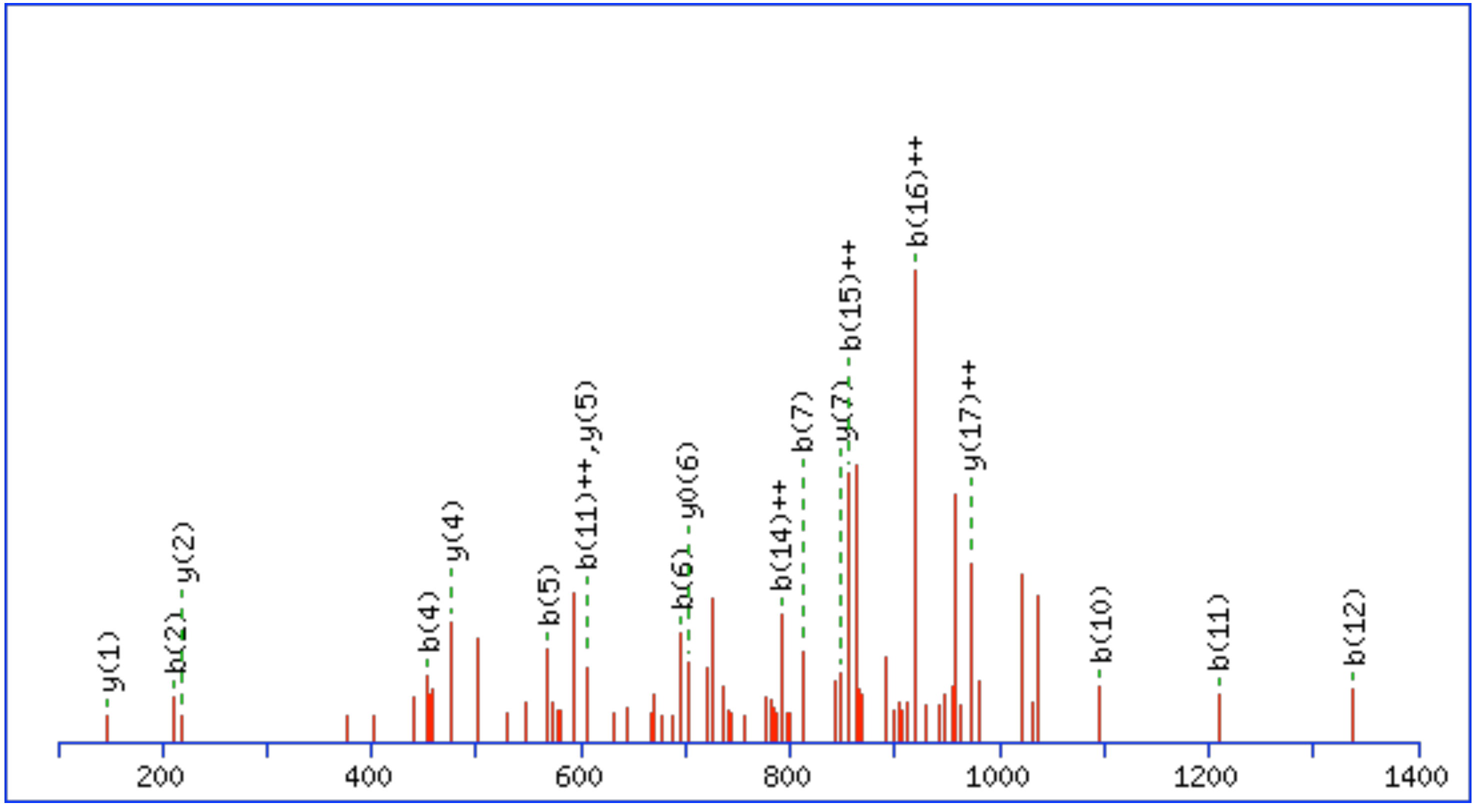
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					**L**							**16**
2	**211.1441**	106.0757					**P**	1744.7759	**872.8916**	1727.7494	864.3783	1726.7654	**863.8863**	**15**
3	**324.2282**	162.6177					**I**	**1647.7232**	824.3652	1630.6966	815.8520	1629.7126	815.3599	**14**
4	**453.2708**	227.1390			435.2602	218.1337	**E**	**1534.6391**	767.8232	1517.6126	759.3099	**1516.6286**	758.8179	**13**

5	**568.2977**	284.6525			550.2871	275.6472	**D**	**1405.5965**	703.3019	1388.5700	694.7886	1387.5860	694.2966	**12**
6	**696.3927**	348.7000	679.3661	340.1867	678.3821	339.6947	**K**	**1290.5696**	645.7884	1273.5430	637.2752	1272.5590	636.7831	**11**
7	**811.4196**	406.2134	794.3931	397.7002	793.4090	397.2082	**D**	1162.4746	581.7409	1145.4481	573.2277	1144.4641	572.7357	**10**
8	868.4411	434.7242	851.4145	426.2109	850.4305	425.7189	**G**	**1047.4477**	524.2275	1030.4211	515.7142	**1029.4371**	515.2222	**9**
9	**981.5251**	491.2662	964.4986	482.7529	963.5146	482.2609	**L**	990.4262	495.7167	973.3997	487.2035	972.4156	486.7115	**8**
10	**1096.5521**	**548.7797**	1079.5255	540.2664	**1078.5415**	539.7744	**D**	877.3421	439.1747	860.3156	430.6614	859.3316	430.1694	**7**
11	**1209.6361**	**605.3217**	1192.6096	596.8084	**1191.6256**	596.3164	**I**	762.3152	381.6612	745.2887	**373.1480**	744.3046	372.6560	**6**
12	**1338.6787**	669.8430	1321.6522	661.3297	**1320.6682**	660.8377	**E**	**649.2311**	325.1192	632.2046	316.6059	631.2206	316.1139	**5**
13	**1453.7057**	**727.3565**	1436.6791	718.8432	1435.6951	718.3512	**D**	**520.1885**	260.5979	503.1620	252.0846	**502.1780**	251.5926	**4**
14	**1581.7643**	**791.3858**	1564.7377	782.8725	1563.7537	782.3805	**Q**	**405.1616**	203.0844	388.1351	194.5712	**387.1510**	194.0792	**3**
15	1710.8069	**855.9071**	1693.7803	847.3938	1692.7963	846.9018	**E**	**277.1030**	139.0552			**259.0925**	130.0499	**2**
16							**E**	**148.0604**	74.5339			130.0499	65.5286	**1**





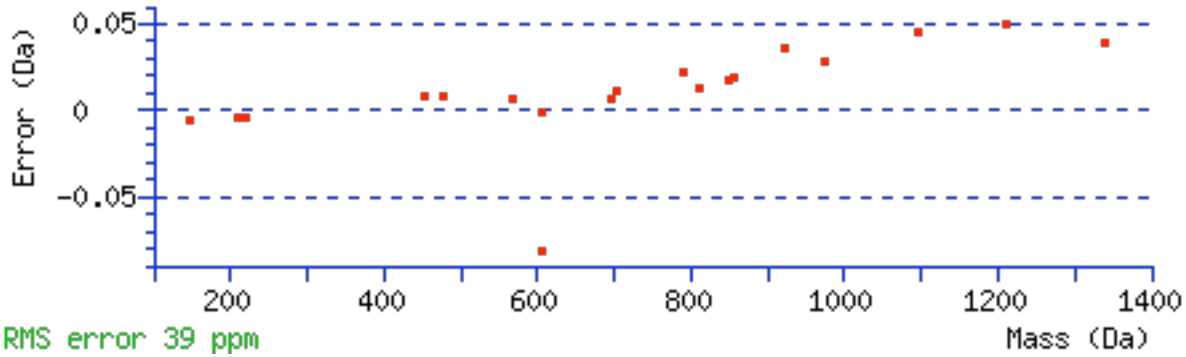
MS/MS Fragmentation of **LPIEDKDGLDIEDQEEAE**
Found in **New_Precursor_FGGANEPM**, (2 exons, 184 aa), EST(CD294941)
Match to Query 782: 2056.962668 from(1029.488610,2+) intensity(309452.0000)
Title: Cmpd 159, +MSn(1030.1290), 28.6 min
Data file Qtof_all.mgf

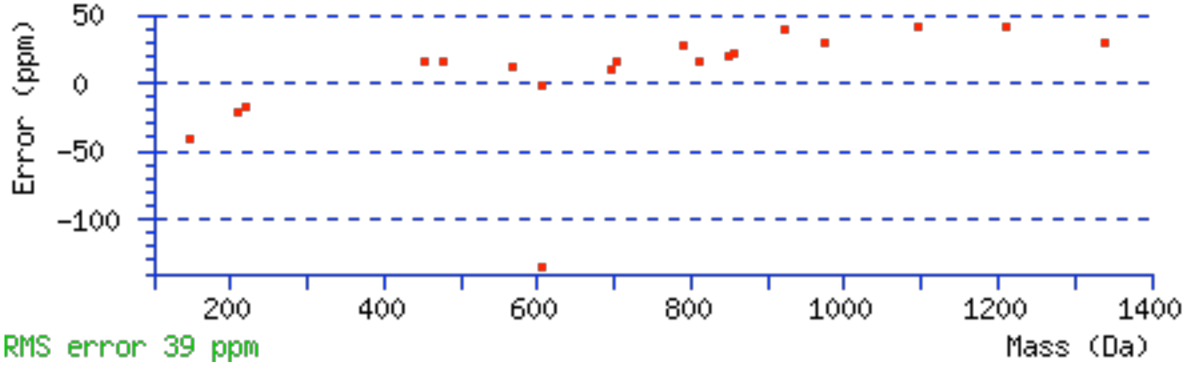


Monoisotopic mass of neutral peptide Mr(calc): 2056.9324 **Ions Score:** 54 **Expect:** 0.039 **Matches (Bold Red):** 19/180 fragment ions using 30 most intense peaks

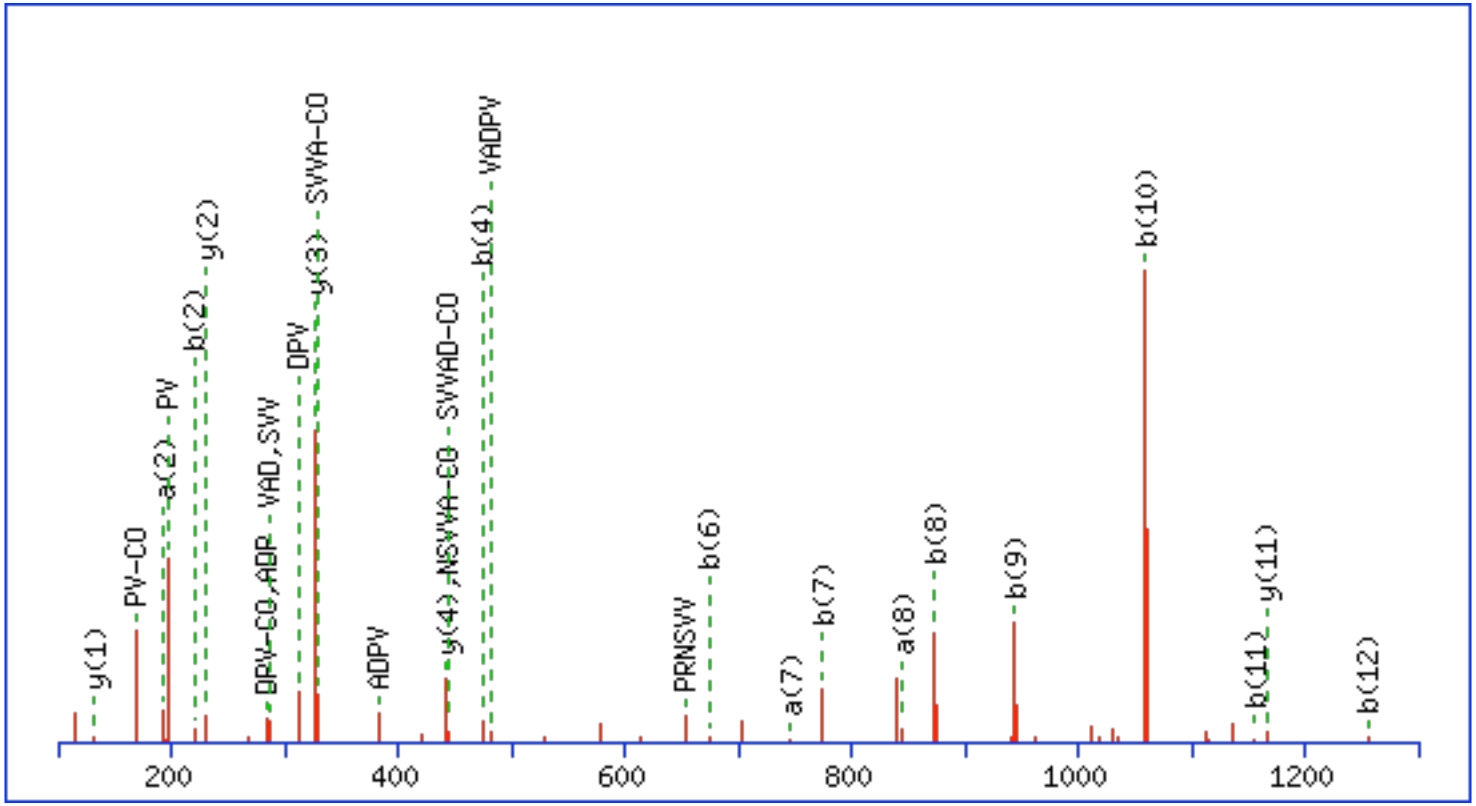
#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	114.0913	57.5493					**L**							**18**
2	**211.1441**	106.0757					**P**	1944.8557	**972.9315**	1927.8291	964.4182	1926.8451	963.9262	**17**
3	324.2282	162.6177					**I**	1847.8029	924.4051	1830.7763	915.8918	1829.7923	915.3998	**16**
4	**453.2708**	227.1390			435.2602	218.1337	**E**	1734.7188	867.8631	1717.6923	859.3498	1716.7083	858.8578	**15**

5	**568.2977**	284.6525			550.2871	275.6472	**D**	1605.6762	803.3418	1588.6497	794.8285	1587.6657	794.3365	**14**
6	**696.3927**	348.7000	679.3661	340.1867	678.3821	339.6947	**K**	1490.6493	745.8283	1473.6227	737.3150	1472.6387	736.8230	**13**
7	**811.4196**	406.2134	794.3931	397.7002	793.4090	397.2082	**D**	1362.5543	681.7808	1345.5278	673.2675	1344.5438	672.7755	**12**
8	868.4411	434.7242	851.4145	426.2109	850.4305	425.7189	**G**	1247.5274	624.2673	1230.5008	615.7541	1229.5168	615.2620	**11**
9	981.5251	491.2662	964.4986	482.7529	963.5146	482.2609	**L**	1190.5059	595.7566	1173.4794	587.2433	1172.4954	586.7513	**10**
10	**1096.5521**	548.7797	1079.5255	540.2664	1078.5415	539.7744	**D**	1077.4219	539.2146	1060.3953	530.7013	1059.4113	530.2093	**9**
11	**1209.6361**	**605.3217**	1192.6096	596.8084	1191.6256	596.3164	**I**	962.3949	481.7011	945.3684	473.1878	944.3843	472.6958	**8**
12	**1338.6787**	669.8430	1321.6522	661.3297	1320.6682	660.8377	**E**	**849.3108**	425.1591	832.2843	416.6458	831.3003	416.1538	**7**
13	1453.7057	727.3565	1436.6791	718.8432	1435.6951	718.3512	**D**	720.2683	360.6378	703.2417	352.1245	**702.2577**	351.6325	**6**
14	1581.7643	**791.3858**	1564.7377	782.8725	1563.7537	782.3805	**Q**	**605.2413**	303.1243	588.2148	294.6110	587.2307	294.1190	**5**
15	1710.8069	**855.9071**	1693.7803	847.3938	1692.7963	846.9018	**E**	**477.1827**	239.0950			459.1722	230.0897	**4**
16	1839.8494	**920.4284**	1822.8229	911.9151	1821.8389	911.4231	**E**	348.1401	174.5737			330.1296	165.5684	**3**
17	1910.8866	955.9469	1893.8600	947.4336	1892.8760	946.9416	**A**	**219.0975**	110.0524			201.0870	101.0471	**2**
18							**E**	**148.0604**	74.5339			130.0499	65.5286	**1**





MS/MS Fragmentation of **GYPRNSVVADPVL**
Found in **New_Precursor_GYPRNSVV**, (2 exons, 135 aa), No EST
Match to Query 150: 1385.435848 from(693.725200,2+) intensity(42.6727)
Data file Maldi_All.mgf



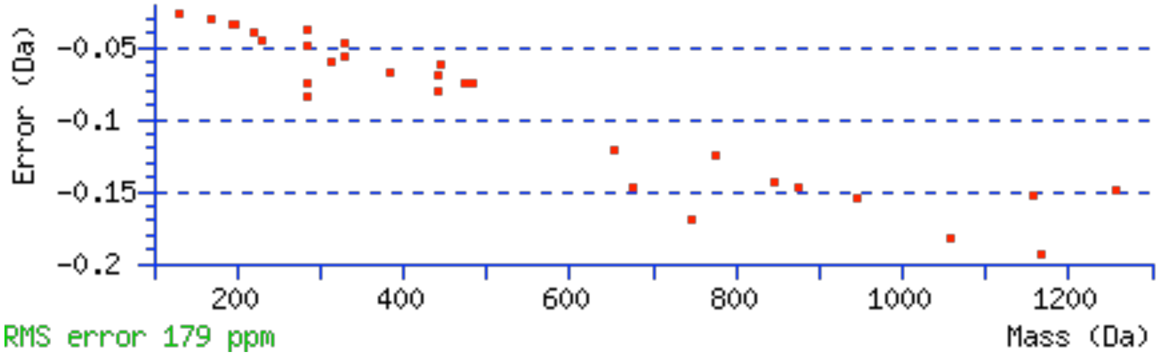
Monoisotopic mass of neutral peptide Mr(calc): 1385.7303 **Ions Score:** 57 **Expect:** 0.04 **Matches (Bold Red):** 32/191 fragment ions using 50 most intense peaks

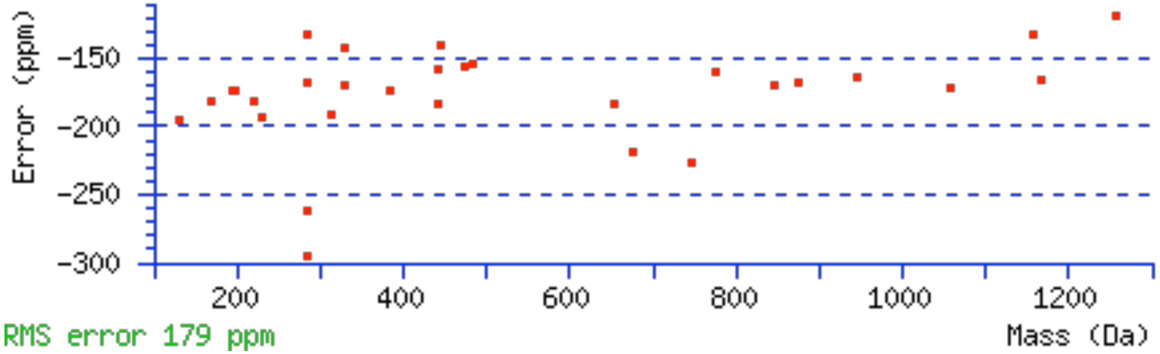
#	Immon.	a	a*	a^0	b	b*	b^0	d	Seq.	v	w	y	y*	y^0	#
1	30.0338	30.0338			58.0287				G						13
2	136.0757	**193.0972**			**221.0921**				Y	1221.6586		1329.7161	1312.6896	1311.7056	12
3	70.0651	290.1499			318.1448				P	1124.6058	1123.6106	**1166.6528**	1149.6262	1148.6422	11
4	129.1135	446.2510	429.2245		**474.2459**	457.2194		361.1870	R	968.5047	967.5095	1069.6000	1052.5735	1051.5895	10

5	87.0553	560.2940	543.2674		588.2889	571.2623		517.2881	**N**			913.4989	896.4724	895.4884	**9**
6	60.0444	647.3260	630.2994	629.3154	**675.3209**	658.2944	657.3103	631.3311	**S**			799.4560		781.4454	**8**
7	72.0808	**746.3944**	729.3678	728.3838	**774.3893**	757.3628	756.3787	732.3787	**V**			712.4240		694.4134	**7**
8	72.0808	**845.4628**	828.4363	827.4522	**873.4577**	856.4312	855.4472	831.4472	**V**			613.3556		595.3450	**6**
9	44.0495	916.4999	899.4734	898.4894	**944.4948**	927.4683	926.4843		**A**			514.2871		496.2766	**5**
10	88.0393	1031.5269	1014.5003	1013.5163	**1059.5218**	1042.4952	1041.5112	987.5370	**D**			**443.2500**		425.2395	**4**
11	70.0651	1128.5796	1111.5531	1110.5691	**1156.5745**	1139.5480	1138.5640	1102.5640	**P**			**328.2231**			**3**
12	72.0808	1227.6480	1210.6215	1209.6375	**1255.6430**	1238.6164	1237.6324	1213.6324	**V**			**231.1703**			**2**
13	86.0964								**L**			**132.1019**			**1**

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
YP	233.1285	261.1234	**YPR**	389.2296	417.2245	**YPRN**	503.2725	531.2674
YPRNS	590.3045	618.2994	**YPRNSV**	689.3729	717.3678	**PR**	226.1662	254.1612
PRN	340.2092	368.2041	**PRNS**	427.2412	455.2361	**PRNSV**	526.3096	554.3045
PRNSVV	625.3780	**653.3729**	**PRNSVVA**	696.4151	724.4100	**RN**	243.1564	271.1513
RNS	330.1884	358.1833	**RNSV**	429.2568	457.2518	**RNSVV**	528.3253	556.3202
RNSVVA	599.3624	627.3573	**NS**	174.0873	202.0822	**NSV**	273.1557	301.1506
NSVV	372.2241	400.2191	**NSVVA**	**443.2613**	471.2562	**NSVVAD**	558.2882	586.2831
NSVVADP	655.3410	683.3359	**SV**	159.1128	187.1077	**SVV**	258.1812	**286.1761**
SVVA	**329.2183**	357.2132	**SVVAD**	**444.2453**	472.2402	**SVVADP**	541.2980	569.2930
SVVADPV	640.3665	668.3614	**VV**	171.1492	199.1441	**VVA**	242.1863	270.1812
VVAD	357.2132	385.2082	**VVADP**	454.2660	**482.2609**	**VVADPV**	553.3344	581.3293
VA	143.1179	171.1128	**VAD**	258.1448	**286.1397**	**VADP**	355.1976	**383.1925**
VADPV	454.2660	**482.2609**	**AD**	159.0764	187.0713	**ADP**	256.1292	**284.1241**
ADPV	355.1976	**383.1925**	**DP**	185.0921	213.0870	**DPV**	**284.1605**	**312.1554**

PV	**169.1335**	**197.1285**						





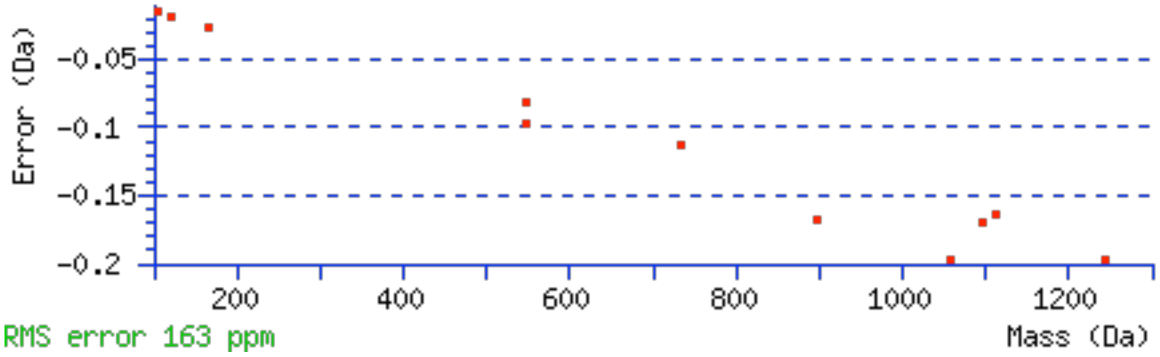
MS/MS Fragmentation of **DAGPHAWYGTGMF**
Found in **New_Precursor_DAGPAWYG**, (2 exons, 235 aa), No EST
Match to Query 164: 1407.338448 from(704.676500,2+) intensity(288.4586)
Data file Maldi_All.mgf

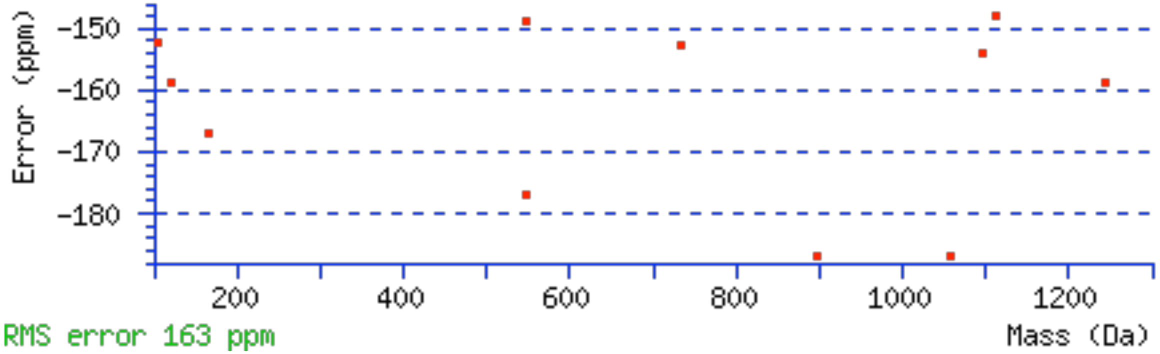
Monoisotopic mass of neutral peptide Mr(calc): 1407.6030 **Variable modifications: C-term :** Amidated (C-term) **Ions Score:** 40 **Expect:** 2.4 **Matches (Bold Red):** 11/159 fragment ions using 16 most intense peaks

#	Immon.	a	a^0	b	b^0	Seq.	y	y^0	#
1	88.0393	88.0393	70.0287	116.0342	98.0237	D			13
2	44.0495	159.0764	141.0659	187.0713	169.0608	A	1293.5833	1275.5728	12
3	30.0338	216.0979	198.0873	244.0928	226.0822	G	1222.5462	1204.5357	11
4	70.0651	313.1506	295.1401	341.1456	323.1350	P	1165.5248	1147.5142	10
5	110.0713	450.2096	432.1990	478.2045	460.1939	H	1068.4720	1050.4614	9
6	44.0495	521.2467	503.2361	**549.2416**	531.2310	A	931.4131	913.4025	8
7	159.0917	707.3260	689.3154	**735.3209**	717.3103	W	860.3760	842.3654	7
8	136.0757	870.3893	852.3787	**898.3842**	880.3737	Y	674.2967	656.2861	6
9	30.0338	927.4108	909.4002	955.4057	937.3951	G	511.2333	493.2228	5
10	74.0600	1028.4585	1010.4479	**1056.4534**	1038.4428	T	454.2119	436.2013	4
11	30.0338	1085.4799	1067.4694	**1113.4748**	**1095.4643**	G	353.1642		3
12	**104.0528**	1216.5204	1198.5098	**1244.5153**	1226.5048	M	296.1427		2
13	**120.0808**					F	**165.1022**		1

Seq	ya	yb	Seq	ya	yb	Seq	ya	yb
AG	101.0709	129.0659	AGP	198.1237	226.1186	AGPH	335.1826	363.1775
AGPHA	406.2197	434.2146	AGPHAW	592.2990	620.2940	GP	127.0866	155.0815
GPH	264.1455	292.1404	GPHA	335.1826	363.1775	GPHAW	521.2619	**549.2568**
GPHAWY	684.3253	712.3202	PH	207.1240	235.1190	PHA	278.1612	306.1561
PHAW	464.2405	492.2354	PHAWY	627.3038	655.2987	PHAWYG	684.3253	712.3202
HA	181.1084	209.1033	HAW	367.1877	395.1826	HAWY	530.2510	558.2459
HAWYG	587.2725	615.2674	HAWYGT	688.3202	716.3151	AW	230.1288	258.1237

AWY	393.1921	421.1870	**AWYG**	450.2136	478.2085	**AWYGT**	551.2613	579.2562
AWYGTG	608.2827	636.2776	**WY**	322.1550	350.1499	**WYG**	379.1765	407.1714
WYGT	480.2241	508.2191	**WYGTG**	537.2456	565.2405	**WYGTGM**	668.2861	696.2810
YG	193.0972	221.0921	**YGT**	294.1448	322.1397	**YGTG**	351.1663	379.1612
YGTGM	482.2068	510.2017	**GT**	131.0815	159.0764	**GTG**	188.1030	216.0979
GTGM	319.1435	347.1384	**TG**	131.0815	159.0764	**TGM**	262.1220	290.1169
GM	161.0743	189.0692						




Error (ppm)
-150
-160
-170
-180
200
400
600
800
1000
1200
Mass (Da)
RMS error 163 ppm