



Mascot Search Results

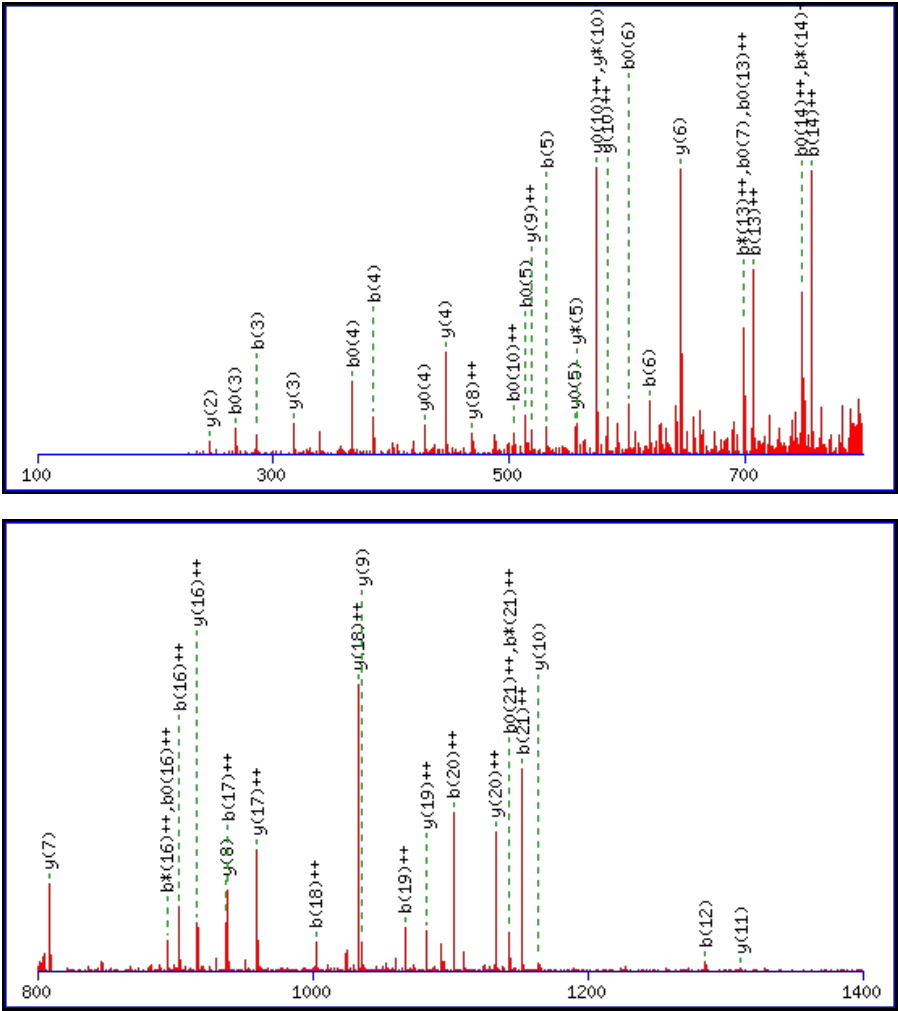
Results Generated by a Script Modified from Mascot Peptide View
by Newman Sze, School of Biological Sciences, Nanyang Technological University

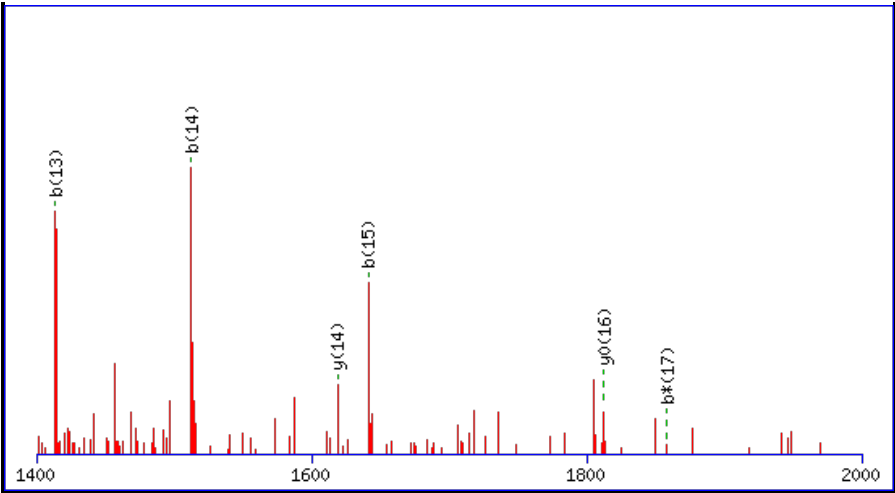
Spectrum No: 1; Query: 54530; Rank: 1

Peptide View

MS/MS Fragmentation of **AITVFSPDGHLFQVEYAQEA**VK
Found in **IPI00024175**, Tax_Id=9606 Gene_Symbol=PSMA7 Isoform 1 of Proteasome subunit alpha type-7

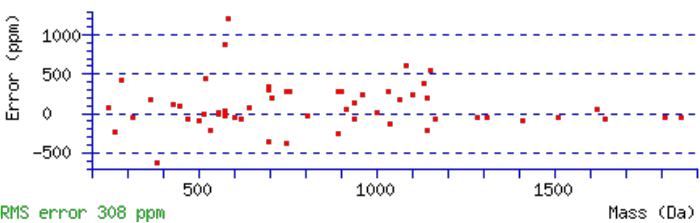
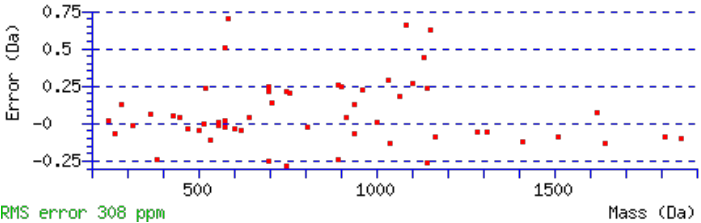
Match to Query 54530: 2448.250902 from(817.090910,3+)
Title: 091224LimSK_Exosome3_06.6797.6797.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2448.2325
Fixed modifications: Carbamidomethyl (C)
Ions Score: 58 Expect: 0.00029
Matches (**Bold Red**): 56/218 fragment ions using 97 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							22
2	185.1285	93.0679					I	2378.2027	1189.6050	2361.1761	1181.0917	2360.1921	1180.5997	21
3	286.1761	143.5917			268.1656	134.5864	T	2265.1186	1133.0630	2248.0921	1124.5497	2247.1081	1124.0577	20
4	385.2445	193.1259			367.2340	184.1206	V	2164.0709	1082.5391	2147.0444	1074.0258	2146.0604	1073.5338	19
5	532.3130	266.6601			514.3024	257.6548	F	2065.0025	1033.0049	2047.9760	1024.4916	2046.9920	1023.9996	18
6	619.3450	310.1761			601.3344	301.1709	S	1917.9341	959.4707	1900.9076	950.9574	1899.9236	950.4654	17
7	716.3978	358.7025			698.3872	349.6972	P	1830.9021	915.9547	1813.8755	907.4414	1812.8915	906.9494	16
8	831.4247	416.2160				813.4141	D	1733.8493	867.4283	1716.8228	858.9150	1715.8388	858.4230	15
9	888.4462	444.7267				870.4356	G	1618.8224	809.9148	1601.7958	801.4016	1600.8118	800.9095	14
10	1025.5051	513.2562				1007.4945	H	1561.8009	781.4041	1544.7744	772.8908	1543.7904	772.3988	13
11	1138.5891	569.7982				1120.5786	L	1424.7420	712.8746	1407.7155	704.3614	1406.7314	703.8694	12
12	1285.6576	643.3324				1267.6470	F	1311.6579	656.3326	1294.6314	647.8193	1293.6474	647.3273	11
13	1413.7161	707.3617	1396.6896	698.8484	1395.7056	698.3564	Q	1164.5895	582.7984	1147.5630	574.2851	1146.5790	573.7931	10
14	1512.7845	756.8959	1495.7580	748.3826	1494.7740	747.8906	V	1036.5310	518.7691	1019.5044	510.2558	1018.5204	509.7638	9
15	1641.8271	821.4172	1624.8006	812.9039	1623.8166	812.4119	E	937.4625	469.2349	920.4360	460.7216	919.4520	460.2296	8
16	1804.8905	902.9489	1787.8639	894.4356	1786.8799	893.9436	Y	808.4199	404.7136	791.3934	396.2003	790.4094	395.7083	7
17	1875.9276	938.4674	1858.9010	929.9542	1857.9170	929.4621	A	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	6
18	2003.9862	1002.4967	1986.9596	993.9834	1985.9756	993.4914	Q	574.3195	287.6634	557.2930	279.1501	556.3089	278.6581	5
19	2133.0287	1067.0180	2116.0022	1058.5047	2115.0182	1058.0127	E	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
20	2204.0659	1102.5366	2187.0393	1094.0233	2186.0553	1093.5313	A	317.2183	159.1128	300.1918	150.5995			3
21	2303.1343	1152.0708	2286.1077	1143.5575	2285.1237	1143.0655	V	246.1812	123.5942	229.1547	115.0810			2
22							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

Score	Mr(calc):	Delta	Sequence

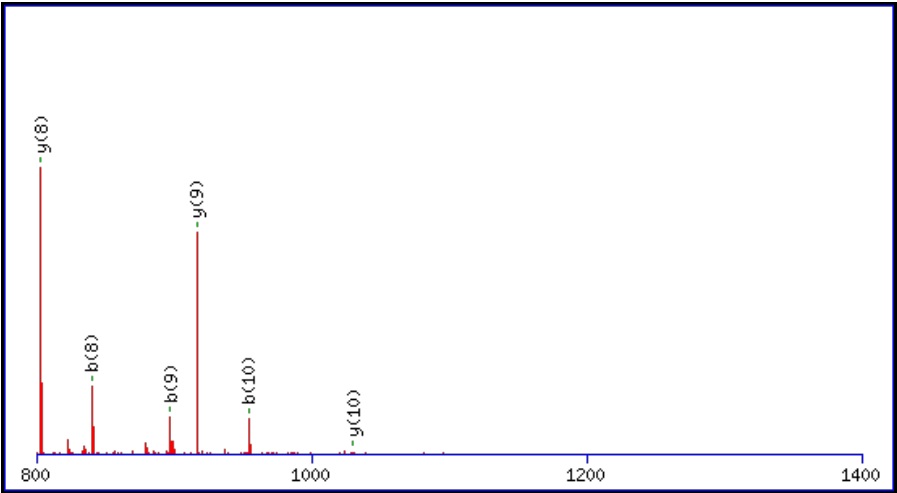
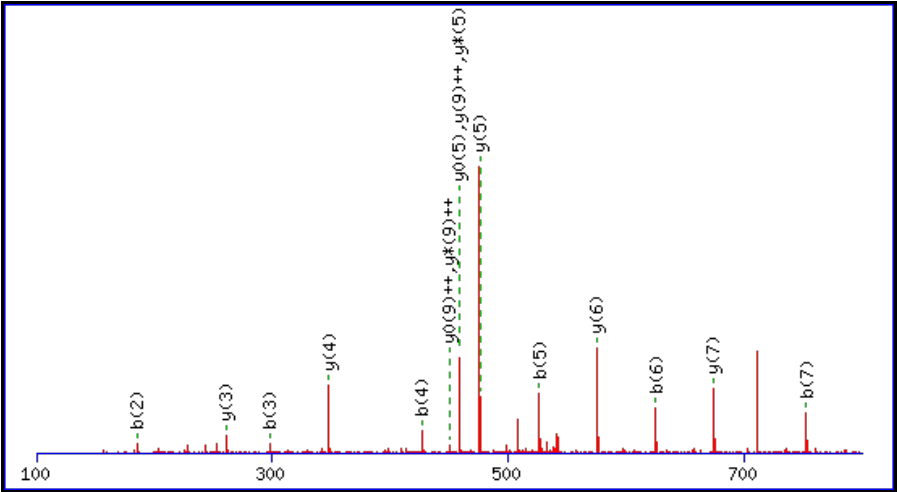
57.9	2448.2325	0.0184	AITVFSPDGHLFQVEYAEAVK
5.0	2448.2301	0.0208	QLEVVHTLDGKEYITPAQISK
4.3	2447.2492	1.0017	HFPGRGADPALGSLPAAGLSGLCAR
4.1	2448.2298	0.0211	YVNGHAKKHYEDAQVPLTNHK
4.1	2448.2301	0.0208	QLEVVHTLDGKEYITPAQISK
2.5	2448.2318	0.0191	LAAEEQFQALVKQMNQTLQDK
1.9	2446.2523	1.9986	FHHLVSPFVGQQVVKTGGSSKK
1.9	2446.2523	1.9986	FHHLVSPFVGQQVVKTGGSSKK
1.6	2448.2279	0.0230	VCSKATSPTSQRGQEVISTPTSK
1.6	2446.2509	2.0000	ELGIETYKVVNSERLVQYVK

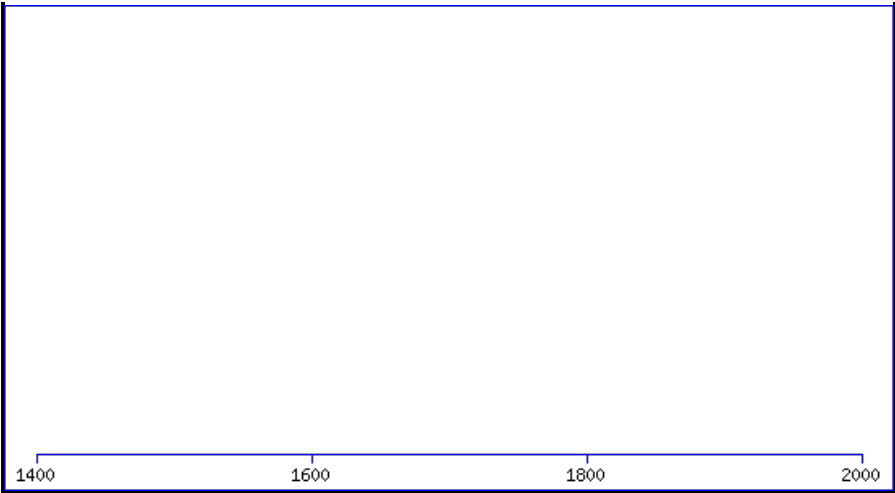
Spectrum No: 2; Query: 4771; Rank: 1

Peptide View

MS/MS Fragmentation of **ALLEVVQSGGK**
Found in **IP100024175**, Tax_Id=9606 Gene_Symbol=PSMA7 Isoform 1 of Proteasome subunit alpha type-7

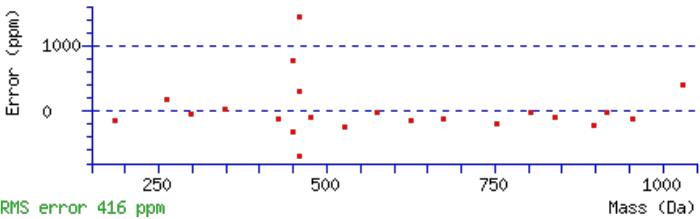
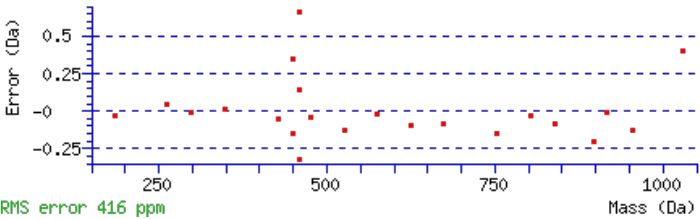
Match to Query 4771: 1099.628208 from(550.821380,2+)
Title: 091224LimSK_Exosome3_06.2231.2231.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1099.6237
Fixed modifications: Carbamidomethyl (C)
Ions Score: 59 Expect: 0.00013
Matches (**Bold Red**): 22/96 fragment ions using 40 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	185.1285	93.0679					L	1029.5939	515.3006	1012.5673	506.7873	1011.5833	506.2953	10
3	298.2125	149.6099					L	916.5098	458.7585	899.4833	450.2453	898.4993	449.7533	9
4	427.2551	214.1312			409.2445	205.1259	E	803.4258	402.2165	786.3992	393.7032	785.4152	393.2112	8
5	526.3235	263.6654			508.3130	254.6601	V	674.3832	337.6952	657.3566	329.1819	656.3726	328.6899	7
6	625.3919	313.1996			607.3814	304.1943	V	575.3148	288.1610	558.2882	279.6477	557.3042	279.1557	6
7	753.4505	377.2289	736.4240	368.7156	735.4400	368.2236	Q	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	5
8	840.4825	420.7449	823.4560	412.2316	822.4720	411.7396	S	348.1878	174.5975	331.1612	166.0842	330.1772	165.5922	4
9	897.5040	449.2556	880.4775	440.7424	879.4934	440.2504	G	261.1557	131.0815	244.1292	122.5682			3
10	954.5255	477.7664	937.4989	469.2531	936.5149	468.7611	G	204.1343	102.5708	187.1077	94.0575			2
11							K	147.1128	74.0600	130.0863	65.5468			1



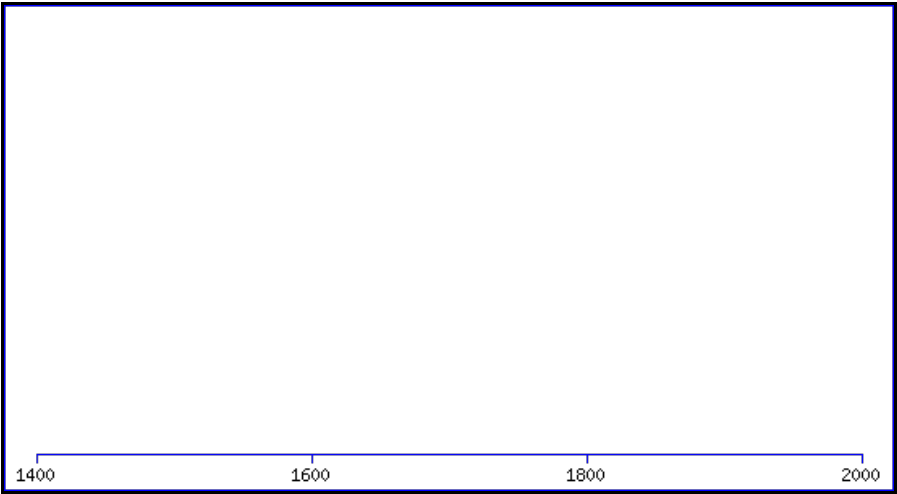
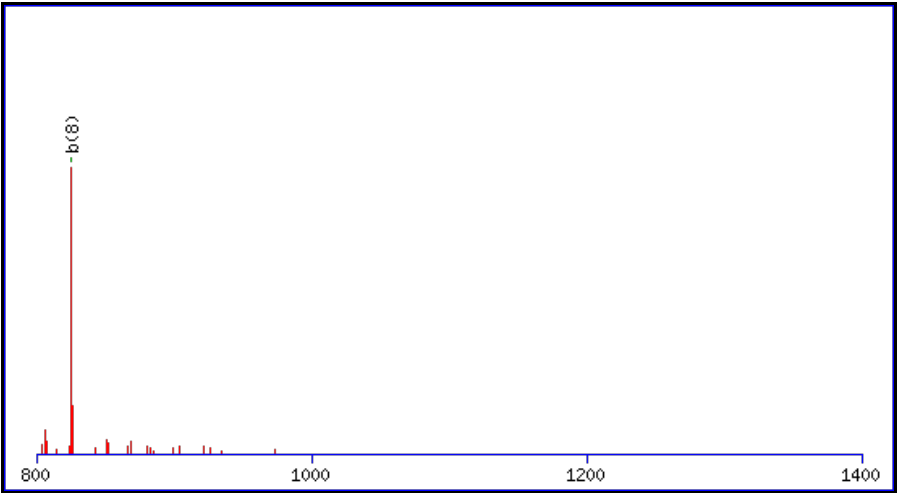
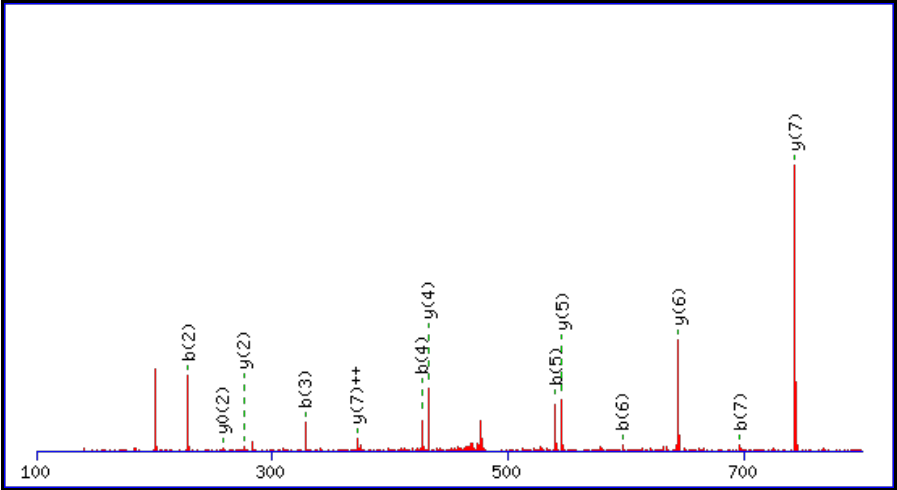
All matches to this query

Score	Mr(calc):	Delta	Sequence
58.6	1099.6237	0.0045	ALLEVVQSGGK
11.3	1099.6349	-0.0067	LALEKERNK
4.1	1099.6237	0.0045	ISQVLGNEIK
3.0	1099.6349	-0.0067	NLKNKIENK
3.0	1099.6349	-0.0067	NLKNKLENK
1.8	1099.6390	-0.0108	NIQGLFAPLK
1.6	1098.6145	1.0137	SKTASKHVNK
1.3	1099.6237	0.0045	AIPKTLKDSQ

Peptide View

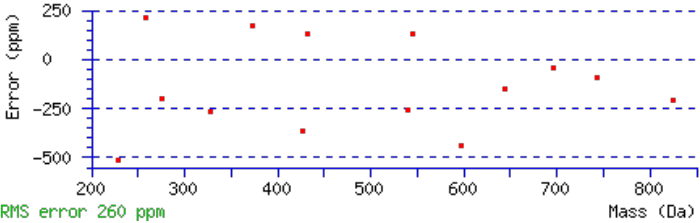
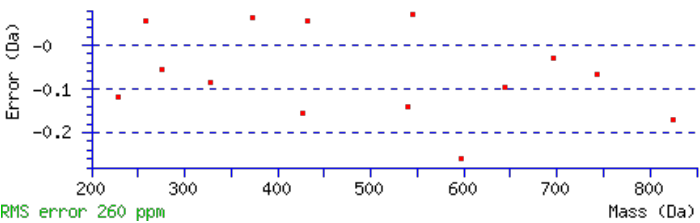
MS/MS Fragmentation of **DIVVLGVEK**
Found in **IPI00024175**, Tax_Id=9606 Gene_Symbol=PSMA7 Isoform 1 of Proteasome subunit alpha type-7

Match to Query 2207: 970.574128 from(486.294340,2+)
Title: 091224LimSK_Exosome3_06.2990.2990.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide **Mr(calc)**: 970.5699
Fixed modifications: Carbamidomethyl (C)
Ions Score: 44 **Expect**: 0.0028
Matches (Bold Red): 14/78 fragment ions using 35 most intense peaks

#	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							9
2	229.1183	115.0628	211.1077	106.0575	I	856.5502	428.7788	839.5237	420.2655	838.5397	419.7735	8
3	328.1867	164.5970	310.1761	155.5917	V	743.4662	372.2367	726.4396	363.7234	725.4556	363.2314	7
4	427.2551	214.1312	409.2445	205.1259	V	644.3978	322.7025	627.3712	314.1892	626.3872	313.6972	6
5	540.3392	270.6732	522.3286	261.6679	L	545.3293	273.1683	528.3028	264.6550	527.3188	264.1630	5
6	597.3606	299.1840	579.3501	290.1787	G	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
7	696.4291	348.7182	678.4185	339.7129	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
8	825.4716	413.2395	807.4611	404.2342	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9					K	147.1128	74.0600	130.0863	65.5468			1



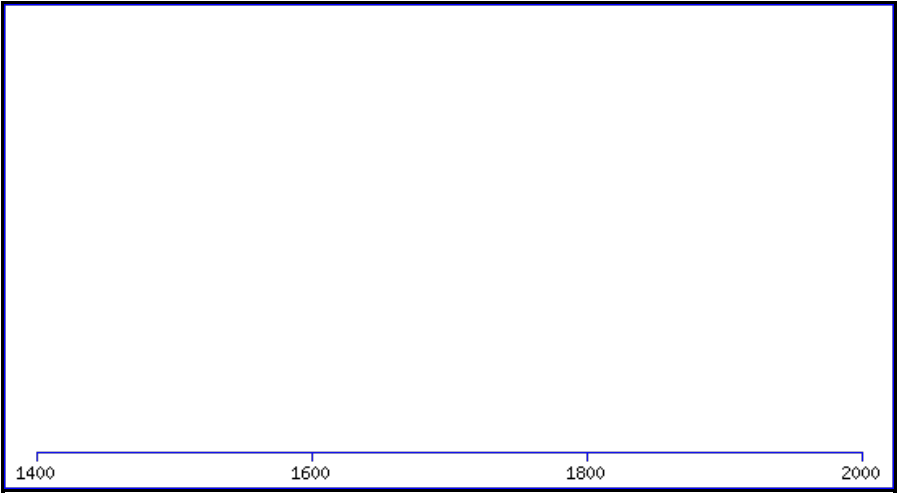
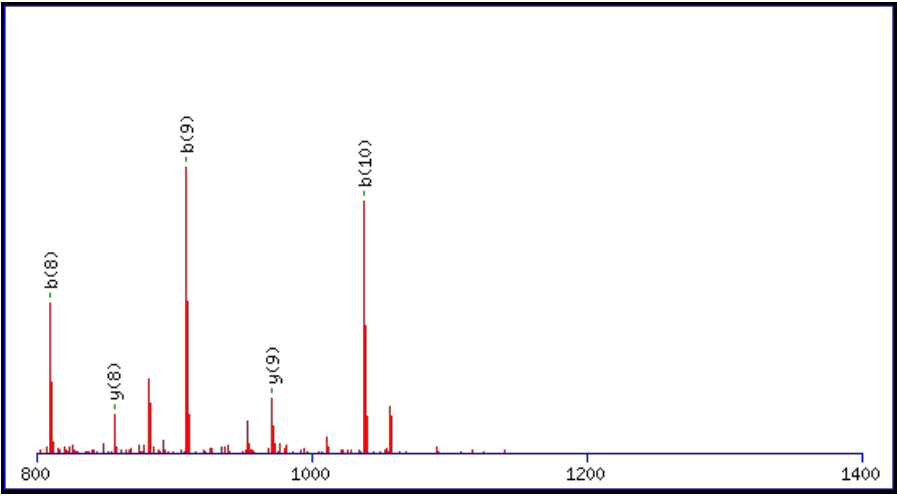
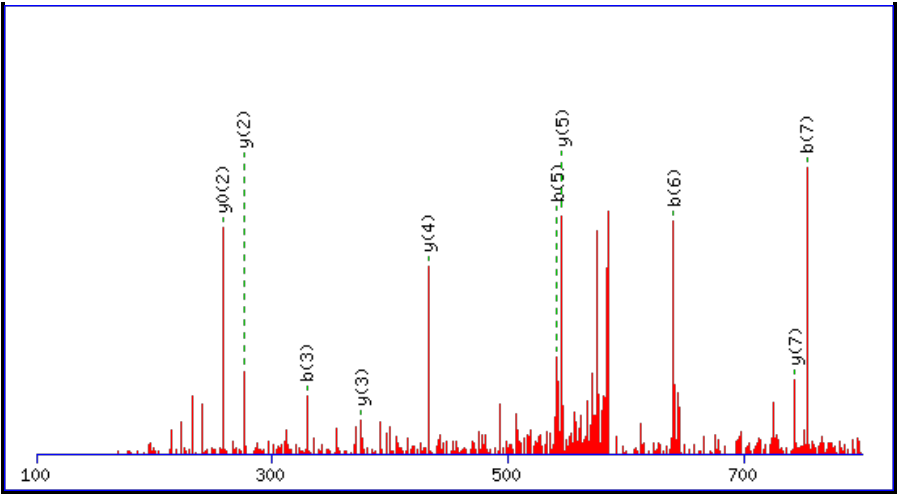
All matches to this query

Score	Mr(calc):	Delta	Sequence
43.8	970.5699	0.0042	DIVVLGVEK
10.1	970.5699	0.0043	IAELLGLDK
8.0	970.5672	0.0069	RNVGIREK
7.7	970.5811	-0.0070	SLLLLEQR
7.2	970.5699	0.0042	IDVGDVILK
5.8	970.5811	-0.0070	ITLLVQER
5.5	970.5811	-0.0070	DVVILGRSL
5.3	969.5720	1.0022	QVVIGGRNK
4.1	970.5699	0.0043	LDLQILEK
2.6	969.5719	1.0022	ARVENIIR

Spectrum No: 4; Query: 7382; Rank: 1

Peptide View

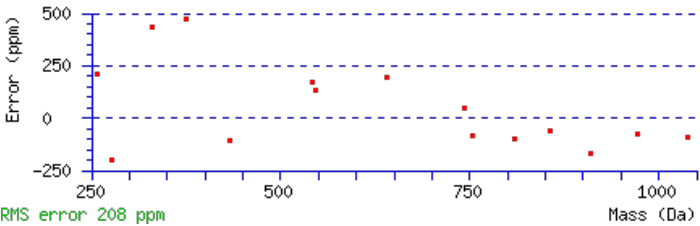
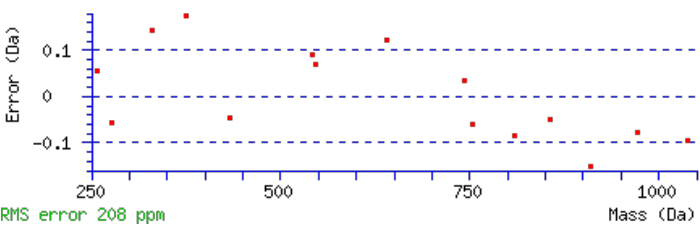
MS/MS Fragmentation of **GRDIVVLGVEK**
Found in **IPI00024175**, Tax_Id=9606 Gene_Symbol=PSMA7 Isoform 1 of Proteasome subunit alpha type-7
Match to Query 7382: 1183.698248 from(592.856400,2+)
Title: 091224LimSK_Exosome3_06.1747.1747.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1183.6925
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 Expect: 0.00033
Matches (Bold Red): 15/112 fragment ions using 36 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	214.1299	107.5686	197.1033	99.0553			R	1127.6783	564.3428	1110.6517	555.8295	1109.6677	555.3375	10
3	329.1568	165.0820	312.1302	156.5688	311.1462	156.0768	D	971.5772	486.2922	954.5506	477.7790	953.5666	477.2869	9
4	442.2409	221.6241	425.2143	213.1108	424.2303	212.6188	I	856.5502	428.7788	839.5237	420.2655	838.5397	419.7735	8
5	541.3093	271.1583	524.2827	262.6450	523.2987	262.1530	V	743.4662	372.2367	726.4396	363.7234	725.4556	363.2314	7
6	640.3777	320.6925	623.3511	312.1792	622.3671	311.6872	V	644.3978	322.7025	627.3712	314.1892	626.3872	313.6972	6

7	753.4618	377.2345	736.4352	368.7212	735.4512	368.2292	L	545.3293	273.1683	528.3028	264.6550	527.3188	264.1630	5
8	810.4832	405.7452	793.4567	397.2320	792.4726	396.7400	G	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
9	909.5516	455.2795	892.5251	446.7662	891.5411	446.2742	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
10	1038.5942	519.8007	1021.5677	511.2875	1020.5837	510.7955	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
11							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

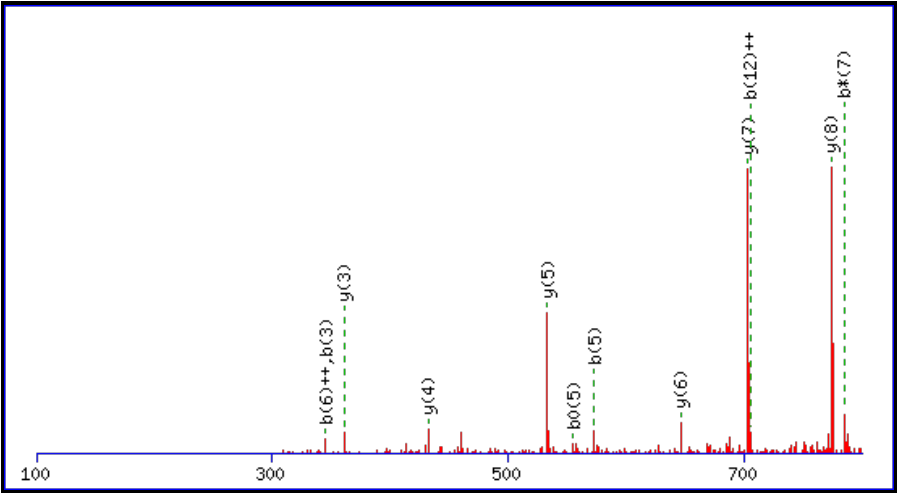
Score	Mr(calc):	Delta	Sequence
51.9	1183.6925	0.0058	GRDIVVLGVEK
14.4	1183.7037	-0.0054	GNLKQVRIEK
12.0	1181.6992	1.9990	QQRKPLREK
11.8	1183.6924	0.0058	AEKQKPEVKK
4.7	1183.7037	-0.0054	RKALDLLNKK
4.6	1183.6965	0.0018	KEVVKPPYPK
3.3	1183.7037	-0.0054	LNTSIPQKRK
2.9	1183.7037	-0.0054	VLKNQDLARK
2.6	1183.6924	0.0058	GREILELVQK
2.5	1183.7037	-0.0054	NNTLVLQVRK

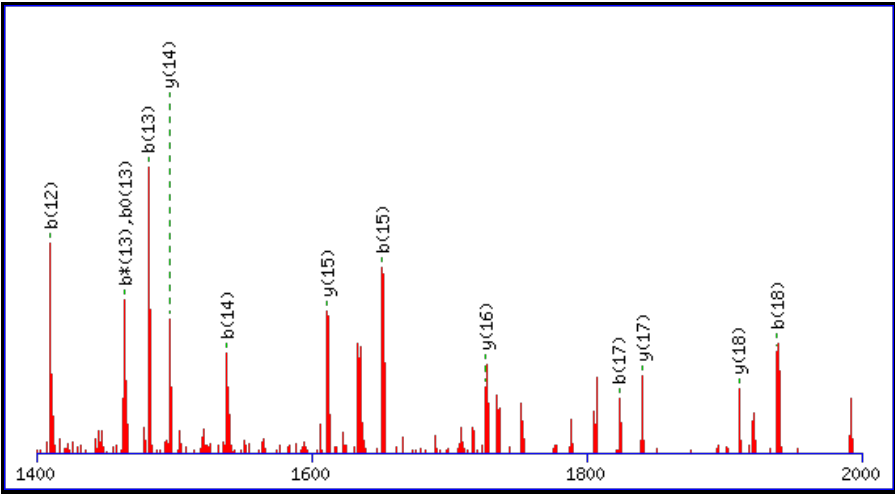
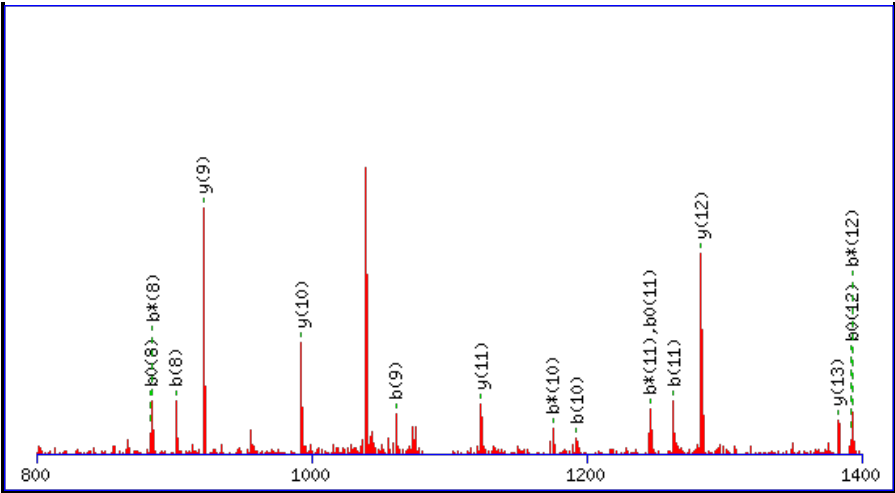
Spectrum No: 5; Query: 46207; Rank: 1

Peptide View

MS/MS Fragmentation of **ICALDDNVCMAFAGLTADAR**
Found in **IP100024175**, Tax_Id=9606 Gene_Symbol=PSMA7 Isoform 1 of Proteasome subunit alpha type-7

Match to Query 46207: 2182.997328 from(1092.505940,2+)
Title: 091224LimSK_Exosome3_06.7435.7435.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

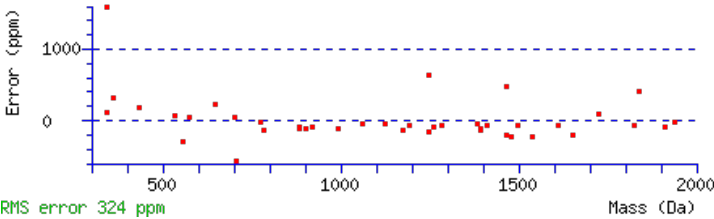
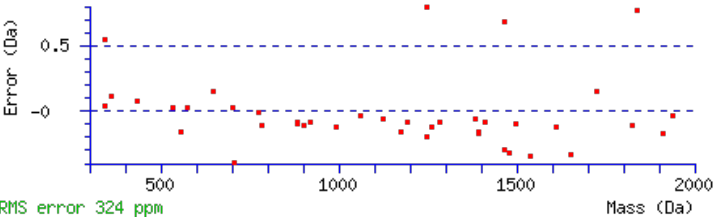




Monoisotopic mass of neutral peptide Mr(calc): 2182.9809
Fixed modifications: Carbamidomethyl (C)
Ions Score: 103 Expect: 1.5e-008
Matches (**Bold Red**): 41/204 fragment ions using 74 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					I							20
2	274.1220	137.5646					C	2070.9042	1035.9557	2053.8776	1027.4424	2052.8936	1026.9504	19
3	345.1591	173.0832					A	1910.8735	955.9404	1893.8470	947.4271	1892.8629	946.9351	18
4	458.2432	229.6252					L	1839.8364	920.4218	1822.8098	911.9086	1821.8258	911.4166	17
5	573.2701	287.1387			555.2595	278.1334	D	1726.7523	863.8798	1709.7258	855.3665	1708.7418	854.8745	16
6	688.2971	344.6522			670.2865	335.6469	D	1611.7254	806.3663	1594.6988	797.8531	1593.7148	797.3611	15
7	802.3400	401.6736	785.3134	393.1604	784.3294	392.6683	N	1496.6984	748.8529	1479.6719	740.3396	1478.6879	739.8476	14
8	901.4084	451.2078	884.3818	442.6946	883.3978	442.2026	V	1382.6555	691.8314	1365.6290	683.3181	1364.6450	682.8261	13
9	1061.4390	531.2232	1044.4125	522.7099	1043.4285	522.2179	C	1283.5871	642.2972	1266.5606	633.7839	1265.5765	633.2919	12
10	1192.4795	596.7434	1175.4530	588.2301	1174.4690	587.7381	M	1123.5565	562.2819	1106.5299	553.7686	1105.5459	553.2766	11
11	1263.5166	632.2620	1246.4901	623.7487	1245.5061	623.2567	A	992.5160	496.7616	975.4894	488.2483	974.5054	487.7563	10
12	1410.5851	705.7962	1393.5585	697.2829	1392.5745	696.7909	F	921.4789	461.2431	904.4523	452.7298	903.4683	452.2378	9
13	1481.6222	741.3147	1464.5956	732.8014	1463.6116	732.3094	A	774.4104	387.7089	757.3839	379.1956	756.3999	378.7036	8
14	1538.6436	769.8255	1521.6171	761.3122	1520.6331	760.8202	G	703.3733	352.1903	686.3468	343.6770	685.3628	343.1850	7
15	1651.7277	826.3675	1634.7011	817.8542	1633.7171	817.3622	L	646.3519	323.6796	629.3253	315.1663	628.3413	314.6743	6
16	1752.7754	876.8913	1735.7488	868.3781	1734.7648	867.8860	T	533.2678	267.1375	516.2413	258.6243	515.2572	258.1323	5
17	1823.8125	912.4099	1806.7859	903.8966	1805.8019	903.4046	A	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	4
18	1938.8394	969.9234	1921.8129	961.4101	1920.8289	960.9181	D	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
19	2009.8765	1005.4419	1992.8500	996.9286	1991.8660	996.4366	A	246.1561	123.5817	229.1295	115.0684			2

20							R	175.1190	88.0631	158.0924	79.5498			1
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All matches to this query

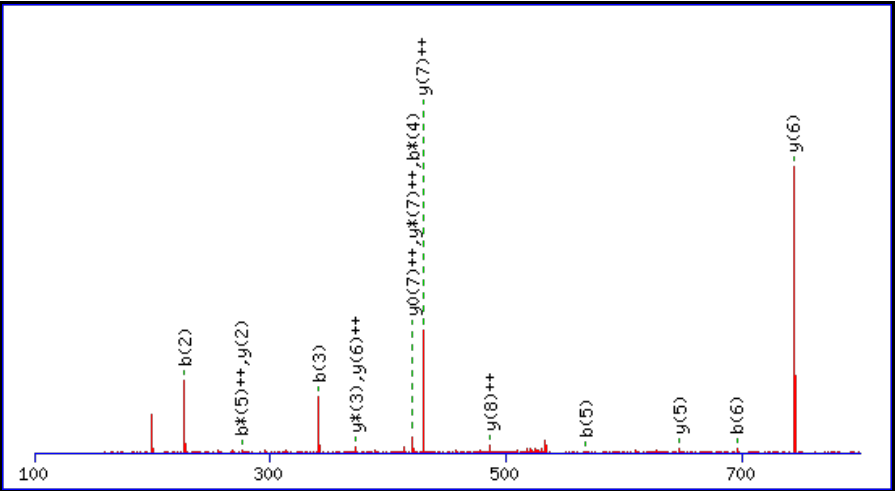
Score	Mr(calc):	Delta	Sequence
102.8	2182.9809	0.0164	ICALDDNVCMAFAGLTADAR
9.8	2180.9830	2.0144	YGMVAQVTQTLKLEDTPK
7.8	2181.9742	1.0232	ITSEMGASQANIRLTSLK
7.8	2181.9742	1.0232	ITSEMGASQANIRLTSLK
7.8	2181.9742	1.0232	ITSEMGASQANIRLTSLK
7.8	2181.9742	1.0232	ITSEMGASQANIRLTSLK
7.8	2181.9742	1.0232	ITSEMGASQANIRLTSLK
7.2	2183.0154	-0.0181	GVNTERSSKLGSNAGNKPCK
6.5	2180.9830	2.0144	YGMVAQVTQTLKLEDTPK
5.4	2181.9782	1.0191	EIKSYMNTAGNSAPSLFLK
4.9	2183.0023	-0.0050	SRFKGMYYLHPGTLDYR

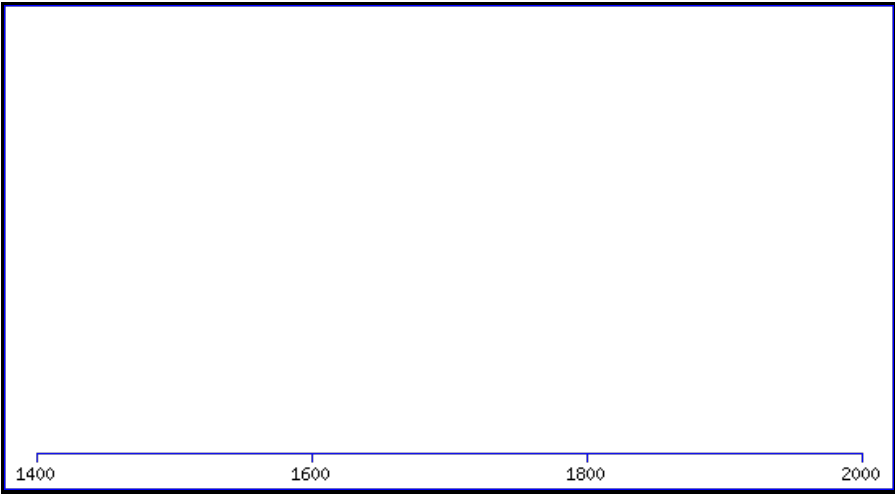
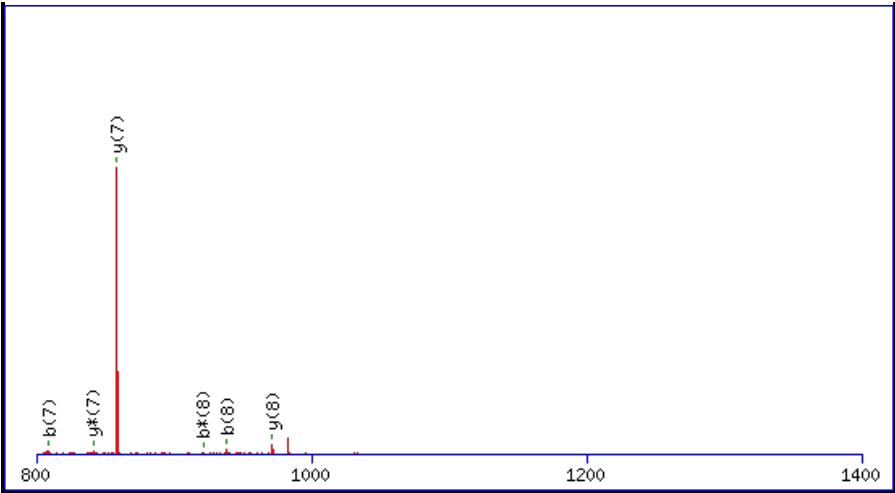
Spectrum No: 6; Query: 4381; Rank: 1

Peptide View

MS/MS Fragmentation of **ILNPEEIEK**
Found in **IPI00024175**, Tax_Id=9606 Gene_Symbol=PSMA7 Isoform 1 of Proteasome subunit alpha type-7

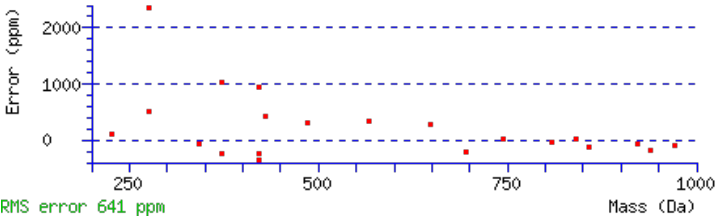
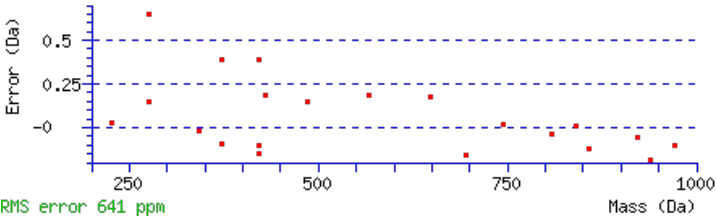
Match to Query 4381: 1083.585948 from(542.800250,2+)
Title: 091224LimSK_Exosome3_06.1889.1889.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1083.5811
Fixed modifications: Carbamidomethyl (C)
Ions Score: 40 Expect: 0.0095
Matches (Bold Red): 21/82 fragment ions using 36 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					I							9
2	227.1754	114.0913					L	971.5044	486.2558	954.4779	477.7426	953.4938	477.2506	8
3	341.2183	171.1128	324.1918	162.5995			N	858.4203	429.7138	841.3938	421.2005	840.4098	420.7085	7
4	438.2711	219.6392	421.2445	211.1259			P	744.3774	372.6923	727.3509	364.1791	726.3668	363.6871	6
5	567.3137	284.1605	550.2871	275.6472	549.3031	275.1552	E	647.3246	324.1660	630.2981	315.6527	629.3141	315.1607	5
6	696.3563	348.6818	679.3297	340.1685	678.3457	339.6765	E	518.2821	259.6447	501.2555	251.1314	500.2715	250.6394	4
7	809.4403	405.2238	792.4138	396.7105	791.4298	396.2185	I	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
8	938.4829	469.7451	921.4564	461.2318	920.4724	460.7398	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
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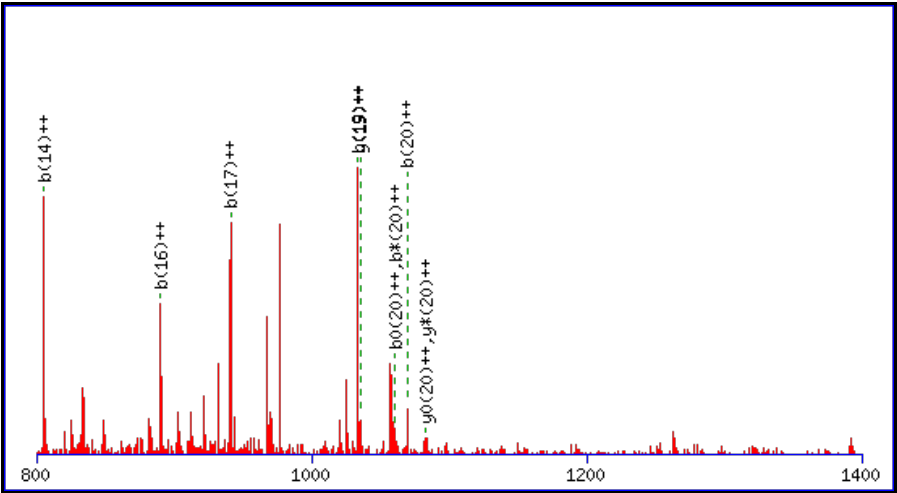
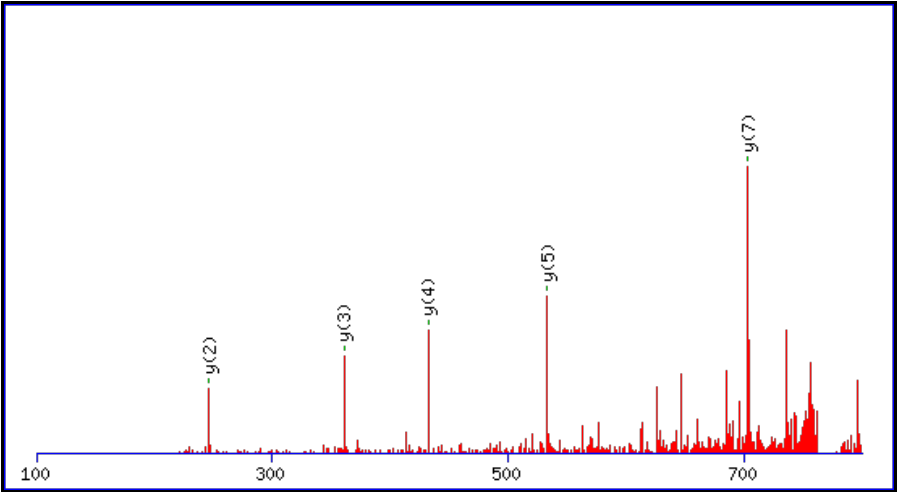
39.8	1083.5811	0.0048	ILNPEEIEK
7.7	1083.5763	0.0097	LLATKAMLK
6.9	1083.5954	-0.0094	ILHKKHTK
6.2	1083.5841	0.0018	ILQLYARK
4.0	1082.5923	0.9937	KILGKMVSK
2.6	1083.5859	0.0001	LLHSSQMLR
2.2	1083.5924	-0.0064	NIQPKVEEK
1.8	1082.5760	1.0099	LLIEGSDYR
0.5	1083.5812	0.0048	EPAVLELEGK
0.4	1083.5924	-0.0064	EPKLNENIK

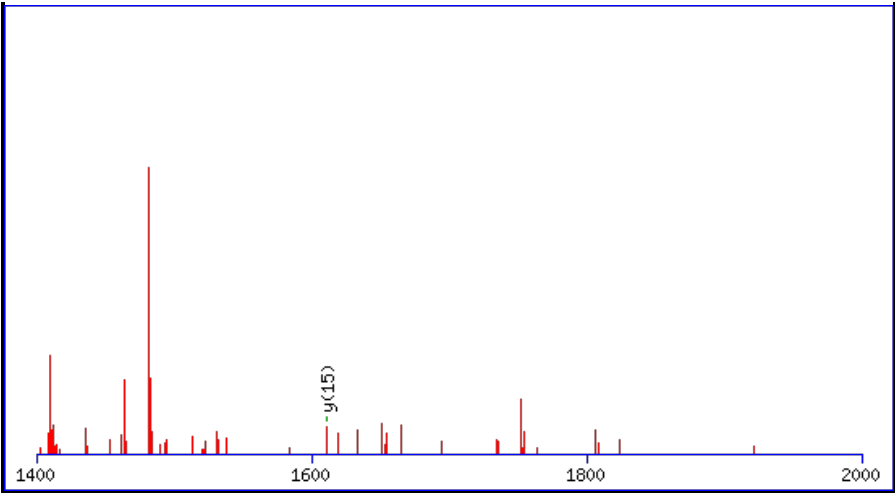
Spectrum No: 7; Query: 51343; Rank: 1

Peptide View

MS/MS Fragmentation of **KICALDDNVCMAFAGLTADAR**
Found in **IP100024175**, Tax_Id=9606 Gene_Symbol=PSMA7 Isoform 1 of Proteasome subunit alpha type-7

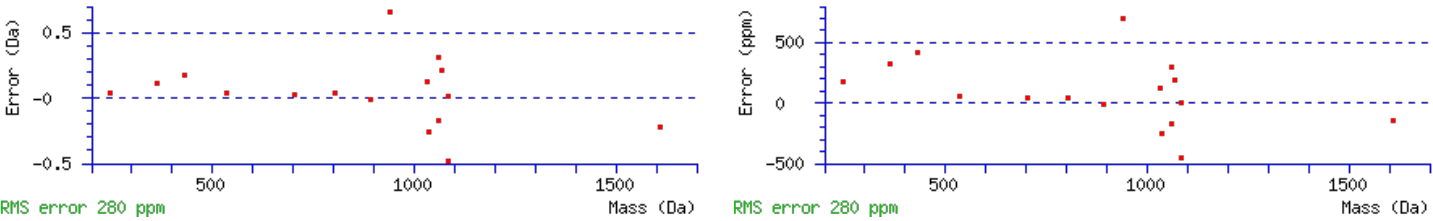
Match to Query 51343: 2311.094622 from(771.372150,3+)
Title: 091224LimSK_Exosome3_06.6940.6940.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2311.0759
Fixed modifications: Carbamidomethyl (C)
Ions Score: 29 Expect: 0.33
Matches (Bold Red): 16/226 fragment ions using 36 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							21
2	242.1863	121.5968	225.1598	113.0835			I	2183.9882	1092.4977	2166.9617	1083.9845	2165.9777	1083.4925	20
3	402.2170	201.6121	385.1904	193.0988			C	2070.9042	1035.9557	2053.8776	1027.4424	2052.8936	1026.9504	19
4	473.2541	237.1307	456.2275	228.6174			A	1910.8735	955.9404	1893.8470	947.4271	1892.8629	946.9351	18
5	586.3381	293.6727	569.3116	285.1594			L	1839.8364	920.4218	1822.8098	911.9086	1821.8258	911.4166	17
6	701.3651	351.1862	684.3385	342.6729	683.3545	342.1809	D	1726.7523	863.8798	1709.7258	855.3665	1708.7418	854.8745	16
7	816.3920	408.6996	799.3655	400.1864	798.3815	399.6944	D	1611.7254	806.3663	1594.6988	797.8531	1593.7148	797.3611	15
8	930.4349	465.7211	913.4084	457.2078	912.4244	456.7158	N	1496.6984	748.8529	1479.6719	740.3396	1478.6879	739.8476	14
9	1029.5034	515.2553	1012.4768	506.7420	1011.4928	506.2500	V	1382.6555	691.8314	1365.6290	683.3181	1364.6450	682.8261	13
10	1189.5340	595.2706	1172.5075	586.7574	1171.5234	586.2654	C	1283.5871	642.2972	1266.5606	633.7839	1265.5765	633.2919	12
11	1320.5745	660.7909	1303.5479	652.2776	1302.5639	651.7856	M	1123.5565	562.2819	1106.5299	553.7686	1105.5459	553.2766	11
12	1391.6116	696.3094	1374.5851	687.7962	1373.6010	687.3042	A	992.5160	496.7616	975.4894	488.2483	974.5054	487.7563	10
13	1538.6800	769.8436	1521.6535	761.3304	1520.6695	760.8384	F	921.4789	461.2431	904.4523	452.7298	903.4683	452.2378	9
14	1609.7171	805.3622	1592.6906	796.8489	1591.7066	796.3569	A	774.4104	387.7089	757.3839	379.1956	756.3999	378.7036	8
15	1666.7386	833.8729	1649.7120	825.3597	1648.7280	824.8677	G	703.3733	352.1903	686.3468	343.6770	685.3628	343.1850	7
16	1779.8227	890.4150	1762.7961	881.9017	1761.8121	881.4097	L	646.3519	323.6796	629.3253	315.1663	628.3413	314.6743	6
17	1880.8703	940.9388	1863.8438	932.4255	1862.8598	931.9335	T	533.2678	267.1375	516.2413	258.6243	515.2572	258.1323	5
18	1951.9075	976.4574	1934.8809	967.9441	1933.8969	967.4521	A	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	4
19	2066.9344	1033.9708	2049.9078	1025.4576	2048.9238	1024.9656	D	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
20	2137.9715	1069.4894	2120.9450	1060.9761	2119.9609	1060.4841	A	246.1561	123.5817	229.1295	115.0684			2
21							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

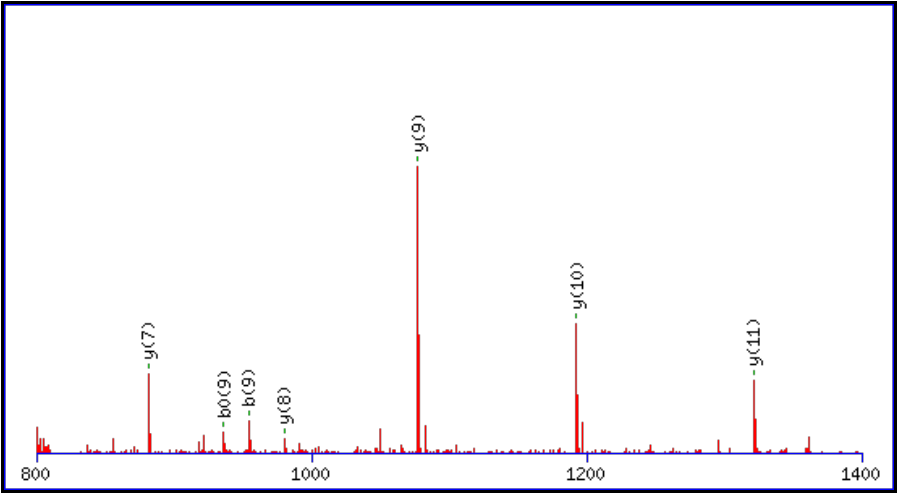
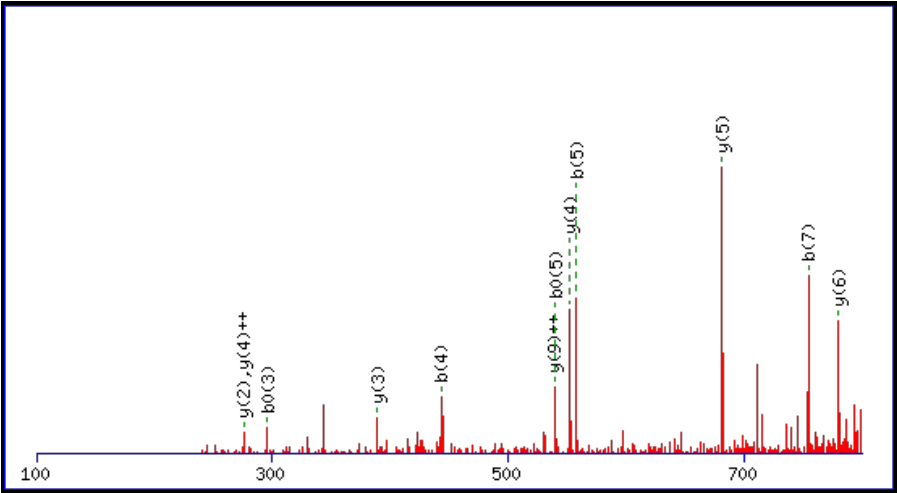
Score	Mr(calc):	Delta	Sequence
29.1	2311.0759	0.0187	KICALDDNVCMAFAGLTADAR

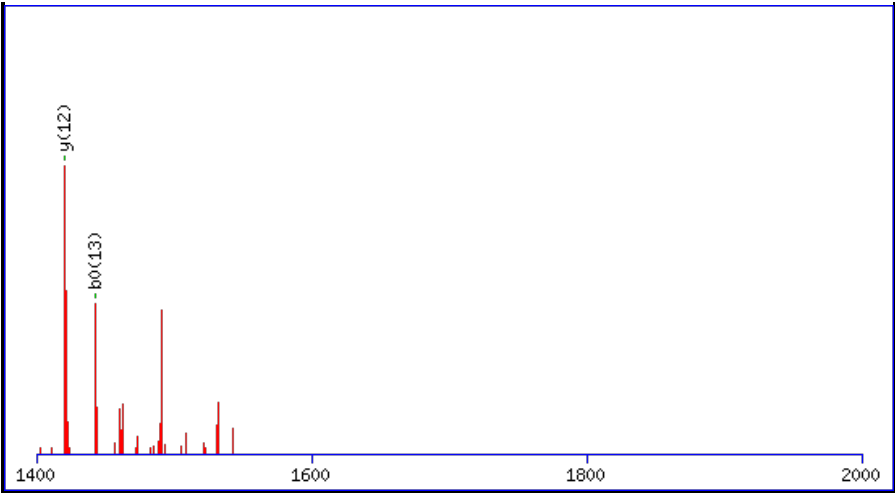
17.7	2311.0959	-0.0013	KRFMLKPYESFEELTGEK
9.2	2311.1032	-0.0086	MGWTGGGLGKSGEGIREPISVK
8.3	2309.0876	2.0071	SGGCFPGSATVHLEQGGTKLVK
7.5	2311.1147	-0.0201	MAAKMEITLSSNTEASSKQER
5.0	2309.0859	2.0087	GNAGDCLANPAVPWGQGVEIER
4.9	2310.1079	0.9867	SRLFVGNLPPDITEEEMRK
4.5	2310.0947	1.0000	RQHGQLWFPEGFKVSEASK
4.2	2310.1039	0.9907	EELARDKCVVIGLQSTGEAR
4.0	2311.1038	-0.0092	QKQSGFFLENKSTYQLWK

Spectrum No: 8; Query: 27223; Rank: 1

Peptide View

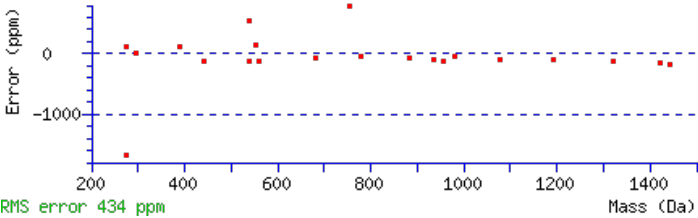
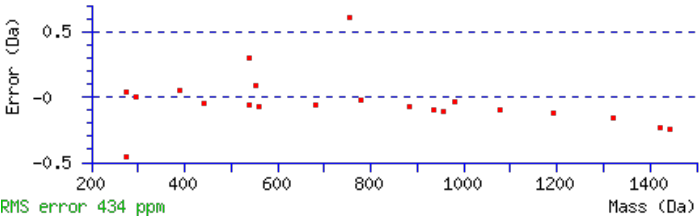
MS/MS Fragmentation of **LTVEDPVTVEYITR**
Found in **IPI00024175**, Tax_Id=9606 Gene_Symbol=PSMA7 Isoform 1 of Proteasome subunit alpha type-7
Match to Query 27223: 1633.866328 from(817.940440,2+)
Title: 091224LimSK_Exosome3_07.5092.5092.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1633.8563
Fixed modifications: Carbamidomethyl (C)
Ions Score: 91 **Expect:** 9.7e-008
Matches (Bold Red): 21/126 fragment ions using 32 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							14
2	215.1390	108.0731	197.1285	99.0679	T	1521.7795	761.3934	1504.7530	752.8801	1503.7690	752.3881	13
3	314.2074	157.6074	296.1969	148.6021	V	1420.7318	710.8696	1403.7053	702.3563	1402.7213	701.8643	12
4	443.2500	222.1287	425.2395	213.1234	E	1321.6634	661.3353	1304.6369	652.8221	1303.6529	652.3301	11
5	558.2770	279.6421	540.2664	270.6368	D	1192.6208	596.8141	1175.5943	588.3008	1174.6103	587.8088	10
6	655.3297	328.1685	637.3192	319.1632	P	1077.5939	539.3006	1060.5673	530.7873	1059.5833	530.2953	9
7	754.3981	377.7027	736.3876	368.6974	V	980.5411	490.7742	963.5146	482.2609	962.5306	481.7689	8
8	855.4458	428.2266	837.4353	419.2213	T	881.4727	441.2400	864.4462	432.7267	863.4621	432.2347	7
9	954.5142	477.7608	936.5037	468.7555	V	780.4250	390.7162	763.3985	382.2029	762.4145	381.7109	6
10	1083.5568	542.2821	1065.5463	533.2768	E	681.3566	341.1819	664.3301	332.6687	663.3461	332.1767	5
11	1246.6202	623.8137	1228.6096	614.8084	Y	552.3140	276.6607	535.2875	268.1474	534.3035	267.6554	4
12	1359.7042	680.3558	1341.6937	671.3505	I	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
13	1460.7519	730.8796	1442.7413	721.8743	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
14					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

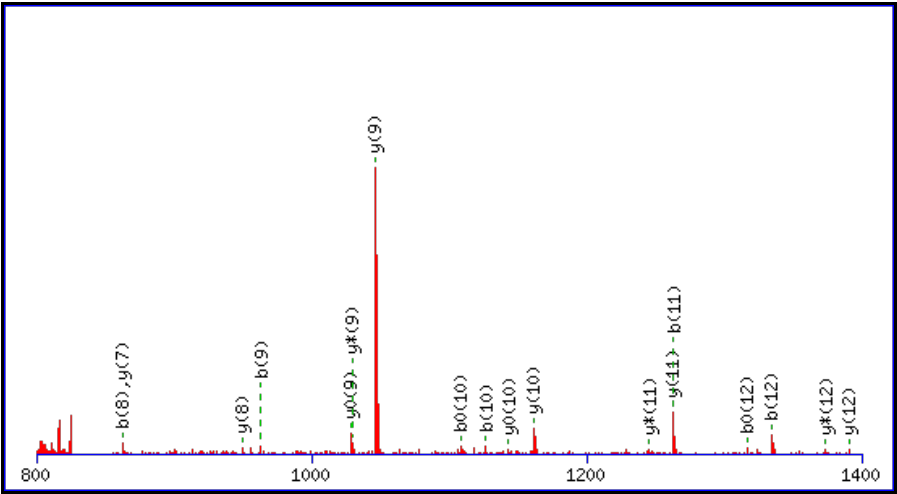
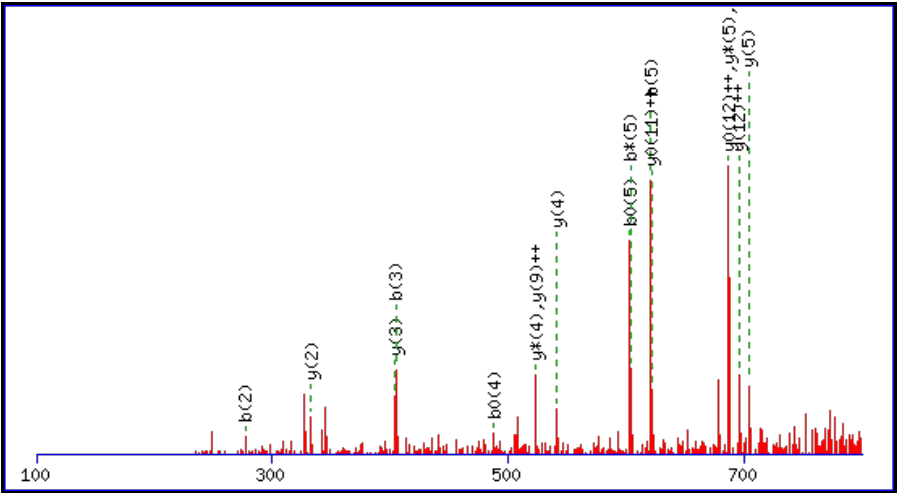
Score	Mr(calc):	Delta	Sequence
91.3	1633.8563	0.0100	LTVEDPVTVEYITR
8.8	1632.8501	1.0162	KFLPSTANRGLPPR
8.8	1632.8501	1.0162	KFLPSTANRGLPPR
8.6	1632.8528	1.0135	TLNINTKYYYVLVI
8.6	1632.8528	1.0135	TLNINTKYYYVLVI
5.2	1632.8528	1.0135	TLNINTKYYYVLVI
2.7	1631.8743	1.9920	RGGAEGSPKLAVYATR
2.3	1633.8665	-0.0002	LQIVNNTRKVDVR

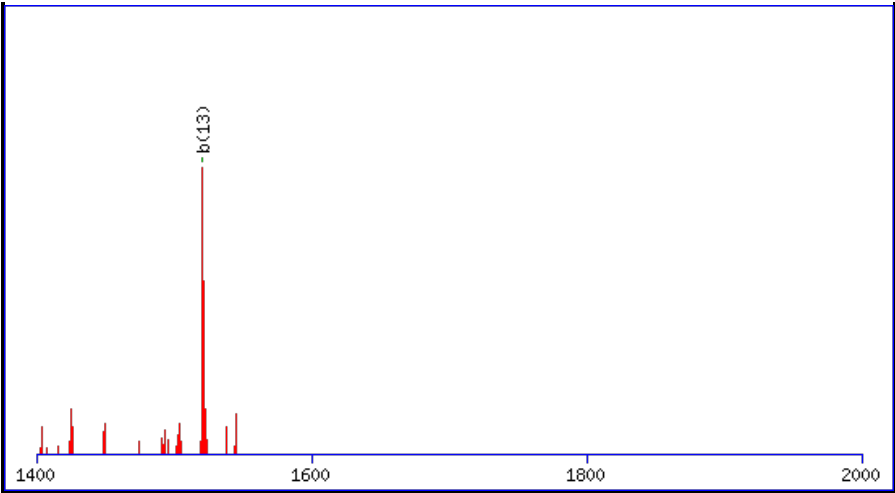
2.3	1631.8661	2.0002	QVRFRLTPPSPVR
1.8	1631.8631	2.0032	VLETLVTVAEEHHR

Spectrum No: 9; Query: 28501; Rank: 1

Peptide View

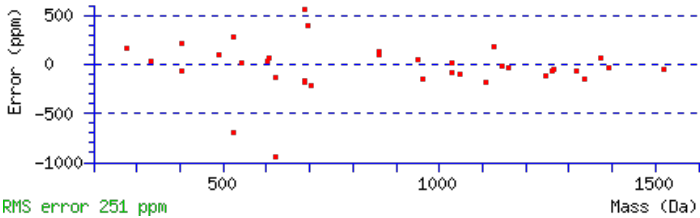
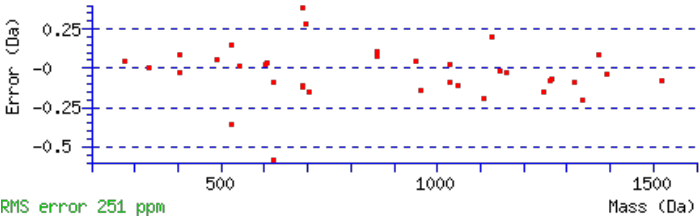
MS/MS Fragmentation of **LYQTDPSGTYHAWK**
Found in **IPI00024175**, Tax_Id=9606 Gene_Symbol=PSMA7 Isoform 1 of Proteasome subunit alpha type-7
Match to Query 28501: 1665.789888 from(833.902220,2+)
Title: 091224LimSK_Exosome3_05.1898.1898.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1665.7787
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 Expect: 0.00087
Matches (Bold Red): 37/136 fragment ions using 71 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							14
2	277.1547	139.0810					Y	1553.7019	777.3546	1536.6754	768.8413	1535.6914	768.3493	13
3	405.2132	203.1103	388.1867	194.5970			Q	1390.6386	695.8229	1373.6121	687.3097	1372.6280	686.8177	12
4	506.2609	253.6341	489.2344	245.1208	488.2504	244.6288	T	1262.5800	631.7937	1245.5535	623.2804	1244.5695	622.7884	11
5	621.2879	311.1476	604.2613	302.6343	603.2773	302.1423	D	1161.5324	581.2698	1144.5058	572.7565	1143.5218	572.2645	10
6	718.3406	359.6740	701.3141	351.1607	700.3301	350.6687	P	1046.5054	523.7563	1029.4789	515.2431	1028.4948	514.7511	9
7	805.3727	403.1900	788.3461	394.6767	787.3621	394.1847	S	949.4526	475.2300	932.4261	466.7167	931.4421	466.2247	8
8	862.3941	431.7007	845.3676	423.1874	844.3836	422.6954	G	862.4206	431.7139	845.3941	423.2007	844.4100	422.7087	7
9	963.4418	482.2245	946.4153	473.7113	945.4312	473.2193	T	805.3992	403.2032	788.3726	394.6899	787.3886	394.1979	6
10	1126.5051	563.7562	1109.4786	555.2429	1108.4946	554.7509	Y	704.3515	352.6794	687.3249	344.1661			5
11	1263.5640	632.2857	1246.5375	623.7724	1245.5535	623.2804	H	541.2881	271.1477	524.2616	262.6344			4
12	1334.6012	667.8042	1317.5746	659.2909	1316.5906	658.7989	A	404.2292	202.6183	387.2027	194.1050			3
13	1520.6805	760.8439	1503.6539	752.3306	1502.6699	751.8386	W	333.1921	167.0997	316.1656	158.5864			2
14							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

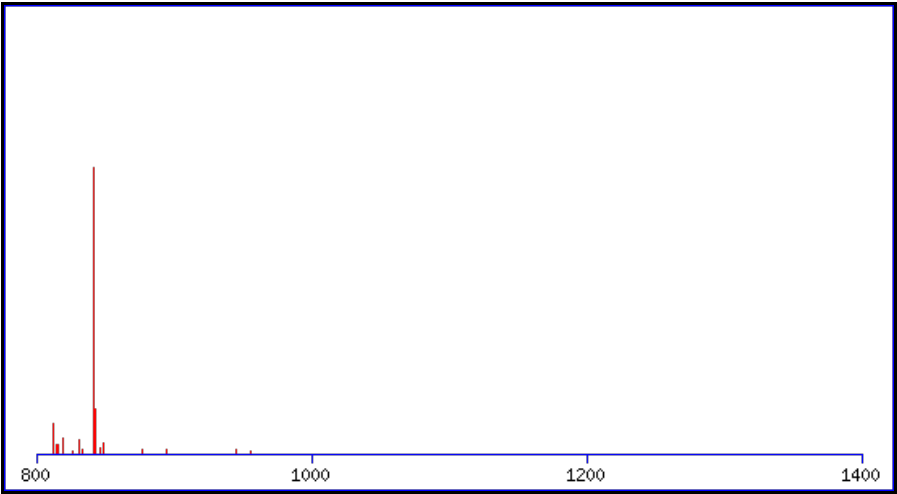
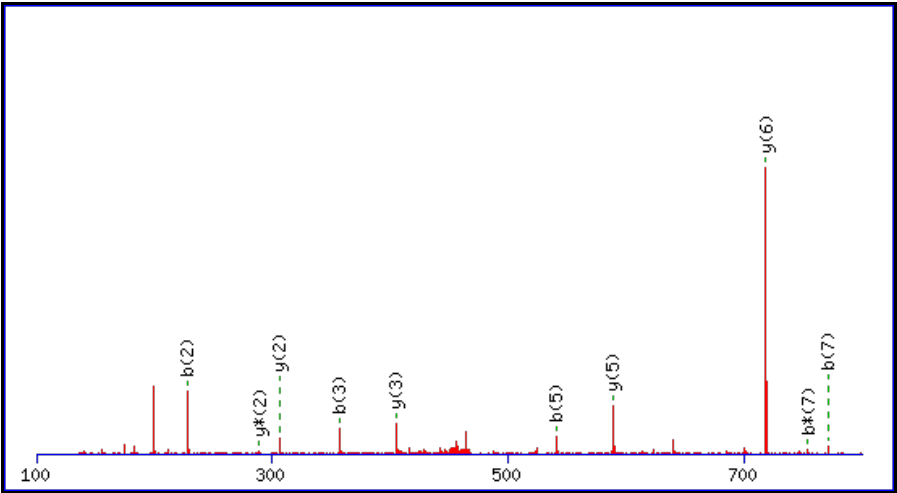
Score	Mr(calc):	Delta	Sequence
53.9	1665.7787	0.0112	LYQTDPSGTYHAWK
10.0	1665.7954	-0.0055	GSSVEMLQDVIDVMK
9.8	1665.7780	0.0118	QQMEERFVASNPSK
8.5	1665.7854	0.0045	NMVYILTITPLK
8.5	1665.7854	0.0045	NMVYILTITPLK
6.2	1665.7767	0.0132	MEIDDLASNVETVSK
5.2	1665.7892	0.0007	GASVIIRFVTNTTK
4.5	1664.7716	1.0183	MQNNIADPEELFK

4.3	1664.7885	1.0014	VDIPPPFDLACITK
3.9	1665.7780	0.0119	GLIQQFTTITEKK

Spectrum No: 10; Query: 1875; Rank: 1

Peptide View

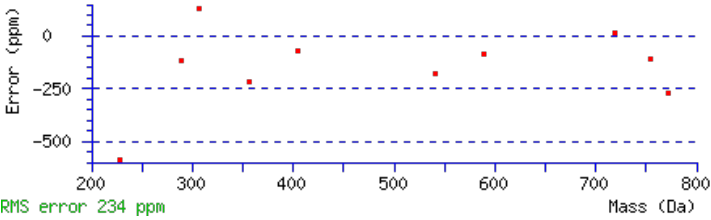
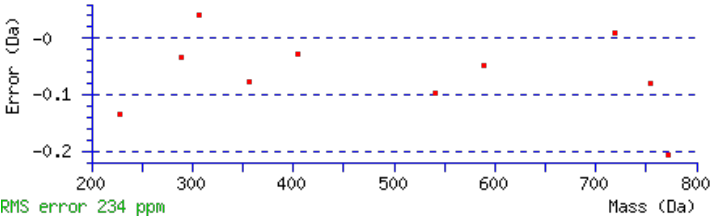
MS/MS Fragmentation of **NIELAVMR**
Found in **IPI00024175**, Tax_Id=9606 Gene_Symbol=PSMA7 Isoform 1 of Proteasome subunit alpha type-7
Match to Query 1875: 944.515768 from(473.265160,2+)
Title: 091224LimSK_Exosome3_06.2979.2979.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 944.5113
Fixed modifications: Carbamidomethyl (C)
Ions Score: 33 **Expect:** 0.063
Matches (Bold Red): 10/70 fragment ions using 17 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							8
2	228.1343	114.5708	211.1077	106.0575			I	831.4757	416.2415	814.4491	407.7282	813.4651	407.2362	7
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	E	718.3916	359.6994	701.3651	351.1862	700.3811	350.6942	6
4	470.2609	235.6341	453.2344	227.1208	452.2504	226.6288	L	589.3490	295.1782	572.3225	286.6649			5
5	541.2980	271.1527	524.2715	262.6394	523.2875	262.1474	A	476.2650	238.6361	459.2384	230.1228			4
6	640.3665	320.6869	623.3399	312.1736	622.3559	311.6816	V	405.2279	203.1176	388.2013	194.6043			3
7	771.4069	386.2071	754.3804	377.6938	753.3964	377.2018	M	306.1594	153.5834	289.1329	145.0701			2
8							R	175.1190	88.0631	158.0924	79.5498			1



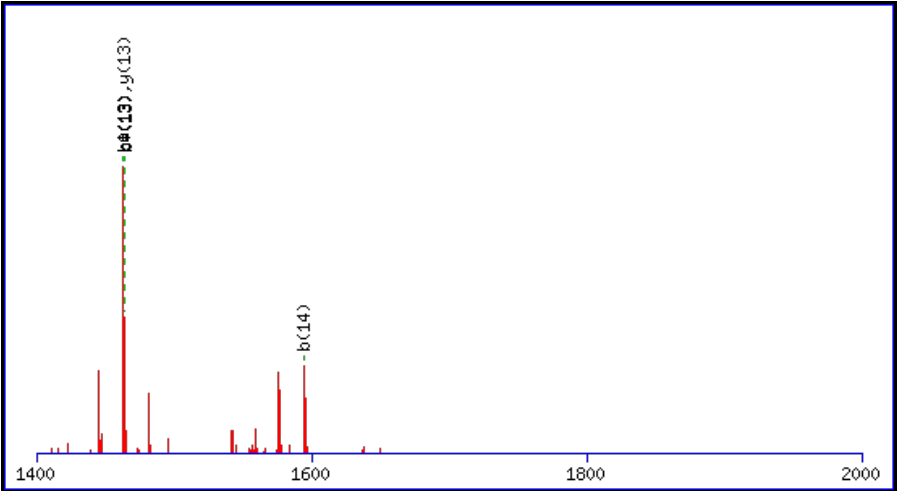
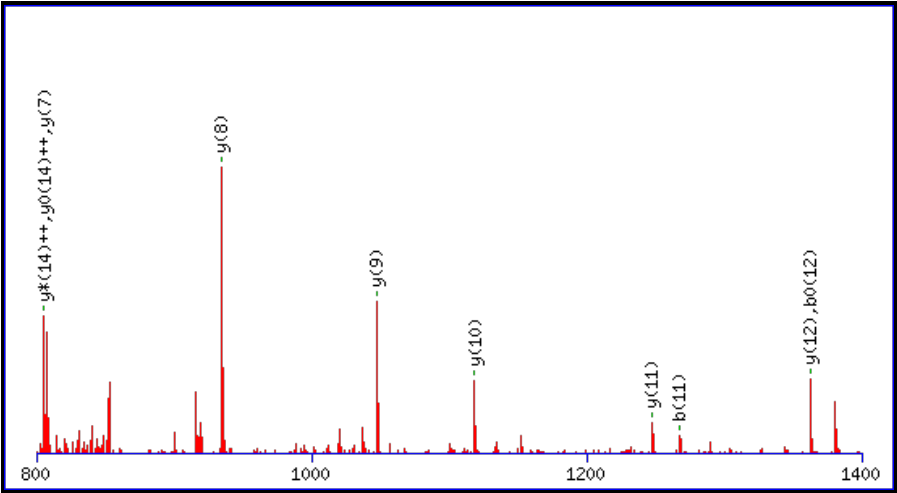
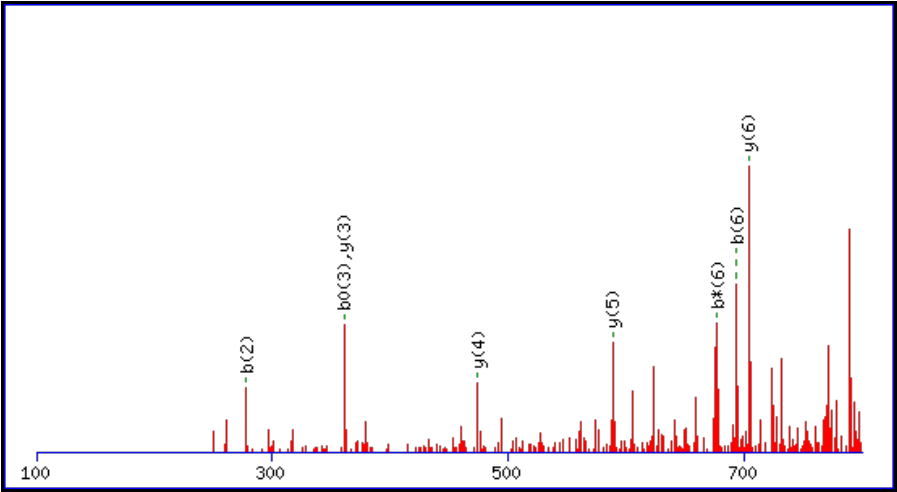
All matches to this query

Score	Mr(calc):	Delta	Sequence
33.2	944.5113	0.0045	NIELAVMR
12.0	944.5151	0.0006	LNARAASSR
8.2	943.5087	1.0071	LLQTGQER
7.1	943.5087	1.0071	EPTKIGSGR
7.1	943.5087	1.0071	EPTKVASGR
5.3	944.5152	0.0006	SSPTRKNR
4.5	944.5179	-0.0021	ITIXPDTSK
4.2	944.5152	0.0006	SSSPGAKRR
4.1	942.5134	2.0023	DGLLGAELR
3.8	943.5100	1.0057	GRQGGRWK

Peptide View

MS/MS Fragmentation of **NYTDEALETDDLTIK**
Found in **IPI00024175**, Tax_Id=9606 Gene_Symbol=PSMA7 Isoform 1 of Proteasome subunit alpha type-7

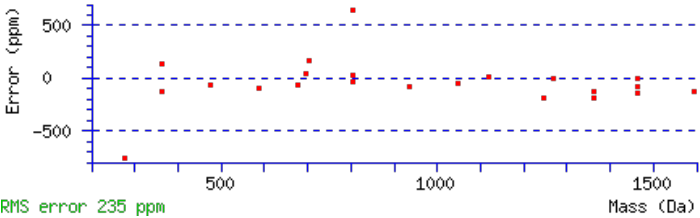
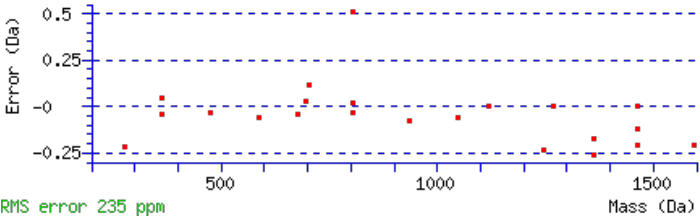
Match to Query 31171: 1739.820948 from(870.917750,2+)
Title: 091224LimSK_Exosome3_06.4135.4135.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide **Mr(calc)**: 1739.8101
Fixed modifications: Carbamidomethyl (C)
Ions Score: 119 Expect: 2.7e-010
Matches (**Bold Red**): 22/160 fragment ions using 18 most intense peaks

		++		++	0	0++		++		++	0	0++	
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#	b	b	b*	b*	b	b	Seq.	y	y	y*	y*	y	y	#
1	115.0502	58.0287	98.0237	49.5155			N							15
2	278.1135	139.5604	261.0870	131.0471			Y	1626.7745	813.8909	1609.7479	805.3776	1608.7639	804.8856	14
3	379.1612	190.0842	362.1347	181.5710	361.1506	181.0790	T	1463.7112	732.3592	1446.6846	723.8459	1445.7006	723.3539	13
4	494.1882	247.5977	477.1616	239.0844	476.1776	238.5924	D	1362.6635	681.8354	1345.6369	673.3221	1344.6529	672.8301	12
5	623.2307	312.1190	606.2042	303.6057	605.2202	303.1137	E	1247.6365	624.3219	1230.6100	615.8086	1229.6260	615.3166	11
6	694.2679	347.6376	677.2413	339.1243	676.2573	338.6323	A	1118.5939	559.8006	1101.5674	551.2873	1100.5834	550.7953	10
7	807.3519	404.1796	790.3254	395.6663	789.3414	395.1743	I	1047.5568	524.2821	1030.5303	515.7688	1029.5463	515.2768	9
8	936.3945	468.7009	919.3680	460.1876	918.3840	459.6956	E	934.4728	467.7400	917.4462	459.2267	916.4622	458.7347	8
9	1037.4422	519.2247	1020.4156	510.7115	1019.4316	510.2195	T	805.4302	403.2187	788.4036	394.7055	787.4196	394.2134	7
10	1152.4691	576.7382	1135.4426	568.2249	1134.4586	567.7329	D	704.3825	352.6949	687.3559	344.1816	686.3719	343.6896	6
11	1267.4961	634.2517	1250.4695	625.7384	1249.4855	625.2464	D	589.3556	295.1814	572.3290	286.6681	571.3450	286.1761	5
12	1380.5801	690.7937	1363.5536	682.2804	1362.5696	681.7884	L	474.3286	237.6679	457.3021	229.1547	456.3180	228.6627	4
13	1481.6278	741.3176	1464.6013	732.8043	1463.6173	732.3123	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
14	1594.7119	797.8596	1577.6853	789.3463	1576.7013	788.8543	I	260.1969	130.6021	243.1703	122.0888			2
15							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

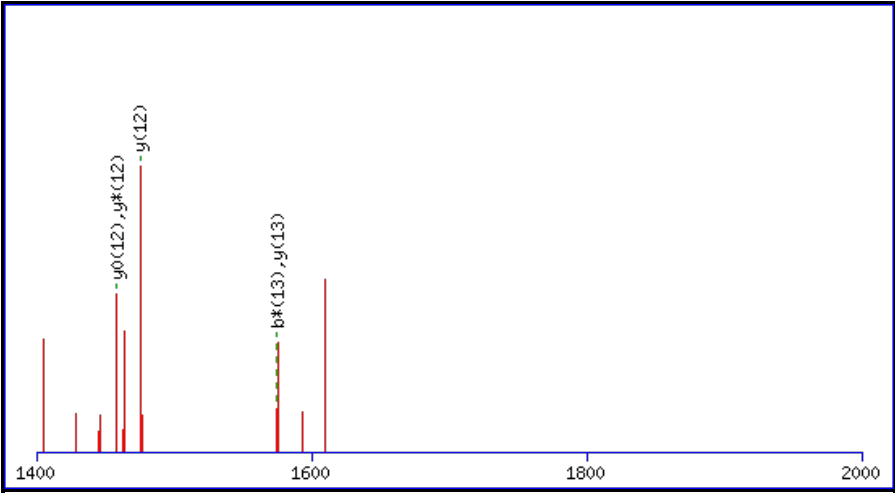
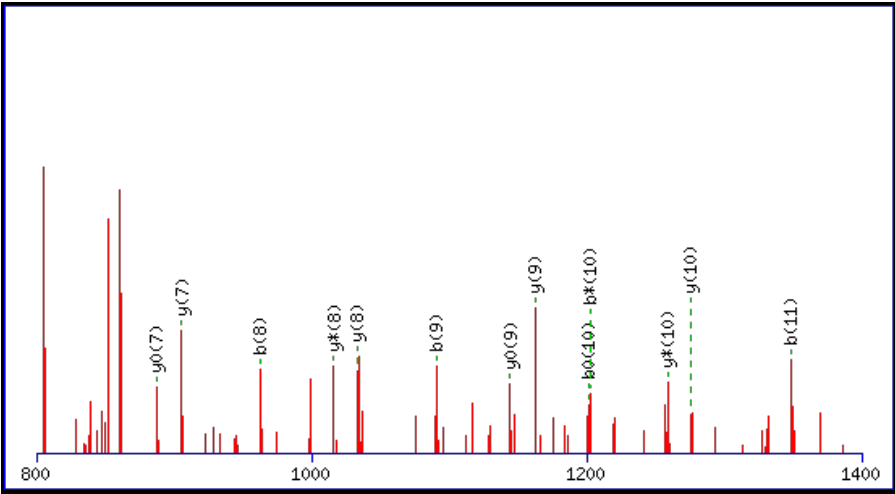
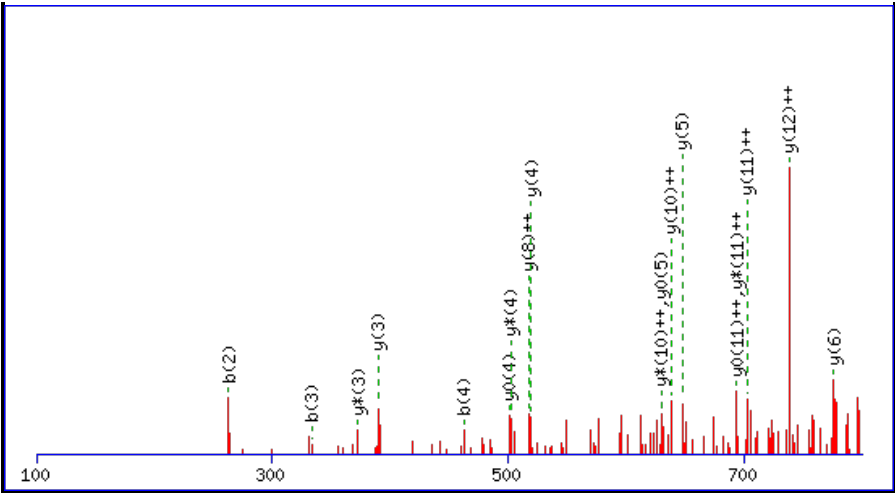
Score	Mr(calc):	Delta	Sequence
119.1	1739.8101	0.0108	NYTDEAIETDDLTIK
9.7	1739.8222	-0.0013	MKQYASPMPTQTVDVK
7.9	1739.8066	0.0144	DEGHRVLIESQMTK
7.2	1739.8335	-0.0125	CNSVKDGAICYKPTK
7.0	1739.8379	-0.0170	FERNFIAQGPYENR
6.3	1739.8284	-0.0074	EKNSTYSKPNSFLK
6.3	1739.8284	-0.0074	EKNSTYSKPNSFLK
6.3	1738.8010	1.0200	KQSTQFSGGPTEDTEK
6.0	1739.8288	-0.0078	TLFEVMATKPETDDK
6.0	1739.8317	-0.0108	YQMPTGIKGPLPNTK

Spectrum No: 12; Query: 31027; Rank: 1

Peptide View

MS/MS Fragmentation of **YVAEIEKEKEENEK**
Found in **IP100024175**, Tax_Id=9606 Gene_Symbol=PSMA7 Isoform 1 of Proteasome subunit alpha type-7

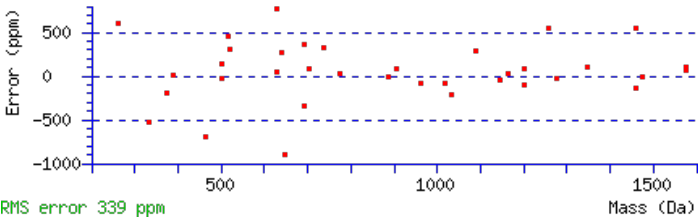
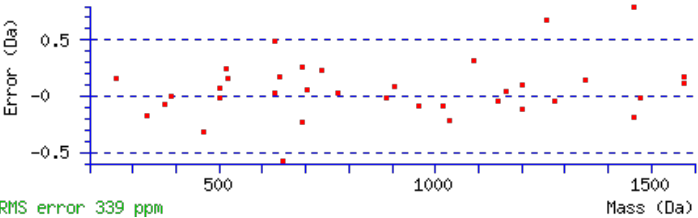
Match to Query 31027: 1736.852568 from(869.433560,2+)
Title: 091224LimSK_Exosome3_06.245.245.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1736.8468
Fixed modifications: Carbamidomethyl (C)
Ions Score: 50 Expect: 0.0023
Matches (**Bold Red**): 36/136 fragment ions using 59 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							14
2	263.1390	132.0731					V	1574.7908	787.8990	1557.7643	779.3858	1556.7802	778.8938	13
3	334.1761	167.5917					A	1475.7224	738.3648	1458.6958	729.8516	1457.7118	729.3596	12
4	463.2187	232.1130			445.2082	223.1077	E	1404.6853	702.8463	1387.6587	694.3330	1386.6747	693.8410	11
5	576.3028	288.6550			558.2922	279.6498	I	1275.6427	638.3250	1258.6161	629.8117	1257.6321	629.3197	10
6	705.3454	353.1763			687.3348	344.1710	E	1162.5586	581.7829	1145.5321	573.2697	1144.5481	572.7777	9

7	833.4403	417.2238	816.4138	408.7105	815.4298	408.2185	K	1033.5160	517.2617	1016.4895	508.7484	1015.5055	508.2564	8
8	962.4829	481.7451	945.4564	473.2318	944.4724	472.7398	E	905.4211	453.2142	888.3945	444.7009	887.4105	444.2089	7
9	1090.5779	545.7926	1073.5514	537.2793	1072.5673	536.7873	K	776.3785	388.6929	759.3519	380.1796	758.3679	379.6876	6
10	1219.6205	610.3139	1202.5939	601.8006	1201.6099	601.3086	E	648.2835	324.6454	631.2570	316.1321	630.2729	315.6401	5
11	1348.6631	674.8352	1331.6365	666.3219	1330.6525	665.8299	E	519.2409	260.1241	502.2144	251.6108	501.2304	251.1188	4
12	1462.7060	731.8566	1445.6795	723.3434	1444.6955	722.8514	N	390.1983	195.6028	373.1718	187.0895	372.1878	186.5975	3
13	1591.7486	796.3779	1574.7221	787.8647	1573.7380	787.3727	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
14							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

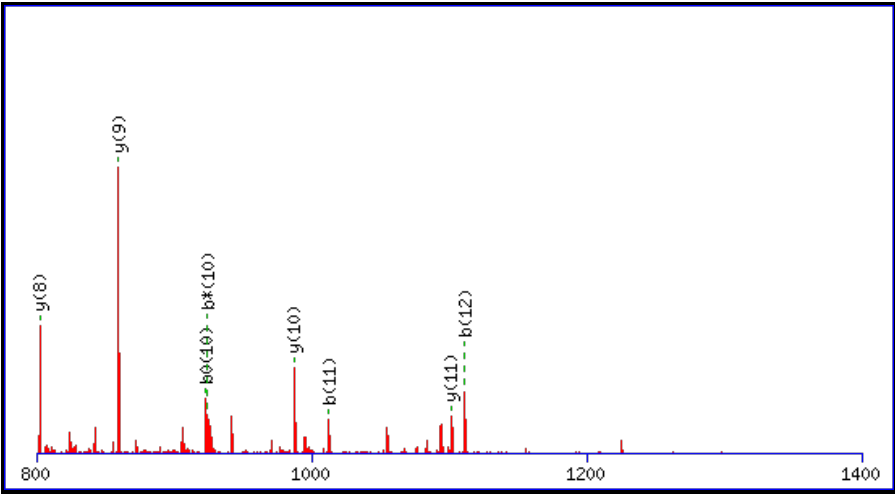
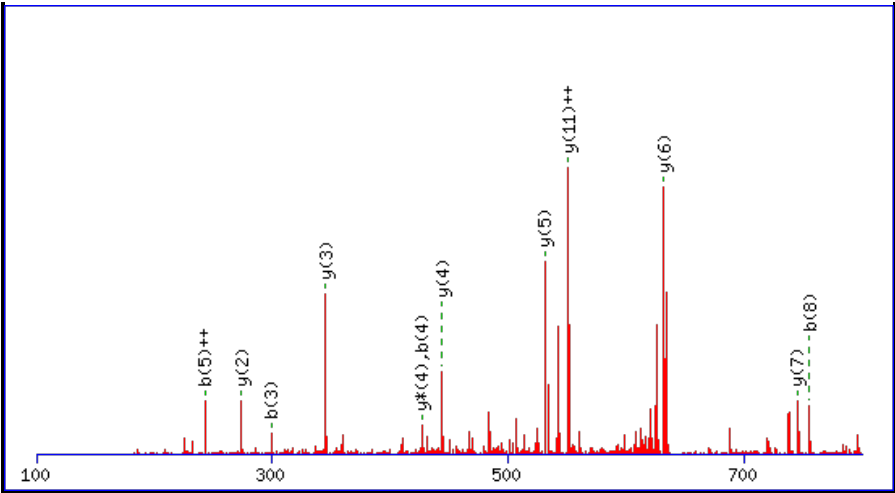
Score	Mr(calc):	Delta	Sequence
49.6	1736.8468	0.0058	YVAEIEKEKEENEK
8.2	1736.8359	0.0167	VYQAVRHNKATENK
7.3	1736.8498	0.0027	YSLIVAQHVEKEGGK
5.0	1735.8553	0.9973	GPSLRLAGVTMGGRRER
4.9	1735.8593	0.9933	YLSQLLMRRSAYR
4.2	1736.8498	0.0027	YSLIVAQHVEKEGGK
3.9	1734.8342	2.0184	FLEYGKDTLQRTGK
3.6	1735.8662	0.9864	ESMAVLEKQDISDKK
3.3	1734.8537	1.9989	SSSSKYFLTSESTRR
3.0	1736.8386	0.0139	LGSGSEGTVYLVSDKK

Spectrum No: 13; Query: 10725; Rank: 1

Peptide View

MS/MS Fragmentation of **AINQGGLTSVAVR**
Found in **IPI00029623**, Tax_Id=9606 Gene_Symbol=PSMA6 Proteasome subunit alpha type-6

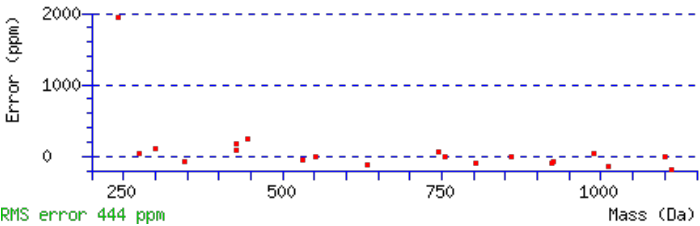
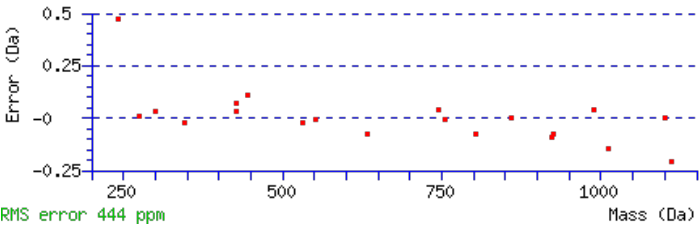
Match to Query 10725: 1284.722048 from(643.368300,2+)
Title: 091224LimSK_Exosome3_07.1898.1898.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1284.7150
Fixed modifications: Carbamidomethyl (C)
Ions Score: 95 Expect: 2.7e-008
Matches (**Bold Red**): 20/118 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	72.0444	36.5258					A							13
2	185.1285	93.0679					I	1214.6852	607.8462	1197.6586	599.3329	1196.6746	598.8409	12
3	299.1714	150.0893	282.1448	141.5761			N	1101.6011	551.3042	1084.5745	542.7909	1083.5905	542.2989	11
4	427.2300	214.1186	410.2034	205.6053			Q	987.5582	494.2827	970.5316	485.7694	969.5476	485.2774	10
5	484.2514	242.6293	467.2249	234.1161			G	859.4996	430.2534	842.4730	421.7402	841.4890	421.2482	9
6	541.2729	271.1401	524.2463	262.6268			G	802.4781	401.7427	785.4516	393.2294	784.4676	392.7374	8

7	654.3570	327.6821	637.3304	319.1688			L	745.4567	373.2320	728.4301	364.7187	727.4461	364.2267	7
8	755.4046	378.2060	738.3781	369.6927	737.3941	369.2007	T	632.3726	316.6899	615.3461	308.1767	614.3620	307.6847	6
9	842.4367	421.7220	825.4101	413.2087	824.4261	412.7167	S	531.3249	266.1661	514.2984	257.6528	513.3144	257.1608	5
10	941.5051	471.2562	924.4785	462.7429	923.4945	462.2509	V	444.2929	222.6501	427.2663	214.1368			4
11	1012.5422	506.7747	995.5156	498.2615	994.5316	497.7694	A	345.2245	173.1159	328.1979	164.6026			3
12	1111.6106	556.3089	1094.5841	547.7957	1093.6000	547.3037	V	274.1874	137.5973	257.1608	129.0840			2
13							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

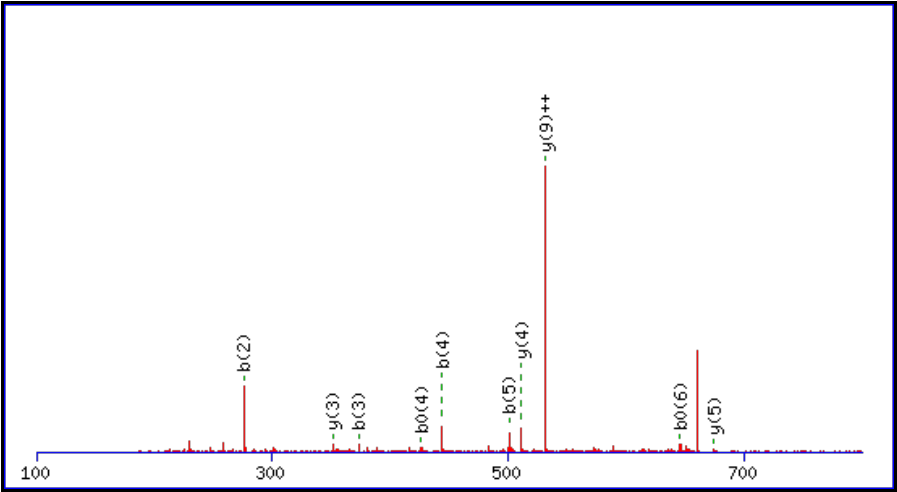
Score	Mr(calc):	Delta	Sequence
94.6	1284.7150	0.0071	AINOGLTSLVAVR
3.7	1284.7224	-0.0003	MKEEVKGIPVR
3.1	1284.7262	-0.0041	LQEVRESIRR
2.5	1284.7150	0.0071	LRELVAGDSAVR
2.2	1284.7262	-0.0042	ERRVLTATPSR
2.0	1284.7262	-0.0041	ELEQVSLRR
1.4	1284.7224	-0.0003	NVVLCLELGR

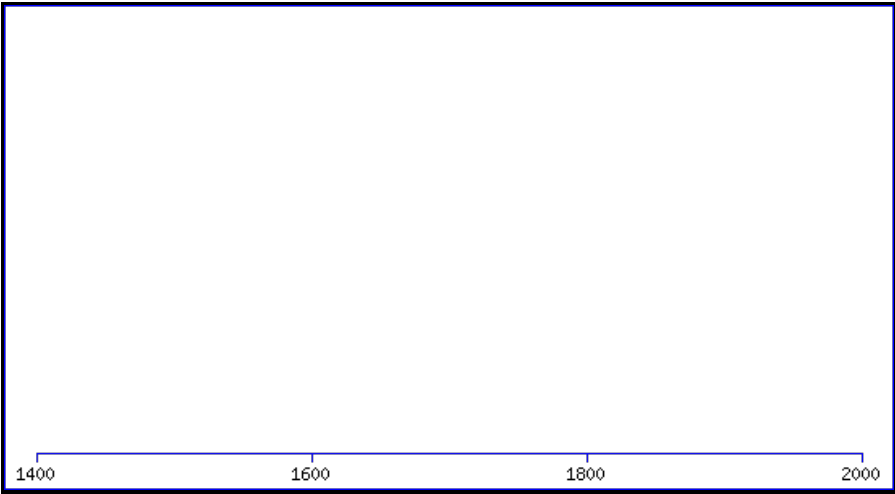
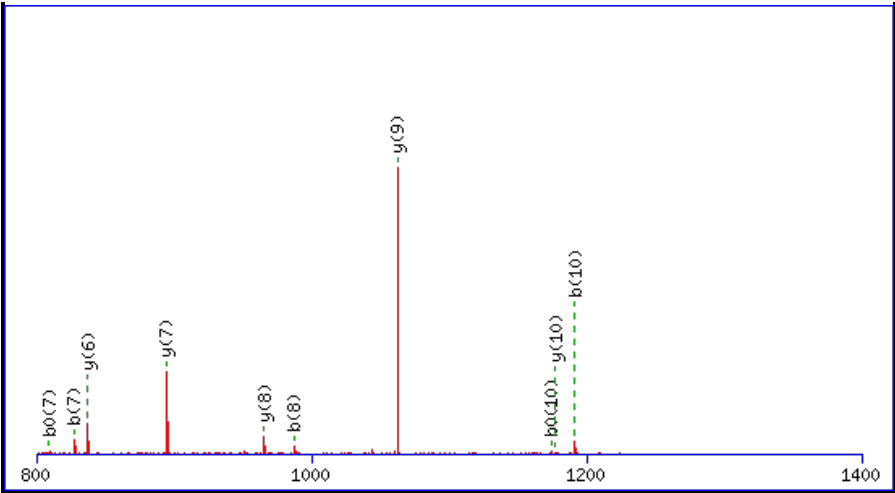
Spectrum No: 14; Query: 12579; Rank: 1

Peptide View

MS/MS Fragmentation of **CDPAGYYCGFK**
Found in **IPI00029623**, Tax_Id=9606 Gene_Symbol=PSMA6 Proteasome subunit alpha type-6

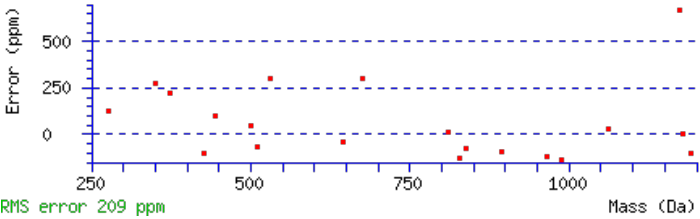
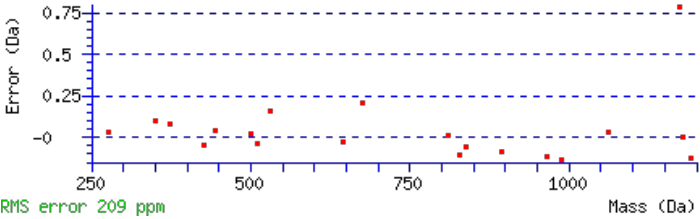
Match to Query 12579: 1336.526908 from(669.270730,2+)
Title: 091224LimSK_Exosome3_06.2429.2429.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1336.5217
Fixed modifications: Carbamidomethyl (C)
Ions Score: 45 Expect: 0.0034
Matches (**Bold Red**): 20/80 fragment ions using 45 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	161.0379	81.0226			C							11
2	276.0649	138.5361	258.0543	129.5308	D	1177.4983	589.2528	1160.4717	580.7395	1159.4877	580.2475	10
3	373.1176	187.0625	355.1071	178.0572	P	1062.4713	531.7393	1045.4448	523.2260			9
4	444.1547	222.5810	426.1442	213.5757	A	965.4186	483.2129	948.3920	474.6996			8
5	501.1762	251.0917	483.1656	242.0865	G	894.3815	447.6944	877.3549	439.1811			7
6	664.2395	332.6234	646.2290	323.6181	Y	837.3600	419.1836	820.3334	410.6704			6
7	827.3029	414.1551	809.2923	405.1498	Y	674.2967	337.6520	657.2701	329.1387			5
8	987.3335	494.1704	969.3230	485.1651	C	511.2333	256.1203	494.2068	247.6070			4
9	1044.3550	522.6811	1026.3444	513.6758	G	351.2027	176.1050	334.1761	167.5917			3
10	1191.4234	596.2153	1173.4128	587.2101	F	294.1812	147.5942	277.1547	139.0810			2
11					K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

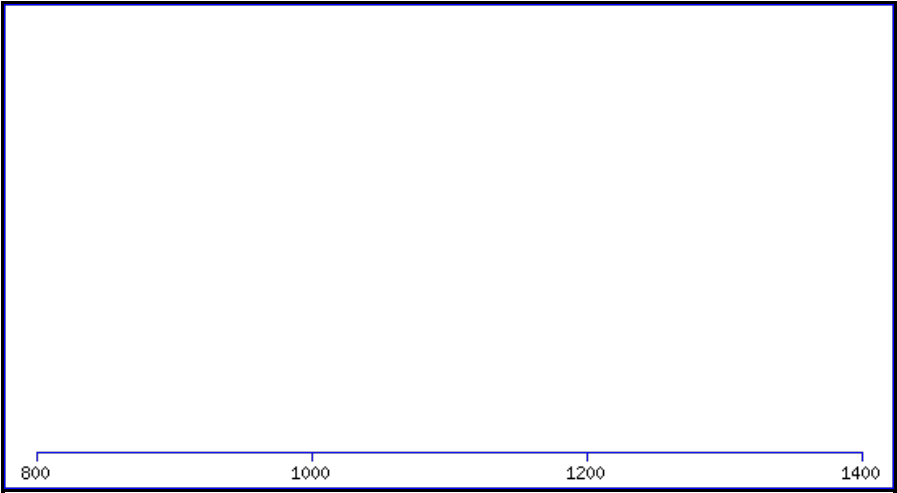
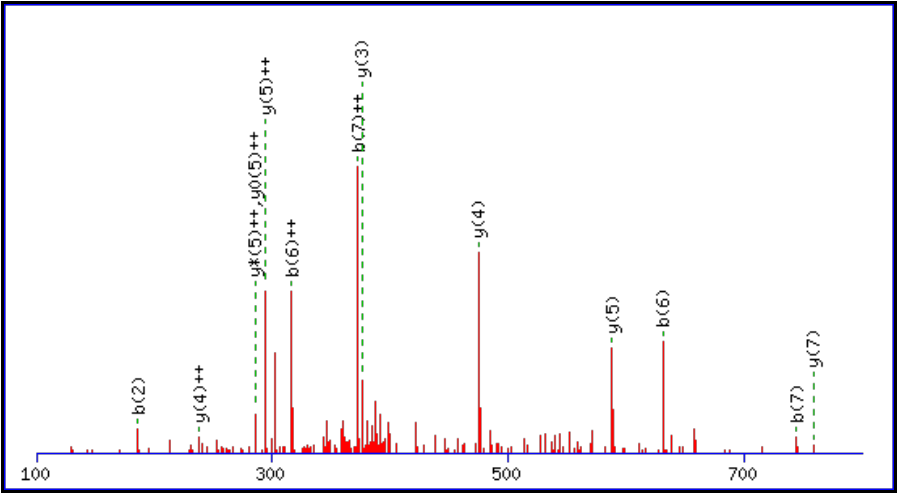
Score	Mr(calc):	Delta	Sequence
45.1	1336.5217	0.0053	CDPAGYYCGFK
26.3	1336.5257	0.0012	YAESLSEAMEK
23.5	1336.5387	-0.0117	MKSTEVLPEK
17.4	1336.5193	0.0076	XCSEFGVQLMGK
14.7	1336.5257	0.0012	YAESLSEAMEK
12.8	1335.5353	0.9916	XCSEFGVQLMGK
12.1	1336.5313	-0.0044	TGGTNTEKLEK
12.1	1336.5313	-0.0044	TGGTNTEKLEK
11.3	1336.5257	0.0012	YAESLSEAMEK
11.1	1336.5313	-0.0044	LGSEIIDSSTR

Spectrum No: 15; Query: 8543; Rank: 1

Peptide View

MS/MS Fragmentation of **GKDCAVIVTQK**
Found in **IP100029623**, Tax_Id=9606 Gene_Symbol=PSMA6 Proteasome subunit alpha type-6

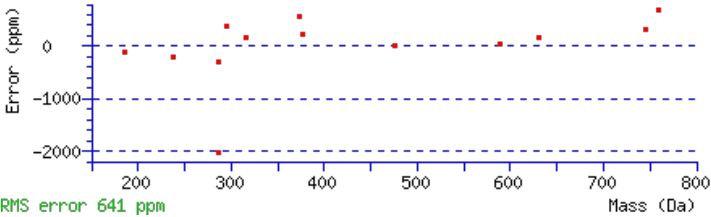
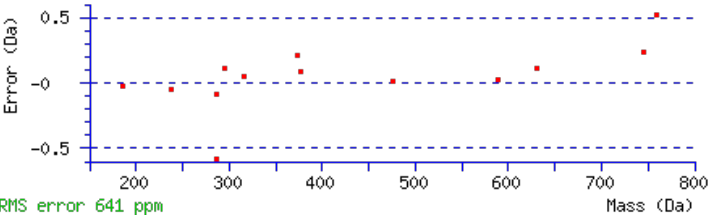
Match to Query 8543: 1217.648952 from(406.890260,3+)
Title: 091224LimSK_Exosome3_06.125.125.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1217.6438
Fixed modifications: Carbamidomethyl (C)
Ions Score: 25 Expect: 0.39
Matches (**Bold Red**): 13/110 fragment ions using 17 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	186.1237	93.5655	169.0972	85.0522			K	1161.6296	581.3184	1144.6031	572.8052	1143.6191	572.3132	10
3	301.1506	151.0790	284.1241	142.5657	283.1401	142.0737	D	1033.5347	517.2710	1016.5081	508.7577	1015.5241	508.2657	9
4	461.1813	231.0943	444.1547	222.5810	443.1707	222.0890	C	918.5077	459.7575	901.4812	451.2442	900.4972	450.7522	8
5	532.2184	266.6128	515.1919	258.0996	514.2078	257.6076	A	758.4771	379.7422	741.4505	371.2289	740.4665	370.7369	7
6	631.2868	316.1470	614.2603	307.6338	613.2763	307.1418	V	687.4400	344.2236	670.4134	335.7103	669.4294	335.2183	6
7	744.3709	372.6891	727.3443	364.1758	726.3603	363.6838	I	588.3715	294.6894	571.3450	286.1761	570.3610	285.6841	5
8	843.4393	422.2233	826.4128	413.7100	825.4287	413.2180	V	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	4
9	944.4870	472.7471	927.4604	464.2339	926.4764	463.7418	T	376.2191	188.6132	359.1925	180.0999	358.2085	179.6079	3
10	1072.5456	536.7764	1055.5190	528.2631	1054.5350	527.7711	Q	275.1714	138.0893	258.1448	129.5761			2
11							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

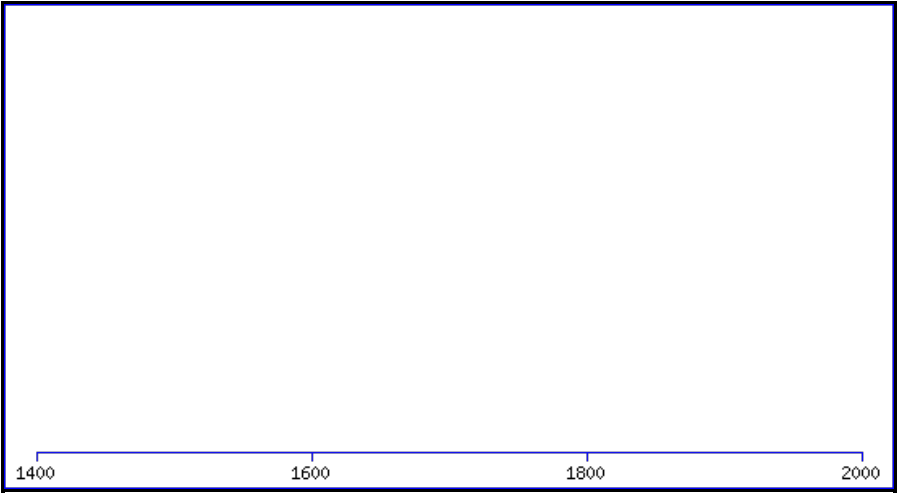
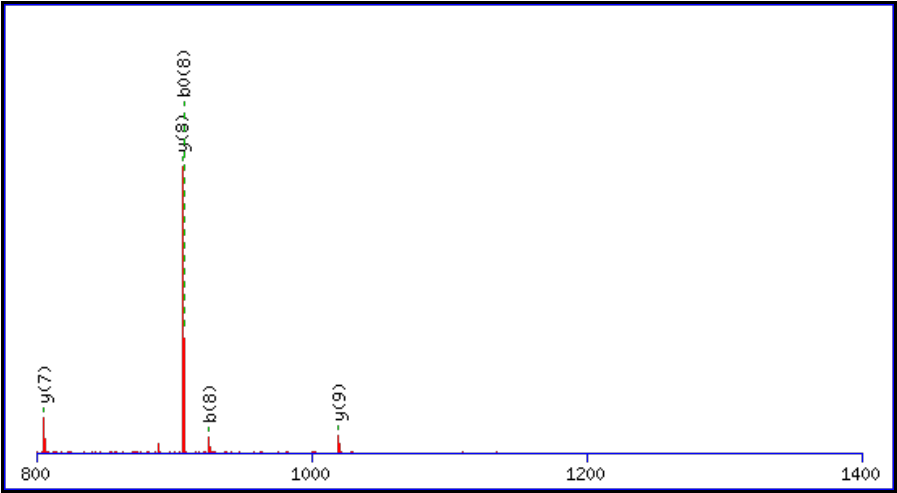
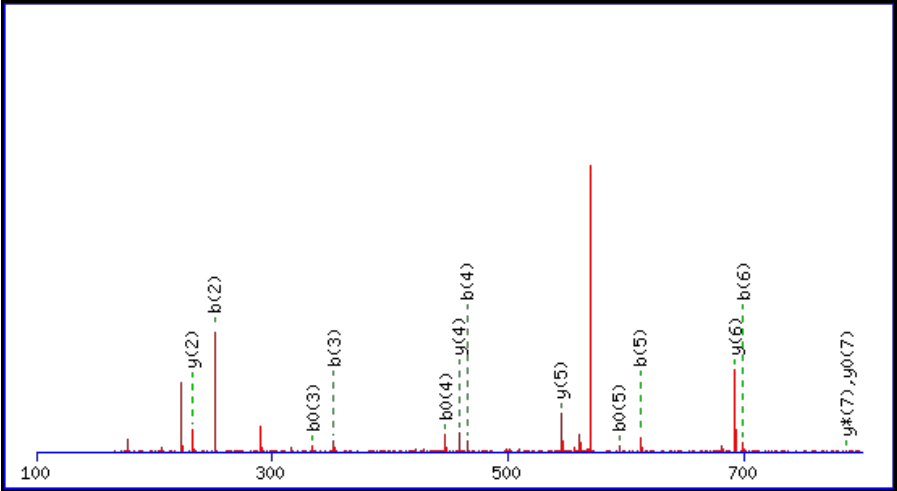
Score	Mr(calc):	Delta	Sequence
25.3	1217.6438	0.0051	GKDCAVIVTQK
17.4	1215.6360	2.0129	FVPEIRDGQR
17.4	1216.6468	1.0021	YVLLSSL SKK
17.4	1216.6468	1.0021	YVLLSSL SKK
15.2	1217.6503	-0.0013	DAVESIEKISK
14.8	1216.6524	0.9965	LAGSSGRGGQTVK
14.4	1217.6438	0.0052	LMDDLLNKTR
14.1	1217.6478	0.0011	NALADELPVMK
11.1	1216.6524	0.9966	DRTQELRTAK
10.6	1216.6403	1.0087	TKRIMITFK

Spectrum No: 16; Query: 6446; Rank: 1

Peptide View

MS/MS Fragmentation of **HITIFSPEGR**
Found in **IPI00029623**, Tax_Id=9606 Gene_Symbol=PSMA6 Proteasome subunit alpha type-6

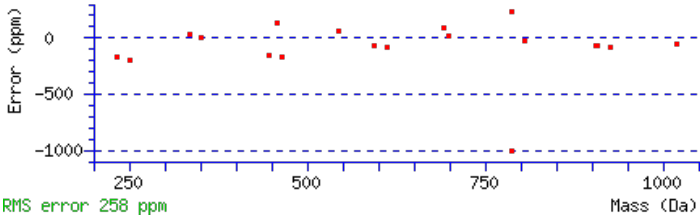
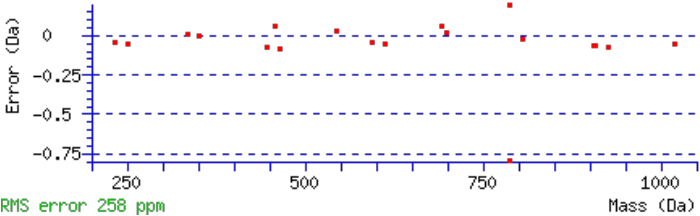
Match to Query 6446: 1155.608408 from(578.811480,2+)
Title: 091224LimSK_Exosome3_06.1790.1790.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1155.6037

Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 Expect: 0.00067
Matches (Bold Red): 19/82 fragment ions using 31 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	138.0662	69.5367			H							10
2	251.1503	126.0788			I	1019.5520	510.2796	1002.5255	501.7664	1001.5415	501.2744	9
3	352.1979	176.6026	334.1874	167.5973	T	906.4680	453.7376	889.4414	445.2243	888.4574	444.7323	8
4	465.2820	233.1446	447.2714	224.1394	I	805.4203	403.2138	788.3937	394.7005	787.4097	394.2085	7
5	612.3504	306.6788	594.3398	297.6736	F	692.3362	346.6717	675.3097	338.1585	674.3257	337.6665	6
6	699.3824	350.1949	681.3719	341.1896	S	545.2678	273.1375	528.2413	264.6243	527.2572	264.1323	5
7	796.4352	398.7212	778.4246	389.7160	P	458.2358	229.6215	441.2092	221.1083	440.2252	220.6162	4
8	925.4778	463.2425	907.4672	454.2373	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
9	982.4993	491.7533	964.4887	482.7480	G	232.1404	116.5738	215.1139	108.0606			2
10					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

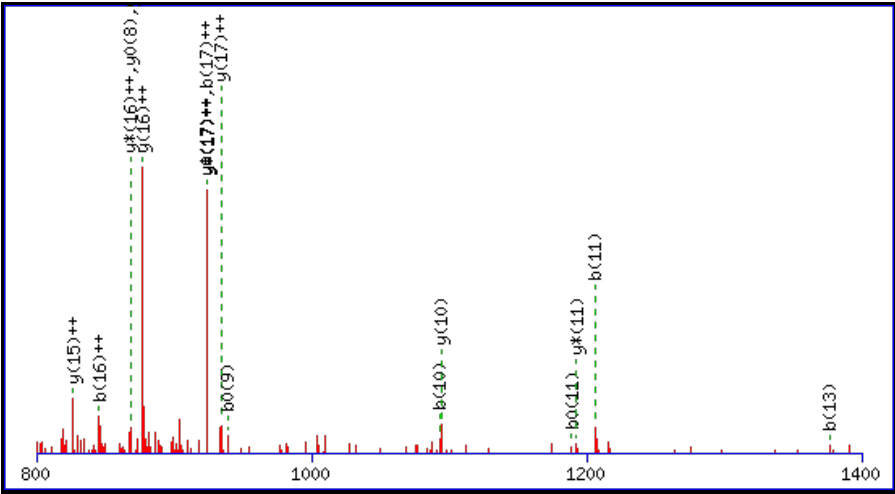
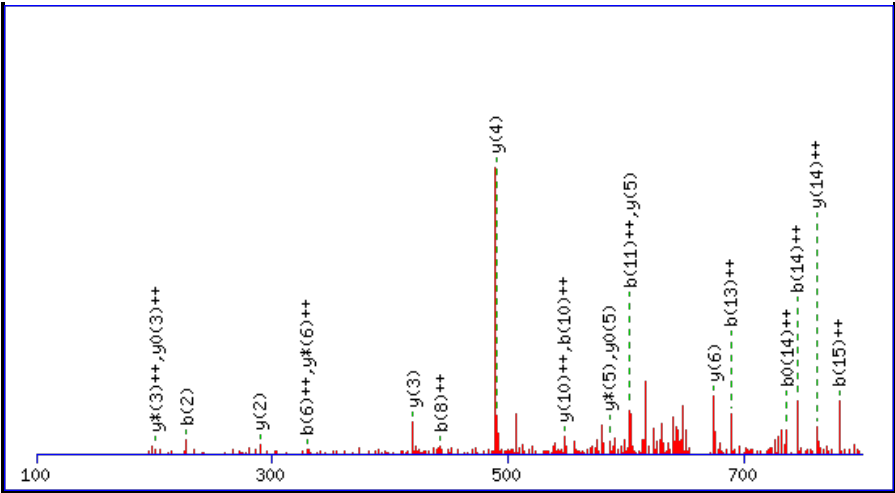
Score	Mr(calc):	Delta	Sequence
52.1	1155.6037	0.0048	HTTIESPEGR
12.3	1155.6070	0.0014	HLTQAVCTVK
7.6	1155.6183	-0.0098	CVPGREILGR
3.1	1155.6182	-0.0098	HLNTIQKMR
3.0	1155.5996	0.0088	HLSDSKSQVR
2.6	1153.6131	1.9953	HITIEDLWK
2.3	1153.6132	1.9952	TFSPTYGLLR

Spectrum No: 17; Query: 39057; Rank: 1

Peptide View

MS/MS Fragmentation of **ILTEAEIDAHLVALAERD**
Found in **IPI00029623**, Tax_Id=9606 Gene_Symbol=PSMA6 Proteasome subunit alpha type-6

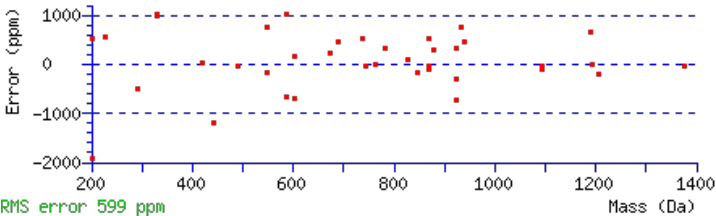
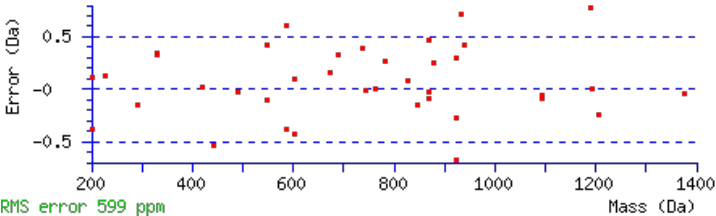
Match to Query 39057: 1978.050432 from(660.357420,3+)
Title: 091224LimSK_Exosome3_06.9882.9882.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1978.0371
Fixed modifications: Carbamidomethyl (C)
Ions Score: 39 Expect: 0.013
Matches (Bold Red): 38/166 fragment ions using 74 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					I							18
2	227.1754	114.0913					L	1865.9603	933.4838	1848.9338	924.9705	1847.9498	924.4785	17
3	328.2231	164.6152			310.2125	155.6099	T	1752.8763	876.9418	1735.8497	868.4285	1734.8657	867.9365	16
4	457.2657	229.1365			439.2551	220.1312	E	1651.8286	826.4179	1634.8020	817.9047	1633.8180	817.4127	15
5	528.3028	264.6550			510.2922	255.6498	A	1522.7860	761.8966	1505.7594	753.3834	1504.7754	752.8914	14
6	657.3454	329.1763			639.3348	320.1710	E	1451.7489	726.3781	1434.7223	717.8648	1433.7383	717.3728	13

7	770.4294	385.7184			752.4189	376.7131	I	1322.7063	661.8568	1305.6797	653.3435	1304.6957	652.8515	12
8	885.4564	443.2318			867.4458	434.2266	D	1209.6222	605.3148	1192.5957	596.8015	1191.6117	596.3095	11
9	956.4935	478.7504			938.4829	469.7451	A	1094.5953	547.8013	1077.5687	539.2880	1076.5847	538.7960	10
10	1093.5524	547.2798			1075.5419	538.2746	H	1023.5582	512.2827	1006.5316	503.7694	1005.5476	503.2774	9
11	1206.6365	603.8219			1188.6259	594.8166	L	886.4993	443.7533	869.4727	435.2400	868.4887	434.7480	8
12	1305.7049	653.3561			1287.6943	644.3508	V	773.4152	387.2112	756.3886	378.6980	755.4046	378.2060	7
13	1376.7420	688.8746			1358.7314	679.8694	A	674.3468	337.6770	657.3202	329.1638	656.3362	328.6717	6
14	1489.8261	745.4167			1471.8155	736.4114	L	603.3097	302.1585	586.2831	293.6452	585.2991	293.1532	5
15	1560.8632	780.9352			1542.8526	771.9299	A	490.2256	245.6164	473.1991	237.1032	472.2150	236.6112	4
16	1689.9058	845.4565			1671.8952	836.4512	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
17	1846.0069	923.5071	1828.9803	914.9938	1827.9963	914.5018	R	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
18							D	134.0448	67.5260			116.0342	58.5207	1



All matches to this query

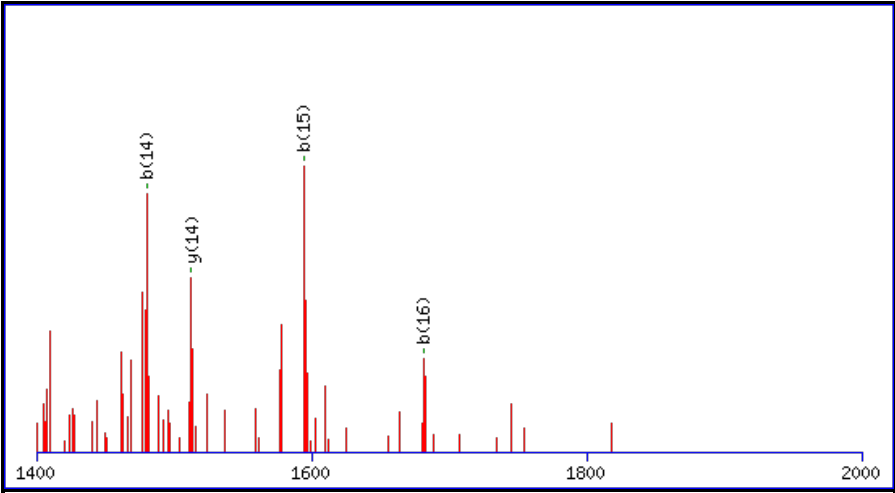
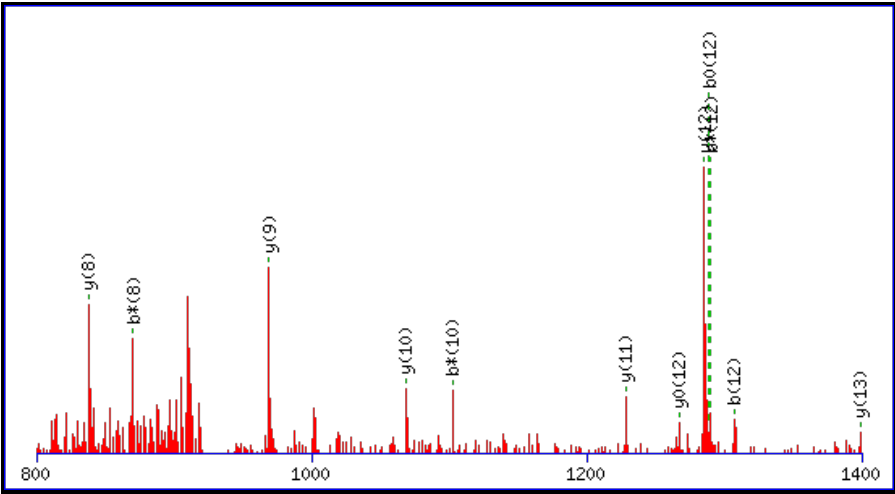
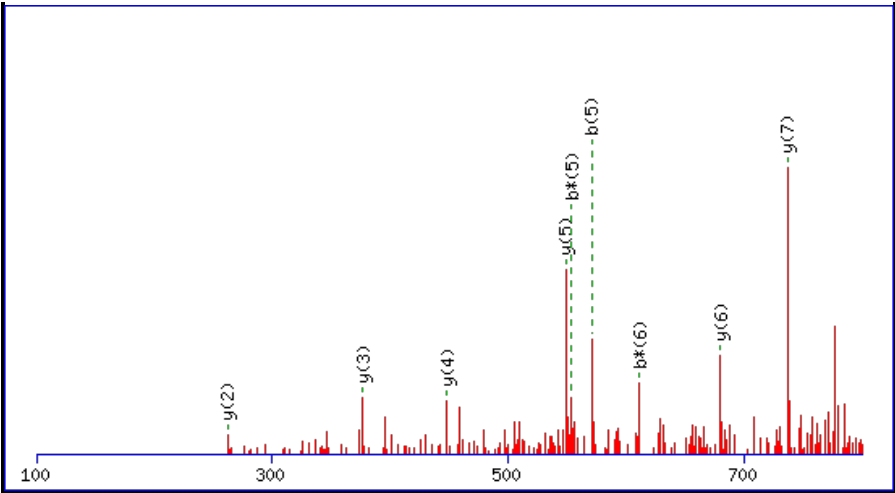
Score	Mr(calc):	Delta	Sequence
39.2	1978.0371	0.0134	ILTEAEIDAHLVALAERD
11.1	1976.0401	2.0103	CTVKPLAFIEGLSDTGLR
10.6	1977.0482	1.0023	ILIEENRKVIAPMLSR
1.7	1978.0553	-0.0049	FTLGTFLRLAALRTYR
1.6	1977.0304	1.0200	SIVRIIGKMLPLEPCR
0.8	1978.0418	0.0087	MAAEALRNRYRNTQAILK
0.8	1978.0645	-0.0140	MFPISVVRPFRKMNEK
0.3	1976.0466	2.0038	EDELTFIKSAHQNVEK
0.3	1976.0327	2.0178	LAGSSAASSPNGQGLQKLYK
0.3	1976.0327	2.0177	FLIDSNGQVITTERLDR

Spectrum No: 18; Query: 35132; Rank: 1

Peptide View

MS/MS Fragmentation of **ITENIGCVMTGMTADSR**
Found in **IP100029623**, Tax_Id=9606 Gene_Symbol=PSMA6 Proteasome subunit alpha type-6

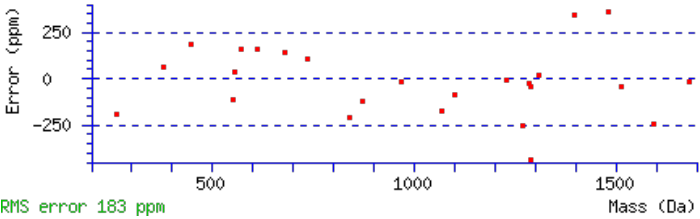
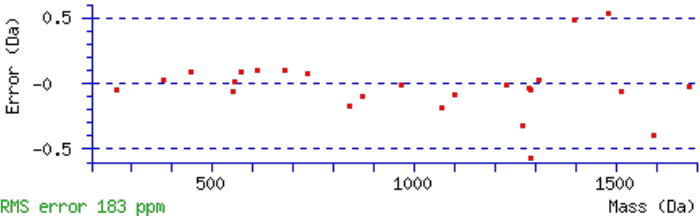
Match to Query 35132: 1854.842608 from(928.428580,2+)
Title: 091224LimSK_Exosome3_06.4869.4869.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1854.8274
Fixed modifications: Carbamidomethyl (C)
Ions Score: 113 Expect: 1.3e-009
Matches (**Bold Red**): 25/182 fragment ions using 41 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					I							17
2	215.1390	108.0731			197.1285	99.0679	T	1742.7506	871.8789	1725.7241	863.3657	1724.7401	862.8737	16
3	344.1816	172.5944			326.1710	163.5892	E	1641.7029	821.3551	1624.6764	812.8418	1623.6924	812.3498	15
4	458.2245	229.6159	441.1980	221.1026	440.2140	220.6106	N	1512.6603	756.8338	1495.6338	748.3205	1494.6498	747.8285	14
5	571.3086	286.1579	554.2821	277.6447	553.2980	277.1527	I	1398.6174	699.8123	1381.5909	691.2991	1380.6069	690.8071	13
6	628.3301	314.6687	611.3035	306.1554	610.3195	305.6634	G	1285.5334	643.2703	1268.5068	634.7570	1267.5228	634.2650	12

7	788.3607	394.6840	771.3342	386.1707	770.3502	385.6787	C	1228.5119	614.7596	1211.4853	606.2463	1210.5013	605.7543	11
8	887.4291	444.2182	870.4026	435.7049	869.4186	435.2129	V	1068.4812	534.7443	1051.4547	526.2310	1050.4707	525.7390	10
9	1018.4696	509.7384	1001.4431	501.2252	1000.4591	500.7332	M	969.4128	485.2101	952.3863	476.6968	951.4023	476.2048	9
10	1119.5173	560.2623	1102.4907	551.7490	1101.5067	551.2570	T	838.3723	419.6898	821.3458	411.1765	820.3618	410.6845	8
11	1176.5388	588.7730	1159.5122	580.2597	1158.5282	579.7677	G	737.3247	369.1660	720.2981	360.6527	719.3141	360.1607	7
12	1307.5792	654.2933	1290.5527	645.7800	1289.5687	645.2880	M	680.3032	340.6552	663.2767	332.1420	662.2926	331.6500	6
13	1408.6269	704.8171	1391.6004	696.3038	1390.6164	695.8118	T	549.2627	275.1350	532.2362	266.6217	531.2522	266.1297	5
14	1479.6640	740.3357	1462.6375	731.8224	1461.6535	731.3304	A	448.2150	224.6112	431.1885	216.0979	430.2045	215.6059	4
15	1594.6910	797.8491	1577.6644	789.3359	1576.6804	788.8438	D	377.1779	189.0926	360.1514	180.5793	359.1674	180.0873	3
16	1681.7230	841.3651	1664.6965	832.8519	1663.7124	832.3599	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
17							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

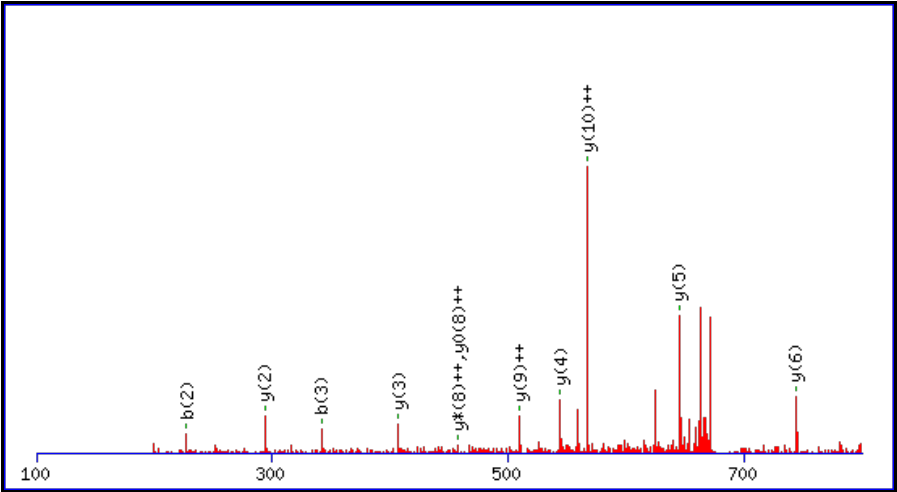
Score	Mr(calc):	Delta	Sequence
112.5	1854.8274	0.0152	ITENIGCVMTGMTADSR
5.2	1854.8587	-0.0161	TSLGKITGNYLGYTCK
1.2	1854.8587	-0.0161	TSLGKITGNYLGYTCK
0.6	1853.8520	0.9906	DGEKSGTVSPQKQSAQK
0.5	1854.8587	-0.0161	TSLGKITGNYLGYTCK

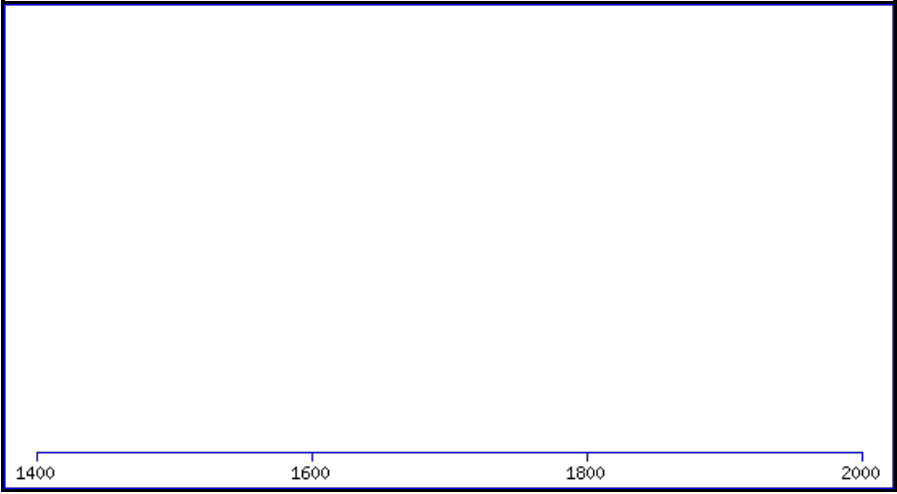
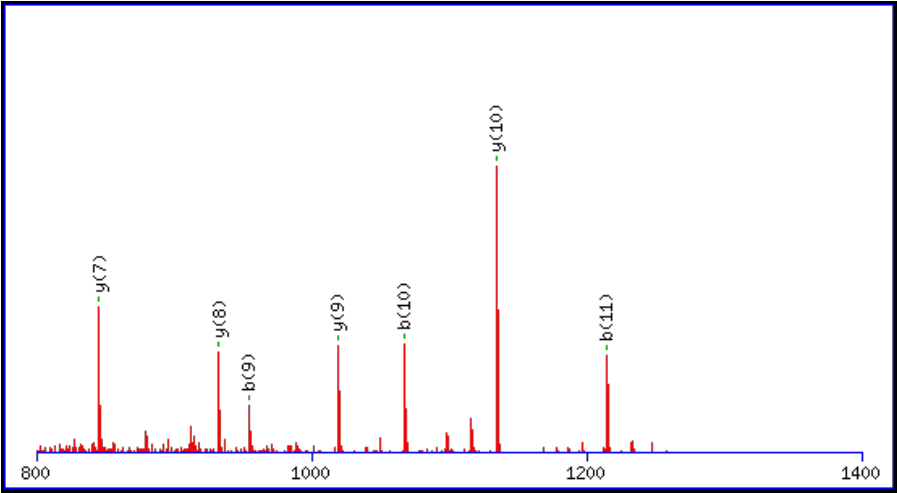
Spectrum No: 19; Query: 13505; Rank: 1

Peptide View

MS/MS Fragmentation of **LLDSSTVTHLFK**
Found in **IPI00029623**, Tax_Id=9606 Gene_Symbol=PSMA6 Proteasome subunit alpha type-6

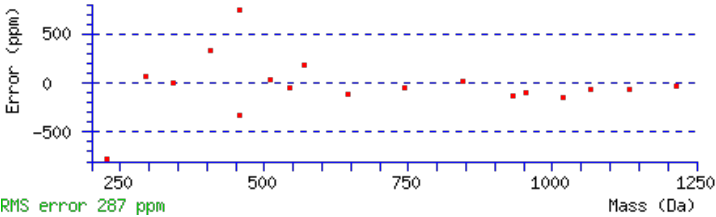
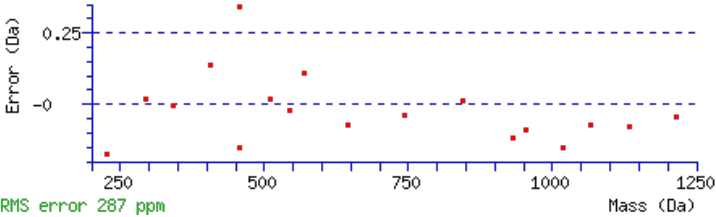
Match to Query 13505: 1359.749188 from(680.881870,2+)
Title: 091224LimSK_Exosome3_06.5181.5181.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1359.7398
Fixed modifications: Carbamidomethyl (C)
Ions Score: 75 Expect: 3.3e-006
Matches (**Bold Red**): 18/98 fragment ions using 26 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							12
2	227.1754	114.0913			L	1247.6630	624.3352	1230.6365	615.8219	1229.6525	615.3299	11
3	342.2023	171.6048	324.1918	162.5995	D	1134.5790	567.7931	1117.5524	559.2798	1116.5684	558.7878	10
4	429.2344	215.1208	411.2238	206.1155	S	1019.5520	510.2796	1002.5255	501.7664	1001.5415	501.2744	9
5	516.2664	258.6368	498.2558	249.6316	S	932.5200	466.7636	915.4934	458.2504	914.5094	457.7584	8
6	617.3141	309.1607	599.3035	300.1554	T	845.4880	423.2476	828.4614	414.7343	827.4774	414.2423	7
7	716.3825	358.6949	698.3719	349.6896	V	744.4403	372.7238	727.4137	364.2105	726.4297	363.7185	6
8	817.4302	409.2187	799.4196	400.2134	T	645.3719	323.1896	628.3453	314.6763	627.3613	314.1843	5
9	954.4891	477.7482	936.4785	468.7429	H	544.3242	272.6657	527.2976	264.1525			4
10	1067.5732	534.2902	1049.5626	525.2849	L	407.2653	204.1363	390.2387	195.6230			3
11	1214.6416	607.8244	1196.6310	598.8191	F	294.1812	147.5942	277.1547	139.0810			2
12					K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

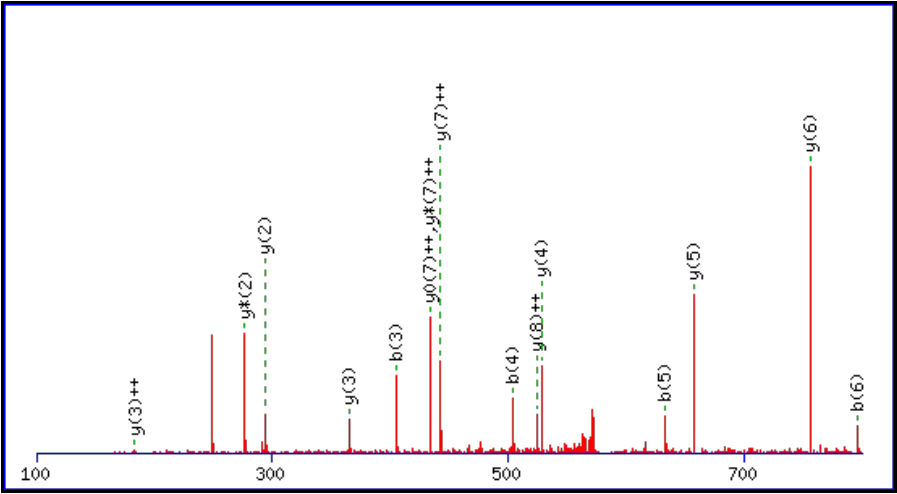
Score	Mr(calc):	Delta	Sequence
75.0	1359.7398	0.0094	LLDSSTVTHLFK
6.9	1359.7544	-0.0052	LAAKSPIRETMK
5.2	1359.7373	0.0119	MIGVTGWFKPPK
4.5	1359.7623	-0.0131	LLINDFGRERK
4.5	1359.7527	-0.0035	ILDLLIPLTNR
2.5	1359.7544	-0.0052	LSERLIQNIMK
2.5	1359.7366	0.0126	TPMRKINPLMK
1.1	1359.7510	-0.0019	HDSITGSLKKEK
0.6	1359.7609	-0.0117	EIVSGLLAHVSSK
0.6	1359.7358	0.0134	ARDTVTSFLAAVK

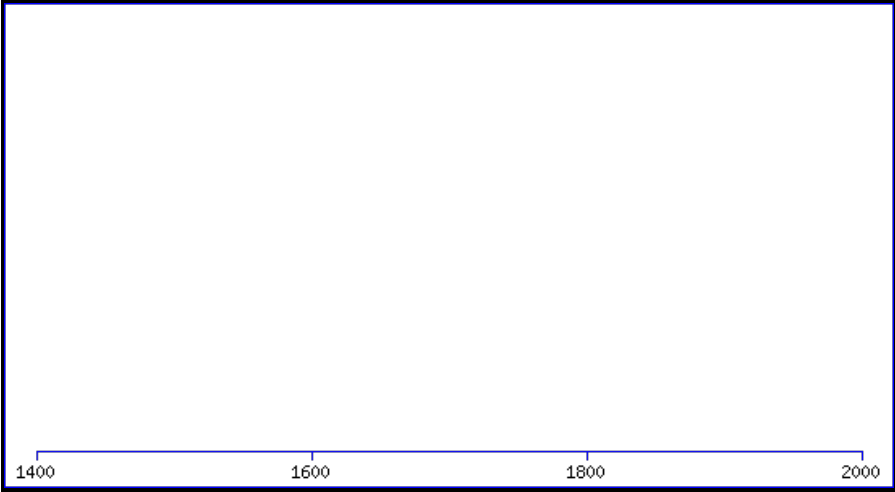
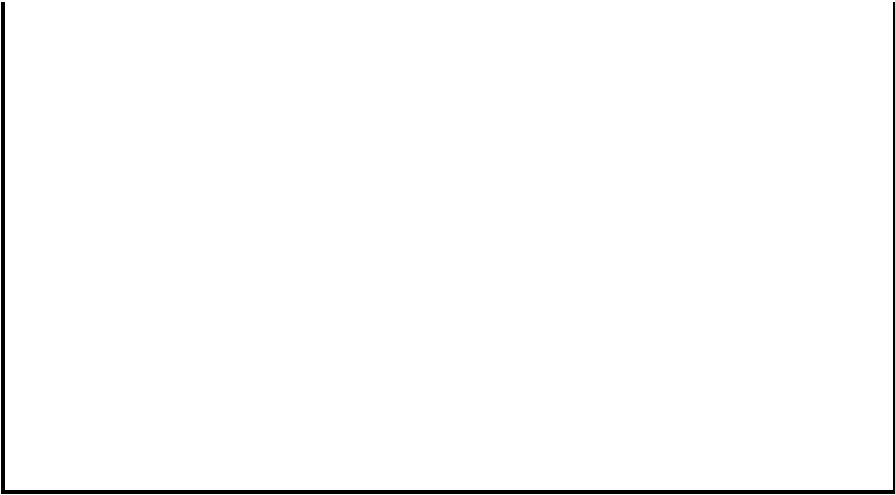
Spectrum No: 20; Query: 6609; Rank: 1

Peptide View

MS/MS Fragmentation of **LYQVEYAFK**
Found in **IPI00029623**, Tax_Id=9606 Gene_Symbol=PSMA6 Proteasome subunit alpha type-6

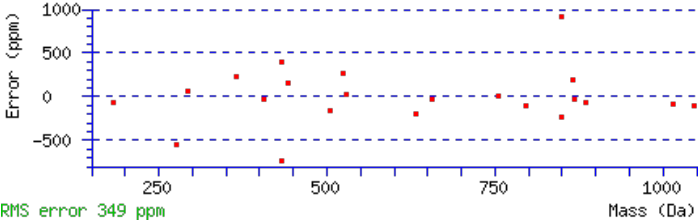
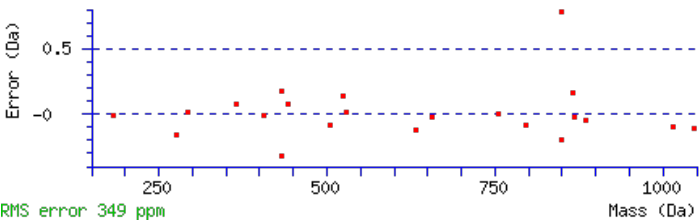
Match to Query 6609: 1159.597848 from(580.806200,2+)
Title: 091224LimSK_Exosome3_06.3990.3990.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1159.5913
Fixed modifications: Carbamidomethyl (C)
Ions Score: 57 Expect: 0.00025
Matches (**Bold Red**): 25/76 fragment ions using 33 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							9
2	277.1547	139.0810					Y	1047.5146	524.2609	1030.4880	515.7477	1029.5040	515.2556	8
3	405.2132	203.1103	388.1867	194.5970			Q	884.4512	442.7293	867.4247	434.2160	866.4407	433.7240	7
4	504.2817	252.6445	487.2551	244.1312			V	756.3927	378.7000	739.3661	370.1867	738.3821	369.6947	6
5	633.3243	317.1658	616.2977	308.6525	615.3137	308.1605	E	657.3243	329.1658	640.2977	320.6525	639.3137	320.1605	5
6	796.3876	398.6974	779.3610	390.1842	778.3770	389.6921	Y	528.2817	264.6445	511.2551	256.1312			4
7	867.4247	434.2160	850.3981	425.7027	849.4141	425.2107	A	365.2183	183.1128	348.1918	174.5995			3
8	1014.4931	507.7502	997.4666	499.2369	996.4825	498.7449	F	294.1812	147.5942	277.1547	139.0810			2
9							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
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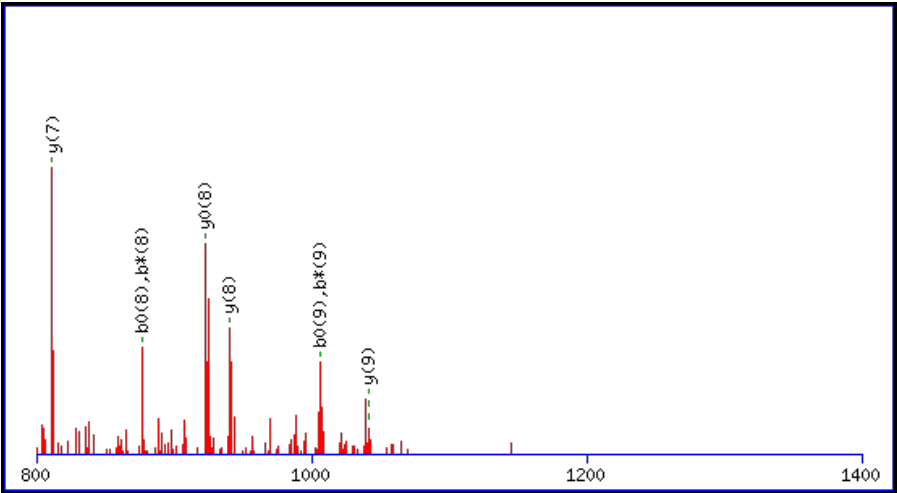
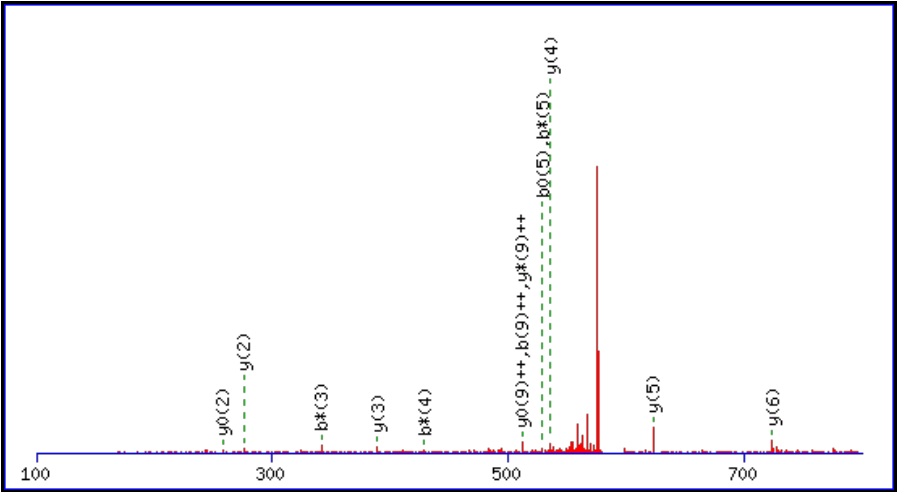
57.4	1159.5913	0.0065	LYQVEYAFK
14.7	1159.5890	0.0089	LYKTLSEVK
14.0	1159.5890	0.0089	LYKTLSEVK
13.1	1159.5986	-0.0007	EFKAGGEVPAR
12.1	1159.5985	-0.0007	ETLRAWQEK
10.7	1158.6049	0.9929	KTFSLVKEK
10.7	1158.6049	0.9929	KTFSLVKEK
8.6	1159.5873	0.0105	YIQAEPPTNK
8.1	1159.6026	-0.0047	EFINHYLPK
6.3	1159.6084	-0.0106	EKQLKEEEK

Spectrum No: 21; Query: 6877; Rank: 1

Peptide View

MS/MS Fragmentation of **QTESTSFLEK**
Found in **IPI00029623**, Tax_Id=9606 Gene_Symbol=PSMA6 Proteasome subunit alpha type-6

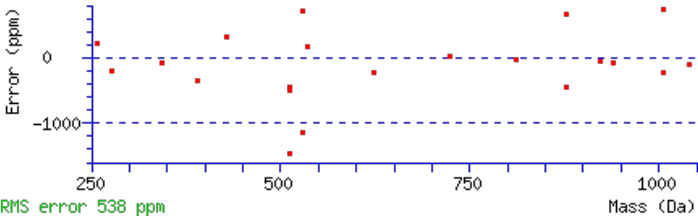
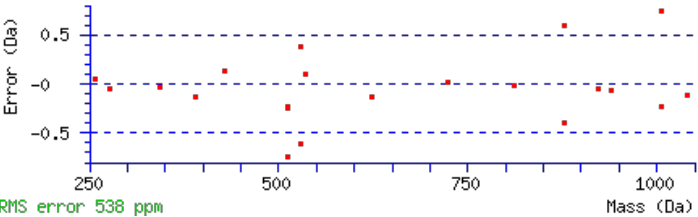
Match to Query 6877: 1168.565848 from(585.290200,2+)
Title: 091224LimSK_Exosome3_07.1131.1131.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1168.5612
Fixed modifications: Carbamidomethyl (C)
Ions Score: 25 Expect: 0.58
Matches (**Bold Red**): 21/104 fragment ions using 52 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.0659	65.0366	112.0393	56.5233			Q							10
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	T	1041.5099	521.2586	1024.4833	512.7453	1023.4993	512.2533	9
3	359.1561	180.0817	342.1296	171.5684	341.1456	171.0764	E	940.4622	470.7347	923.4357	462.2215	922.4516	461.7295	8
4	446.1882	223.5977	429.1616	215.0844	428.1776	214.5924	S	811.4196	406.2134	794.3931	397.7002	793.4090	397.2082	7
5	547.2358	274.1216	530.2093	265.6083	529.2253	265.1163	T	724.3876	362.6974	707.3610	354.1842	706.3770	353.6921	6
6	634.2679	317.6376	617.2413	309.1243	616.2573	308.6323	S	623.3399	312.1736	606.3134	303.6603	605.3293	303.1683	5
7	781.3363	391.1718	764.3097	382.6585	763.3257	382.1665	F	536.3079	268.6576	519.2813	260.1443	518.2973	259.6523	4
8	894.4203	447.7138	877.3938	439.2005	876.4098	438.7085	L	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
9	1023.4629	512.2351	1006.4364	503.7218	1005.4524	503.2298	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
10							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

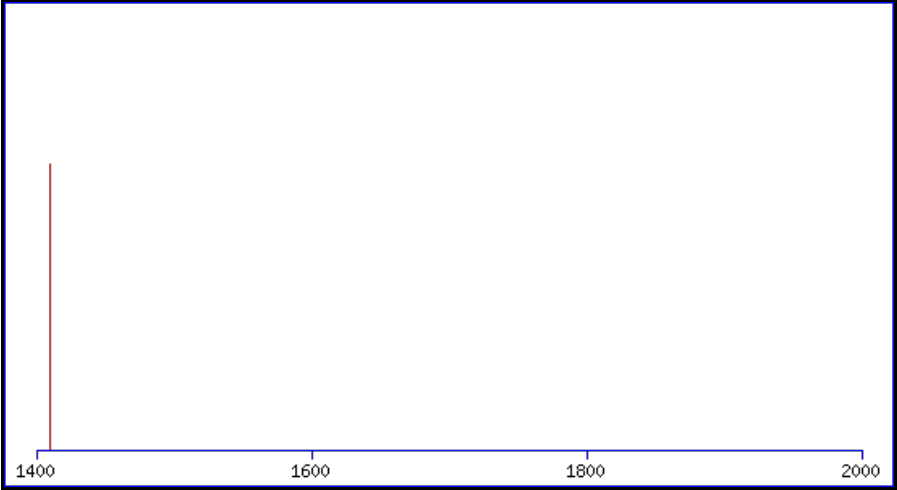
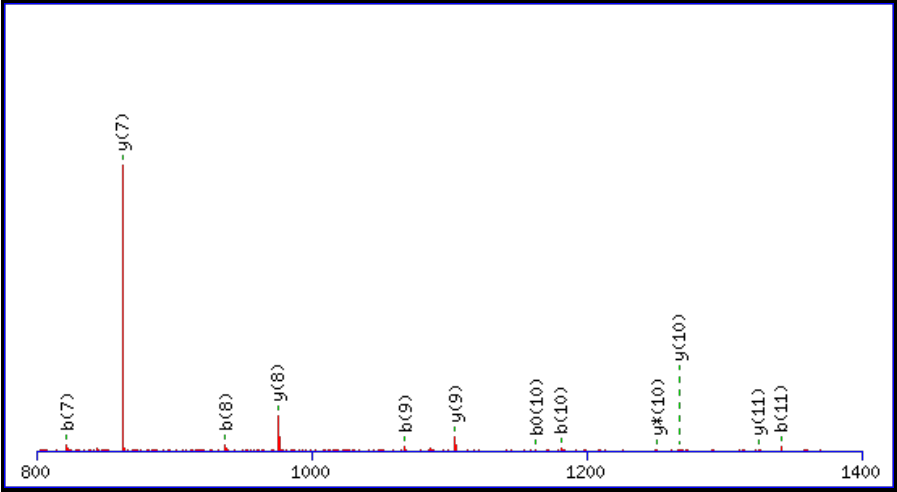
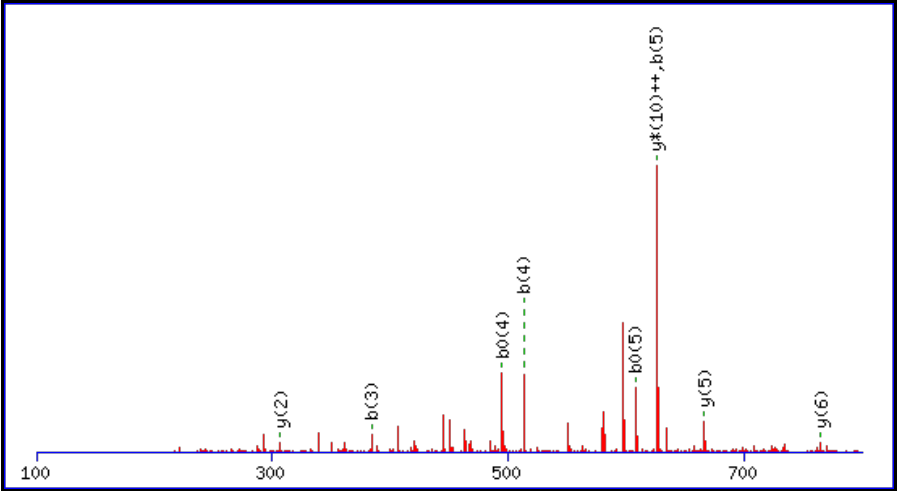
Score	Mr(calc):	Delta	Sequence
25.1	1168.5612	0.0047	QTESTSELEK
11.1	1168.5741	-0.0082	EKTEGVVSIK
10.0	1168.5601	0.0057	AARSAAGASSLK
9.5	1167.5509	1.0149	XQSRTGARAK
9.2	1168.5740	-0.0082	ESVLGEKSLK
8.9	1167.5594	1.0065	DKGKFEDMAK
8.3	1168.5641	0.0017	RLASSWLEK
8.0	1167.5723	0.9936	MAAVKTLNPK
7.5	1167.5509	1.0149	DLNTRARSR
7.4	1168.5641	0.0017	RLASSWLEK

Spectrum No: 22; Query: 19659; Rank: 1

Peptide View

MS/MS Fragmentation of **YGYEIPVDMLCK**
Found in **IPI00029623**, Tax_Id=9606 Gene_Symbol=PSMA6 Proteasome subunit alpha type-6

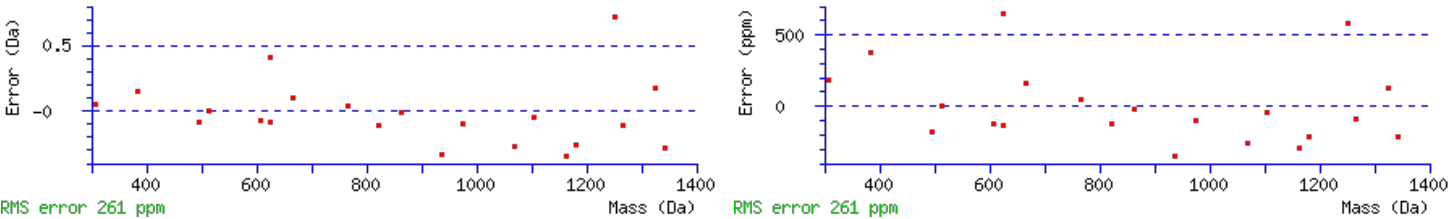
Match to Query 19659: 1486.690048 from(744.352300,2+)
Title: 091224LimSK_Exosome3_06.5785.5785.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1486.6836
Fixed modifications: Carbamidomethyl (C)
Ions Score: 67 Expect: 4.4e-005

Matches (Bold Red): 21/96 fragment ions using 37 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389			Y							12
2	221.0921	111.0497			G	1324.6276	662.8174	1307.6010	654.3042	1306.6170	653.8121	11
3	384.1554	192.5813			Y	1267.6061	634.3067	1250.5796	625.7934	1249.5955	625.3014	10
4	513.1980	257.1026	495.1874	248.0974	E	1104.5428	552.7750	1087.5162	544.2618	1086.5322	543.7697	9
5	626.2821	313.6447	608.2715	304.6394	I	975.5002	488.2537	958.4736	479.7405	957.4896	479.2484	8
6	723.3348	362.1710	705.3243	353.1658	P	862.4161	431.7117	845.3896	423.1984	844.4056	422.7064	7
7	822.4032	411.7053	804.3927	402.7000	V	765.3634	383.1853	748.3368	374.6720	747.3528	374.1800	6
8	937.4302	469.2187	919.4196	460.2134	D	666.2949	333.6511	649.2684	325.1378	648.2844	324.6458	5
9	1068.4707	534.7390	1050.4601	525.7337	M	551.2680	276.1376	534.2415	267.6244			4
10	1181.5547	591.2810	1163.5442	582.2757	L	420.2275	210.6174	403.2010	202.1041			3
11	1341.5854	671.2963	1323.5748	662.2910	C	307.1435	154.0754	290.1169	145.5621			2
12					K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

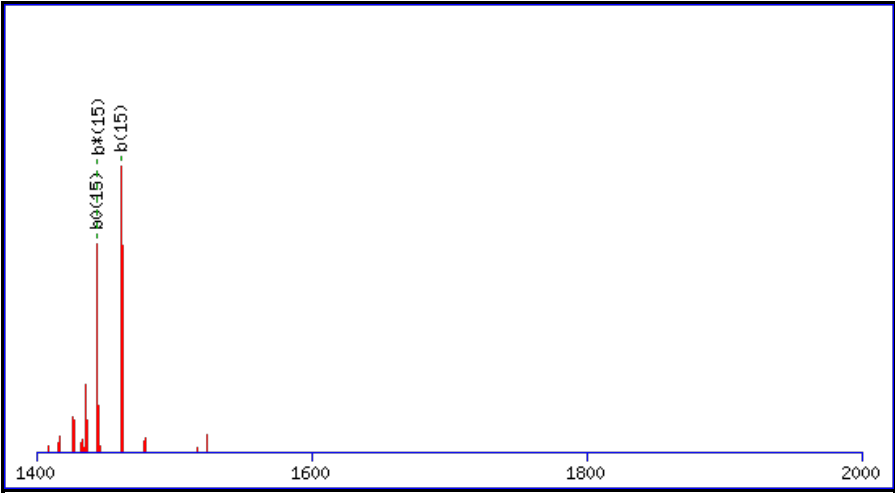
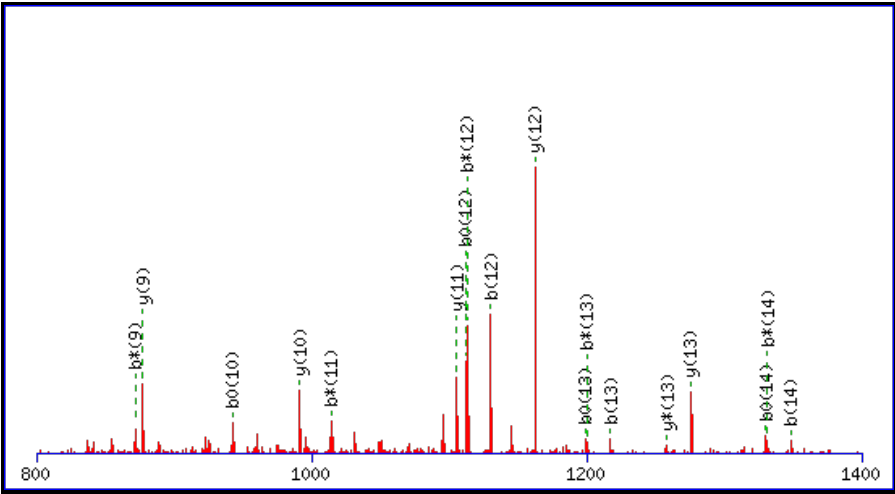
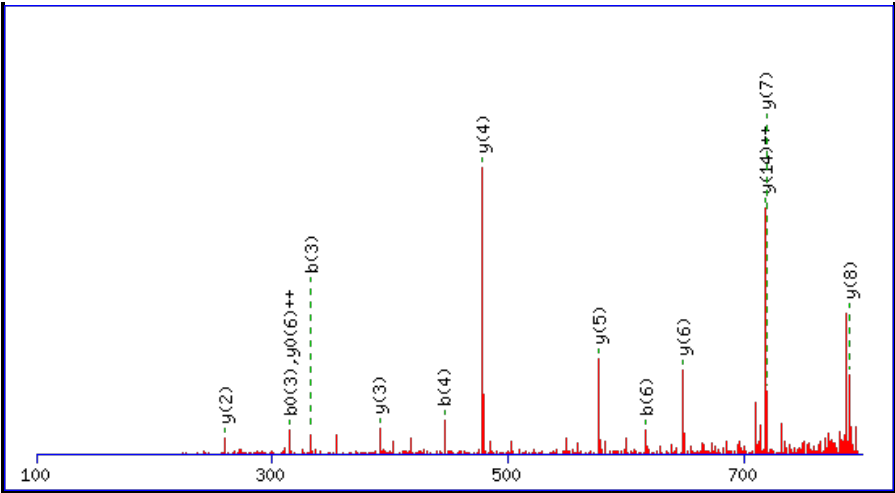
Score	Mr(calc):	Delta	Sequence
66.6	1486.6836	0.0064	YGYEIPVDMLCK
14.2	1485.6993	0.9907	AVKDLASPLIGRS
6.9	1486.6929	-0.0029	ARGPQSPPGSSAAK
6.9	1486.6929	-0.0029	ARGPQSPPGSSAAK
6.6	1486.6833	0.0067	AITSPLAAGSKPSK
5.7	1486.6907	-0.0007	LPATSMAIPLIGK
5.6	1486.6833	0.0067	AITSPLAAGSKPSK
4.0	1484.6813	2.0087	AFNWSSSLTKHK
4.0	1484.6813	2.0087	AFNWSSSLTKHK
3.0	1486.6830	0.0070	NSHRIGPHQSEK

Spectrum No: 23; Query: 25974; Rank: 1

Peptide View

MS/MS Fragmentation of **ATCIGNNSAAVSM**LK
Found in **IPI00299155**, Tax_Id=9606 Gene_Symbol=PSMA4 Proteasome subunit alpha type-4

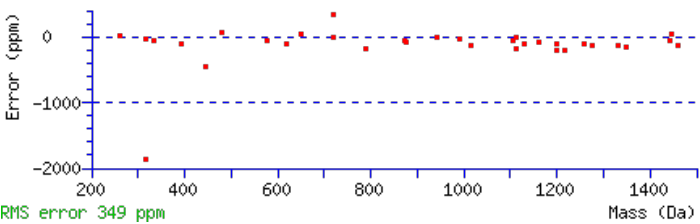
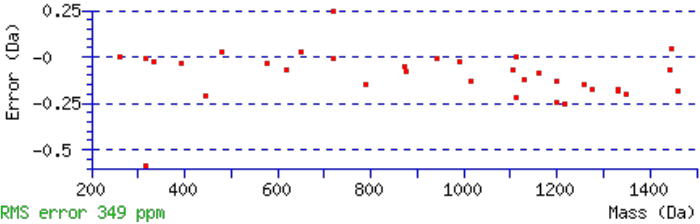
Match to Query 25974: 1606.790368 from(804.402460,2+)
Title: 091224LimSK_Exosome3_06.3300.3300.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1606.7807
Fixed modifications: Carbamidomethyl (C)
Ions Score: 101 Expect: 1.6e-008
Matches (Bold Red): 34/162 fragment ions using 48 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							16
2	173.0921	87.0497			155.0815	78.0444	T	1536.7509	768.8791	1519.7243	760.3658	1518.7403	759.8738	15
3	333.1227	167.0650			315.1122	158.0597	C	1435.7032	718.3552	1418.6766	709.8420	1417.6926	709.3500	14
4	446.2068	223.6070			428.1962	214.6017	I	1275.6725	638.3399	1258.6460	629.8266	1257.6620	629.3346	13
5	503.2282	252.1178			485.2177	243.1125	G	1162.5885	581.7979	1145.5619	573.2846	1144.5779	572.7926	12
6	617.2712	309.1392	600.2446	300.6260	599.2606	300.1339	N	1105.5670	553.2871	1088.5405	544.7739	1087.5565	544.2819	11

7	731.3141	366.1607	714.2876	357.6474	713.3035	357.1554	N	991.5241	496.2657	974.4975	487.7524	973.5135	487.2604	10
8	818.3461	409.6767	801.3196	401.1634	800.3356	400.6714	S	877.4812	439.2442	860.4546	430.7309	859.4706	430.2389	9
9	889.3832	445.1953	872.3567	436.6820	871.3727	436.1900	A	790.4491	395.7282	773.4226	387.2149	772.4386	386.7229	8
10	960.4204	480.7138	943.3938	472.2005	942.4098	471.7085	A	719.4120	360.2096	702.3855	351.6964	701.4015	351.2044	7
11	1031.4575	516.2324	1014.4309	507.7191	1013.4469	507.2271	A	648.3749	324.6911	631.3484	316.1778	630.3643	315.6858	6
12	1130.5259	565.7666	1113.4993	557.2533	1112.5153	556.7613	V	577.3378	289.1725	560.3112	280.6593	559.3272	280.1673	5
13	1217.5579	609.2826	1200.5314	600.7693	1199.5473	600.2773	S	478.2694	239.6383	461.2428	231.1251	460.2588	230.6330	4
14	1348.5984	674.8028	1331.5718	666.2896	1330.5878	665.7976	M	391.2374	196.1223	374.2108	187.6090			3
15	1461.6825	731.3449	1444.6559	722.8316	1443.6719	722.3396	L	260.1969	130.6021	243.1703	122.0888			2
16							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

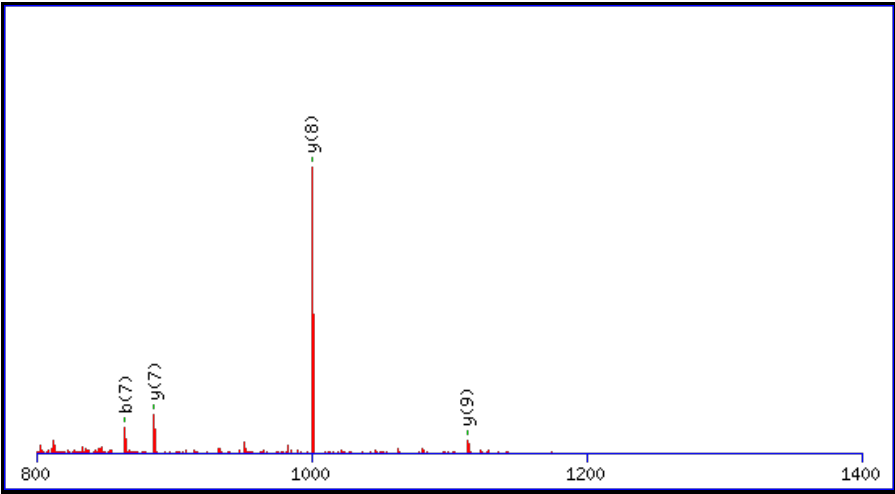
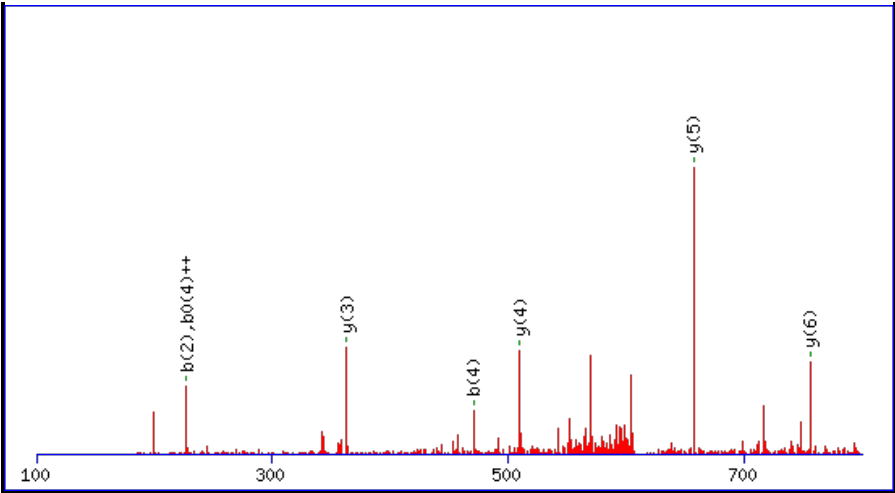
Score	Mr(calc):	Delta	Sequence
100.9	1606.7807	0.0097	ATCIGNNSAAAVSMLK
15.4	1606.7838	0.0065	YINSTLPNDSENIK
10.3	1606.7913	-0.0009	FVGTDPASDEVVLMK
9.4	1606.8058	-0.0155	NSLQKMLEVCELK
9.3	1606.7991	-0.0088	FQDSSQWLQIDLK
8.1	1605.8007	0.9896	MYQGHMQVVGVTLK
7.9	1606.7774	0.0130	VCTSVTHSFISAGNK
6.0	1605.8007	0.9896	MYQGHMQVVGVTLK
3.6	1606.8025	-0.0121	SLTTSQYLMHEVAK
2.7	1606.7908	-0.0005	LGFSKITYREWK

Spectrum No: 24; Query: 8739; Rank: 1

Peptide View

MS/MS Fragmentation of **LLDEVFFSEK**
Found in **IP100299155**, Tax_Id=9606 Gene_Symbol=PSMA4 Proteasome subunit alpha type-4

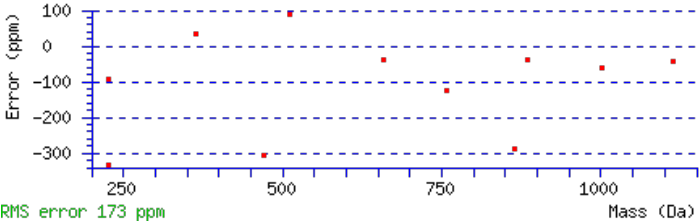
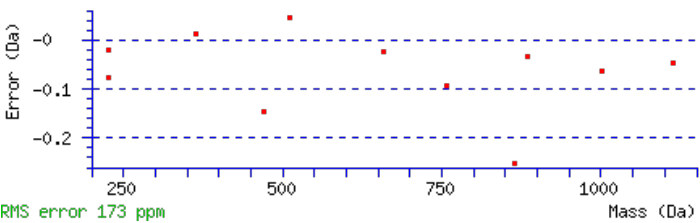
Match to Query 8739: 1225.629288 from(613.821920,2+)
Title: 091224LimSK_Exosome3_06.5499.5499.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1225.6230
Fixed modifications: Carbamidomethyl (C)
Ions Score: 73 Expect: 8.2e-006
Matches (**Bold Red**): 11/84 fragment ions using 11 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							10
2	227.1754	114.0913			L	1113.5463	557.2768	1096.5197	548.7635	1095.5357	548.2715	9
3	342.2023	171.6048	324.1918	162.5995	D	1000.4622	500.7347	983.4357	492.2215	982.4516	491.7295	8
4	471.2449	236.1261	453.2344	227.1208	E	885.4353	443.2213	868.4087	434.7080	867.4247	434.2160	7
5	570.3134	285.6603	552.3028	276.6550	V	756.3927	378.7000	739.3661	370.1867	738.3821	369.6947	6
6	717.3818	359.1945	699.3712	350.1892	F	657.3243	329.1658	640.2977	320.6525	639.3137	320.1605	5

7	864.4502	432.7287	846.4396	423.7234	F	510.2558	255.6316	493.2293	247.1183	492.2453	246.6263	4
8	951.4822	476.2447	933.4716	467.2395	S	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
9	1080.5248	540.7660	1062.5142	531.7608	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
10					K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

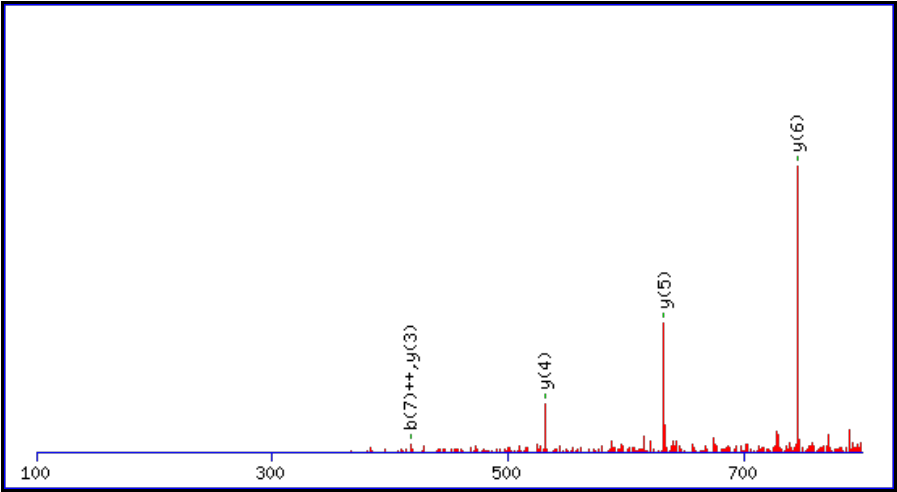
Score	Mr(calc):	Delta	Sequence
72.6	1225.6230	0.0062	LLDEVFSEK
6.8	1223.6275	2.0018	NKKVDAAASIK
5.1	1225.6302	-0.0010	VHSEVASLQEK
3.6	1225.6343	-0.0050	EPFPPSSPLOK
3.1	1225.6349	-0.0057	LIHDTNMRAR
2.5	1224.6172	1.0121	MPDPAKSAPAPK
2.1	1224.6340	0.9953	KLTGAVRSSAR
2.1	1224.6340	0.9953	KLTGAVRSSAR
1.6	1225.6292	0.0001	SLRIASRSTR
1.5	1225.6254	0.0039	ILSACVLSKR

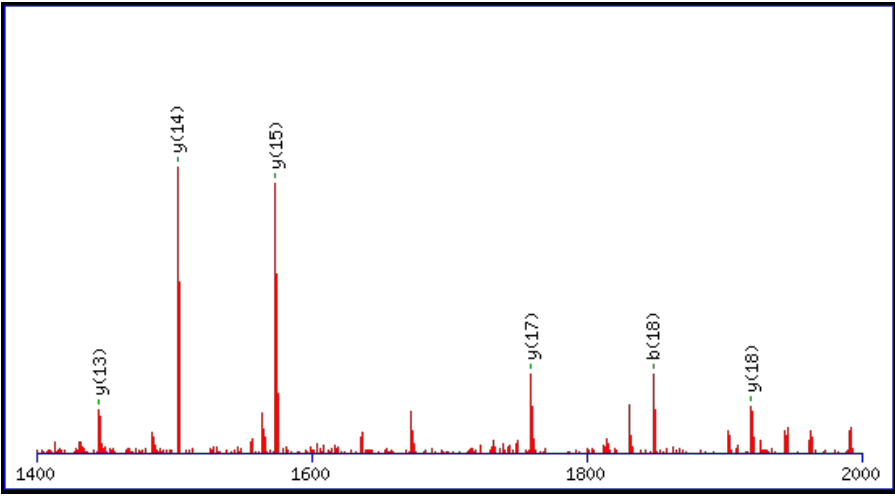
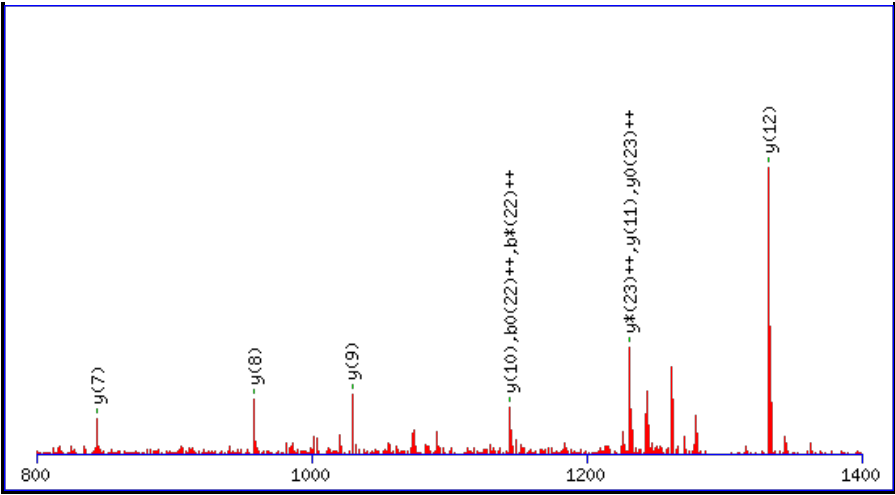
Spectrum No: 25; Query: 58319; Rank: 1

Peptide View

MS/MS Fragmentation of **LNEDMACSVAGITSDANVLTNELR**
Found in **IPI00299155**, Tax_Id=9606 Gene_Symbol=PSMA4 Proteasome subunit alpha type-4

Match to Query 58319: 2592.237888 from(1297.126220,2+)
Title: 091224LimSK_Exosome3_05.7610.7610.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

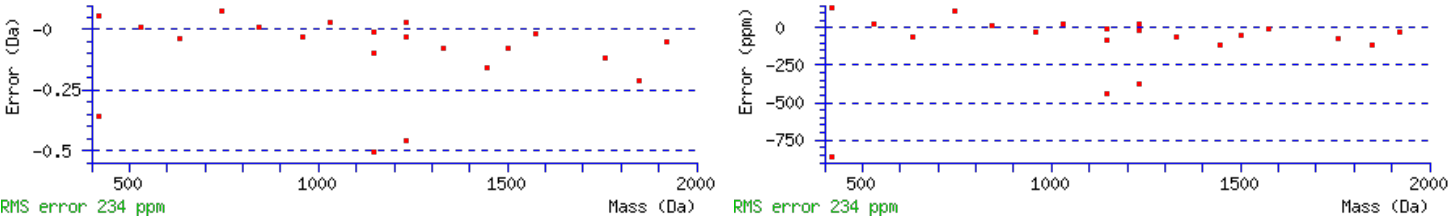




Monoisotopic mass of neutral peptide Mr(calc): 2592.2159
Fixed modifications: Carbamidomethyl (C)
Ions Score: 144 Expect: 9.4e-013
Matches (Bold Red): 21/266 fragment ions using 24 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							24
2	228.1343	114.5708	211.1077	106.0575			N	2480.1392	1240.5732	2463.1126	1232.0600	2462.1286	1231.5679	23
3	357.1769	179.0921	340.1503	170.5788	339.1663	170.0868	E	2366.0963	1183.5518	2349.0697	1175.0385	2348.0857	1174.5465	22
4	472.2038	236.6055	455.1773	228.0923	454.1932	227.6003	D	2237.0537	1119.0305	2220.0271	1110.5172	2219.0431	1110.0252	21
5	603.2443	302.1258	586.2177	293.6125	585.2337	293.1205	M	2122.0267	1061.5170	2105.0002	1053.0037	2104.0162	1052.5117	20
6	674.2814	337.6443	657.2549	329.1311	656.2708	328.6391	A	1990.9862	995.9968	1973.9597	987.4835	1972.9757	986.9915	19
7	834.3121	417.6597	817.2855	409.1464	816.3015	408.6544	C	1919.9491	960.4782	1902.9226	951.9649	1901.9386	951.4729	18
8	921.3441	461.1757	904.3175	452.6624	903.3335	452.1704	S	1759.9185	880.4629	1742.8919	871.9496	1741.9079	871.4576	17
9	1020.4125	510.7099	1003.3859	502.1966	1002.4019	501.7046	V	1672.8864	836.9469	1655.8599	828.4336	1654.8759	827.9416	16
10	1091.4496	546.2284	1074.4231	537.7152	1073.4390	537.2232	A	1573.8180	787.4127	1556.7915	778.8994	1555.8075	778.4074	15
11	1148.4711	574.7392	1131.4445	566.2259	1130.4605	565.7339	G	1502.7809	751.8941	1485.7544	743.3808	1484.7703	742.8888	14
12	1261.5551	631.2812	1244.5286	622.7679	1243.5446	622.2759	I	1445.7594	723.3834	1428.7329	714.8701	1427.7489	714.3781	13
13	1362.6028	681.8050	1345.5763	673.2918	1344.5922	672.7998	T	1332.6754	666.8413	1315.6488	658.3281	1314.6648	657.8360	12
14	1449.6348	725.3211	1432.6083	716.8078	1431.6243	716.3158	S	1231.6277	616.3175	1214.6012	607.8042	1213.6171	607.3122	11
15	1564.6618	782.8345	1547.6352	774.3213	1546.6512	773.8292	D	1144.5957	572.8015	1127.5691	564.2882	1126.5851	563.7962	10
16	1635.6989	818.3531	1618.6724	809.8398	1617.6883	809.3478	A	1029.5687	515.2880	1012.5422	506.7747	1011.5582	506.2827	9
17	1749.7418	875.3746	1732.7153	866.8613	1731.7313	866.3693	N	958.5316	479.7694	941.5051	471.2562	940.5211	470.7642	8
18	1848.8102	924.9088	1831.7837	916.3955	1830.7997	915.9035	V	844.4887	422.7480	827.4621	414.2347	826.4781	413.7427	7
19	1961.8943	981.4508	1944.8678	972.9375	1943.8837	972.4455	L	745.4203	373.2138	728.3937	364.7005	727.4097	364.2085	6

20	2062.9420	1031.9746	2045.9154	1023.4614	2044.9314	1022.9693	T	632.3362	316.6717	615.3097	308.1585	614.3257	307.6665	5
21	2176.9849	1088.9961	2159.9584	1080.4828	2158.9743	1079.9908	N	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	4
22	2306.0275	1153.5174	2289.0010	1145.0041	2288.0169	1144.5121	E	417.2456	209.1264	400.2191	200.6132	399.2350	200.1212	3
23	2419.1116	1210.0594	2402.0850	1201.5461	2401.1010	1201.0541	L	288.2030	144.6051	271.1765	136.0919			2
24							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

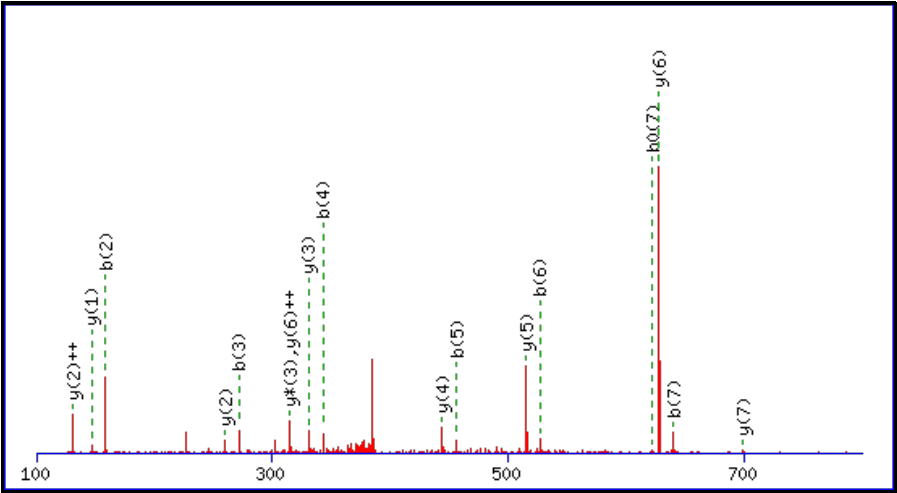
Score	Mr(calc):	Delta	Sequence
144.4	2592.2159	0.0219	LNEDMACSVAGITSDANVLTNELR
5.3	2590.2388	1.9991	NADLTVHRLGALSLGDGGTTATNEK
4.5	2592.2389	-0.0010	YIWICWFAALAAGGAYIAGVSPR
4.1	2590.2332	2.0046	EPAPTPPKGTAPTTLKEPAPTPK
3.9	2592.2287	0.0092	VSKVILPLTLSISPCFESHEK
2.9	2591.2219	1.0160	QSARKPLLGLPSYMLQSEELR
1.9	2592.2226	0.0153	HANRANKCIFEVSILTWSR
1.9	2592.2226	0.0153	HANRANKCIFEVSILTWSR
1.7	2592.2185	0.0194	VMSAQLTMAKTSGAMPTGSMKAVAK
1.7	2592.2185	0.0194	VMSAQLTMAKTSGAMPTGSMKAVAK

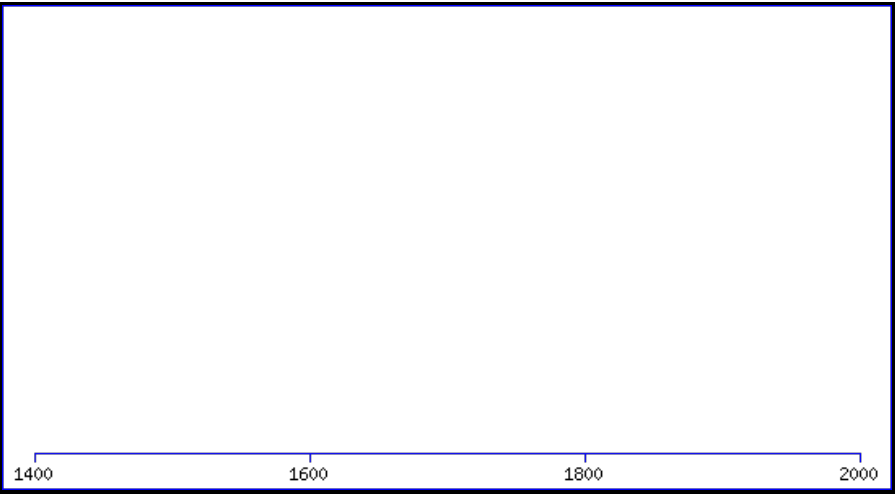
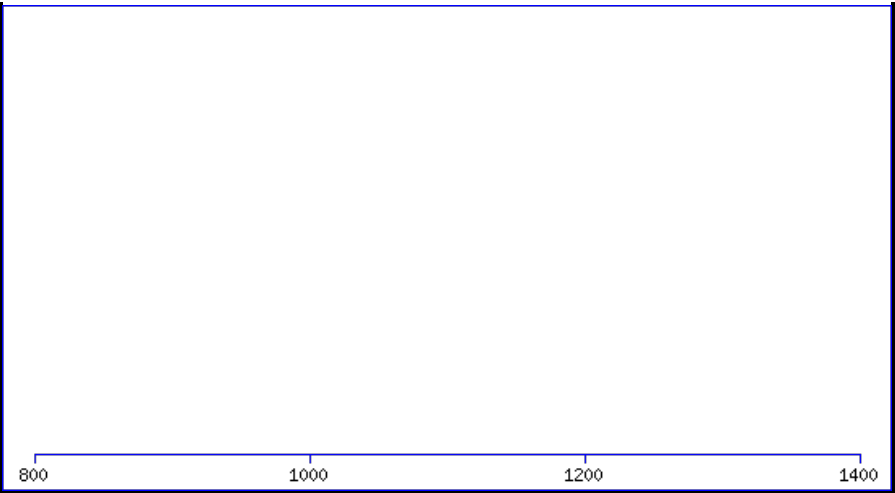
Spectrum No: 26; Query: 215; Rank: 1

Peptide View

MS/MS Fragmentation of **SALALAIK**
Found in **IP100299155**, Tax_Id=9606 Gene_Symbol=PSMA4 Proteasome subunit alpha type-4

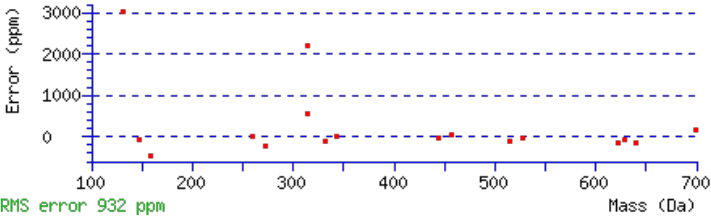
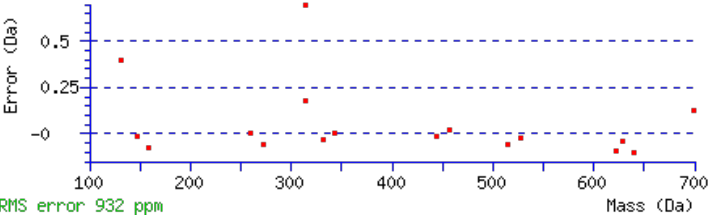
Match to Query 215: 785.504788 from(393.759670,2+)
Title: 091224LimSK_Exosome3_06.2155.2155.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 785.5011
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 **Expect:** 0.00029
Matches (Bold Red): 17/56 fragment ions using 34 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	88.0393	44.5233	70.0287	35.5180	S					8
2	159.0764	80.0418	141.0659	71.0366	A	699.4763	350.2418	682.4498	341.7285	7
3	272.1605	136.5839	254.1499	127.5786	L	628.4392	314.7233	611.4127	306.2100	6
4	343.1976	172.1024	325.1870	163.0972	A	515.3552	258.1812	498.3286	249.6679	5
5	456.2817	228.6445	438.2711	219.6392	L	444.3180	222.6627	427.2915	214.1494	4
6	527.3188	264.1630	509.3082	255.1577	A	331.2340	166.1206	314.2074	157.6074	3
7	640.4028	320.7051	622.3923	311.6998	I	260.1969	130.6021	243.1703	122.0888	2
8					K	147.1128	74.0600	130.0863	65.5468	1



All matches to this query

Score	Mr(calc):	Delta	Sequence
51.8	785.5011	0.0037	SALALAIK

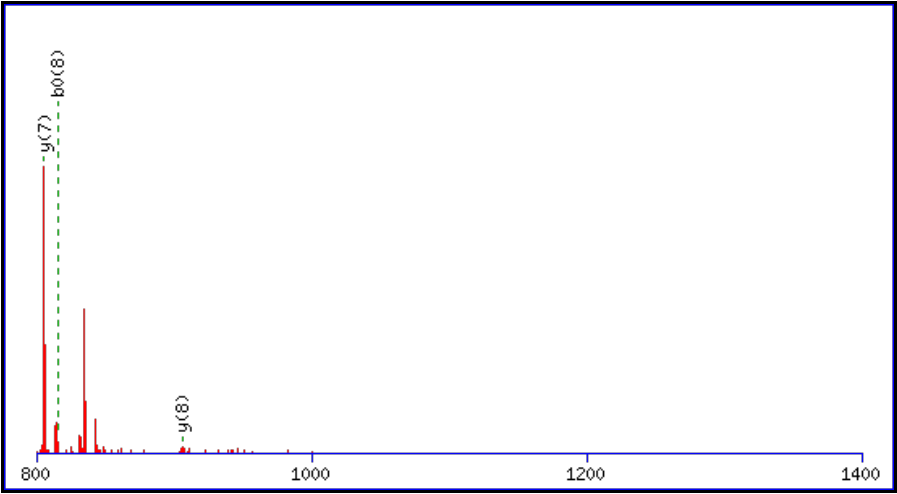
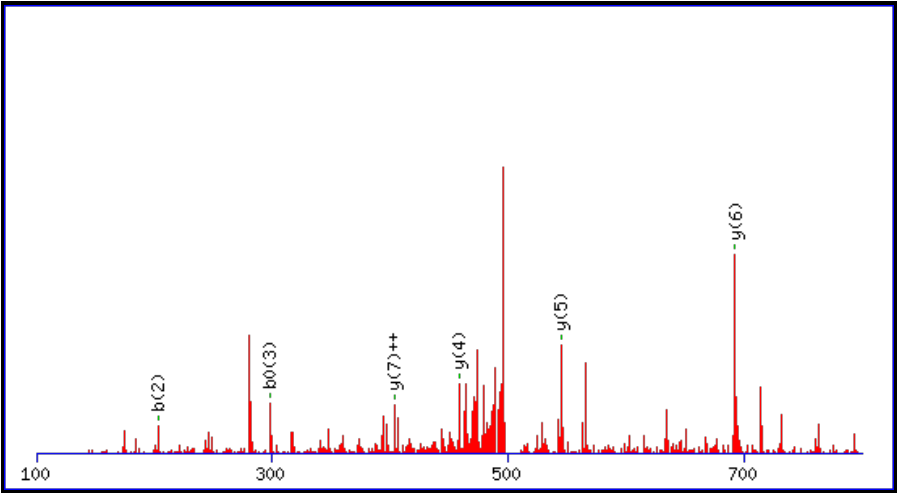
24.6	785.5011	0.0037	GLTLAALK
21.2	785.5123	-0.0075	GTLVRIK
20.2	783.4966	2.0081	RLSPALK
17.5	785.5123	-0.0075	TGLIRVK
17.0	785.5123	-0.0075	GTRVLLK
16.6	785.5123	-0.0075	XSRLALK
13.9	785.5123	-0.0075	KKQAALK
11.5	785.5123	-0.0075	SRVAILK
8.6	785.5011	0.0037	KVDALLK

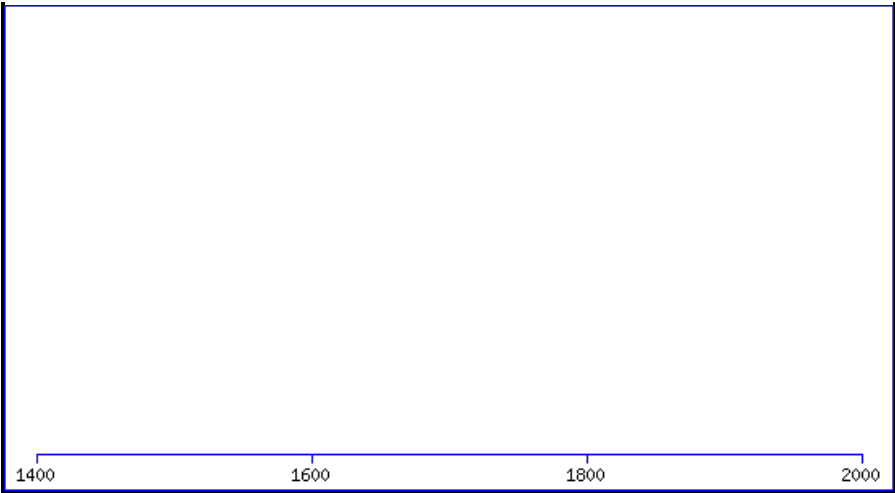
Spectrum No: 27; Query: 2884; Rank: 1

Peptide View

MS/MS Fragmentation of **TTIFSPEGR**
Found in **IPI00299155**, Tax_Id=9606 Gene_Symbol=PSMA4 Proteasome subunit alpha type-4

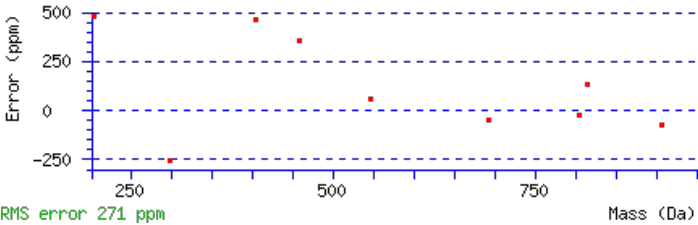
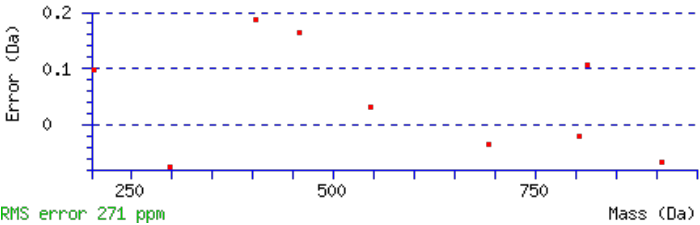
Match to Query 2884: 1006.513488 from(504.264020,2+)
Title: 091224LimSK_Exosome3_06.1415.1415.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1006.5084
Fixed modifications: Carbamidomethyl (C)
Ions Score: 22 Expect: 0.91
Matches (**Bold Red**): 9/76 fragment ions using 33 most intense peaks

#	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							9
2	203.1026	102.0550	185.0921	93.0497	T	906.4680	453.7376	889.4414	445.2243	888.4574	444.7323	8
3	316.1867	158.5970	298.1761	149.5917	I	805.4203	403.2138	788.3937	394.7005	787.4097	394.2085	7
4	463.2551	232.1312	445.2445	223.1259	F	692.3362	346.6717	675.3097	338.1585	674.3257	337.6665	6
5	550.2871	275.6472	532.2766	266.6419	S	545.2678	273.1375	528.2413	264.6243	527.2572	264.1323	5
6	647.3399	324.1736	629.3293	315.1683	P	458.2358	229.6215	441.2092	221.1083	440.2252	220.6162	4
7	776.3825	388.6949	758.3719	379.6896	E	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
8	833.4040	417.2056	815.3934	408.2003	G	232.1404	116.5738	215.1139	108.0606			2
9					R	175.1190	88.0631	158.0924	79.5498			1



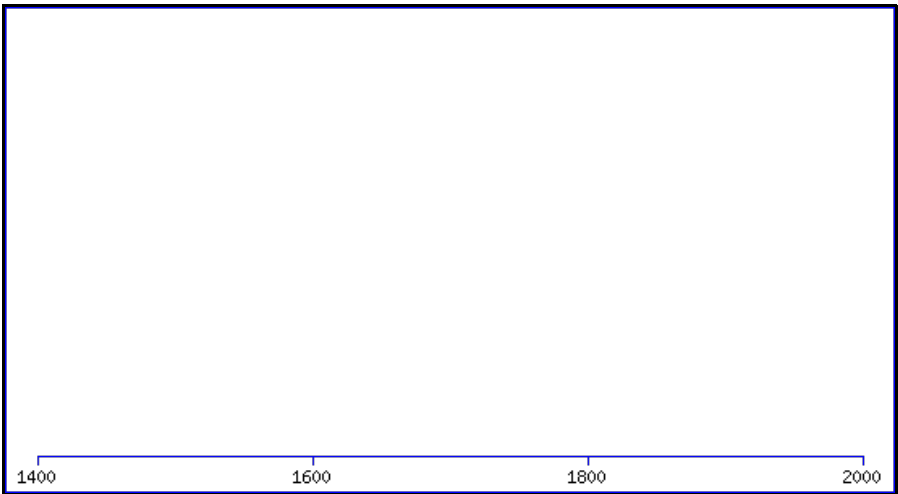
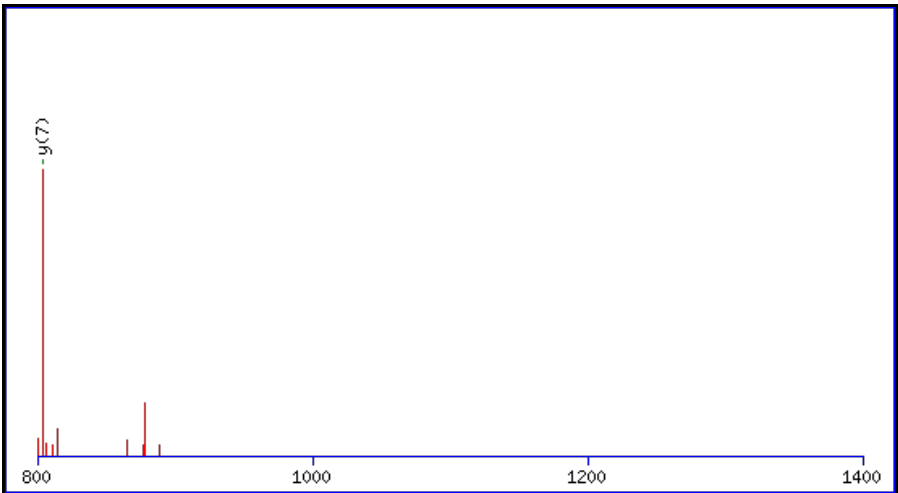
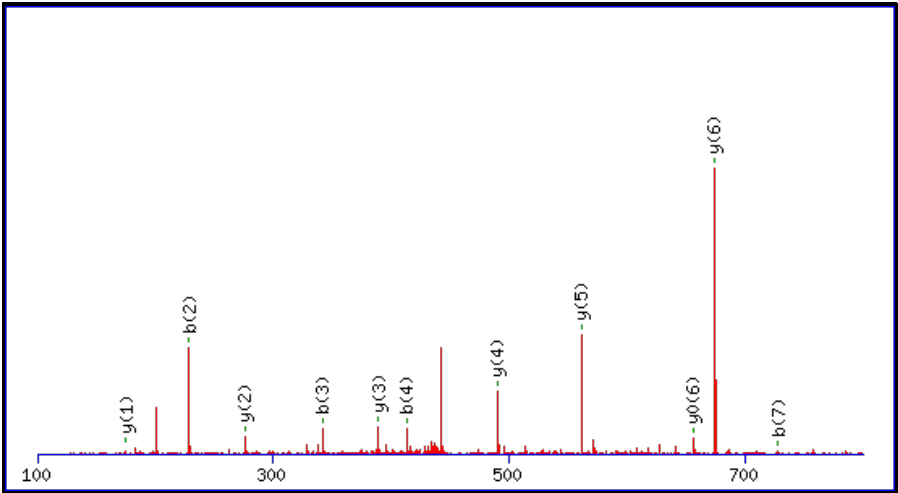
All matches to this query

Score	Mr(calc):	Delta	Sequence
21.6	1006.5084	0.0051	TTIESPEGR
5.3	1005.5178	0.9957	TGRLPFCR
5.2	1004.5147	1.9988	SLLCMPIR
4.6	1004.5152	1.9983	LSIGHHGER
4.0	1004.5080	2.0055	EAPSEWIR
3.9	1005.5026	1.0109	GGSMGQGLRK
2.2	1005.5025	1.0109	MGGKQSTAAR
1.4	1006.5229	-0.0095	KCSSSVAIR
1.1	1006.5052	0.0083	MMALVRDR
1.1	1006.5052	0.0083	MMALVRDR

Peptide View

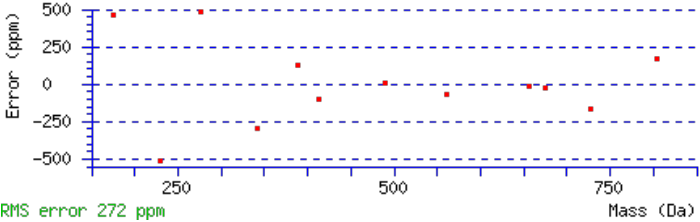
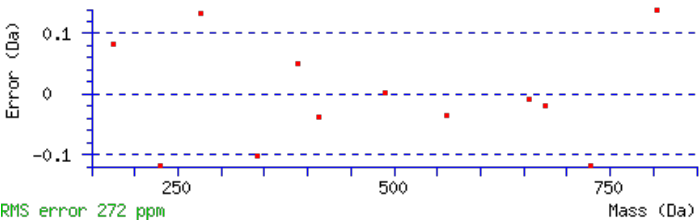
MS/MS Fragmentation of **VEIATLTR**
Found in **IPI00299155**, Tax_Id=9606 Gene_Symbol=PSMA4 Proteasome subunit alpha type-4

Match to Query 1296: 901.526888 from(451.770720,2+)
Title: 091224LimSK_Exosome3_07.1534.1534.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 901.5233
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 Expect: 0.00054
Matches (**Bold Red**): 12/66 fragment ions using 28 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415			V							8
2	229.1183	115.0628	211.1077	106.0575	E	803.4621	402.2347	786.4356	393.7214	785.4516	393.2294	7
3	342.2023	171.6048	324.1918	162.5995	I	674.4196	337.7134	657.3930	329.2001	656.4090	328.7081	6
4	413.2395	207.1234	395.2289	198.1181	A	561.3355	281.1714	544.3089	272.6581	543.3249	272.1661	5
5	514.2871	257.6472	496.2766	248.6419	T	490.2984	245.6528	473.2718	237.1396	472.2878	236.6475	4
6	627.3712	314.1892	609.3606	305.1840	L	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
7	728.4189	364.7131	710.4083	355.7078	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
8					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

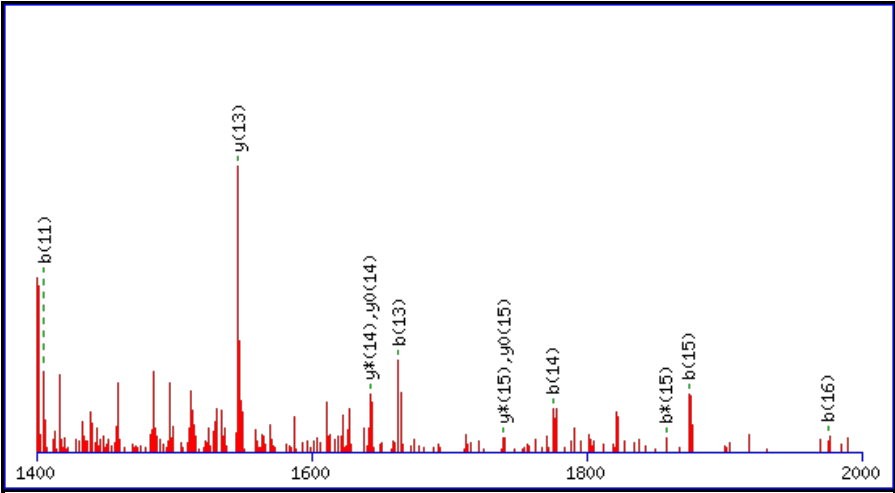
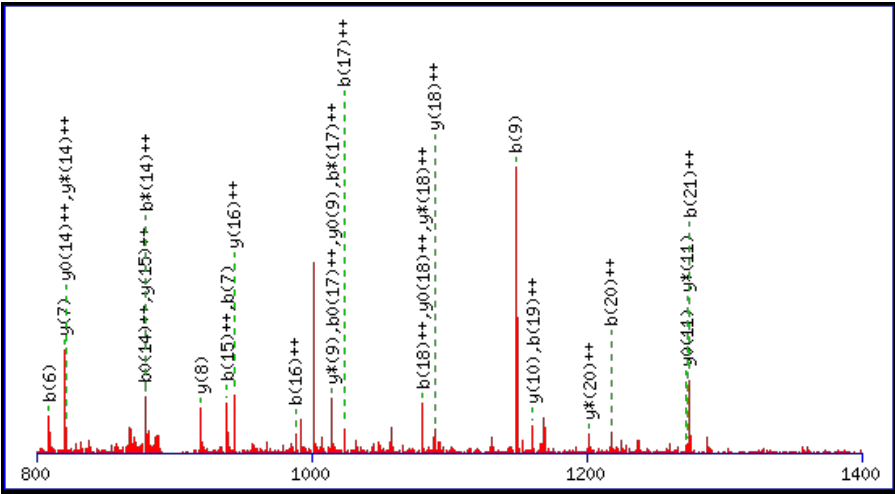
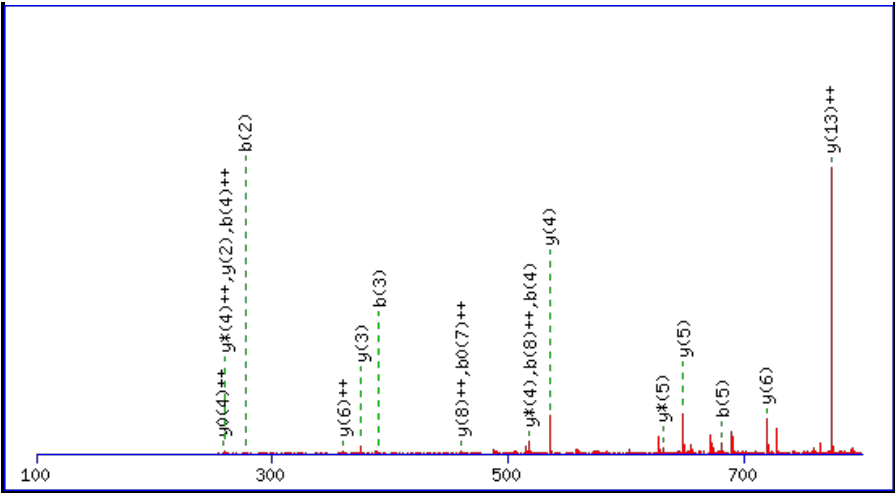
Score	Mr(calc):	Delta	Sequence
52.4	901.5233	0.0036	VEIATLTR
20.4	901.5233	0.0036	VTLVDVTR
15.2	900.5280	0.9989	GAVIATELK
12.2	901.5233	0.0036	DLVISISR
9.4	900.5181	1.0088	LNLWISR
8.2	901.5345	-0.0076	LVQKTASR
8.1	900.5181	1.0088	KVLWEAR
8.1	901.5233	0.0036	LDLSAKQK
6.2	900.5280	0.9989	AEKLEIAK
5.4	899.5188	2.0080	ILREVDR

Spectrum No: 29; Query: 60146; Rank: 1

Peptide View

MS/MS Fragmentation of **YLLQYQEPIPCQLVTALCDIK**
Found in **IP100299155**, Tax_Id=9606 Gene_Symbol=PSMA4 Proteasome subunit alpha type-4

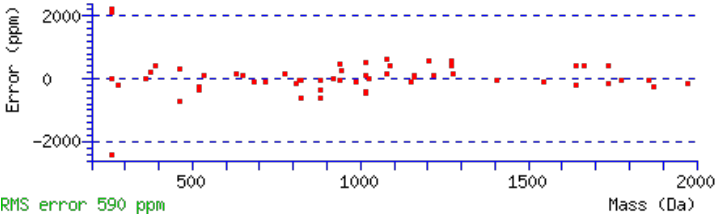
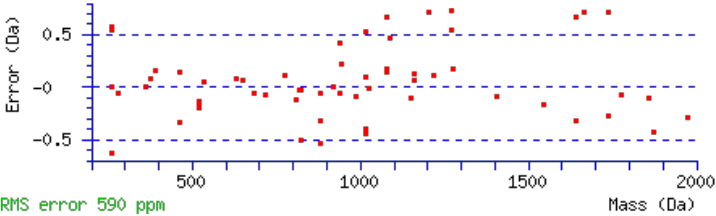
Match to Query 60146: 2693.362302 from(898.794710,3+)
Title: 091224LimSK_Exosome3_05.8322.8322.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 2693.3444
Fixed modifications: Carbamidomethyl (C)
Ions Score: 55 Expect: 0.00058
Matches (**Bold Red**): 59/230 fragment ions using 115 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							22
2	277.1547	139.0810					L	2531.2884	1266.1478	2514.2619	1257.6346	2513.2778	1257.1426	21
3	390.2387	195.6230					L	2418.2043	1209.6058	2401.1778	1201.0925	2400.1938	1200.6005	20
4	518.2973	259.6523	501.2708	251.1390			Q	2305.1203	1153.0638	2288.0937	1144.5505	2287.1097	1144.0585	19
5	681.3606	341.1840	664.3341	332.6707			Y	2177.0617	1089.0345	2160.0352	1080.5212	2159.0511	1080.0292	18
6	809.4192	405.2132	792.3927	396.7000			Q	2013.9984	1007.5028	1996.9718	998.9896	1995.9878	998.4975	17

7	938.4618	469.7345	921.4353	461.2213	920.4512	460.7293	E	1885.9398	943.4735	1868.9133	934.9603	1867.9292	934.4683	16
8	1035.5146	518.2609	1018.4880	509.7477	1017.5040	509.2556	P	1756.8972	878.9522	1739.8707	870.4390	1738.8866	869.9470	15
9	1148.5986	574.8030	1131.5721	566.2897	1130.5881	565.7977	I	1659.8444	830.4259	1642.8179	821.9126	1641.8339	821.4206	14
10	1245.6514	623.3293	1228.6249	614.8161	1227.6408	614.3241	P	1546.7604	773.8838	1529.7338	765.3706	1528.7498	764.8785	13
11	1405.6821	703.3447	1388.6555	694.8314	1387.6715	694.3394	C	1449.7076	725.3574	1432.6811	716.8442	1431.6971	716.3522	12
12	1534.7246	767.8660	1517.6981	759.3527	1516.7141	758.8607	E	1289.6770	645.3421	1272.6504	636.8288	1271.6664	636.3368	11
13	1662.7832	831.8952	1645.7567	823.3820	1644.7727	822.8900	Q	1160.6344	580.8208	1143.6078	572.3076	1142.6238	571.8155	10
14	1775.8673	888.4373	1758.8407	879.9240	1757.8567	879.4320	L	1032.5758	516.7915	1015.5492	508.2783	1014.5652	507.7863	9
15	1874.9357	937.9715	1857.9092	929.4582	1856.9251	928.9662	V	919.4917	460.2495	902.4652	451.7362	901.4812	451.2442	8
16	1975.9834	988.4953	1958.9568	979.9821	1957.9728	979.4900	T	820.4233	410.7153	803.3968	402.2020	802.4128	401.7100	7
17	2047.0205	1024.0139	2029.9939	1015.5006	2029.0099	1015.0086	A	719.3756	360.1915	702.3491	351.6782	701.3651	351.1862	6
18	2160.1046	1080.5559	2143.0780	1072.0426	2142.0940	1071.5506	L	648.3385	324.6729	631.3120	316.1596	630.3280	315.6676	5
19	2320.1352	1160.5712	2303.1087	1152.0580	2302.1246	1151.5660	C	535.2545	268.1309	518.2279	259.6176	517.2439	259.1256	4
20	2435.1621	1218.0847	2418.1356	1209.5714	2417.1516	1209.0794	D	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
21	2548.2462	1274.6267	2531.2197	1266.1135	2530.2356	1265.6215	I	260.1969	130.6021	243.1703	122.0888			2
22							K	147.1128	74.0600	130.0863	65.5468			1



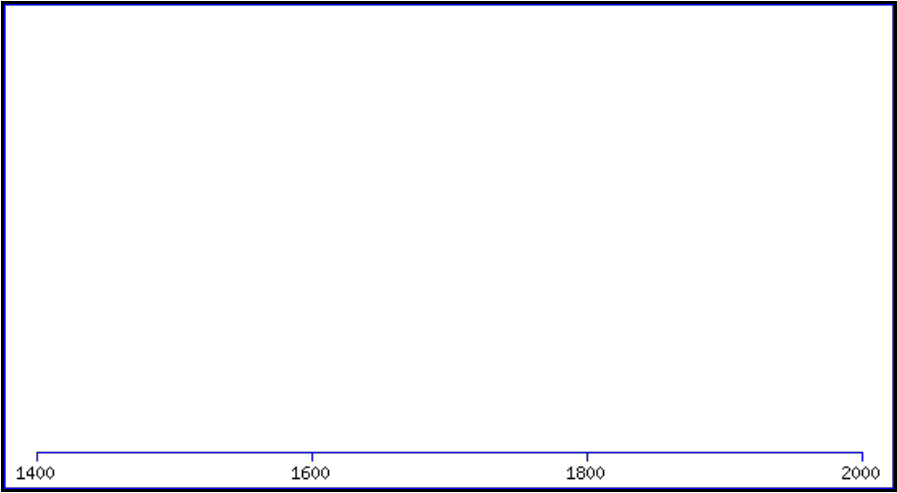
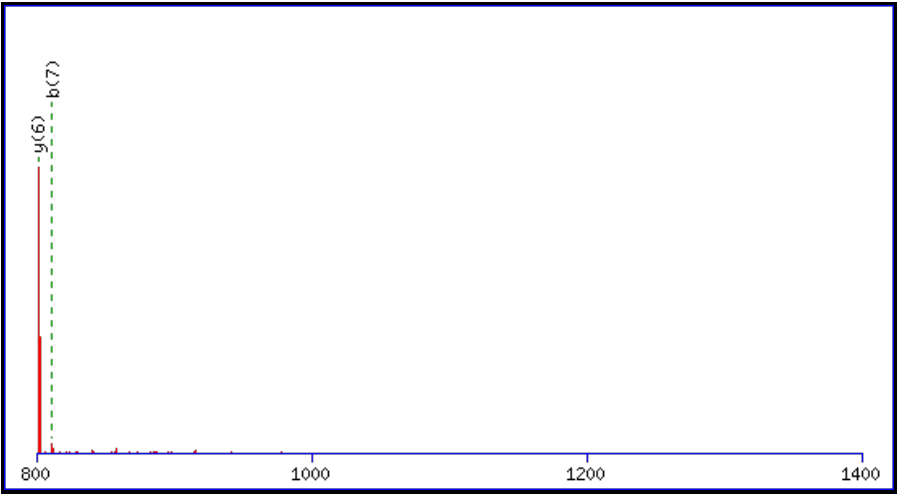
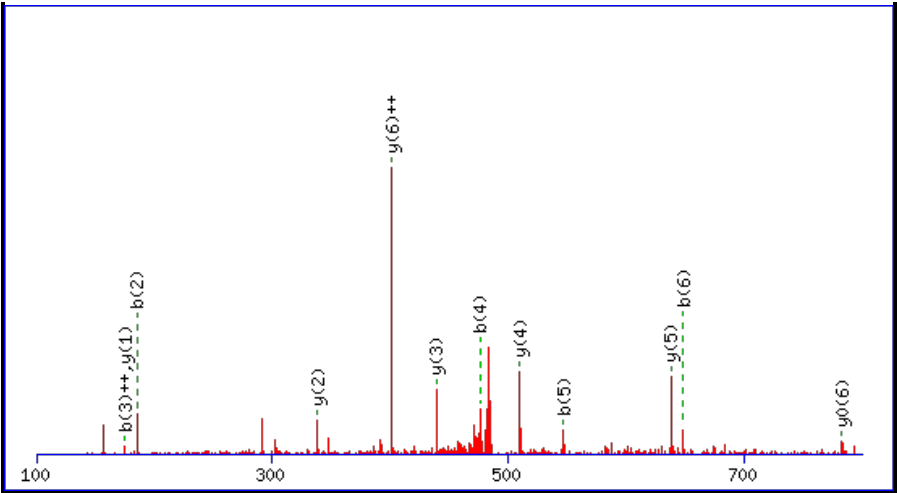
All matches to this query

Score	Mr(calc):	Delta	Sequence
55.0	2693.3444	0.0179	YLLQYQEPIPCQLVTALCDIK
14.4	2692.3765	0.9858	TGVFLFTASSGGLPTDEITFAKLLK
10.8	2692.3765	0.9858	TGVFLFTASSGGLPTDEITFAKLLK
10.8	2692.3765	0.9858	TGVFLFTASSGGLPTDEITFAKLLK
9.7	2692.3765	0.9858	TGVFLFTASSGGLPTDEITFAKLLK
4.8	2691.3737	1.9886	TMAFHGLLNDGTVGIFRGNQMRLLK
4.1	2693.3538	0.0085	NHYYVGAERKQLAGSLSLSETQVK
3.9	2692.3765	0.9858	TGVFLFTASSGGLPTDEITFAKLLK
3.5	2693.3370	0.0253	VPAEEPANELPMNEIEAWKAAEKK
3.0	2692.3853	0.9770	TLTLIEKGSQSVQKFTLSNVLLK

Spectrum No: 30; Query: 2493; Rank: 1

Peptide View

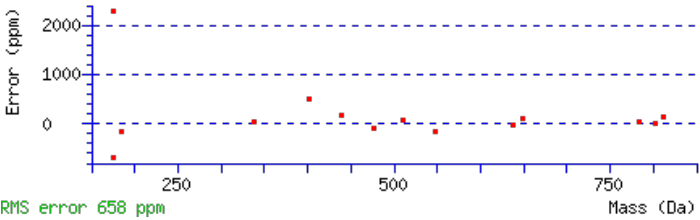
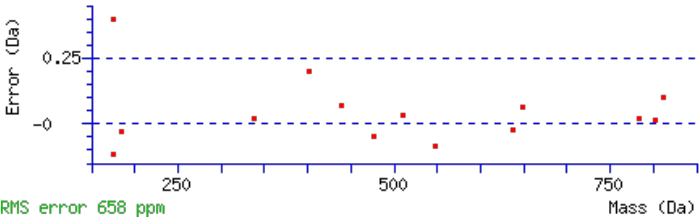
MS/MS Fragmentation of **AIYQATYR**
Found in **IPI00479306**, Tax_Id=9606 Gene_Symbol=PSMB5 Proteasome subunit beta type-5
Match to Query 2493: 984.507028 from(493.260790,2+)
Title: 091224LimSK_Exosome3_07.804.804.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 984.5029
Fixed modifications: Carbamidomethyl (C)
Ions Score: 36 Expect: 0.028
Matches (Bold Red): 14/64 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	72.0444	36.5258					A							8
2	185.1285	93.0679					I	914.4730	457.7402	897.4465	449.2269	896.4625	448.7349	7
3	348.1918	174.5995					Y	801.3890	401.1981	784.3624	392.6849	783.3784	392.1928	6
4	476.2504	238.6288	459.2238	230.1155			Q	638.3257	319.6665	621.2991	311.1532	620.3151	310.6612	5
5	547.2875	274.1474	530.2609	265.6341			A	510.2671	255.6372	493.2405	247.1239	492.2565	246.6319	4
6	648.3352	324.6712	631.3086	316.1579	630.3246	315.6659	T	439.2300	220.1186	422.2034	211.6053	421.2194	211.1133	3

7	811.3985	406.2029	794.3719	397.6896	793.3879	397.1976	Y	338.1823	169.5948	321.1557	161.0815			2
8							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

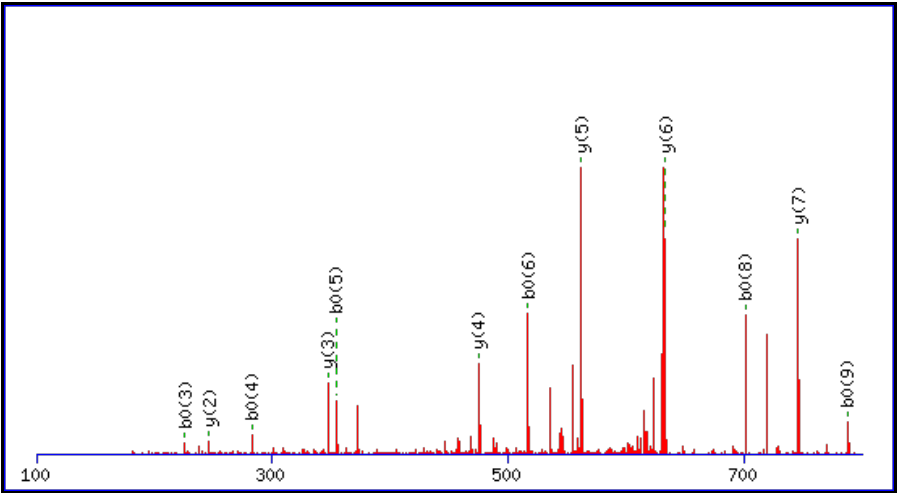
Score	Mr(calc):	Delta	Sequence
35.8	984.5029	0.0042	AIYQATYR
6.2	984.5101	-0.0030	QRPQATER
5.9	982.5097	1.9974	YKHDKR
5.2	982.5018	2.0052	KCGKAYTR
4.4	983.4971	1.0100	SNLMVHQR
4.3	984.5101	-0.0031	SPRQQVDR
4.1	984.5101	-0.0031	KSAGGTTAHR
4.0	982.5100	1.9970	TKLLVSDK
3.5	984.5141	-0.0071	QYTVRYR
3.2	984.5005	0.0065	TVKTVTTR

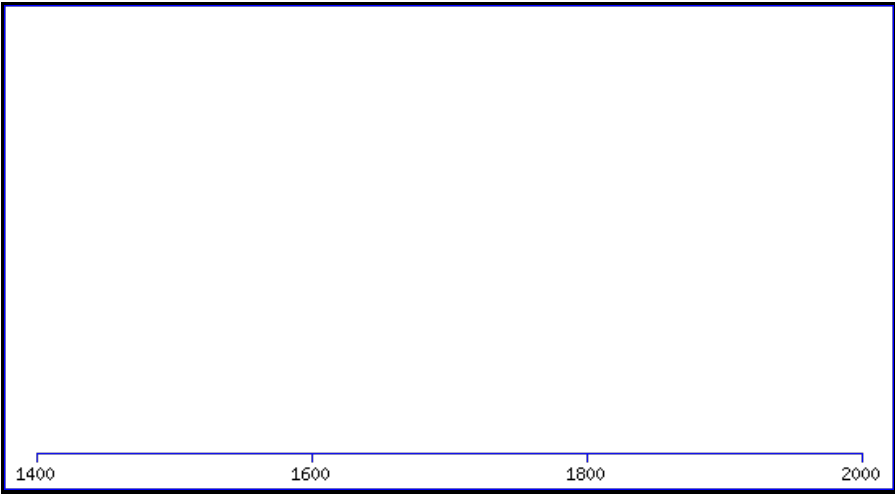
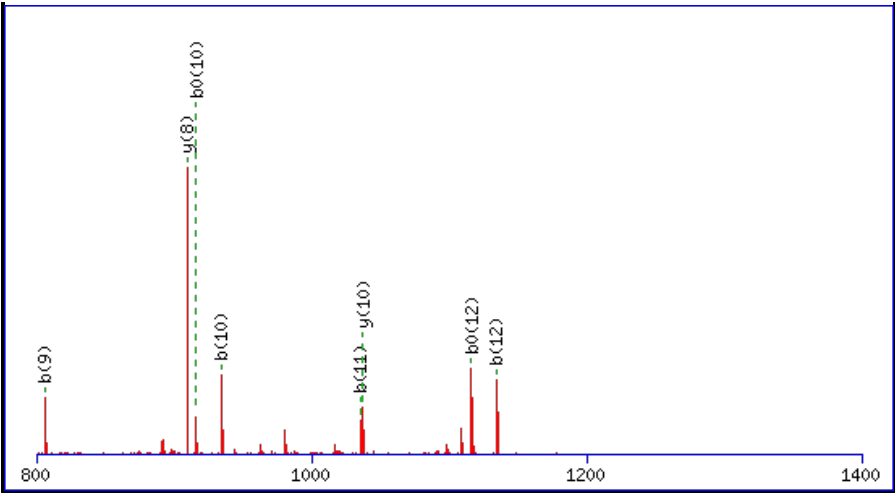
Spectrum No: 31; Query: 10547; Rank: 1

Peptide View

MS/MS Fragmentation of **ATAGAYIASQTVK**
Found in **IPI00383971**, Tax_Id=9606 Gene_Symbol=PSMB5 proteasome beta 5 subunit isoform 3

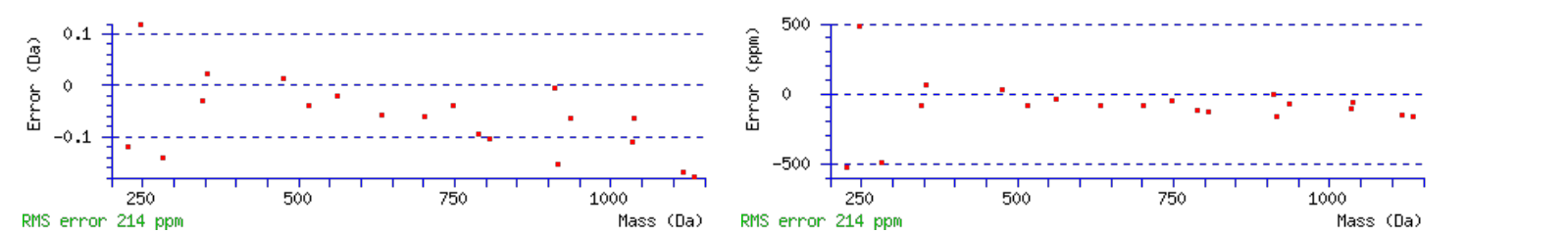
Match to Query 10547: 1279.682928 from(640.848740,2+)
Title: 091224LimSK_Exosome3_07.1335.1335.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1279.6772
Fixed modifications: Carbamidomethyl (C)
Ions Score: 75 Expect: 4e-006
Matches (Bold Red): 20/120 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	72.0444	36.5258					A							13
2	173.0921	87.0497			155.0815	78.0444	T	1209.6474	605.3273	1192.6208	596.8141	1191.6368	596.3220	12
3	244.1292	122.5682			226.1186	113.5629	A	1108.5997	554.8035	1091.5732	546.2902	1090.5891	545.7982	11
4	301.1506	151.0790			283.1401	142.0737	G	1037.5626	519.2849	1020.5360	510.7717	1019.5520	510.2796	10
5	372.1878	186.5975			354.1772	177.5922	A	980.5411	490.7742	963.5146	482.2609	962.5306	481.7689	9
6	535.2511	268.1292			517.2405	259.1239	Y	909.5040	455.2556	892.4775	446.7424	891.4934	446.2504	8
7	648.3352	324.6712			630.3246	315.6659	I	746.4407	373.7240	729.4141	365.2107	728.4301	364.7187	7
8	719.3723	360.1898			701.3617	351.1845	A	633.3566	317.1819	616.3301	308.6687	615.3461	308.1767	6
9	806.4043	403.7058			788.3937	394.7005	S	562.3195	281.6634	545.2930	273.1501	544.3089	272.6581	5
10	934.4629	467.7351	917.4363	459.2218	916.4523	458.7298	Q	475.2875	238.1474	458.2609	229.6341	457.2769	229.1421	4
11	1035.5106	518.2589	1018.4840	509.7456	1017.5000	509.2536	T	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
12	1134.5790	567.7931	1117.5524	559.2798	1116.5684	558.7878	V	246.1812	123.5942	229.1547	115.0810			2
13							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

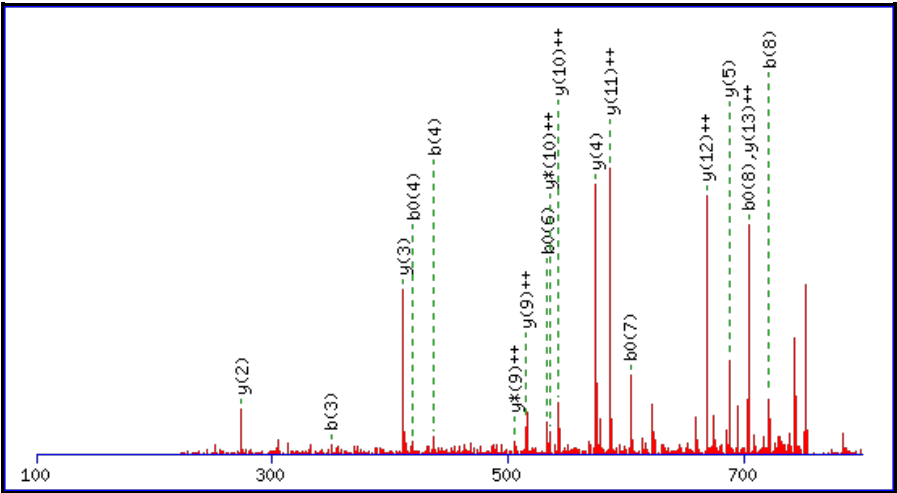
Score	Mr(calc):	Delta	Sequence
75.3	1279.6772	0.0057	ATAGAYIASQTVK
19.9	1279.6901	-0.0072	KPTQASITKVK
14.3	1279.6901	-0.0072	KPTQASITKVK
8.8	1279.6772	0.0057	NVFTVSASSIOK
7.6	1277.6723	2.0106	VMMAELEKTVK
6.7	1277.6857	1.9973	ARLQSPATKVK
6.6	1277.6857	1.9973	ARLQSPATKVK
6.1	1279.6880	-0.0050	LIKSMESVMVK
3.8	1279.6880	-0.0050	LIKSMESVMVK
1.6	1279.6788	0.0041	ELSLKGDVVK

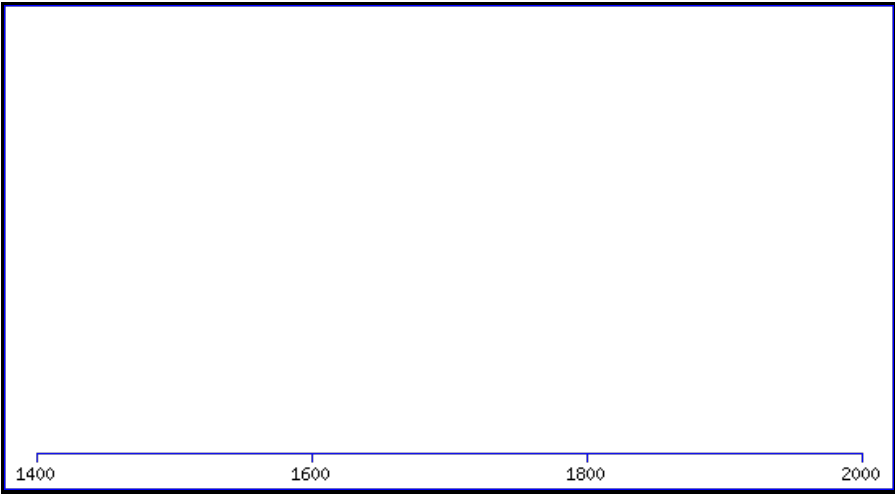
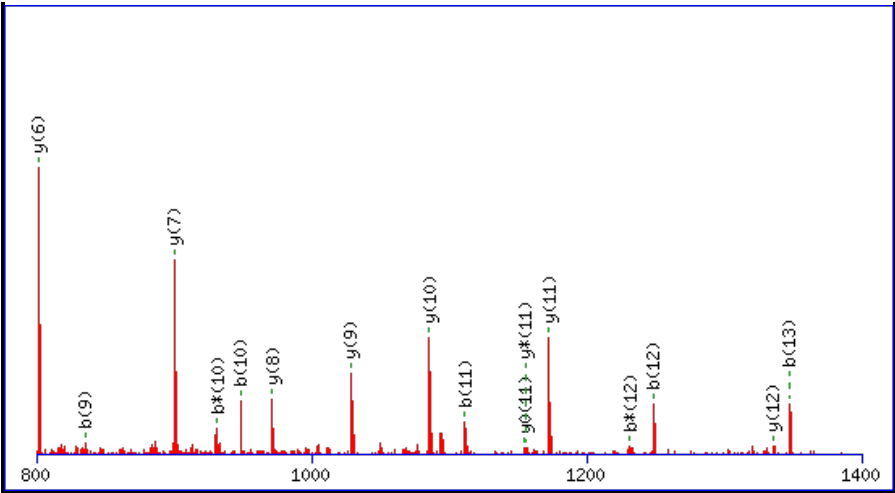
Spectrum No: 32; Query: 21296; Rank: 1

Peptide View

MS/MS Fragmentation of **DAYSGGAVNLYHVR**
Found in **IP100479306**, Tax_Id=9606 Gene_Symbol=PSMB5 Proteasome subunit beta type-5

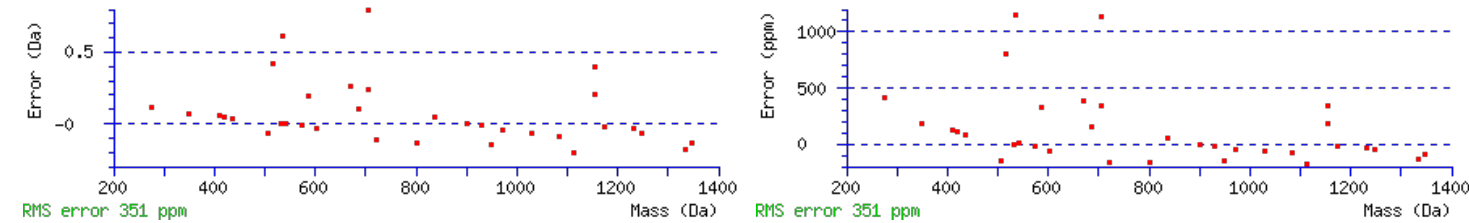
Match to Query 21296: 1520.747688 from(761.381120,2+)
Title: 091224LimSK_Exosome3_07.2739.2739.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1520.7372
Fixed modifications: Carbamidomethyl (C)
Ions Score: 73 Expect: 9.6e-006
Matches (**Bold Red**): 34/120 fragment ions using 67 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							14
2	187.0713	94.0393			169.0608	85.0340	A	1406.7175	703.8624	1389.6910	695.3491	1388.7070	694.8571	13
3	350.1347	175.5710			332.1241	166.5657	Y	1335.6804	668.3438	1318.6539	659.8306	1317.6698	659.3386	12
4	437.1667	219.0870			419.1561	210.0817	S	1172.6171	586.8122	1155.5905	578.2989	1154.6065	577.8069	11
5	494.1882	247.5977			476.1776	238.5924	G	1085.5851	543.2962	1068.5585	534.7829			10
6	551.2096	276.1084			533.1991	267.1032	G	1028.5636	514.7854	1011.5370	506.2722			9
7	622.2467	311.6270			604.2362	302.6217	A	971.5421	486.2747	954.5156	477.7614			8
8	721.3151	361.1612			703.3046	352.1559	V	900.5050	450.7561	883.4785	442.2429			7
9	835.3581	418.1827	818.3315	409.6694	817.3475	409.1774	N	801.4366	401.2219	784.4100	392.7087			6
10	948.4421	474.7247	931.4156	466.2114	930.4316	465.7194	L	687.3937	344.2005	670.3671	335.6872			5
11	1111.5055	556.2564	1094.4789	547.7431	1093.4949	547.2511	Y	574.3096	287.6584	557.2831	279.1452			4
12	1248.5644	624.7858	1231.5378	616.2726	1230.5538	615.7805	H	411.2463	206.1268	394.2197	197.6135			3
13	1347.6328	674.3200	1330.6062	665.8068	1329.6222	665.3148	V	274.1874	137.5973	257.1608	129.0840			2
14							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

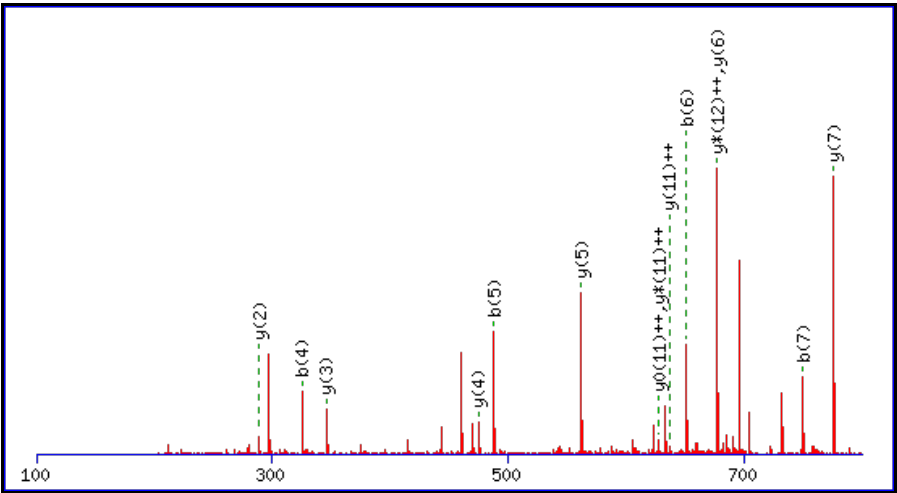
Score	Mr(calc):	Delta	Sequence
73.2	1520.7372	0.0105	DAYSGGAVNLYHVR
6.8	1520.7501	-0.0024	IHSPSPHKQVPSK
2.9	1520.7471	0.0006	VNEKYSTLPAEDR
2.5	1519.7396	1.0081	GSGKPPGVPASSKSGK
2.4	1519.7552	0.9925	IAENIMKSNIDK
1.9	1519.7396	1.0081	GSGKPPGVPASSKSGK
1.9	1520.7479	-0.0002	LAKNMEEMFHKK
0.5	1519.7297	1.0180	AFSAHSSLVTHKR
0.2	1520.7599	-0.0123	TPPKSSQELLSVR
0.2	1520.7599	-0.0123	TPPKSSQELLSVR

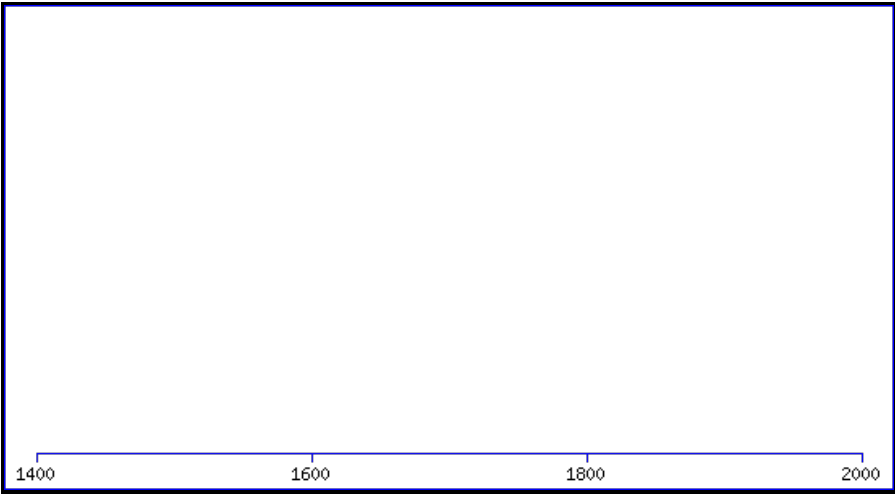
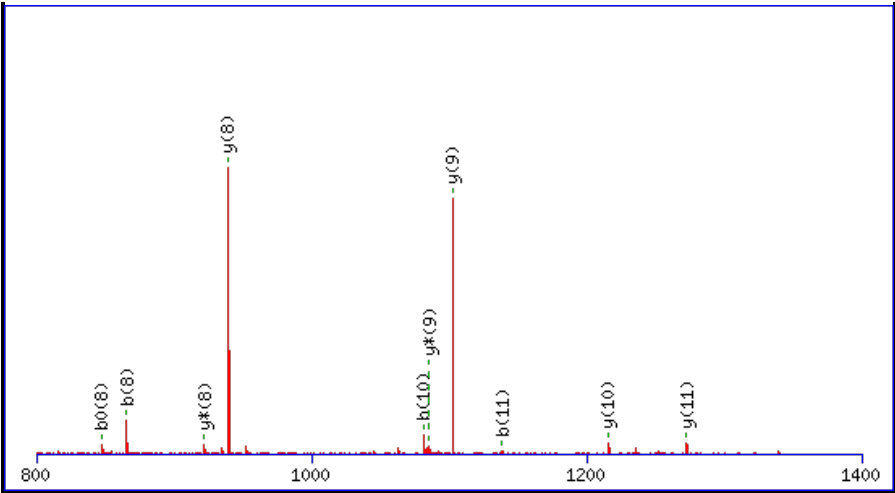
Spectrum No: 33; Query: 16441; Rank: 1

Peptide View

MS/MS Fragmentation of **GPGLYYVDSEGNR**
Found in **IPI00479306**, Tax_Id=9606 Gene_Symbol=PSMB5 Proteasome subunit beta type-5

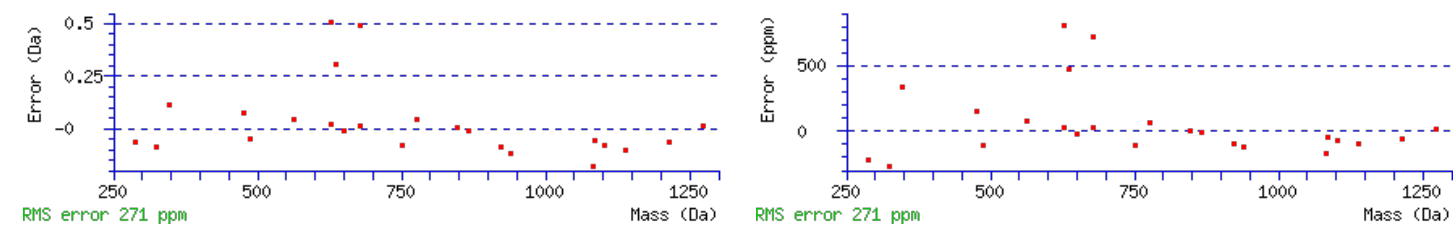
Match to Query 16441: 1425.659468 from(713.837010,2+)
Title: 091224LimSK_Exosome3_07.2142.2142.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1425.6525
Fixed modifications: Carbamidomethyl (C)
Ions Score: 72 Expect: 1.3e-005
Matches (Bold Red): 24/102 fragment ions using 46 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	155.0815	78.0444					P	1369.6383	685.3228	1352.6117	676.8095	1351.6277	676.3175	12
3	212.1030	106.5551					G	1272.5855	636.7964	1255.5590	628.2831	1254.5749	627.7911	11
4	325.1870	163.0972					L	1215.5640	608.2857	1198.5375	599.7724	1197.5535	599.2804	10
5	488.2504	244.6288					Y	1102.4800	551.7436	1085.4534	543.2304	1084.4694	542.7383	9
6	651.3137	326.1605					Y	939.4166	470.2120	922.3901	461.6987	921.4061	461.2067	8
7	750.3821	375.6947					V	776.3533	388.6803	759.3268	380.1670	758.3428	379.6750	7
8	865.4090	433.2082			847.3985	424.2029	D	677.2849	339.1461	660.2584	330.6328	659.2743	330.1408	6
9	952.4411	476.7242			934.4305	467.7189	S	562.2580	281.6326	545.2314	273.1193	544.2474	272.6273	5
10	1081.4837	541.2455			1063.4731	532.2402	E	475.2259	238.1166	458.1994	229.6033	457.2154	229.1113	4
11	1138.5051	569.7562			1120.4946	560.7509	G	346.1833	173.5953	329.1568	165.0820			3
12	1252.5481	626.7777	1235.5215	618.2644	1234.5375	617.7724	N	289.1619	145.0846	272.1353	136.5713			2
13							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

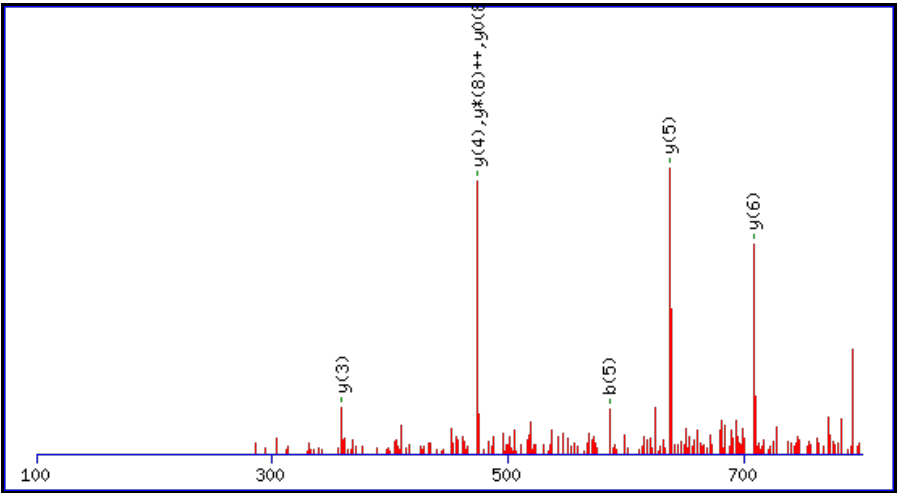
Score	Mr(calc):	Delta	Sequence
72.0	1425.6525	0.0070	GPGLYYVDSEGNR
8.1	1423.6578	2.0017	MKHVTVGRNMR
4.4	1425.6736	-0.0141	XTDPVDVVPQDGR
2.4	1425.6493	0.0102	CQGPAPSPSPCLR
0.7	1423.6531	2.0064	SVTHANALTVMGK
0.7	1423.6531	2.0064	SVTHANALTVMGK
0.5	1424.6602	0.9993	AAARDYTFFKR
0.4	1425.6687	-0.0092	LLTSQELQMQR
0.4	1425.6687	-0.0092	LLTSQELQMQR
0.2	1425.6574	0.0020	LLSYMEGELEAR

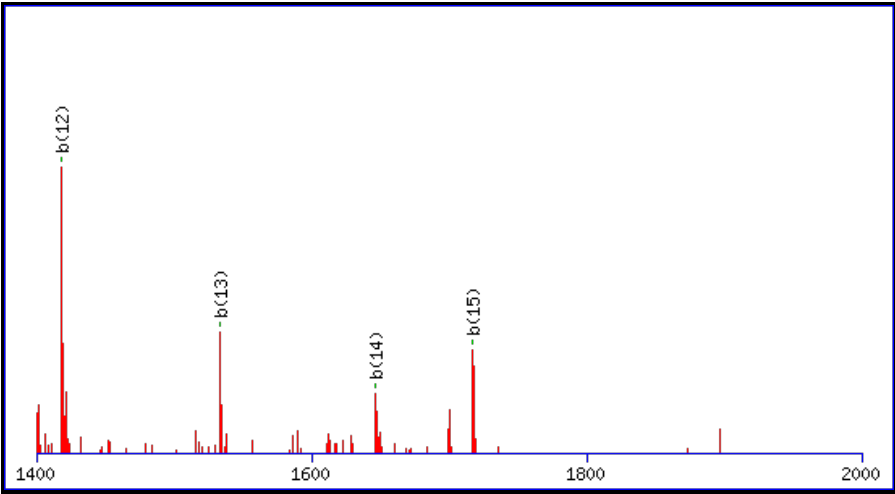
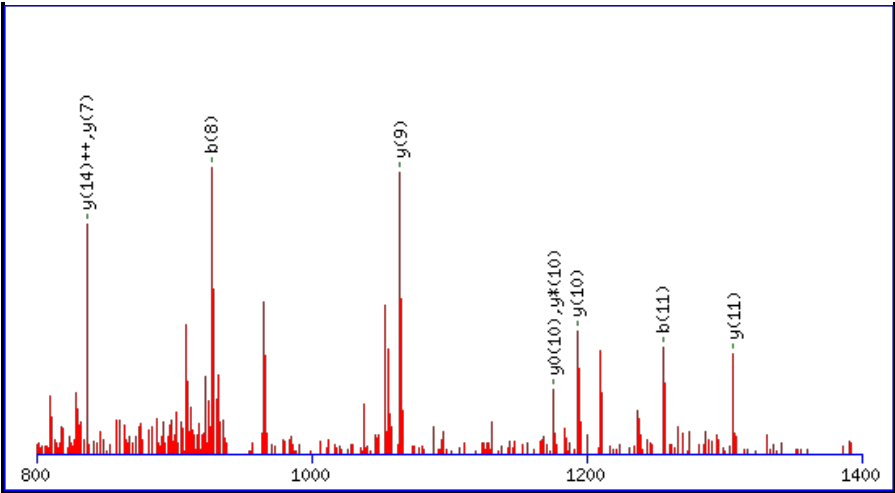
Spectrum No: 34; Query: 36207; Rank: 1

Peptide View

MS/MS Fragmentation of **GYSYDLEVEQAYDLAR**
Found in **IPI00479306**, Tax_Id=9606 Gene_Symbol=PSMB5 Proteasome subunit beta type-5

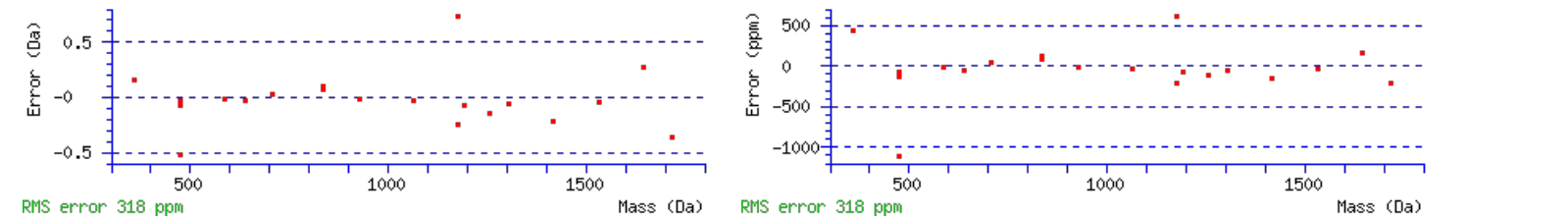
Match to Query 36207: 1890.875988 from(946.445270,2+)
Title: 091224LimSK_Exosome3_07.6197.6197.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1890.8635
Fixed modifications: Carbamidomethyl (C)
Ions Score: 83 Expect: 1.2e-006
Matches (**Bold Red**): 20/152 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							16
2	221.0921	111.0497					Y	1834.8494	917.9283	1817.8228	909.4151	1816.8388	908.9230	15
3	308.1241	154.5657			290.1135	145.5604	S	1671.7861	836.3967	1654.7595	827.8834	1653.7755	827.3914	14
4	471.1874	236.0974			453.1769	227.0921	Y	1584.7540	792.8807	1567.7275	784.3674	1566.7435	783.8754	13
5	586.2144	293.6108			568.2038	284.6055	D	1421.6907	711.3490	1404.6642	702.8357	1403.6801	702.3437	12
6	699.2984	350.1529			681.2879	341.1476	L	1306.6638	653.8355	1289.6372	645.3222	1288.6532	644.8302	11
7	828.3410	414.6742			810.3305	405.6689	E	1193.5797	597.2935	1176.5531	588.7802	1175.5691	588.2882	10
8	927.4094	464.2084			909.3989	455.2031	V	1064.5371	532.7722	1047.5106	524.2589	1046.5265	523.7669	9
9	1056.4520	528.7297			1038.4415	519.7244	E	965.4687	483.2380	948.4421	474.7247	947.4581	474.2327	8
10	1184.5106	592.7589	1167.4841	584.2457	1166.5000	583.7537	Q	836.4261	418.7167	819.3995	410.2034	818.4155	409.7114	7
11	1255.5477	628.2775	1238.5212	619.7642	1237.5372	619.2722	A	708.3675	354.6874	691.3410	346.1741	690.3570	345.6821	6
12	1418.6111	709.8092	1401.5845	701.2959	1400.6005	700.8039	Y	637.3304	319.1688	620.3039	310.6556	619.3198	310.1636	5
13	1533.6380	767.3226	1516.6114	758.8094	1515.6274	758.3174	D	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
14	1646.7221	823.8647	1629.6955	815.3514	1628.7115	814.8594	L	359.2401	180.1237	342.2136	171.6104			3
15	1717.7592	859.3832	1700.7326	850.8700	1699.7486	850.3779	A	246.1561	123.5817	229.1295	115.0684			2
16							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

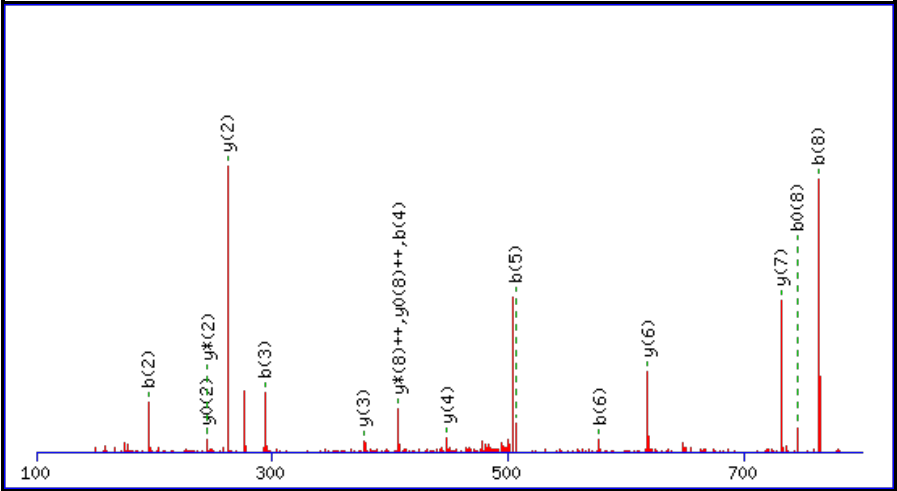
Score	Mr(calc):	Delta	Sequence
82.9	1890.8635	0.0124	GYSYDLEVEQAYDLAR
16.8	1888.8833	1.9927	PQTESLGLTHEPAGAQR
16.8	1888.8833	1.9927	PQTESLGLTHEPAGAQR
15.2	1890.8893	-0.0133	LLIYDASKLEAGVPSR
12.6	1890.8688	0.0072	MRPYRESPLLARAR
10.2	1889.8745	1.0015	LSPAGASPGPQSASSRGQR
9.5	1889.8668	1.0092	MFETMAIEIEQLLAR
8.6	1888.8833	1.9927	PQTESLGLTHEPAGAQR
7.8	1890.8949	-0.0189	QLIRETSTHQLNSER
6.8	1890.8599	0.0161	THHTGTGHTQTHRER

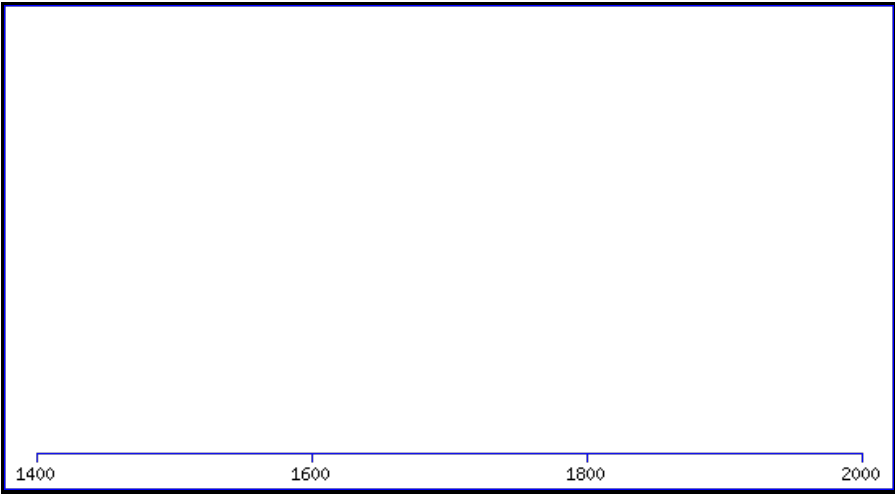
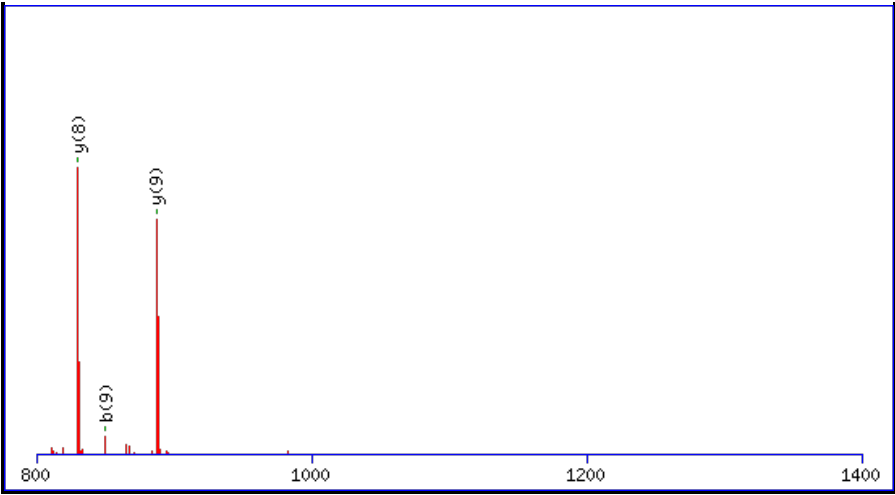
Spectrum No: 35; Query: 3147; Rank: 1

Peptide View

MS/MS Fragmentation of **HGVIVAADSR**
Found in **IPI00383971**, Tax_Id=9606 Gene_Symbol=PSMB5 proteasome beta 5 subunit isoform 3

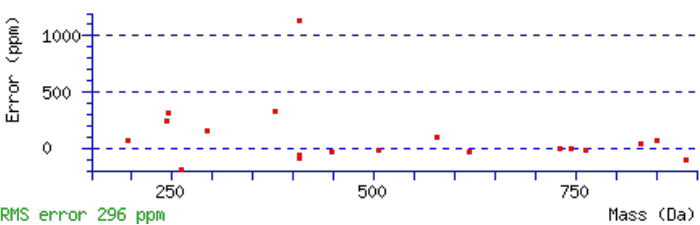
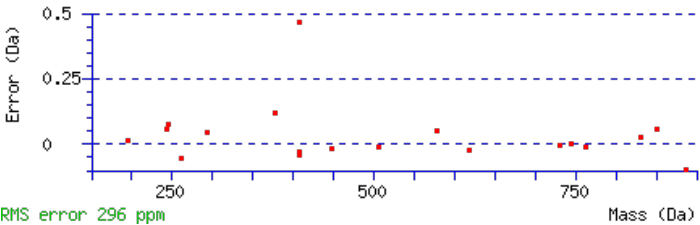
Match to Query 3147: 1023.549968 from(512.782260,2+)
Title: 091224LimSK_Exosome3_07.231.231.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1023.5461
Fixed modifications: Carbamidomethyl (C)
Ions Score: 67 Expect: 2.1e-005
Matches (Bold Red): 19/74 fragment ions using 27 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	138.0662	69.5367			H							10
2	195.0877	98.0475			G	887.4945	444.2509	870.4680	435.7376	869.4839	435.2456	9
3	294.1561	147.5817			V	830.4730	415.7402	813.4465	407.2269	812.4625	406.7349	8
4	407.2401	204.1237			I	731.4046	366.2060	714.3781	357.6927	713.3941	357.2007	7
5	506.3085	253.6579			V	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	6
6	577.3457	289.1765			A	519.2522	260.1297	502.2256	251.6164	501.2416	251.1244	5
7	648.3828	324.6950			A	448.2150	224.6112	431.1885	216.0979	430.2045	215.6059	4
8	763.4097	382.2085	745.3991	373.2032	D	377.1779	189.0926	360.1514	180.5793	359.1674	180.0873	3
9	850.4417	425.7245	832.4312	416.7192	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
10					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query



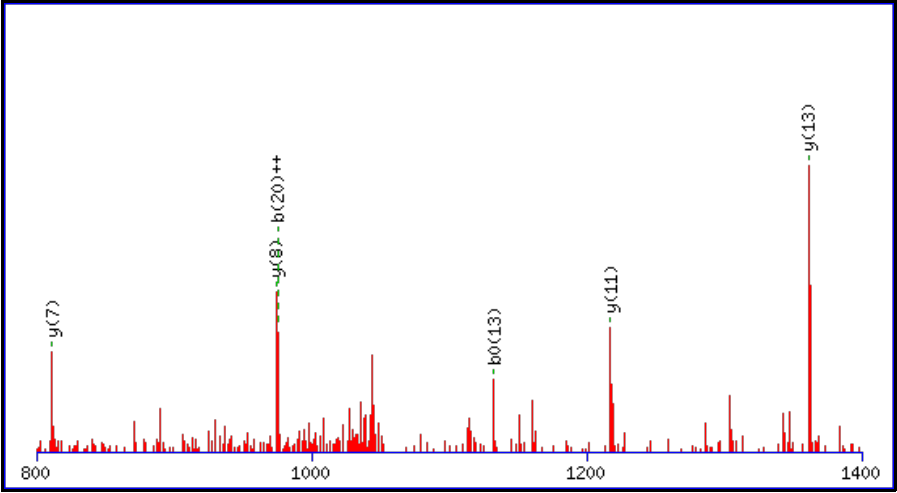
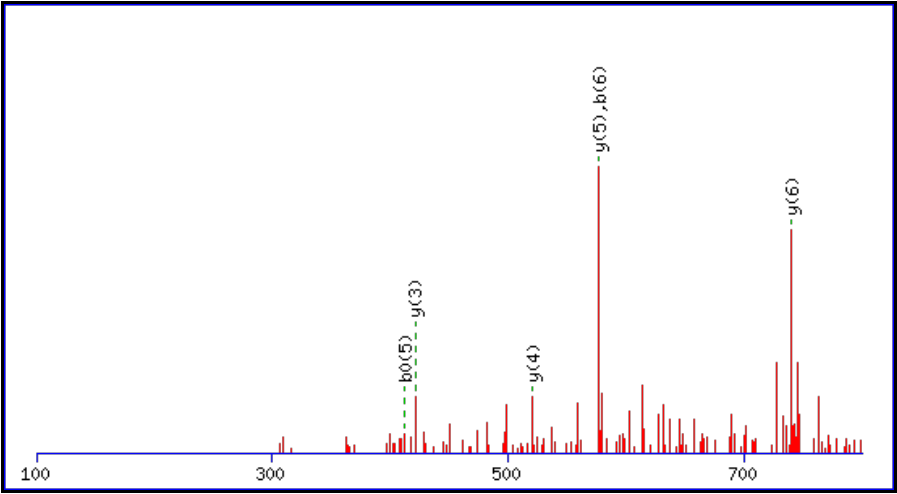
Score	Mr(calc):	Delta	Sequence
67.0	1023.5461	0.0038	HGVIVAADSR
10.4	1023.5461	0.0038	YSRGVLSSR
8.1	1023.5569	-0.0069	MKVKMLSR
7.6	1023.5423	0.0077	KDDKMLFK
6.1	1021.5444	2.0056	YQLTLEQK
6.0	1021.5444	2.0056	FKTELEQK
5.5	1021.5444	2.0056	LYKQLDDK
4.3	1022.5430	1.0070	KNSLSSIMK
3.7	1021.5457	2.0042	AGIRYWTR
3.6	1021.5444	2.0055	DKTVGDFLK

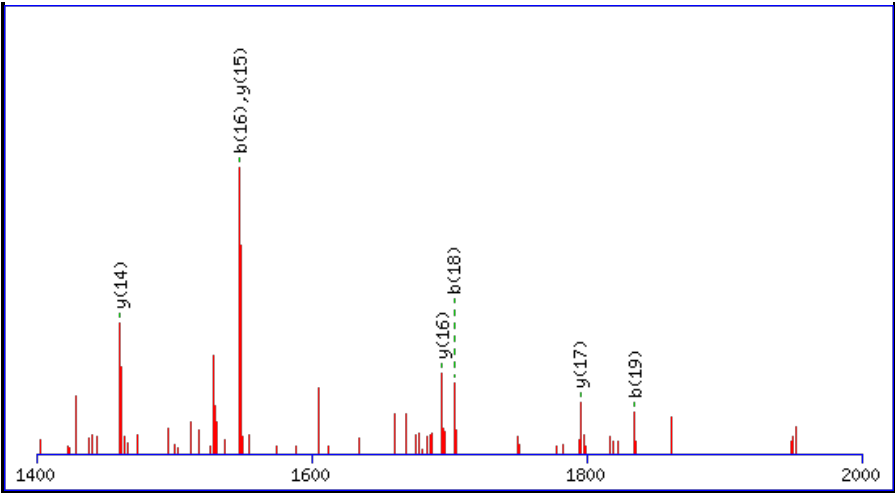
Spectrum No: 36; Query: 44178; Rank: 1

Peptide View

MS/MS Fragmentation of **ISGATFSVGSGSVYAYGVMDR**
Found in **IPI00479306**, Tax_Id=9606 Gene_Symbol=PSMB5 Proteasome subunit beta type-5

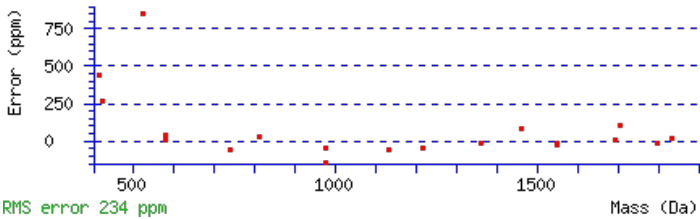
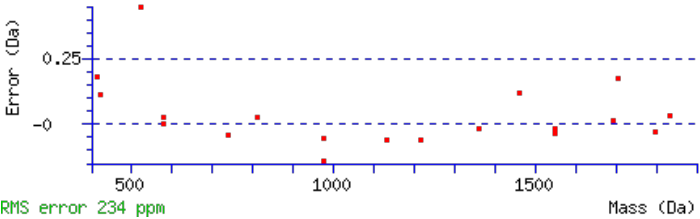
Match to Query 44178: 2123.007708 from(1062.511130,2+)
Title: 091224LimSK_Exosome3_07.6355.6355.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2122.9994
Fixed modifications: Carbamidomethyl (C)
Ions Score: 93 Expect: 1.4e-007
Matches (**Bold Red**): 19/196 fragment ions using 25 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							21
2	201.1234	101.0653	183.1128	92.0600	S	2010.9226	1005.9649	1993.8960	997.4516	1992.9120	996.9596	20
3	258.1448	129.5761	240.1343	120.5708	G	1923.8905	962.4489	1906.8640	953.9356	1905.8800	953.4436	19
4	329.1819	165.0946	311.1714	156.0893	A	1866.8691	933.9382	1849.8425	925.4249	1848.8585	924.9329	18
5	430.2296	215.6185	412.2191	206.6132	T	1795.8320	898.4196	1778.8054	889.9063	1777.8214	889.4143	17
6	577.2980	289.1527	559.2875	280.1474	F	1694.7843	847.8958	1677.7577	839.3825	1676.7737	838.8905	16
7	664.3301	332.6687	646.3195	323.6634	S	1547.7159	774.3616	1530.6893	765.8483	1529.7053	765.3563	15
8	763.3985	382.2029	745.3879	373.1976	V	1460.6838	730.8456	1443.6573	722.3323	1442.6733	721.8403	14
9	820.4199	410.7136	802.4094	401.7083	G	1361.6154	681.3114	1344.5889	672.7981	1343.6049	672.3061	13
10	907.4520	454.2296	889.4414	445.2243	S	1304.5940	652.8006	1287.5674	644.2873	1286.5834	643.7953	12
11	964.4734	482.7404	946.4629	473.7351	G	1217.5619	609.2846	1200.5354	600.7713	1199.5514	600.2793	11
12	1051.5055	526.2564	1033.4949	517.2511	S	1160.5405	580.7739	1143.5139	572.2606	1142.5299	571.7686	10
13	1150.5739	575.7906	1132.5633	566.7853	V	1073.5084	537.2579	1056.4819	528.7446	1055.4979	528.2526	9
14	1313.6372	657.3222	1295.6266	648.3170	Y	974.4400	487.7237	957.4135	479.2104	956.4295	478.7184	8
15	1384.6743	692.8408	1366.6638	683.8355	A	811.3767	406.1920	794.3502	397.6787	793.3661	397.1867	7
16	1547.7377	774.3725	1529.7271	765.3672	Y	740.3396	370.6734	723.3130	362.1602	722.3290	361.6681	6
17	1604.7591	802.8832	1586.7486	793.8779	G	577.2763	289.1418	560.2497	280.6285	559.2657	280.1365	5
18	1703.8275	852.4174	1685.8170	843.4121	V	520.2548	260.6310	503.2282	252.1178	502.2442	251.6258	4
19	1834.8680	917.9376	1816.8574	908.9324	M	421.1864	211.0968	404.1598	202.5836	403.1758	202.0915	3
20	1949.8950	975.4511	1931.8844	966.4458	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
21					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
92.7	2122.9994	0.0083	ISGATESVGSGSVYAYGVMDR

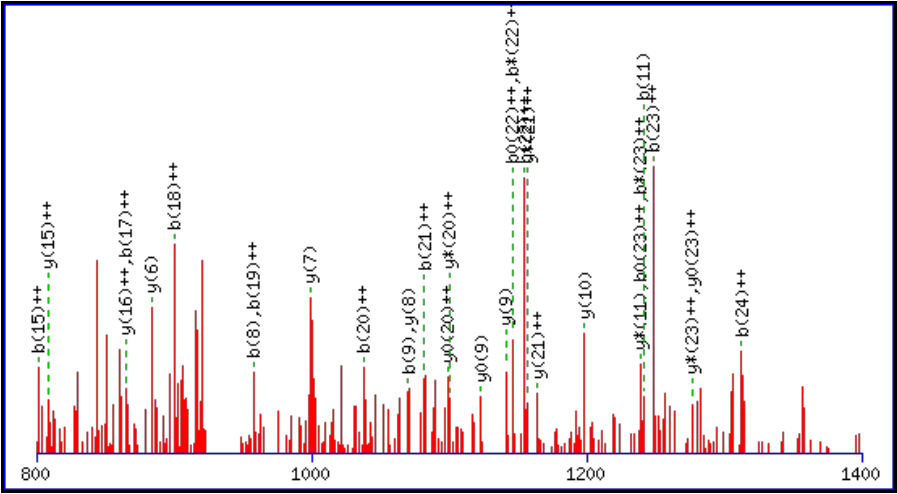
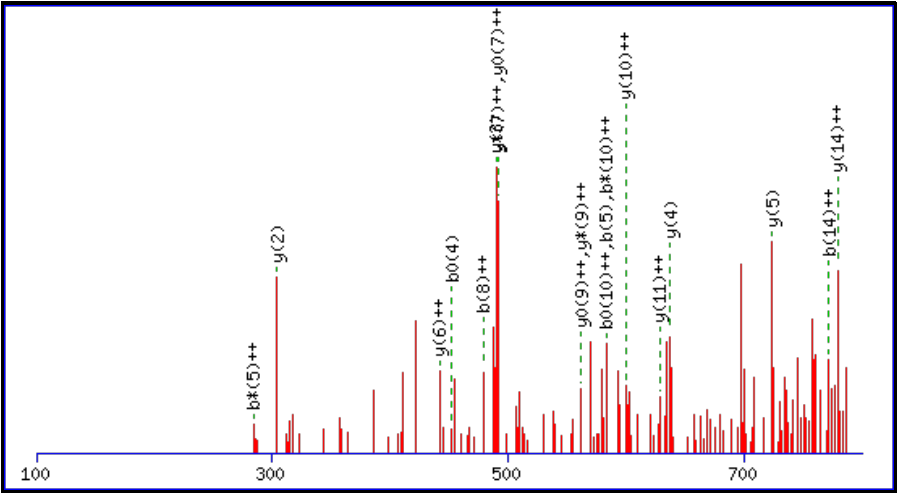
8.3	2122.9942	0.0135	AKPSLLSRV GALTNTLSR
6.7	2120.9923	2.0154	MLSFWWPLALILATQR
6.3	2123.0049	0.0029	XTSAPPTLGQPKGV SASQDR
5.5	2123.0010	0.0067	IYAMNSEGLGEPALVPGTPK
5.4	2123.0252	-0.0175	CFIVGADNVNSKOMQOIR
5.3	2123.0049	0.0029	XTSAPPTLGQPKGV SASQDR
4.7	2123.0049	0.0029	XTSAPPTLGQPKGV SASQDR
4.1	2120.9921	2.0156	RFNYVVRALPLASEGNR
4.1	2123.0038	0.0039	QTPHLGEQRRTTASLLR

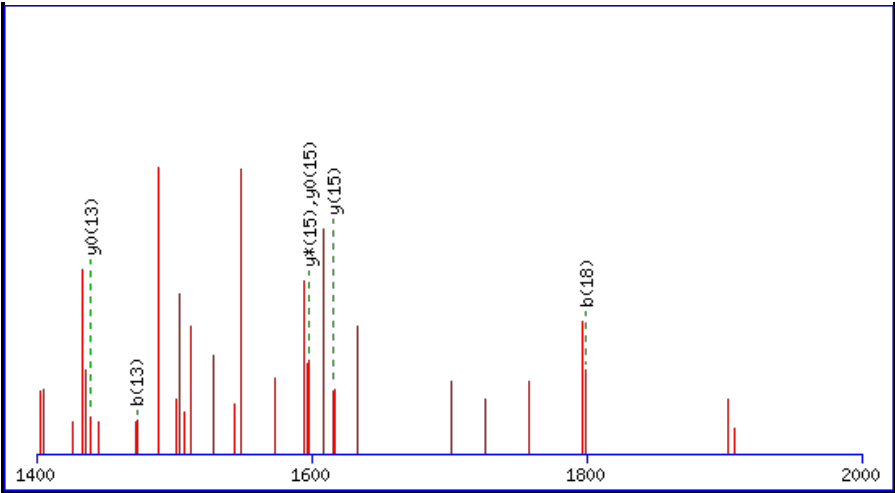
Spectrum No: 37; Query: 61596; Rank: 1

Peptide View

MS/MS Fragmentation of **KVIEINPYLLGT MAGGAADCSFWER**
Found in **IPI00383971**, Tax_Id=9606 Gene_Symbol=PSMB5 proteasome beta 5 subunit isoform 3

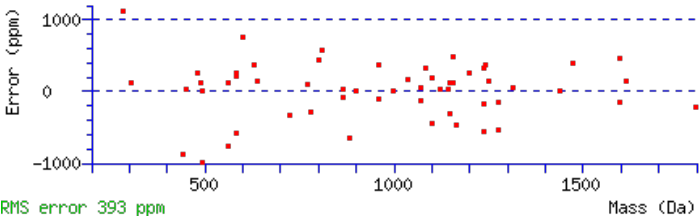
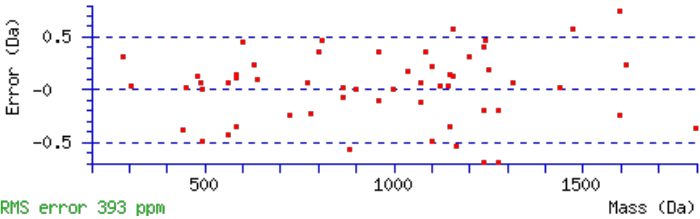
Match to Query 61596: 2798.372742 from(933.798190,3+)
Title: 091224LimSK_Exosome3_08.7700.7700.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2797.3567
Fixed modifications: Carbamidomethyl (C)
Ions Score: 27 Expect: 0.52
Matches (**Bold Red**): 56/280 fragment ions using 131 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							25
2	228.1707	114.5890	211.1441	106.0757			V	2670.2691	1335.6382	2653.2425	1327.1249	2652.2585	1326.6329	24
3	341.2547	171.1310	324.2282	162.6177			I	2571.2007	1286.1040	2554.1741	1277.5907	2553.1901	1277.0987	23
4	470.2973	235.6523	453.2708	227.1390	452.2867	226.6470	E	2458.1166	1229.5619	2441.0900	1221.0487	2440.1060	1220.5567	22
5	583.3814	292.1943	566.3548	283.6811	565.3708	283.1890	I	2329.0740	1165.0406	2312.0475	1156.5274	2311.0634	1156.0354	21
6	697.4243	349.2158	680.3978	340.7025	679.4137	340.2105	N	2215.9899	1108.4986	2198.9634	1099.9853	2197.9794	1099.4933	20
7	794.4771	397.7422	777.4505	389.2289	776.4665	388.7369	P	2101.9470	1051.4771	2084.9205	1042.9639	2083.9364	1042.4719	19
8	957.5404	479.2738	940.5138	470.7606	939.5298	470.2686	Y	2004.8942	1002.9508	1987.8677	994.4375	1986.8837	993.9455	18
9	1070.6245	535.8159	1053.5979	527.3026	1052.6139	526.8106	L	1841.8309	921.4191	1824.8044	912.9058	1823.8204	912.4138	17
10	1183.7085	592.3579	1166.6820	583.8446	1165.6980	583.3526	L	1728.7469	864.8771	1711.7203	856.3638	1710.7363	855.8718	16
11	1240.7300	620.8686	1223.7034	612.3554	1222.7194	611.8633	G	1615.6628	808.3350	1598.6362	799.8218	1597.6522	799.3298	15
12	1341.7777	671.3925	1324.7511	662.8792	1323.7671	662.3872	T	1558.6413	779.8243	1541.6148	771.3110	1540.6308	770.8190	14
13	1472.8181	736.9127	1455.7916	728.3994	1454.8076	727.9074	M	1457.5936	729.3005	1440.5671	720.7872	1439.5831	720.2952	13
14	1543.8553	772.4313	1526.8287	763.9180	1525.8447	763.4260	A	1326.5532	663.7802	1309.5266	655.2669	1308.5426	654.7749	12
15	1600.8767	800.9420	1583.8502	792.4287	1582.8662	791.9367	G	1255.5160	628.2617	1238.4895	619.7484	1237.5055	619.2564	11
16	1657.8982	829.4527	1640.8716	820.9395	1639.8876	820.4475	G	1198.4946	599.7509	1181.4680	591.2377	1180.4840	590.7456	10
17	1728.9353	864.9713	1711.9088	856.4580	1710.9247	855.9660	A	1141.4731	571.2402	1124.4466	562.7269	1123.4626	562.2349	9
18	1799.9724	900.4898	1782.9459	891.9766	1781.9619	891.4846	A	1070.4360	535.7216	1053.4095	527.2084	1052.4254	526.7164	8
19	1914.9994	958.0033	1897.9728	949.4900	1896.9888	948.9980	D	999.3989	500.2031	982.3723	491.6898	981.3883	491.1978	7
20	2075.0300	1038.0186	2058.0035	1029.5054	2057.0194	1029.0134	C	884.3719	442.6896	867.3454	434.1763	866.3614	433.6843	6
21	2162.0620	1081.5347	2145.0355	1073.0214	2144.0515	1072.5294	S	724.3413	362.6743	707.3148	354.1610	706.3307	353.6690	5
22	2309.1305	1155.0689	2292.1039	1146.5556	2291.1199	1146.0636	F	637.3093	319.1583	620.2827	310.6450	619.2987	310.1530	4
23	2495.2098	1248.1085	2478.1832	1239.5952	2477.1992	1239.1032	W	490.2409	245.6241	473.2143	237.1108	472.2303	236.6188	3
24	2624.2524	1312.6298	2607.2258	1304.1165	2606.2418	1303.6245	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
25							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

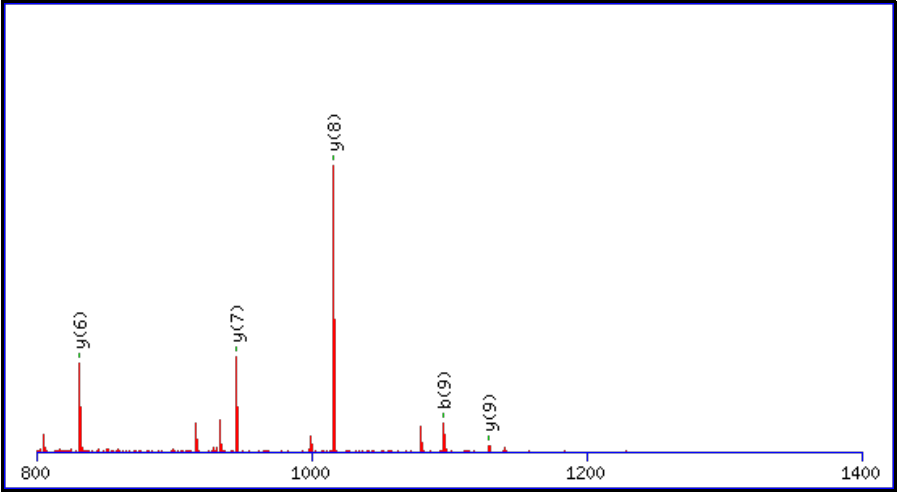
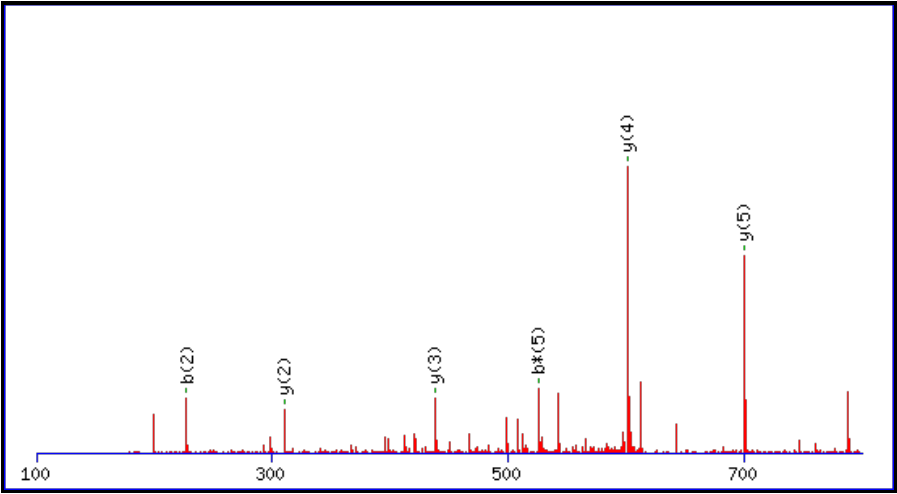
Score	Mr(calc):	Delta	Sequence
26.5	2797.3567	1.0160	KVIEINPYLLGTMAGGAADCSFWER
18.1	2798.3962	-0.0235	LPEEHARFYAAEICIALNFLHER
15.3	2797.3800	0.9927	FQDVGPQAPVGSVYQKTNAVSEIKR
11.5	2797.3565	1.0162	GEGGQMARIASESAGSDPLERLPWQR
10.6	2796.3881	1.9846	LGDSSDLLSPGGPGPPLPMSSPGLGKKR
9.1	2797.3800	0.9927	FQDVGPQAPVGSVYQKTNAVSEIKR
8.6	2797.3800	0.9927	FQDVGPQAPVGSVYQKTNAVSEIKR
8.6	2797.3800	0.9927	FQDVGPQAPVGSVYQKTNAVSEIKR
7.8	2797.3452	1.0275	YDELYAALTALLAAGSQLDTVRRK
7.6	2796.3881	1.9846	LGDSSDLLSPGGPGPPLPMSSPGLGKKR

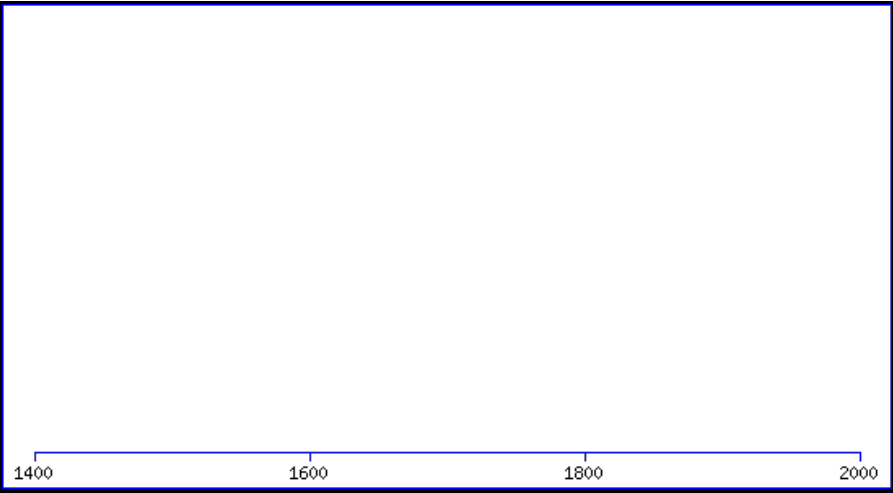
Spectrum No: 38; Query: 9350; Rank: 1

Peptide View

MS/MS Fragmentation of **LLANMVYQYK**
Found in **IP100383971**, Tax_Id=9606 Gene_Symbol=PSMB5 proteasome beta 5 subunit isoform 3

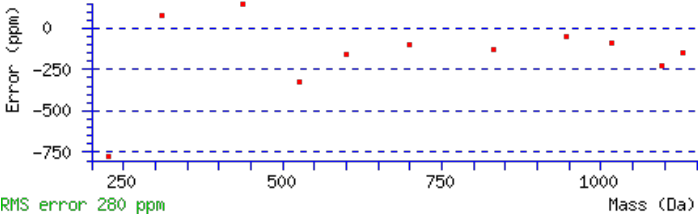
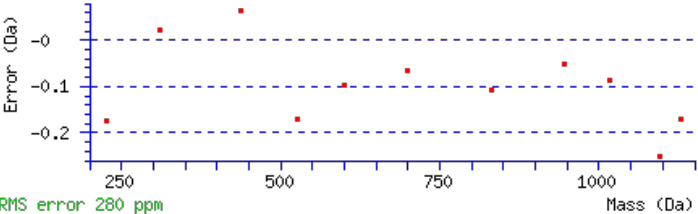
Match to Query 9350: 1241.653808 from(621.834180,2+)
Title: 091224LimSK_Exosome3_07.3815.3815.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1241.6478
Fixed modifications: Carbamidomethyl (C)
Ions Score: 67 Expect: 2.3e-005
Matches (**Bold Red**): 11/66 fragment ions using 20 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	#
1	114.0913	57.5493			L					10
2	227.1754	114.0913			L	1129.5710	565.2892	1112.5445	556.7759	9
3	298.2125	149.6099			A	1016.4870	508.7471	999.4604	500.2339	8
4	412.2554	206.6314	395.2289	198.1181	N	945.4499	473.2286	928.4233	464.7153	7
5	543.2959	272.1516	526.2694	263.6383	M	831.4069	416.2071	814.3804	407.6938	6
6	642.3643	321.6858	625.3378	313.1725	V	700.3665	350.6869	683.3399	342.1736	5
7	805.4277	403.2175	788.4011	394.7042	Y	601.2980	301.1527	584.2715	292.6394	4
8	933.4863	467.2468	916.4597	458.7335	Q	438.2347	219.6210	421.2082	211.1077	3
9	1096.5496	548.7784	1079.5230	540.2652	Y	310.1761	155.5917	293.1496	147.0784	2
10					K	147.1128	74.0600	130.0863	65.5468	1



All matches to this query

Score	Mr(calc):	Delta	Sequence
67.0	1241.6478	0.0060	LLANMVYQYK
0.7	1239.6476	2.0062	TLLSGSASVVVK
0.2	1239.6360	2.0178	GRLANQYYQK

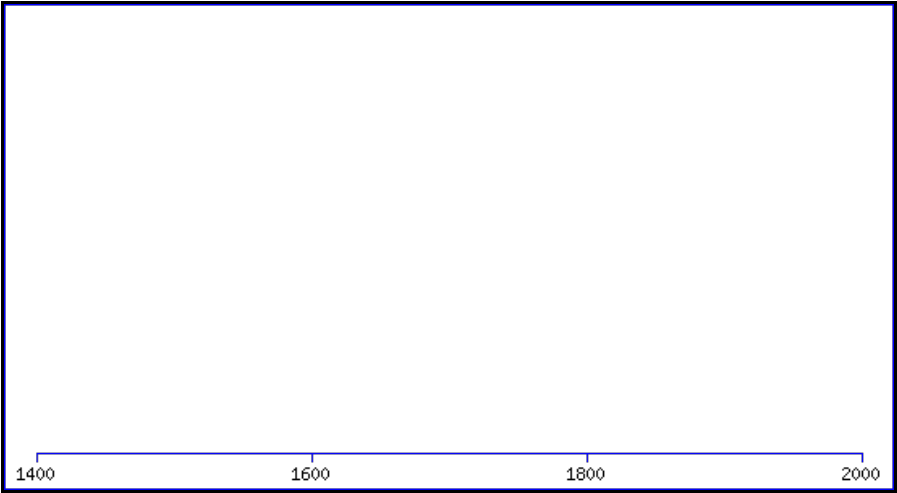
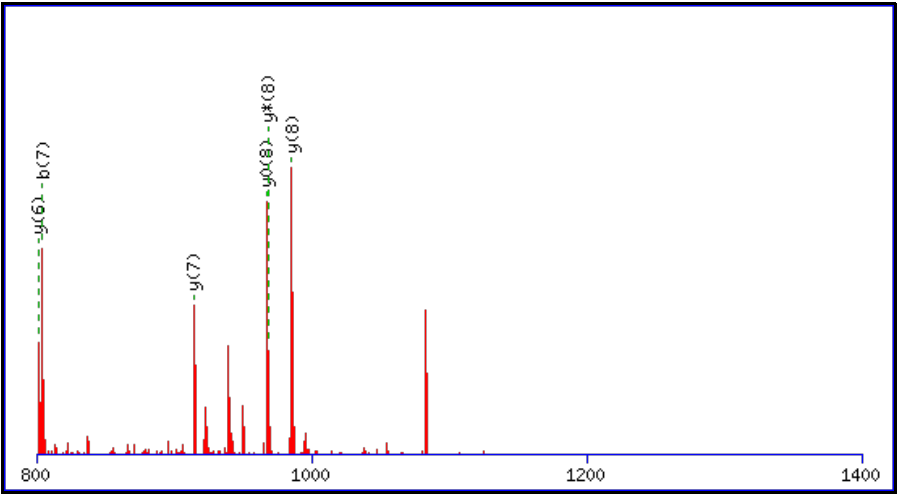
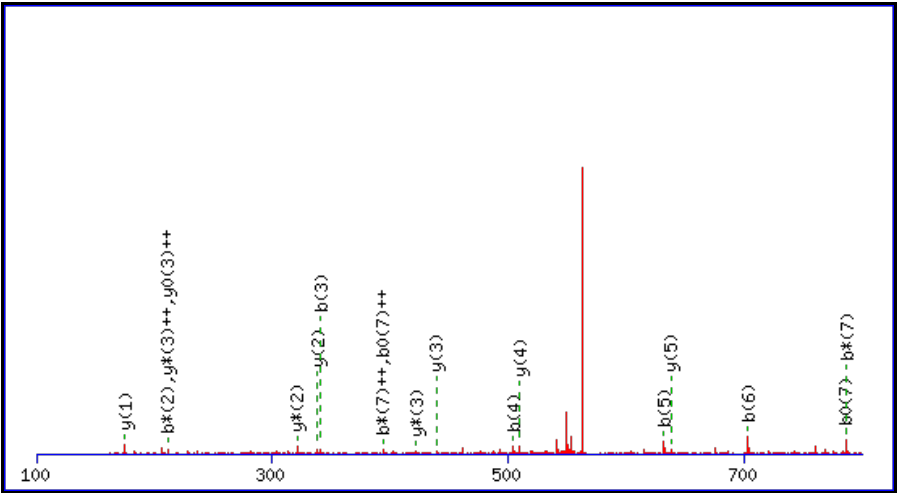
Spectrum No: 39; Query: 5936; Rank: 1

Peptide View

MS/MS Fragmentation of **RAIYQATYR**
Found in **IPI00479306**, Tax_Id=9606 Gene_Symbol=PSMB5 Proteasome subunit beta type-5

Match to Query 5936: 1140.607388 from(571.310970,2+)

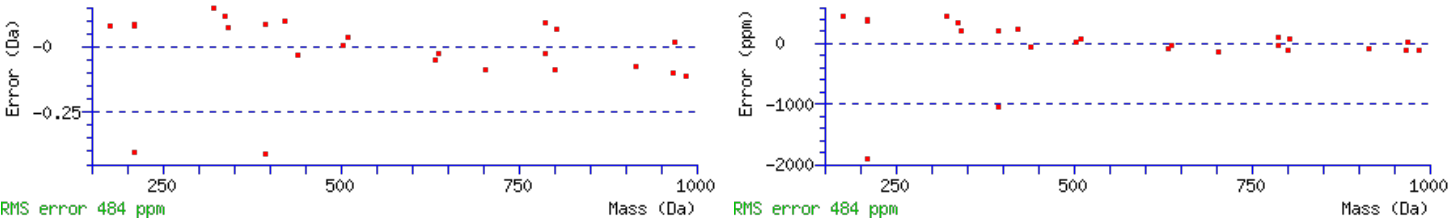
Title: 091224LimSK_Exosome3_07.561.561.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1140.6040
Fixed modifications: Carbamidomethyl (C)
Ions Score: 39 Expect: 0.013
Matches (Bold Red): 25/80 fragment ions using 50 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							9
2	228.1455	114.5764	211.1190	106.0631			A	985.5102	493.2587	968.4836	484.7454	967.4996	484.2534	8
3	341.2296	171.1184	324.2030	162.6051			I	914.4730	457.7402	897.4465	449.2269	896.4625	448.7349	7
4	504.2929	252.6501	487.2663	244.1368			Y	801.3890	401.1981	784.3624	392.6849	783.3784	392.1928	6

5	632.3515	316.6794	615.3249	308.1661			Q	638.3257	319.6665	621.2991	311.1532	620.3151	310.6612	5
6	703.3886	352.1979	686.3620	343.6847			A	510.2671	255.6372	493.2405	247.1239	492.2565	246.6319	4
7	804.4363	402.7218	787.4097	394.2085	786.4257	393.7165	T	439.2300	220.1186	422.2034	211.6053	421.2194	211.1133	3
8	967.4996	484.2534	950.4730	475.7402	949.4890	475.2482	Y	338.1823	169.5948	321.1557	161.0815			2
9							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

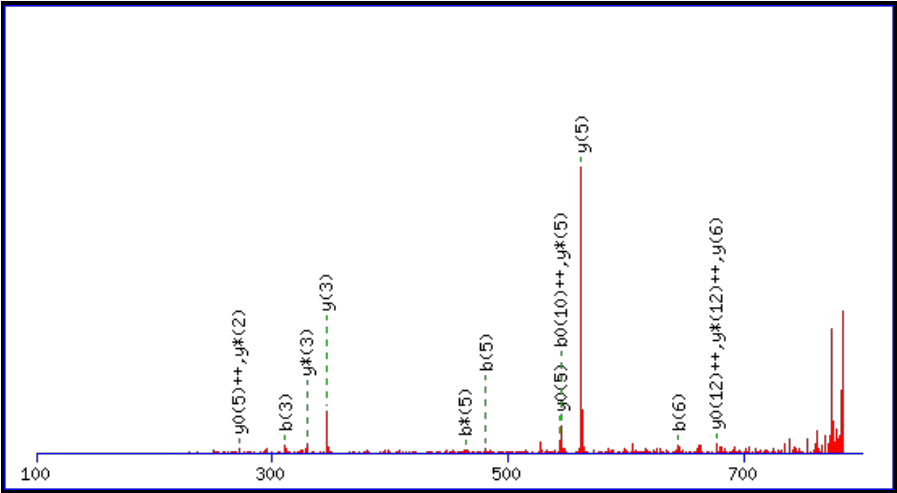
Score	Mr(calc):	Delta	Sequence
39.4	1140.6040	0.0034	RAIYQATYR
23.1	1138.6095	1.9979	GPGKPLQEGTR
12.8	1139.6087	0.9987	LLXPPPGNYR
9.0	1140.5961	0.0113	YSSQIMLKR
8.9	1139.5975	1.0099	GDYLKELER
7.8	1140.6179	-0.0105	LIIEYAYTR
6.0	1139.6087	0.9986	GPQGPPPAGLLH
5.2	1139.6104	0.9970	KILVFPSR
4.8	1139.6047	1.0027	GKEGSALSHVR
4.7	1140.5961	0.0113	IAPGLPGCQTK

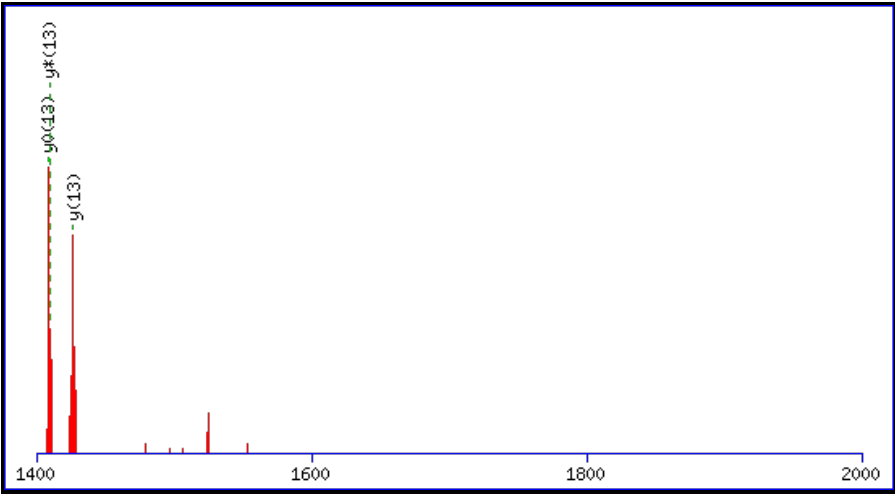
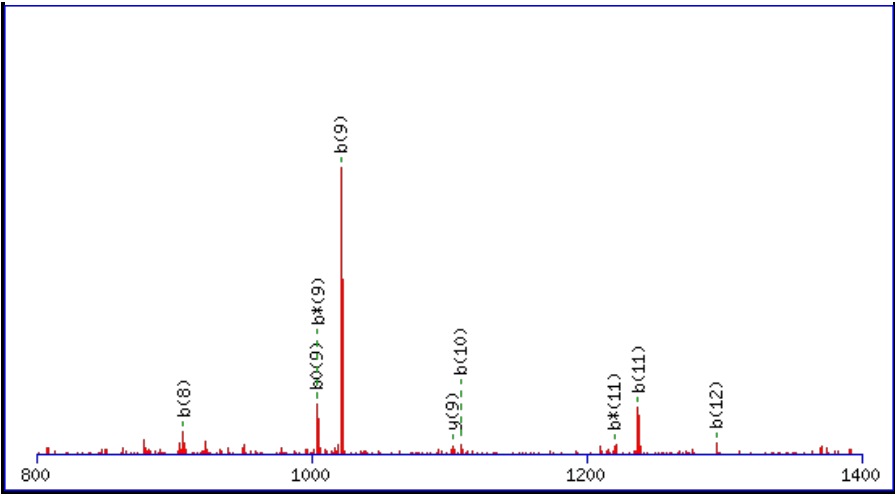
Spectrum No: 40; Query: 24678; Rank: 1

Peptide View

MS/MS Fragmentation of **RGPGLYYVDSEGNR**
Found in **IPI00479306**, Tax_Id=9606 Gene_Symbol=PSMB5 Proteasome subunit beta type-5

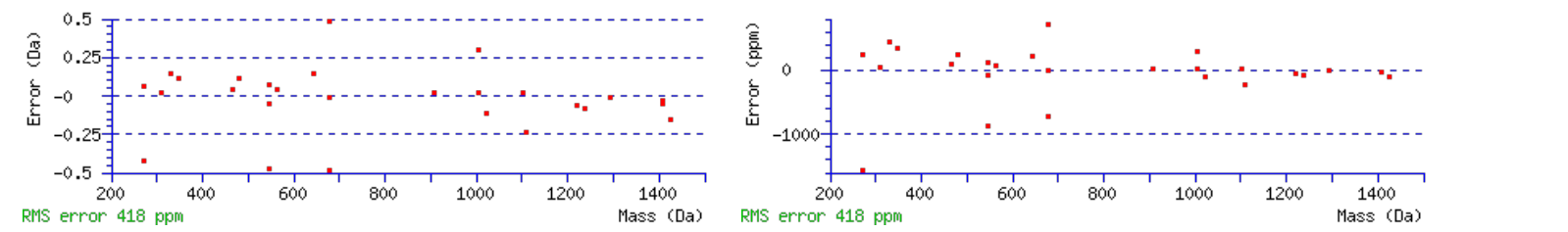
Match to Query 24678: 1581.765588 from(791.890070,2+)
Title: 091224LimSK_Exosome3_07.1767.1767.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1581.7536
Fixed modifications: Carbamidomethyl (C)
Ions Score: 58 Expect: 0.00031
Matches (Bold Red): 28/134 fragment ions using 57 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							14
2	214.1299	107.5686	197.1033	99.0553			G	1426.6597	713.8335	1409.6332	705.3202	1408.6492	704.8282	13
3	311.1826	156.0949	294.1561	147.5817			P	1369.6383	685.3228	1352.6117	676.8095	1351.6277	676.3175	12
4	368.2041	184.6057	351.1775	176.0924			G	1272.5855	636.7964	1255.5590	628.2831	1254.5749	627.7911	11
5	481.2881	241.1477	464.2616	232.6344			L	1215.5640	608.2857	1198.5375	599.7724	1197.5535	599.2804	10
6	644.3515	322.6794	627.3249	314.1661			Y	1102.4800	551.7436	1085.4534	543.2304	1084.4694	542.7383	9
7	807.4148	404.2110	790.3883	395.6978			Y	939.4166	470.2120	922.3901	461.6987	921.4061	461.2067	8
8	906.4832	453.7452	889.4567	445.2320			V	776.3533	388.6803	759.3268	380.1670	758.3428	379.6750	7
9	1021.5102	511.2587	1004.4836	502.7454	1003.4996	502.2534	D	677.2849	339.1461	660.2584	330.6328	659.2743	330.1408	6
10	1108.5422	554.7747	1091.5156	546.2615	1090.5316	545.7694	S	562.2580	281.6326	545.2314	273.1193	544.2474	272.6273	5
11	1237.5848	619.2960	1220.5582	610.7828	1219.5742	610.2907	E	475.2259	238.1166	458.1994	229.6033	457.2154	229.1113	4
12	1294.6062	647.8068	1277.5797	639.2935	1276.5957	638.8015	G	346.1833	173.5953	329.1568	165.0820			3
13	1408.6492	704.8282	1391.6226	696.3149	1390.6386	695.8229	N	289.1619	145.0846	272.1353	136.5713			2
14							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

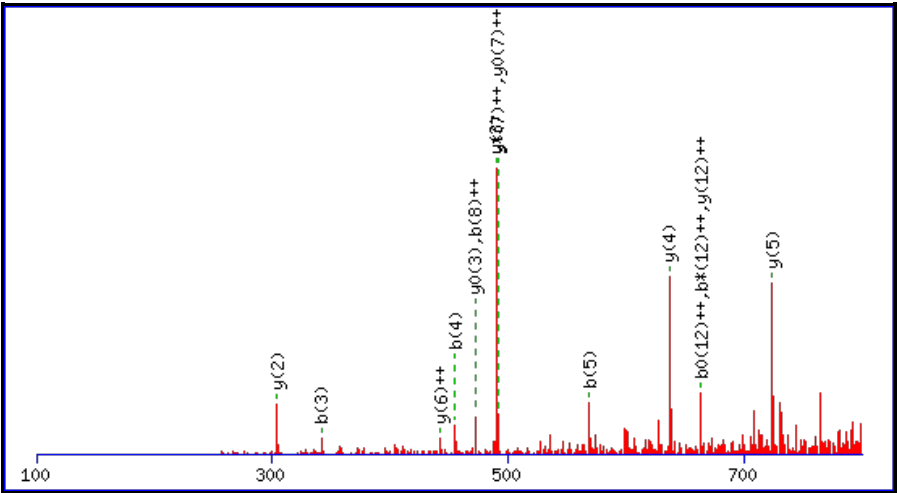
Score	Mr(calc):	Delta	Sequence
57.8	1581.7536	0.0120	RGPGLYYVDSEGNR
10.4	1581.7651	0.0005	SLPPSDSKKTVESK
10.4	1581.7651	0.0005	XLPPSDSKKTVESK
9.8	1581.7651	0.0005	SLPPSDSKKTVESK
9.8	1581.7651	0.0005	XLPPSDSKKTVESK
7.2	1580.7534	1.0121	GGMIVDPLRSGEPR
6.6	1581.7569	0.0087	ECGKSFSSLGNLQR
3.2	1579.7743	1.9913	GNSLWGFEKAGSSNQK
2.7	1581.7810	-0.0154	MVAAAAATEARLRR
2.4	1581.7722	-0.0066	HPWLQDEDMKRK

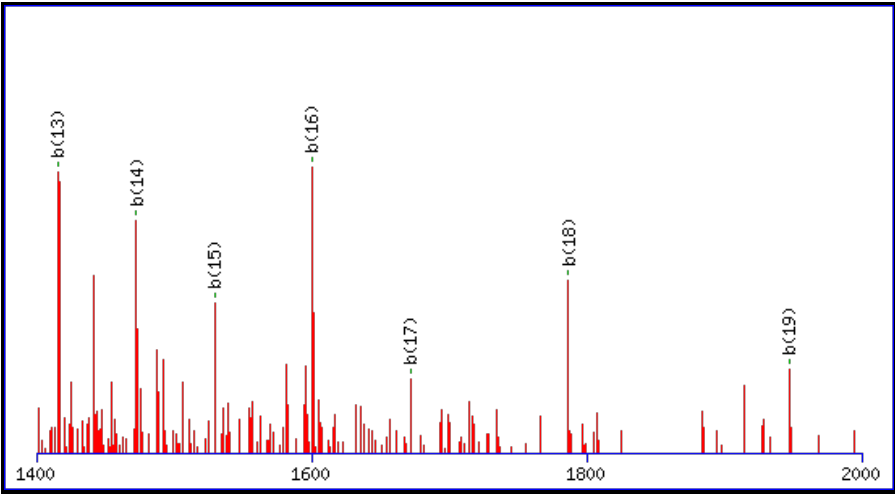
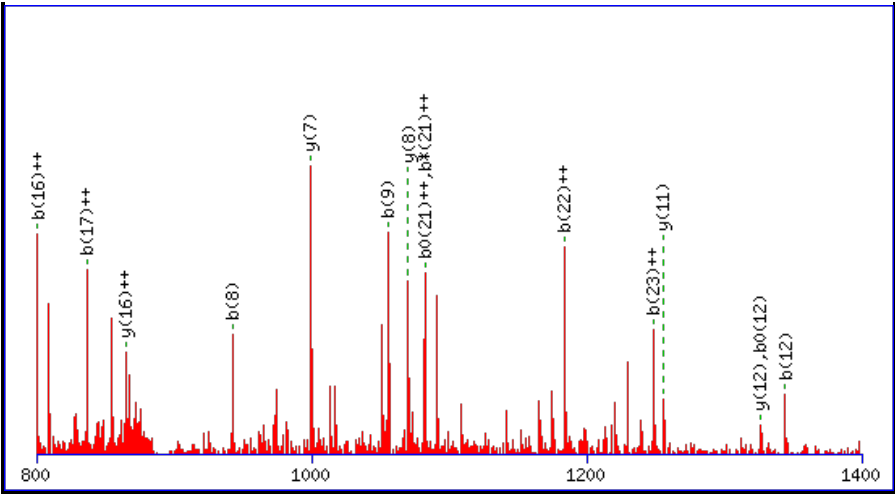
Spectrum No: 41; Query: 59664; Rank: 1

Peptide View

MS/MS Fragmentation of **VIEINPYLLGTMAGGAADCSFWER**
Found in **IP100383971**, Tax_Id=9606 Gene_Symbol=PSMB5 proteasome beta 5 subunit isoform 3

Match to Query 59664: 2669.281422 from(890.767750,3+)
Title: 091224LimSK_Exosome3_07.8862.8862.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

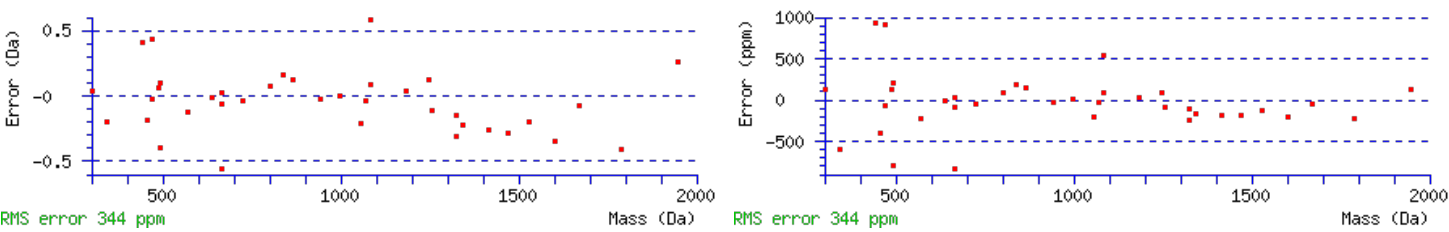




Monoisotopic mass of neutral peptide Mr(calc): 2669.2618
Fixed modifications: Carbamidomethyl (C)
Ions Score: 105 Expect: 8.9e-009
Matches (Bold Red): 37/262 fragment ions using 42 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							24
2	213.1598	107.0835					I	2571.2007	1286.1040	2554.1741	1277.5907	2553.1901	1277.0987	23
3	342.2023	171.6048			324.1918	162.5995	E	2458.1166	1229.5619	2441.0900	1221.0487	2440.1060	1220.5567	22
4	455.2864	228.1468			437.2758	219.1416	I	2329.0740	1165.0406	2312.0475	1156.5274	2311.0634	1156.0354	21
5	569.3293	285.1683	552.3028	276.6550	551.3188	276.1630	N	2215.9899	1108.4986	2198.9634	1099.9853	2197.9794	1099.4933	20
6	666.3821	333.6947	649.3556	325.1814	648.3715	324.6894	P	2101.9470	1051.4771	2084.9205	1042.9639	2083.9364	1042.4719	19
7	829.4454	415.2264	812.4189	406.7131	811.4349	406.2211	Y	2004.8942	1002.9508	1987.8677	994.4375	1986.8837	993.9455	18
8	942.5295	471.7684	925.5029	463.2551	924.5189	462.7631	L	1841.8309	921.4191	1824.8044	912.9058	1823.8204	912.4138	17
9	1055.6136	528.3104	1038.5870	519.7971	1037.6030	519.3051	L	1728.7469	864.8771	1711.7203	856.3638	1710.7363	855.8718	16
10	1112.6350	556.8211	1095.6085	548.3079	1094.6245	547.8159	G	1615.6628	808.3350	1598.6362	799.8218	1597.6522	799.3298	15
11	1213.6827	607.3450	1196.6562	598.8317	1195.6721	598.3397	T	1558.6413	779.8243	1541.6148	771.3110	1540.6308	770.8190	14
12	1344.7232	672.8652	1327.6966	664.3520	1326.7126	663.8599	M	1457.5936	729.3005	1440.5671	720.7872	1439.5831	720.2952	13
13	1415.7603	708.3838	1398.7338	699.8705	1397.7497	699.3785	A	1326.5532	663.7802	1309.5266	655.2669	1308.5426	654.7749	12
14	1472.7818	736.8945	1455.7552	728.3812	1454.7712	727.8892	G	1255.5160	628.2617	1238.4895	619.7484	1237.5055	619.2564	11
15	1529.8032	765.4053	1512.7767	756.8920	1511.7927	756.4000	G	1198.4946	599.7509	1181.4680	591.2377	1180.4840	590.7456	10
16	1600.8403	800.9238	1583.8138	792.4105	1582.8298	791.9185	A	1141.4731	571.2402	1124.4466	562.7269	1123.4626	562.2349	9
17	1671.8775	836.4424	1654.8509	827.9291	1653.8669	827.4371	A	1070.4360	535.7216	1053.4095	527.2084	1052.4254	526.7164	8
18	1786.9044	893.9558	1769.8779	885.4426	1768.8938	884.9506	D	999.3989	500.2031	982.3723	491.6898	981.3883	491.1978	7
19	1946.9350	973.9712	1929.9085	965.4579	1928.9245	964.9659	C	884.3719	442.6896	867.3454	434.1763	866.3614	433.6843	6

20	2033.9671	1017.4872	2016.9405	1008.9739	2015.9565	1008.4819	S	724.3413	362.6743	707.3148	354.1610	706.3307	353.6690	5
21	2181.0355	1091.0214	2164.0089	1082.5081	2163.0249	1082.0161	F	637.3093	319.1583	620.2827	310.6450	619.2987	310.1530	4
22	2367.1148	1184.0610	2350.0883	1175.5478	2349.1042	1175.0558	W	490.2409	245.6241	473.2143	237.1108	472.2303	236.6188	3
23	2496.1574	1248.5823	2479.1308	1240.0691	2478.1468	1239.5771	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
24							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

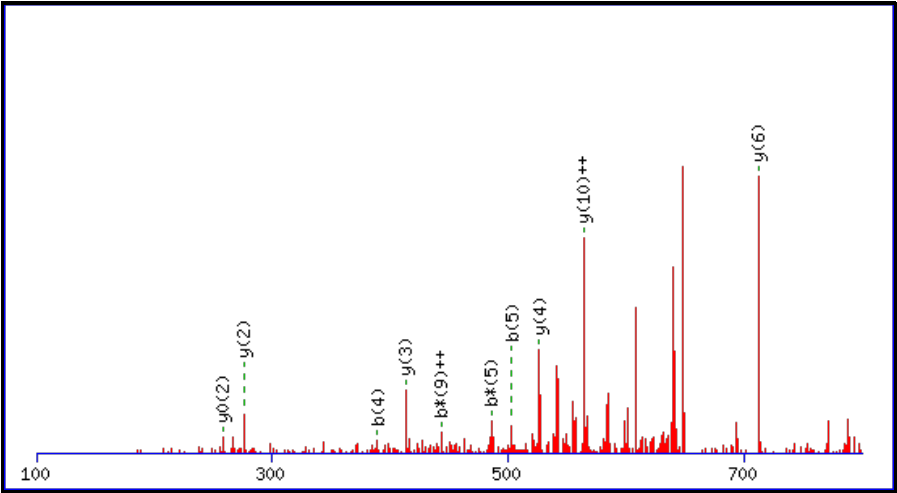
Score	Mr(calc):	Delta	Sequence
104.9	2669.2618	0.0196	VIEINPYLLGTMAGGAADCSFWER
8.1	2667.2727	2.0087	HYTSQELKDECALVPRTLATK
8.1	2667.2727	2.0087	HYTSQELKDECALVPRTLATK
8.1	2669.2840	-0.0026	SPAVPSSLGGRTWSLRALISGGGAR
8.1	2669.2840	-0.0026	SPAVPSSLGGRTWSLRALISGGGAR
8.1	2669.2840	-0.0026	SPAVPSSLGGRTWSLRALISGGGAR
7.6	2667.2808	2.0006	DFILTVSIVIGVGGCWFAYTQNK
6.8	2667.2727	2.0087	HYTSQELKDECALVPRTLATK
6.7	2669.3067	-0.0253	VNLQNNPGAMEHEHMKLFRAQR
5.6	2667.2515	2.0299	SQYLQKFSPELLGKGLAALDGPK

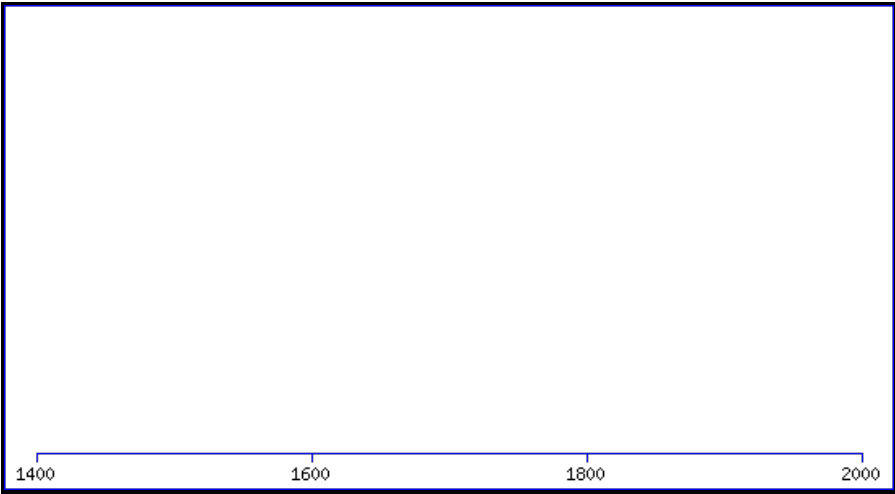
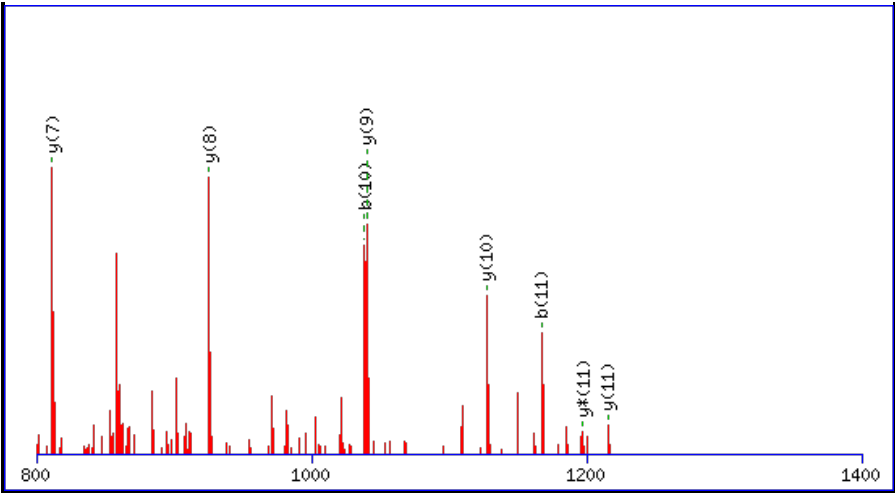
Spectrum No: 42; Query: 11753; Rank: 1

Peptide View

MS/MS Fragmentation of **VSSDNVADLHEK**
Found in **IP100479306**, Tax_Id=9606 Gene_Symbol=PSMB5 Proteasome subunit beta type-5

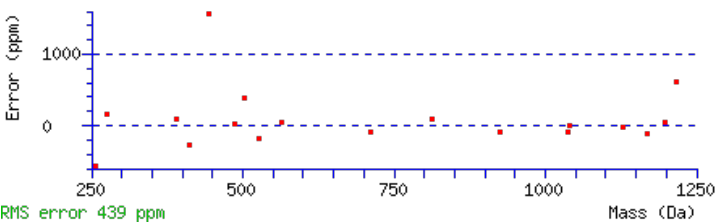
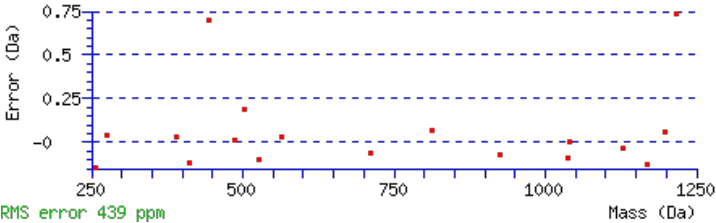
Match to Query 11753: 1312.631088 from(657.322820,2+)
Title: 091224LimSK_Exosome3_07.320.320.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1312.6259
Fixed modifications: Carbamidomethyl (C)
Ions Score: 77 Expect: 3.5e-006
Matches (Bold Red): 18/120 fragment ions using 27 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							12
2	187.1077	94.0575			169.0972	85.0522	S	1214.5648	607.7860	1197.5382	599.2727	1196.5542	598.7807	11
3	274.1397	137.5735			256.1292	128.5682	S	1127.5327	564.2700	1110.5062	555.7567	1109.5222	555.2647	10
4	389.1667	195.0870			371.1561	186.0817	D	1040.5007	520.7540	1023.4742	512.2407	1022.4901	511.7487	9
5	503.2096	252.1084	486.1831	243.5952	485.1991	243.1032	N	925.4738	463.2405	908.4472	454.7272	907.4632	454.2352	8
6	602.2780	301.6427	585.2515	293.1294	584.2675	292.6374	V	811.4308	406.2191	794.4043	397.7058	793.4203	397.2138	7
7	673.3151	337.1612	656.2886	328.6479	655.3046	328.1559	A	712.3624	356.6849	695.3359	348.1716	694.3519	347.6796	6
8	788.3421	394.6747	771.3155	386.1614	770.3315	385.6694	D	641.3253	321.1663	624.2988	312.6530	623.3148	312.1610	5
9	901.4262	451.2167	884.3996	442.7034	883.4156	442.2114	L	526.2984	263.6528	509.2718	255.1396	508.2878	254.6475	4
10	1038.4851	519.7462	1021.4585	511.2329	1020.4745	510.7409	H	413.2143	207.1108	396.1878	198.5975	395.2037	198.1055	3
11	1167.5277	584.2675	1150.5011	575.7542	1149.5171	575.2622	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
12							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

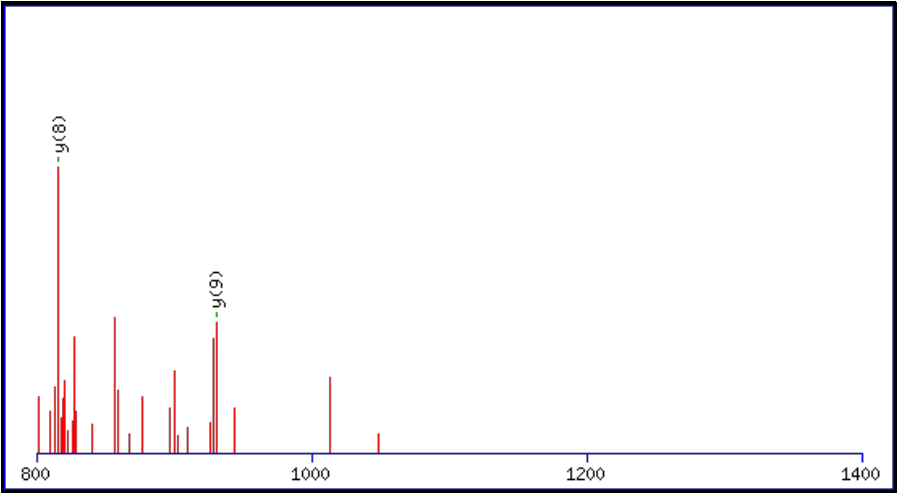
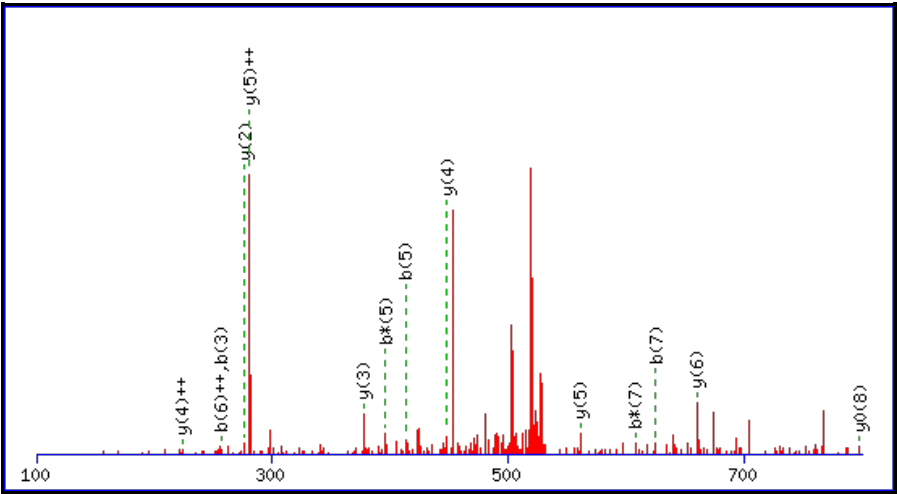
Score	Mr(calc):	Delta	Sequence
76.7	1312.6259	0.0052	VSSDNVADLHEK
17.2	1312.6372	-0.0061	VTGSAGTTEPHTR
13.4	1312.6388	-0.0077	SGTSATLGITGLR
13.1	1310.6272	2.0039	NSTAWLLLGIS
9.8	1312.6388	-0.0077	SVKNSITQQTK
9.2	1312.6340	-0.0029	SVRMASRMTR
8.7	1312.6306	0.0005	EGRLOQGNMHK
8.4	1312.6411	-0.0100	EIEQSWKHEK
7.5	1312.6349	-0.0038	VSSMPIELLTK
7.4	1312.6428	-0.0117	GAFLDKPKTEK

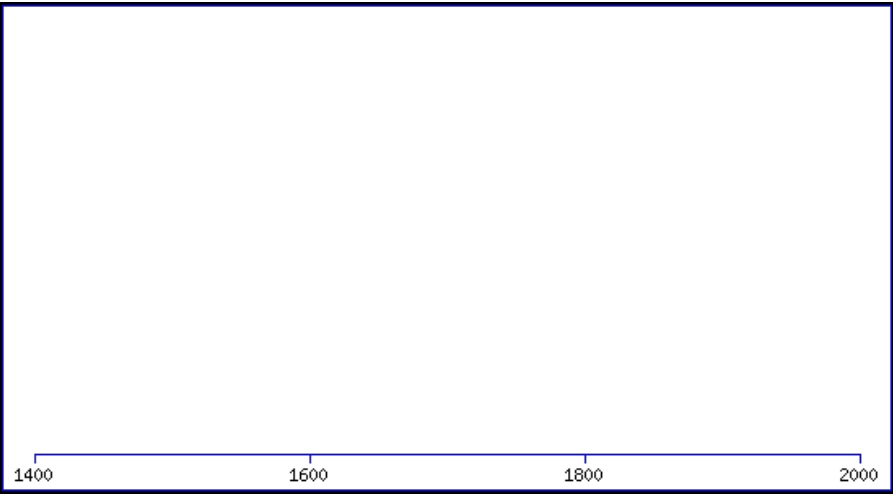
Spectrum No: 43; Query: 4059; Rank: 1

Peptide View

MS/MS Fragmentation of **AANGVVLATEK**
Found in **IPI00219622**, Tax_Id=9606 Gene_Symbol=PSMA2 Proteasome subunit alpha type-2

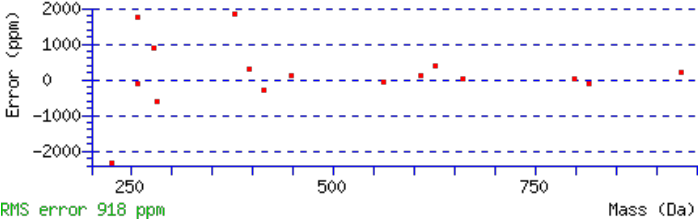
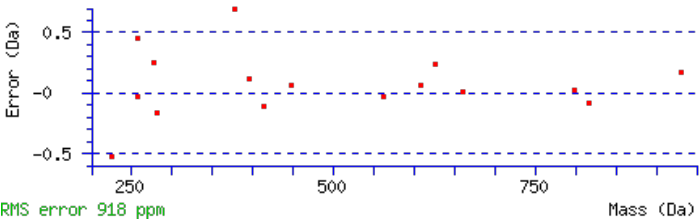
Match to Query 4059: 1071.597168 from(536.805860,2+)
Title: 091224LimSK_Exosome3_06.531.531.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1071.5924
Fixed modifications: Carbamidomethyl (C)
Ions Score: 21 Expect: 0.88
Matches (**Bold Red**): 16/98 fragment ions using 58 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	143.0815	72.0444					A	1001.5626	501.2849	984.5360	492.7717	983.5520	492.2796	10
3	257.1244	129.0659	240.0979	120.5526			N	930.5255	465.7664	913.4989	457.2531	912.5149	456.7611	9
4	314.1459	157.5766	297.1193	149.0633			G	816.4825	408.7449	799.4560	400.2316	798.4720	399.7396	8
5	413.2143	207.1108	396.1878	198.5975			V	759.4611	380.2342	742.4345	371.7209	741.4505	371.2289	7
6	512.2827	256.6450	495.2562	248.1317			V	660.3927	330.7000	643.3661	322.1867	642.3821	321.6947	6
7	625.3668	313.1870	608.3402	304.6738			L	561.3243	281.1658	544.2977	272.6525	543.3137	272.1605	5
8	696.4039	348.7056	679.3774	340.1923			A	448.2402	224.6237	431.2136	216.1105	430.2296	215.6185	4
9	797.4516	399.2294	780.4250	390.7162	779.4410	390.2241	T	377.2031	189.1052	360.1765	180.5919	359.1925	180.0999	3
10	926.4942	463.7507	909.4676	455.2375	908.4836	454.7454	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
11							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

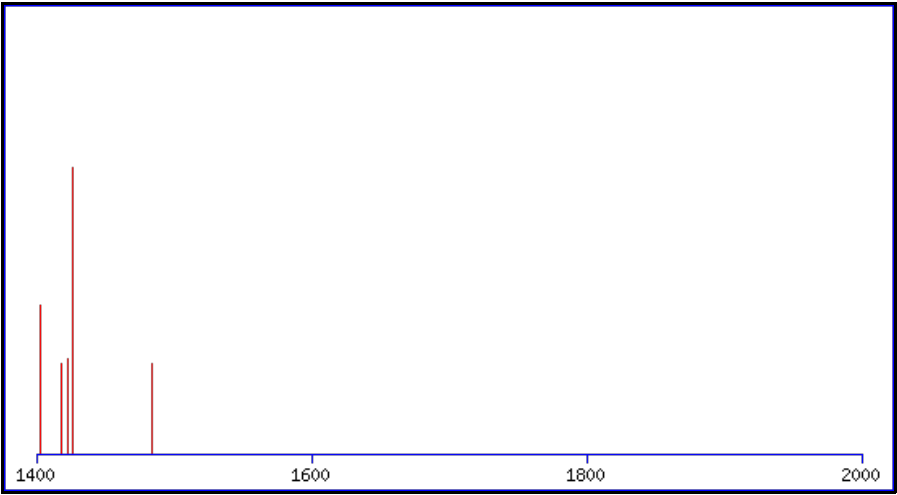
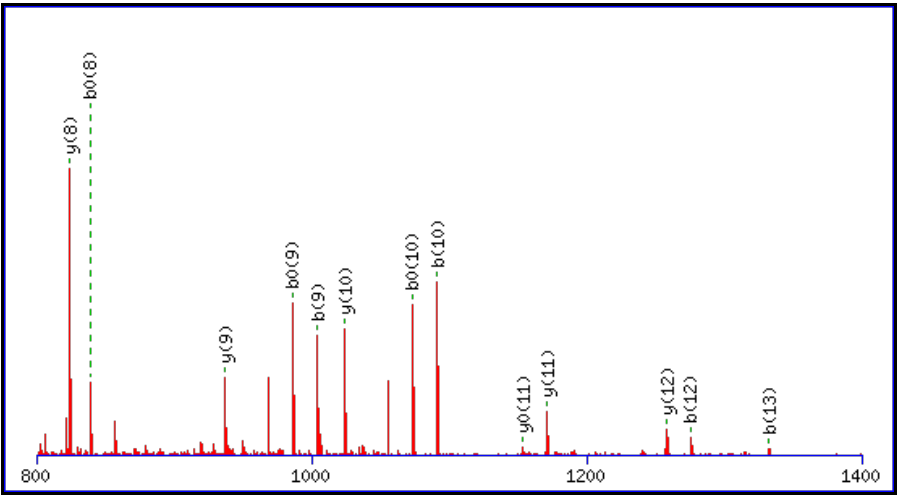
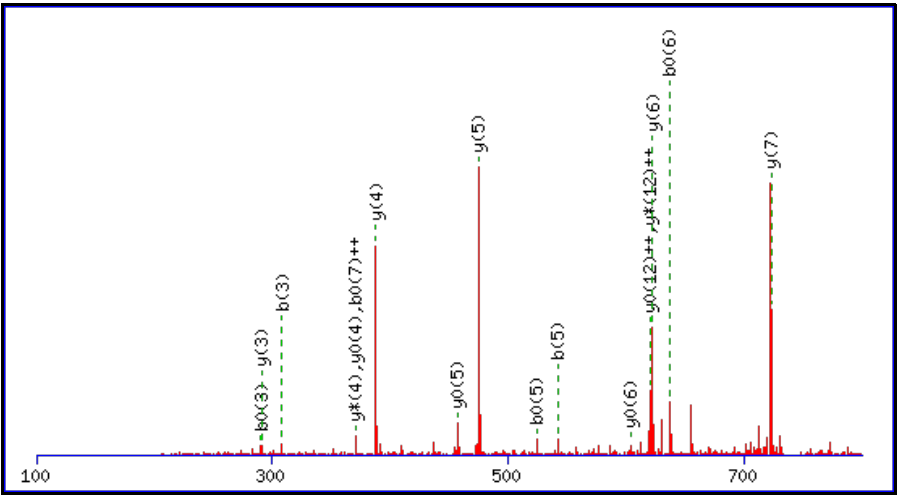
Score	Mr(calc):	Delta	Sequence
20.8	1071.5924	0.0048	AANGVVLATEK

Spectrum No: 44; Query: 19275; Rank: 1

Peptide View

MS/MS Fragmentation of **GYSFSLTTFSPSGK**
Found in **IP100219622**, Tax_Id=9606 Gene_Symbol=PSMA2 Proteasome subunit alpha type-2

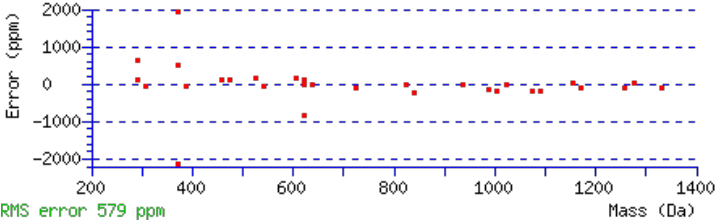
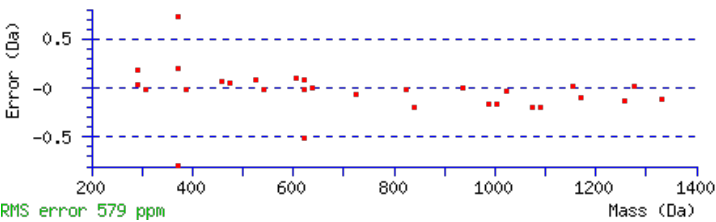
Match to Query 19275: 1477.716268 from(739.865410,2+)
Title: 091224LimSK_Exosome3_06.5477.5477.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1477.7089
Fixed modifications: Carbamidomethyl (C)
Ions Score: 76 Expect: 4.4e-006
Matches (Bold Red): 30/122 fragment ions using 47 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			G							14
2	221.0921	111.0497			Y	1421.6947	711.3510	1404.6682	702.8377	1403.6842	702.3457	13
3	308.1241	154.5657	290.1135	145.5604	S	1258.6314	629.8193	1241.6048	621.3061	1240.6208	620.8141	12
4	455.1925	228.0999	437.1819	219.0946	F	1171.5994	586.3033	1154.5728	577.7900	1153.5888	577.2980	11
5	542.2245	271.6159	524.2140	262.6106	S	1024.5310	512.7691	1007.5044	504.2558	1006.5204	503.7638	10

6	655.3086	328.1579	637.2980	319.1527	L	937.4989	469.2531	920.4724	460.7398	919.4884	460.2478	9
7	756.3563	378.6818	738.3457	369.6765	T	824.4149	412.7111	807.3883	404.1978	806.4043	403.7058	8
8	857.4040	429.2056	839.3934	420.2003	T	723.3672	362.1872	706.3406	353.6740	705.3566	353.1819	7
9	1004.4724	502.7398	986.4618	493.7345	F	622.3195	311.6634	605.2930	303.1501	604.3089	302.6581	6
10	1091.5044	546.2558	1073.4938	537.2506	S	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	5
11	1188.5572	594.7822	1170.5466	585.7769	P	388.2191	194.6132	371.1925	186.0999	370.2085	185.6079	4
12	1275.5892	638.2982	1257.5786	629.2930	S	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
13	1332.6107	666.8090	1314.6001	657.8037	G	204.1343	102.5708	187.1077	94.0575			2
14					K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

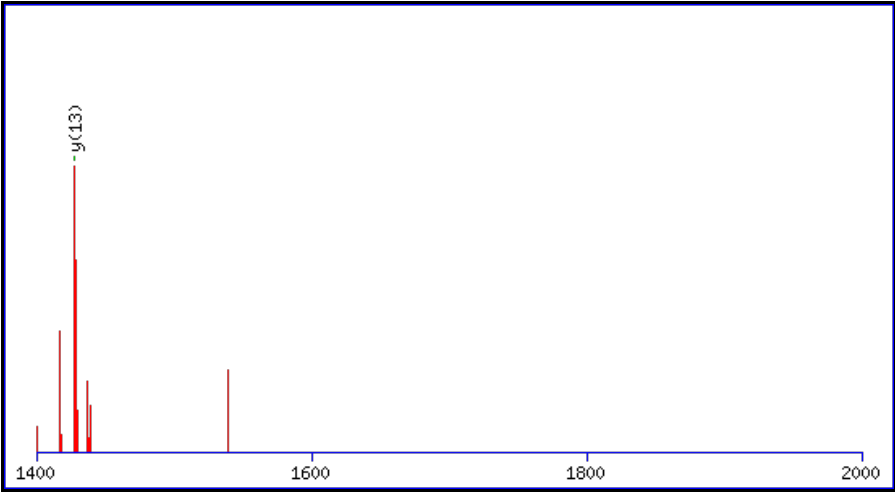
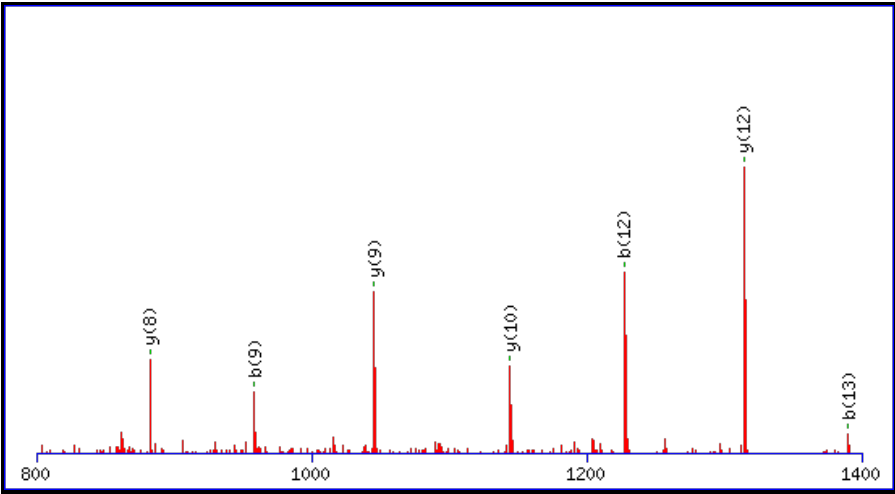
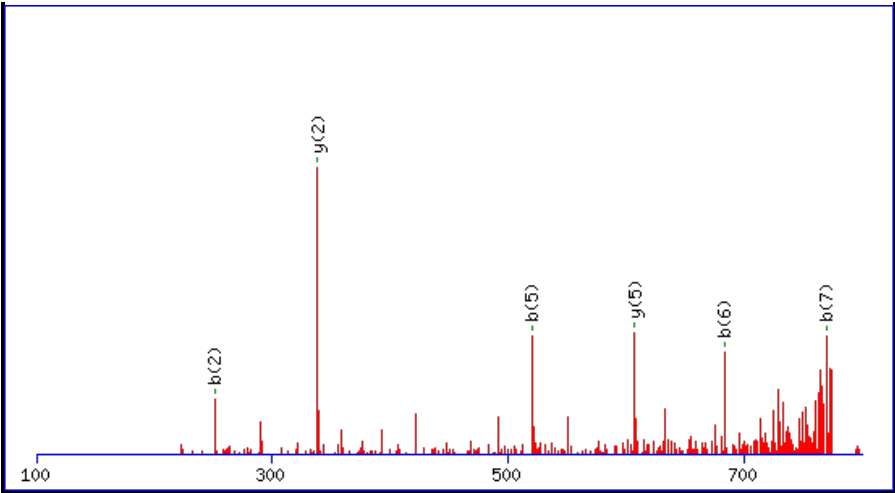
Score	Mr(calc):	Delta	Sequence
76.4	1477.7089	0.0073	GYSESLTTESPSGK
12.0	1475.7061	2.0101	VKFASLEFSPGSK
7.1	1477.7040	0.0122	VLLSFGKAFECK
6.1	1477.7040	0.0123	GYLQMSPLFKAK
5.7	1477.7290	-0.0127	RSSLPNGEGLQLK
5.7	1477.7290	-0.0127	RSSLPNGEGLQLK
5.4	1477.7112	0.0050	MLLAPPSTPSRGR
5.4	1477.7112	0.0050	MLLAPPSTPSRGR
4.6	1477.7040	0.0122	YGAICGFGLSLIK
3.8	1476.7143	1.0019	MAAPSDGFKPRER

Spectrum No: 45; Query: 23954; Rank: 1

Peptide View

MS/MS Fragmentation of **HIGLVYSGMGPDYR**
Found in **IP100219622**, Tax_Id=9606 Gene_Symbol=PSMA2 Proteasome subunit alpha type-2

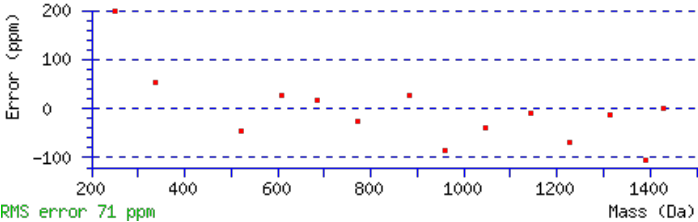
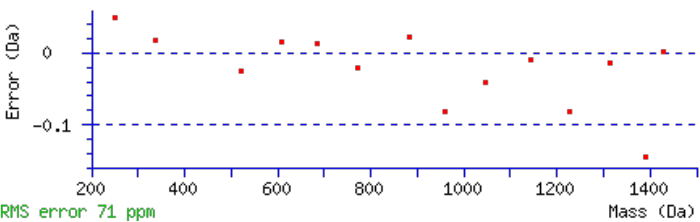
Match to Query 23954: 1563.760388 from(782.887470,2+)
Title: 091224LimSK_Exosome3_06.3980.3980.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1563.7504
Fixed modifications: Carbamidomethyl (C)
Ions Score: 72 Expect: 1.3e-005
Matches (**Bold Red**): 14/114 fragment ions using 19 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	138.0662	69.5367			H							14
2	251.1503	126.0788			I	1427.6988	714.3530	1410.6722	705.8397	1409.6882	705.3477	13
3	308.1717	154.5895			G	1314.6147	657.8110	1297.5882	649.2977	1296.6041	648.8057	12
4	421.2558	211.1315			L	1257.5932	629.3003	1240.5667	620.7870	1239.5827	620.2950	11
5	520.3242	260.6657			V	1144.5092	572.7582	1127.4826	564.2449	1126.4986	563.7529	10
6	683.3875	342.1974			Y	1045.4408	523.2240	1028.4142	514.7107	1027.4302	514.2187	9

7	770.4196	385.7134	752.4090	376.7081	S	882.3774	441.6924	865.3509	433.1791	864.3669	432.6871	8
8	827.4410	414.2241	809.4305	405.2189	G	795.3454	398.1763	778.3189	389.6631	777.3348	389.1711	7
9	958.4815	479.7444	940.4709	470.7391	M	738.3239	369.6656	721.2974	361.1523	720.3134	360.6603	6
10	1015.5030	508.2551	997.4924	499.2498	G	607.2835	304.1454	590.2569	295.6321	589.2729	295.1401	5
11	1112.5557	556.7815	1094.5452	547.7762	P	550.2620	275.6346	533.2354	267.1214	532.2514	266.6293	4
12	1227.5827	614.2950	1209.5721	605.2897	D	453.2092	227.1083	436.1827	218.5950	435.1987	218.1030	3
13	1390.6460	695.8266	1372.6354	686.8214	Y	338.1823	169.5948	321.1557	161.0815			2
14					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

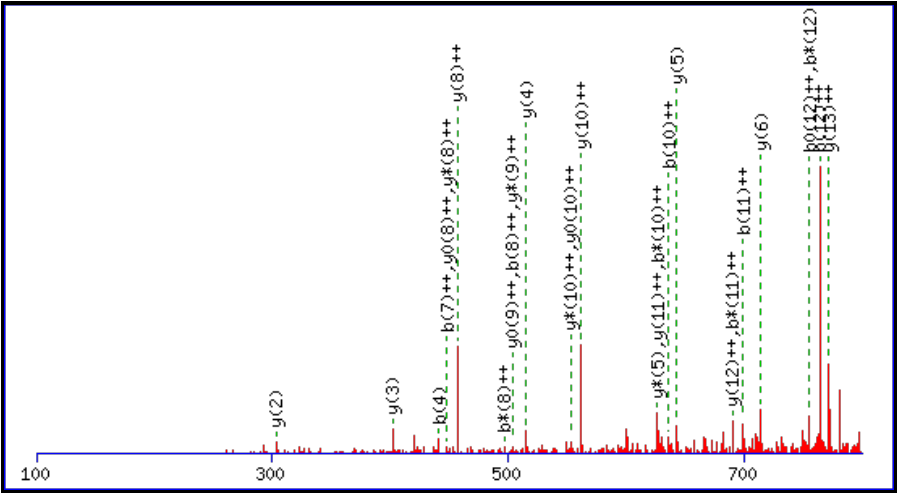
Score	Mr(calc):	Delta	Sequence
71.6	1563.7504	0.0100	HIGLVYSGMGPDYR
9.4	1563.7715	-0.0111	EDFKQMSPGIQR
4.3	1563.7631	-0.0027	RTITHSRLGNSSR
0.3	1563.7586	0.0018	VVEKAKYSLDSVF
0.3	1563.7586	0.0018	VVEKAKYSLDSVF
0.1	1561.7649	1.9955	VILTCTVIYCIK
0.1	1563.7517	0.0087	YIYMHIHSHAHR

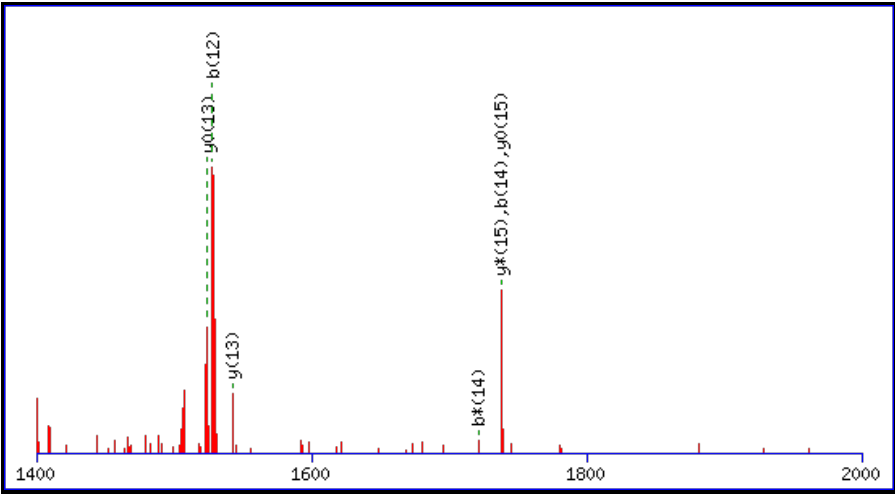
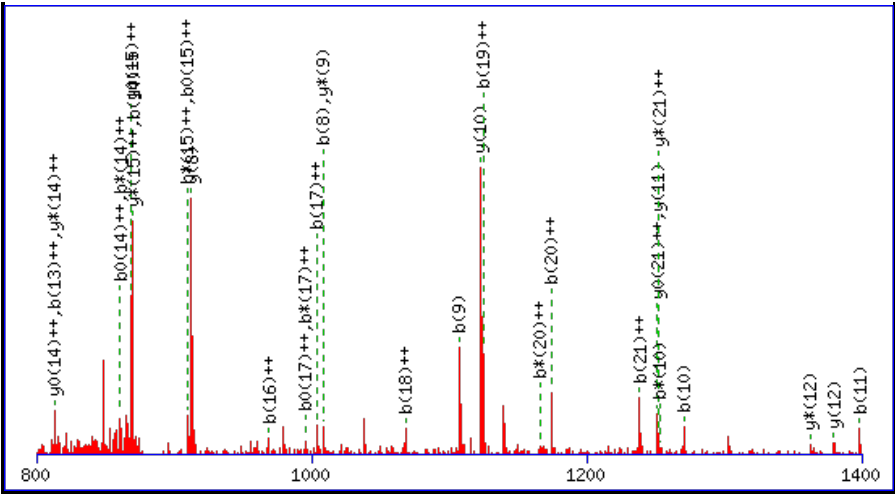
Spectrum No: 46; Query: 59196; Rank: 1

Peptide View

MS/MS Fragmentation of **KLAQQYYLVYQEPIPTAQLVQR**
Found in **IPI00219622**, Tax_Id=9606 Gene_Symbol=PSMA2 Proteasome subunit alpha type-2

Match to Query 59196: 2648.452752 from(883.824860,3+)
Title: 091224LimSK_Exosome3_07.6329.6329.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

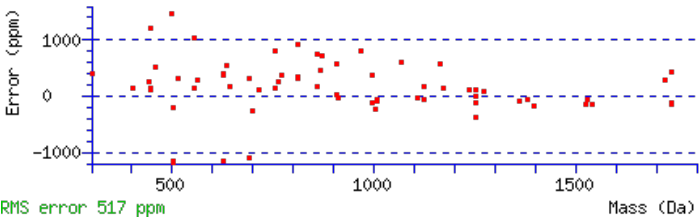
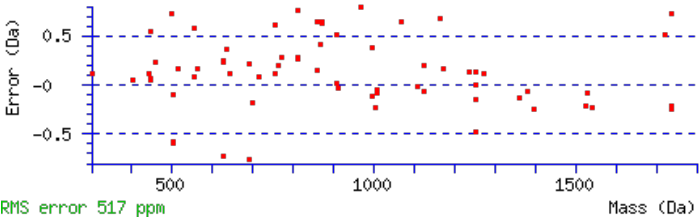




Monoisotopic mass of neutral peptide Mr(calc): 2648.4326
Fixed modifications: Carbamidomethyl (C)
Ions Score: 44 Expect: 0.0018
Matches (Bold Red): 67/218 fragment ions using 128 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							22
2	242.1863	121.5968	225.1598	113.0835			L	2521.3449	1261.1761	2504.3184	1252.6628	2503.3344	1252.1708	21
3	313.2234	157.1153	296.1969	148.6021			A	2408.2609	1204.6341	2391.2343	1196.1208	2390.2503	1195.6288	20
4	441.2820	221.1446	424.2554	212.6314			Q	2337.2238	1169.1155	2320.1972	1160.6022	2319.2132	1160.1102	19
5	569.3406	285.1739	552.3140	276.6607			Q	2209.1652	1105.0862	2192.1386	1096.5730	2191.1546	1096.0809	18
6	732.4039	366.7056	715.3774	358.1923			Y	2081.1066	1041.0569	2064.0801	1032.5437	2063.0960	1032.0517	17
7	895.4672	448.2373	878.4407	439.7240			Y	1918.0433	959.5253	1901.0167	951.0120	1900.0327	950.5200	16
8	1008.5513	504.7793	991.5247	496.2660			L	1754.9799	877.9936	1737.9534	869.4803	1736.9694	868.9883	15
9	1107.6197	554.3135	1090.5932	545.8002			V	1641.8959	821.4516	1624.8693	812.9383	1623.8853	812.4463	14
10	1270.6830	635.8452	1253.6565	627.3319			Y	1542.8275	771.9174	1525.8009	763.4041	1524.8169	762.9121	13
11	1398.7416	699.8744	1381.7151	691.3612			Q	1379.7641	690.3857	1362.7376	681.8724	1361.7536	681.3804	12
12	1527.7842	764.3957	1510.7577	755.8825	1509.7736	755.3905	E	1251.7056	626.3564	1234.6790	617.8431	1233.6950	617.3511	11
13	1624.8370	812.9221	1607.8104	804.4089	1606.8264	803.9168	P	1122.6630	561.8351	1105.6364	553.3218	1104.6524	552.8298	10
14	1737.9210	869.4642	1720.8945	860.9509	1719.9105	860.4589	I	1025.6102	513.3087	1008.5837	504.7955	1007.5996	504.3035	9
15	1834.9738	917.9905	1817.9473	909.4773	1816.9632	908.9853	P	912.5261	456.7667	895.4996	448.2534	894.5156	447.7614	8
16	1936.0215	968.5144	1918.9949	960.0011	1918.0109	959.5091	T	815.4734	408.2403	798.4468	399.7271	797.4628	399.2350	7
17	2007.0586	1004.0329	1990.0320	995.5197	1989.0480	995.0277	A	714.4257	357.7165	697.3992	349.2032			6
18	2135.1172	1068.0622	2118.0906	1059.5489	2117.1066	1059.0569	Q	643.3886	322.1979	626.3620	313.6847			5
19	2248.2012	1124.6043	2231.1747	1116.0910	2230.1907	1115.5990	L	515.3300	258.1686	498.3035	249.6554			4

20	2347.2696	1174.1385	2330.2431	1165.6252	2329.2591	1165.1332	V	402.2459	201.6266	385.2194	193.1133			3
21	2475.3282	1238.1678	2458.3017	1229.6545	2457.3177	1229.1625	Q	303.1775	152.0924	286.1510	143.5791			2
22							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

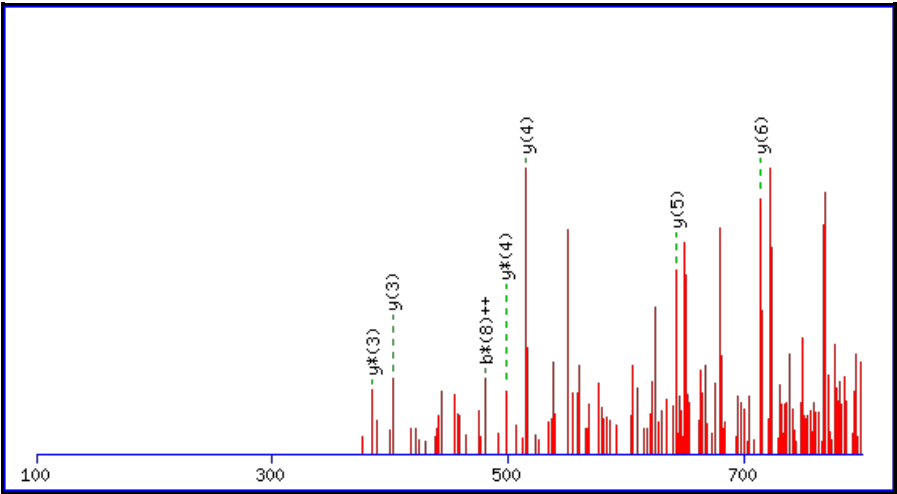
Score	Mr(calc):	Delta	Sequence
43.7	2648.4326	0.0202	KLAQQYYLVYQEPIPTAQLVQR
7.6	2647.4495	1.0033	ISYLMIALTVVGCIEHWLLRAR
4.9	2647.4293	1.0235	GSSDVQELQORIGOLLIHLOEKEK
2.5	2648.4320	0.0208	VTIAELGVQLVAGMSLSLQPHRADK
1.3	2648.4277	0.0250	AHLTGWLMTLKKTFVLAPSSVLR
1.1	2648.4286	0.0242	NALTGILTQFEQIVAVENASTRQK
0.3	2646.4277	2.0250	SSVFLGNSIMSQKFESLILLMLR

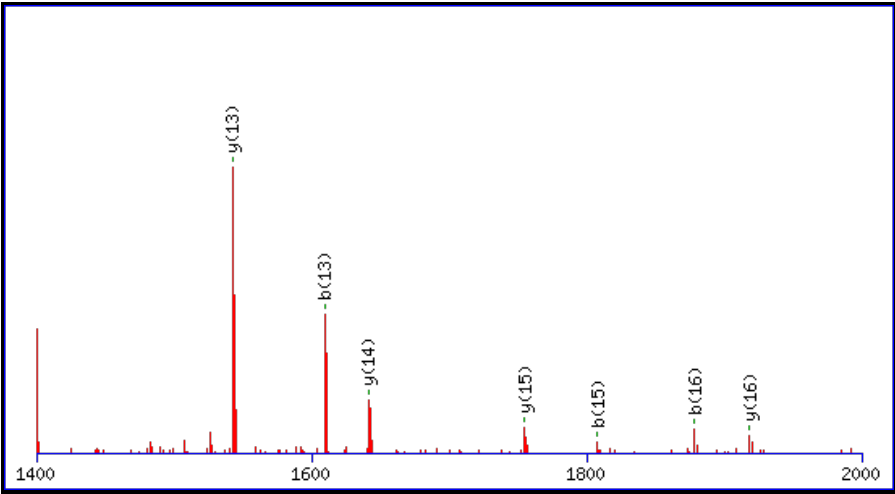
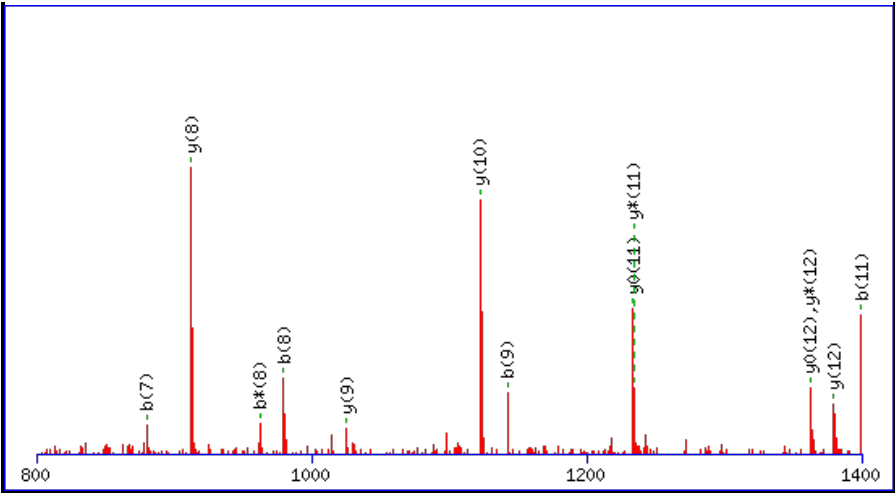
Spectrum No: 47; Query: 56429; Rank: 1

Peptide View

MS/MS Fragmentation of **LAQQYYLVYQEPIPTAQLVQR**
Found in **IP100219622**, Tax_Id=9606 Gene_Symbol=PSMA2 Proteasome subunit alpha type-2

Match to Query 56429: 2520.356868 from(1261.185710,2+)
Title: 091224LimSK_Exosome3_06.6454.6454.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

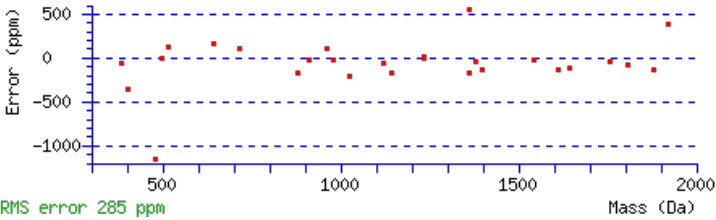
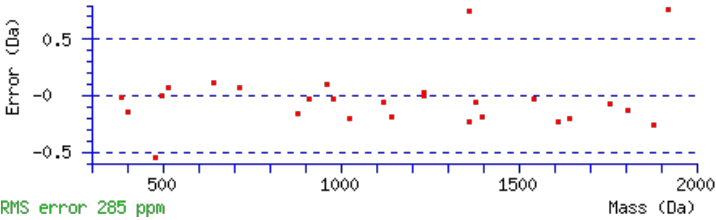




Monoisotopic mass of neutral peptide Mr(calc): 2520.3376
Fixed modifications: Carbamidomethyl (C)
Ions Score: 65 Expect: 2.3e-005
Matches (Bold Red): 27/204 fragment ions using 59 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							21
2	185.1285	93.0679					A	2408.2609	1204.6341	2391.2343	1196.1208	2390.2503	1195.6288	20
3	313.1870	157.0972	296.1605	148.5839			Q	2337.2238	1169.1155	2320.1972	1160.6022	2319.2132	1160.1102	19
4	441.2456	221.1264	424.2191	212.6132			Q	2209.1652	1105.0862	2192.1386	1096.5730	2191.1546	1096.0809	18
5	604.3089	302.6581	587.2824	294.1448			Y	2081.1066	1041.0569	2064.0801	1032.5437	2063.0960	1032.0517	17
6	767.3723	384.1898	750.3457	375.6765			Y	1918.0433	959.5253	1901.0167	951.0120	1900.0327	950.5200	16
7	880.4563	440.7318	863.4298	432.2185			L	1754.9799	877.9936	1737.9534	869.4803	1736.9694	868.9883	15
8	979.5247	490.2660	962.4982	481.7527			V	1641.8959	821.4516	1624.8693	812.9383	1623.8853	812.4463	14
9	1142.5881	571.7977	1125.5615	563.2844			Y	1542.8275	771.9174	1525.8009	763.4041	1524.8169	762.9121	13
10	1270.6467	635.8270	1253.6201	627.3137			Q	1379.7641	690.3857	1362.7376	681.8724	1361.7536	681.3804	12
11	1399.6892	700.3483	1382.6627	691.8350	1381.6787	691.3430	E	1251.7056	626.3564	1234.6790	617.8431	1233.6950	617.3511	11
12	1496.7420	748.8746	1479.7155	740.3614	1478.7314	739.8694	P	1122.6630	561.8351	1105.6364	553.3218	1104.6524	552.8298	10
13	1609.8261	805.4167	1592.7995	796.9034	1591.8155	796.4114	I	1025.6102	513.3087	1008.5837	504.7955	1007.5996	504.3035	9
14	1706.8788	853.9431	1689.8523	845.4298	1688.8683	844.9378	P	912.5261	456.7667	895.4996	448.2534	894.5156	447.7614	8
15	1807.9265	904.4669	1790.9000	895.9536	1789.9160	895.4616	T	815.4734	408.2403	798.4468	399.7271	797.4628	399.2350	7
16	1878.9636	939.9855	1861.9371	931.4722	1860.9531	930.9802	A	714.4257	357.7165	697.3992	349.2032			6
17	2007.0222	1004.0147	1989.9957	995.5015	1989.0116	995.0095	Q	643.3886	322.1979	626.3620	313.6847			5
18	2120.1063	1060.5568	2103.0797	1052.0435	2102.0957	1051.5515	L	515.3300	258.1686	498.3035	249.6554			4
19	2219.1747	1110.0910	2202.1481	1101.5777	2201.1641	1101.0857	V	402.2459	201.6266	385.2194	193.1133			3

20	2347.2333	1174.1203	2330.2067	1165.6070	2329.2227	1165.1150	Q	303.1775	152.0924	286.1510	143.5791			2
21							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

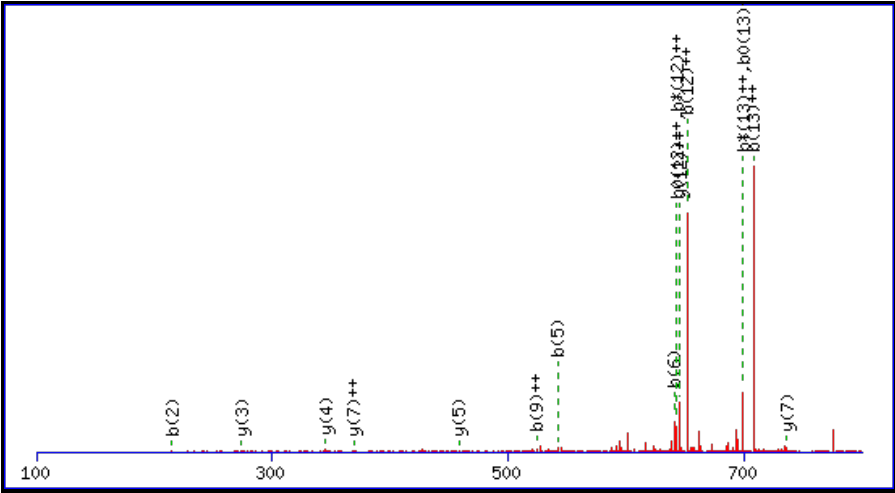
Score	Mr(calc):	Delta	Sequence
65.1	2520.3376	0.0192	LAQOYYLVYQEPIPTAQLVQR
3.2	2518.3501	2.0068	WQLALAVGAPLLLGAGAIYLSR
0.4	2519.3400	1.0168	DLAVVLETAPILTALDIEVDRR

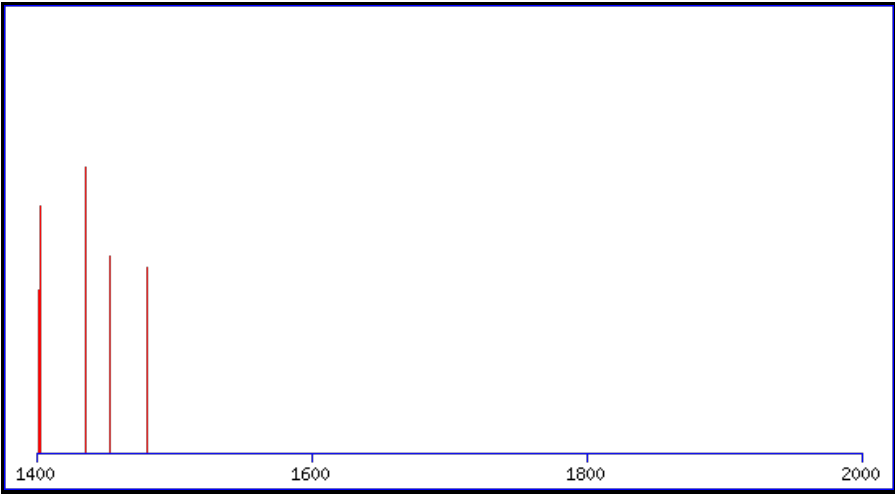
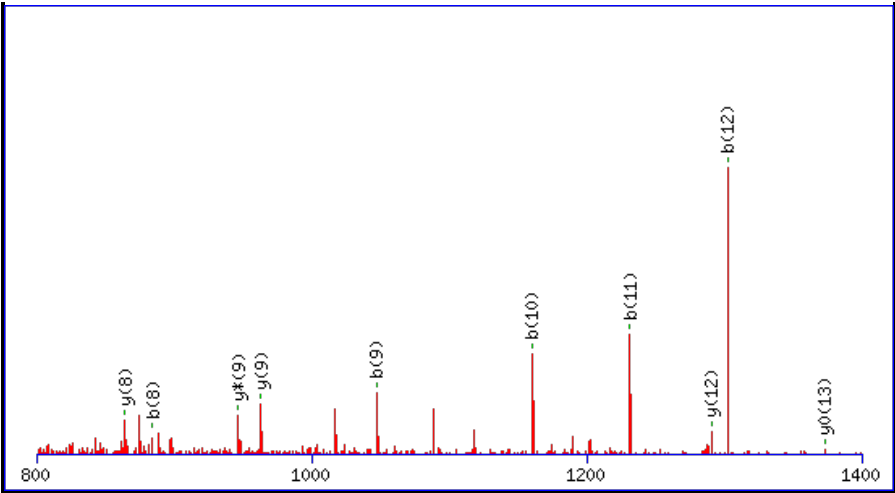
Spectrum No: 48; Query: 20380; Rank: 1

Peptide View

MS/MS Fragmentation of **LTPTEVKDYLA**
Found in **IPI00219622**, Tax_Id=9606 Gene_Symbol=PSMA2 Proteasome subunit alpha type-2

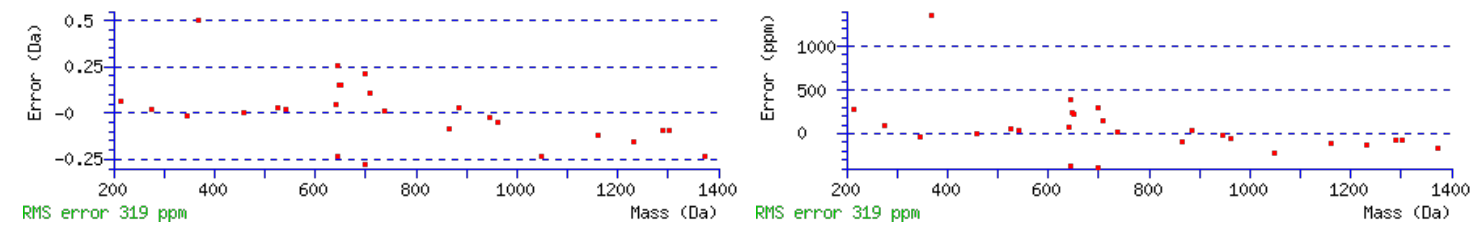
Match to Query 20380: 1503.826388 from(752.920470,2+)
Title: 091224LimSK_Exosome3_06.7667.7667.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1503.8184
Fixed modifications: Carbamidomethyl (C)
Ions Score: 23 Expect: 0.45
Matches (**Bold Red**): 27/116 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							14
2	215.1390	108.0731			197.1285	99.0679	T	1391.7417	696.3745	1374.7151	687.8612	1373.7311	687.3692	13
3	312.1918	156.5995			294.1812	147.5942	P	1290.6940	645.8506	1273.6674	637.3374	1272.6834	636.8454	12
4	413.2395	207.1234			395.2289	198.1181	T	1193.6412	597.3243	1176.6147	588.8110	1175.6307	588.3190	11
5	542.2821	271.6447			524.2715	262.6394	E	1092.5936	546.8004	1075.5670	538.2871	1074.5830	537.7951	10
6	641.3505	321.1789			623.3399	312.1736	V	963.5510	482.2791	946.5244	473.7658	945.5404	473.2738	9
7	769.4454	385.2264	752.4189	376.7131	751.4349	376.2211	K	864.4825	432.7449	847.4560	424.2316	846.4720	423.7396	8
8	884.4724	442.7398	867.4458	434.2266	866.4618	433.7345	D	736.3876	368.6974			718.3770	359.6921	7
9	1047.5357	524.2715	1030.5092	515.7582	1029.5251	515.2662	Y	621.3606	311.1840					6
10	1160.6198	580.8135	1143.5932	572.3002	1142.6092	571.8082	L	458.2973	229.6523					5
11	1231.6569	616.3321	1214.6303	607.8188	1213.6463	607.3268	A	345.2132	173.1103					4
12	1302.6940	651.8506	1285.6674	643.3374	1284.6834	642.8454	A	274.1761	137.5917					3
13	1415.7781	708.3927	1398.7515	699.8794	1397.7675	699.3874	I	203.1390	102.0731					2
14							A	90.0550	45.5311					1



All matches to this query

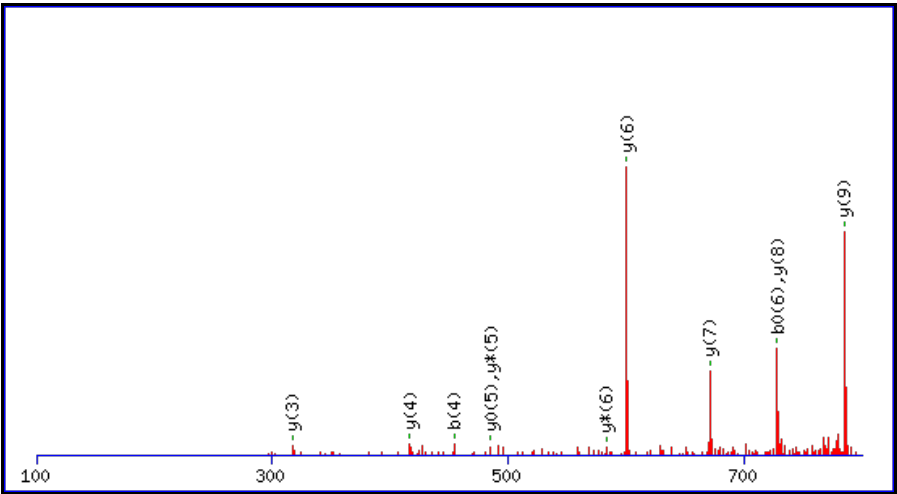
Score	Mr(calc):	Delta	Sequence
23.3	1503.8184	0.0080	LTPTEVKDYLA AIA
2.3	1502.8239	1.0025	SNLREVAQMLKSK
1.9	1501.8286	1.9978	SNIREIEKLCLK
1.2	1501.8075	2.0189	ASLALCAFVAVPQR

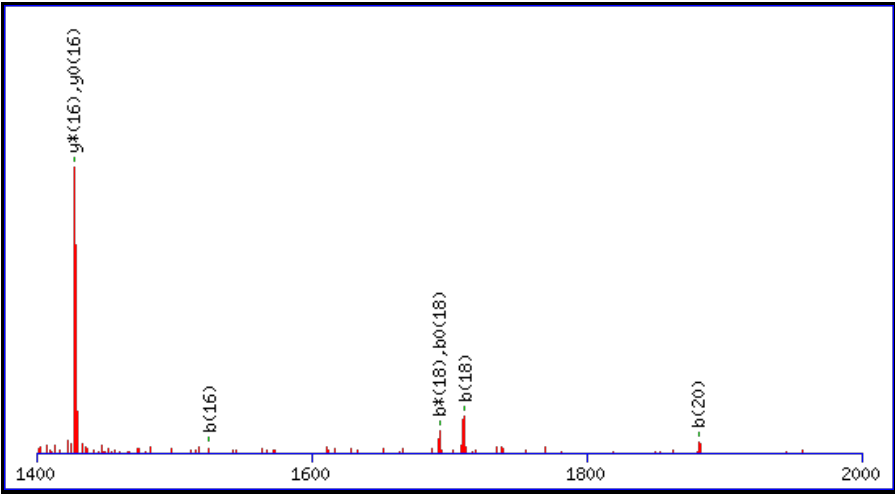
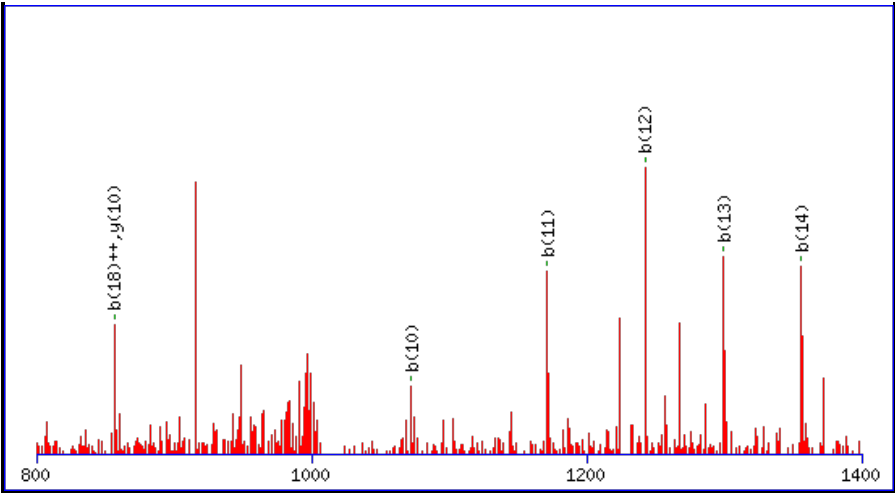
Spectrum No: 49; Query: 40917; Rank: 1

Peptide View

MS/MS Fragmentation of **LVQIEYALAAVAGGAPSVGIK**
Found in **IP100219622**, Tax_Id=9606 Gene_Symbol=PSMA2 Proteasome subunit alpha type-2

Match to Query 40917: 2026.158968 from(1014.086760,2+)
Title: 091224LimSK_Exosome3_06.8096.8096.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

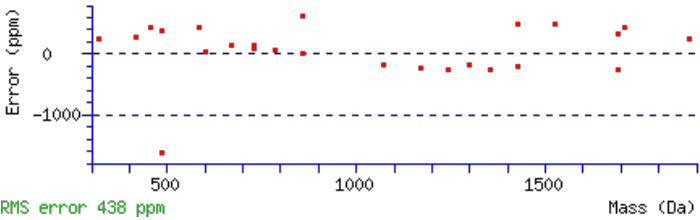
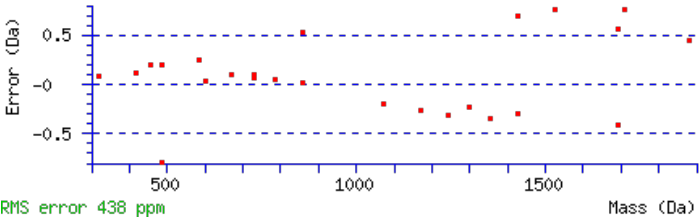




Monoisotopic mass of neutral peptide Mr(calc): 2026.1463
Fixed modifications: Carbamidomethyl (C)
Ions Score: 77 Expect: 5.8e-007
Matches (Bold Red): 27/220 fragment ions using 44 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493					L							21
2	213.1598	107.0835					V	1914.0695	957.5384	1897.0429	949.0251	1896.0589	948.5331	20
3	341.2183	171.1128	324.1918	162.5995			Q	1815.0011	908.0042	1797.9745	899.4909	1796.9905	898.9989	19
4	454.3024	227.6548	437.2758	219.1416			I	1686.9425	843.9749	1669.9160	835.4616	1668.9319	834.9696	18
5	583.3450	292.1761	566.3184	283.6629	565.3344	283.1709	E	1573.8584	787.4329	1556.8319	778.9196	1555.8479	778.4276	17
6	746.4083	373.7078	729.3818	365.1945	728.3978	364.7025	Y	1444.8158	722.9116	1427.7893	714.3983	1426.8053	713.9063	16
7	817.4454	409.2264	800.4189	400.7131	799.4349	400.2211	A	1281.7525	641.3799	1264.7260	632.8666	1263.7419	632.3746	15
8	930.5295	465.7684	913.5029	457.2551	912.5189	456.7631	L	1210.7154	605.8613	1193.6889	597.3481	1192.7048	596.8561	14
9	1001.5666	501.2869	984.5401	492.7737	983.5560	492.2817	A	1097.6313	549.3193	1080.6048	540.8060	1079.6208	540.3140	13
10	1072.6037	536.8055	1055.5772	528.2922	1054.5932	527.8002	A	1026.5942	513.8007	1009.5677	505.2875	1008.5837	504.7955	12
11	1171.6721	586.3397	1154.6456	577.8264	1153.6616	577.3344	V	955.5571	478.2822	938.5306	469.7689	937.5465	469.2769	11
12	1242.7093	621.8583	1225.6827	613.3450	1224.6987	612.8530	A	856.4887	428.7480	839.4621	420.2347	838.4781	419.7427	10
13	1299.7307	650.3690	1282.7042	641.8557	1281.7202	641.3637	G	785.4516	393.2294	768.4250	384.7162	767.4410	384.2241	9
14	1356.7522	678.8797	1339.7256	670.3665	1338.7416	669.8744	G	728.4301	364.7187	711.4036	356.2054	710.4196	355.7134	8
15	1427.7893	714.3983	1410.7627	705.8850	1409.7787	705.3930	A	671.4087	336.2080	654.3821	327.6947	653.3981	327.2027	7
16	1524.8421	762.9247	1507.8155	754.4114	1506.8315	753.9194	P	600.3715	300.6894	583.3450	292.1761	582.3610	291.6841	6
17	1611.8741	806.4407	1594.8475	797.9274	1593.8635	797.4354	S	503.3188	252.1630	486.2922	243.6498	485.3082	243.1577	5
18	1710.9425	855.9749	1693.9160	847.4616	1692.9319	846.9696	V	416.2867	208.6470	399.2602	200.1337			4
19	1767.9640	884.4856	1750.9374	875.9723	1749.9534	875.4803	G	317.2183	159.1128	300.1918	150.5995			3

20	1881.0480	941.0277	1864.0215	932.5144	1863.0375	932.0224	I	260.1969	130.6021	243.1703	122.0888			2
21							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

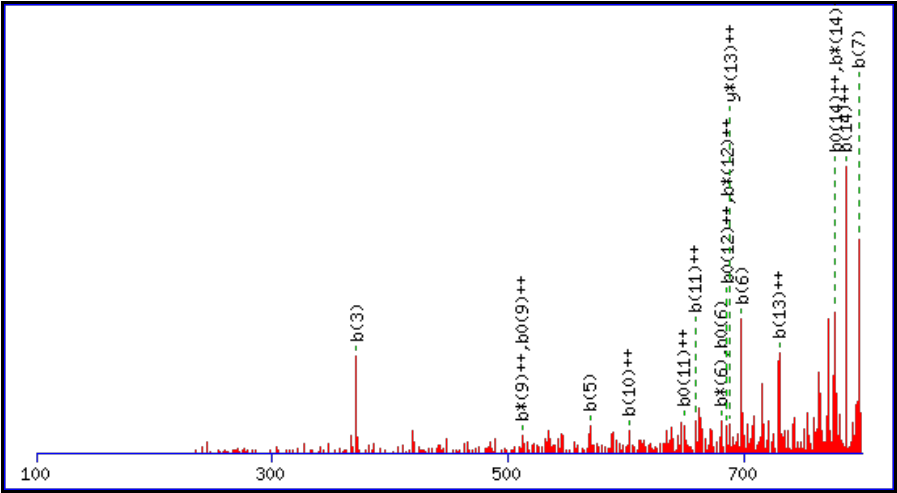
Score	Mr(calc):	Delta	Sequence
77.2	2026.1463	0.0127	LVQIEYALAAVAGGAPSVGIK
11.5	2026.1649	-0.0059	ELIMIAGGNQSILLWIKK
9.5	2026.1575	0.0015	NLVPPKSSSEANVAAATPAIK
4.8	2025.1443	1.0147	GSTAVGIRGLTADARVVINR
2.4	2026.1786	-0.0197	LQTSSVLVSGLRGLGVEIAK
0.3	2025.1735	0.9855	LSPVTYKLQPGNKPSRLK

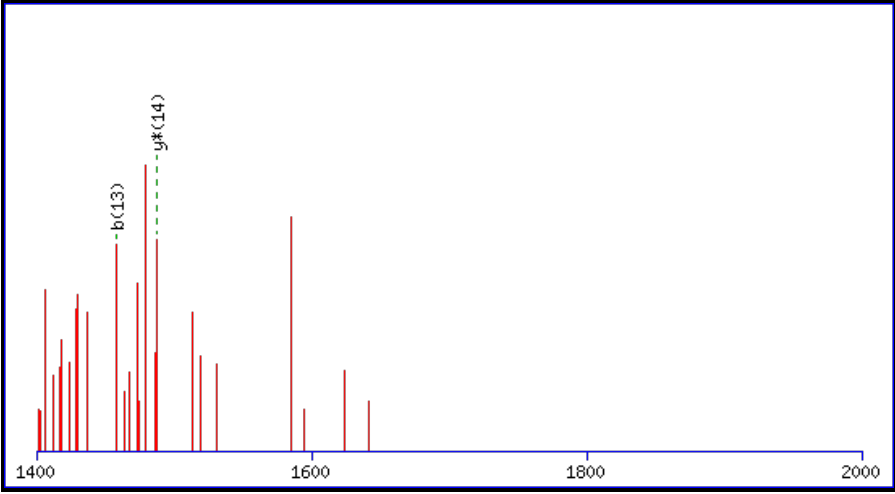
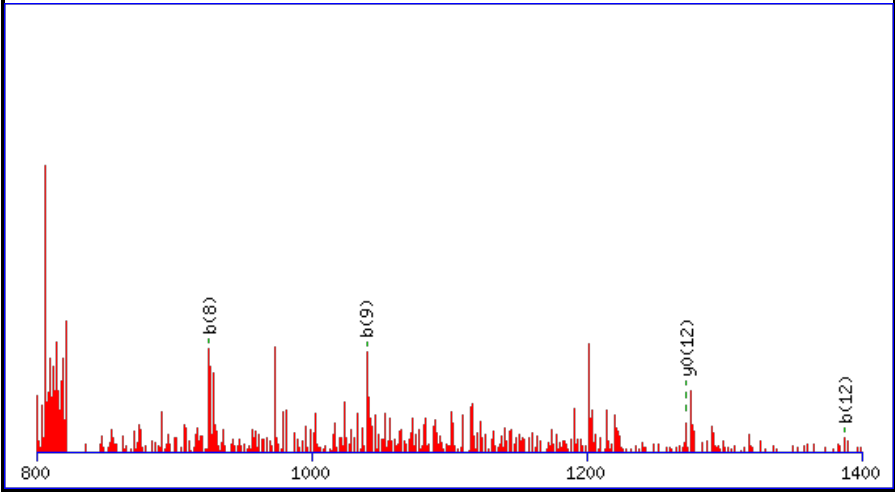
Spectrum No: 50; Query: 28329; Rank: 1

Peptide View

MS/MS Fragmentation of **RLTPTEVKDYLAAlA**
Found in **IP100219622**, Tax_Id=9606 Gene_Symbol=PSMA2 Proteasome subunit alpha type-2

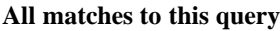
Match to Query 28329: 1659.931528 from(830.973040,2+)
Title: 091224LimSK_Exosome3_06.6854.6854.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1659.9195
Fixed modifications: Carbamidomethyl (C)
Ions Score: 29 Expect: 0.079
Matches (**Bold Red**): 24/138 fragment ions using 66 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							15
2	270.1925	135.5999	253.1659	127.0866			L	1504.8257	752.9165	1487.7992	744.4032	1486.8152	743.9112	14
3	371.2401	186.1237	354.2136	177.6104	353.2296	177.1184	T	1391.7417	696.3745	1374.7151	687.8612	1373.7311	687.3692	13
4	468.2929	234.6501	451.2663	226.1368	450.2823	225.6448	P	1290.6940	645.8506	1273.6674	637.3374	1272.6834	636.8454	12
5	569.3406	285.1739	552.3140	276.6607	551.3300	276.1686	T	1193.6412	597.3243	1176.6147	588.8110	1175.6307	588.3190	11
6	698.3832	349.6952	681.3566	341.1819	680.3726	340.6899	E	1092.5936	546.8004	1075.5670	538.2871	1074.5830	537.7951	10
7	797.4516	399.2294	780.4250	390.7162	779.4410	390.2241	V	963.5510	482.2791	946.5244	473.7658	945.5404	473.2738	9
8	925.5465	463.2769	908.5200	454.7636	907.5360	454.2716	K	864.4825	432.7449	847.4560	424.2316	846.4720	423.7396	8
9	1040.5735	520.7904	1023.5469	512.2771	1022.5629	511.7851	D	736.3876	368.6974			718.3770	359.6921	7
10	1203.6368	602.3220	1186.6103	593.8088	1185.6263	593.3168	Y	621.3606	311.1840					6
11	1316.7209	658.8641	1299.6943	650.3508	1298.7103	649.8588	L	458.2973	229.6523					5
12	1387.7580	694.3826	1370.7314	685.8694	1369.7474	685.3774	A	345.2132	173.1103					4
13	1458.7951	729.9012	1441.7686	721.3879	1440.7845	720.8959	A	274.1761	137.5917					3
14	1571.8792	786.4432	1554.8526	777.9299	1553.8686	777.4379	I	203.1390	102.0731					2
15							A	90.0550	45.5311					1



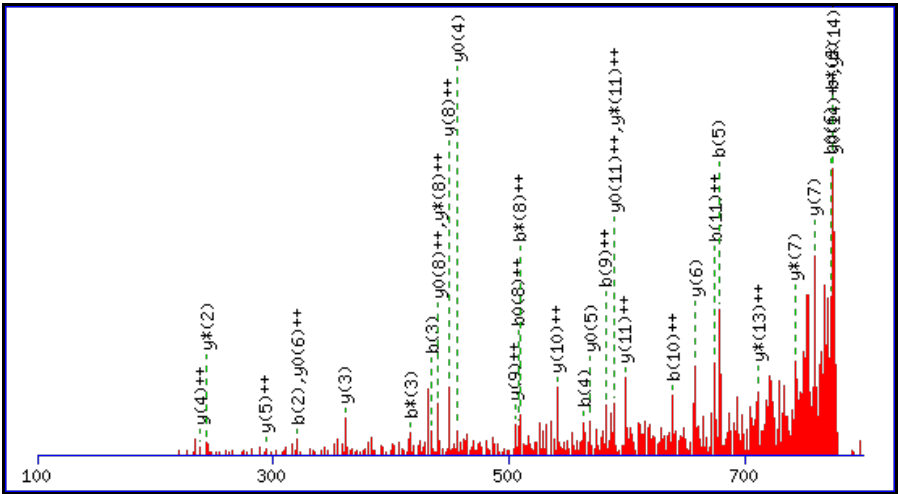
Score	Mr(calc):	Delta	Sequence
28.8	1659.9195	0.0120	RLTPTEVKDYLAAIA
1.1	1659.9437	-0.0121	IKKISKPPVVQTSR
0.9	1659.9437	-0.0121	IKKISKPPVVQTSR
0.2	1658.9233	1.0083	SQPLLIPTTGRKLR

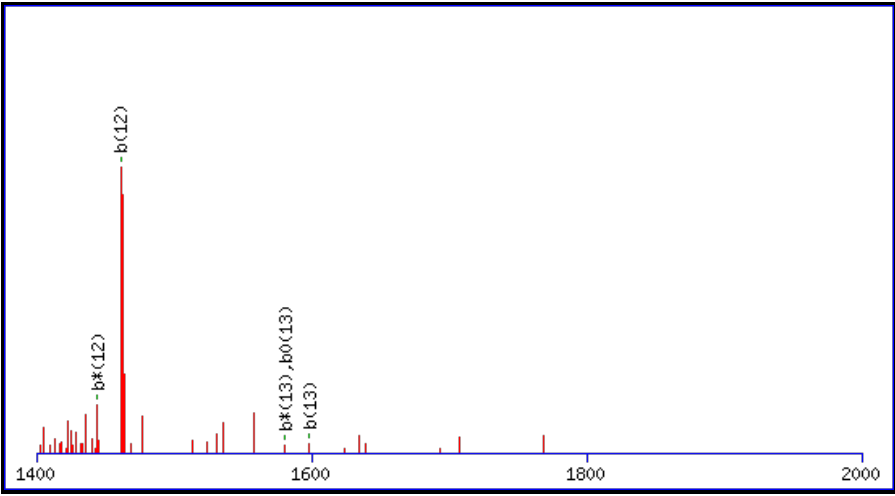
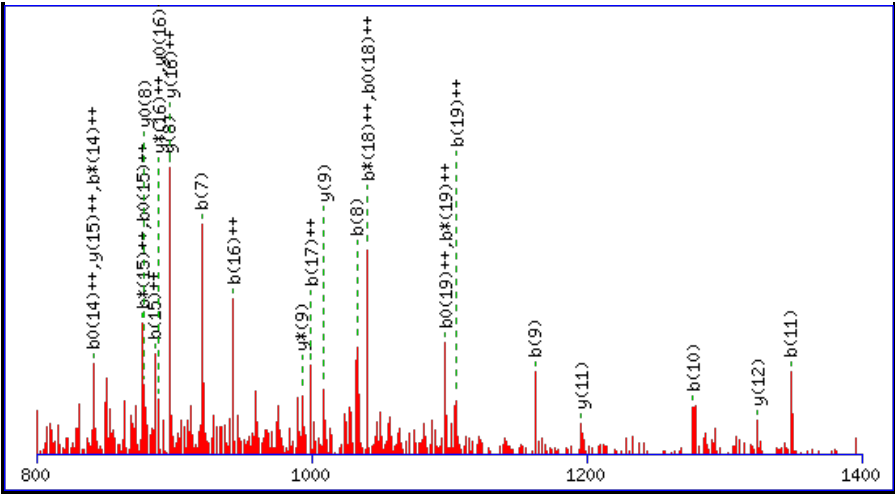
Spectrum No: 51; Query: 52630; Rank: 1

Peptide View

MS/MS Fragmentation of **RYNEDLELEDAIHTAILTK**
Found in **IPI00219622**, Tax_Id=9606 Gene_Symbol=PSMA2 Proteasome subunit alpha type-2

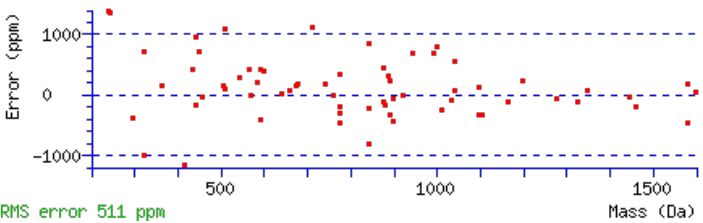
Match to Query 52630: 2356.247982 from(786.423270,3+)
Title: 091224LimSK_Exosome3_06.8753.8753.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2356.2274
Fixed modifications: Carbamidomethyl (C)
Ions Score: 40 Expect: 0.011
Matches (**Bold Red**): 65/218 fragment ions using 136 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							20
2	320.1717	160.5895	303.1452	152.0762			Y	2201.1336	1101.0704	2184.1071	1092.5572	2183.1230	1092.0652	19
3	434.2146	217.6110	417.1881	209.0977			N	2038.0703	1019.5388	2021.0437	1011.0255	2020.0597	1010.5335	18
4	563.2572	282.1323	546.2307	273.6190	545.2467	273.1270	E	1924.0274	962.5173	1907.0008	954.0040	1906.0168	953.5120	17
5	678.2842	339.6457	661.2576	331.1325	660.2736	330.6404	D	1794.9848	897.9960	1777.9582	889.4827	1776.9742	888.9907	16
6	791.3682	396.1878	774.3417	387.6745	773.3577	387.1825	L	1679.9578	840.4825	1662.9313	831.9693	1661.9472	831.4773	15
7	920.4108	460.7091	903.3843	452.1958	902.4003	451.7038	E	1566.8738	783.9405	1549.8472	775.4272	1548.8632	774.9352	14
8	1033.4949	517.2511	1016.4684	508.7378	1015.4843	508.2458	L	1437.8312	719.4192	1420.8046	710.9059	1419.8206	710.4139	13
9	1162.5375	581.7724	1145.5109	573.2591	1144.5269	572.7671	E	1324.7471	662.8772	1307.7205	654.3639	1306.7365	653.8719	12
10	1277.5644	639.2859	1260.5379	630.7726	1259.5539	630.2806	D	1195.7045	598.3559	1178.6780	589.8426	1177.6939	589.3506	11
11	1348.6016	674.8044	1331.5750	666.2911	1330.5910	665.7991	A	1080.6776	540.8424	1063.6510	532.3291	1062.6670	531.8371	10
12	1461.6856	731.3464	1444.6591	722.8332	1443.6750	722.3412	I	1009.6404	505.3239	992.6139	496.8106	991.6299	496.3186	9
13	1598.7445	799.8759	1581.7180	791.3626	1580.7340	790.8706	H	896.5564	448.7818	879.5298	440.2686	878.5458	439.7765	8
14	1699.7922	850.3997	1682.7657	841.8865	1681.7816	841.3945	T	759.4975	380.2524	742.4709	371.7391	741.4869	371.2471	7
15	1770.8293	885.9183	1753.8028	877.4050	1752.8188	876.9130	A	658.4498	329.7285	641.4232	321.2153	640.4392	320.7233	6
16	1883.9134	942.4603	1866.8868	933.9471	1865.9028	933.4550	I	587.4127	294.2100	570.3861	285.6967	569.4021	285.2047	5
17	1996.9974	999.0024	1979.9709	990.4891	1978.9869	989.9971	L	474.3286	237.6679	457.3021	229.1547	456.3180	228.6627	4
18	2098.0451	1049.5262	2081.0186	1041.0129	2080.0346	1040.5209	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
19	2211.1292	1106.0682	2194.1026	1097.5550	2193.1186	1097.0630	L	260.1969	130.6021	243.1703	122.0888			2

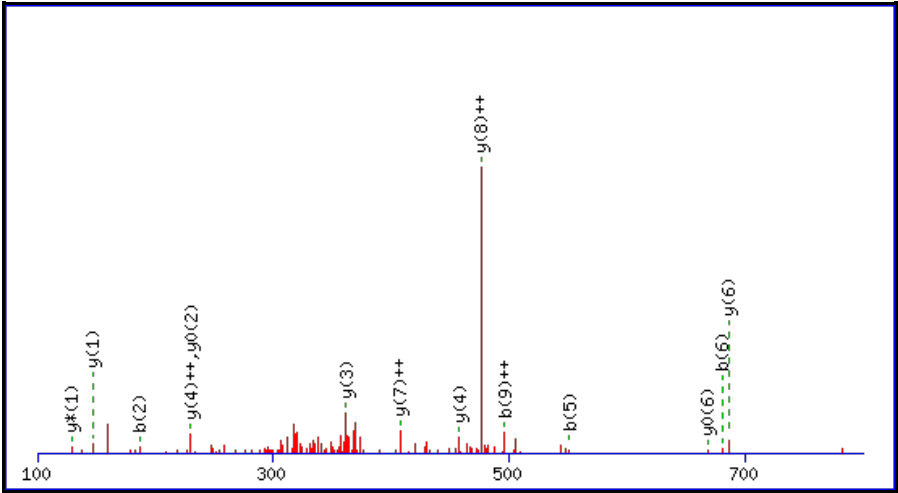


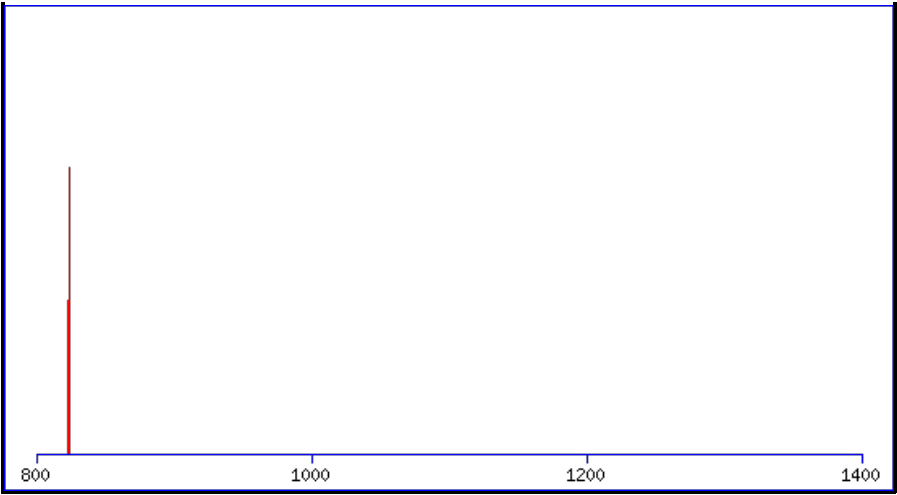
Score	Mr(calc):	Delta	Sequence
40.1	2356.2274	0.0206	RYNEDLELEDAIHTAILTLK
5.3	2356.2589	-0.0109	MLLPLPPQSSKPVPKKSQSSK
4.6	2354.2376	2.0104	TVARGPVAPSKVATTSVITVK
1.6	2354.2627	1.9852	IQNTLQKAKIPLVTNEECQK
0.5	2355.2506	0.9974	QQLPGQSRLSKQSGSLGLSQEK

Spectrum No: 52; Query: 5850; Rank: 1

MS/MS Fragmentation of **SVHKVEPI**TK
Found in **IPI00219622**, Tax_Id=9606 Gene_Symbol=PSMA2 Proteasome subunit alpha type-2

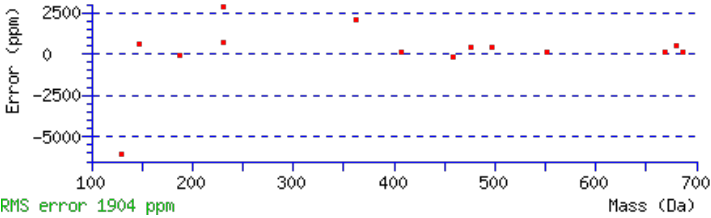
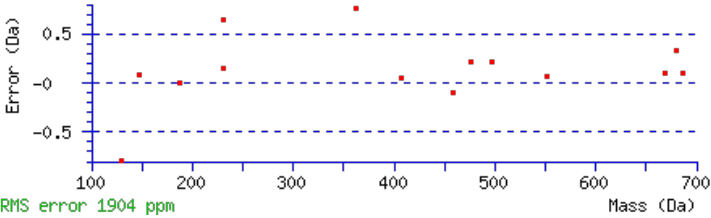
Match to Query 5850: 1136.658762 from(379.893530,3+)
Title: 091224LimSK_Exosome3_06.60.60.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1136.6554
Fixed modifications: Carbamidomethyl (C)
Ions Score: 20 Expect: 0.38
Matches (Bold Red): 14/100 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	88.0393	44.5233			70.0287	35.5180	S							10
2	187.1077	94.0575			169.0972	85.0522	V	1050.6306	525.8189	1033.6041	517.3057	1032.6200	516.8137	9
3	324.1666	162.5870			306.1561	153.5817	H	951.5622	476.2847	934.5356	467.7715	933.5516	467.2795	8
4	452.2616	226.6344	435.2350	218.1212	434.2510	217.6292	K	814.5033	407.7553	797.4767	399.2420	796.4927	398.7500	7
5	551.3300	276.1686	534.3035	267.6554	533.3194	267.1634	V	686.4083	343.7078	669.3818	335.1945	668.3978	334.7025	6
6	680.3726	340.6899	663.3461	332.1767	662.3620	331.6847	E	587.3399	294.1736	570.3134	285.6603	569.3293	285.1683	5
7	777.4254	389.2163	760.3988	380.7030	759.4148	380.2110	P	458.2973	229.6523	441.2708	221.1390	440.2867	220.6470	4
8	890.5094	445.7584	873.4829	437.2451	872.4989	436.7531	I	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
9	991.5571	496.2822	974.5306	487.7689	973.5465	487.2769	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
10							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query



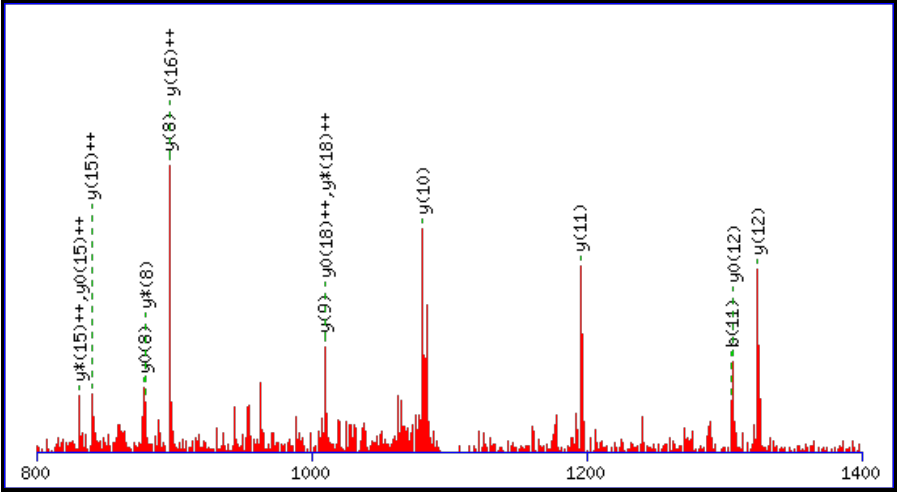
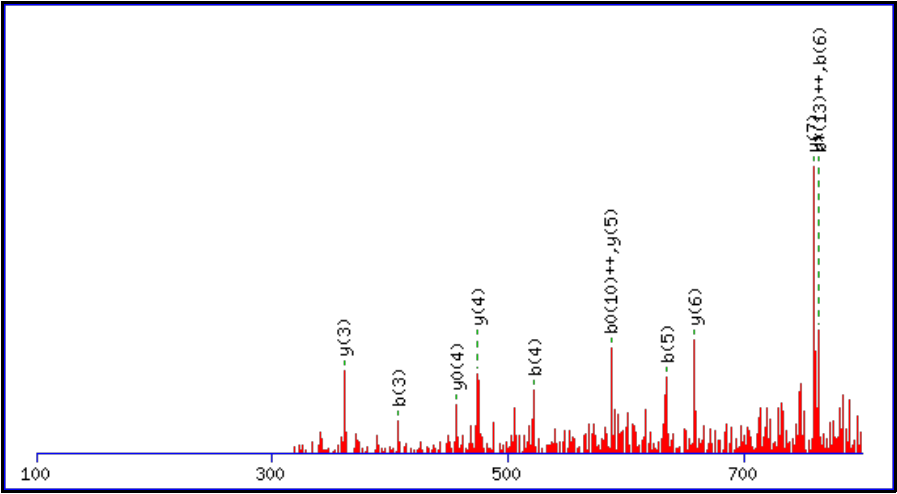
Score	Mr(calc):	Delta	Sequence
20.4	1136.6554	0.0034	SVHKVEPITK
12.5	1135.6574	1.0014	EGARAHLKVR
5.0	1134.6471	2.0117	AIPMYKIATK
4.7	1134.6413	2.0174	SVVALKTPIK
2.9	1136.6627	-0.0040	KKFTMIEIK
2.6	1135.6574	1.0014	SVLIQHQR
2.3	1136.6666	-0.0078	VHREIVSGLK
1.4	1136.6666	-0.0078	GKAHPGKTIK
1.4	1136.6554	0.0034	LALEVTVHQQ
1.3	1136.6526	0.0061	XARKLAGATGR

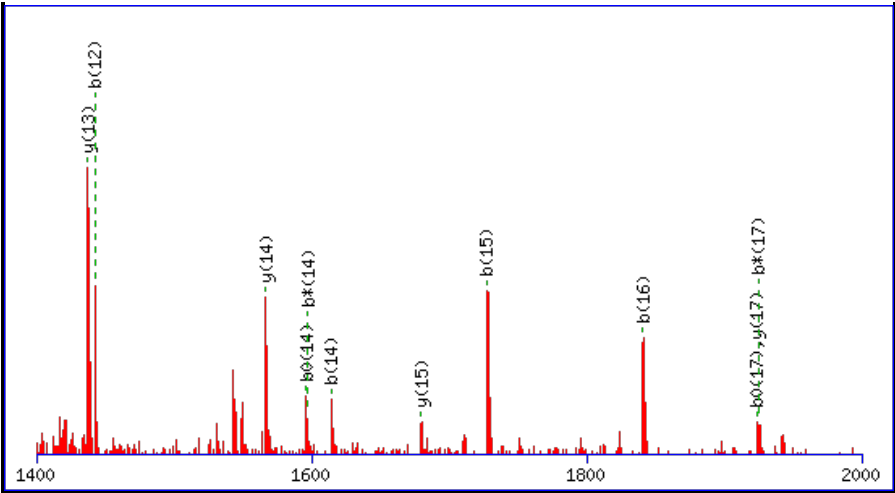
Spectrum No: 53; Query: 46805; Rank: 1

Peptide View

MS/MS Fragmentation of **YNEDLELEDIAHTAILTLK**
Found in **IPI00219622**, Tax_Id=9606 Gene_Symbol=PSMA2 Proteasome subunit alpha type-2

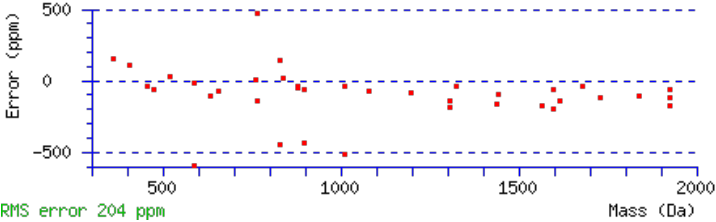
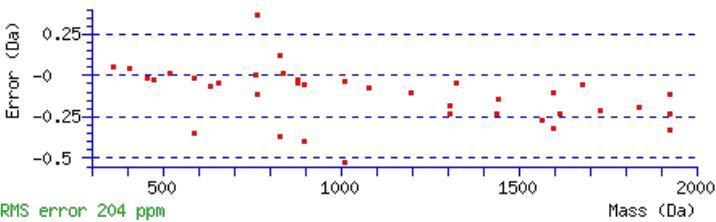
Match to Query 46805: 2200.145168 from(1101.079860,2+)
Title: 091224LimSK_Exosome3_06.8735.8735.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2200.1263
Fixed modifications: Carbamidomethyl (C)
Ions Score: 126 Expect: 3.7e-011
Matches (**Bold Red**): 39/206 fragment ions using 45 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							19
2	278.1135	139.5604	261.0870	131.0471			N	2038.0703	1019.5388	2021.0437	1011.0255	2020.0597	1010.5335	18
3	407.1561	204.0817	390.1296	195.5684	389.1456	195.0764	E	1924.0274	962.5173	1907.0008	954.0040	1906.0168	953.5120	17
4	522.1831	261.5952	505.1565	253.0819	504.1725	252.5899	D	1794.9848	897.9960	1777.9582	889.4827	1776.9742	888.9907	16
5	635.2671	318.1372	618.2406	309.6239	617.2566	309.1319	L	1679.9578	840.4825	1662.9313	831.9693	1661.9472	831.4773	15
6	764.3097	382.6585	747.2832	374.1452	746.2992	373.6532	E	1566.8738	783.9405	1549.8472	775.4272	1548.8632	774.9352	14
7	877.3938	439.2005	860.3672	430.6873	859.3832	430.1953	L	1437.8312	719.4192	1420.8046	710.9059	1419.8206	710.4139	13
8	1006.4364	503.7218	989.4098	495.2086	988.4258	494.7165	E	1324.7471	662.8772	1307.7205	654.3639	1306.7365	653.8719	12
9	1121.4633	561.2353	1104.4368	552.7220	1103.4528	552.2300	D	1195.7045	598.3559	1178.6780	589.8426	1177.6939	589.3506	11
10	1192.5004	596.7539	1175.4739	588.2406	1174.4899	587.7486	A	1080.6776	540.8424	1063.6510	532.3291	1062.6670	531.8371	10
11	1305.5845	653.2959	1288.5580	644.7826	1287.5739	644.2906	I	1009.6404	505.3239	992.6139	496.8106	991.6299	496.3186	9
12	1442.6434	721.8253	1425.6169	713.3121	1424.6329	712.8201	H	896.5564	448.7818	879.5298	440.2686	878.5458	439.7765	8
13	1543.6911	772.3492	1526.6645	763.8359	1525.6805	763.3439	T	759.4975	380.2524	742.4709	371.7391	741.4869	371.2471	7
14	1614.7282	807.8677	1597.7017	799.3545	1596.7176	798.8625	A	658.4498	329.7285	641.4232	321.2153	640.4392	320.7233	6
15	1727.8123	864.4098	1710.7857	855.8965	1709.8017	855.4045	I	587.4127	294.2100	570.3861	285.6967	569.4021	285.2047	5
16	1840.8963	920.9518	1823.8698	912.4385	1822.8858	911.9465	L	474.3286	237.6679	457.3021	229.1547	456.3180	228.6627	4
17	1941.9440	971.4756	1924.9175	962.9624	1923.9334	962.4704	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
18	2055.0281	1028.0177	2038.0015	1019.5044	2037.0175	1019.0124	L	260.1969	130.6021	243.1703	122.0888			2
19							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
125.8	2200.1263	0.0189	YNEDLELEDAIHTAILTLK
3.1	2200.1528	-0.0076	YPIINYTFTSGLSGVLGAATR
2.3	2200.1575	-0.0124	LAWLHPGVKPCSVEGLGQR

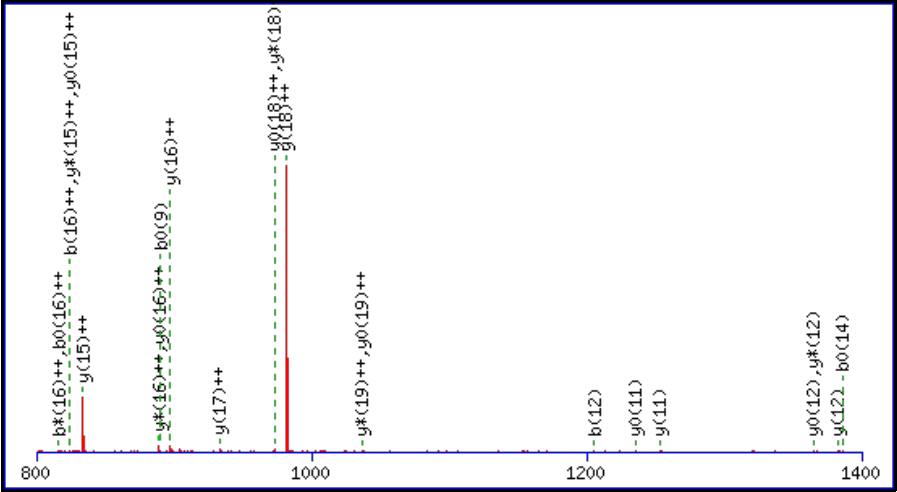
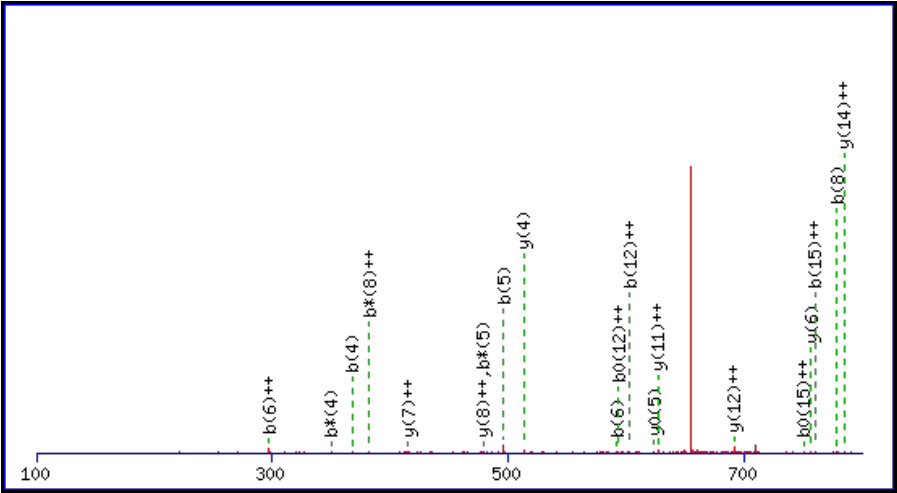
2.2	2199.1300	1.0151	TIHSNQTVVIPENVNITLK
2.2	2199.1300	1.0151	TIHSNQTVVIPENVNITLK
1.8	2200.1261	0.0190	RMSVLVRKPEGAICLYTK
1.8	2200.1261	0.0190	RMSVLVRKPEGAICLYTK
1.2	2199.1349	1.0103	MKVLWAALLVTFLAGCQAK
0.8	2199.1487	0.9965	TSAMLTVRALPIKFTEGLR

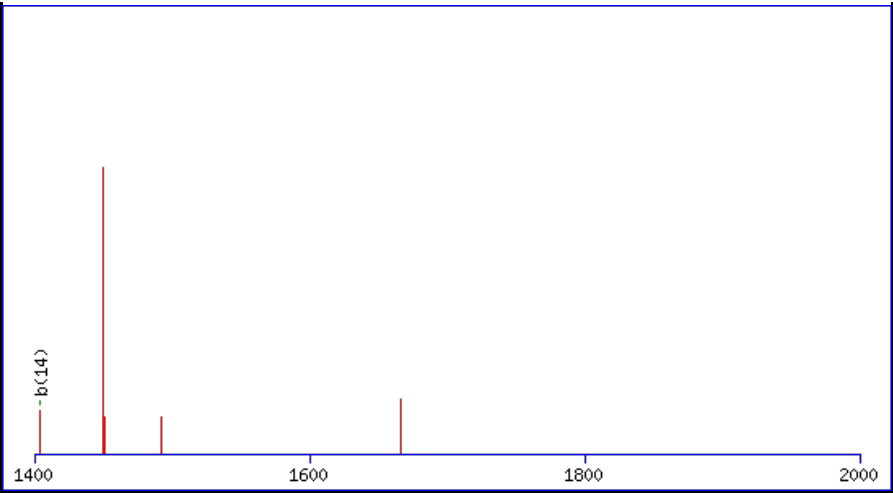
Spectrum No: 54; Query: 45395; Rank: 1

Peptide View

MS/MS Fragmentation of **AQPAQPADEPAEKADPEMEH**
Found in **IPI00016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1

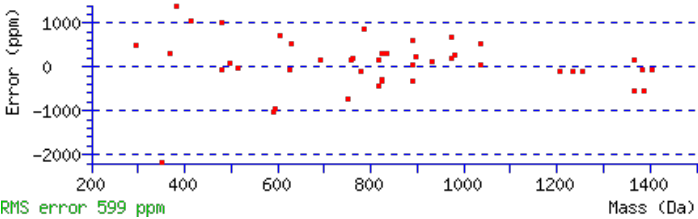
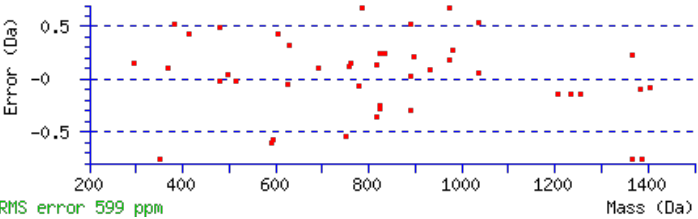
Match to Query 45395: 2159.953032 from(720.991620,3+)
Title: 091224LimSK_Exosome3_05.874.874.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2159.9429
Fixed modifications: Carbamidomethyl (C)
Ions Score: 24 Expect: 1
Matches (Bold Red): 45/196 fragment ions using 103 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							20
2	200.1030	100.5551	183.0764	92.0418			Q	2089.9131	1045.4602	2072.8866	1036.9469	2071.9026	1036.4549	19
3	297.1557	149.0815	280.1292	140.5682			P	1961.8545	981.4309	1944.8280	972.9176	1943.8440	972.4256	18
4	368.1928	184.6001	351.1663	176.0868			A	1864.8018	932.9045	1847.7752	924.3913	1846.7912	923.8992	17
5	496.2514	248.6293	479.2249	240.1161			Q	1793.7647	897.3860	1776.7381	888.8727	1775.7541	888.3807	16
6	593.3042	297.1557	576.2776	288.6425			P	1665.7061	833.3567	1648.6795	824.8434	1647.6955	824.3514	15
7	664.3413	332.6743	647.3148	324.1610			A	1568.6533	784.8303	1551.6268	776.3170	1550.6428	775.8250	14
8	779.3682	390.1878	762.3417	381.6745	761.3577	381.1825	D	1497.6162	749.3117	1480.5897	740.7985	1479.6057	740.3065	13
9	908.4108	454.7091	891.3843	446.1958	890.4003	445.7038	E	1382.5893	691.7983	1365.5627	683.2850	1364.5787	682.7930	12
10	1005.4636	503.2354	988.4371	494.7222	987.4530	494.2302	P	1253.5467	627.2770	1236.5201	618.7637	1235.5361	618.2717	11
11	1076.5007	538.7540	1059.4742	530.2407	1058.4902	529.7487	A	1156.4939	578.7506	1139.4674	570.2373	1138.4834	569.7453	10
12	1205.5433	603.2753	1188.5168	594.7620	1187.5327	594.2700	E	1085.4568	543.2320	1068.4303	534.7188	1067.4462	534.2268	9
13	1333.6383	667.3228	1316.6117	658.8095	1315.6277	658.3175	K	956.4142	478.7107	939.3877	470.1975	938.4036	469.7055	8
14	1404.6754	702.8413	1387.6488	694.3281	1386.6648	693.8360	A	828.3192	414.6633			810.3087	405.6580	7
15	1519.7023	760.3548	1502.6758	751.8415	1501.6918	751.3495	D	757.2821	379.1447			739.2716	370.1394	6
16	1648.7449	824.8761	1631.7184	816.3628	1630.7344	815.8708	E	642.2552	321.6312			624.2446	312.6259	5
17	1745.7977	873.4025	1728.7711	864.8892	1727.7871	864.3972	P	513.2126	257.1099			495.2020	248.1047	4
18	1876.8382	938.9227	1859.8116	930.4094	1858.8276	929.9174	M	416.1598	208.5836			398.1493	199.5783	3
19	2005.8808	1003.4440	1988.8542	994.9307	1987.8702	994.4387	E	285.1193	143.0633			267.1088	134.0580	2
20							H	156.0768	78.5420					1



All matches to this query

Score	Mr(calc):	Delta	Sequence
24.0	2159.9429	0.0101	AQPAQPADEPAEKADEPMEH
9.6	2157.9432	2.0099	LLASWVSGSSGRSGGEMRK

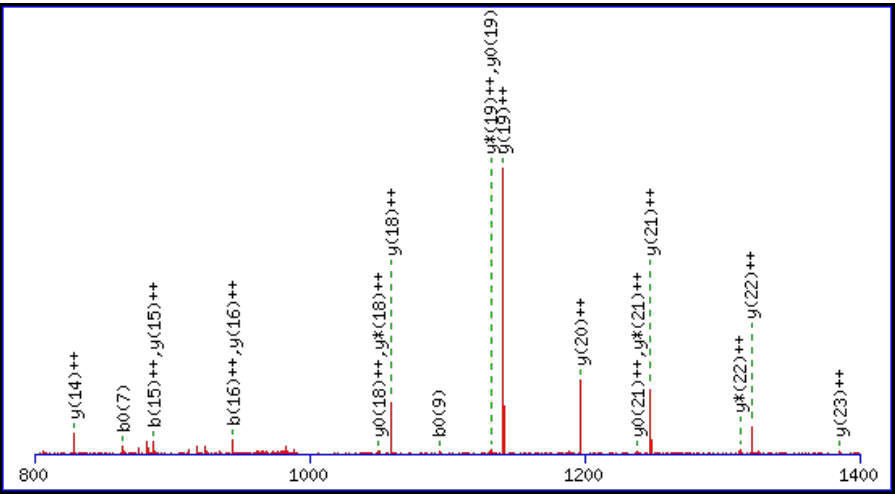
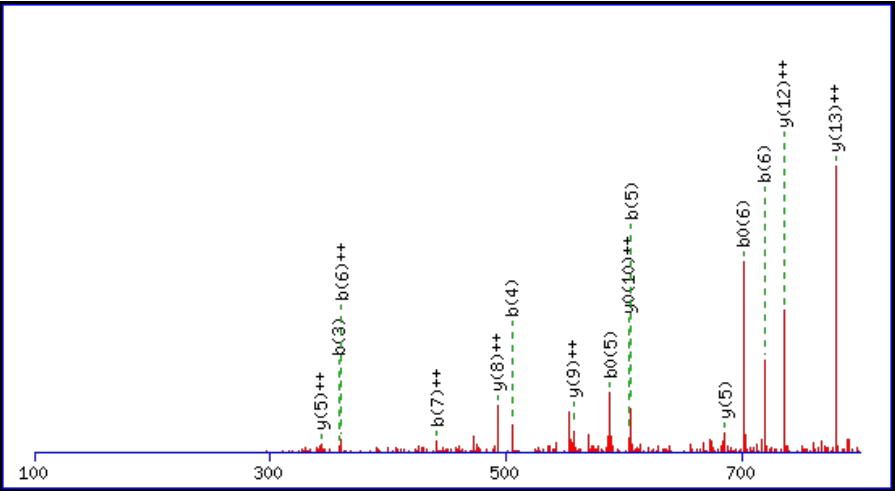
9.1	2159.9574	-0.0043	YSFFVAMGYLTICHISR
8.3	2157.9432	2.0099	LLASWVSGSSGRSGGFMRK
8.0	2157.9476	2.0055	XSHGTKMMTPEVLAEAYGK
7.9	2157.9402	2.0129	SAQELPQVEAYSPSACSVR
7.2	2157.9670	1.9860	VASSDLVNMGISVVSYTLK
7.2	2157.9670	1.9860	VASSDLVNMGISVVSYTLK
6.8	2157.9418	2.0112	LGGTSLSLVMEVNSGIYR
6.8	2158.9337	1.0193	TAENVRALSTEEKGEGYK

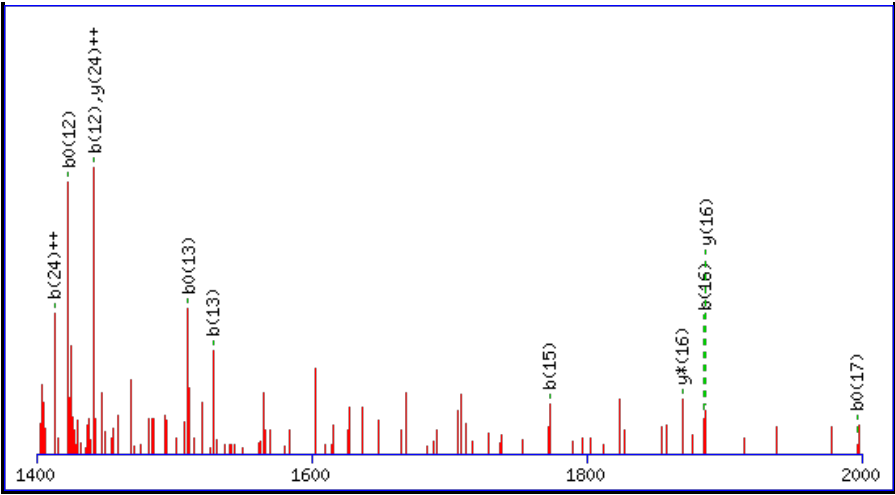
Spectrum No: 55; Query: 65422; Rank: 1

Peptide View

MS/MS Fragmentation of **DLEFTIYDDDDVSPFLEGLEERPQR**
Found in **IPI00016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1

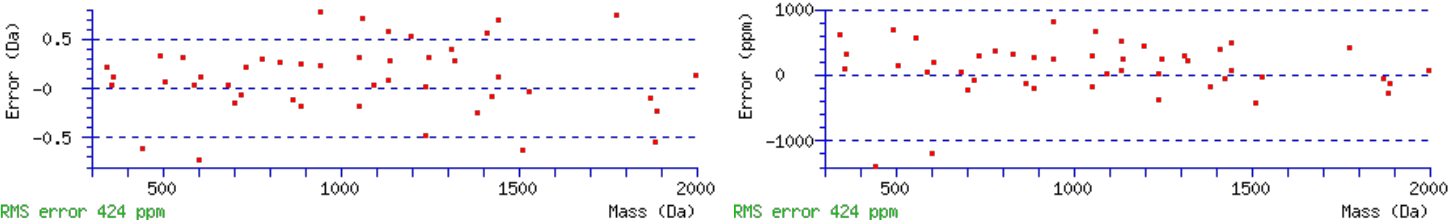
Match to Query 65422: 2997.408372 from(1000.143400,3+)
Title: 091224LimSK_Exosome3_06.8382.8382.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2997.3880
Fixed modifications: Carbamidomethyl (C)
Ions Score: 77 Expect: 5.9e-006
Matches (**Bold Red**): 46/238 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	116.0342	58.5207			98.0237	49.5155	D							25
2	229.1183	115.0628			211.1077	106.0575	L	2883.3683	1442.1878	2866.3418	1433.6745	2865.3577	1433.1825	24
3	358.1609	179.5841			340.1503	170.5788	E	2770.2842	1385.6458	2753.2577	1377.1325	2752.2737	1376.6405	23
4	505.2293	253.1183			487.2187	244.1130	F	2641.2417	1321.1245	2624.2151	1312.6112	2623.2311	1312.1192	22
5	606.2770	303.6421			588.2664	294.6368	T	2494.1732	1247.5903	2477.1467	1239.0770	2476.1627	1238.5850	21
6	719.3610	360.1842			701.3505	351.1789	I	2393.1256	1197.0664	2376.0990	1188.5531	2375.1150	1188.0611	20
7	882.4244	441.7158			864.4138	432.7105	Y	2280.0415	1140.5244	2263.0149	1132.0111	2262.0309	1131.5191	19
8	997.4513	499.2293			979.4407	490.2240	D	2116.9782	1058.9927	2099.9516	1050.4794	2098.9676	1049.9874	18
9	1112.4782	556.7428			1094.4677	547.7375	D	2001.9512	1001.4793	1984.9247	992.9660	1983.9407	992.4740	17
10	1227.5052	614.2562			1209.4946	605.2510	D	1886.9243	943.9658	1869.8977	935.4525	1868.9137	934.9605	16
11	1342.5321	671.7697			1324.5216	662.7644	D	1771.8973	886.4523	1754.8708	877.9390	1753.8868	877.4470	15
12	1441.6005	721.3039			1423.5900	712.2986	V	1656.8704	828.9388	1639.8438	820.4256	1638.8598	819.9336	14
13	1528.6326	764.8199			1510.6220	755.8146	S	1557.8020	779.4046	1540.7754	770.8914	1539.7914	770.3993	13
14	1625.6853	813.3463			1607.6748	804.3410	P	1470.7700	735.8886	1453.7434	727.3753	1452.7594	726.8833	12
15	1772.7538	886.8805			1754.7432	877.8752	F	1373.7172	687.3622	1356.6906	678.8490	1355.7066	678.3570	11
16	1885.8378	943.4225			1867.8273	934.4173	L	1226.6488	613.8280	1209.6222	605.3148	1208.6382	604.8227	10
17	2014.8804	1007.9438			1996.8698	998.9386	E	1113.5647	557.2860	1096.5382	548.7727	1095.5541	548.2807	9
18	2071.9019	1036.4546			2053.8913	1027.4493	G	984.5221	492.7647	967.4956	484.2514	966.5116	483.7594	8
19	2184.9859	1092.9966			2166.9754	1083.9913	L	927.5007	464.2540	910.4741	455.7407	909.4901	455.2487	7
20	2314.0285	1157.5179			2296.0180	1148.5126	E	814.4166	407.7119	797.3900	399.1987	796.4060	398.7067	6
21	2443.0711	1222.0392			2425.0606	1213.0339	E	685.3740	343.1906	668.3474	334.6774	667.3634	334.1854	5
22	2599.1722	1300.0898	2582.1457	1291.5765	2581.1617	1291.0845	R	556.3314	278.6693	539.3049	270.1561			4
23	2696.2250	1348.6161	2679.1985	1340.1029	2678.2144	1339.6109	P	400.2303	200.6188	383.2037	192.1055			3
24	2824.2836	1412.6454	2807.2570	1404.1322	2806.2730	1403.6401	Q	303.1775	152.0924	286.1510	143.5791			2
25							R	175.1190	88.0631	158.0924	79.5498			1



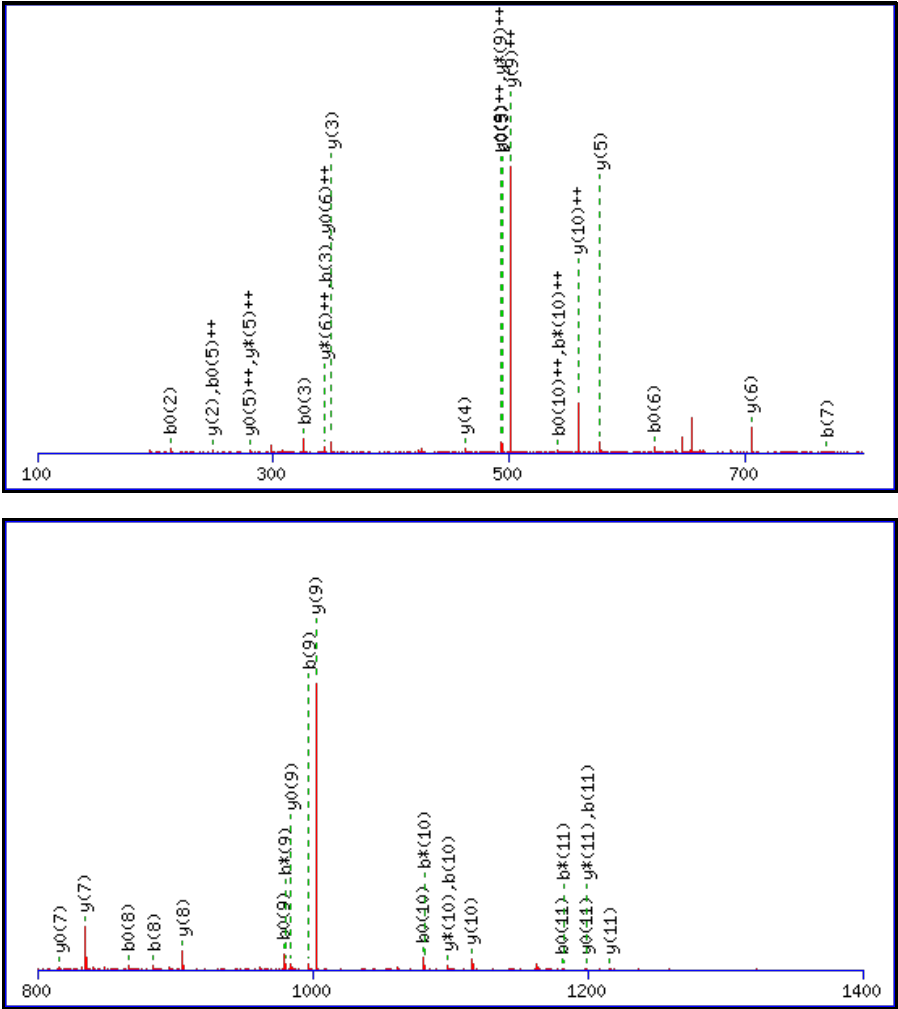
Score	Mr(calcd):	Delta	Sequence
77.2	2997.3880	0.0204	DLEFTIYDDDDVSPFLEGLEERPQR
8.8	2997.4356	-0.0272	ICGSPCPAVWPDVIKLPYFNTMKPK
8.8	2997.4356	-0.0272	LCGSPCPAVWPDVIKLPYFNTMKPK
7.7	2997.3919	0.0164	ETFMKTSLQTVDLRLAQLLEELSNR
7.7	2997.3919	0.0164	ETFMKTSLQTVDLRLAQLLEELSNR
7.6	2996.3908	1.0176	FGDEMPARYGGGGSGAAAGVVVGSGGGRGAGGSR
6.7	2995.3959	2.0124	YLYMDEADRLNMDFETEVDKILK
6.0	2995.4222	1.9861	LGNPEEGORMRLSSAPSAQDFESILGK
5.6	2996.3795	1.0289	NYKVMAAENIPENPLKYLPNIDK
5.6	2997.3860	0.0224	MLIRHKMTHNPNRPLAECQFCHK

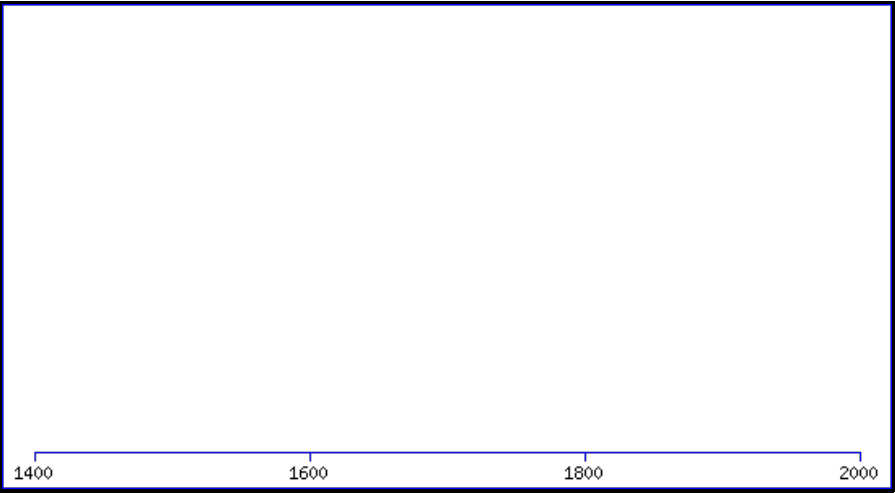
Spectrum No: 56; Query: 12922; Rank: 1

Peptide View

MS/MS Fragmentation of **ETLPAEQDLTK**
Found in **IPI00016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1

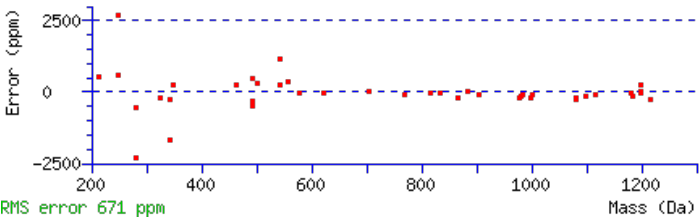
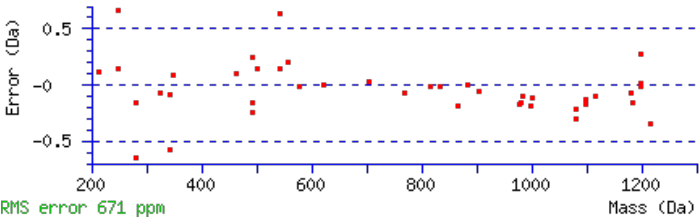
Match to Query 12922: 1344.683928 from(673.349240,2+)
Title: 091224LimSK_Exosome3_05.1782.1782.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1344.6773
Fixed modifications: Carbamidomethyl (C)
Ions Score: 78 Expect: 3e-006
Matches (Bold Red): 43/118 fragment ions using 53 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							12
2	231.0975	116.0524			213.0870	107.0471	T	1216.6420	608.8246	1199.6154	600.3113	1198.6314	599.8193	11
3	344.1816	172.5944			326.1710	163.5892	L	1115.5943	558.3008	1098.5677	549.7875	1097.5837	549.2955	10
4	441.2344	221.1208			423.2238	212.1155	P	1002.5102	501.7587	985.4837	493.2455	984.4997	492.7535	9
5	512.2715	256.6394			494.2609	247.6341	A	905.4575	453.2324	888.4309	444.7191	887.4469	444.2271	8
6	641.3141	321.1607			623.3035	312.1554	E	834.4203	417.7138	817.3938	409.2005	816.4098	408.7085	7
7	769.3727	385.1900	752.3461	376.6767	751.3621	376.1847	Q	705.3777	353.1925	688.3512	344.6792	687.3672	344.1872	6
8	884.3996	442.7034	867.3731	434.1902	866.3890	433.6982	D	577.3192	289.1632	560.2926	280.6499	559.3086	280.1579	5
9	997.4837	499.2455	980.4571	490.7322	979.4731	490.2402	L	462.2922	231.6498	445.2657	223.1365	444.2817	222.6445	4
10	1098.5313	549.7693	1081.5048	541.2560	1080.5208	540.7640	T	349.2082	175.1077	332.1816	166.5944	331.1976	166.1024	3
11	1199.5790	600.2932	1182.5525	591.7799	1181.5685	591.2879	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
12							K	147.1128	74.0600	130.0863	65.5468			1



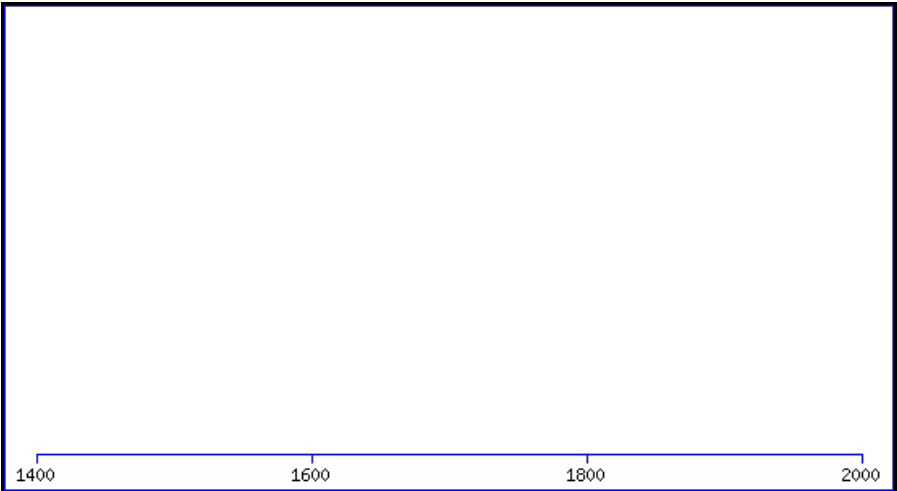
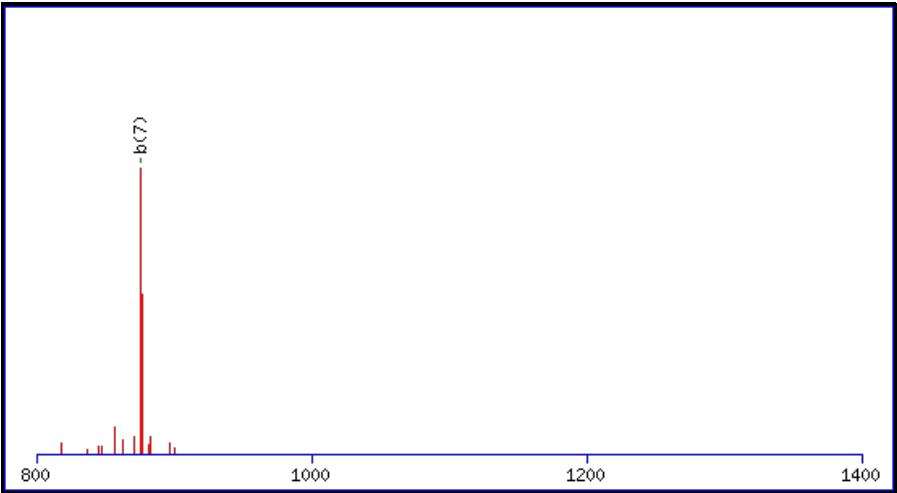
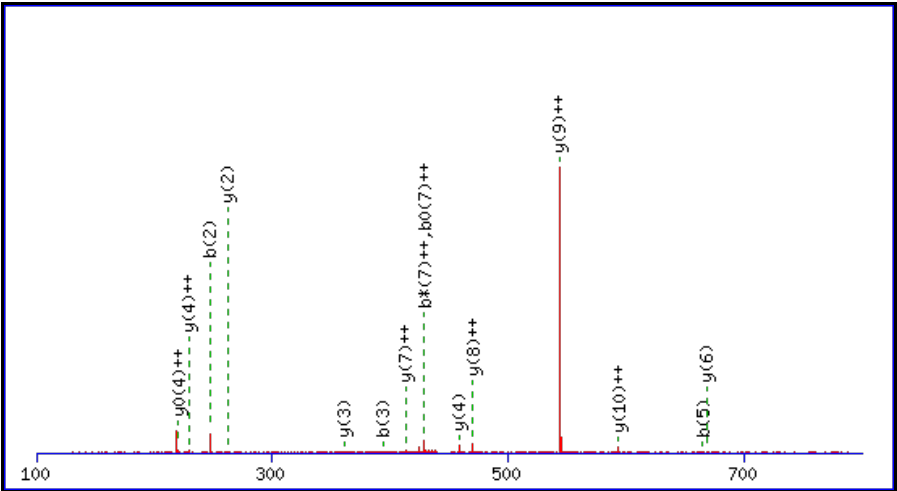
All matches to this query

Score	Mr(calc):	Delta	Sequence
77.8	1344.6773	0.0067	ETLPAEQDLTTK
11.2	1342.6646	2.0193	DLLAPPSPALGGR
10.2	1344.6915	-0.0075	DPLSAPALRLGR
8.3	1344.6737	0.0102	MNVSPVPLRR
7.9	1342.6881	1.9958	EVLEGLDYLHR
7.5	1343.6711	1.0128	LLGPGGRPSSPAR
7.0	1344.6819	0.0021	KTSKIASLIPK
6.8	1342.6662	2.0177	KVPVSVNLLSK
6.6	1344.6819	0.0021	KTSKIASLIPK
6.5	1344.6826	0.0013	DVERFEKGYGK

Spectrum No: 57; Query: 12473; Rank: 1

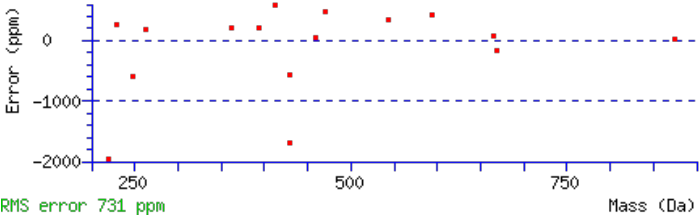
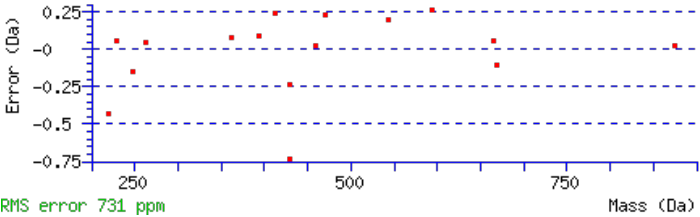
Peptide View

MS/MS Fragmentation of **FVFDRPLPVSR**
Found in **IPI00016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1
Match to Query 12473: 1331.742972 from(444.921600,3+)
Title: 091224LimSK_Exosome3_06.4388.4388.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1331.7350
Fixed modifications: Carbamidomethyl (C)
Ions Score: 29 Expect: 0.11
Matches (**Bold Red**): 16/104 fragment ions using 33 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							11
2	247.1441	124.0757					V	1185.6739	593.3406	1168.6473	584.8273	1167.6633	584.3353	10
3	394.2125	197.6099					F	1086.6055	543.8064	1069.5789	535.2931	1068.5949	534.8011	9
4	509.2395	255.1234			491.2289	246.1181	D	939.5370	470.2722	922.5105	461.7589	921.5265	461.2669	8
5	665.3406	333.1739	648.3140	324.6606	647.3300	324.1686	R	824.5101	412.7587	807.4835	404.2454	806.4995	403.7534	7
6	762.3933	381.7003	745.3668	373.1870	744.3828	372.6950	P	668.4090	334.7081	651.3824	326.1949	650.3984	325.7028	6
7	875.4774	438.2423	858.4509	429.7291	857.4668	429.2371	L	571.3562	286.1817	554.3297	277.6685	553.3457	277.1765	5
8	972.5302	486.7687	955.5036	478.2554	954.5196	477.7634	P	458.2722	229.6397	441.2456	221.1264	440.2616	220.6344	4
9	1071.5986	536.3029	1054.5720	527.7897	1053.5880	527.2976	V	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
10	1158.6306	579.8189	1141.6041	571.3057	1140.6200	570.8137	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
11							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

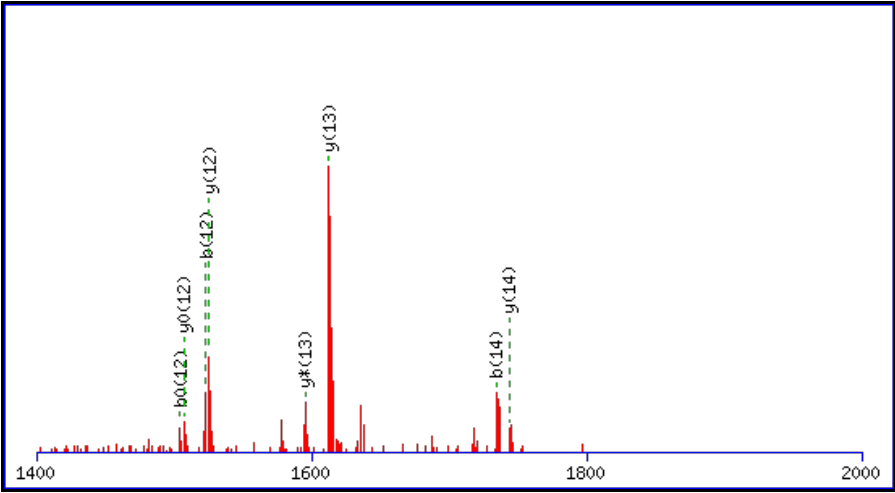
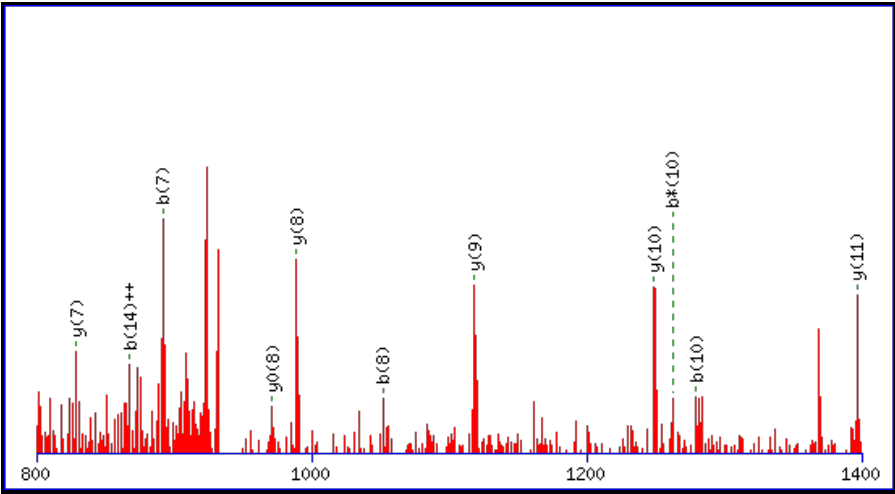
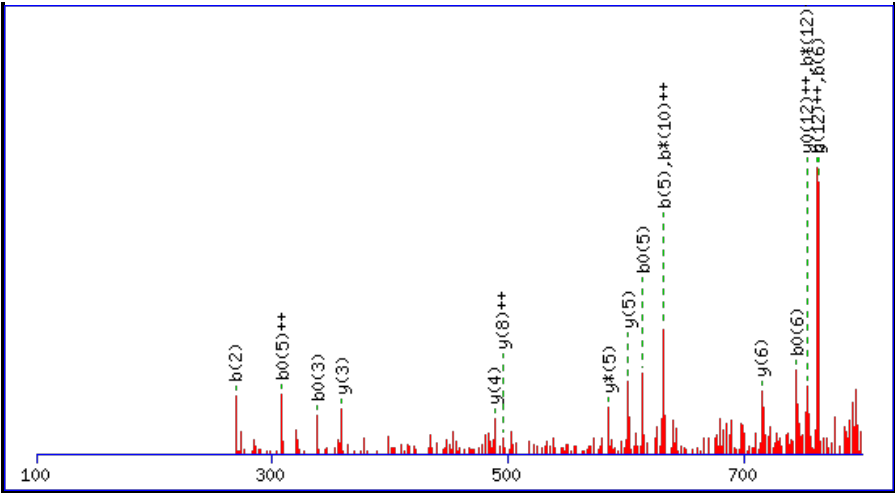
Score	Mr(calc):	Delta	Sequence
29.1	1331.7350	0.0080	FVFDRPLPVS R
8.4	1329.7252	2.0178	QTVSQVVNAKE K
6.6	1331.7561	-0.0131	QIPPRPPEGLT K
6.5	1330.7503	0.9927	MVAVNLATGKRR
5.9	1330.7486	0.9944	KLSNAPRPLKK
5.1	1329.7405	2.0025	RSFLGQKDPALV
5.1	1331.7534	-0.0104	LELAGAPHGRRR
5.0	1329.7252	2.0178	VSEEVEKGRAVK
4.8	1331.7449	-0.0019	AFLVIADSLQQK
4.8	1330.7486	0.9944	XHVITALRVKK

Spectrum No: 58; Query: 35891; Rank: 1

Peptide View

MS/MS Fragmentation of **HMSEFMECNLNELVK**
Found in **IP100016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1

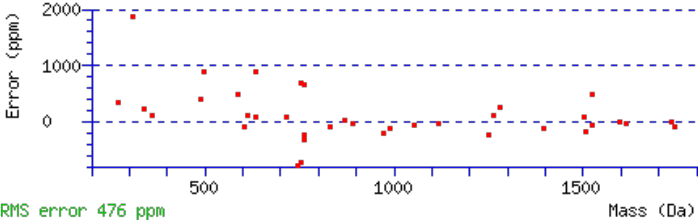
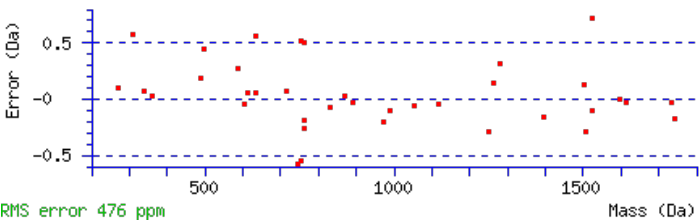
Match to Query 35891: 1879.841868 from(940.928210,2+)
Title: 091224LimSK_Exosome3_06.5841.5841.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1879.8266
Fixed modifications: Carbamidomethyl (C)
Ions Score: 62 Expect: 0.00017
Matches (Bold Red): 37/142 fragment ions using 80 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	138.0662	69.5367					H							15
2	269.1067	135.0570					M	1743.7750	872.3912	1726.7485	863.8779	1725.7645	863.3859	14
3	356.1387	178.5730			338.1281	169.5677	S	1612.7346	806.8709	1595.7080	798.3576	1594.7240	797.8656	13
4	485.1813	243.0943			467.1707	234.0890	E	1525.7025	763.3549	1508.6760	754.8416	1507.6920	754.3496	12
5	632.2497	316.6285			614.2391	307.6232	F	1396.6599	698.8336	1379.6334	690.3203	1378.6494	689.8283	11
6	763.2902	382.1487			745.2796	373.1435	M	1249.5915	625.2994	1232.5650	616.7861	1231.5810	616.2941	10

7	892.3328	446.6700			874.3222	437.6647	E	1118.5510	559.7792	1101.5245	551.2659	1100.5405	550.7739	9
8	1052.3634	526.6854			1034.3529	517.6801	C	989.5084	495.2579	972.4819	486.7446	971.4979	486.2526	8
9	1166.4064	583.7068	1149.3798	575.1935	1148.3958	574.7015	N	829.4778	415.2425	812.4512	406.7293	811.4672	406.2373	7
10	1279.4904	640.2489	1262.4639	631.7356	1261.4799	631.2436	L	715.4349	358.2211	698.4083	349.7078	697.4243	349.2158	6
11	1393.5334	697.2703	1376.5068	688.7570	1375.5228	688.2650	N	602.3508	301.6790	585.3243	293.1658	584.3402	292.6738	5
12	1522.5759	761.7916	1505.5494	753.2783	1504.5654	752.7863	E	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
13	1635.6600	818.3336	1618.6335	809.8204	1617.6494	809.3284	L	359.2653	180.1363	342.2387	171.6230			3
14	1734.7284	867.8678	1717.7019	859.3546	1716.7179	858.8626	V	246.1812	123.5942	229.1547	115.0810			2
15							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

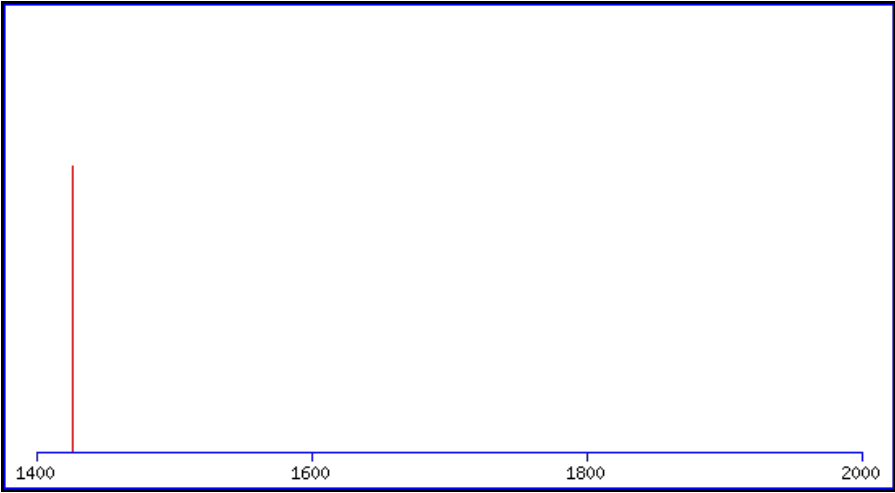
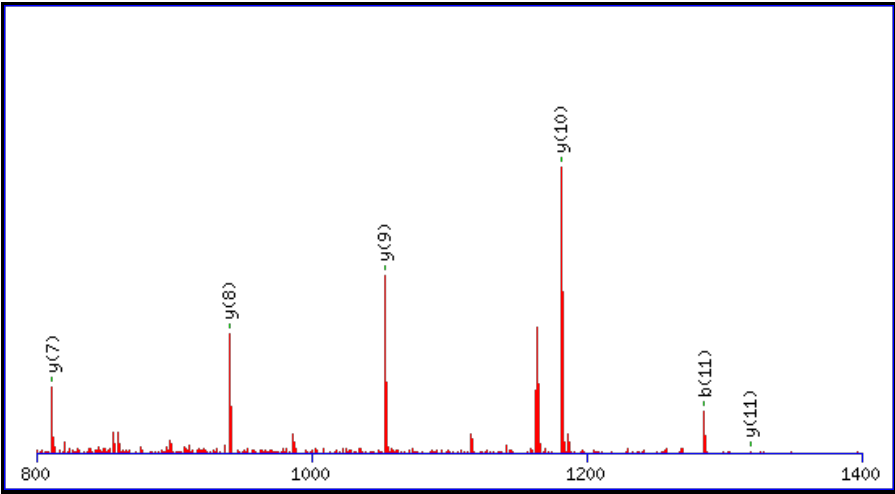
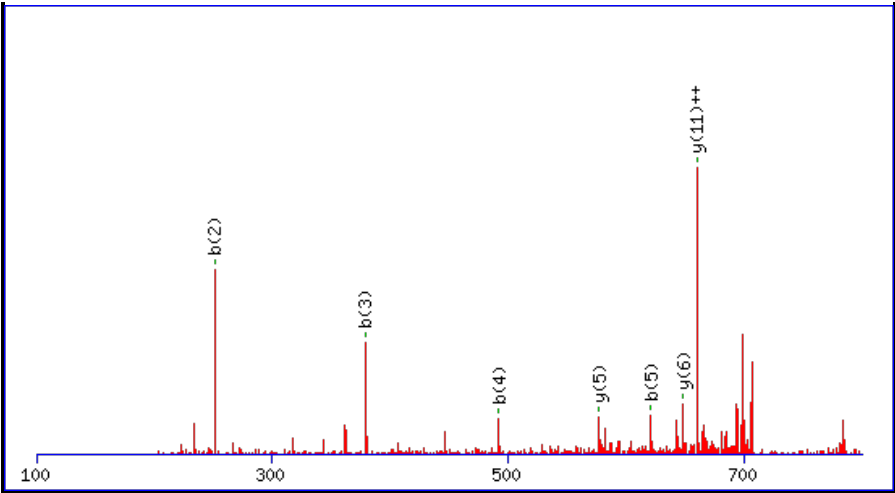
Score	Mr(calc):	Delta	Sequence
61.6	1879.8266	0.0152	HMSEFMECNLNELVK
5.1	1879.8270	0.0148	KFAHVEDSDLIYK
4.7	1879.8499	-0.0080	ISDQNASGAPPMTVREK
4.7	1879.8499	-0.0080	ISDQNASGAPPMTVREK
2.8	1879.8481	-0.0063	KSVPRNSLESAEYLK
2.1	1879.8369	0.0049	GENVFGSAEIIASLSVK
1.0	1878.8334	1.0085	GSRGGNTSSSHGSAGPKQK
0.5	1878.8336	1.0083	QTMPRPYTFQVSSGGK
0.2	1878.8223	1.0196	CFEISDADNKVVEAGK

Spectrum No: 59; Query: 16758; Rank: 1

Peptide View

MS/MS Fragmentation of **IHQIEYAMEAVK**
Found in **IPI00016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1

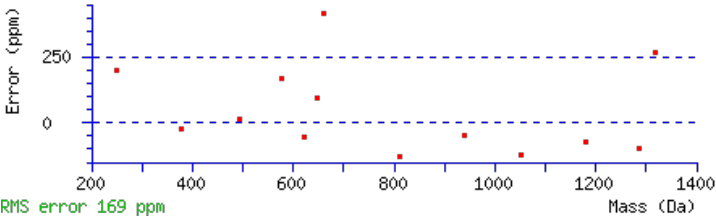
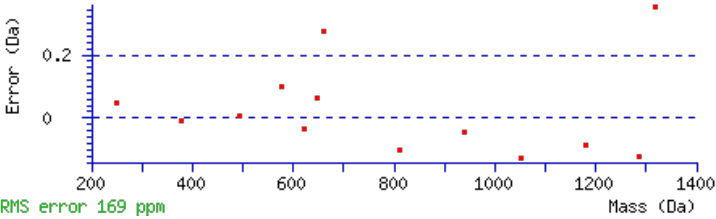
Match to Query 16758: 1430.732288 from(716.373420,2+)
Title: 091224LimSK_Exosome3_05.2499.2499.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1430.7227
Fixed modifications: Carbamidomethyl (C)
Ions Score: 49 Expect: 0.0022
Matches (**Bold Red**): 13/114 fragment ions using 20 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					I							12
2	251.1503	126.0788					H	1318.6460	659.8266	1301.6195	651.3134	1300.6354	650.8214	11
3	379.2088	190.1081	362.1823	181.5948			Q	1181.5871	591.2972	1164.5605	582.7839	1163.5765	582.2919	10
4	492.2929	246.6501	475.2663	238.1368			I	1053.5285	527.2679	1036.5020	518.7546	1035.5179	518.2626	9
5	621.3355	311.1714	604.3089	302.6581	603.3249	302.1661	E	940.4444	470.7259	923.4179	462.2126	922.4339	461.7206	8
6	784.3988	392.7030	767.3723	384.1898	766.3883	383.6978	Y	811.4019	406.2046	794.3753	397.6913	793.3913	397.1993	7

7	855.4359	428.2216	838.4094	419.7083	837.4254	419.2163	A	648.3385	324.6729	631.3120	316.1596	630.3280	315.6676	6
8	986.4764	493.7418	969.4499	485.2286	968.4659	484.7366	M	577.3014	289.1543	560.2749	280.6411	559.2908	280.1491	5
9	1115.5190	558.2631	1098.4925	549.7499	1097.5084	549.2579	E	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
10	1186.5561	593.7817	1169.5296	585.2684	1168.5456	584.7764	A	317.2183	159.1128	300.1918	150.5995			3
11	1285.6245	643.3159	1268.5980	634.8026	1267.6140	634.3106	V	246.1812	123.5942	229.1547	115.0810			2
12							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

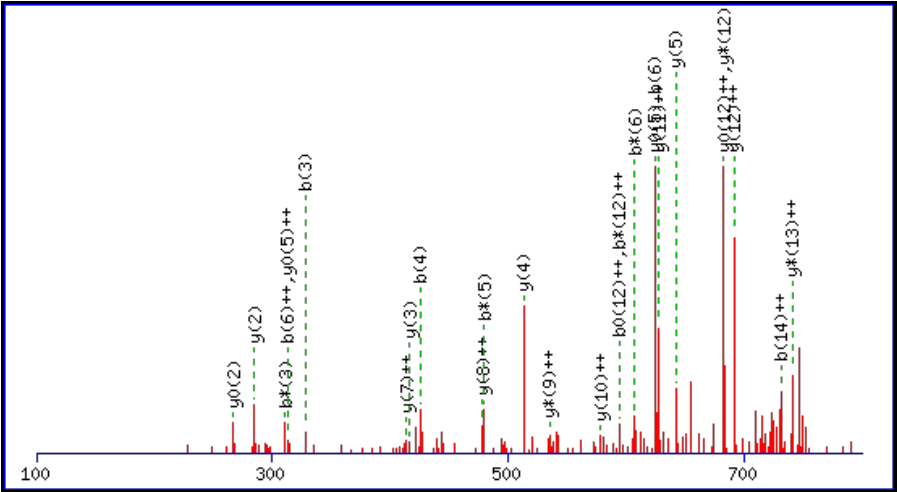
Score	Mr(calc):	Delta	Sequence
49.0	1430.7227	0.0095	IHQIEYAMEAVK
13.1	1430.7395	-0.0072	QHLLSLQORTK
6.8	1430.7184	0.0139	IHGVLTHYQKR
6.6	1430.7395	-0.0072	QHLLSLQORTK
6.5	1430.7184	0.0139	HLQSLHKFVSR
6.4	1430.7340	-0.0017	IHTGEKPYKCAK
6.0	1430.7184	0.0139	IHGVLTHYQKR
5.2	1430.7307	0.0016	LHTEGNPEKQDK
4.1	1430.7340	-0.0017	IHTKEQPYKCK
3.4	1430.7252	0.0071	EQAEIQIKEESK

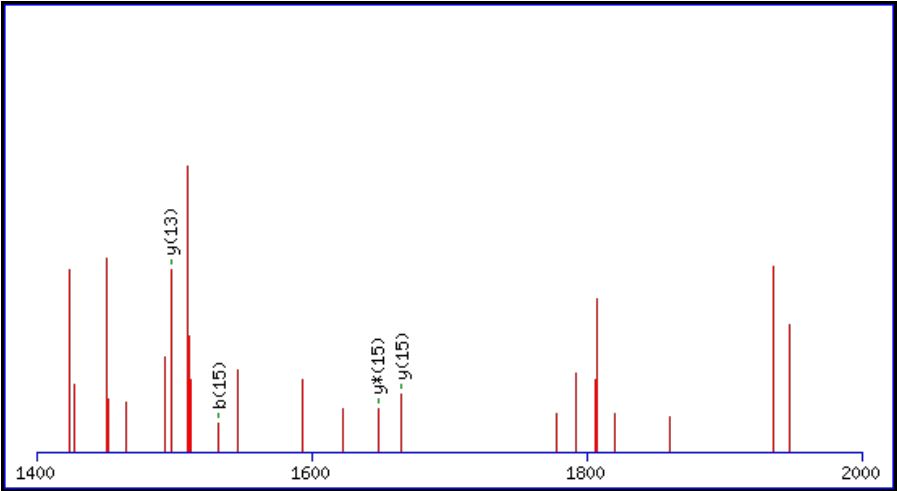
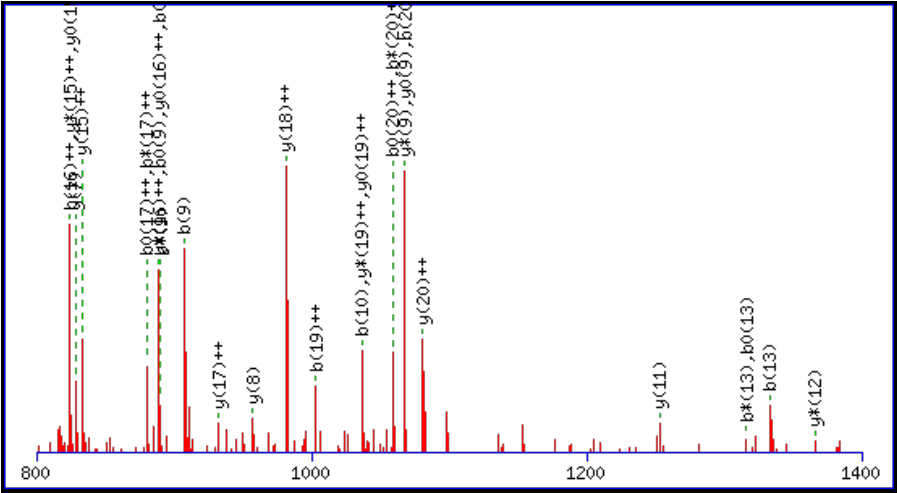
Spectrum No: 60; Query: 50562; Rank: 1

Peptide View

MS/MS Fragmentation of **KAQPAQPADEPAEKADPEMEH**
Found in **IPI00016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1

Match to Query 50562: 2288.047242 from(763.689690,3+)
Title: 091224LimSK_Exosome3_05.523.523.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

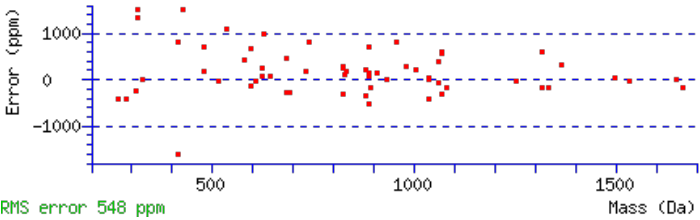
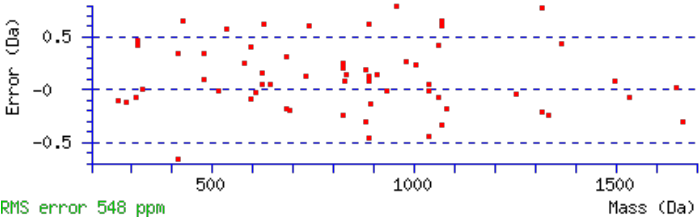




Monoisotopic mass of neutral peptide Mr(calc): 2288.0379
Fixed modifications: Carbamidomethyl (C)
Ions Score: 45 Expect: 0.01
Matches (**Bold Red**): 61/208 fragment ions using 102 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	129.1022	65.0548	112.0757	56.5415			K							21
2	200.1394	100.5733	183.1128	92.0600			A	2160.9502	1080.9788	2143.9237	1072.4655	2142.9397	1071.9735	20
3	328.1979	164.6026	311.1714	156.0893			Q	2089.9131	1045.4602	2072.8866	1036.9469	2071.9026	1036.4549	19
4	425.2507	213.1290	408.2241	204.6157			P	1961.8545	981.4309	1944.8280	972.9176	1943.8440	972.4256	18
5	496.2878	248.6475	479.2613	240.1343			A	1864.8018	932.9045	1847.7752	924.3913	1846.7912	923.8992	17
6	624.3464	312.6768	607.3198	304.1636			Q	1793.7647	897.3860	1776.7381	888.8727	1775.7541	888.3807	16
7	721.3992	361.2032	704.3726	352.6899			P	1665.7061	833.3567	1648.6795	824.8434	1647.6955	824.3514	15
8	792.4363	396.7218	775.4097	388.2085			A	1568.6533	784.8303	1551.6268	776.3170	1550.6428	775.8250	14
9	907.4632	454.2352	890.4367	445.7220	889.4526	445.2300	D	1497.6162	749.3117	1480.5897	740.7985	1479.6057	740.3065	13
10	1036.5058	518.7565	1019.4793	510.2433	1018.4952	509.7513	E	1382.5893	691.7983	1365.5627	683.2850	1364.5787	682.7930	12
11	1133.5586	567.2829	1116.5320	558.7696	1115.5480	558.2776	P	1253.5467	627.2770	1236.5201	618.7637	1235.5361	618.2717	11
12	1204.5957	602.8015	1187.5691	594.2882	1186.5851	593.7962	A	1156.4939	578.7506	1139.4674	570.2373	1138.4834	569.7453	10
13	1333.6383	667.3228	1316.6117	658.8095	1315.6277	658.3175	E	1085.4568	543.2320	1068.4303	534.7188	1067.4462	534.2268	9
14	1461.7332	731.3703	1444.7067	722.8570	1443.7227	722.3650	K	956.4142	478.7107	939.3877	470.1975	938.4036	469.7055	8
15	1532.7703	766.8888	1515.7438	758.3755	1514.7598	757.8835	A	828.3192	414.6633			810.3087	405.6580	7
16	1647.7973	824.4023	1630.7707	815.8890	1629.7867	815.3970	D	757.2821	379.1447			739.2716	370.1394	6
17	1776.8399	888.9236	1759.8133	880.4103	1758.8293	879.9183	E	642.2552	321.6312			624.2446	312.6259	5
18	1873.8926	937.4500	1856.8661	928.9367	1855.8821	928.4447	P	513.2126	257.1099			495.2020	248.1047	4
19	2004.9331	1002.9702	1987.9066	994.4569	1986.9226	993.9649	M	416.1598	208.5836			398.1493	199.5783	3

20	2133.9757	1067.4915	2116.9492	1058.9782	2115.9652	1058.4862	E	285.1193	143.0633			267.1088	134.0580	2
21							H	156.0768	78.5420					1



All matches to this query

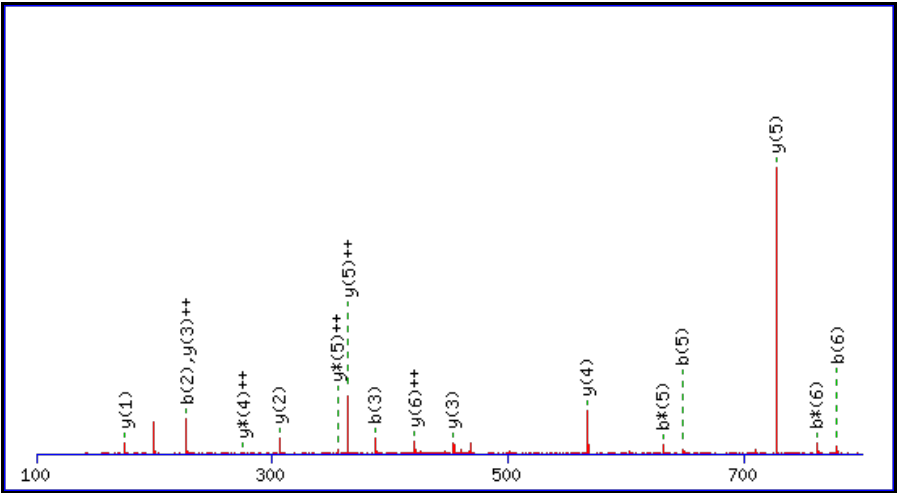
Score	Mr(calc):	Delta	Sequence
44.5	2288.0379	0.0094	KAQPAQPADEPAEKADPEMEH
9.0	2288.0686	-0.0213	GGADVSGGVSAPDISLGEGHLSVK
7.3	2287.0572	0.9900	KISPKGVDIVMDPLGGSDTAK
4.8	2287.0498	0.9975	QGLKSPQESLSDLGAIESLR
4.2	2286.0318	2.0155	NLPTKEQNFSHSISENFSK
4.2	2286.0318	2.0155	NLPTKEQNFSHSISENFSK
3.9	2287.0368	1.0105	WVNAQFSKEYQKHMETF
3.3	2288.0459	0.0013	MIGPTHGQMTVTRLVNTLK
3.3	2286.0384	2.0088	DVQSLSLRIMLAIEILTK
2.9	2287.0572	0.9900	KISPKGVDIVMDPLGGSDTAK

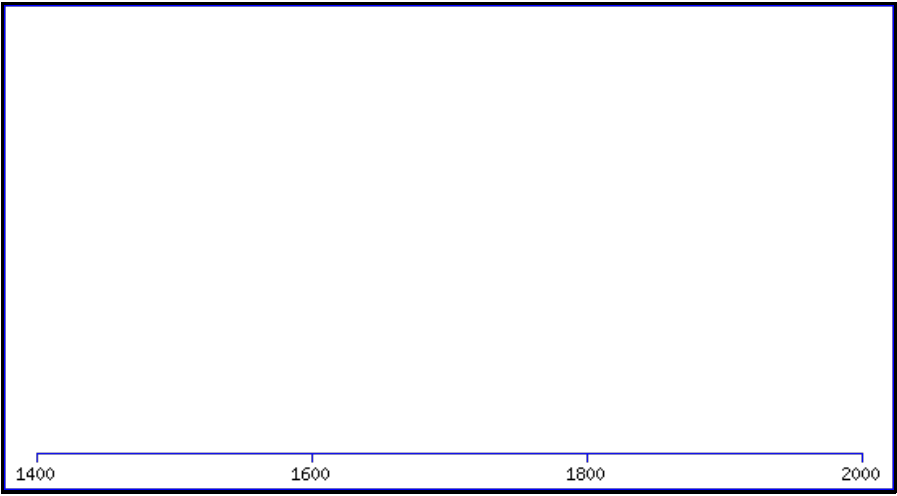
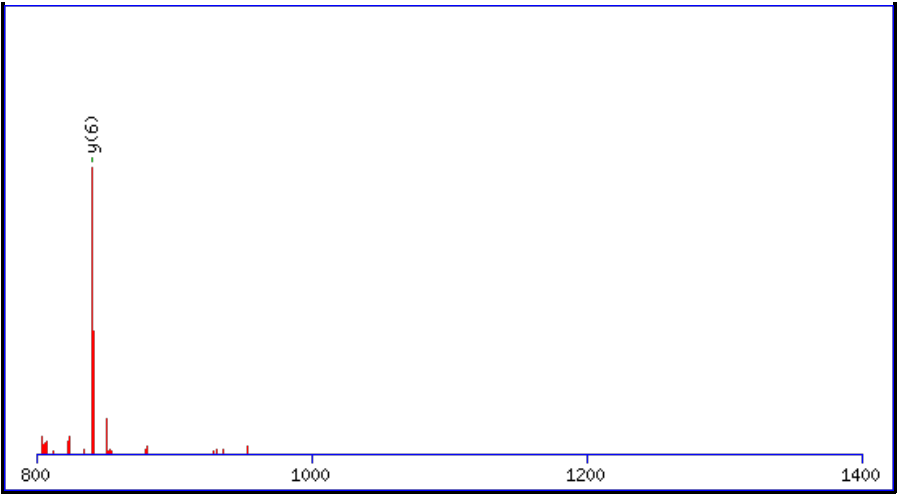
Spectrum No: 61; Query: 1985; Rank: 1

Peptide View

MS/MS Fragmentation of **LLCNFMR**
Found in **IPI00016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1

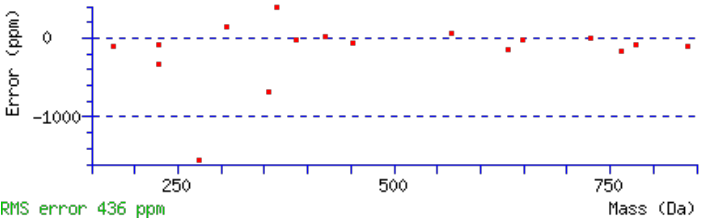
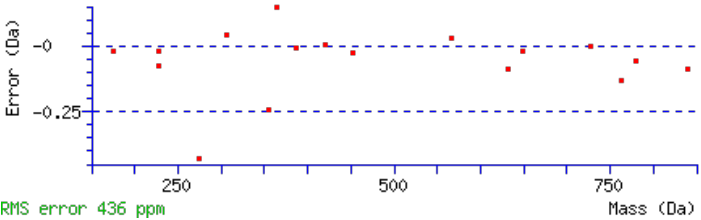
Match to Query 1985: 952.466588 from(477.240570,2+)
Title: 091224LimSK_Exosome3_06.3045.3045.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 952.4623
Fixed modifications: Carbamidomethyl (C)
Ions Score: 45 Expect: 0.0048
Matches (Bold Red): 17/42 fragment ions using 26 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	114.0913	57.5493			L					7
2	227.1754	114.0913			L	840.3855	420.6964	823.3589	412.1831	6
3	387.2061	194.1067			C	727.3014	364.1544	710.2749	355.6411	5
4	501.2490	251.1281	484.2224	242.6149	N	567.2708	284.1390	550.2442	275.6258	4
5	648.3174	324.6623	631.2908	316.1491	F	453.2279	227.1176	436.2013	218.6043	3
6	779.3579	390.1826	762.3313	381.6693	M	306.1594	153.5834	289.1329	145.0701	2
7					R	175.1190	88.0631	158.0924	79.5498	1



All matches to this query

Score	Mr(calc):	Delta	Sequence
44.8	952.4623	0.0043	LLCNFMR
19.1	952.4743	-0.0077	IIQISSGR

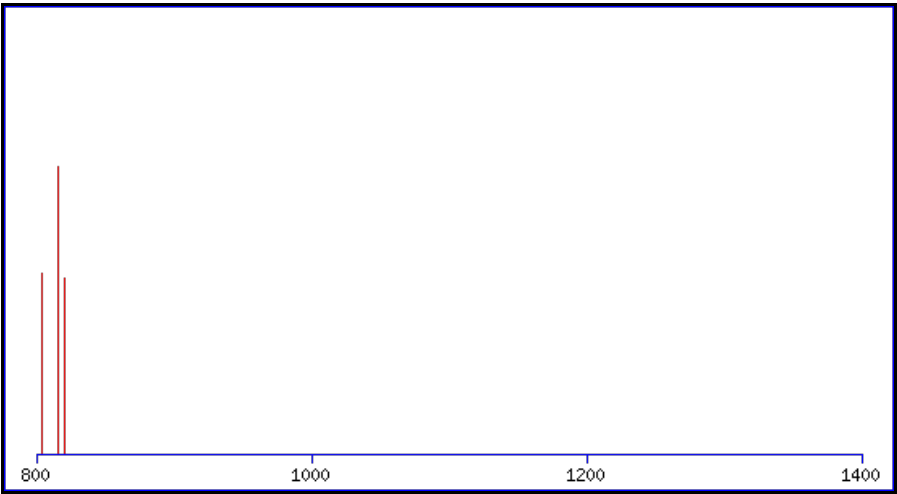
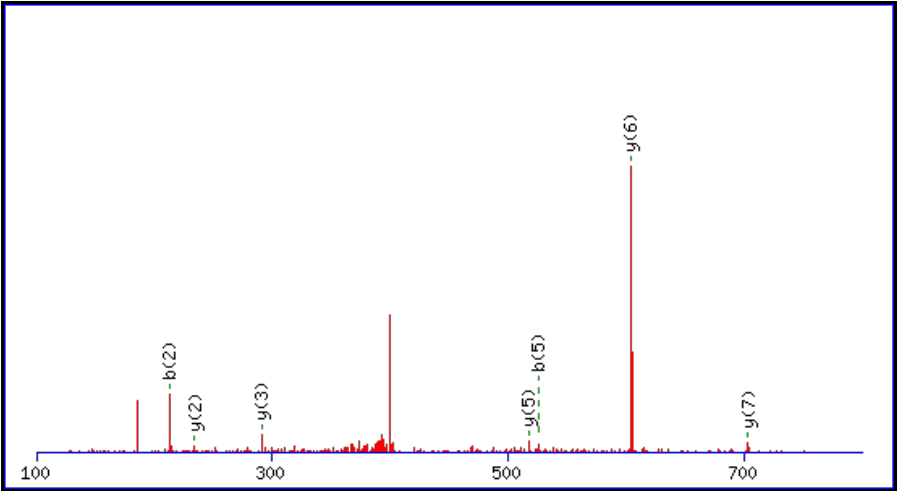
16.9	952.4743	-0.0077	LLSNAISR
15.6	952.4743	-0.0077	LLVQTGSR
14.4	952.4630	0.0036	LIEETR
14.3	952.4743	-0.0077	IIQISSGR
13.8	952.4743	-0.0077	LLVQTGSR
13.1	951.4539	1.0127	GSGGRGLLVG
12.2	952.4630	0.0036	LLELETR
10.2	952.4743	-0.0077	LLEKSQR

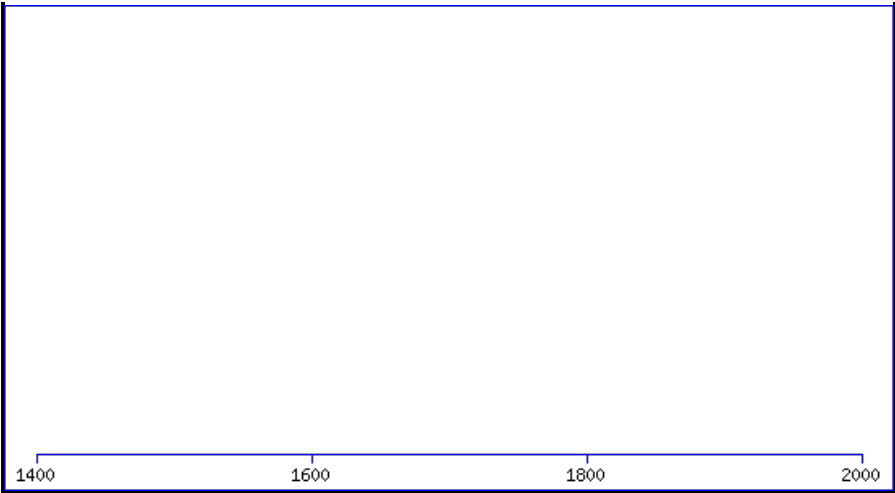
Spectrum No: 62; Query: 398; Rank: 1

Peptide View

MS/MS Fragmentation of **LVSLIGSK**
Found in **IPI00016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1

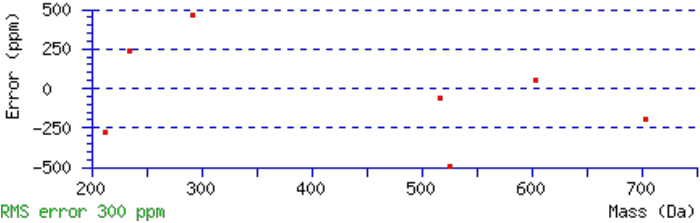
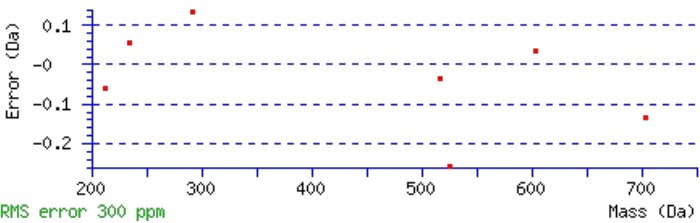
Match to Query 398: 815.515368 from(408.764960,2+)
Title: 091224LimSK_Exosome3_06.1657.1657.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 815.5116
Fixed modifications: Carbamidomethyl (C)
Ions Score: 38 Expect: 0.0067
Matches (**Bold Red**): 7/64 fragment ions using 15 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							8
2	213.1598	107.0835			V	703.4349	352.2211	686.4083	343.7078	685.4243	343.2158	7
3	300.1918	150.5995	282.1812	141.5942	S	604.3665	302.6869	587.3399	294.1736	586.3559	293.6816	6
4	413.2758	207.1416	395.2653	198.1363	L	517.3344	259.1709	500.3079	250.6576	499.3239	250.1656	5
5	526.3599	263.6836	508.3493	254.6783	I	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	4
6	583.3814	292.1943	565.3708	283.1890	G	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
7	670.4134	335.7103	652.4028	326.7051	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
8					K	147.1128	74.0600	130.0863	65.5468			1



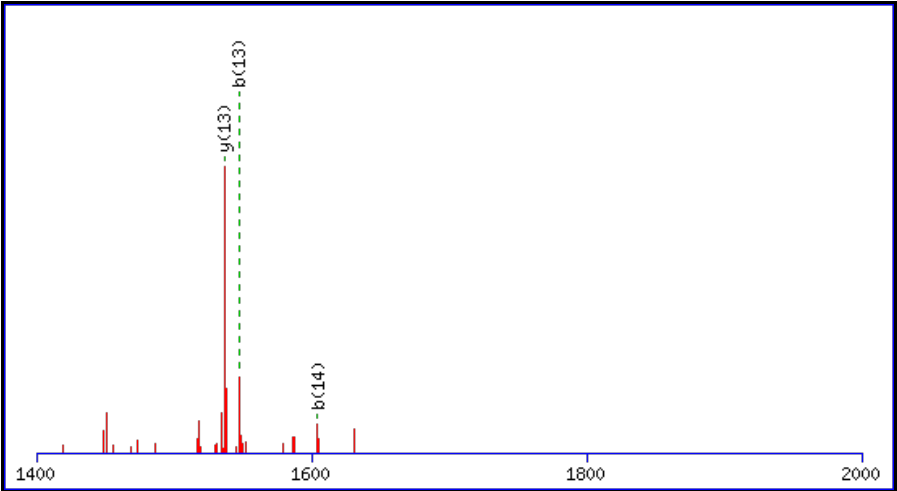
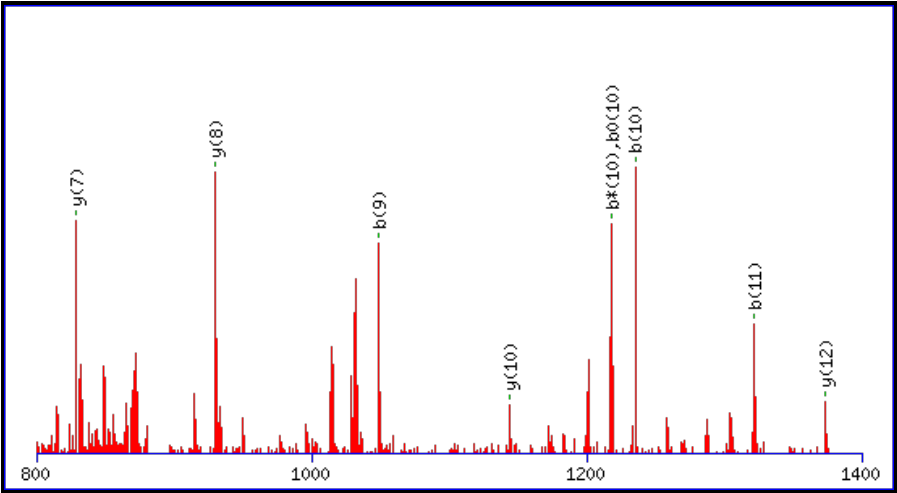
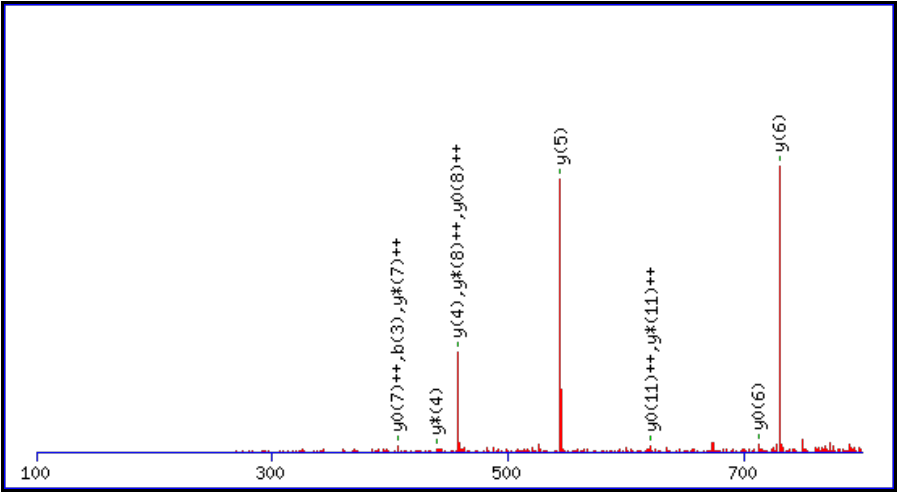
All matches to this query

Score	Mr(calc):	Delta	Sequence
37.7	815.5116	0.0037	LVSLIGSK
18.3	815.5116	0.0037	IVSISLGK
10.4	815.5116	0.0037	VISKLEK
8.2	815.5116	0.0037	IVELSKK
8.2	815.5116	0.0037	IVTVEKK
8.2	815.5116	0.0037	LYVTKEK
7.7	813.5072	2.0082	LPSTLRK
6.4	813.5072	2.0082	AILQKNK
5.3	815.5229	-0.0075	ISLLRSK
3.2	815.5229	-0.0075	LSVLRTK

Peptide View

MS/MS Fragmentation of **NQYDNDVTWSPQGR**
Found in **IPI00016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1

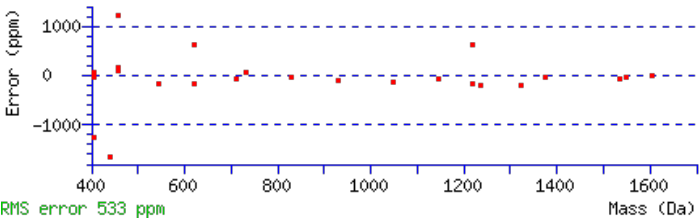
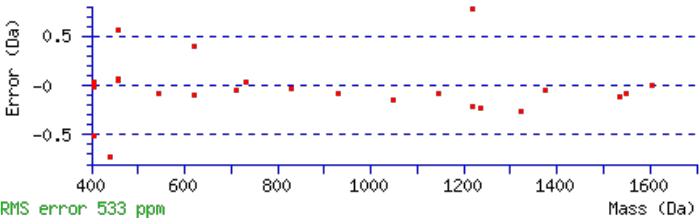
Match to Query 32590: 1777.813028 from(889.913790,2+)
Title: 091224LimSK_Exosome3_07.3191.3191.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide **Mr(calc):** 1777.8020
Fixed modifications: Carbamidomethyl (C)
Ions Score: 72 **Expect:** 1.4e-005
Matches (Bold Red): 24/154 fragment ions using 37 most intense peaks

		++		++	0	0++			++		++	0	0++	
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#	b	b	b*	b*	b	b	Seq.	y	y	y*	y*	y	y	#
1	115.0502	58.0287	98.0237	49.5155			N							15
2	243.1088	122.0580	226.0822	113.5448			Q	1664.7663	832.8868	1647.7398	824.3735	1646.7558	823.8815	14
3	406.1721	203.5897	389.1456	195.0764			Y	1536.7077	768.8575	1519.6812	760.3442	1518.6972	759.8522	13
4	521.1991	261.1032	504.1725	252.5899	503.1885	252.0979	D	1373.6444	687.3258	1356.6179	678.8126	1355.6339	678.3206	12
5	635.2420	318.1246	618.2154	309.6114	617.2314	309.1193	N	1258.6175	629.8124	1241.5909	621.2991	1240.6069	620.8071	11
6	750.2689	375.6381	733.2424	367.1248	732.2584	366.6328	D	1144.5745	572.7909	1127.5480	564.2776	1126.5640	563.7856	10
7	849.3373	425.1723	832.3108	416.6590	831.3268	416.1670	V	1029.5476	515.2774	1012.5211	506.7642	1011.5370	506.2722	9
8	950.3850	475.6961	933.3585	467.1829	932.3745	466.6909	T	930.4792	465.7432	913.4526	457.2300	912.4686	456.7380	8
9	1049.4534	525.2304	1032.4269	516.7171	1031.4429	516.2251	V	829.4315	415.2194	812.4050	406.7061	811.4209	406.2141	7
10	1235.5327	618.2700	1218.5062	609.7567	1217.5222	609.2647	W	730.3631	365.6852	713.3366	357.1719	712.3525	356.6799	6
11	1322.5648	661.7860	1305.5382	653.2727	1304.5542	652.7807	S	544.2838	272.6455	527.2572	264.1323	526.2732	263.6402	5
12	1419.6175	710.3124	1402.5910	701.7991	1401.6070	701.3071	P	457.2518	229.1295	440.2252	220.6162			4
13	1547.6761	774.3417	1530.6496	765.8284	1529.6655	765.3364	Q	360.1990	180.6031	343.1724	172.0899			3
14	1604.6976	802.8524	1587.6710	794.3392	1586.6870	793.8471	G	232.1404	116.5738	215.1139	108.0606			2
15							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

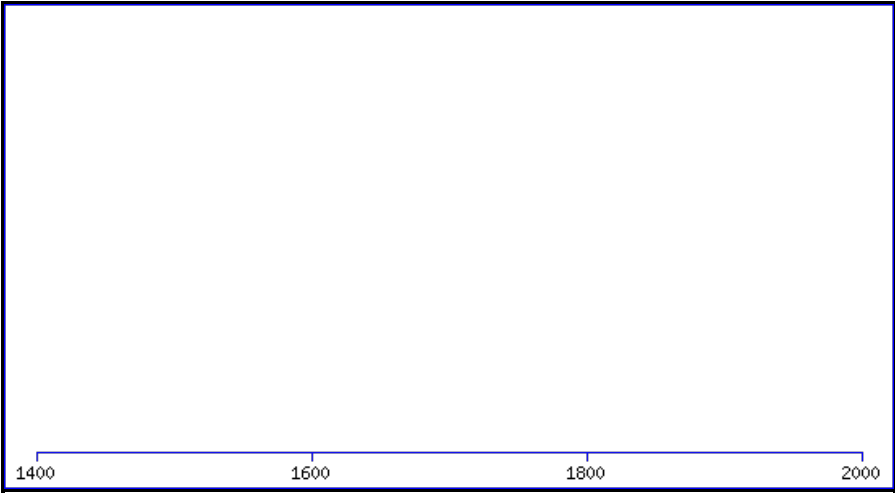
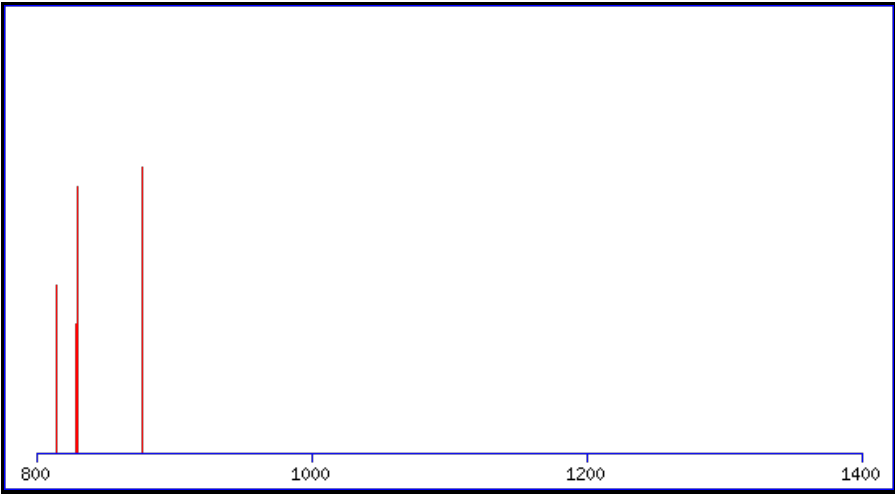
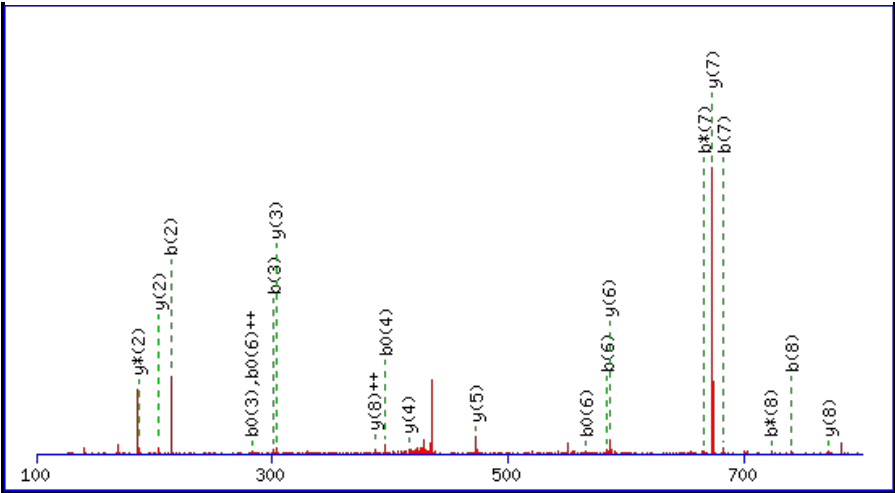
Score	Mr(calc):	Delta	Sequence
72.5	1777.8020	0.0110	NOYDNDVTWSPQGR
9.4	1775.7909	2.0222	XLKMETPGMTTPSLK
6.6	1777.8221	-0.0091	VPERGVGNSGDSVRGGR
5.0	1775.8239	1.9891	XLKMETPGMTTPSLK
5.0	1775.7909	2.0222	XLKMETPGMTTPSLK
4.5	1776.8068	1.0062	MKSLPCLLLSAQTR
3.9	1775.7930	2.0200	SGSSPLGVVTKAASMPK
3.7	1777.8294	-0.0164	MDLAGARPRPGLSEGR
3.6	1776.8043	1.0087	SIHEQDTNVNNSVLK
3.5	1775.7930	2.0200	SGSSPLGVVTKAASMPK

Spectrum No: 64; Query: 1100; Rank: 1

Peptide View

MS/MS Fragmentation of **NVSIGIVGK**
Found in **IP100016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1

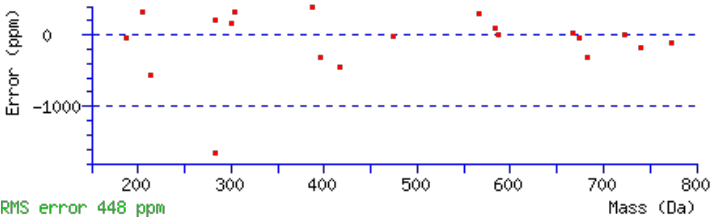
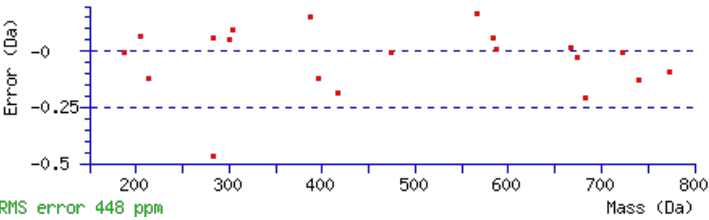
Match to Query 1100: 885.532028 from(443.773290,2+)
Title: 091224LimSK_Exosome3_06.1634.1634.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 885.5284
Fixed modifications: Carbamidomethyl (C)
Ions Score: 45 Expect: 0.0027
Matches (**Bold Red**): 20/80 fragment ions using 45 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							9
2	214.1186	107.5629	197.0921	99.0497			V	772.4927	386.7500	755.4662	378.2367	754.4822	377.7447	8
3	301.1506	151.0790	284.1241	142.5657	283.1401	142.0737	S	673.4243	337.2158	656.3978	328.7025	655.4137	328.2105	7
4	414.2347	207.6210	397.2082	199.1077	396.2241	198.6157	I	586.3923	293.6998	569.3657	285.1865			6
5	471.2562	236.1317	454.2296	227.6185	453.2456	227.1264	G	473.3082	237.1577	456.2817	228.6445			5
6	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	I	416.2867	208.6470	399.2602	200.1337			4

7	683.4087	342.2080	666.3821	333.6947	665.3981	333.2027	V	303.2027	152.1050	286.1761	143.5917			3
8	740.4301	370.7187	723.4036	362.2054	722.4195	361.7134	G	204.1343	102.5708	187.1077	94.0575			2
9							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

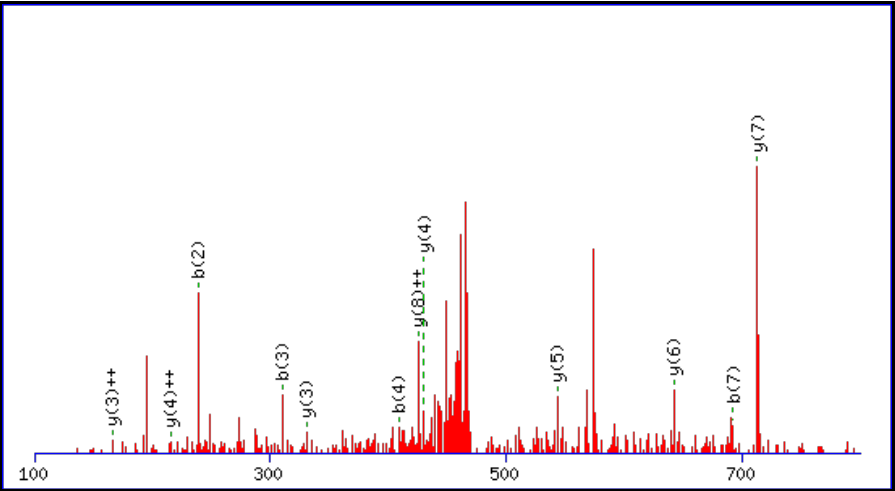
Score	Mr(calc):	Delta	Sequence
44.6	885.5284	0.0037	NVSIGIVGK
10.7	884.5232	1.0088	WLLGIAGR
7.3	885.5283	0.0037	DALQKALK
6.5	885.5284	0.0037	LVIQTQGK
6.0	885.5284	0.0037	GELTVVLR
4.9	884.5232	1.0088	WLLGQLR
3.3	884.5232	1.0088	VLWLAQR
2.9	885.5297	0.0024	WLRGARK
2.9	885.5297	0.0024	WRQLRK
2.3	885.5396	-0.0076	GVGKSAIVR

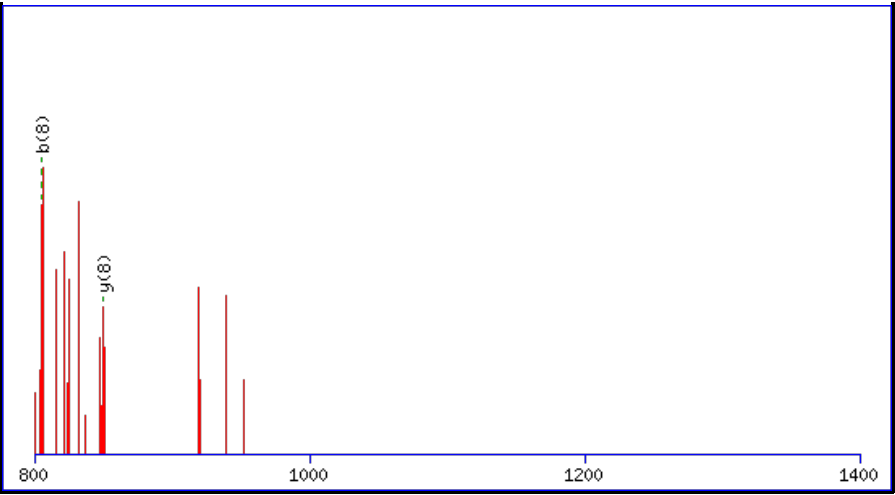
Spectrum No: 65; Query: 1975; Rank: 1

Peptide View

MS/MS Fragmentation of **THAVLVALK**
Found in **IP100016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1

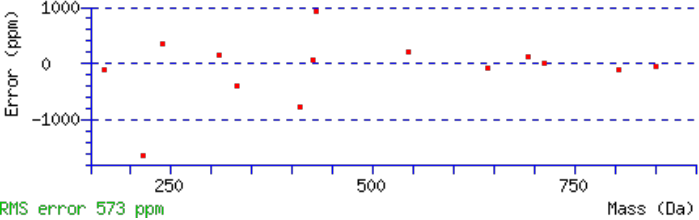
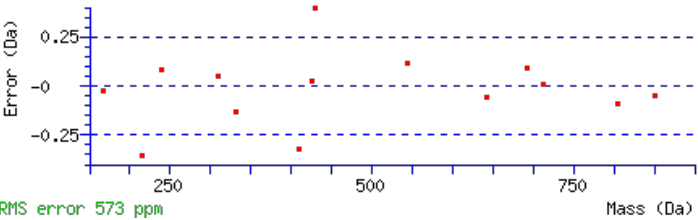
Match to Query 1975: 950.595808 from(476.305180,2+)
Title: 091224LimSK_Exosome3_06.1003.1003.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 950.5913
Fixed modifications: Carbamidomethyl (C)
Ions Score: 23 Expect: 0.062
Matches (**Bold Red**): 14/64 fragment ions using 63 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	102.0550	51.5311	84.0444	42.5258	T					9
2	239.1139	120.0606	221.1033	111.0553	H	850.5509	425.7791	833.5244	417.2658	8
3	310.1510	155.5791	292.1404	146.5738	A	713.4920	357.2496	696.4654	348.7364	7
4	409.2194	205.1133	391.2088	196.1081	V	642.4549	321.7311	625.4283	313.2178	6
5	522.3035	261.6554	504.2929	252.6501	L	543.3865	272.1969	526.3599	263.6836	5
6	621.3719	311.1896	603.3613	302.1843	V	430.3024	215.6548	413.2758	207.1416	4
7	692.4090	346.7081	674.3984	337.7028	A	331.2340	166.1206	314.2074	157.6074	3
8	805.4931	403.2502	787.4825	394.2449	L	260.1969	130.6021	243.1703	122.0888	2
9					K	147.1128	74.0600	130.0863	65.5468	1



All matches to this query

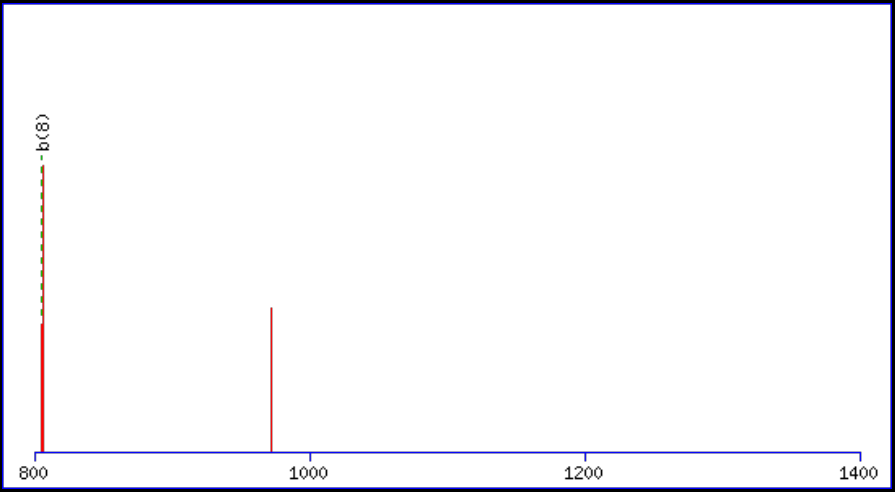
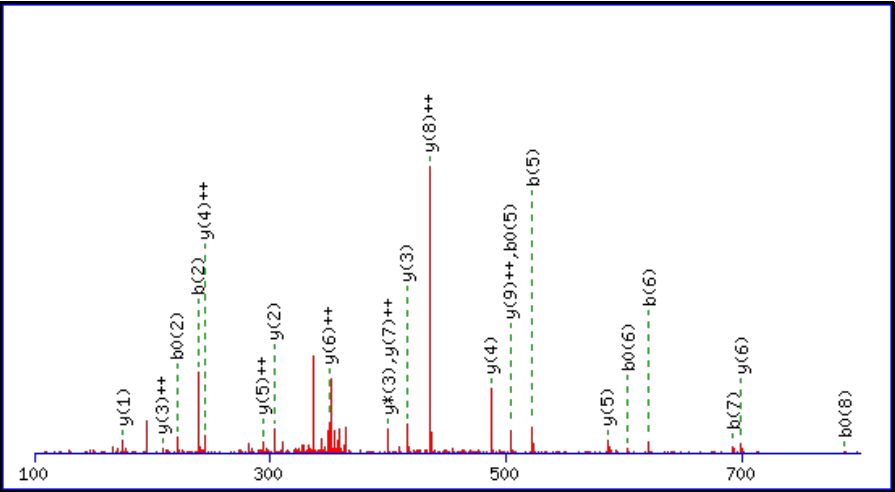
Score	Mr(calc):	Delta	Sequence
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22.6	950.5913	0.0045	THAVLVALK
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Spectrum No: 66; Query: 4930; Rank: 1

Peptide View

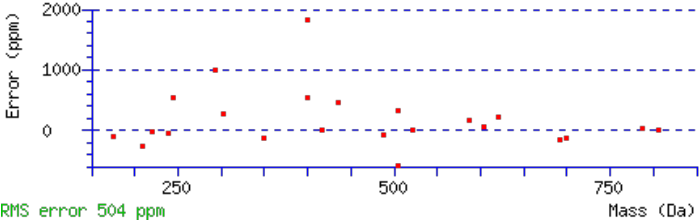
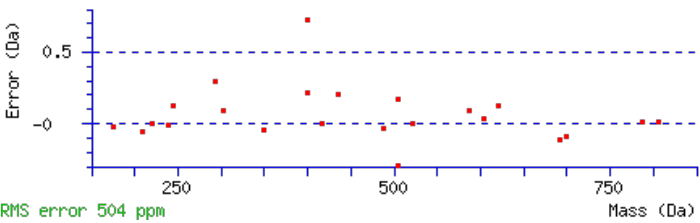
MS/MS Fragmentation of **THAVLVALKR**
Found in **IPI00016832**, Tax_Id=9606 Gene_Symbol=PSMA1 Isoform Short of Proteasome subunit alpha type-1
Match to Query 4930: 1106.697102 from(369.906310,3+)
Title: 091224LimSK_Exosome3_05.720.720.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1106.6924
Fixed modifications: Carbamidomethyl (C)
Ions Score: 43 Expect: 0.0004
Matches (**Bold Red**): 23/74 fragment ions using 44 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	102.0550	51.5311			84.0444	42.5258	T					10
2	239.1139	120.0606			221.1033	111.0553	H	1006.6520	503.8296	989.6255	495.3164	9
3	310.1510	155.5791			292.1404	146.5738	A	869.5931	435.3002	852.5665	426.7869	8
4	409.2194	205.1133			391.2088	196.1081	V	798.5560	399.7816	781.5294	391.2684	7
5	522.3035	261.6554			504.2929	252.6501	L	699.4876	350.2474	682.4610	341.7341	6
6	621.3719	311.1896			603.3613	302.1843	V	586.4035	293.7054	569.3770	285.1921	5
7	692.4090	346.7081			674.3984	337.7028	A	487.3351	244.1712	470.3085	235.6579	4
8	805.4931	403.2502			787.4825	394.2449	L	416.2980	208.6526	399.2714	200.1394	3
9	933.5880	467.2976	916.5615	458.7844	915.5774	458.2924	K	303.2139	152.1106	286.1874	143.5973	2
10							R	175.1190	88.0631	158.0924	79.5498	1



All matches to this query

Score	Mr(calc):	Delta	Sequence
43.5	1106.6924	0.0047	THAVLVALKR
4.8	1105.6859	1.0112	IYLSNLKKK
1.9	1105.6859	1.0112	ALHLLAVLEK

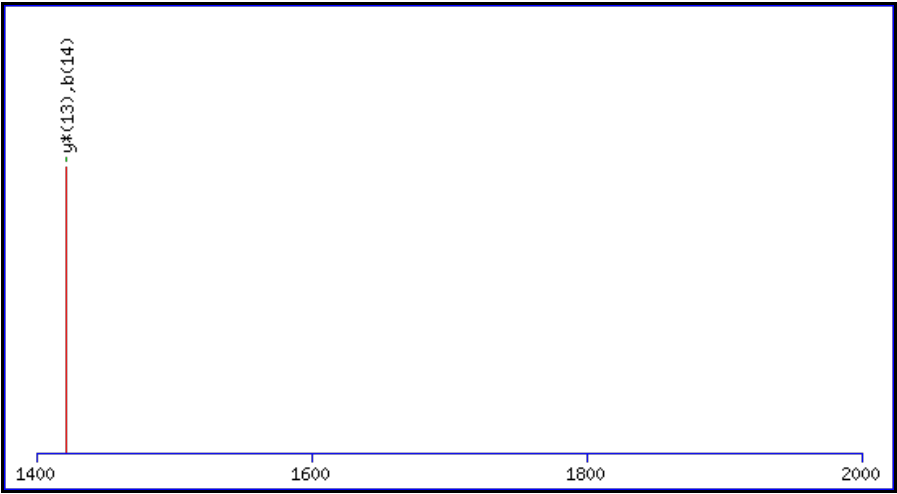
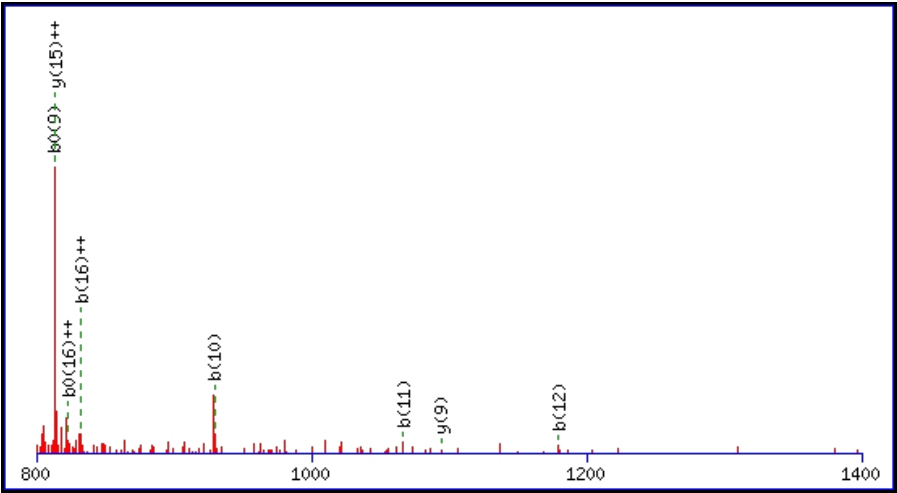
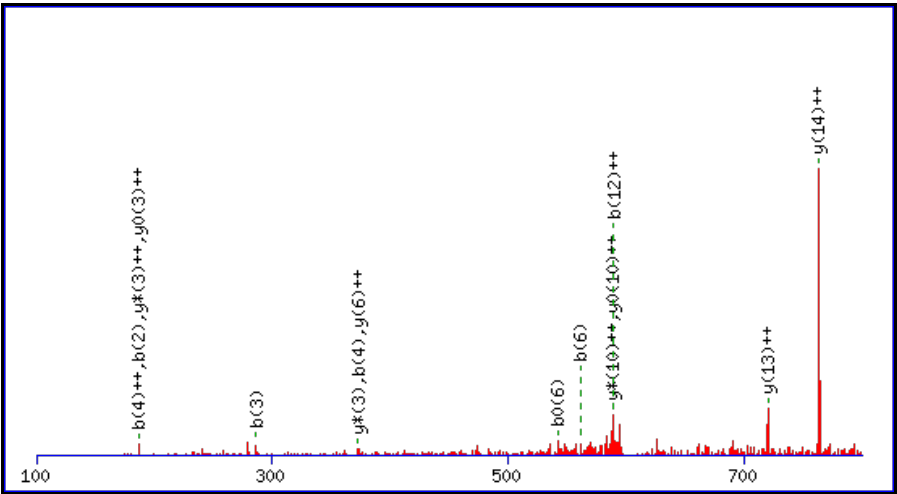
Spectrum No: 67; Query: 33737; Rank: 1

Peptide View

MS/MS Fragmentation of **DAVSGMGVIVHIEKDK**
Found in **IP100028004**, Tax_Id=9606 Gene_Symbol=PSMB3 Proteasome subunit beta type-3

Match to Query 33737: 1810.975902 from(604.665910,3+)
Title: 091224LimSK_Exosome3_06.7253.7253.3.dta

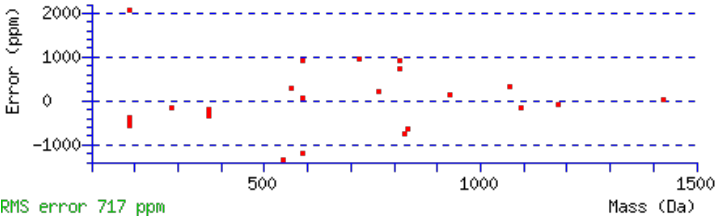
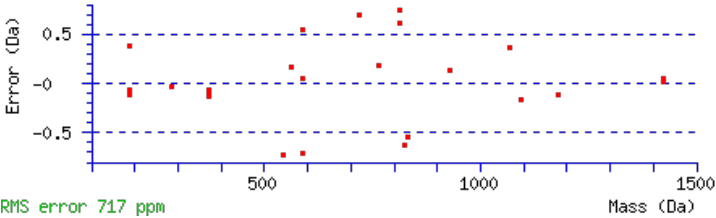
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1809.9659
Fixed modifications: Carbamidomethyl (C)
Ions Score: 25 Expect: 0.29
Matches (Bold Red): 25/162 fragment ions using 58 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							17
2	187.0713	94.0393			169.0608	85.0340	A	1695.9462	848.4767	1678.9197	839.9635	1677.9356	839.4715	16
3	286.1397	143.5735			268.1292	134.5682	V	1624.9091	812.9582	1607.8825	804.4449	1606.8985	803.9529	15
4	373.1718	187.0895			355.1612	178.0842	S	1525.8407	763.4240	1508.8141	754.9107	1507.8301	754.4187	14
5	430.1932	215.6003			412.1827	206.5950	G	1438.8086	719.9080	1421.7821	711.3947	1420.7981	710.9027	13

6	561.2337	281.1205			543.2232	272.1152	M	1381.7872	691.3972	1364.7606	682.8840	1363.7766	682.3919	12
7	618.2552	309.6312			600.2446	300.6259	G	1250.7467	625.8770	1233.7201	617.3637	1232.7361	616.8717	11
8	717.3236	359.1654			699.3130	350.1602	V	1193.7252	597.3663	1176.6987	588.8530	1175.7147	588.3610	10
9	830.4077	415.7075			812.3971	406.7022	I	1094.6568	547.8320	1077.6303	539.3188	1076.6463	538.8268	9
10	929.4761	465.2417			911.4655	456.2364	V	981.5728	491.2900	964.5462	482.7767	963.5622	482.2847	8
11	1066.5350	533.7711			1048.5244	524.7659	H	882.5043	441.7558	865.4778	433.2425	864.4938	432.7505	7
12	1179.6191	590.3132			1161.6085	581.3079	I	745.4454	373.2264	728.4189	364.7131	727.4349	364.2211	6
13	1292.7031	646.8552			1274.6926	637.8499	I	632.3614	316.6843	615.3348	308.1710	614.3508	307.6790	5
14	1421.7457	711.3765			1403.7351	702.3712	E	519.2773	260.1423	502.2508	251.6290	501.2667	251.1370	4
15	1549.8407	775.4240	1532.8141	766.9107	1531.8301	766.4187	K	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	3
16	1664.8676	832.9374	1647.8411	824.4242	1646.8571	823.9322	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
17							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

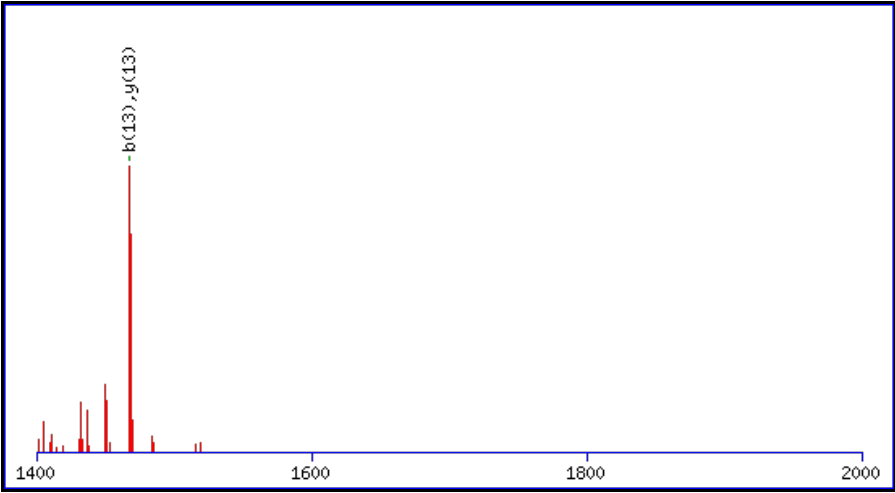
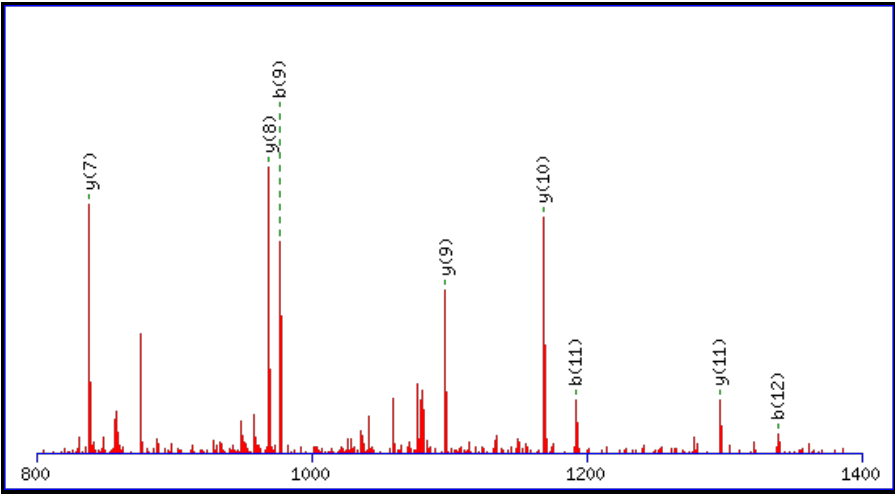
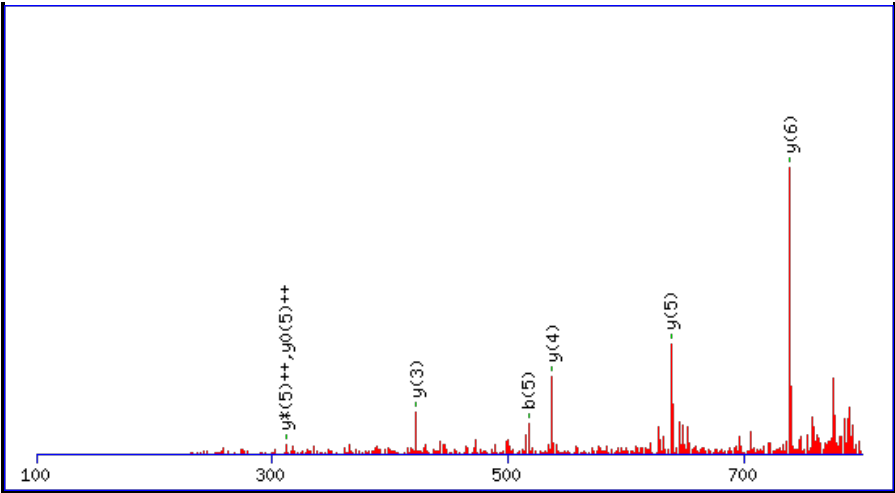
Score	Mr(calc):	Delta	Sequence
25.1	1809.9659	1.0100	DAVSGMGVIVHIIKDK
9.2	1810.9690	0.0069	WVVDLDRGLVLNAEGR
7.2	1810.9649	0.0110	EALGKAKDANNGNLQLR
5.0	1810.9703	0.0056	XVFSNHALRRLQER
2.6	1810.9876	-0.0117	LGFNVTLSLFMRNKR
2.1	1810.9764	-0.0005	HSFSVSSCVIPLPIR
1.7	1808.9858	1.9901	ALQQFLYVQMAKELK
0.6	1809.9697	1.0062	QGVSPKPLQSSRPSQSK
0.2	1810.9901	-0.0142	EGGLKLIQIODNGTGIR

Spectrum No: 68; Query: 26203; Rank: 1

Peptide View

MS/MS Fragmentation of **FGIQAQMVTTFQK**
Found in **IPI00028004**, Tax_Id=9606 Gene_Symbol=PSMB3 Proteasome subunit beta type-3

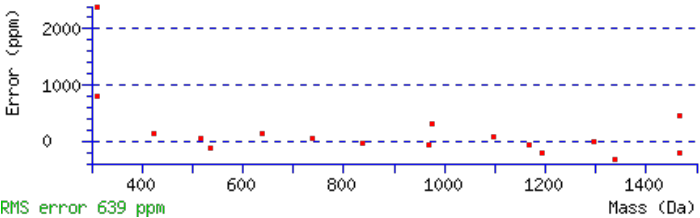
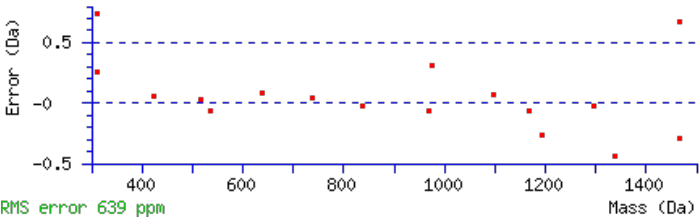
Match to Query 26203: 1612.803968 from(807.409260,2+)
Title: 091224LimSK_Exosome3_06.4983.4983.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1612.7919
Fixed modifications: Carbamidomethyl (C)
Ions Score: 107 Expect: 3.6e-009
Matches (**Bold Red**): 17/128 fragment ions using 17 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							14
2	205.0972	103.0522					G	1466.7308	733.8690	1449.7042	725.3558	1448.7202	724.8638	13
3	318.1812	159.5942					I	1409.7093	705.3583	1392.6828	696.8450	1391.6988	696.3530	12
4	446.2398	223.6235	429.2132	215.1103			Q	1296.6253	648.8163	1279.5987	640.3030	1278.6147	639.8110	11
5	517.2769	259.1421	500.2504	250.6288			A	1168.5667	584.7870	1151.5401	576.2737	1150.5561	575.7817	10
6	645.3355	323.1714	628.3089	314.6581			Q	1097.5296	549.2684	1080.5030	540.7552	1079.5190	540.2631	9

7	776.3760	388.6916	759.3494	380.1784			M	969.4710	485.2391	952.4444	476.7259	951.4604	476.2339	8
8	875.4444	438.2258	858.4178	429.7126			V	838.4305	419.7189	821.4040	411.2056	820.4199	410.7136	7
9	976.4921	488.7497	959.4655	480.2364	958.4815	479.7444	T	739.3621	370.1847	722.3355	361.6714	721.3515	361.1794	6
10	1077.5397	539.2735	1060.5132	530.7602	1059.5292	530.2682	T	638.3144	319.6608	621.2879	311.1476	620.3039	310.6556	5
11	1192.5667	596.7870	1175.5401	588.2737	1174.5561	587.7817	D	537.2667	269.1370	520.2402	260.6237	519.2562	260.1317	4
12	1339.6351	670.3212	1322.6086	661.8079	1321.6245	661.3159	F	422.2398	211.6235	405.2132	203.1103			3
13	1467.6937	734.3505	1450.6671	725.8372	1449.6831	725.3452	Q	275.1714	138.0893	258.1448	129.5761			2
14							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

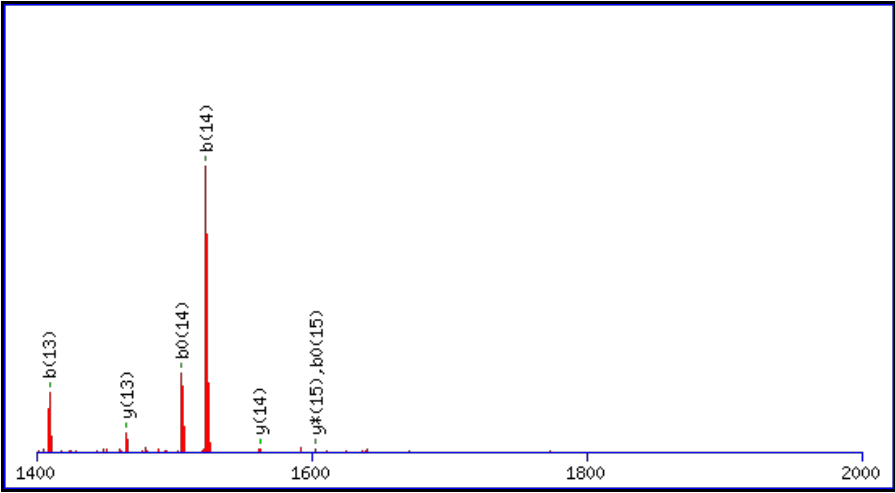
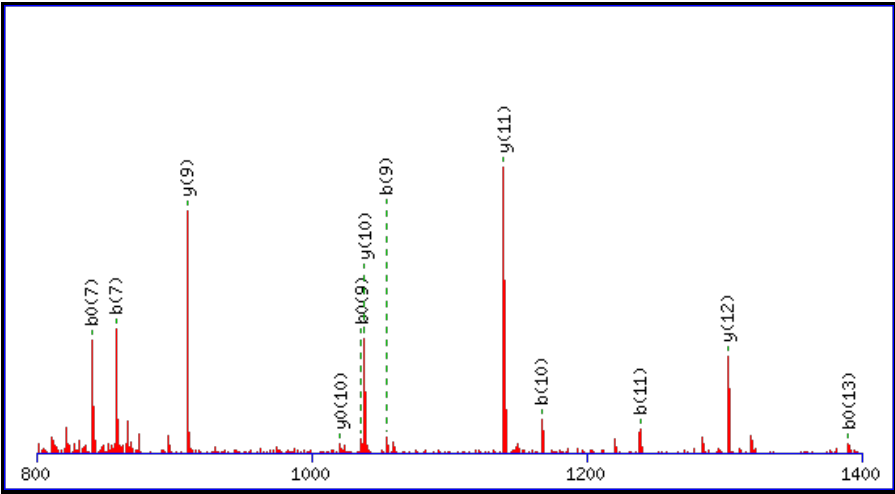
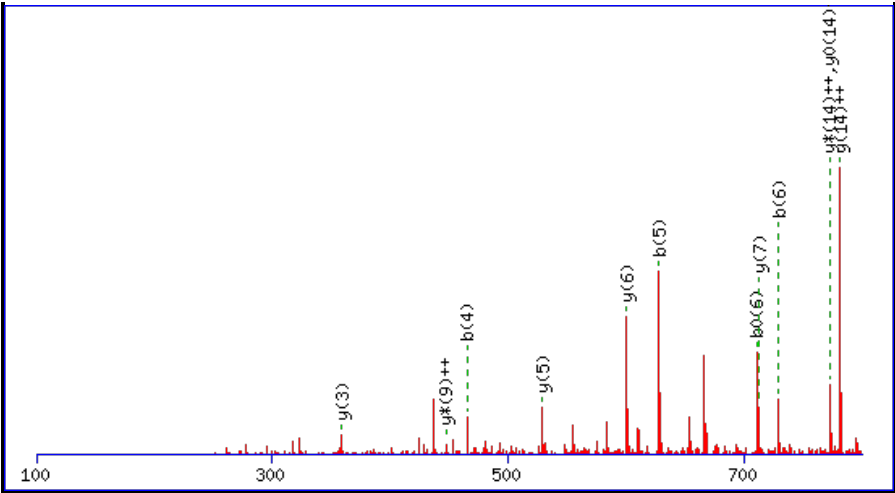
Score	Mr(calc):	Delta	Sequence
107.2	1612.7919	0.0120	FGIQAQMVTTDFQK
8.2	1610.7851	2.0189	CNTNTAIELKLVR
6.4	1612.8178	-0.0138	MATGCTLPQLPRPR
6.1	1612.7902	0.0138	IYYTGKYQSLGIK
5.9	1610.7851	2.0189	CNTNTAIELKLVR
5.9	1612.7902	0.0138	IYYTGKYQSLGIK
5.8	1612.8056	-0.0017	THSPSSKDEQSIGLK
4.9	1612.7902	0.0138	IYYTGKYQSLGIK
4.2	1612.7902	0.0138	IYYTGKYQSLGIK
3.8	1612.8130	-0.0091	MSPALQDLSQPEGLK

Spectrum No: 69; Query: 32090; Rank: 1

Peptide View

MS/MS Fragmentation of **FGPYYTEPVIAGLDPK**
Found in **IPI00028004**, Tax_Id=9606 Gene_Symbol=PSMB3 Proteasome subunit beta type-3

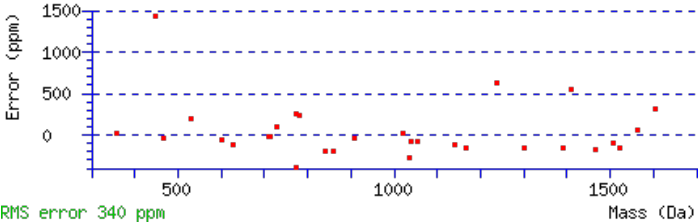
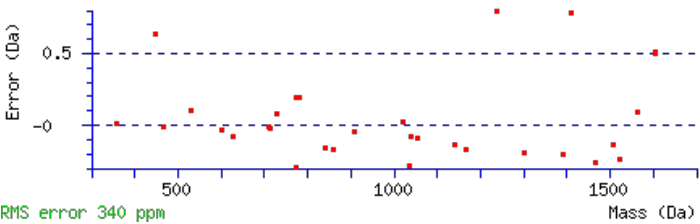
Match to Query 32090: 1765.904368 from(883.959460,2+)
Title: 091224LimSK_Exosome3_07.6121.6121.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1765.8927
Fixed modifications: Carbamidomethyl (C)
Ions Score: 47 Expect: 0.0035
Matches (**Bold Red**): 31/136 fragment ions using 67 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415			F							16
2	205.0972	103.0522			G	1619.8316	810.4194	1602.8050	801.9061	1601.8210	801.4141	15
3	302.1499	151.5786			P	1562.8101	781.9087	1545.7835	773.3954	1544.7995	772.9034	14
4	465.2132	233.1103			Y	1465.7573	733.3823	1448.7308	724.8690	1447.7468	724.3770	13
5	628.2766	314.6419			Y	1302.6940	651.8506	1285.6674	643.3374	1284.6834	642.8454	12
6	729.3243	365.1658	711.3137	356.1605	T	1139.6307	570.3190	1122.6041	561.8057	1121.6201	561.3137	11

7	858.3668	429.6871	840.3563	420.6818	E	1038.5830	519.7951	1021.5564	511.2819	1020.5724	510.7898	10
8	955.4196	478.2134	937.4090	469.2082	P	909.5404	455.2738	892.5138	446.7606	891.5298	446.2686	9
9	1054.4880	527.7477	1036.4775	518.7424	V	812.4876	406.7475	795.4611	398.2342	794.4771	397.7422	8
10	1167.5721	584.2897	1149.5615	575.2844	I	713.4192	357.2132	696.3927	348.7000	695.4087	348.2080	7
11	1238.6092	619.8082	1220.5986	610.8030	A	600.3352	300.6712	583.3086	292.1579	582.3246	291.6659	6
12	1295.6307	648.3190	1277.6201	639.3137	G	529.2980	265.1527	512.2715	256.6394	511.2875	256.1474	5
13	1408.7147	704.8610	1390.7042	695.8557	L	472.2766	236.6419	455.2500	228.1287	454.2660	227.6366	4
14	1523.7417	762.3745	1505.7311	753.3692	D	359.1925	180.0999	342.1660	171.5866	341.1819	171.0946	3
15	1620.7944	810.9009	1602.7839	801.8956	P	244.1656	122.5864	227.1390	114.0731			2
16					K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

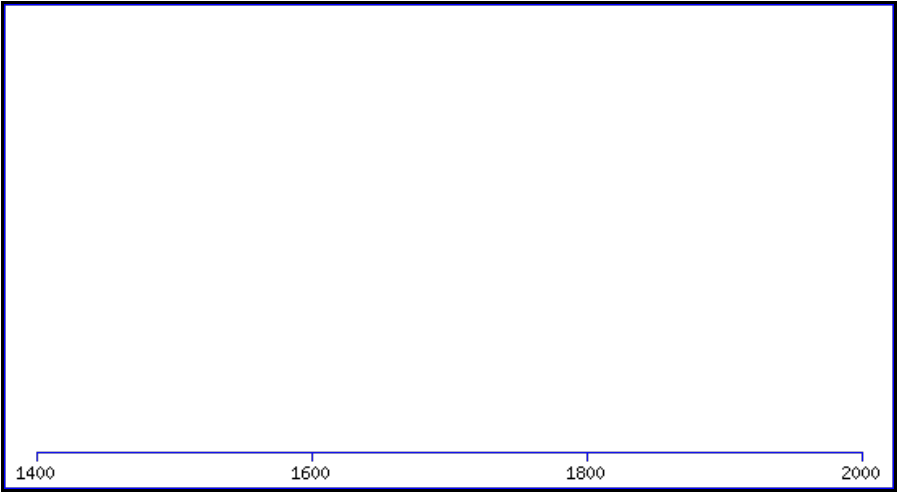
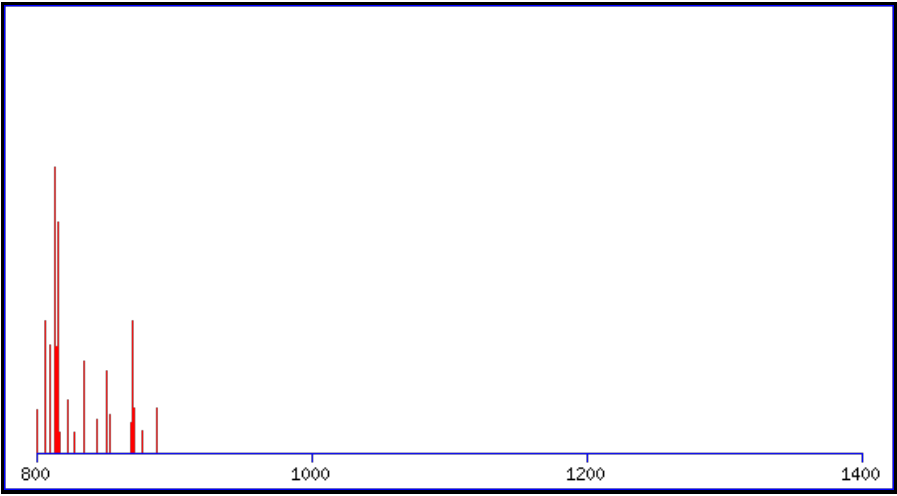
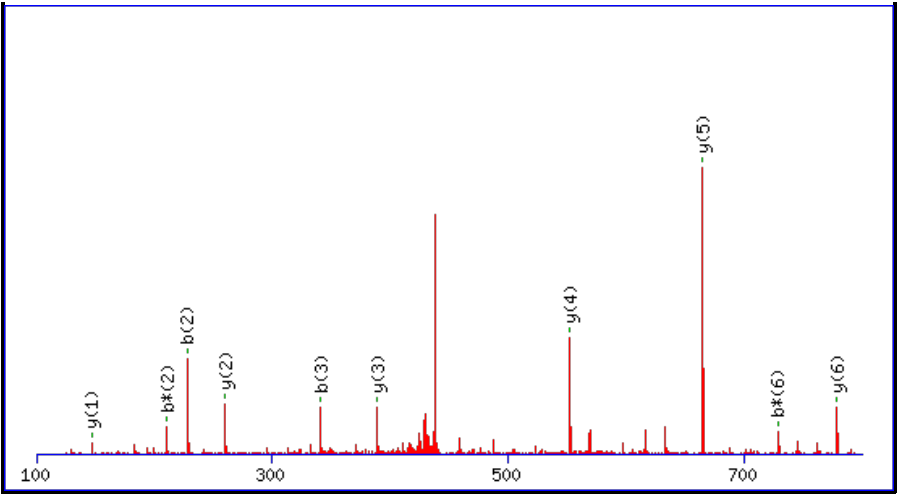
Score	Mr(calc):	Delta	Sequence
47.0	1765.8927	0.0117	FGPYYTEPVIAGLDPK
16.5	1763.9070	1.9973	SGGGEQLDILSVGILVK
5.6	1765.9161	-0.0117	EILQIMNKTISKPR
5.4	1765.8975	0.0069	IEATKKAESEIQAIR
5.3	1763.9110	1.9934	LQLYKLEIPDPDK
3.2	1765.8910	0.0134	RAGLLTGLGLTCDALR
2.8	1765.8975	0.0069	IEATKKAESEIQAIR
1.9	1764.9135	0.9909	VSNGLKAIRVEAVSDK
0.3	1764.9135	0.9909	ELRKAIEGSVTAQGVK
0.1	1764.8867	1.0177	DRNGTHLDAGTVEPKR

Spectrum No: 70; Query: 1153; Rank: 1

Peptide View

MS/MS Fragmentation of **LNLYELK**
Found in **IPI00028004**, Tax_Id=9606 Gene_Symbol=PSMB3 Proteasome subunit beta type-3

Match to Query 1153: 891.511088 from(446.762820,2+)
Title: 091224LimSK_Exosome3_07.3190.3190.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide **Mr(calc):** 891.5065
Fixed modifications: Carbamidomethyl (C)
Ions Score: 51 Expect: 0.00062
Matches (**Bold Red**): 10/58 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	114.0913	57.5493					L							7
2	228.1343	114.5708	211.1077	106.0575			N	779.4298	390.2185	762.4032	381.7053	761.4192	381.2132	6
3	341.2183	171.1128	324.1918	162.5995			L	665.3869	333.1971	648.3603	324.6838	647.3763	324.1918	5
4	504.2817	252.6445	487.2551	244.1312			Y	552.3028	276.6550	535.2762	268.1418	534.2922	267.6498	4
5	633.3243	317.1658	616.2977	308.6525	615.3137	308.1605	E	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
6	746.4083	373.7078	729.3818	365.1945	728.3978	364.7025	L	260.1969	130.6021	243.1703	122.0888			2

7

K

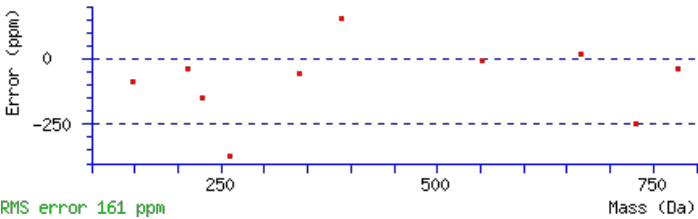
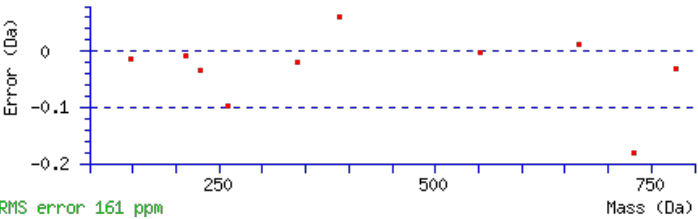
147.1128

74.0600

130.0863

65.5468

1



All matches to this query

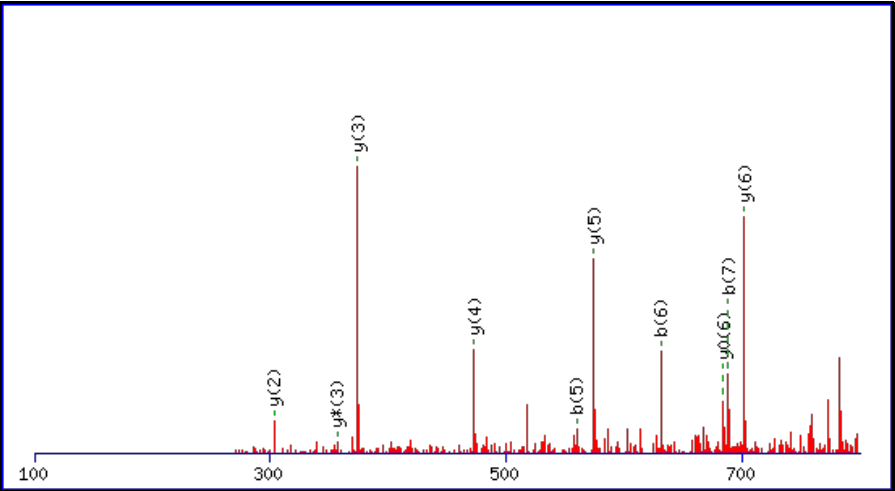
Score	Mr(calc):	Delta	Sequence
50.9	891.5065	0.0046	LNLYELK
36.6	891.5065	0.0045	VQLYELK
18.5	891.5065	0.0046	NLYLEIK
17.0	891.5065	0.0046	INYLIEK
16.7	891.5178	-0.0067	INVQKYK
16.4	891.5065	0.0046	YNLLELK
15.4	891.5065	0.0045	LVAGEYLK
15.4	891.5065	0.0045	IIDLGYAK
14.8	891.5065	0.0045	IIGDAYLK
10.0	891.5178	-0.0067	QVPNPLPK

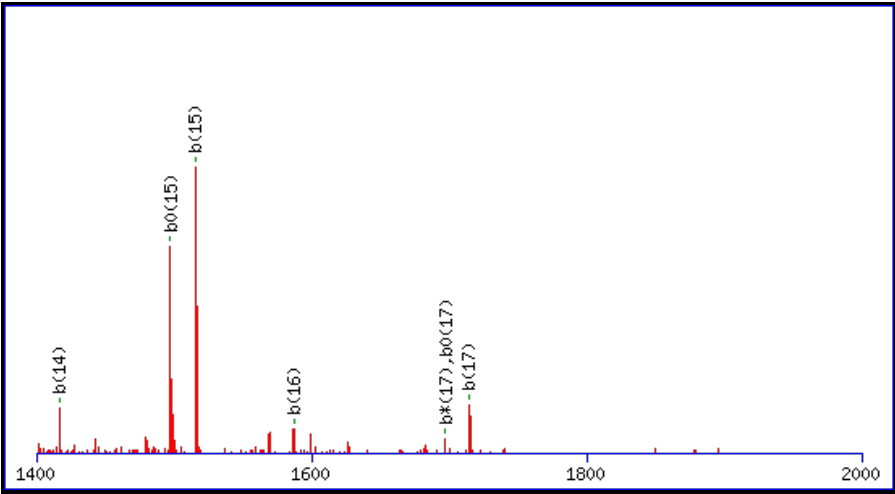
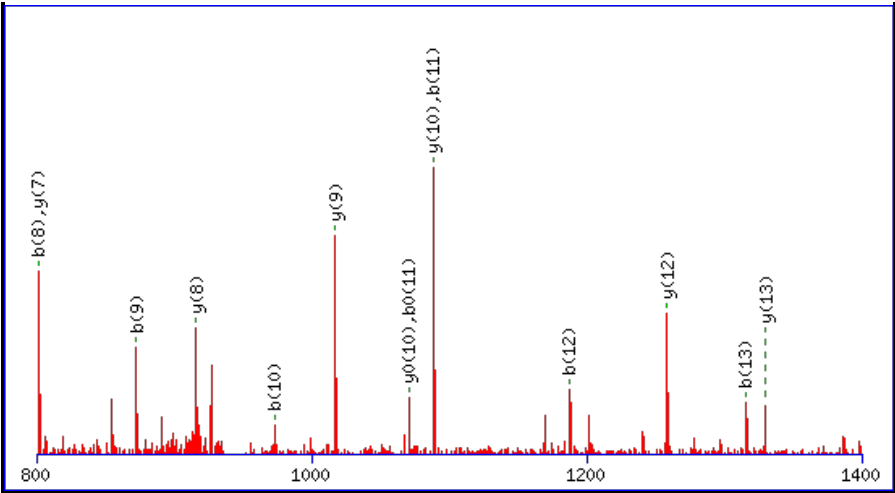
Spectrum No: 71; Query: 36128; Rank: 1

Peptide View

MS/MS Fragmentation of **LYIGLAGLATDVQTVAQR**
Found in **IPI00028004**, Tax_Id=9606 Gene_Symbol=PSMB3 Proteasome subunit beta type-3

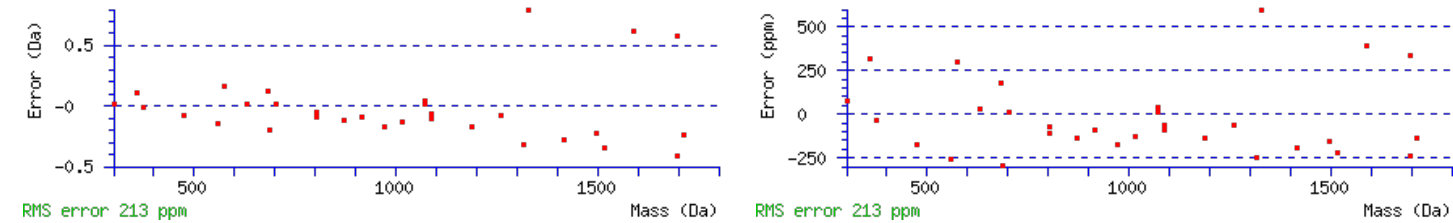
Match to Query 36128: 1888.053788 from(945.034170,2+)
Title: 091224LimSK_Exosome3_06.7721.7721.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1888.0418
Fixed modifications: Carbamidomethyl (C)
Ions Score: 97 Expect: 1.1e-008
Matches (Bold Red): 31/154 fragment ions using 50 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	277.1547	139.0810					Y	1775.9650	888.4862	1758.9385	879.9729	1757.9545	879.4809	17
3	390.2387	195.6230					I	1612.9017	806.9545	1595.8752	798.4412	1594.8911	797.9492	16
4	447.2602	224.1337					G	1499.8176	750.4125	1482.7911	741.8992	1481.8071	741.4072	15
5	560.3443	280.6758					L	1442.7962	721.9017	1425.7696	713.3884	1424.7856	712.8964	14
6	631.3814	316.1943					A	1329.7121	665.3597	1312.6856	656.8464	1311.7015	656.3544	13
7	688.4028	344.7051					G	1258.6750	629.8411	1241.6484	621.3279	1240.6644	620.8359	12
8	801.4869	401.2471					L	1201.6535	601.3304	1184.6270	592.8171	1183.6430	592.3251	11
9	872.5240	436.7656					A	1088.5695	544.7884	1071.5429	536.2751	1070.5589	535.7831	10
10	973.5717	487.2895			955.5611	478.2842	T	1017.5324	509.2698	1000.5058	500.7565	999.5218	500.2645	9
11	1088.5986	544.8030			1070.5881	535.7977	D	916.4847	458.7460	899.4581	450.2327	898.4741	449.7407	8
12	1187.6671	594.3372			1169.6565	585.3319	V	801.4577	401.2325	784.4312	392.7192	783.4472	392.2272	7
13	1315.7256	658.3665	1298.6991	649.8532	1297.7151	649.3612	Q	702.3893	351.6983	685.3628	343.1850	684.3787	342.6930	6
14	1416.7733	708.8903	1399.7468	700.3770	1398.7627	699.8850	T	574.3307	287.6690	557.3042	279.1557	556.3202	278.6637	5
15	1515.8417	758.4245	1498.8152	749.9112	1497.8312	749.4192	V	473.2831	237.1452	456.2565	228.6319			4
16	1586.8788	793.9431	1569.8523	785.4298	1568.8683	784.9378	A	374.2146	187.6110	357.1881	179.0977			3
17	1714.9374	857.9723	1697.9109	849.4591	1696.9269	848.9671	Q	303.1775	152.0924	286.1510	143.5791			2
18							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

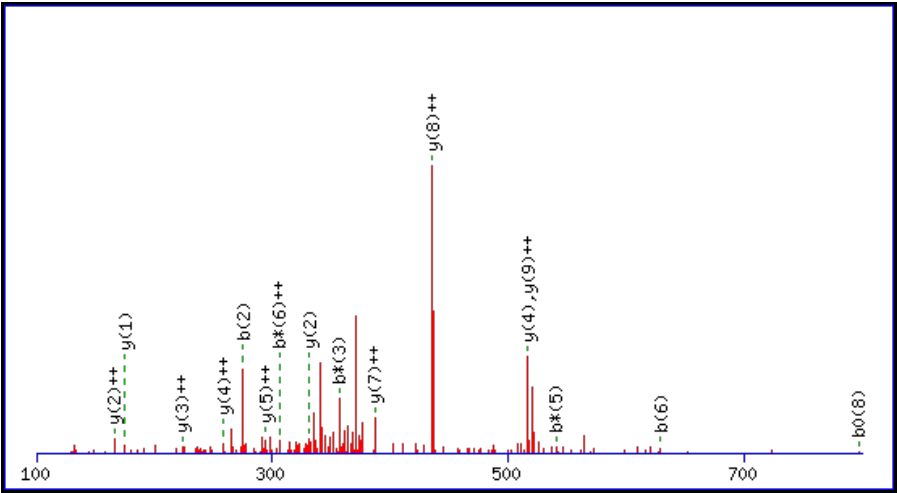
Score	Mr(calc):	Delta	Sequence
97.0	1888.0418	0.0120	LYIGLAGLATDVQTVAQR
13.1	1886.0560	1.9978	TAPSLVMVLSWKSGVRR
4.8	1886.0414	2.0124	GALLDFLWDLNAAIAKR
4.0	1888.0683	-0.0145	FNEVGKILGPQGNTIKR
3.8	1888.0643	-0.0105	GHGPTVGLLLSRGASPTLR
2.1	1887.0578	0.9960	AKNGTGKSGAYLIPLER
2.0	1888.0492	0.0046	MLLSLPFLQDAIQKK
1.8	1888.0431	0.0107	RLWGFESLLIRGAAGR
1.2	1887.0578	0.9960	NALEVDLGYLIITAARR

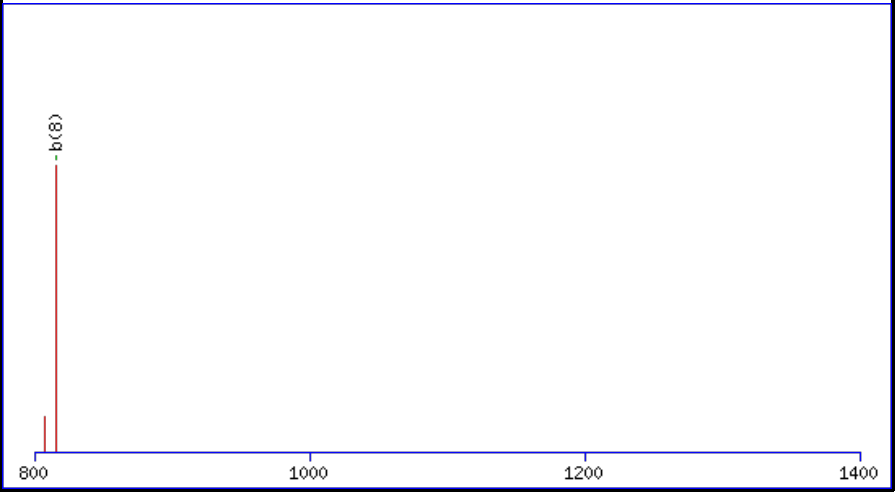
Spectrum No: 72; Query: 6084; Rank: 1

Peptide View

MS/MS Fragmentation of **NCVAIAADRR**
Found in **IP100028004**, Tax_Id=9606 Gene_Symbol=PSMB3 Proteasome subunit beta type-3

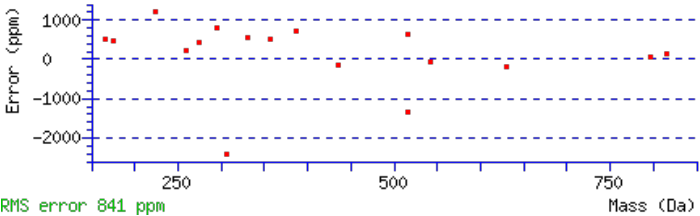
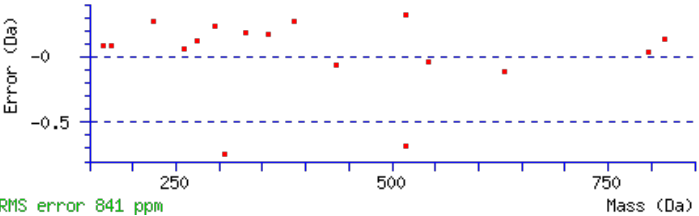
Match to Query 6084: 1144.581252 from(382.534360,3+)
Title: 091224LimSK_Exosome3_06.134.134.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1144.5771
Fixed modifications: Carbamidomethyl (C)
Ions Score: 25 Expect: 0.49
Matches (Bold Red): 17/90 fragment ions using 39 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							10
2	275.0809	138.0441	258.0543	129.5308			C	1031.5415	516.2744	1014.5149	507.7611	1013.5309	507.2691	9
3	374.1493	187.5783	357.1227	179.0650			V	871.5108	436.2591	854.4843	427.7458	853.5003	427.2538	8
4	445.1864	223.0968	428.1598	214.5836			A	772.4424	386.7248	755.4159	378.2116	754.4318	377.7196	7
5	558.2704	279.6389	541.2439	271.1256			I	701.4053	351.2063	684.3787	342.6930	683.3947	342.2010	6
6	629.3076	315.1574	612.2810	306.6441			A	588.3212	294.6643	571.2947	286.1510	570.3107	285.6590	5
7	700.3447	350.6760	683.3181	342.1627			A	517.2841	259.1457	500.2576	250.6324	499.2736	250.1404	4
8	815.3716	408.1894	798.3451	399.6762	797.3610	399.1842	D	446.2470	223.6271	429.2205	215.1139	428.2364	214.6219	3
9	971.4727	486.2400	954.4462	477.7267	953.4622	477.2347	R	331.2201	166.1137	314.1935	157.6004			2
10							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query



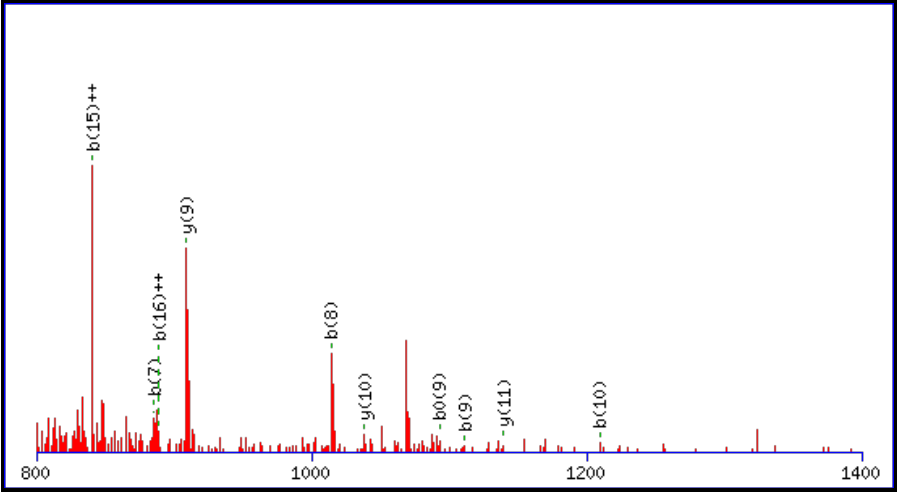
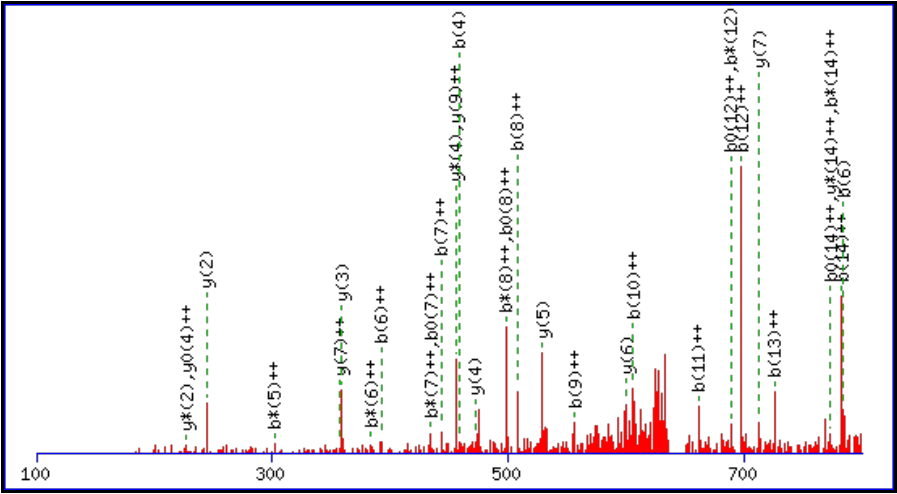
Score	Mr(calc):	Delta	Sequence
24.9	1144.5771	0.0041	NCVAIAADDR
11.7	1144.5771	0.0042	MAAAAAAGEARR
11.4	1142.5696	2.0116	SSVKSLSISR
9.8	1144.5910	-0.0098	SLMSSTAPPVR
9.4	1144.5699	0.0114	MLSAHWEKK
9.1	1143.5801	1.0011	RPLTEPPVR
8.1	1143.5884	0.9929	AEEAVNEVKR
7.8	1144.5836	-0.0024	ELEEKADDR
7.7	1142.5849	1.9964	VVLKSTFNR
7.0	1144.5924	-0.0111	LCGALGWRGR

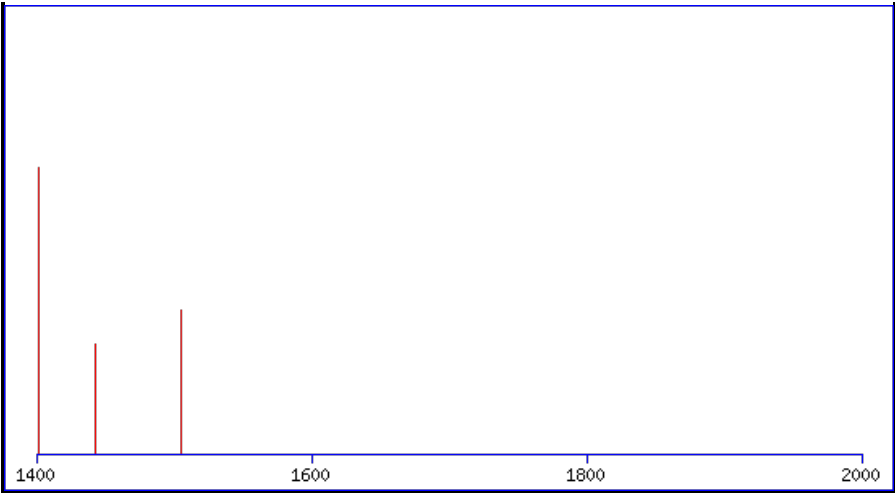
Spectrum No: 73; Query: 37082; Rank: 1

Peptide View

MS/MS Fragmentation of **RFGPYYTEPVIAGLDPK**
Found in **IPI00028004**, Tax_Id=9606 Gene_Symbol=PSMB3 Proteasome subunit beta type-3

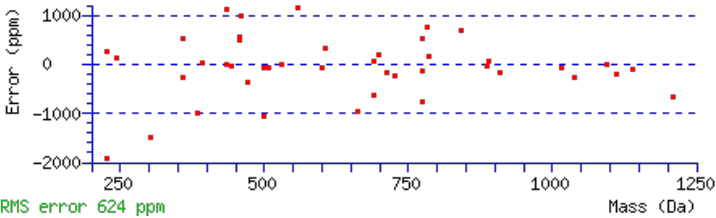
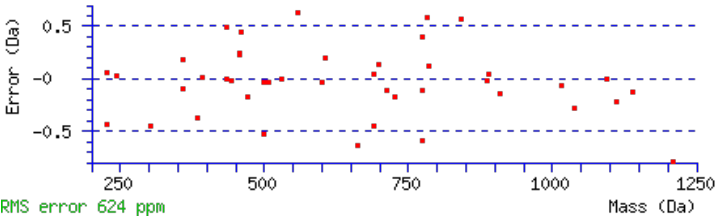
Match to Query 37082: 1923.006462 from(642.009430,3+)
Title: 091224LimSK_Exosome3_06.5711.5711.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1921.9938
Fixed modifications: Carbamidomethyl (C)
Ions Score: 34 Expect: 0.062
Matches (**Bold Red**): 43/176 fragment ions using 129 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							17
2	304.1768	152.5920	287.1503	144.0788			F	1766.9000	883.9536	1749.8734	875.4403	1748.8894	874.9483	16
3	361.1983	181.1028	344.1717	172.5895			G	1619.8316	810.4194	1602.8050	801.9061	1601.8210	801.4141	15
4	458.2510	229.6292	441.2245	221.1159			P	1562.8101	781.9087	1545.7835	773.3954	1544.7995	772.9034	14
5	621.3144	311.1608	604.2878	302.6475			Y	1465.7573	733.3823	1448.7308	724.8690	1447.7468	724.3770	13
6	784.3777	392.6925	767.3511	384.1792			Y	1302.6940	651.8506	1285.6674	643.3374	1284.6834	642.8454	12
7	885.4254	443.2163	868.3988	434.7030	867.4148	434.2110	T	1139.6307	570.3190	1122.6041	561.8057	1121.6201	561.3137	11
8	1014.4680	507.7376	997.4414	499.2243	996.4574	498.7323	E	1038.5830	519.7951	1021.5564	511.2819	1020.5724	510.7898	10
9	1111.5207	556.2640	1094.4942	547.7507	1093.5102	547.2587	P	909.5404	455.2738	892.5138	446.7606	891.5298	446.2686	9
10	1210.5891	605.7982	1193.5626	597.2849	1192.5786	596.7929	V	812.4876	406.7475	795.4611	398.2342	794.4771	397.7422	8
11	1323.6732	662.3402	1306.6467	653.8270	1305.6626	653.3350	I	713.4192	357.2132	696.3927	348.7000	695.4087	348.2080	7
12	1394.7103	697.8588	1377.6838	689.3455	1376.6998	688.8535	A	600.3352	300.6712	583.3086	292.1579	582.3246	291.6659	6
13	1451.7318	726.3695	1434.7052	717.8563	1433.7212	717.3642	G	529.2980	265.1527	512.2715	256.6394	511.2875	256.1474	5
14	1564.8158	782.9116	1547.7893	774.3983	1546.8053	773.9063	L	472.2766	236.6419	455.2500	228.1287	454.2660	227.6366	4
15	1679.8428	840.4250	1662.8162	831.9118	1661.8322	831.4197	D	359.1925	180.0999	342.1660	171.5866	341.1819	171.0946	3
16	1776.8956	888.9514	1759.8690	880.4381	1758.8850	879.9461	P	244.1656	122.5864	227.1390	114.0731			2
17							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
33.6	1921.9938	1.0127	REFPYYTEPVIAGLDPK
8.9	1922.0125	0.9939	DKTEKPDTVQLLTVKK
6.7	1920.9839	2.0226	LDKLSVLRLSVSYLR
6.2	1922.9900	0.0165	KARDMLGLEETQVILK
4.0	1920.9839	2.0226	LDKLSVLRLSVSYLR

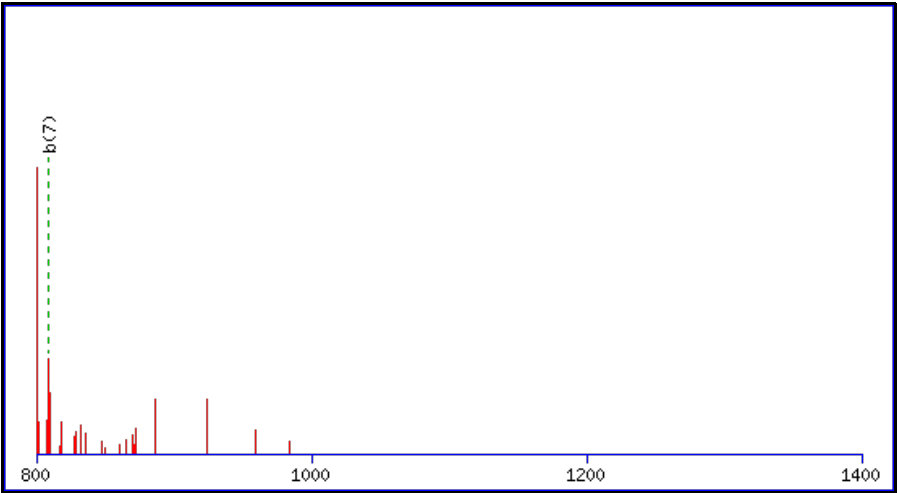
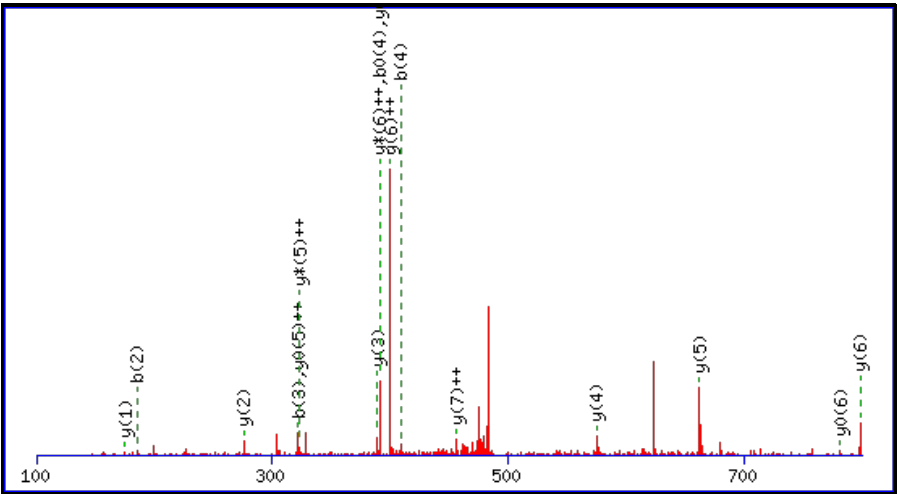
2.1	1921.9874	1.0191	TQGSEKAALQLQLNTIK
2.0	1921.9874	1.0191	KSEVENGPSVVTRILK
1.8	1923.0248	-0.0183	TXQDNPIALSPGPVSLR
1.8	1922.9884	0.0181	TXQDNPIALSPGPVSLR
1.0	1921.9874	1.0191	KSEVENGPSVVTRILK

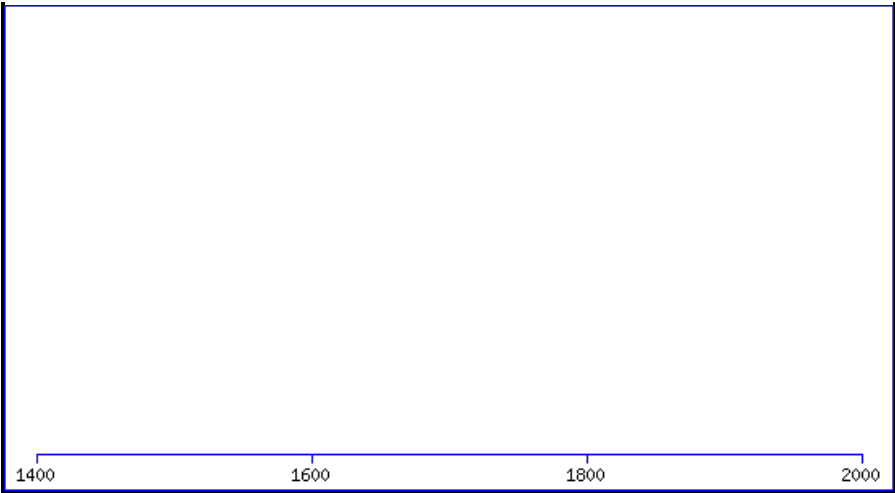
Spectrum No: 74; Query: 2474; Rank: 1

Peptide View

MS/MS Fragmentation of **AIHSWLTR**
Found in **IP100555956**, Tax_Id=9606 Gene_Symbol=PSMB4 Proteasome subunit beta type-4

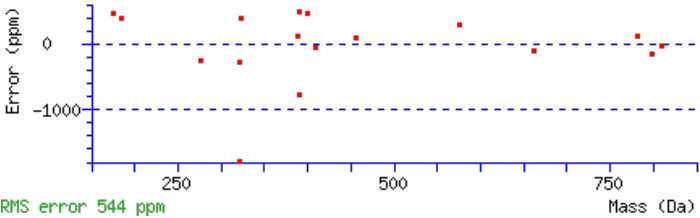
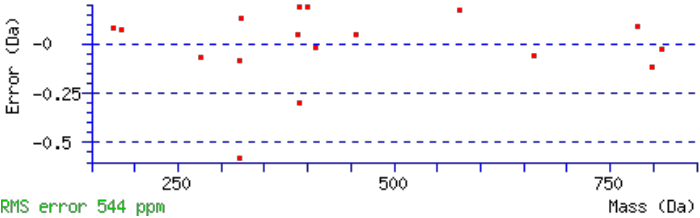
Match to Query 2474: 982.538708 from(492.276630,2+)
Title: 091224LimSK_Exosome3_06.1343.1343.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 982.5348
Fixed modifications: Carbamidomethyl (C)
Ions Score: 25 **Expect:** 0.26
Matches (Bold Red): 18/62 fragment ions using 53 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							8
2	185.1285	93.0679			I	912.5050	456.7561	895.4785	448.2429	894.4944	447.7509	7
3	322.1874	161.5973			H	799.4209	400.2141	782.3944	391.7008	781.4104	391.2088	6
4	409.2194	205.1133	391.2088	196.1081	S	662.3620	331.6847	645.3355	323.1714	644.3515	322.6794	5
5	595.2987	298.1530	577.2881	289.1477	W	575.3300	288.1686	558.3035	279.6554	557.3194	279.1634	4
6	708.3828	354.6950	690.3722	345.6897	L	389.2507	195.1290	372.2241	186.6157	371.2401	186.1237	3
7	809.4304	405.2189	791.4199	396.2136	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
8					R	175.1190	88.0631	158.0924	79.5498			1



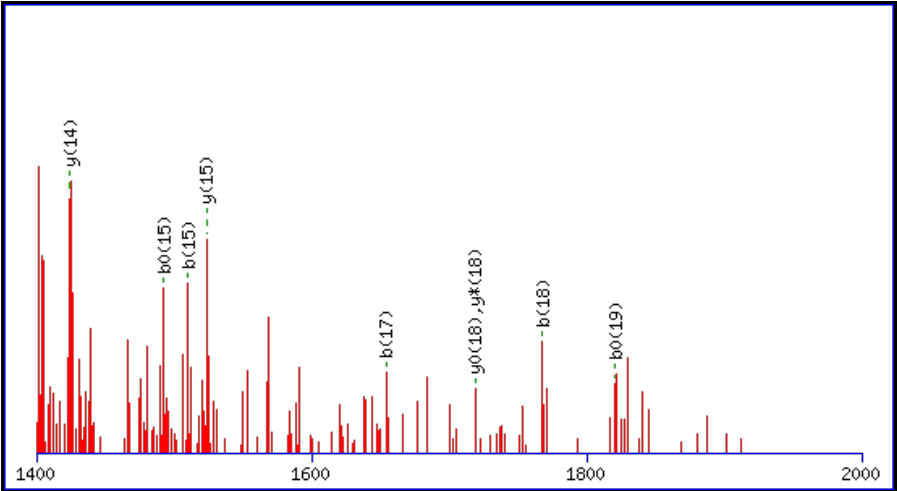
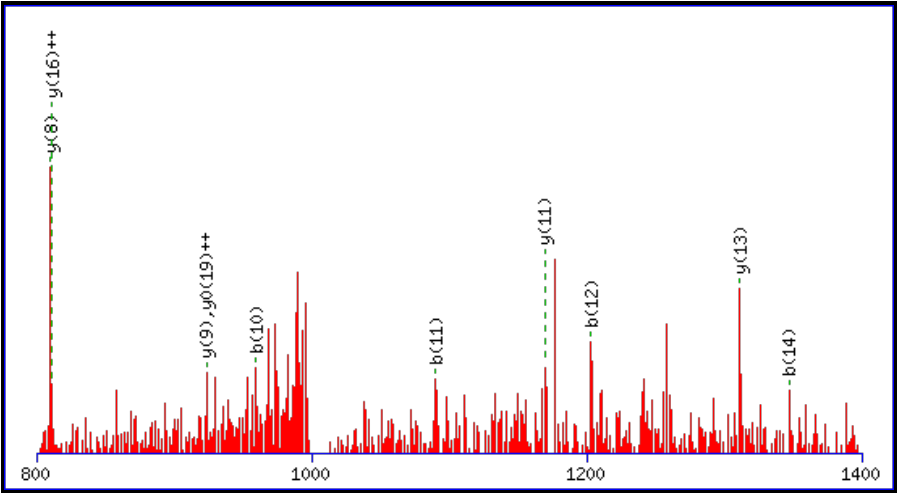
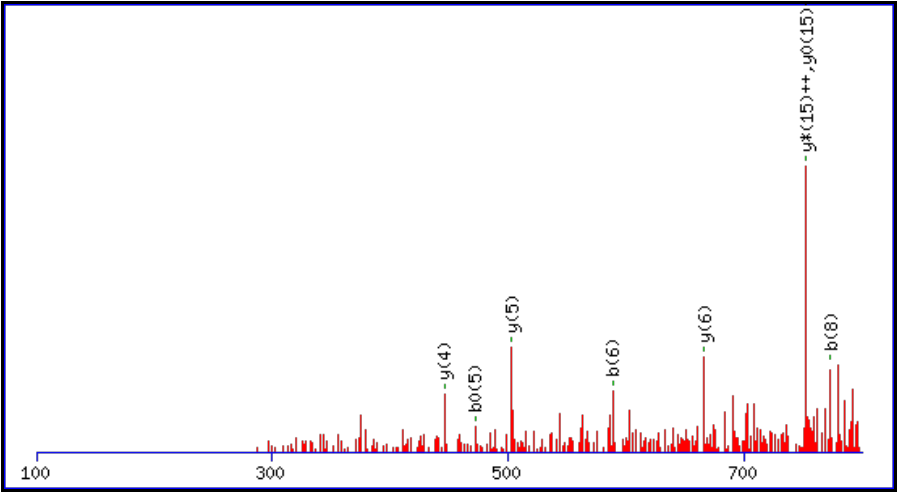
All matches to this query

Score	Mr(calc):	Delta	Sequence
24.9	982.5348	0.0039	AIHSWLTR
8.4	982.5420	-0.0033	RATHSAGKR
6.7	981.5260	1.0127	LLISLTR
6.3	982.5348	0.0039	RFSISFAR
5.8	981.5260	1.0127	ILTITVSR
5.4	982.5348	0.0039	EKKNGSER
5.3	982.5447	-0.0060	LAPLAEDVR
4.8	982.5447	-0.0060	ILPQDLER
1.5	981.5260	1.0127	LLISLTR
1.5	982.5388	-0.0001	ALRFWYK

Peptide View

MS/MS Fragmentation of **FEGGVVIAADMLGSYGLAR**
Found in **IPI00555956**, Tax_Id=9606 Gene_Symbol=PSMB4 Proteasome subunit beta type-4

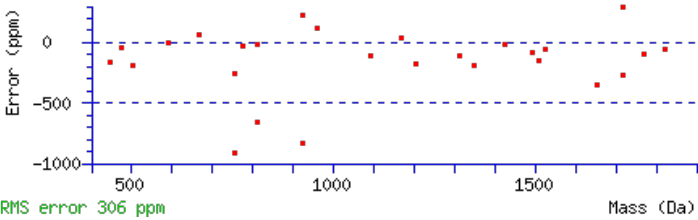
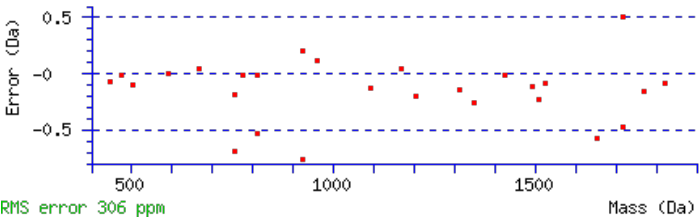
Match to Query 40349: 2012.019688 from(1007.017120,2+)
Title: 091224LimSK_Exosome3_06.9282.9282.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 2012.0037
Fixed modifications: Carbamidomethyl (C)
Ions Score: 43 Expect: 0.0085
Matches (**Bold Red**): 28/182 fragment ions using 60 most intense peaks

		++	0	0++		++		++	0	0++	
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#	b	b	b	b	Seq.	y	y	y*	y*	y	y	#
1	148.0757	74.5415			F							20
2	277.1183	139.0628	259.1077	130.0575	E	1865.9426	933.4749	1848.9160	924.9617	1847.9320	924.4696	19
3	334.1397	167.5735	316.1292	158.5682	G	1736.9000	868.9536	1719.8734	860.4404	1718.8894	859.9483	18
4	391.1612	196.0842	373.1506	187.0790	G	1679.8785	840.4429	1662.8520	831.9296	1661.8680	831.4376	17
5	490.2296	245.6185	472.2191	236.6132	V	1622.8571	811.9322	1605.8305	803.4189	1604.8465	802.9269	16
6	589.2980	295.1527	571.2875	286.1474	V	1523.7886	762.3980	1506.7621	753.8847	1505.7781	753.3927	15
7	702.3821	351.6947	684.3715	342.6894	I	1424.7202	712.8638	1407.6937	704.3505	1406.7097	703.8585	14
8	773.4192	387.2132	755.4087	378.2080	A	1311.6362	656.3217	1294.6096	647.8084	1293.6256	647.3164	13
9	844.4563	422.7318	826.4458	413.7265	A	1240.5990	620.8032	1223.5725	612.2899	1222.5885	611.7979	12
10	959.4833	480.2453	941.4727	471.2400	D	1169.5619	585.2846	1152.5354	576.7713	1151.5514	576.2793	11
11	1090.5238	545.7655	1072.5132	536.7602	M	1054.5350	527.7711	1037.5084	519.2579	1036.5244	518.7659	10
12	1203.6078	602.3075	1185.5973	593.3023	L	923.4945	462.2509	906.4680	453.7376	905.4839	453.2456	9
13	1260.6293	630.8183	1242.6187	621.8130	G	810.4104	405.7089	793.3839	397.1956	792.3999	396.7036	8
14	1347.6613	674.3343	1329.6507	665.3290	S	753.3890	377.1981	736.3624	368.6849	735.3784	368.1928	7
15	1510.7246	755.8660	1492.7141	746.8607	Y	666.3570	333.6821	649.3304	325.1688	648.3464	324.6768	6
16	1567.7461	784.3767	1549.7355	775.3714	G	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	5
17	1654.7781	827.8927	1636.7676	818.8874	S	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
18	1767.8622	884.4347	1749.8516	875.4295	L	359.2401	180.1237	342.2136	171.6104			3
19	1838.8993	919.9533	1820.8887	910.9480	A	246.1561	123.5817	229.1295	115.0684			2
20					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

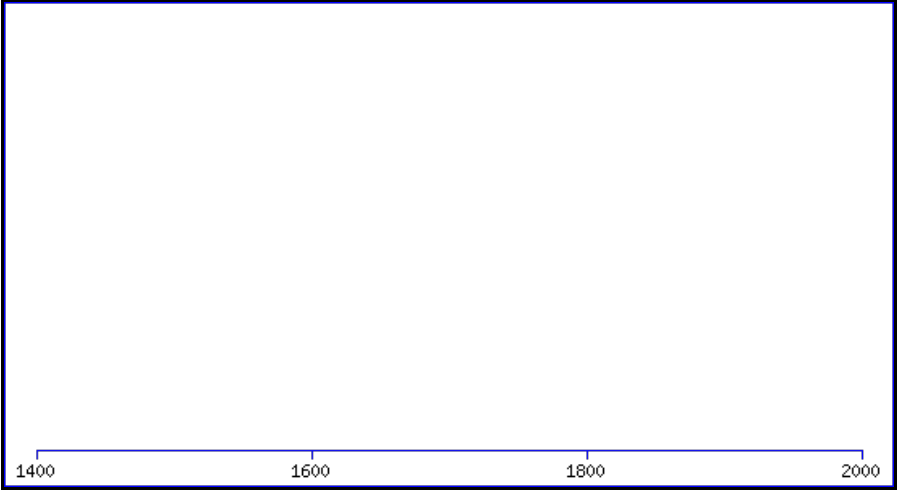
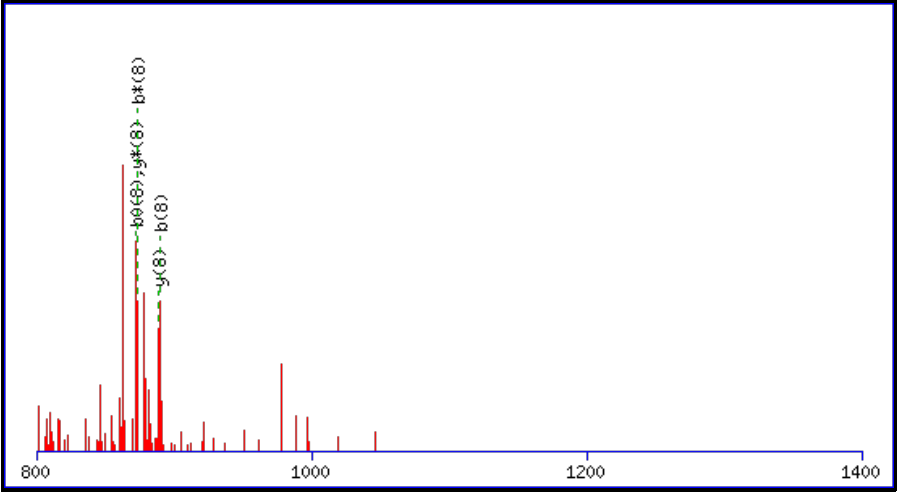
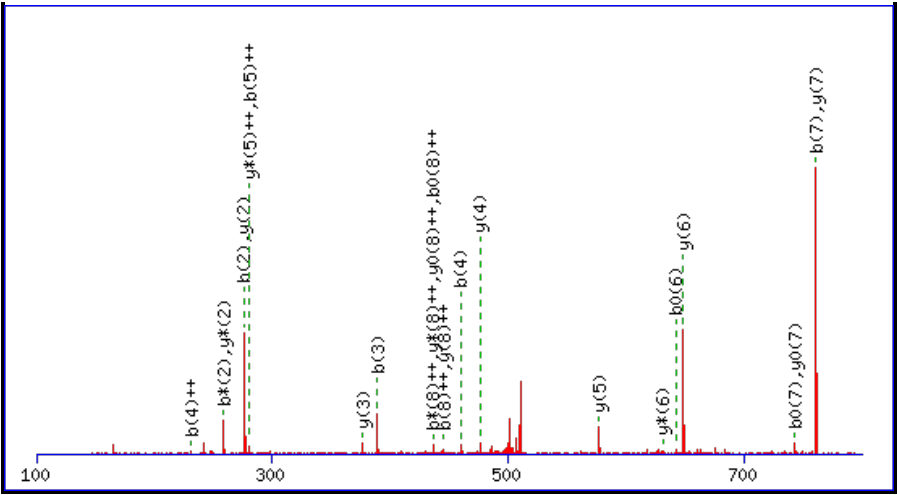
Score	Mr(calc):	Delta	Sequence
43.2	2012.0037	0.0160	FEGGVVIAADMLGSYGSLAR

Spectrum No: 76; Query: 3424; Rank: 1

Peptide View

MS/MS Fragmentation of **FQIATVTEK**
Found in **IP100555956**, Tax_Id=9606 Gene_Symbol=PSMB4 Proteasome subunit beta type-4

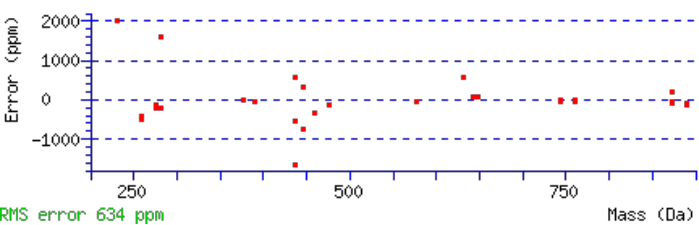
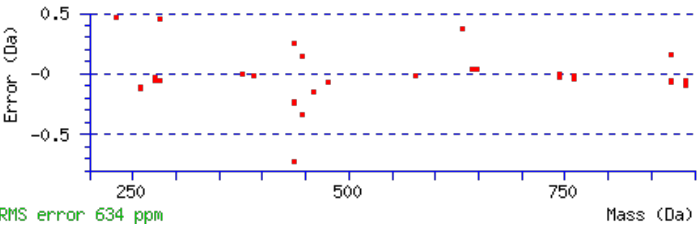
Match to Query 3424: 1035.565248 from(518.789900,2+)
Title: 091224LimSK_Exosome3_06.1901.1901.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1035.5601
Fixed modifications: Carbamidomethyl (C)
Ions Score: 35 Expect: 0.035
Matches (Bold Red): 30/84 fragment ions using 59 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							9
2	276.1343	138.5708	259.1077	130.0575			Q	889.4989	445.2531	872.4724	436.7398	871.4884	436.2478	8
3	389.2183	195.1128	372.1918	186.5995			I	761.4403	381.2238	744.4138	372.7105	743.4298	372.2185	7
4	460.2554	230.6314	443.2289	222.1181			A	648.3563	324.6818	631.3297	316.1685	630.3457	315.6765	6
5	561.3031	281.1552	544.2766	272.6419	543.2926	272.1499	T	577.3192	289.1632	560.2926	280.6499	559.3086	280.1579	5
6	660.3715	330.6894	643.3450	322.1761	642.3610	321.6841	V	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4

7	761.4192	381.2132	744.3927	372.7000	743.4087	372.2080	T	377.2031	189.1052	360.1765	180.5919	359.1925	180.0999	3
8	890.4618	445.7345	873.4353	437.2213	872.4512	436.7293	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

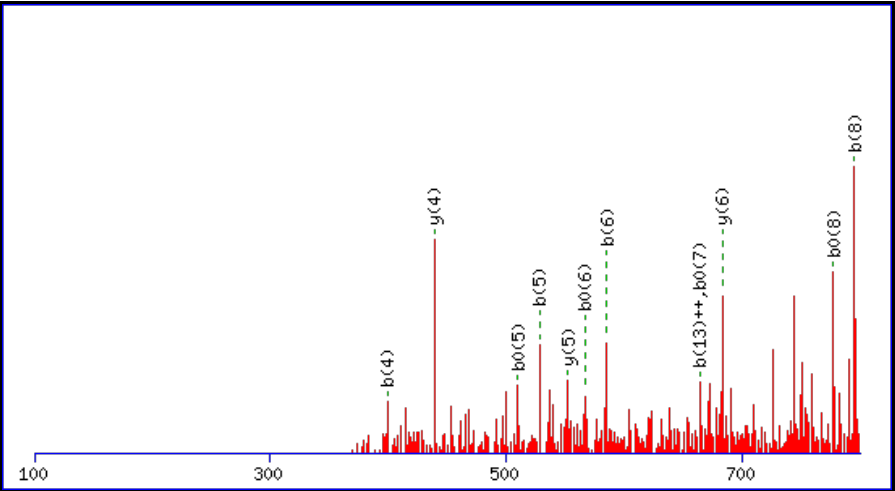
Score	Mr(calc):	Delta	Sequence
35.0	1035.5601	0.0052	FQIATVTEK
18.1	1035.5600	0.0052	VAAYDKLEK
17.8	1035.5600	0.0052	EKIDASVEK
13.3	1034.5525	1.0127	GAITQPLKK
13.1	1035.5729	-0.0077	LKETPKIK
11.8	1035.5713	-0.0060	GFASITTAR
11.7	1035.5600	0.0052	EEKDFLKK
11.1	1035.5753	-0.0101	EFQPFLKK
9.9	1035.5712	-0.0060	AYREKIEK
9.9	1035.5713	-0.0060	EKVQYLTR

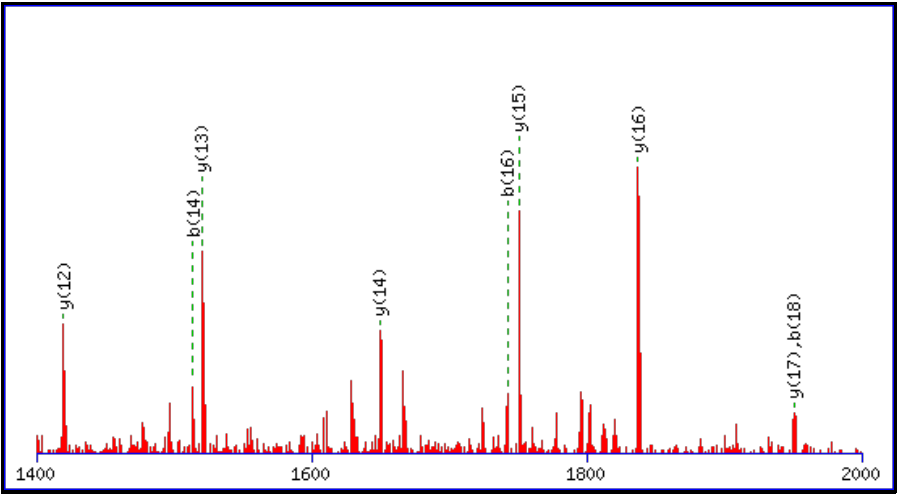
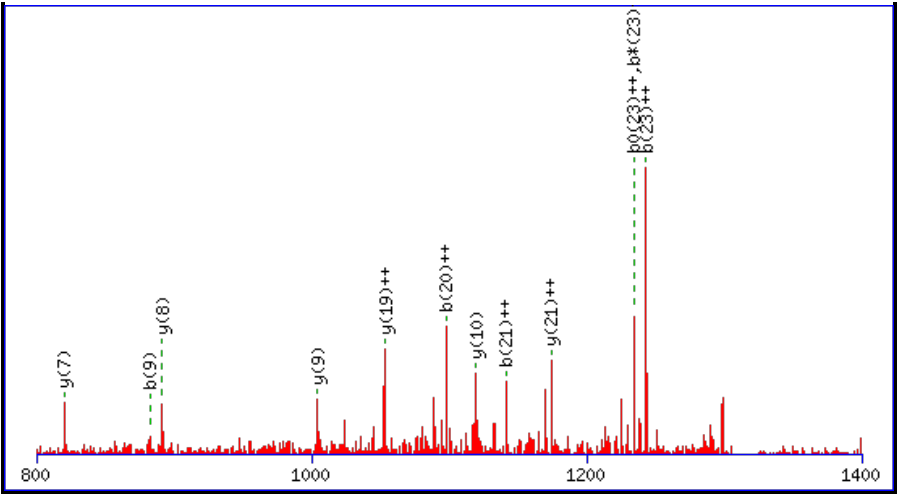
Spectrum No: 77; Query: 59024; Rank: 1

Peptide View

MS/MS Fragmentation of **GVEIEGPLSTETNWDIAHMISGFE**
Found in **IP100555956**, Tax_Id=9606 Gene_Symbol=PSMB4 Proteasome subunit beta type-4

Match to Query 59024: 2631.238388 from(1316.626470,2+)
Title: 091224LimSK_Exosome3_06.8778.8778.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

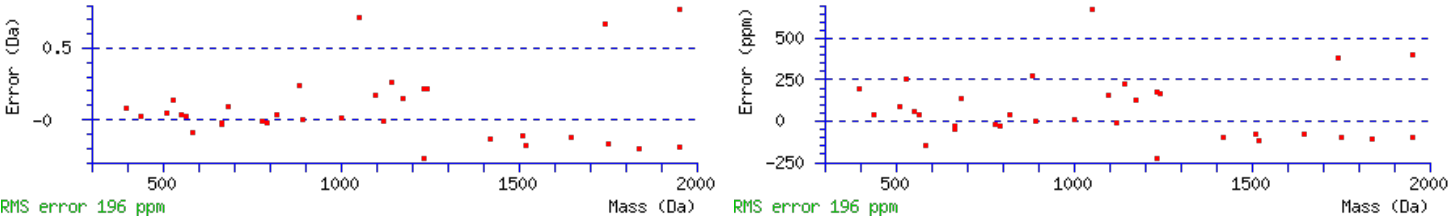




Monoisotopic mass of neutral peptide Mr(calc): 2631.2163
Fixed modifications: Carbamidomethyl (C)
Ions Score: 78 Expect: 4.6e-006
Matches (**Bold Red**): 33/226 fragment ions using 60 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							24
2	157.0972	79.0522					V	2575.2021	1288.1047	2558.1755	1279.5914	2557.1915	1279.0994	23
3	286.1397	143.5735			268.1292	134.5682	E	2476.1337	1238.5705	2459.1071	1230.0572	2458.1231	1229.5652	22
4	399.2238	200.1155			381.2132	191.1103	I	2347.0911	1174.0492	2330.0645	1165.5359	2329.0805	1165.0439	21
5	528.2664	264.6368			510.2558	255.6316	E	2234.0070	1117.5072	2216.9805	1108.9939	2215.9965	1108.5019	20
6	585.2879	293.1476			567.2773	284.1423	G	2104.9644	1052.9859	2087.9379	1044.4726	2086.9539	1043.9806	19
7	682.3406	341.6740			664.3301	332.6687	P	2047.9430	1024.4751	2030.9164	1015.9618	2029.9324	1015.4698	18
8	795.4247	398.2160			777.4141	389.2107	L	1950.8902	975.9487	1933.8637	967.4355	1932.8796	966.9435	17
9	882.4567	441.7320			864.4462	432.7267	S	1837.8061	919.4067	1820.7796	910.8934	1819.7956	910.4014	16
10	983.5044	492.2558			965.4938	483.2506	T	1750.7741	875.8907	1733.7476	867.3774	1732.7635	866.8854	15
11	1112.5470	556.7771			1094.5364	547.7719	E	1649.7264	825.3669	1632.6999	816.8536	1631.7159	816.3616	14
12	1213.5947	607.3010			1195.5841	598.2957	T	1520.6838	760.8456	1503.6573	752.3323	1502.6733	751.8403	13
13	1327.6376	664.3224	1310.6111	655.8092	1309.6270	655.3172	N	1419.6362	710.3217	1402.6096	701.8084	1401.6256	701.3164	12
14	1513.7169	757.3621	1496.6904	748.8488	1495.7064	748.3568	W	1305.5932	653.3003			1287.5827	644.2950	11
15	1628.7439	814.8756	1611.7173	806.3623	1610.7333	805.8703	D	1119.5139	560.2606			1101.5034	551.2553	10
16	1741.8279	871.4176	1724.8014	862.9043	1723.8174	862.4123	I	1004.4870	502.7471			986.4764	493.7418	9
17	1812.8650	906.9362	1795.8385	898.4229	1794.8545	897.9309	A	891.4029	446.2051			873.3923	437.1998	8
18	1949.9239	975.4656	1932.8974	966.9523	1931.9134	966.4603	H	820.3658	410.6865			802.3552	401.6813	7
19	2080.9644	1040.9859	2063.9379	1032.4726	2062.9539	1031.9806	M	683.3069	342.1571			665.2963	333.1518	6

20	2194.0485	1097.5279	2177.0219	1089.0146	2176.0379	1088.5226	I	552.2664	276.6368			534.2558	267.6316	5
21	2281.0805	1141.0439	2264.0540	1132.5306	2263.0700	1132.0386	S	439.1823	220.0948			421.1718	211.0895	4
22	2338.1020	1169.5546	2321.0754	1161.0414	2320.0914	1160.5493	G	352.1503	176.5788			334.1397	167.5735	3
23	2485.1704	1243.0888	2468.1439	1234.5756	2467.1598	1234.0836	F	295.1288	148.0681			277.1183	139.0628	2
24							E	148.0604	74.5339			130.0499	65.5286	1



All matches to this query

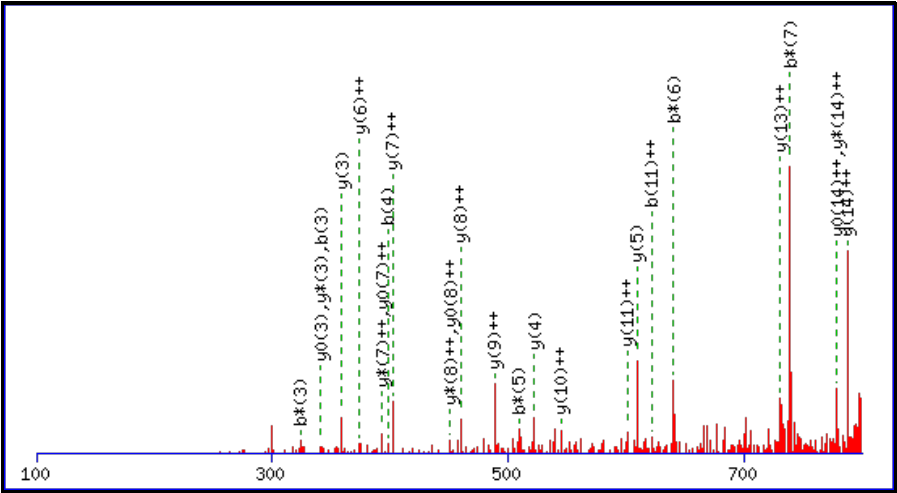
Score	Mr(calc):	Delta	Sequence
78.2	2631.2163	0.0221	GVEIEGPLSTETNWDIAHMSGFE
11.9	2630.2506	0.9878	SVPPSPPERPSLATASQNGAPALVK
9.6	2630.2506	0.9878	SVPPSPPERPSLATASQNGAPALVK
5.6	2630.2506	0.9878	SVPPSPPERPSLATASQNGAPALVK
5.3	2630.2418	0.9966	QVEPLDPPAGSAPGEHVFVKGYEK
3.5	2630.2159	1.0224	SSKRPASPYGEADGEVAMVTSRQK
3.5	2630.2159	1.0224	SSKRPASPYGEADGEVAMVTSRQK
3.2	2631.2169	0.0215	SLEVGTVMTLFYSKKSQRPER
3.2	2631.2169	0.0215	SLEVGTVMTLFYSKKSQRPER
2.6	2630.2159	1.0224	SSKRPASPYGEADGEVAMVTSRQK

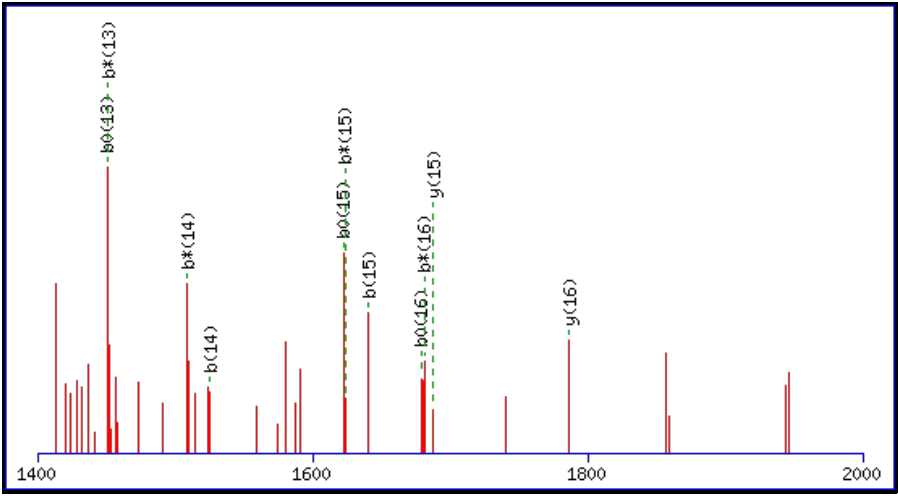
Spectrum No: 78; Query: 54324; Rank: 1

Peptide View

MS/MS Fragmentation of **QVLGQMVIDEELLGDGHSYSPR**
Found in **IP100555956**, Tax_Id=9606 Gene_Symbol=PSMB4 Proteasome subunit beta type-4

Match to Query 54324: 2442.199722 from(815.073850,3+)
Title: 091224LimSK_Exosome3_06.6600.6600.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

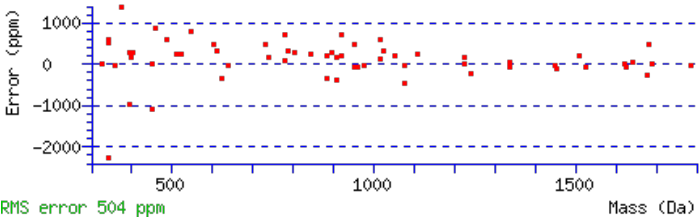
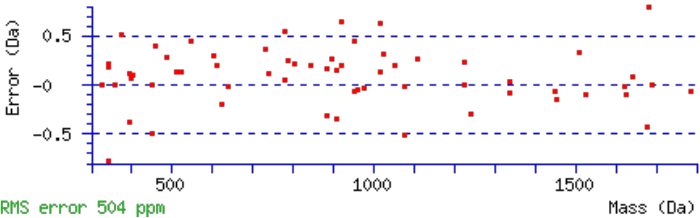




Monoisotopic mass of neutral peptide Mr(calc): 2442.1849
 Fixed modifications: Carbamidomethyl (C)
 Ions Score: 66 Expect: 5.3e-005
 Matches (**Bold Red**): 62/232 fragment ions using 110 most intense peaks

[illegible]

20	2172.0278	1086.5175	2155.0012	1078.0042	2154.0172	1077.5122	S	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
21	2269.0805	1135.0439	2252.0540	1126.5306	2251.0700	1126.0386	P	272.1717	136.5895	255.1452	128.0762			2
22							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

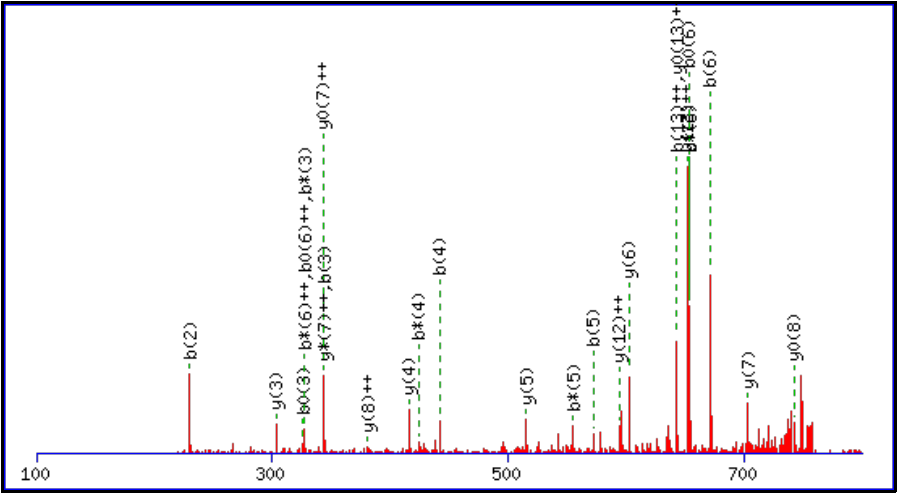
Score	Mr(calc):	Delta	Sequence
66.5	2442.1849	0.0148	QVLGQMVIDEELLGDGHSYSR
5.1	2441.2193	0.9805	VLRATGRAQALVTDLGTAELAR
4.4	2441.1910	1.0087	FEKINEGRMPGTVHSSWHSVK
3.8	2441.2064	0.9933	QDSAAHLGKLSKSTAPGHTSQLK
3.8	2441.2064	0.9933	QDSAAHLGKLSKSTAPGHTSQLK
2.8	2441.1839	1.0158	PPSLSPQLLVADSSPSSTAPSPAR
2.4	2442.2040	-0.0043	RGWNTTSQRYSNVIQPSSESK
2.1	2441.2193	0.9805	VLRATGRAQALVTDLGTAELAR
1.7	2442.1879	0.0118	EYRPHLVDAQAMLLNVSGHVK
1.7	2440.2064	1.9933	KAILTMTQLYKVALQWMVK

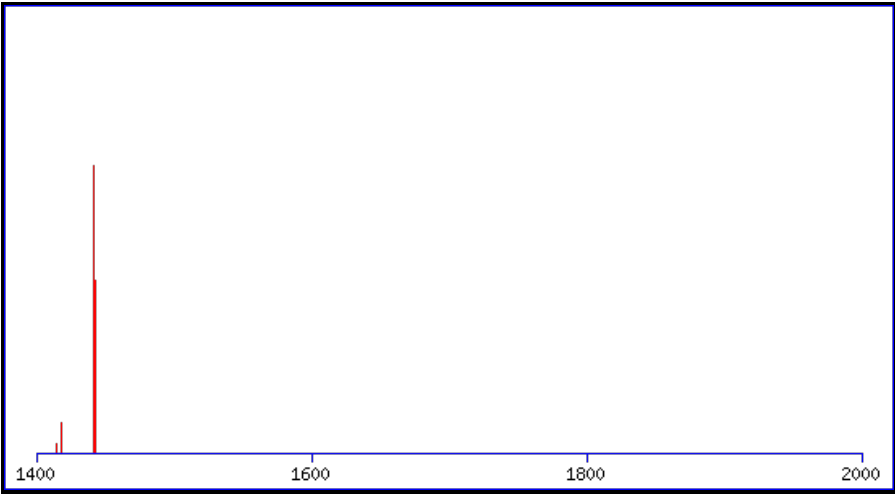
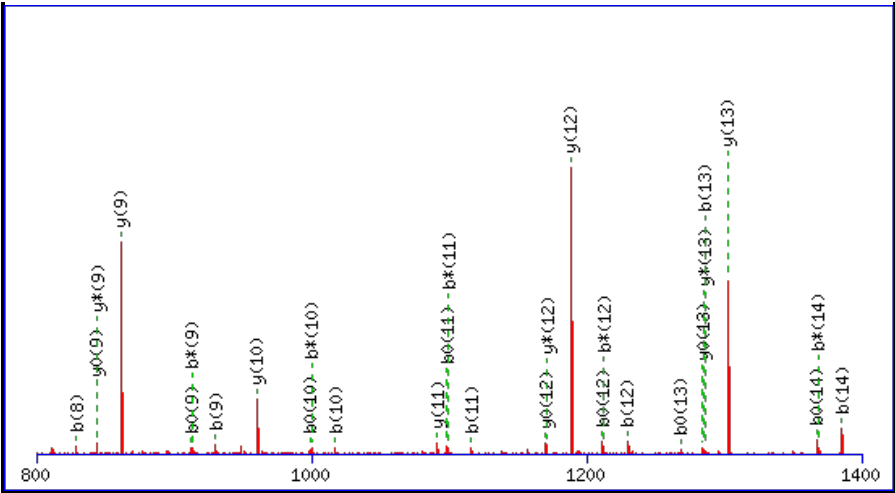
Spectrum No: 79; Query: 22048; Rank: 1

Peptide View

MS/MS Fragmentation of **TQNPMVTGTSVLGVK**
Found in **IP100555956**, Tax_Id=9606 Gene_Symbol=PSMB4 Proteasome subunit beta type-4

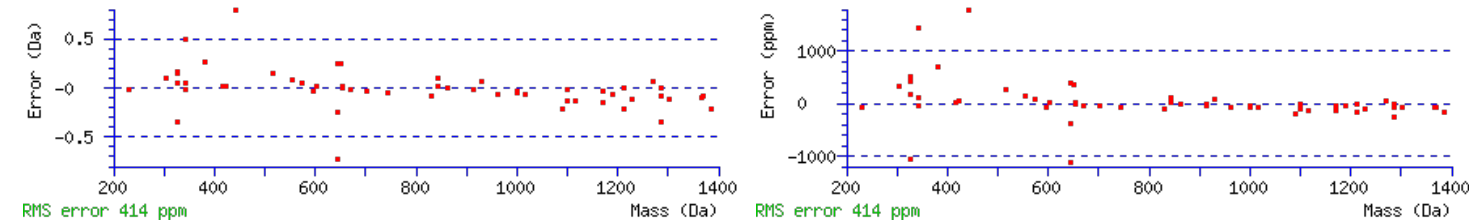
Match to Query 22048: 1530.816668 from(766.415610,2+)
Title: 091224LimSK_Exosome3_06.3921.3921.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1530.8076
Fixed modifications: Carbamidomethyl (C)
Ions Score: 69 Expect: 1.6e-005
Matches (**Bold Red**): 56/156 fragment ions using 100 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							15
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	1430.7672	715.8872	1413.7406	707.3740	1412.7566	706.8819	14
3	344.1565	172.5819	327.1299	164.0686	326.1459	163.5766	N	1302.7086	651.8579	1285.6821	643.3447	1284.6980	642.8527	13
4	441.2092	221.1083	424.1827	212.5950	423.1987	212.1030	P	1188.6657	594.8365	1171.6391	586.3232	1170.6551	585.8312	12
5	572.2497	286.6285	555.2232	278.1152	554.2391	277.6232	M	1091.6129	546.3101	1074.5864	537.7968	1073.6023	537.3048	11
6	671.3181	336.1627	654.2916	327.6494	653.3076	327.1574	V	960.5724	480.7899	943.5459	472.2766	942.5619	471.7846	10
7	772.3658	386.6865	755.3393	378.1733	754.3552	377.6813	T	861.5040	431.2556	844.4775	422.7424	843.4934	422.2504	9
8	829.3873	415.1973	812.3607	406.6840	811.3767	406.1920	G	760.4563	380.7318	743.4298	372.2185	742.4458	371.7265	8
9	930.4349	465.7211	913.4084	457.2078	912.4244	456.7158	T	703.4349	352.2211	686.4083	343.7078	685.4243	343.2158	7
10	1017.4670	509.2371	1000.4404	500.7239	999.4564	500.2318	S	602.3872	301.6972	585.3606	293.1840	584.3766	292.6919	6
11	1116.5354	558.7713	1099.5088	550.2581	1098.5248	549.7660	V	515.3552	258.1812	498.3286	249.6679			5
12	1229.6195	615.3134	1212.5929	606.8001	1211.6089	606.3081	L	416.2867	208.6470	399.2602	200.1337			4
13	1286.6409	643.8241	1269.6144	635.3108	1268.6303	634.8188	G	303.2027	152.1050	286.1761	143.5917			3
14	1385.7093	693.3583	1368.6828	684.8450	1367.6988	684.3530	V	246.1812	123.5942	229.1547	115.0810			2
15							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

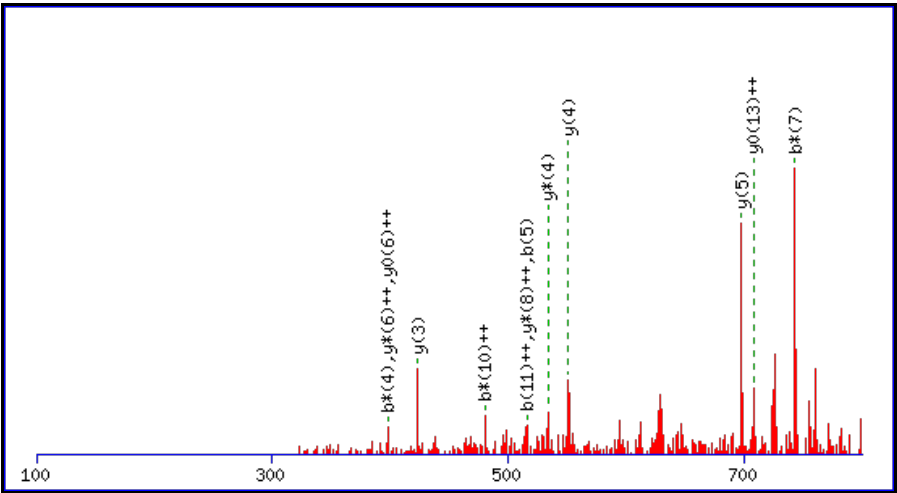
Score	Mr(calc):	Delta	Sequence
69.1	1530.8076	0.0091	TQNPMVTGTSVLGVK
12.8	1528.8097	2.0070	LNNDLVGSTENLLK
6.2	1528.8167	2.0000	KVIPYIASQFRK
5.3	1530.8076	0.0091	DLIVMLRDTDVNK
4.6	1530.8188	-0.0021	MVVQTASQASPLKR
3.9	1529.8161	1.0005	LQTLQSENSNLRK
3.5	1530.8194	-0.0028	PIAFNEPLSFLQR
3.5	1530.8187	-0.0020	QTLKSLIKLSK
2.7	1530.8266	-0.0100	SSWSSLGRAPSLKR
0.9	1530.8208	-0.0041	FFLYVLGHSRHR

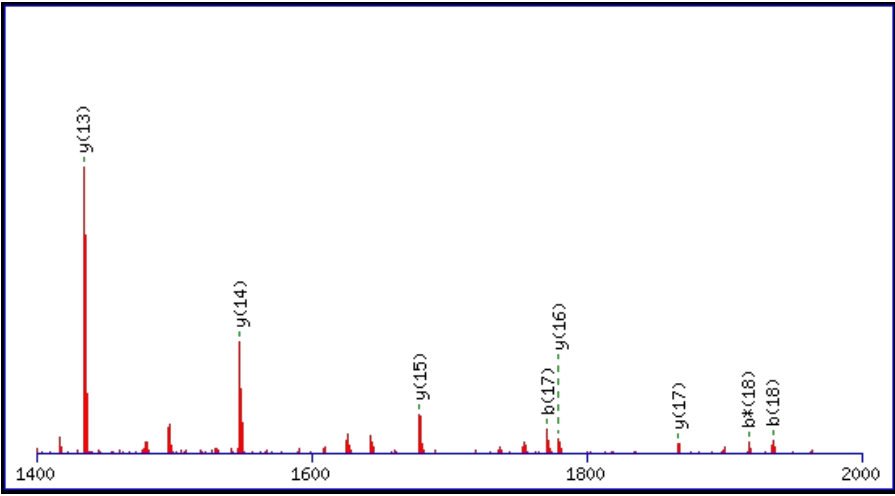
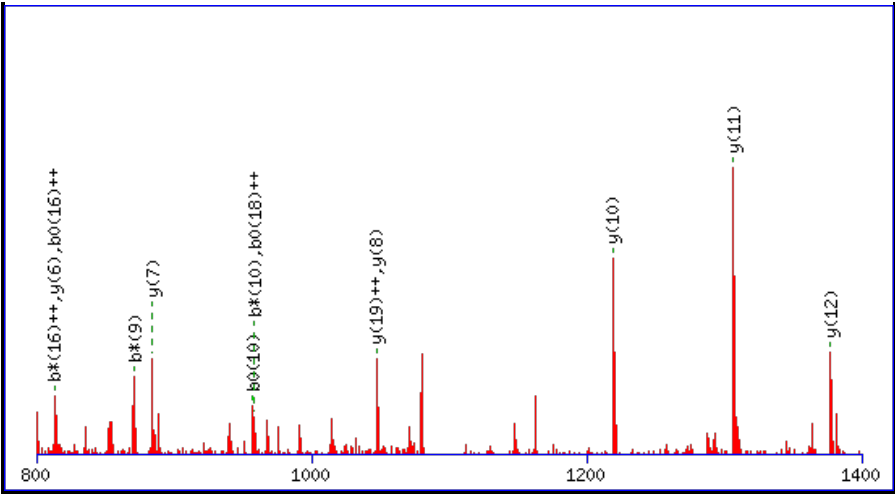
Spectrum No: 80; Query: 46479; Rank: 1

Peptide View

MS/MS Fragmentation of **VNNSTMLGASGDYADFQYLK**
Found in **IPI00555956**, Tax_Id=9606 Gene_Symbol=PSMB4 Proteasome subunit beta type-4

Match to Query 46479: 2193.019848 from(1097.517200,2+)
Title: 091224LimSK_Exosome3_06.5930.5930.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

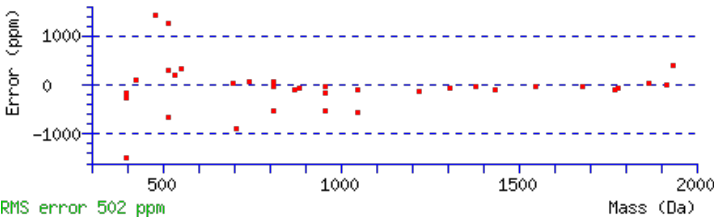
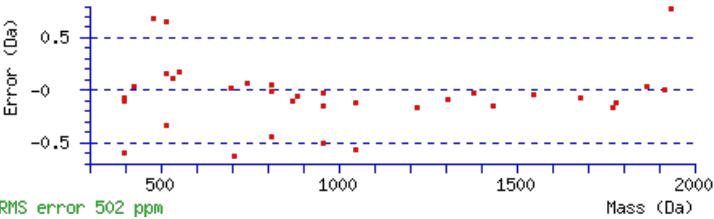




Monoisotopic mass of neutral peptide Mr(calc): 2193.0048
Fixed modifications: Carbamidomethyl (C)
Ions Score: 122 Expect: 1.7e-010
Matches (**Bold Red**): 34/210 fragment ions using 37 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							20
2	214.1186	107.5629	197.0921	99.0497			N	2094.9437	1047.9755	2077.9171	1039.4622	2076.9331	1038.9702	19
3	328.1615	164.5844	311.1350	156.0711			N	1980.9008	990.9540	1963.8742	982.4407	1962.8902	981.9487	18
4	415.1936	208.1004	398.1670	199.5871	397.1830	199.0951	S	1866.8578	933.9326	1849.8313	925.4193	1848.8473	924.9273	17
5	516.2413	258.6243	499.2147	250.1110	498.2307	249.6190	T	1779.8258	890.4165	1762.7993	881.9033	1761.8153	881.4113	16
6	647.2817	324.1445	630.2552	315.6312	629.2712	315.1392	M	1678.7781	839.8927	1661.7516	831.3794	1660.7676	830.8874	15
7	760.3658	380.6865	743.3393	372.1733	742.3552	371.6813	L	1547.7377	774.3725	1530.7111	765.8592	1529.7271	765.3672	14
8	817.3873	409.1973	800.3607	400.6840	799.3767	400.1920	G	1434.6536	717.8304	1417.6270	709.3172	1416.6430	708.8251	13
9	888.4244	444.7158	871.3978	436.2026	870.4138	435.7105	A	1377.6321	689.3197	1360.6056	680.8064	1359.6216	680.3144	12
10	975.4564	488.2318	958.4299	479.7186	957.4458	479.2266	S	1306.5950	653.8011	1289.5685	645.2879	1288.5844	644.7959	11
11	1032.4779	516.7426	1015.4513	508.2293	1014.4673	507.7373	G	1219.5630	610.2851	1202.5364	601.7719	1201.5524	601.2798	10
12	1147.5048	574.2560	1130.4783	565.7428	1129.4942	565.2508	D	1162.5415	581.7744	1145.5150	573.2611	1144.5310	572.7691	9
13	1310.5681	655.7877	1293.5416	647.2744	1292.5576	646.7824	Y	1047.5146	524.2609	1030.4880	515.7477	1029.5040	515.2556	8
14	1381.6053	691.3063	1364.5787	682.7930	1363.5947	682.3010	A	884.4512	442.7293	867.4247	434.2160	866.4407	433.7240	7
15	1496.6322	748.8197	1479.6057	740.3065	1478.6216	739.8145	D	813.4141	407.2107	796.3876	398.6974	795.4036	398.2054	6
16	1643.7006	822.3539	1626.6741	813.8407	1625.6900	813.3487	F	698.3872	349.6972	681.3606	341.1840			5
17	1771.7592	886.3832	1754.7326	877.8700	1753.7486	877.3780	Q	551.3188	276.1630	534.2922	267.6498			4
18	1934.8225	967.9149	1917.7960	959.4016	1916.8120	958.9096	Y	423.2602	212.1337	406.2336	203.6205			3
19	2047.9066	1024.4569	2030.8800	1015.9437	2029.8960	1015.4516	L	260.1969	130.6021	243.1703	122.0888			2

20							K	147.1128	74.0600	130.0863	65.5468			1
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All matches to this query

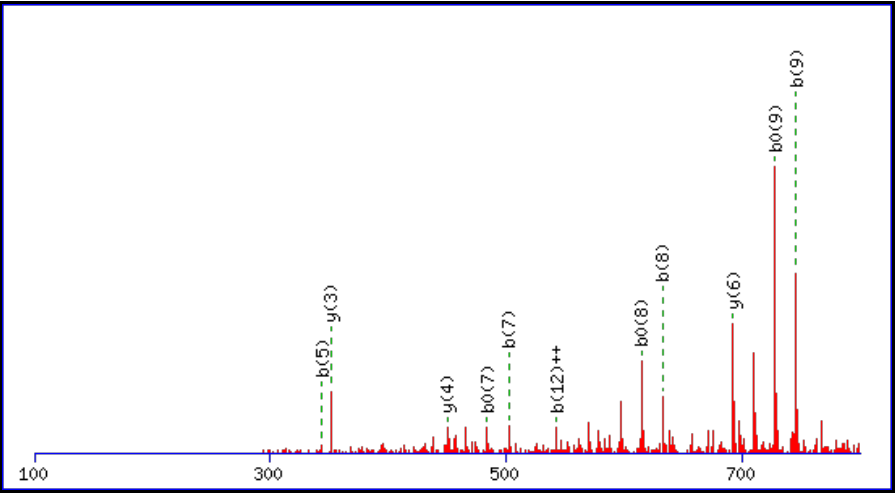
Score	Mr(calc):	Delta	Sequence
122.3	2193.0048	0.0150	VNNSTMLGASGDYADFQYLK
7.7	2191.0211	1.9987	EKKWWQSEGLDHVSIR
5.2	2193.0098	0.0100	EKVADMTSVLDPNKMYLK
2.9	2191.0324	1.9875	GGQRATPSWREAGLGAWPSK
2.9	2191.0324	1.9875	GGQRATPSWREAGLGAWPSK
2.6	2191.0216	1.9983	DQSEPVWDMTTQKVQQQK
2.0	2192.0310	0.9888	DTLLTRHRAPGWTQMTTR
1.7	2193.0098	0.0100	EKVADMTSVLDPNKMYLK
1.6	2191.0054	2.0144	EEILKTTFCICGLERDK
1.6	2191.0054	2.0144	EEILKTTFCICGLERDK

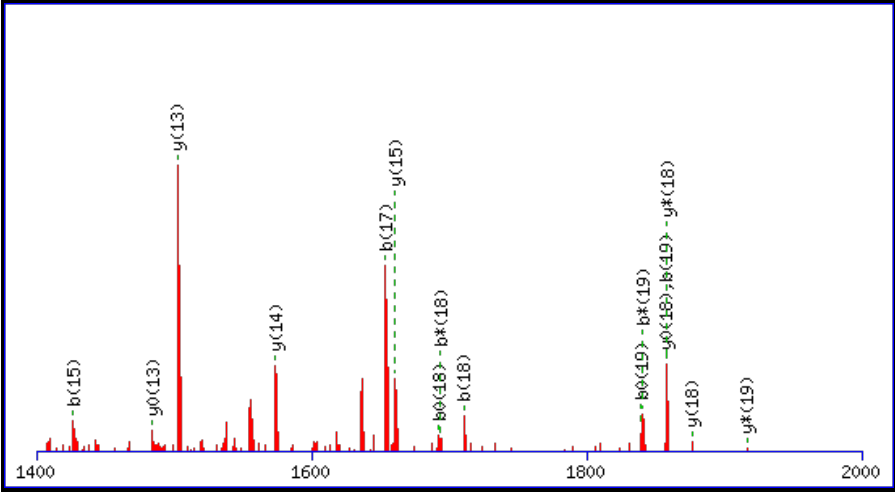
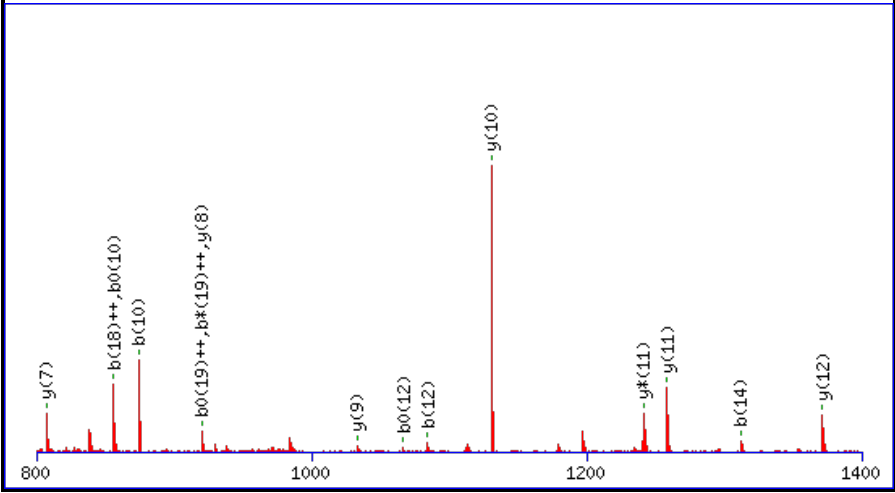
Spectrum No: 81; Query: 40090; Rank: 1

Peptide View

MS/MS Fragmentation of **AGGSASAMLQPLLDNQVGFK**
Found in **IPI00025019**, Tax_Id=9606 Gene_Symbol=PSMB1 Proteasome subunit beta type-1

Match to Query 40090: 2003.027728 from(1002.521140,2+)
Title: 091224LimSK_Exosome3_07.6973.6973.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

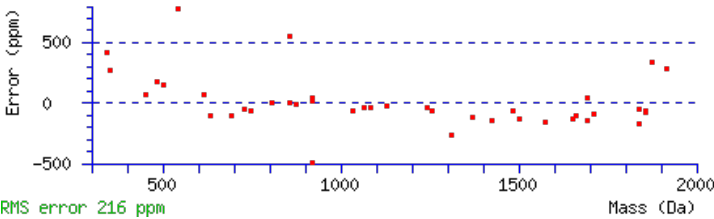
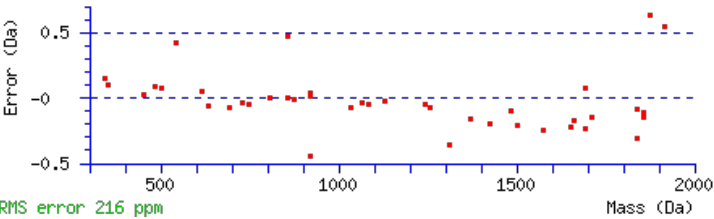




Monoisotopic mass of neutral peptide Mr(calc): 2003.0146
Fixed modifications: Carbamidomethyl (C)
Ions Score: 93 Expect: 8.9e-008
Matches (Bold Red): 42/192 fragment ions using 62 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258					A							20
2	129.0659	65.0366					G	1932.9848	966.9960	1915.9582	958.4828	1914.9742	957.9907	19
3	186.0873	93.5473					G	1875.9633	938.4853	1858.9368	929.9720	1857.9527	929.4800	18
4	273.1193	137.0633			255.1088	128.0580	S	1818.9418	909.9746	1801.9153	901.4613	1800.9313	900.9693	17
5	344.1565	172.5819			326.1459	163.5766	A	1731.9098	866.4585	1714.8833	857.9453	1713.8993	857.4533	16
6	431.1885	216.0979			413.1779	207.0926	S	1660.8727	830.9400	1643.8462	822.4267	1642.8621	821.9347	15
7	502.2256	251.6164			484.2150	242.6112	A	1573.8407	787.4240	1556.8141	778.9107	1555.8301	778.4187	14
8	633.2661	317.1367			615.2555	308.1314	M	1502.8036	751.9054	1485.7770	743.3921	1484.7930	742.9001	13
9	746.3502	373.6787			728.3396	364.6734	L	1371.7631	686.3852	1354.7365	677.8719	1353.7525	677.3799	12
10	874.4087	437.7080	857.3822	429.1947	856.3982	428.7027	Q	1258.6790	629.8431	1241.6525	621.3299	1240.6684	620.8379	11
11	971.4615	486.2344	954.4349	477.7211	953.4509	477.2291	P	1130.6204	565.8139	1113.5939	557.3006	1112.6099	556.8086	10
12	1084.5456	542.7764	1067.5190	534.2631	1066.5350	533.7711	L	1033.5677	517.2875	1016.5411	508.7742	1015.5571	508.2822	9
13	1197.6296	599.3184	1180.6031	590.8052	1179.6191	590.3132	L	920.4836	460.7454	903.4571	452.2322	902.4730	451.7402	8
14	1312.6566	656.8319	1295.6300	648.3186	1294.6460	647.8266	D	807.3995	404.2034	790.3730	395.6901	789.3890	395.1981	7
15	1426.6995	713.8534	1409.6729	705.3401	1408.6889	704.8481	N	692.3726	346.6899	675.3461	338.1767			6
16	1554.7581	777.8827	1537.7315	769.3694	1536.7475	768.8774	Q	578.3297	289.6685	561.3031	281.1552			5
17	1653.8265	827.4169	1636.7999	818.9036	1635.8159	818.4116	V	450.2711	225.6392	433.2445	217.1259			4
18	1710.8479	855.9276	1693.8214	847.4143	1692.8374	846.9223	G	351.2027	176.1050	334.1761	167.5917			3
19	1857.9164	929.4618	1840.8898	920.9485	1839.9058	920.4565	F	294.1812	147.5942	277.1547	139.0810			2

20						K	147.1128	74.0600	130.0863	65.5468				1
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All matches to this query

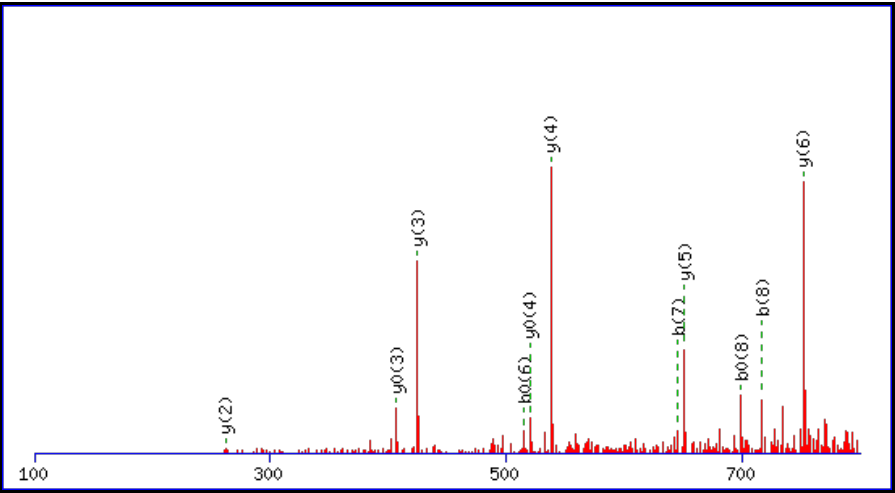
Score	Mr(calc):	Delta	Sequence
92.7	2003.0146	0.0131	AGGSASAMLQPLLDNQVGFK
0.8	2003.0364	-0.0086	FNAHEFATLVIDILSDAK
0.7	2002.0361	0.9917	HTLTRNLDVQLLDTKR
0.7	2002.0361	0.9917	HTLTRNLDVQLLDTKR
0.7	2001.0379	1.9899	QTASQVEQPIITQGSSVTK

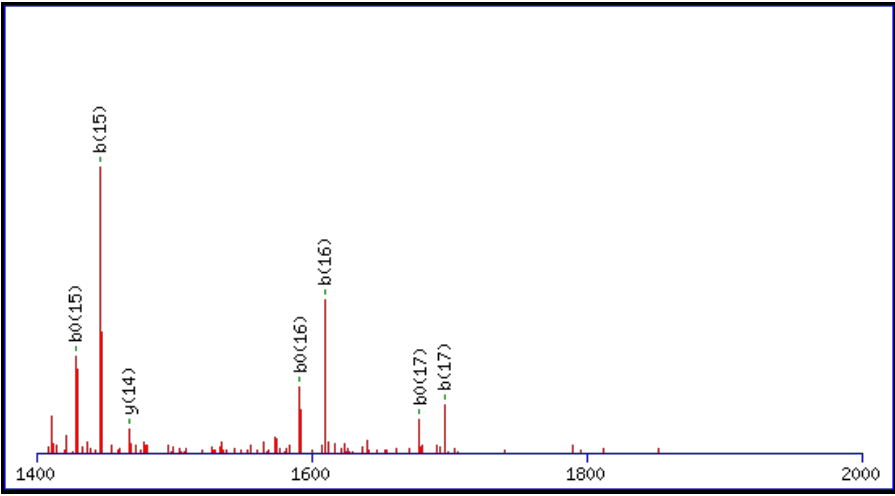
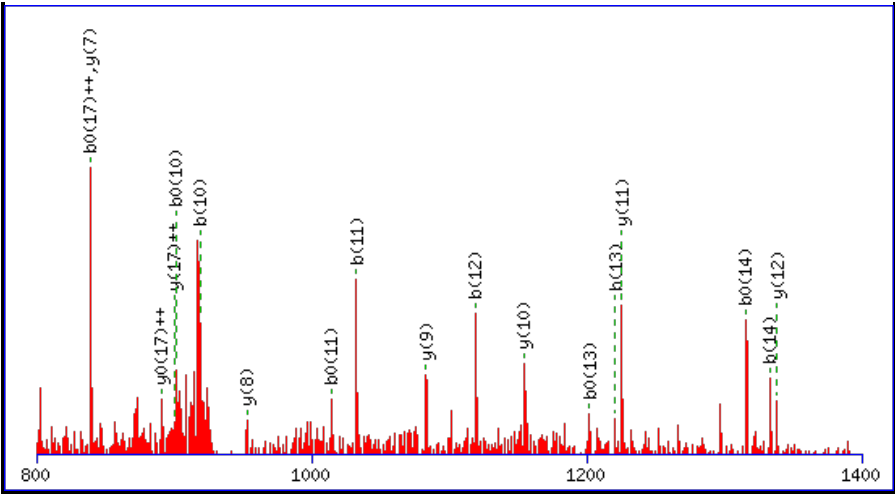
Spectrum No: 82; Query: 35592; Rank: 1

Peptide View

MS/MS Fragmentation of **AMTTGAIAAMLSTILYSR**
Found in **IP100025019**, Tax_Id=9606 Gene_Symbol=PSMB1 Proteasome subunit beta type-1

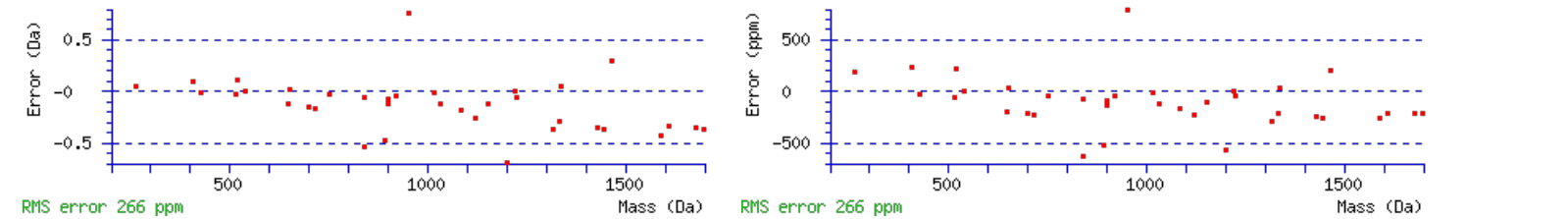
Match to Query 35592: 1869.985348 from(935.999950,2+)
Title: 091224LimSK_Exosome3_07.9275.9275.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1869.9692
Fixed modifications: Carbamidomethyl (C)
Ions Score: 70 Expect: 1.3e-005
Matches (**Bold Red**): 36/164 fragment ions using 84 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							18
2	203.0849	102.0461			M	1799.9394	900.4733	1782.9129	891.9601	1781.9288	891.4681	17
3	304.1326	152.5699	286.1220	143.5646	T	1668.8989	834.9531	1651.8724	826.4398	1650.8884	825.9478	16
4	405.1802	203.0938	387.1697	194.0885	T	1567.8512	784.4293	1550.8247	775.9160	1549.8407	775.4240	15
5	462.2017	231.6045	444.1911	222.5992	G	1466.8036	733.9054	1449.7770	725.3921	1448.7930	724.9001	14
6	533.2388	267.1230	515.2282	258.1178	A	1409.7821	705.3947	1392.7556	696.8814	1391.7715	696.3894	13
7	646.3229	323.6651	628.3123	314.6598	I	1338.7450	669.8761	1321.7184	661.3629	1320.7344	660.8708	12
8	717.3600	359.1836	699.3494	350.1784	A	1225.6609	613.3341	1208.6344	604.8208	1207.6504	604.3288	11
9	788.3971	394.7022	770.3865	385.6969	A	1154.6238	577.8155	1137.5973	569.3023	1136.6132	568.8103	10
10	919.4376	460.2224	901.4270	451.2171	M	1083.5867	542.2970	1066.5601	533.7837	1065.5761	533.2917	9
11	1032.5217	516.7645	1014.5111	507.7592	L	952.5462	476.7767	935.5197	468.2635	934.5356	467.7715	8
12	1119.5537	560.2805	1101.5431	551.2752	S	839.4621	420.2347	822.4356	411.7214	821.4516	411.2294	7
13	1220.6014	610.8043	1202.5908	601.7990	T	752.4301	376.7187	735.4036	368.2054	734.4196	367.7134	6
14	1333.6854	667.3463	1315.6749	658.3411	I	651.3824	326.1949	634.3559	317.6816	633.3719	317.1896	5
15	1446.7695	723.8884	1428.7589	714.8831	L	538.2984	269.6528	521.2718	261.1396	520.2878	260.6475	4
16	1609.8328	805.4200	1591.8223	796.4148	Y	425.2143	213.1108	408.1878	204.5975	407.2037	204.1055	3
17	1696.8648	848.9361	1678.8543	839.9308	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
18					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

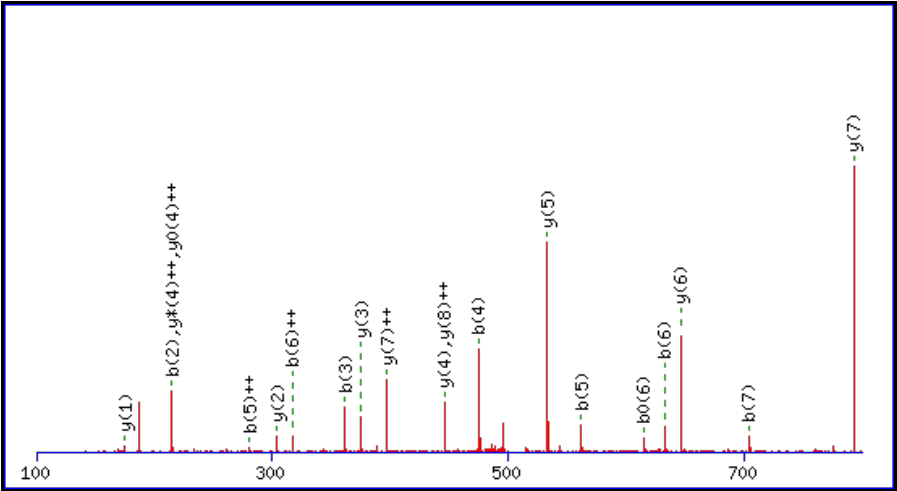
Score	Mr(calc):	Delta	Sequence
69.8	1869.9692	0.0161	AMTTGAIAAMLSTILYSR
5.7	1868.9761	1.0093	NLVDPITHDLIISLAR
4.2	1869.9737	0.0116	LWIEQYGTVEILNHR
3.5	1869.9727	0.0126	VHVKTHHGVPLPQVSR
3.2	1868.9734	1.0120	EPLTRIRNNSAIHR
2.3	1869.9809	0.0044	LRHVYTPSQTLEDRR
1.4	1869.9870	-0.0017	MPTVTVPQLELDVGLSR
1.3	1868.9857	0.9996	GQERPGIQGVPQLSFTR
0.9	1869.9697	0.0156	QPQAGLSQANFTLGPVSR
0.9	1869.9826	0.0028	SIKAPATPASATLGRPPR

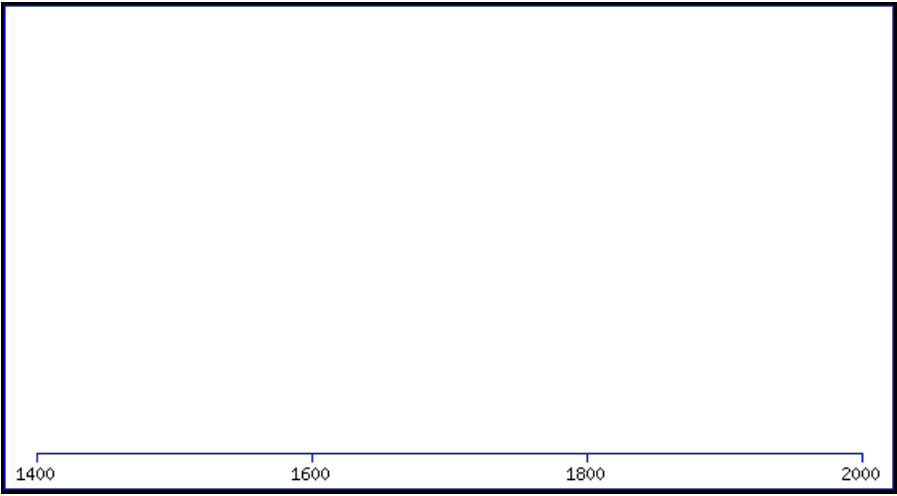
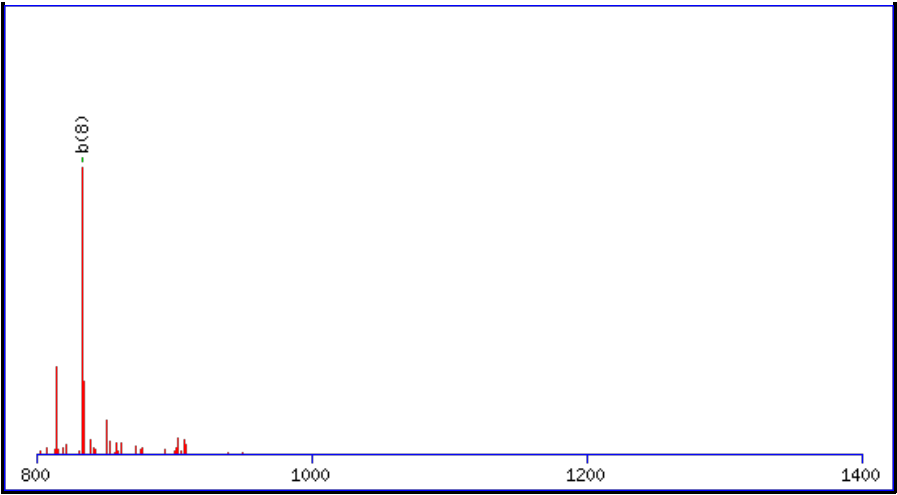
Spectrum No: 83; Query: 2883; Rank: 1

Peptide View

MS/MS Fragmentation of **DVFISAAER**
Found in **IP100025019**, Tax_Id=9606 Gene_Symbol=PSMB1 Proteasome subunit beta type-1

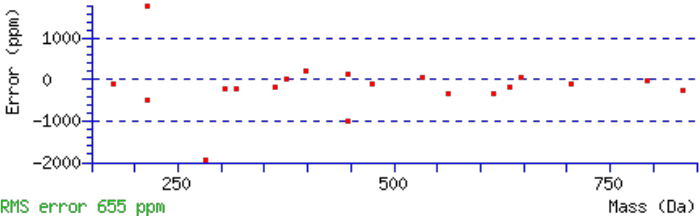
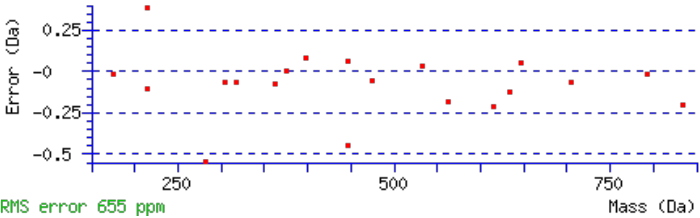
Match to Query 2883: 1006.513348 from(504.263950,2+)
Title: 091224LimSK_Exosome3_07.1952.1952.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1006.5083
Fixed modifications: Carbamidomethyl (C)
Ions Score: 57 Expect: 0.00026
Matches (**Bold Red**): 21/78 fragment ions using 29 most intense peaks

#	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							9
2	215.1026	108.0550	197.0921	99.0497	V	892.4887	446.7480	875.4621	438.2347	874.4781	437.7427	8
3	362.1710	181.5892	344.1605	172.5839	F	793.4203	397.2138	776.3937	388.7005	775.4097	388.2085	7
4	475.2551	238.1312	457.2445	229.1259	I	646.3519	323.6796	629.3253	315.1663	628.3413	314.6743	6
5	562.2871	281.6472	544.2766	272.6419	S	533.2678	267.1375	516.2413	258.6243	515.2572	258.1323	5
6	633.3243	317.1658	615.3137	308.1605	A	446.2358	223.6215	429.2092	215.1083	428.2252	214.6162	4
7	704.3614	352.6843	686.3508	343.6790	A	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
8	833.4040	417.2056	815.3934	408.2003	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
9					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
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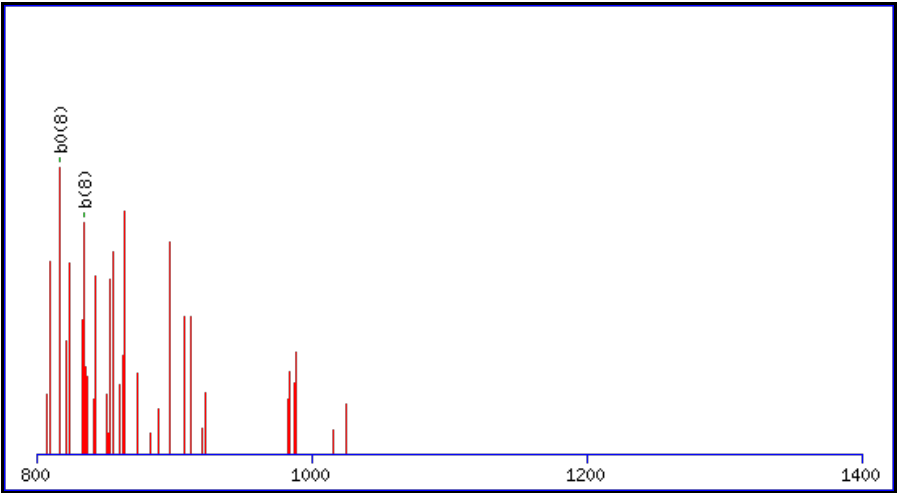
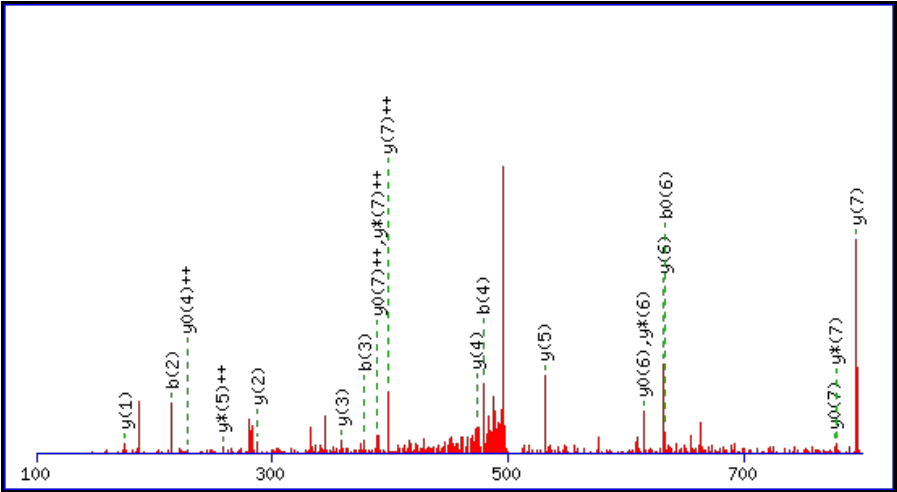
56.9	1006.5083	0.0050	DVFISAAER
11.2	1006.5084	0.0050	DVAEVTAFR
11.2	1006.5083	0.0050	FLNVTEER
11.0	1004.5073	2.0060	VLCKGSGER
10.3	1005.5145	0.9989	GRFGEVWR
9.1	1006.5229	-0.0096	VNMSEKKR
7.7	1005.5165	0.9969	VIMITGDNK
5.7	1005.5121	1.0013	VPLTRGQR
5.1	1004.5096	2.0038	IFLTYIR
5.1	1006.5117	0.0016	MIDAVVTSR

Spectrum No: 84; Query: 2914; Rank: 1

Peptide View

MS/MS Fragmentation of **DVYTGDAIR**
Found in **IP100025019**, Tax_Id=9606 Gene_Symbol=PSMB1 Proteasome subunit beta type-1

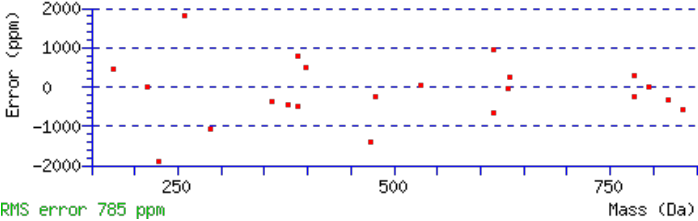
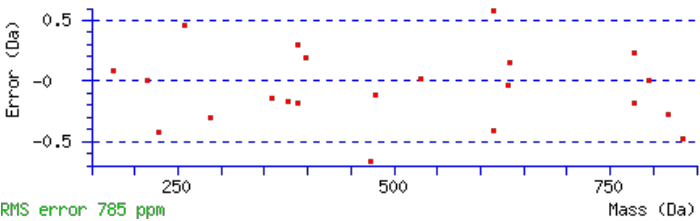
Match to Query 2914: 1008.492288 from(505.253420,2+)
Title: 091224LimSK_Exosome3_07.1243.1243.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1008.4876
Fixed modifications: Carbamidomethyl (C)
Ions Score: 21 Expect: 0.95
Matches (**Bold Red**): 22/74 fragment ions using 81 most intense peaks

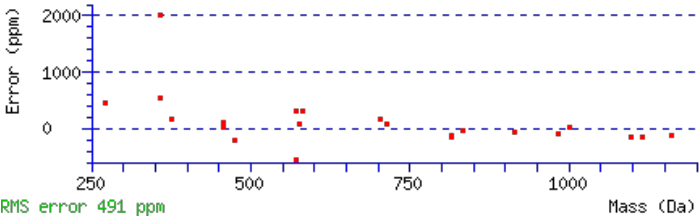
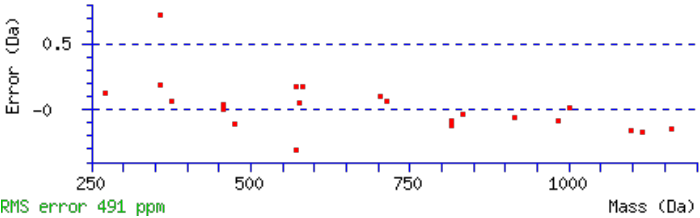
#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	116.0342	58.5207	98.0237	49.5155	D							9
2	215.1026	108.0550	197.0921	99.0497	V	894.4680	447.7376	877.4414	439.2243	876.4574	438.7323	8
3	378.1660	189.5866	360.1554	180.5813	Y	795.3995	398.2034	778.3730	389.6901	777.3890	389.1981	7
4	479.2136	240.1105	461.2031	231.1052	T	632.3362	316.6717	615.3097	308.1585	614.3257	307.6665	6
5	536.2351	268.6212	518.2245	259.6159	G	531.2885	266.1479	514.2620	257.6346	513.2780	257.1426	5
6	651.2620	326.1347	633.2515	317.1294	D	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
7	722.2992	361.6532	704.2886	352.6479	A	359.2401	180.1237	342.2136	171.6104			3
8	835.3832	418.1953	817.3727	409.1900	L	288.2030	144.6051	271.1765	136.0919			2
9					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
20.8	1008.4876	0.0047	DVYTGDALR
8.4	1008.4866	0.0057	GRGVNTLGR
8.2	1007.4841	1.0082	KTFTLYR
7.1	1006.4822	2.0101	GPGTRGARR
6.7	1007.4801	1.0122	GKPPLSSSR
6.5	1008.4876	0.0046	VDYGDVSVR
6.3	1008.5005	-0.0082	ALLTLADGR
6.0	1008.4906	0.0017	TLTPWRR
6.0	1008.4876	0.0047	ITVDDYGAR
5.0	1007.4801	1.0122	VLGAPATSGR

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							11
2	187.0713	94.0393			169.0608	85.0340	G	1159.6430	580.3251	1142.6164	571.8118	1141.6324	571.3198	10
3	300.1554	150.5813			282.1448	141.5761	I	1102.6215	551.8144	1085.5949	543.3011	1084.6109	542.8091	9
4	456.2565	228.6319	439.2300	220.1186	438.2459	219.6266	R	989.5374	495.2724	972.5109	486.7591	971.5269	486.2671	8
5	585.2991	293.1532	568.2726	284.6399	567.2885	284.1479	E	833.4363	417.2218	816.4098	408.7085	815.4258	408.2165	7
6	714.3417	357.6745	697.3151	349.1612	696.3311	348.6692	E	704.3937	352.7005	687.3672	344.1872	686.3832	343.6952	6
7	815.3894	408.1983	798.3628	399.6851	797.3788	399.1930	T	575.3511	288.1792	558.3246	279.6659	557.3406	279.1739	5
8	914.4578	457.7325	897.4312	449.2193	896.4472	448.7272	V	474.3035	237.6554	457.2769	229.1421	456.2929	228.6501	4
9	1001.4898	501.2485	984.4633	492.7353	983.4792	492.2433	S	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3
10	1114.5739	557.7906	1097.5473	549.2773	1096.5633	548.7853	L	288.2030	144.6051	271.1765	136.0919			2
11							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
47.7	1287.6783	0.0080	EGIREETVSLR
16.8	1287.6823	0.0040	SSEAVIWEVLR
14.3	1287.6823	0.0040	TDKELIDWLR
12.3	1287.6952	-0.0089	GPALSLLTPAIR
12.2	1286.6718	1.0145	EIPSLDQEKTK
10.6	1287.6952	-0.0089	GPALSLLTPAIR
9.3	1287.6758	0.0105	QHLLFMSQIR
9.2	1287.6782	0.0080	EASPAAKTKETR
6.9	1287.6857	0.0006	NQMNLLTLDVK
6.1	1287.6783	0.0080	EGTEASLQIRGK

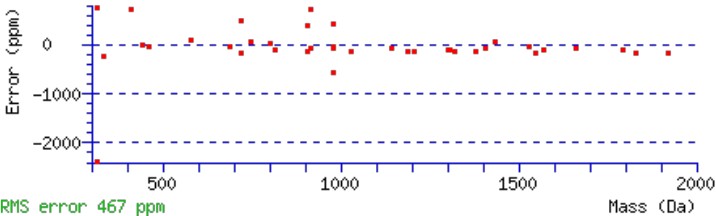
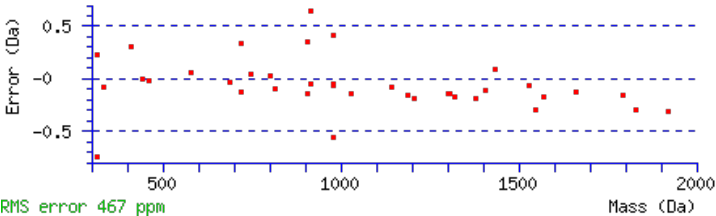
Spectrum No: 86; Query: 44191; Rank: 1

Peptide View

MS/MS Fragmentation of **FFPYVYNIIGGLDEEGK**
Found in **IPI00025019**, Tax_Id=9606 Gene_Symbol=PSMB1 Proteasome subunit beta type-1

Match to Query 44191: 2123.042028 from(1062.528290,2+)
Title: 091224LimSK_Exosome3_07.8986.8986.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

7	980.4553	490.7313					Y	1307.6478	654.3275	1290.6212	645.8142	1289.6372	645.3222	12
8	1094.4982	547.7527	1077.4716	539.2395			N	1144.5844	572.7959	1127.5579	564.2826	1126.5739	563.7906	11
9	1207.5823	604.2948	1190.5557	595.7815			I	1030.5415	515.7744	1013.5150	507.2611	1012.5310	506.7691	10
10	1320.6663	660.8368	1303.6398	652.3235			I	917.4575	459.2324	900.4309	450.7191	899.4469	450.2271	9
11	1377.6878	689.3475	1360.6612	680.8343			G	804.3734	402.6903	787.3468	394.1771	786.3628	393.6850	8
12	1434.7093	717.8583	1417.6827	709.3450			G	747.3519	374.1796	730.3254	365.6663	729.3414	365.1743	7
13	1547.7933	774.4003	1530.7668	765.8870			L	690.3305	345.6689	673.3039	337.1556	672.3199	336.6636	6
14	1662.8203	831.9138	1645.7937	823.4005	1644.8097	822.9085	D	577.2464	289.1268	560.2198	280.6136	559.2358	280.1216	5
15	1791.8629	896.4351	1774.8363	887.9218	1773.8523	887.4298	E	462.2195	231.6134	445.1929	223.1001	444.2089	222.6081	4
16	1920.9054	960.9564	1903.8789	952.4431	1902.8949	951.9511	E	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
17	1977.9269	989.4671	1960.9004	980.9538	1959.9163	980.4618	G	204.1343	102.5708	187.1077	94.0575			2
18							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

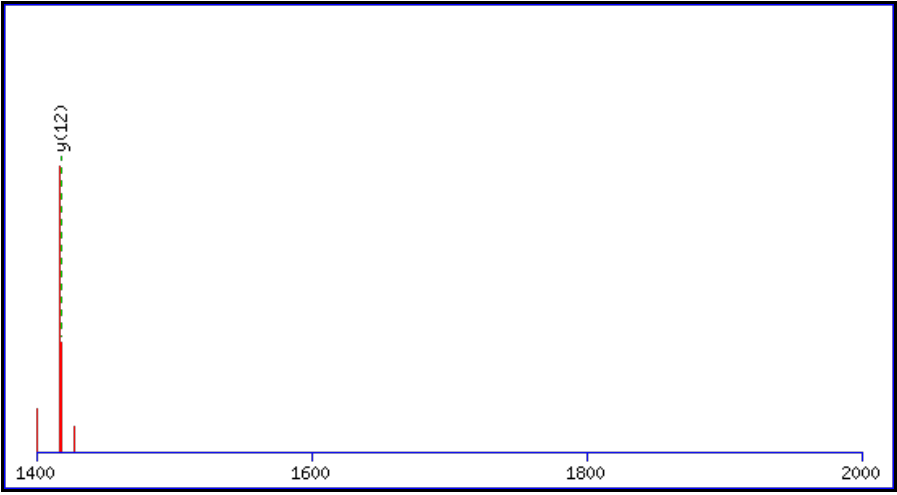
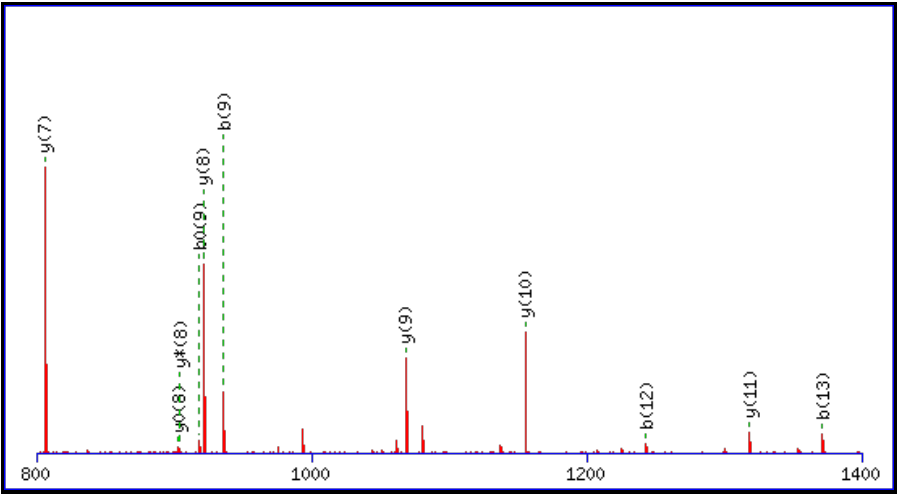
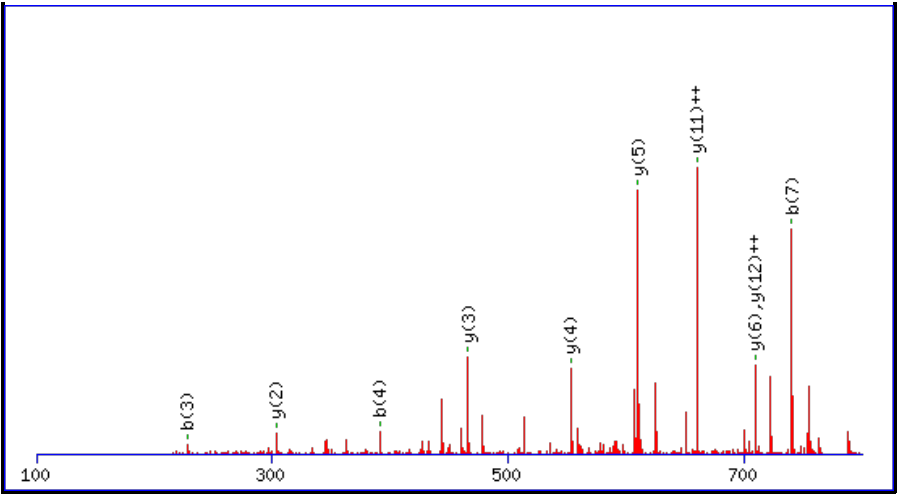
Score	Mr(calc):	Delta	Sequence
83.8	2123.0251	0.0169	FFPYVYVNIIGGLDEEGK
10.8	2123.0364	0.0056	GSMGPMGPSPDLSHIKQGRR
5.8	2123.0535	-0.0115	IAIQOTYSWTNQIDISDK
4.6	2123.0470	-0.0049	QFSDVLDQISRNEKMWK
3.7	2123.0446	-0.0025	XSLMGLGDIISQQLVERR
3.6	2123.0364	0.0056	GSMGPMGPSPDLSHIKQGRR
3.5	2122.0267	1.0154	MASRSMRLLLLLSCLAK
3.3	2121.0412	2.0008	KSLMDIPESQSEQDFVLR
2.4	2122.0306	1.0115	AFLMASQYQQPHEANKF
0.9	2121.0272	2.0148	LLSSLGIDTRNILETGNK

Spectrum No: 87; Query: 22776; Rank: 1

Peptide View

MS/MS Fragmentation of **GAVYSFDPVGSYQR**
Found in **IP100025019**, Tax_Id=9606 Gene_Symbol=PSMB1 Proteasome subunit beta type-1

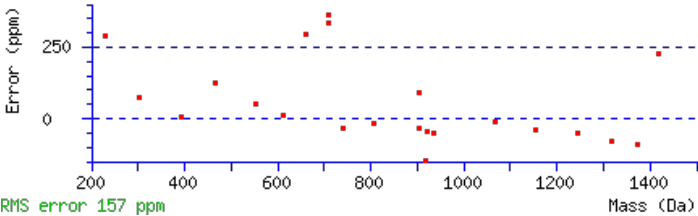
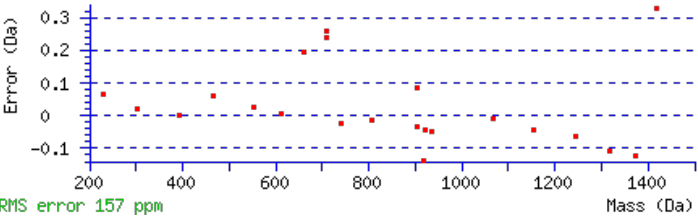
Match to Query 22776: 1544.732648 from(773.373600,2+)
Title: 091224LimSK_Exosome3_07.3814.3814.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1544.7260
Fixed modifications: Carbamidomethyl (C)
Ions Score: 101 Expect: 1.8e-008
Matches (Bold Red): 22/118 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							14
2	129.0659	65.0366					A	1488.7118	744.8595	1471.6852	736.3462	1470.7012	735.8542	13
3	228.1343	114.5708					V	1417.6747	709.3410	1400.6481	700.8277	1399.6641	700.3357	12
4	391.1976	196.1024					Y	1318.6062	659.8068	1301.5797	651.2935	1300.5957	650.8015	11
5	478.2296	239.6185			460.2191	230.6132	S	1155.5429	578.2751	1138.5164	569.7618	1137.5323	569.2698	10
6	625.2980	313.1527			607.2875	304.1474	F	1068.5109	534.7591	1051.4843	526.2458	1050.5003	525.7538	9

7	740.3250	370.6661			722.3144	361.6608	D	921.4425	461.2249	904.4159	452.7116	903.4319	452.2196	8
8	837.3777	419.1925			819.3672	410.1872	P	806.4155	403.7114	789.3890	395.1981	788.4050	394.7061	7
9	936.4462	468.7267			918.4356	459.7214	V	709.3628	355.1850	692.3362	346.6717	691.3522	346.1797	6
10	993.4676	497.2375			975.4571	488.2322	G	610.2944	305.6508	593.2678	297.1375	592.2838	296.6455	5
11	1080.4997	540.7535			1062.4891	531.7482	S	553.2729	277.1401	536.2463	268.6268	535.2623	268.1348	4
12	1243.5630	622.2851			1225.5524	613.2798	Y	466.2409	233.6241	449.2143	225.1108			3
13	1371.6216	686.3144	1354.5950	677.8011	1353.6110	677.3091	Q	303.1775	152.0924	286.1510	143.5791			2
14							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
100.5	1544.7260	0.0067	GAVYSFDPVGSYQR
8.0	1542.7249	2.0077	FCDRVQDAYTLR
6.5	1544.7357	-0.0030	KVVAVSMHPGPGMR
4.8	1543.7395	0.9931	ETAASLLQAGYKGR
4.5	1544.7236	0.0091	SFQDSLEDIKKR
4.4	1544.7364	-0.0038	KPATLSQIGTNKK
4.2	1544.7388	-0.0062	YKTHVDTVLAYR
4.1	1543.7283	1.0043	TLRYVPEESKDK
4.1	1543.7283	1.0043	TLRYVPEESKDK
3.8	1544.7388	-0.0062	YKTHVDTVLAYR

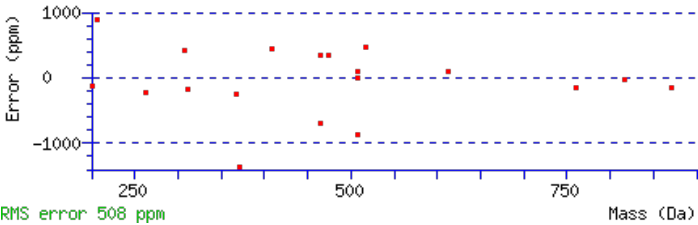
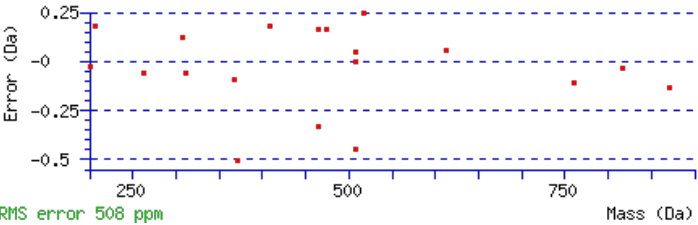
Spectrum No: 88; Query: 6117; Rank: 1

Peptide View

MS/MS Fragmentation of **LSEGF**SIHTR
Found in **IPI00025019**, Tax_Id=9606 Gene_Symbol=PSMB1 Proteasome subunit beta type-1

Match to Query 6117: 1145.589882 from(382.870570,3+)
Title: 091224LimSK_Exosome3_07.3308.3308.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

7	734.3719	367.6896	716.3614	358.6843	I	526.3096	263.6584	509.2831	255.1452	508.2990	254.6532	4
8	871.4308	436.2191	853.4203	427.2138	H	413.2255	207.1164	396.1990	198.6031	395.2150	198.1111	3
9	972.4785	486.7429	954.4680	477.7376	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
10					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

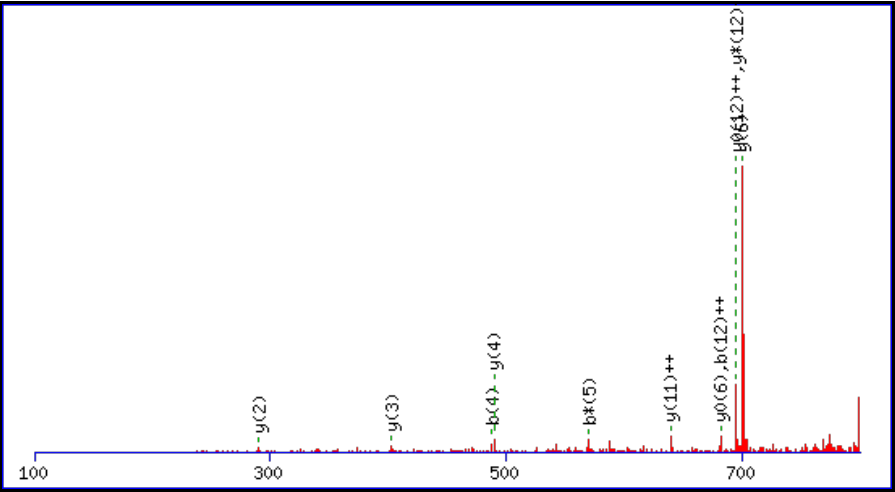
Score	Mr(calc):	Delta	Sequence
37.6	1145.5829	0.0070	LSEGFSIHTR
12.2	1144.5976	0.9923	ISQLVDVDEK
8.0	1143.5745	2.0154	ERVGEGGRER
7.2	1144.5754	1.0145	TPRPPALGTR
6.7	1144.5754	1.0145	ISPGIRGTHK
5.8	1144.5794	1.0105	TKFWKTVR
5.4	1144.5754	1.0145	TPSPARPALR
5.1	1144.5893	1.0006	TYGITGVKVK
4.9	1145.5928	-0.0029	DGDCLKTQIEK
4.8	1143.5884	2.0015	GVQLDSAGLER

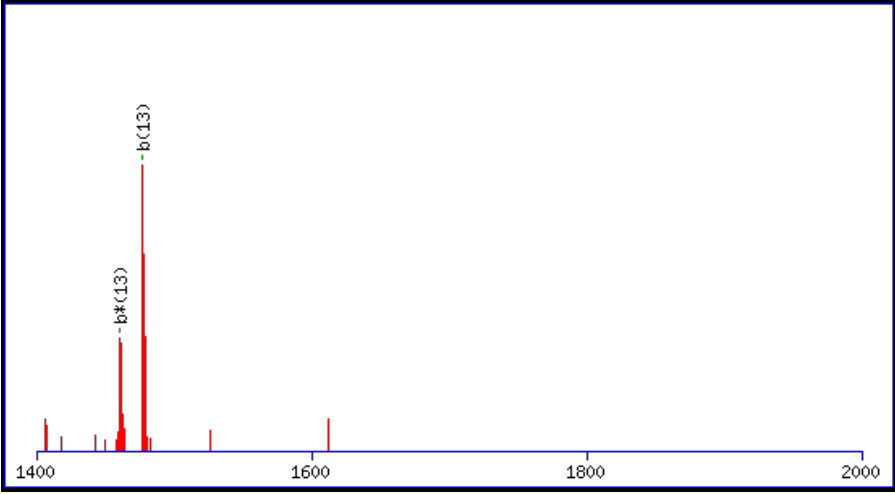
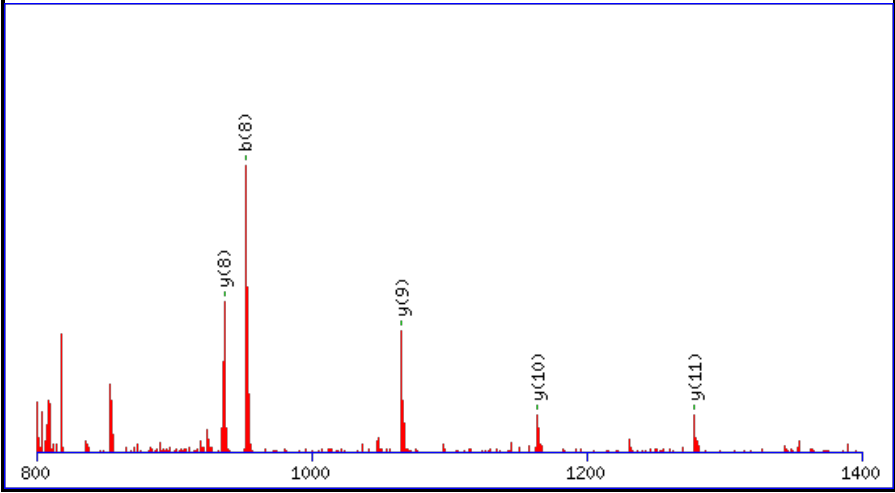
Spectrum No: 89; Query: 27970; Rank: 1

Peptide View

MS/MS Fragmentation of **NMQNVEHVPLSLDR**
Found in **IPI00025019**, Tax_Id=9606 Gene_Symbol=PSMB1 Proteasome subunit beta type-1

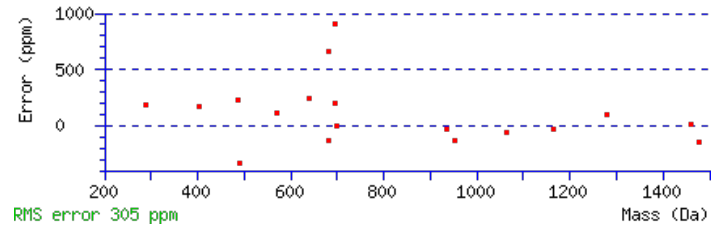
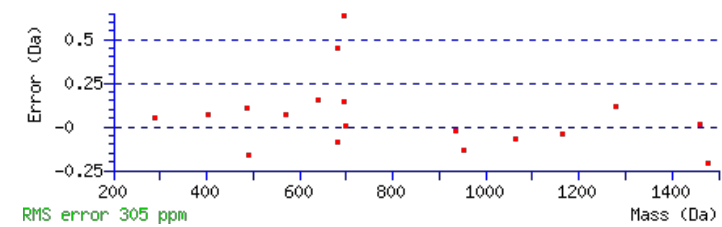
Match to Query 27970: 1650.826928 from(826.420740,2+)
Title: 091224LimSK_Exosome3_07.3635.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1650.8148
Fixed modifications: Carbamidomethyl (C)
Ions Score: 70 Expect: 2.1e-005
Matches (Bold Red): 18/144 fragment ions using 27 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							14
2	246.0907	123.5490	229.0641	115.0357			M	1537.7791	769.3932	1520.7526	760.8799	1519.7686	760.3879	13
3	374.1493	187.5783	357.1227	179.0650			Q	1406.7387	703.8730	1389.7121	695.3597	1388.7281	694.8677	12
4	488.1922	244.5997	471.1656	236.0865			N	1278.6801	639.8437	1261.6535	631.3304	1260.6695	630.8384	11
5	587.2606	294.1339	570.2341	285.6207			V	1164.6371	582.8222	1147.6106	574.3089	1146.6266	573.8169	10
6	716.3032	358.6552	699.2767	350.1420	698.2926	349.6500	E	1065.5687	533.2880	1048.5422	524.7747	1047.5582	524.2827	9
7	853.3621	427.1847	836.3356	418.6714	835.3515	418.1794	H	936.5261	468.7667	919.4996	460.2534	918.5156	459.7614	8
8	952.4305	476.7189	935.4040	468.2056	934.4200	467.7136	V	799.4672	400.2373	782.4407	391.7240	781.4567	391.2320	7
9	1049.4833	525.2453	1032.4567	516.7320	1031.4727	516.2400	P	700.3988	350.7030	683.3723	342.1898	682.3882	341.6978	6
10	1162.5674	581.7873	1145.5408	573.2740	1144.5568	572.7820	L	603.3461	302.1767	586.3195	293.6634	585.3355	293.1714	5
11	1249.5994	625.3033	1232.5728	616.7901	1231.5888	616.2980	S	490.2620	245.6346	473.2354	237.1214	472.2514	236.6293	4
12	1362.6834	681.8454	1345.6569	673.3321	1344.6729	672.8401	L	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
13	1477.7104	739.3588	1460.6838	730.8456	1459.6998	730.3535	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
14							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

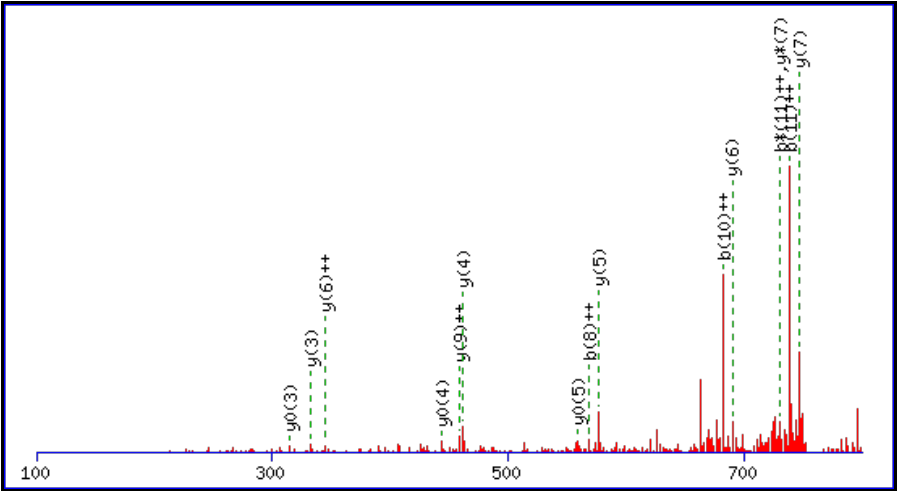
Score	Mr(calc):	Delta	Sequence
69.8	1650.8148	0.0122	NMQNVEHVPLSLDR
7.8	1650.8416	-0.0146	VLEKQLPGSMTIQK
7.3	1648.8355	1.9914	GLHMKLDHDLSLDR
7.3	1650.8416	-0.0146	VLEKQLPGSMTIQK
6.6	1650.8131	0.0139	RFVAVPEGIPTETR
5.8	1650.8131	0.0139	RFVAVPEGIPTETR
3.8	1650.8416	-0.0146	SPLVLQSILSLMDR
3.2	1650.8160	0.0109	RHSIISVLPWKR
3.2	1650.8260	0.0009	GLPGADGRAGVMGPPGSR
3.1	1648.8321	1.9948	GNDNWLVRYEKQK

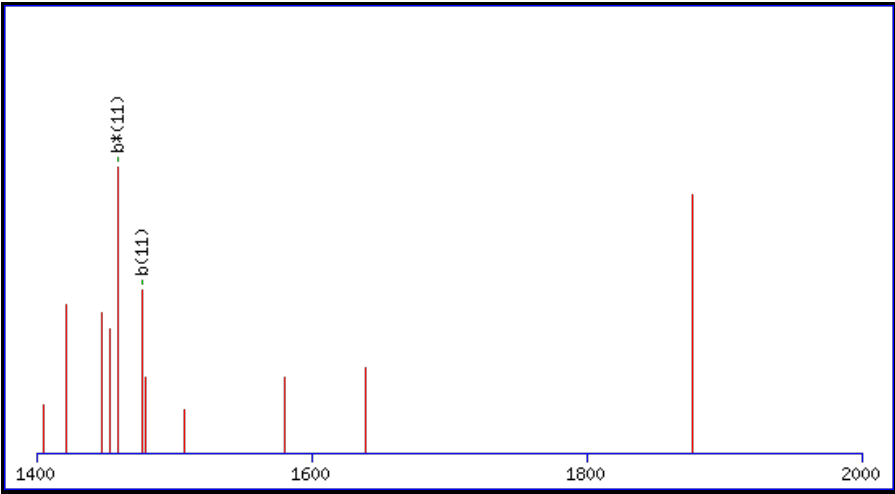
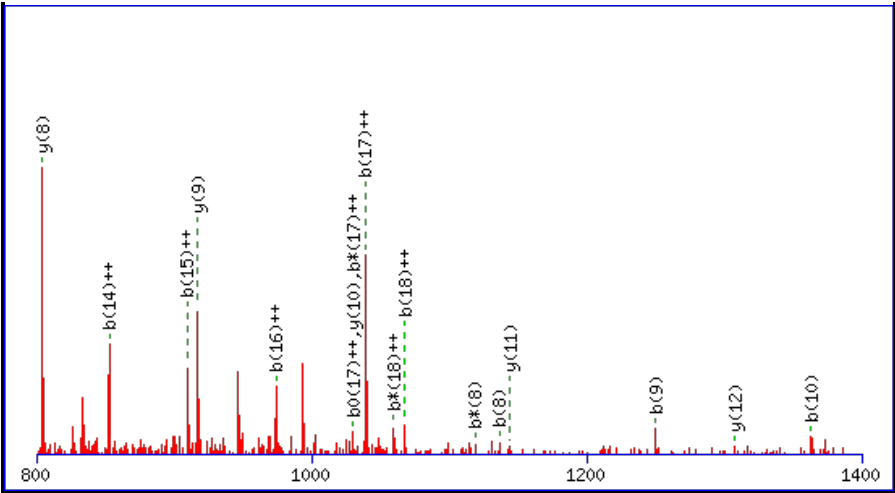
Spectrum No: 90; Query: 50223; Rank: 1

Peptide View

MS/MS Fragmentation of **RFFPYVYVNIIGGLDEEGK**
Found in **IPI00025019**, Tax_Id=9606 Gene_Symbol=PSMB1 Proteasome subunit beta type-1

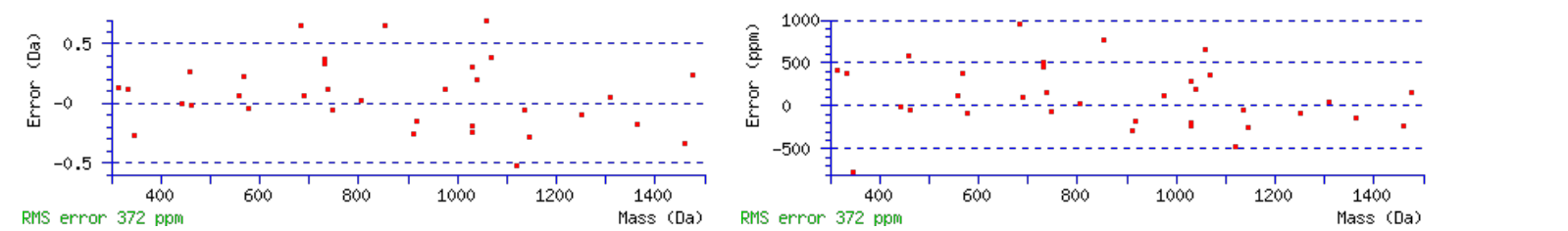
Match to Query 50223: 2279.141292 from(760.721040,3+)
Title: 091224LimSK_Exosome3_08.8210.8210.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2279.1263
Fixed modifications: Carbamidomethyl (C)
Ions Score: 36 Expect: 0.046
Matches (Bold Red): 34/184 fragment ions using 77 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							19
2	304.1768	152.5920	287.1503	144.0788			F	2124.0324	1062.5199	2107.0059	1054.0066	2106.0219	1053.5146	18
3	451.2452	226.1262	434.2187	217.6130			F	1976.9640	988.9856	1959.9375	980.4724	1958.9535	979.9804	17
4	548.2980	274.6526	531.2714	266.1394			P	1829.8956	915.4514	1812.8691	906.9382	1811.8850	906.4462	16
5	711.3613	356.1843	694.3348	347.6710			Y	1732.8428	866.9251	1715.8163	858.4118	1714.8323	857.9198	15
6	874.4246	437.7160	857.3981	429.2027			Y	1569.7795	785.3934	1552.7530	776.8801	1551.7690	776.3881	14
7	973.4931	487.2502	956.4665	478.7369			V	1406.7162	703.8617	1389.6896	695.3485	1388.7056	694.8564	13
8	1136.5564	568.7818	1119.5298	560.2686			Y	1307.6478	654.3275	1290.6212	645.8142	1289.6372	645.3222	12
9	1250.5993	625.8033	1233.5728	617.2900			N	1144.5844	572.7959	1127.5579	564.2826	1126.5739	563.7906	11
10	1363.6834	682.3453	1346.6568	673.8320			I	1030.5415	515.7744	1013.5150	507.2611	1012.5310	506.7691	10
11	1476.7674	738.8874	1459.7409	730.3741			I	917.4575	459.2324	900.4309	450.7191	899.4469	450.2271	9
12	1533.7889	767.3981	1516.7623	758.8848			G	804.3734	402.6903	787.3468	394.1771	786.3628	393.6850	8
13	1590.8104	795.9088	1573.7838	787.3955			G	747.3519	374.1796	730.3254	365.6663	729.3414	365.1743	7
14	1703.8944	852.4509	1686.8679	843.9376			L	690.3305	345.6689	673.3039	337.1556	672.3199	336.6636	6
15	1818.9214	909.9643	1801.8948	901.4510	1800.9108	900.9590	D	577.2464	289.1268	560.2198	280.6136	559.2358	280.1216	5
16	1947.9640	974.4856	1930.9374	965.9723	1929.9534	965.4803	E	462.2195	231.6134	445.1929	223.1001	444.2089	222.6081	4
17	2077.0066	1039.0069	2059.9800	1030.4936	2058.9960	1030.0016	E	333.1769	167.0921	316.1503	158.5788	315.1663	158.0868	3
18	2134.0280	1067.5176	2117.0015	1059.0044	2116.0175	1058.5124	G	204.1343	102.5708	187.1077	94.0575			2
19							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

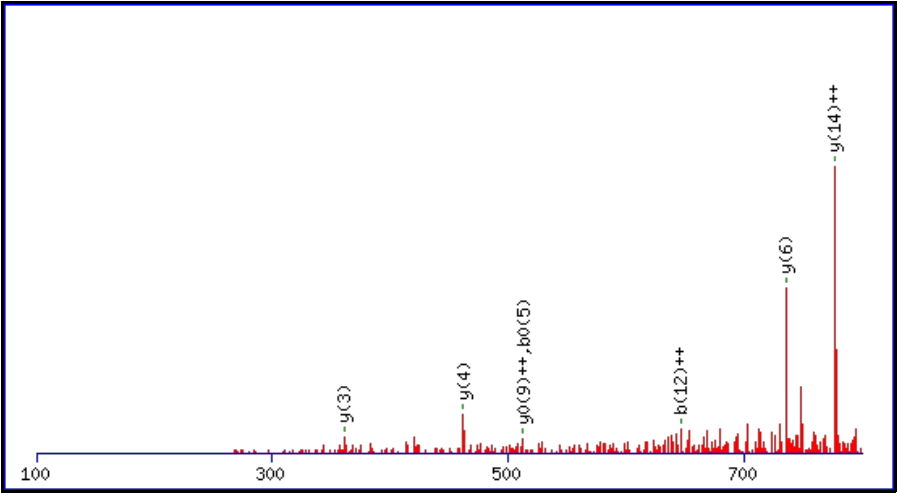
Score	Mr(calc):	Delta	Sequence
36.3	2279.1263	0.0150	RFFPYVYVNIIGGLDEEGK
8.6	2279.1440	-0.0027	LSINTHPSQKPLSITVRTK
8.3	2277.1165	2.0248	XLEKNVKEVLEDFAEEDGEK
7.2	2277.1365	2.0048	NSDQDVALKLAQERAEIVAK
7.0	2279.1596	-0.0183	IINDLLARSIGMVEVNTVVK
6.6	2277.1478	1.9935	ITLQTRLNQEALEDRLER
6.6	2277.1478	1.9935	ITLQTRLNQEALEDRLER
5.9	2278.1286	1.0127	FYFVSSADLLDILSKGAQPK
5.5	2278.1409	1.0004	SMSLDMGQPSQANTKKLLGTR
5.3	2277.1328	2.0085	TVTSSTEKGLIVYCVTSPKK

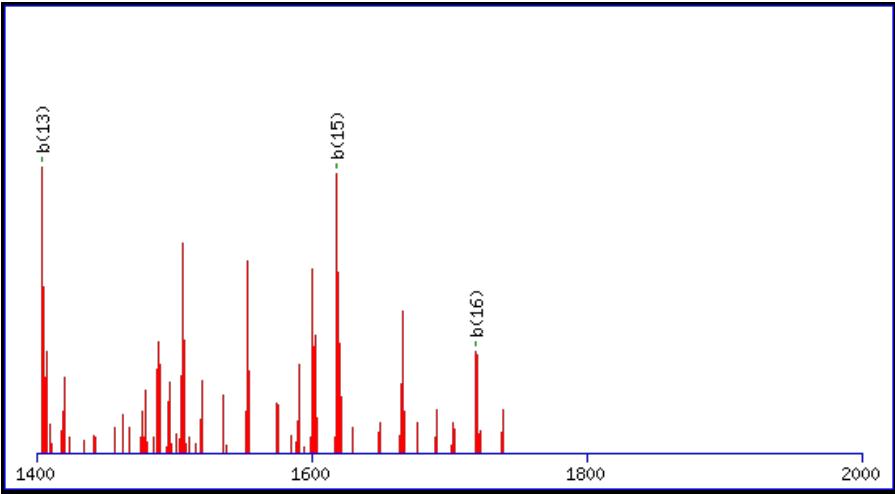
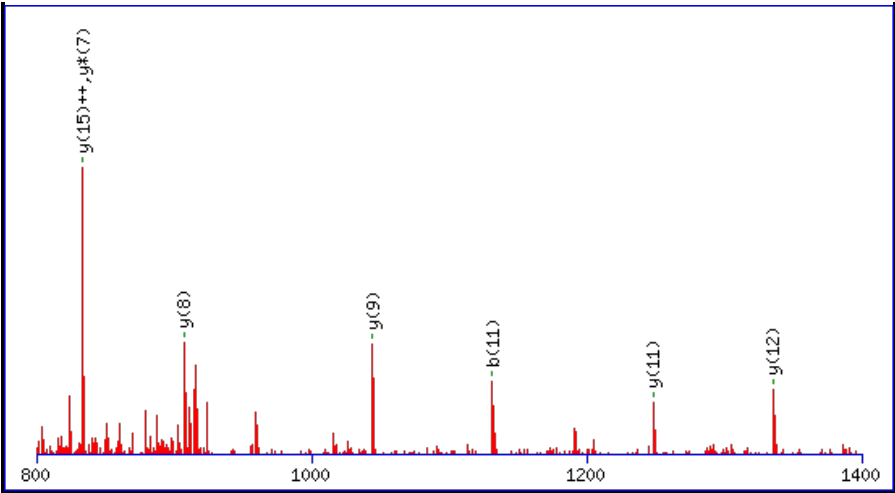
Spectrum No: 91; Query: 35461; Rank: 1

Peptide View

MS/MS Fragmentation of **TVIGCSGFHGDCLTLTK**
Found in **IPI00025019**, Tax_Id=9606 Gene_Symbol=PSMB1 Proteasome subunit beta type-1

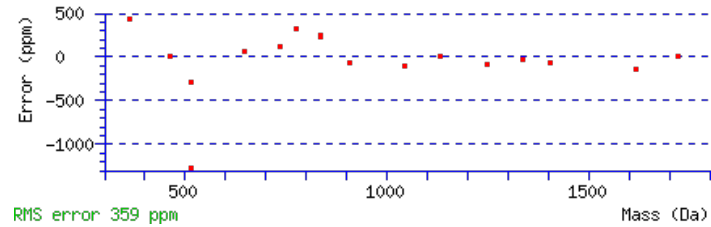
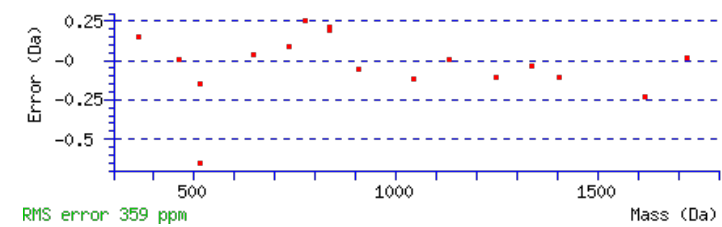
Match to Query 35461: 1864.894248 from(933.454400,2+)
Title: 091224LimSK_Exosome3_07.3982.3982.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1864.8812
Fixed modifications: Carbamidomethyl (C)
Ions Score: 56 Expect: 0.00064
Matches (Bold Red): 17/158 fragment ions using 28 most intense peaks

#	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							17
2	201.1234	101.0653	183.1128	92.0600	V	1764.8408	882.9240	1747.8142	874.4107	1746.8302	873.9187	16
3	314.2074	157.6074	296.1969	148.6021	I	1665.7723	833.3898	1648.7458	824.8765	1647.7618	824.3845	15
4	371.2289	186.1181	353.2183	177.1128	G	1552.6883	776.8478	1535.6617	768.3345	1534.6777	767.8425	14
5	531.2595	266.1334	513.2490	257.1281	C	1495.6668	748.3370	1478.6403	739.8238	1477.6562	739.3318	13
6	618.2916	309.6494	600.2810	300.6441	S	1335.6362	668.3217	1318.6096	659.8084	1317.6256	659.3164	12
7	675.3130	338.1602	657.3025	329.1549	G	1248.6041	624.8057	1231.5776	616.2924	1230.5936	615.8004	11
8	822.3815	411.6944	804.3709	402.6891	F	1191.5827	596.2950	1174.5561	587.7817	1173.5721	587.2897	10
9	959.4404	480.2238	941.4298	471.2185	H	1044.5143	522.7608	1027.4877	514.2475	1026.5037	513.7555	9
10	1016.4618	508.7346	998.4513	499.7293	G	907.4553	454.2313	890.4288	445.7180	889.4448	445.2260	8
11	1131.4888	566.2480	1113.4782	557.2427	D	850.4339	425.7206	833.4073	417.2073	832.4233	416.7153	7
12	1291.5194	646.2633	1273.5089	637.2581	C	735.4069	368.2071	718.3804	359.6938	717.3964	359.2018	6
13	1404.6035	702.8054	1386.5929	693.8001	L	575.3763	288.1918	558.3497	279.6785	557.3657	279.1865	5
14	1505.6512	753.3292	1487.6406	744.3239	T	462.2922	231.6498	445.2657	223.1365	444.2817	222.6445	4
15	1618.7352	809.8713	1600.7247	800.8660	L	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
16	1719.7829	860.3951	1701.7723	851.3898	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
17					K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

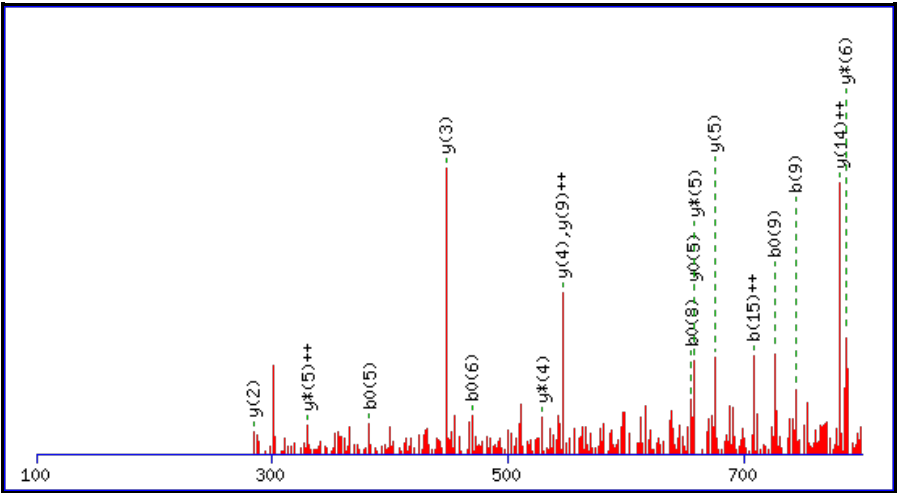
Score	Mr(calc):	Delta	Sequence
55.7	1864.8812	0.0131	TVIGCSGEHGDCLTLTK
5.8	1864.9100	-0.0158	AKILIDSIYKVTEGR
3.5	1864.9118	-0.0175	LSLSLSPSPQTGKPSMR
3.3	1862.9000	1.9943	RSLPTGSPTRPTASEAR
2.0	1864.8932	0.0011	SRDSQVPVTSSVVPEAK
1.6	1864.8989	-0.0047	GLDKMFLSSVSGHGETK
1.1	1864.8866	0.0077	TVTLSIALGKVASPLR
1.1	1862.8849	2.0094	SFQVTKEIISECKSK
0.7	1864.8961	-0.0019	VSEFLRNVRLNLTTK
0.5	1862.8849	2.0094	SFQVTKEIISECKSK

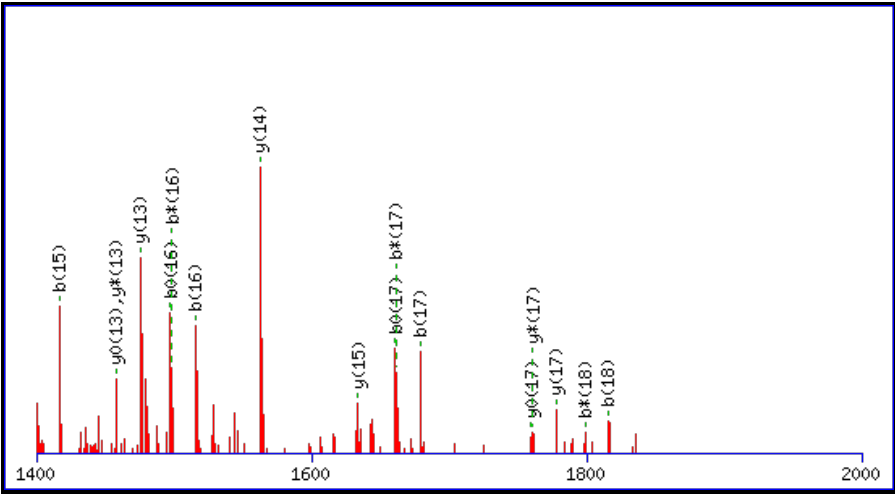
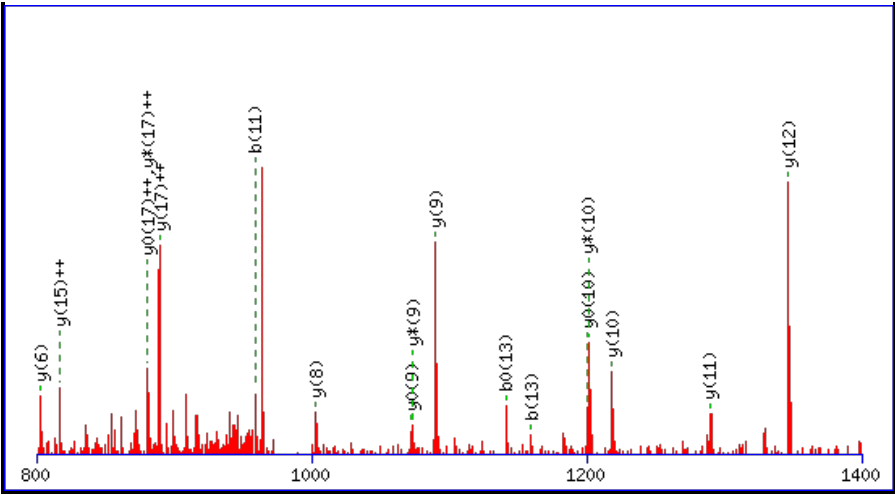
Spectrum No: 92; Query: 38393; Rank: 1

Peptide View

MS/MS Fragmentation of **AIGSASEGAQSSLQEVYHK**
Found in **IPI00291922**, Tax_Id=9606 Gene_Symbol=PSMA5 Proteasome subunit alpha type-5

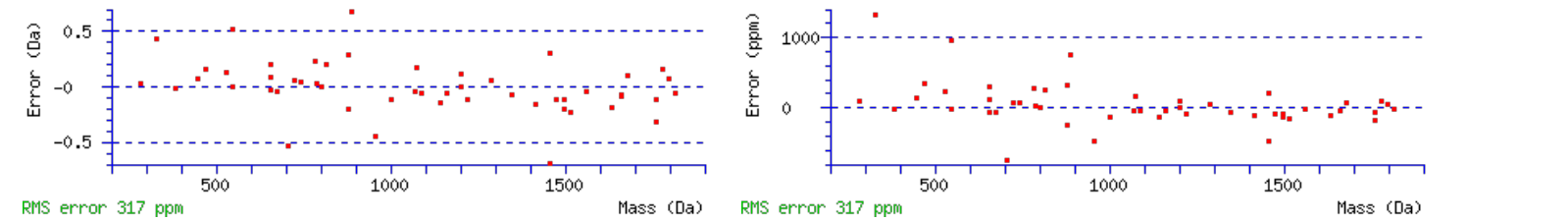
Match to Query 38393: 1960.962328 from(981.488440,2+)
Title: 091224LimSK_Exosome3_05.2179.2179.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1960.9490
Fixed modifications: Carbamidomethyl (C)
Ions Score: 93 Expect: 1.1e-007
Matches (Bold Red): 51/184 fragment ions using 83 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							19
2	185.1285	93.0679					I	1890.9192	945.9632	1873.8926	937.4500	1872.9086	936.9580	18
3	242.1499	121.5786					G	1777.8351	889.4212	1760.8086	880.9079	1759.8246	880.4159	17
4	329.1819	165.0946			311.1714	156.0893	S	1720.8137	860.9105	1703.7871	852.3972	1702.8031	851.9052	16
5	400.2191	200.6132			382.2085	191.6079	A	1633.7816	817.3945	1616.7551	808.8812	1615.7711	808.3892	15
6	487.2511	244.1292			469.2405	235.1239	S	1562.7445	781.8759	1545.7180	773.3626	1544.7340	772.8706	14
7	616.2937	308.6505			598.2831	299.6452	E	1475.7125	738.3599	1458.6860	729.8466	1457.7019	729.3546	13
8	673.3151	337.1612			655.3046	328.1559	G	1346.6699	673.8386	1329.6434	665.3253	1328.6593	664.8333	12
9	744.3523	372.6798			726.3417	363.6745	A	1289.6484	645.3279	1272.6219	636.8146	1271.6379	636.3226	11
10	872.4108	436.7091	855.3843	428.1958	854.4003	427.7038	Q	1218.6113	609.8093	1201.5848	601.2960	1200.6008	600.8040	10
11	959.4429	480.2251	942.4163	471.7118	941.4323	471.2198	S	1090.5528	545.7800	1073.5262	537.2667	1072.5422	536.7747	9
12	1046.4749	523.7411	1029.4483	515.2278	1028.4643	514.7358	S	1003.5207	502.2640	986.4942	493.7507	985.5102	493.2587	8
13	1159.5590	580.2831	1142.5324	571.7698	1141.5484	571.2778	L	916.4887	458.7480	899.4621	450.2347	898.4781	449.7427	7
14	1287.6175	644.3124	1270.5910	635.7991	1269.6070	635.3071	Q	803.4046	402.2060	786.3781	393.6927	785.3941	393.2007	6
15	1416.6601	708.8337	1399.6336	700.3204	1398.6496	699.8284	E	675.3461	338.1767	658.3195	329.6634	657.3355	329.1714	5
16	1515.7285	758.3679	1498.7020	749.8546	1497.7180	749.3626	V	546.3035	273.6554	529.2769	265.1421			4
17	1678.7919	839.8996	1661.7653	831.3863	1660.7813	830.8943	Y	447.2350	224.1212	430.2085	215.6079			3
18	1815.8508	908.4290	1798.8242	899.9158	1797.8402	899.4237	H	284.1717	142.5895	267.1452	134.0762			2
19							K	147.1128	74.0600	130.0863	65.5468			1



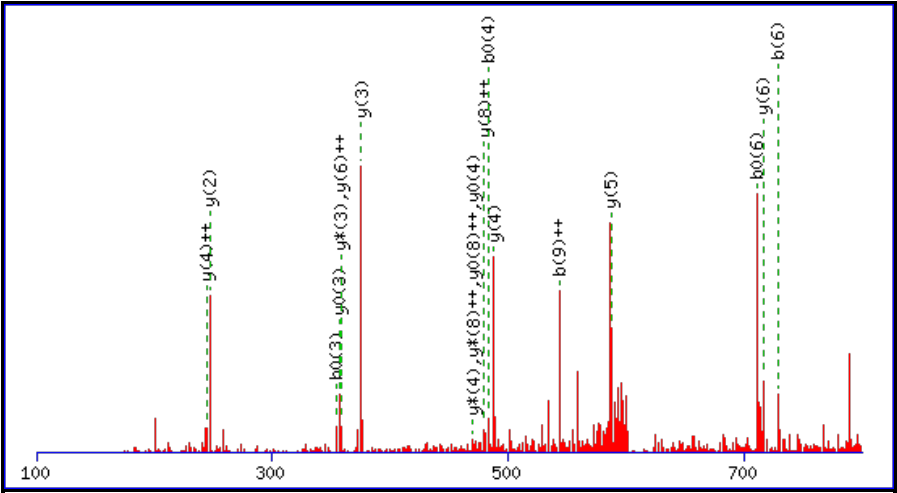
All matches to this query

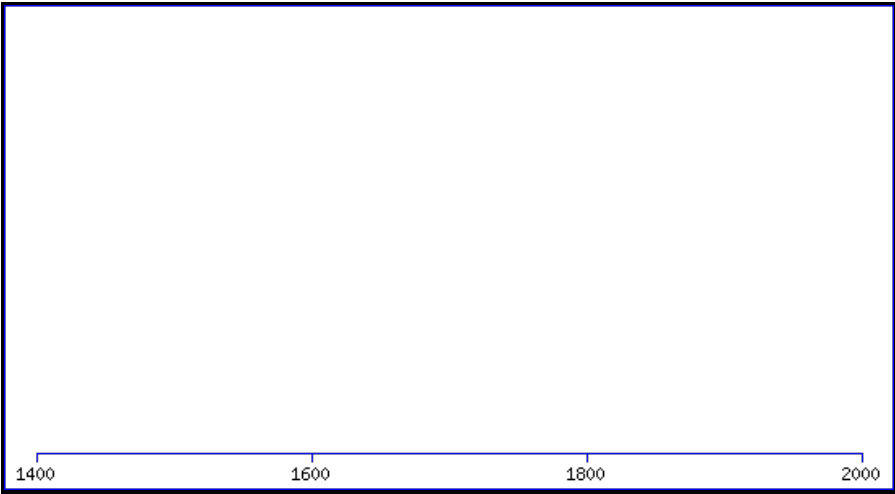
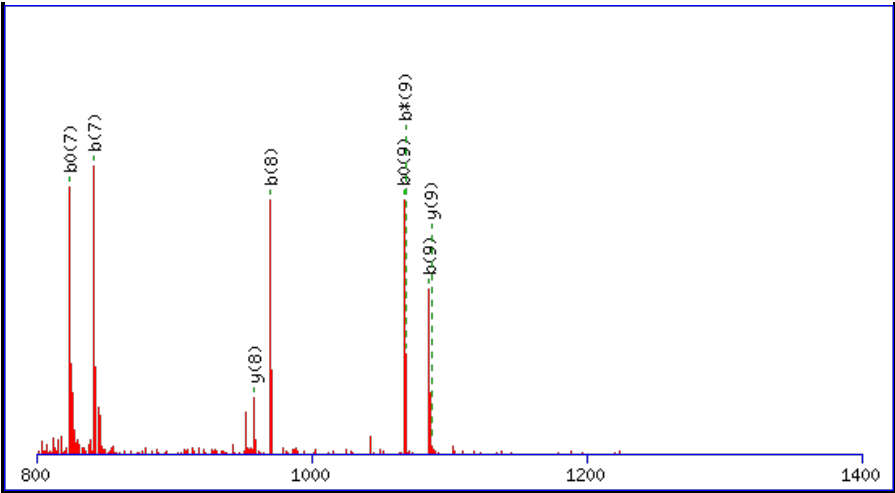
Score	Mr(calc):	Delta	Sequence
93.4	1960.9490	0.0133	AIGSASEGAQSSLQEVYHK
4.0	1960.9710	-0.0087	QLSAQGQMTQLCELINK
4.0	1960.9636	-0.0013	SMNDISLTPNTDQRKNK
2.9	1960.9547	0.0077	VSEAKPSQYYELQVLK
2.9	1960.9547	0.0077	VSEAKPSQYYELQVLK
1.8	1960.9520	0.0103	RPHGDIYGINQALGATAK
1.8	1960.9809	-0.0186	SFHHLWPQGQWASKPR

Spectrum No: 93; Query: 8487; Rank: 1

Peptide View

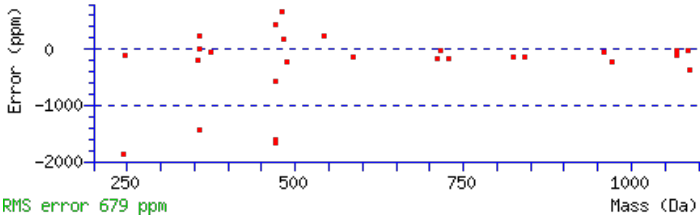
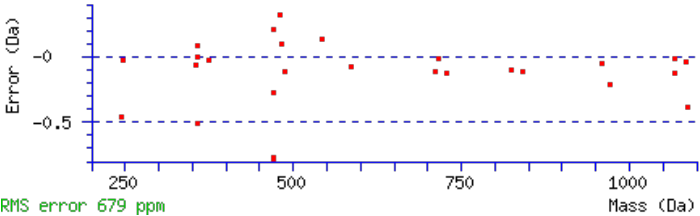
MS/MS Fragmentation of **EELEEVIKDI**
Found in **IPI00291922**, Tax_Id=9606 Gene_Symbol=PSMA5 Proteasome subunit alpha type-5
Match to Query 8487: 1215.629328 from(608.821940,2+)
Title: 091224LimSK_Exosome3_06.6218.6218.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1215.6234
Fixed modifications: Carbamidomethyl (C)
Ions Score: 43 Expect: 0.0068
Matches (Bold Red): 27/88 fragment ions using 48 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							10
2	259.0925	130.0499			241.0819	121.0446	E	1087.5881	544.2977	1070.5616	535.7844	1069.5776	535.2924	9
3	372.1765	186.5919			354.1660	177.5866	L	958.5455	479.7764	941.5190	471.2631	940.5350	470.7711	8
4	501.2191	251.1132			483.2086	242.1079	E	845.4615	423.2344	828.4349	414.7211	827.4509	414.2291	7
5	630.2617	315.6345			612.2511	306.6292	E	716.4189	358.7131	699.3923	350.1998	698.4083	349.7078	6
6	729.3301	365.1687			711.3196	356.1634	V	587.3763	294.1918	570.3497	285.6785	569.3657	285.1865	5
7	842.4142	421.7107			824.4036	412.7055	I	488.3079	244.6576	471.2813	236.1443	470.2973	235.6523	4
8	970.5092	485.7582	953.4826	477.2449	952.4986	476.7529	K	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
9	1085.5361	543.2717	1068.5095	534.7584	1067.5255	534.2664	D	247.1288	124.0681			229.1183	115.0628	2
10							I	132.1019	66.5546					1



All matches to this query



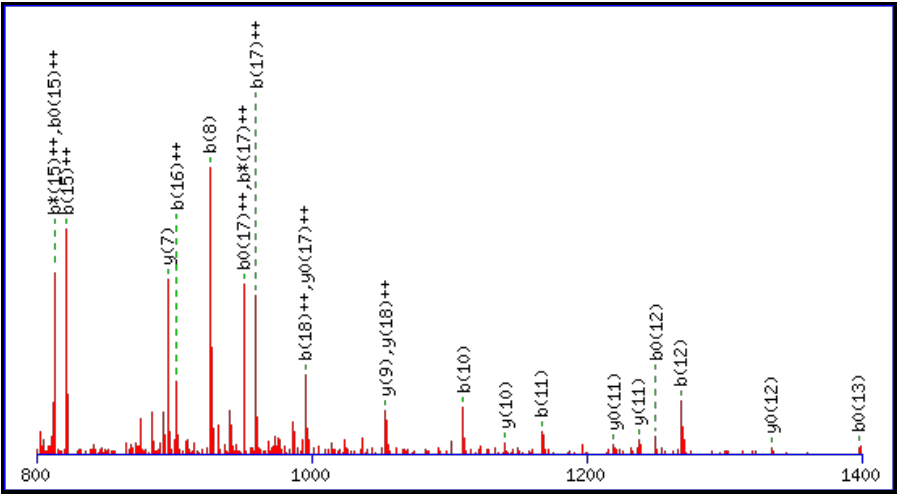
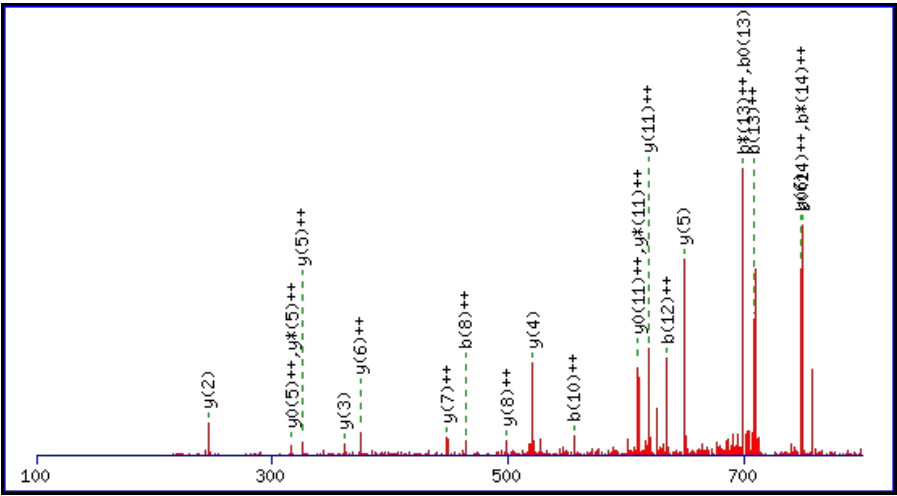
Score	Mr(calc):	Delta	Sequence
43.5	1215.6234	0.0059	EELEEVIKDI
16.8	1213.6294	1.9999	MVKLVWKS
14.5	1214.6329	0.9964	IQMINGSDLPK
13.5	1214.6367	0.9926	DKERAELAAGR
13.3	1213.6107	2.0186	YTPKEQLKK
11.8	1215.6281	0.0012	MIQDSGKVNPK
9.9	1215.6281	0.0012	MALTPTNLNNK
9.4	1213.6190	2.0103	EVEEKQPEVK
8.0	1215.6394	-0.0100	MAPERVASLSR
7.3	1213.6199	2.0095	GAVAMAPEMLPK

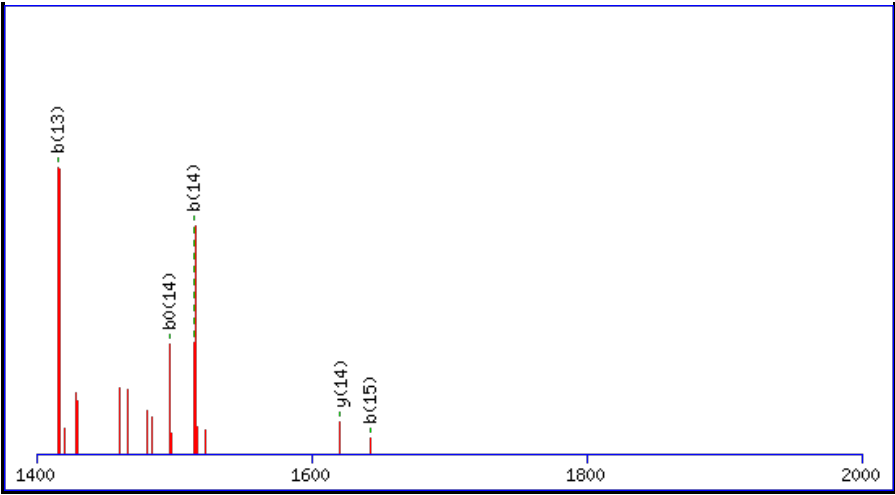
Spectrum No: 94; Query: 45554; Rank: 1

Peptide View

MS/MS Fragmentation of **GPQLFHMDPSGTFVQCDAR**
Found in **IPI00291922**, Tax_Id=9606 Gene_Symbol=PSMA5 Proteasome subunit alpha type-5

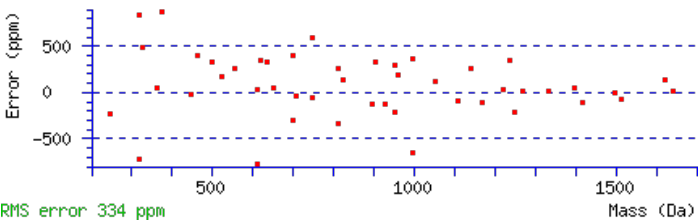
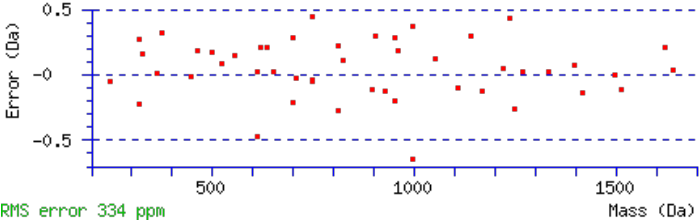
Match to Query 45554: 2161.979982 from(721.667270,3+)
Title: 091224LimSK_Exosome3_07.5269.5269.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2161.9674
Fixed modifications: Carbamidomethyl (C)
Ions Score: 61 Expect: 0.00023
Matches (Bold Red): 49/194 fragment ions using 61 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							19
2	155.0815	78.0444					P	2105.9532	1053.4802	2088.9266	1044.9669	2087.9426	1044.4749	18
3	283.1401	142.0737	266.1135	133.5604			Q	2008.9004	1004.9538	1991.8738	996.4406	1990.8898	995.9486	17
4	396.2241	198.6157	379.1976	190.1024			L	1880.8418	940.9245	1863.8153	932.4113	1862.8313	931.9193	16
5	543.2926	272.1499	526.2660	263.6366			F	1767.7578	884.3825	1750.7312	875.8692	1749.7472	875.3772	15
6	680.3515	340.6794	663.3249	332.1661			H	1620.6893	810.8483	1603.6628	802.3350	1602.6788	801.8430	14
7	811.3920	406.1996	794.3654	397.6863			M	1483.6304	742.3189	1466.6039	733.8056	1465.6199	733.3136	13
8	926.4189	463.7131	909.3924	455.1998	908.4083	454.7078	D	1352.5899	676.7986	1335.5634	668.2853	1334.5794	667.7933	12
9	1023.4717	512.2395	1006.4451	503.7262	1005.4611	503.2342	P	1237.5630	619.2851	1220.5365	610.7719	1219.5524	610.2799	11
10	1110.5037	555.7555	1093.4771	547.2422	1092.4931	546.7502	S	1140.5102	570.7588	1123.4837	562.2455	1122.4997	561.7535	10
11	1167.5252	584.2662	1150.4986	575.7529	1149.5146	575.2609	G	1053.4782	527.2427	1036.4517	518.7295	1035.4676	518.2375	9
12	1268.5728	634.7901	1251.5463	626.2768	1250.5623	625.7848	T	996.4567	498.7320	979.4302	490.2187	978.4462	489.7267	8
13	1415.6412	708.3243	1398.6147	699.8110	1397.6307	699.3190	F	895.4091	448.2082	878.3825	439.6949	877.3985	439.2029	7
14	1514.7097	757.8585	1497.6831	749.3452	1496.6991	748.8532	V	748.3407	374.6740	731.3141	366.1607	730.3301	365.6687	6
15	1642.7682	821.8878	1625.7417	813.3745	1624.7577	812.8825	Q	649.2722	325.1398	632.2457	316.6265	631.2617	316.1345	5
16	1802.7989	901.9031	1785.7723	893.3898	1784.7883	892.8978	C	521.2137	261.1105	504.1871	252.5972	503.2031	252.1052	4
17	1917.8258	959.4166	1900.7993	950.9033	1899.8153	950.4113	D	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
18	1988.8629	994.9351	1971.8364	986.4218	1970.8524	985.9298	A	246.1561	123.5817	229.1295	115.0684			2
19							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
61.0	2161.9674	0.0126	GPQLFHMDPSGTFVQCDAR
12.6	2160.9633	1.0167	SAKYSEAWQSKEEMENTK
10.0	2159.9840	1.9960	FPRMSPLQDVSTIGSR

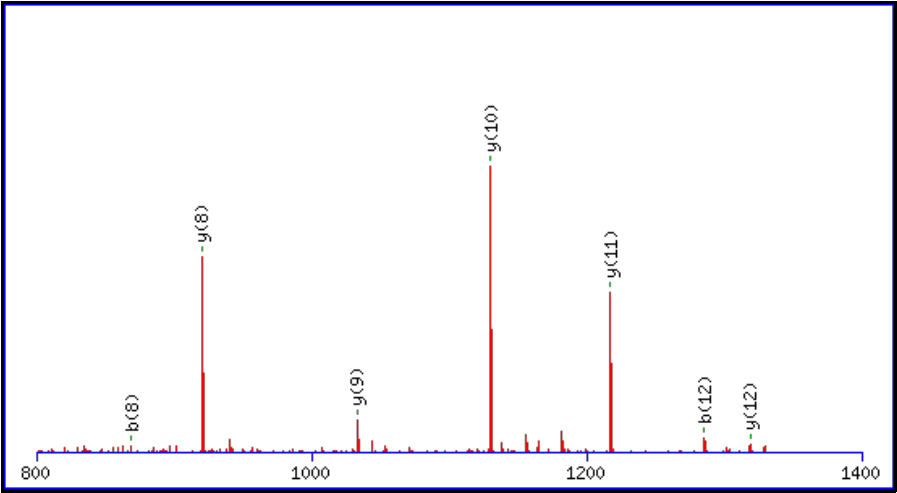
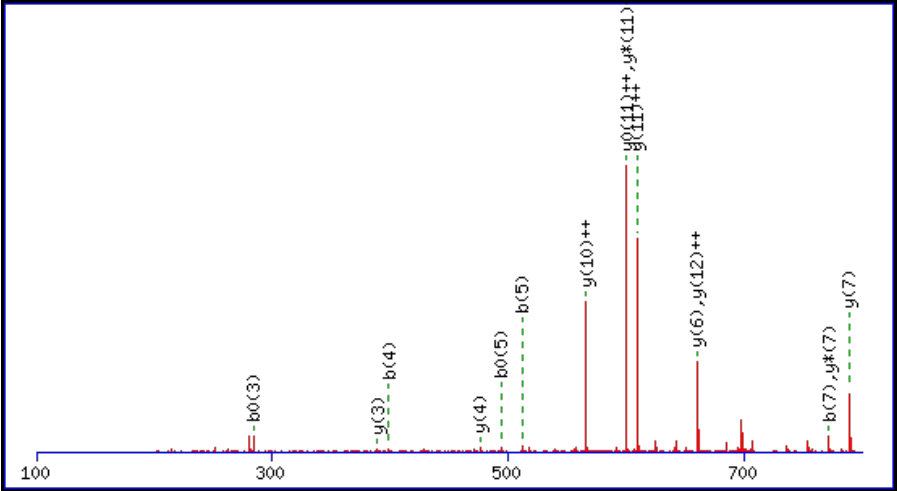
9.7	2161.9843	-0.0044	NSGEVMTVGINAIKEITAR
9.4	2162.0015	-0.0215	IYAAMMIMDYYKQSKVK
8.8	2161.9633	0.0166	MRRLFQTCDDGDGDGYISR
8.6	2159.9759	2.0040	ENYLEATVWIHGDNEENK
5.9	2161.9861	-0.0061	LVASESQTVGSM TVGSMRAR
5.8	2161.9861	-0.0061	LVASESQTVGSM TVGSMRAR
5.7	2161.9861	-0.0061	LVASESQTVGSM TVGSMRAR

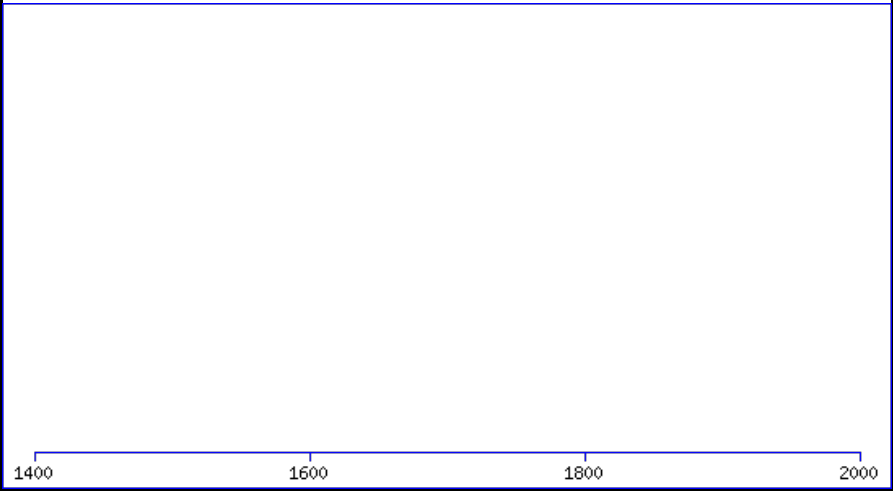
Spectrum No: 95; Query: 16765; Rank: 1

Peptide View

MS/MS Fragmentation of **ITSPLMEPSSIEK**
Found in **IPI00291922**, Tax_Id=9606 Gene_Symbol=PSMA5 Proteasome subunit alpha type-5

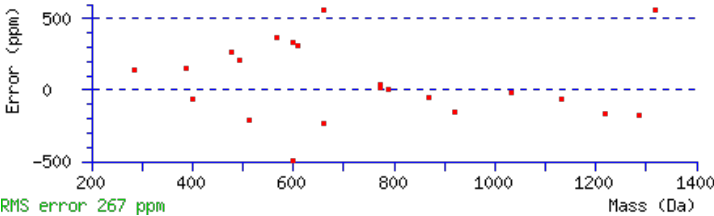
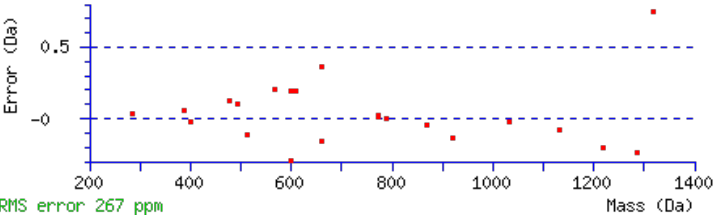
Match to Query 16765: 1430.739968 from(716.377260,2+)
Title: 091224LimSK_Exosome3_06.3321.3321.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1430.7327
Fixed modifications: Carbamidomethyl (C)
Ions Score: 77 Expect: 3e-006
Matches (**Bold Red**): 22/116 fragment ions using 33 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							13
2	215.1390	108.0731	197.1285	99.0679	T	1318.6559	659.8316	1301.6293	651.3183	1300.6453	650.8263	12
3	302.1710	151.5892	284.1605	142.5839	S	1217.6082	609.3077	1200.5817	600.7945	1199.5976	600.3025	11
4	399.2238	200.1155	381.2132	191.1103	P	1130.5762	565.7917	1113.5496	557.2785	1112.5656	556.7864	10
5	512.3079	256.6576	494.2973	247.6523	L	1033.5234	517.2653	1016.4969	508.7521	1015.5129	508.2601	9
6	643.3484	322.1778	625.3378	313.1725	M	920.4394	460.7233	903.4128	452.2100	902.4288	451.7180	8
7	772.3910	386.6991	754.3804	377.6938	E	789.3989	395.2031	772.3723	386.6898	771.3883	386.1978	7
8	869.4437	435.2255	851.4332	426.2202	P	660.3563	330.6818	643.3297	322.1685	642.3457	321.6765	6
9	956.4757	478.7415	938.4652	469.7362	S	563.3035	282.1554	546.2770	273.6421	545.2930	273.1501	5
10	1043.5078	522.2575	1025.4972	513.2522	S	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
11	1156.5918	578.7996	1138.5813	569.7943	I	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
12	1285.6344	643.3209	1267.6239	634.3156	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
13					K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

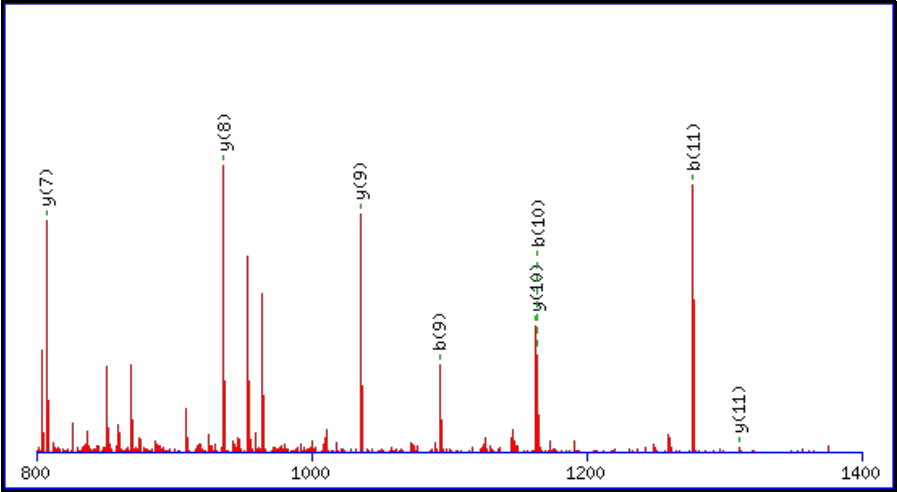
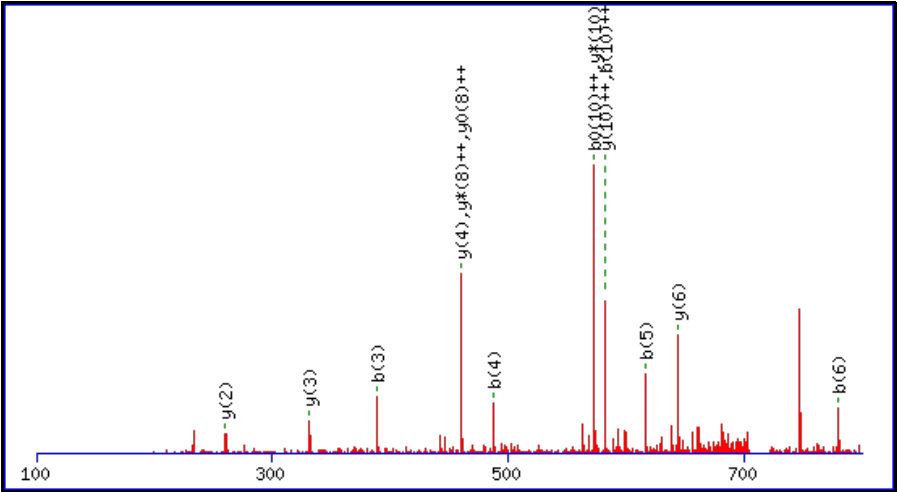
Score	Mr(calc):	Delta	Sequence
77.0	1430.7327	0.0073	ITSPLMEPSSIEK
17.1	1429.7460	0.9940	VNSPIRMKNGNGK
6.0	1429.7330	1.0070	ALVLNTPNNPLGK
4.2	1430.7283	0.0117	ELQIVRTLDDHK
2.8	1429.7330	1.0070	NIANSLPNVALPK
2.5	1430.7518	-0.0118	NADVNVLPIDHK
1.7	1430.7307	0.0093	WPDVOYQILGGR
1.6	1429.7500	0.9900	NVSQLPATWRMK
1.3	1430.7518	-0.0118	ITTTDEFKHLAR

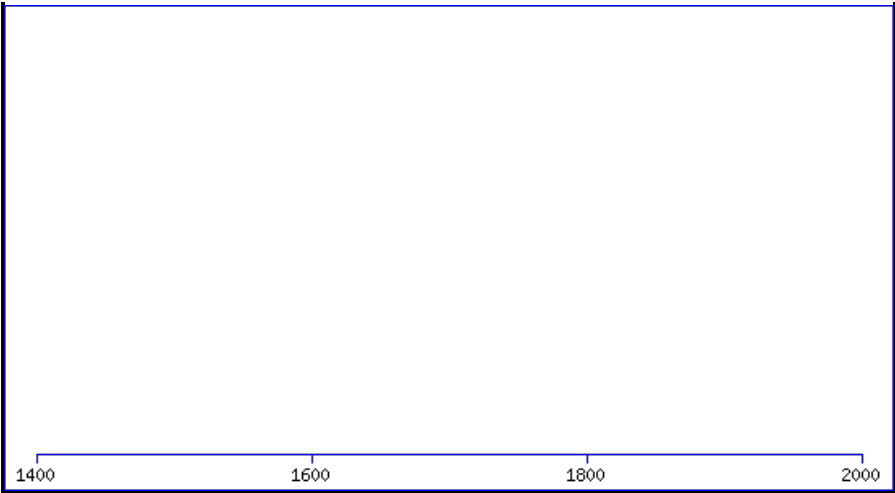
0.9	1428.7249	2.0151	DPYATSVGHLIEK
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Spectrum No: 96; Query: 16335; Rank: 1

Peptide View

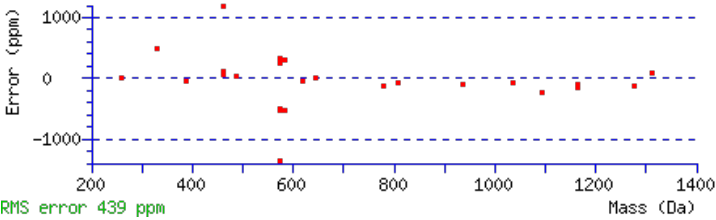
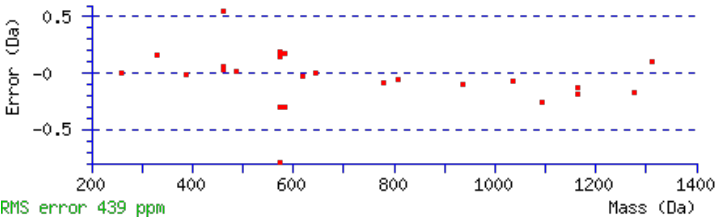
MS/MS Fragmentation of **LFQVEYAIEAIK**
Found in **IPI00291922**, Tax_Id=9606 Gene_Symbol=PSMA5 Proteasome subunit alpha type-5
Match to Query 16335: 1422.784928 from(712.399740,2+)
Title: 091224LimSK_Exosome3_06.6995.6995.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1422.7758
Fixed modifications: Carbamidomethyl (C)
Ions Score: 85 Expect: 2.4e-007
Matches (**Bold Red**): 25/114 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	114.0913	57.5493					L							12
2	261.1598	131.0835					F	1310.6991	655.8532	1293.6725	647.3399	1292.6885	646.8479	11
3	389.2183	195.1128	372.1918	186.5995			Q	1163.6307	582.3190	1146.6041	573.8057	1145.6201	573.3137	10
4	488.2867	244.6470	471.2602	236.1337			V	1035.5721	518.2897	1018.5455	509.7764	1017.5615	509.2844	9
5	617.3293	309.1683	600.3028	300.6550	599.3188	300.1630	E	936.5037	468.7555	919.4771	460.2422	918.4931	459.7502	8
6	780.3927	390.7000	763.3661	382.1867	762.3821	381.6947	Y	807.4611	404.2342	790.4345	395.7209	789.4505	395.2289	7
7	851.4298	426.2185	834.4032	417.7053	833.4192	417.2132	A	644.3978	322.7025	627.3712	314.1892	626.3872	313.6972	6
8	964.5138	482.7606	947.4873	474.2473	946.5033	473.7553	I	573.3606	287.1840	556.3341	278.6707	555.3501	278.1787	5
9	1093.5564	547.2819	1076.5299	538.7686	1075.5459	538.2766	E	460.2766	230.6419	443.2500	222.1287	442.2660	221.6366	4
10	1164.5936	582.8004	1147.5670	574.2871	1146.5830	573.7951	A	331.2340	166.1206	314.2074	157.6074			3
11	1277.6776	639.3424	1260.6511	630.8292	1259.6671	630.3372	I	260.1969	130.6021	243.1703	122.0888			2
12							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

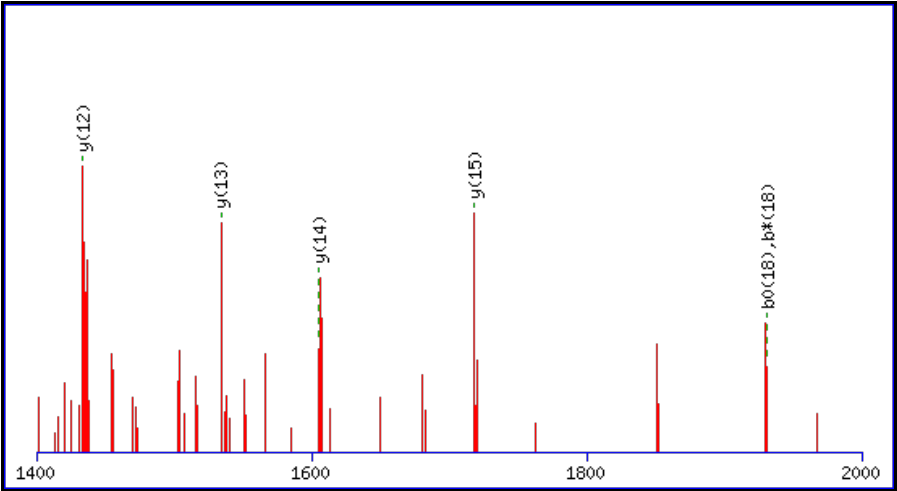
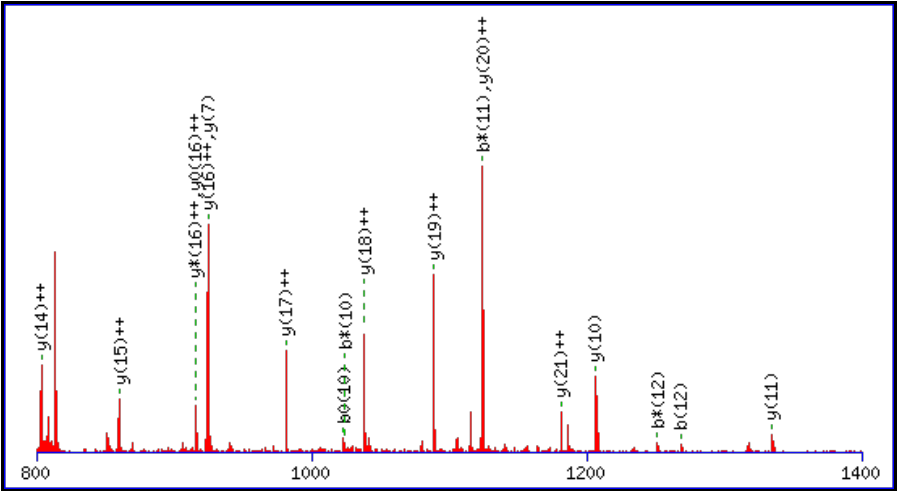
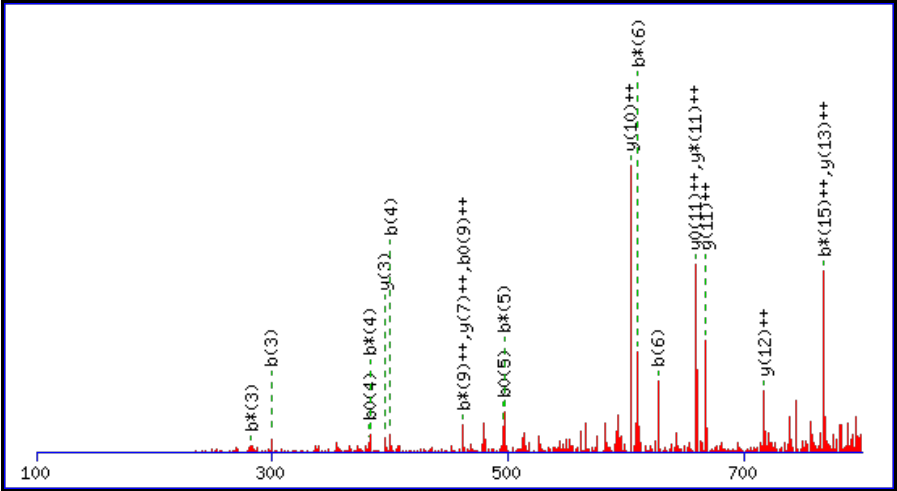
Score	Mr(calc):	Delta	Sequence
85.4	1422.7758	0.0091	LFQVEYAIEAIK
8.6	1422.7904	-0.0055	IMKGLNAYLEKK
7.5	1422.7732	0.0118	QFGHPQIEARIK
7.3	1420.7899	1.9951	EQARLKAHVVD R
6.9	1422.7752	0.0098	MLKGISSSSLKEK
5.3	1422.7878	-0.0028	VGHRMNIERALK
5.0	1422.7710	0.0139	VVWMQTL LILK
4.9	1422.7718	0.0131	AALDSPPGALAE LAK
4.7	1422.7718	0.0131	AHLEEISALVVDK
4.5	1422.7983	-0.0134	FLSRTFALAE LR

Spectrum No: 97; Query: 55322; Rank: 1

Peptide View

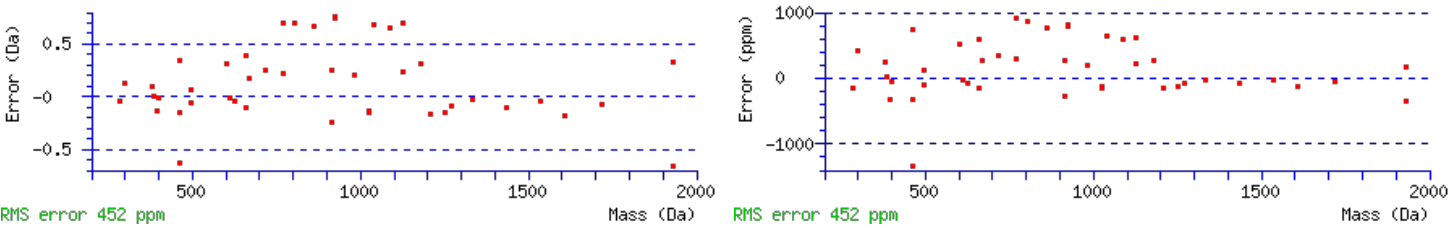
MS/MS Fragmentation of **LNATNIELATVQPGQNFMFTK**
Found in **IPI00291922**, Tax_Id=9606 Gene_Symbol=PSMA5 Proteasome subunit alpha type-5

Match to Query 55322: 2473.259292 from(825.427040,3+)
Title: 091224LimSK_Exosome3_06.6229.6229.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 2473.2424
Fixed modifications: Carbamidomethyl (C)
Ions Score: 74 Expect: 7.1e-006
Matches (Bold Red): 44/242 fragment ions using 69 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							22
2	228.1343	114.5708	211.1077	106.0575			N	2361.1656	1181.0864	2344.1390	1172.5732	2343.1550	1172.0812	21
3	299.1714	150.0893	282.1448	141.5761			A	2247.1227	1124.0650	2230.0961	1115.5517	2229.1121	1115.0597	20
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	T	2176.0856	1088.5464	2159.0590	1080.0331	2158.0750	1079.5411	19
5	514.2620	257.6346	497.2354	249.1214	496.2514	248.6293	N	2075.0379	1038.0226	2058.0113	1029.5093	2057.0273	1029.0173	18
6	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	I	1960.9949	981.0011	1943.9684	972.4878	1942.9844	971.9958	17
7	756.3886	378.6980	739.3621	370.1847	738.3781	369.6927	E	1847.9109	924.4591	1830.8843	915.9458	1829.9003	915.4538	16
8	869.4727	435.2400	852.4462	426.7267	851.4621	426.2347	L	1718.8683	859.9378	1701.8417	851.4245	1700.8577	850.9325	15
9	940.5098	470.7585	923.4833	462.2453	922.4993	461.7533	A	1605.7842	803.3958	1588.7577	794.8825	1587.7737	794.3905	14
10	1041.5575	521.2824	1024.5310	512.7691	1023.5469	512.2771	T	1534.7471	767.8772	1517.7206	759.3639	1516.7365	758.8719	13
11	1140.6259	570.8166	1123.5994	562.3033	1122.6154	561.8113	V	1433.6994	717.3534	1416.6729	708.8401	1415.6889	708.3481	12
12	1268.6845	634.8459	1251.6579	626.3326	1250.6739	625.8406	Q	1334.6310	667.8191	1317.6045	659.3059	1316.6205	658.8139	11
13	1365.7373	683.3723	1348.7107	674.8590	1347.7267	674.3670	P	1206.5724	603.7899	1189.5459	595.2766	1188.5619	594.7846	10
14	1422.7587	711.8830	1405.7322	703.3697	1404.7482	702.8777	G	1109.5197	555.2635	1092.4931	546.7502	1091.5091	546.2582	9
15	1550.8173	775.9123	1533.7908	767.3990	1532.8067	766.9070	Q	1052.4982	526.7527	1035.4717	518.2395	1034.4876	517.7475	8
16	1664.8602	832.9338	1647.8337	824.4205	1646.8497	823.9285	N	924.4396	462.7235	907.4131	454.2102	906.4291	453.7182	7
17	1811.9286	906.4680	1794.9021	897.9547	1793.9181	897.4627	F	810.3967	405.7020	793.3702	397.1887	792.3861	396.6967	6
18	1948.9876	974.9974	1931.9610	966.4841	1930.9770	965.9921	H	663.3283	332.1678	646.3017	323.6545	645.3177	323.1625	5
19	2080.0280	1040.5177	2063.0015	1032.0044	2062.0175	1031.5124	M	526.2694	263.6383	509.2428	255.1251	508.2588	254.6330	4
20	2227.0965	1114.0519	2210.0699	1105.5386	2209.0859	1105.0466	F	395.2289	198.1181	378.2023	189.6048	377.2183	189.1128	3
21	2328.1441	1164.5757	2311.1176	1156.0624	2310.1336	1155.5704	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
22							K	147.1128	74.0600	130.0863	65.5468			1

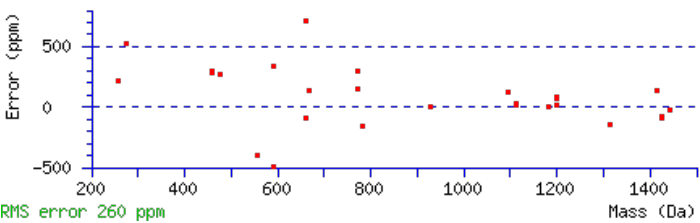
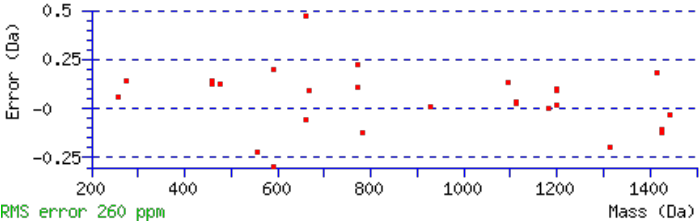


All matches to this query

Score	Mr(calc):	Delta	Sequence
74.1	2473.2424	0.0169	LNATNIELATVQPGQNFHMETK
12.0	2471.2322	2.0271	RGGLEVALQVQVLDTPGYPHSR
9.4	2472.2373	1.0220	LKTGPEGALGSEKNGVPARPGTEK
1.1	2471.2515	2.0078	HVGPSFVRKEFQNNFVIVK
0.4	2473.2512	0.0081	KVLGRGGEAASGGLAPPAVAMVTER
0.3	2471.2557	2.0036	QPGASPSQERKPTGVSVIYWER
0.3	2471.2560	2.0033	GELIPISPSTEVGSGIGTPPSVLK
0.3	2473.2465	0.0128	GSTGGVAPESLTLVLSAASPLVDPR
0.2	2473.2730	-0.0137	IGPIATPDYIQNAPGLPKTRSGK
0.1	2471.2445	2.0148	GDIGIGIAGENGLPGPPGPQGPPEGYK

file:///Z:/temp/LimSK/MascotFig/Exosome3/Exosome3_001.html[3/26/2012 1:35:34 PM]

#	b	b ⁺⁺	b [*]	b ^{***}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{***}	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							14
2	270.1925	135.5999	253.1659	127.0866			I	1431.7400	716.3736	1414.7134	707.8603	1413.7294	707.3683	13
3	371.2401	186.1237	354.2136	177.6104	353.2296	177.1184	T	1318.6559	659.8316	1301.6293	651.3183	1300.6453	650.8263	12
4	458.2722	229.6397	441.2456	221.1264	440.2616	220.6344	S	1217.6082	609.3077	1200.5817	600.7945	1199.5977	600.3025	11
5	555.3249	278.1661	538.2984	269.6528	537.3144	269.1608	P	1130.5762	565.7917	1113.5496	557.2785	1112.5656	556.7864	10
6	668.4090	334.7081	651.3824	326.1949	650.3984	325.7028	L	1033.5234	517.2653	1016.4969	508.7521	1015.5129	508.2601	9
7	799.4495	400.2284	782.4229	391.7151	781.4389	391.2231	M	920.4394	460.7233	903.4128	452.2100	902.4288	451.7180	8
8	928.4921	464.7497	911.4655	456.2364	910.4815	455.7444	E	789.3989	395.2031	772.3723	386.6898	771.3883	386.1978	7
9	1025.5448	513.2761	1008.5183	504.7628	1007.5343	504.2708	P	660.3563	330.6818	643.3297	322.1685	642.3457	321.6765	6
10	1112.5769	556.7921	1095.5503	548.2788	1094.5663	547.7868	S	563.3035	282.1554	546.2770	273.6421	545.2930	273.1501	5
11	1199.6089	600.3081	1182.5823	591.7948	1181.5983	591.3028	S	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
12	1312.6929	656.8501	1295.6664	648.3368	1294.6824	647.8448	I	389.2395	195.1234	372.2129	186.6101	371.2289	186.1181	3
13	1441.7355	721.3714	1424.7090	712.8581	1423.7250	712.3661	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
14							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

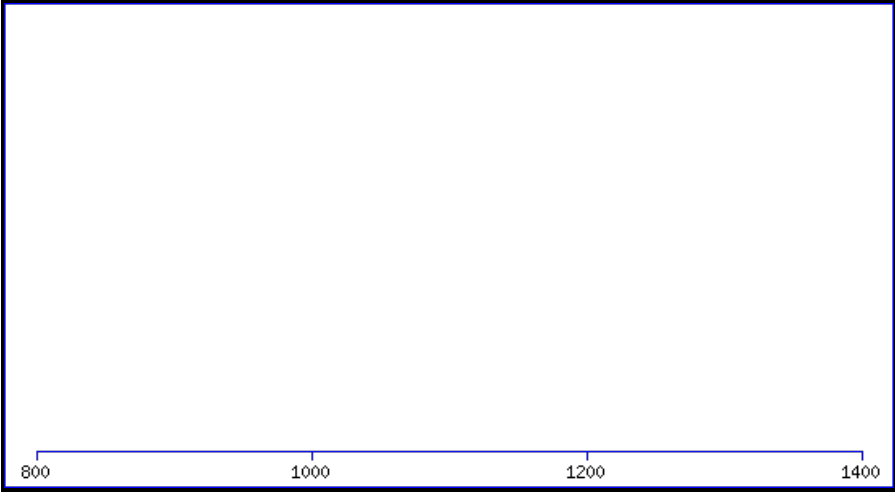
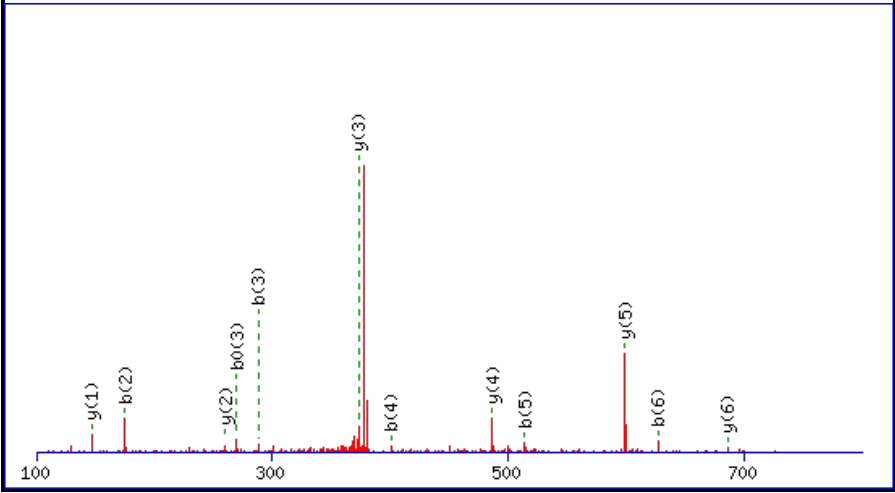
Score	Mr(calc):	Delta	Sequence
36.0	1586.8338	0.0099	RITSPLMEPSSIEK
9.9	1585.8415	1.0022	QFKKMLTSAILAR
8.1	1586.8338	0.0099	GMPETLGQVAKALEK
5.9	1586.8545	-0.0108	DHSIQIKIGKLQK
5.7	1586.8507	-0.0070	KIAVISTKLFMEK
5.2	1586.8562	-0.0126	GSLAMSIQRGSLVPR
5.1	1586.8507	-0.0070	KIAVISTKLFMEK
5.1	1585.8464	0.9973	DGAYLDNPPKGALKK
4.6	1585.8246	1.0191	EHLTASMSRVALQK
4.4	1586.8515	-0.0079	KEVAETSAGPSVVSVK

Spectrum No: 99; Query: 181; Rank: 1

Peptide View

MS/MS Fragmentation of **SSLILK**
Found in **IPI00291922**, Tax_Id=9606 Gene_Symbol=PSMA5 Proteasome subunit alpha type-5

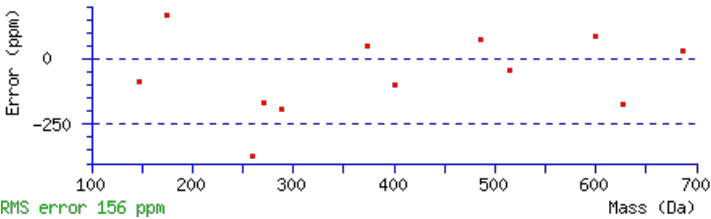
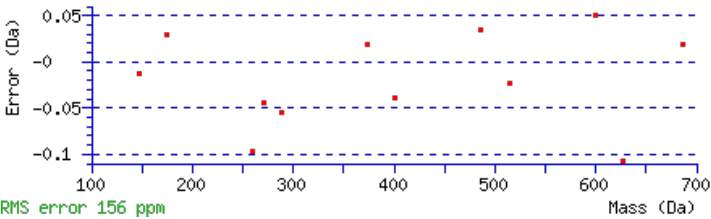
Match to Query 181: 772.509268 from(387.261910,2+)
Title: 091224LimSK_Exosome3_06.2488.2488.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 772.5058
Fixed modifications: Carbamidomethyl (C)
Ions Score: 50 Expect: 0.00026
Matches (**Bold Red**): 12/50 fragment ions using 24 most intense peaks

#	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							7
2	175.0713	88.0393	157.0608	79.0340	S	686.4811	343.7442	669.4545	335.2309	668.4705	334.7389	6
3	288.1554	144.5813	270.1448	135.5761	L	599.4491	300.2282	582.4225	291.7149			5
4	401.2395	201.1234	383.2289	192.1181	I	486.3650	243.6861	469.3384	235.1729			4
5	514.3235	257.6654	496.3130	248.6601	I	373.2809	187.1441	356.2544	178.6308			3
6	627.4076	314.2074	609.3970	305.2021	L	260.1969	130.6021	243.1703	122.0888			2

7					K	147.1128	74.0600	130.0863	65.5468			1
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All matches to this query

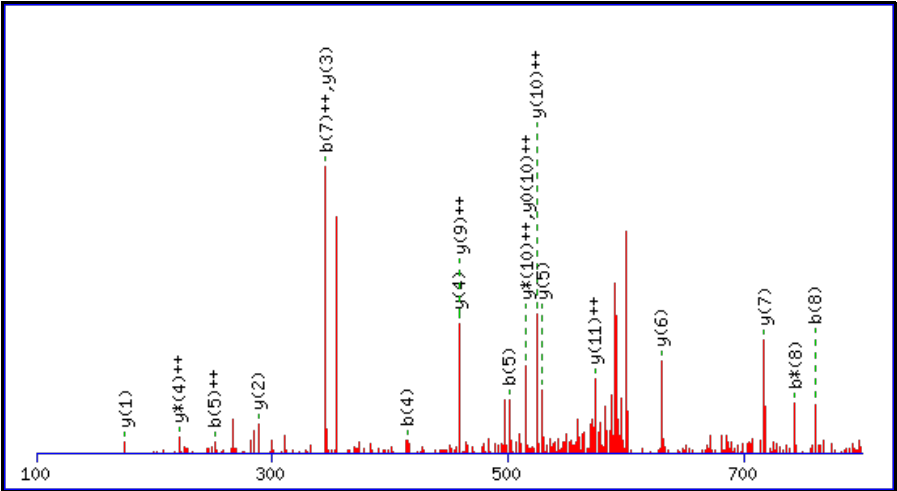
Score	Mr(calc):	Delta	Sequence
50.0	772.5058	0.0035	SSLILK
32.8	772.5058	0.0035	SLSLLLK
32.8	772.5058	0.0034	SVTLLIK
14.4	770.5014	2.0079	ERLLLK
11.3	770.5014	2.0079	EKILR
11.3	770.5014	2.0079	KELLR
10.3	770.5014	2.0079	NGLVKIK
9.2	772.5058	0.0035	ISISLLK
8.9	771.5079	1.0014	RSRLLK
8.3	770.5014	2.0079	ASVLLIR

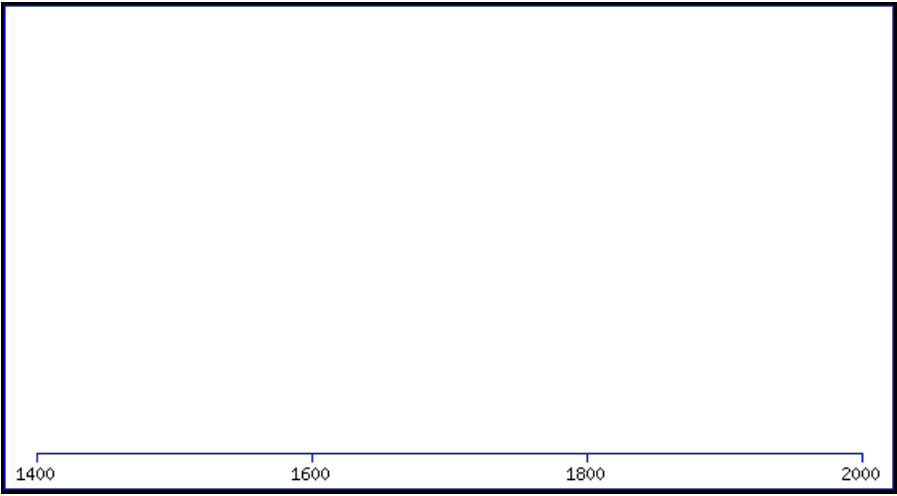
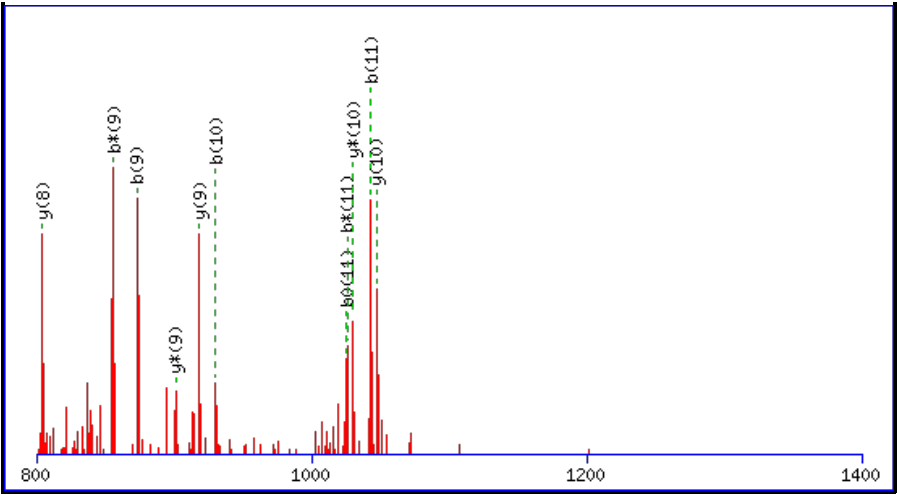
Spectrum No: 100; Query: 8522; Rank: 1

Peptide View

MS/MS Fragmentation of **AVENSSTAIGIR**
Found in **IPI00171199**, Tax_Id=9606 Gene_Symbol=PSMA3 Isoform 2 of Proteasome subunit alpha type-3

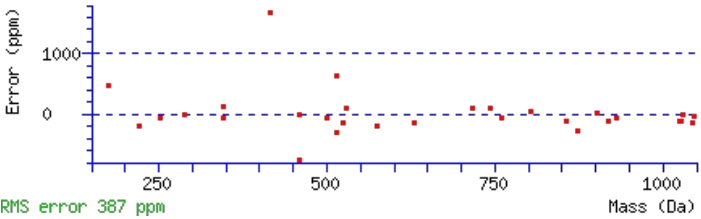
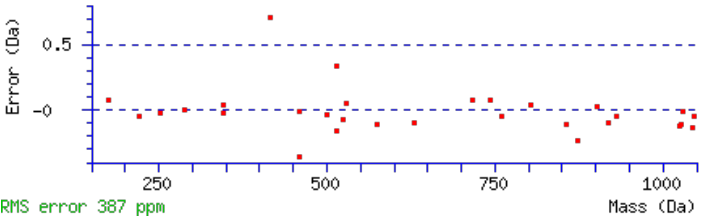
Match to Query 8522: 1216.646368 from(609.330460,2+)
Title: 091224LimSK_Exosome3_06.994.994.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1216.6411
Fixed modifications: Carbamidomethyl (C)
Ions Score: 90 Expect: 1.4e-007
Matches (Bold Red): 30/112 fragment ions using 48 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							12
2	171.1128	86.0600					V	1146.6113	573.8093	1129.5848	565.2960	1128.6008	564.8040	11
3	300.1554	150.5813			282.1448	141.5761	E	1047.5429	524.2751	1030.5164	515.7618	1029.5323	515.2698	10
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	N	918.5003	459.7538	901.4738	451.2405	900.4898	450.7485	9
5	501.2304	251.1188	484.2038	242.6055	483.2198	242.1135	S	804.4574	402.7323	787.4308	394.2191	786.4468	393.7271	8
6	588.2624	294.6348	571.2358	286.1216	570.2518	285.6295	S	717.4254	359.2163	700.3988	350.7030	699.4148	350.2110	7
7	689.3101	345.1587	672.2835	336.6454	671.2995	336.1534	T	630.3933	315.7003	613.3668	307.1870	612.3828	306.6950	6
8	760.3472	380.6772	743.3206	372.1640	742.3366	371.6719	A	529.3457	265.1765	512.3191	256.6632			5
9	873.4312	437.2193	856.4047	428.7060	855.4207	428.2140	I	458.3085	229.6579	441.2820	221.1446			4
10	930.4527	465.7300	913.4262	457.2167	912.4421	456.7247	G	345.2245	173.1159	328.1979	164.6026			3
11	1043.5368	522.2720	1026.5102	513.7587	1025.5262	513.2667	I	288.2030	144.6051	271.1765	136.0919			2
12							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

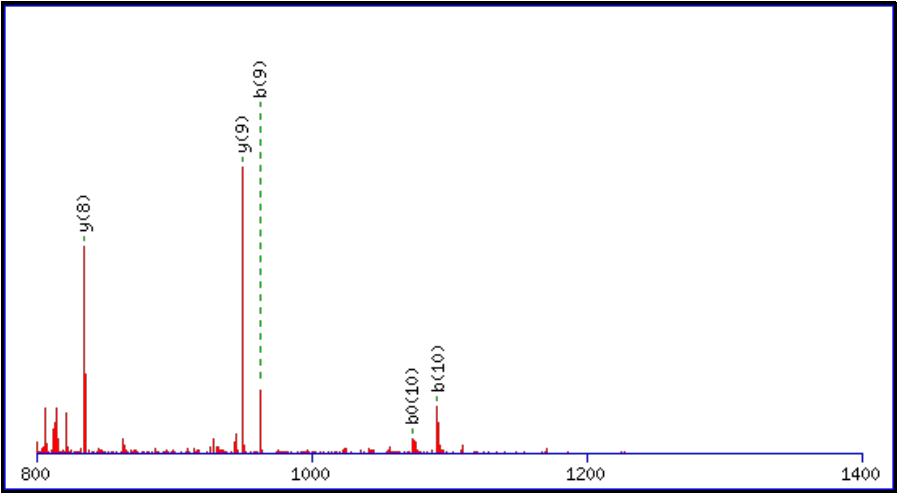
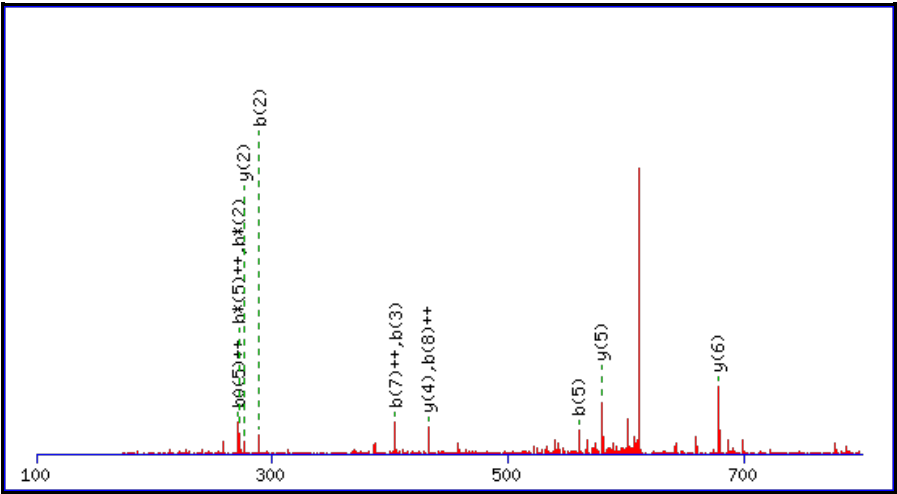
Score	Mr(calc):	Delta	Sequence
89.9	1216.6411	0.0052	AVENSSTAIGIR
15.3	1215.6489	0.9975	ARLPLPGSGLR
13.8	1216.6346	0.0118	VAEATRMLNGR
12.0	1215.6360	1.0104	RDWTAELGIR
11.7	1216.6425	0.0039	WTGRDLASRR
6.5	1216.6411	0.0052	ADTLNGSLSALR
6.5	1216.6387	0.0077	TLNQWVMGIR
6.4	1215.6376	1.0087	ATPLVAGPAALR
6.2	1216.6524	-0.0060	SSLVNNRTQAK
5.5	1216.6524	-0.0060	TRSTGQLELGR

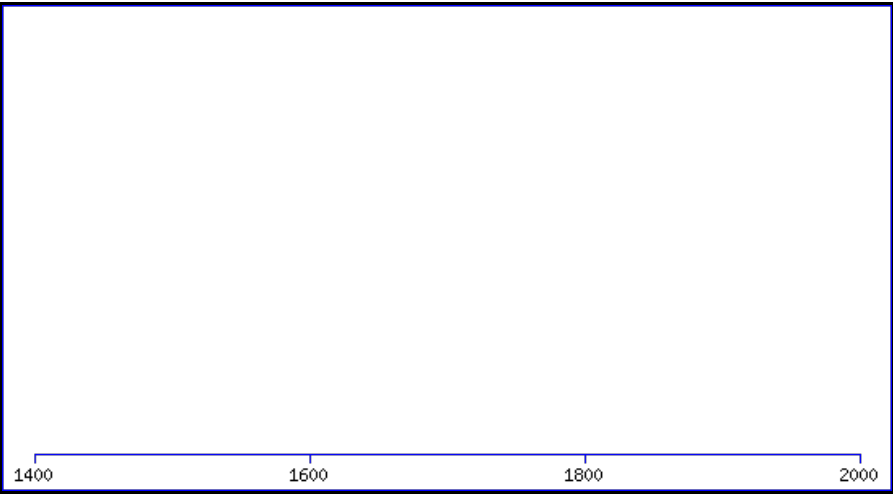
Spectrum No: 101; Query: 9178; Rank: 1

Peptide View

MS/MS Fragmentation of **CKDGVVFGVEK**
Found in **IPI00171199**, Tax_Id=9606 Gene_Symbol=PSMA3 Isoform 2 of Proteasome subunit alpha type-3

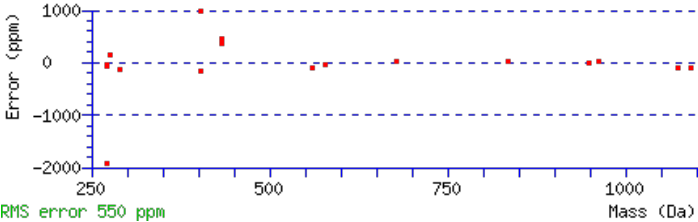
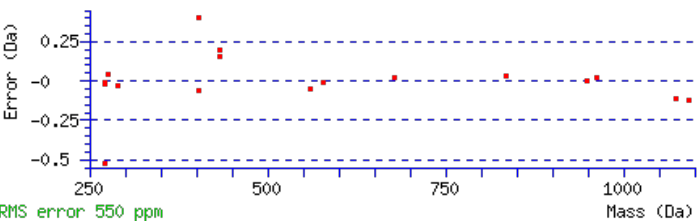
Match to Query 9178: 1236.623628 from(619.319090,2+)
Title: 091224LimSK_Exosome3_05.1172.1172.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1236.6173
Fixed modifications: Carbamidomethyl (C)
Ions Score: 38 Expect: 0.023
Matches (**Bold Red**): 17/112 fragment ions using 36 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	161.0379	81.0226					C							11
2	289.1329	145.0701	272.1063	136.5568			K	1077.5939	539.3006	1060.5673	530.7873	1059.5833	530.2953	10
3	404.1598	202.5836	387.1333	194.0703	386.1493	193.5783	D	949.4989	475.2531	932.4724	466.7398	931.4884	466.2478	9
4	461.1813	231.0943	444.1547	222.5810	443.1707	222.0890	G	834.4720	417.7396	817.4454	409.2264	816.4614	408.7343	8
5	560.2497	280.6285	543.2232	272.1152	542.2391	271.6232	V	777.4505	389.2289	760.4240	380.7156	759.4400	380.2236	7
6	659.3181	330.1627	642.2916	321.6494	641.3076	321.1574	V	678.3821	339.6947	661.3556	331.1814	660.3715	330.6894	6
7	806.3865	403.6969	789.3600	395.1836	788.3760	394.6916	F	579.3137	290.1605	562.2871	281.6472	561.3031	281.1552	5
8	863.4080	432.2076	846.3815	423.6944	845.3974	423.2024	G	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
9	962.4764	481.7418	945.4499	473.2286	944.4658	472.7366	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
10	1091.5190	546.2631	1074.4925	537.7499	1073.5084	537.2579	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
11							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

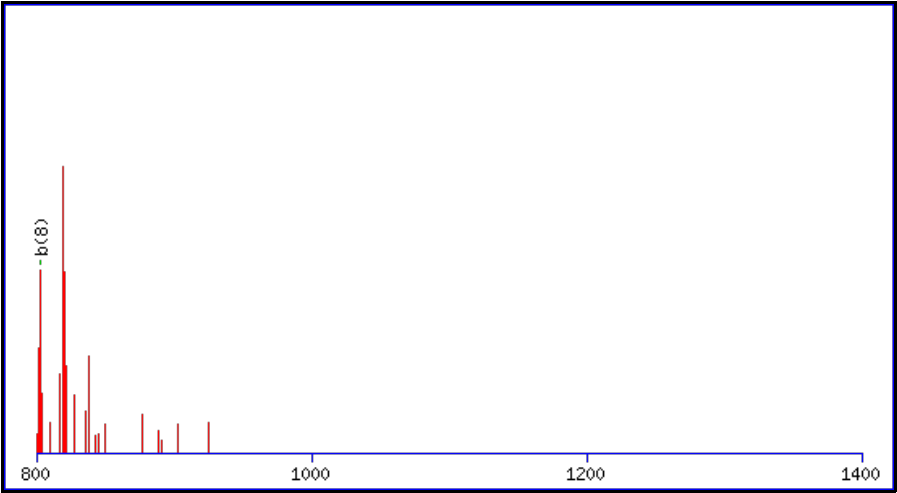
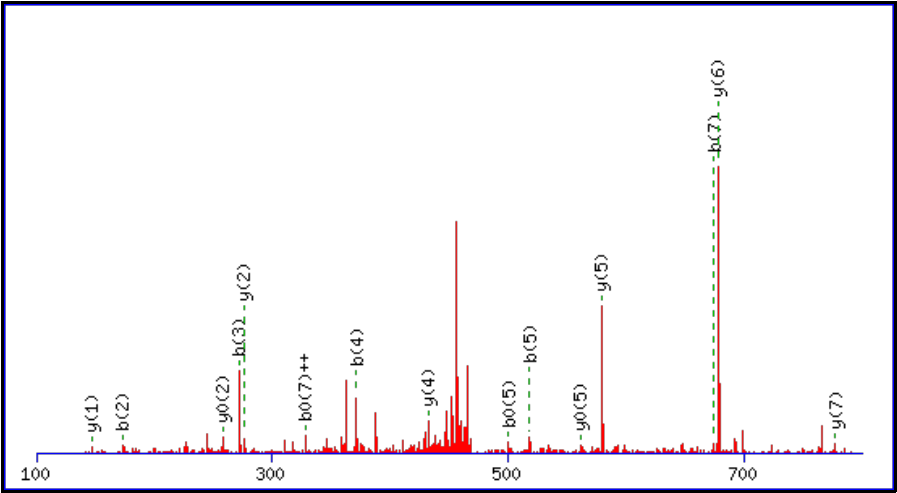
Score	Mr(calc):	Delta	Sequence
38.1	1236.6173	0.0063	CKDGVVFGVEK
16.2	1236.6285	-0.0048	CKDKYGKPNK
9.0	1235.6153	1.0083	SGGNSRVTRMR
6.9	1236.6227	0.0009	DTQPRKATLK
5.7	1236.6227	0.0009	RGTGLGLOGDIK
3.9	1236.6251	-0.0015	WSLYKQQR
3.6	1236.6350	-0.0114	VISQISADNYK
3.2	1236.6340	-0.0103	GRSKGILNGQK
2.9	1236.6285	-0.0049	MGLAGFTKQER
2.5	1236.6350	-0.0114	TNYVENLKEK

Spectrum No: 102; Query: 1933; Rank: 1

Peptide View

MS/MS Fragmentation of **DGVVFGVEK**
Found in **IPI00171199**, Tax_Id=9606 Gene_Symbol=PSMA3 Isoform 2 of Proteasome subunit alpha type-3

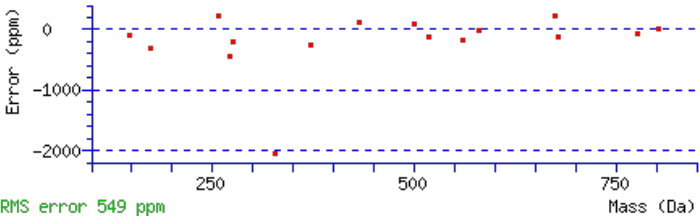
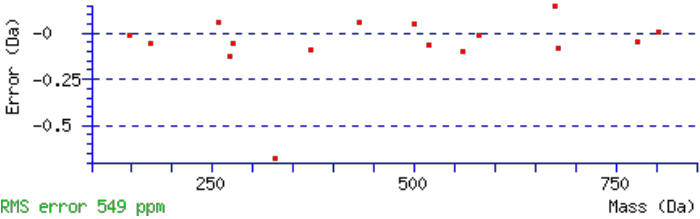
Match to Query 1933: 948.496728 from(475.255640,2+)
Title: 091224LimSK_Exosome3_07.1949.1949.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 948.4917

Fixed modifications: Carbamidomethyl (C)
Ions Score: 27 Expect: 0.28
Matches (**Bold Red**): 16/78 fragment ions using 55 most intense peaks

#	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							9
2	173.0557	87.0315	155.0451	78.0262	G	834.4720	417.7396	817.4454	409.2264	816.4614	408.7343	8
3	272.1241	136.5657	254.1135	127.5604	V	777.4505	389.2289	760.4240	380.7156	759.4400	380.2236	7
4	371.1925	186.0999	353.1819	177.0946	V	678.3821	339.6947	661.3556	331.1814	660.3715	330.6894	6
5	518.2609	259.6341	500.2504	250.6288	F	579.3137	290.1605	562.2871	281.6472	561.3031	281.1552	5
6	575.2824	288.1448	557.2718	279.1396	G	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
7	674.3508	337.6790	656.3402	328.6738	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
8	803.3934	402.2003	785.3828	393.1951	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
9					K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

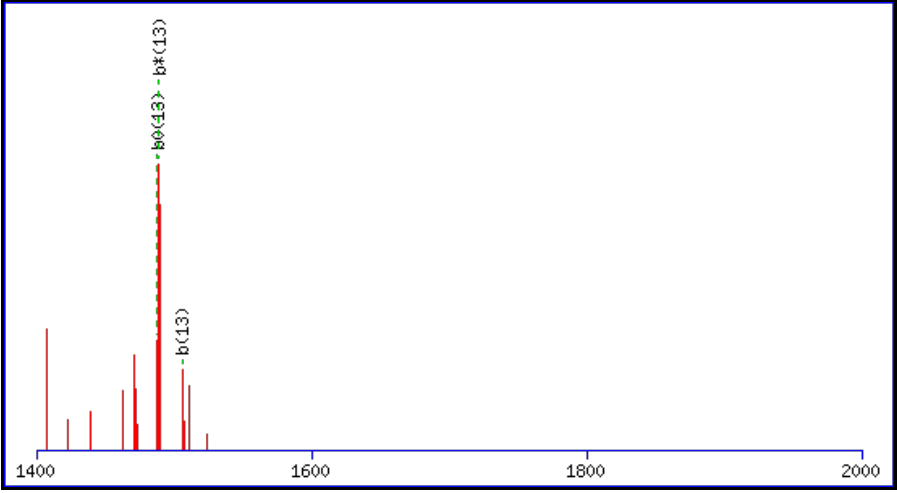
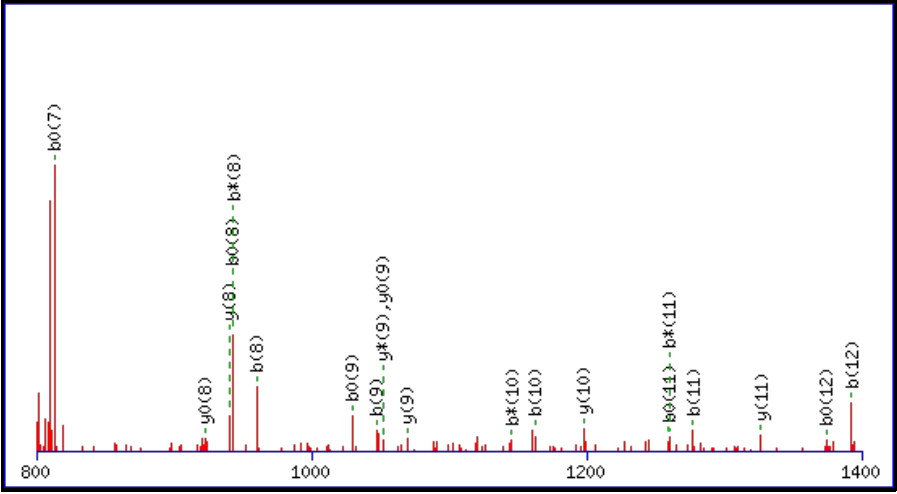
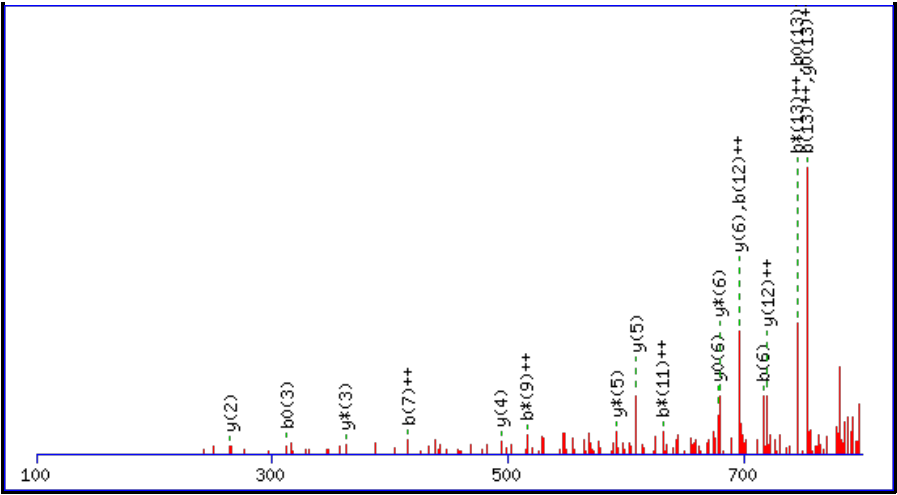
Score	Mr(calc):	Delta	Sequence
27.0	948.4917	0.0051	DGVVFGVEK
8.2	948.4950	0.0017	KMTSPLEK
5.8	948.4916	0.0051	ENILFGEK
4.9	946.4946	2.0021	AVIAWMEK
4.8	948.4906	0.0061	GRGLLTPR
4.4	947.4924	1.0043	AVTDQTVSK
4.2	946.4906	2.0062	ACQKAIEK
4.1	947.4953	1.0014	KVKQH TK
3.9	947.4841	1.0126	ASLLTVHK
3.7	946.4832	2.0136	TEREREK

Spectrum No: 103; Query: 28119; Rank: 1

Peptide View

MS/MS Fragmentation of **ESLKEEDESDDDNM**
Found in **IPI00171199**, Tax_Id=9606 Gene_Symbol=PSMA3 Isoform 2 of Proteasome subunit alpha type-3

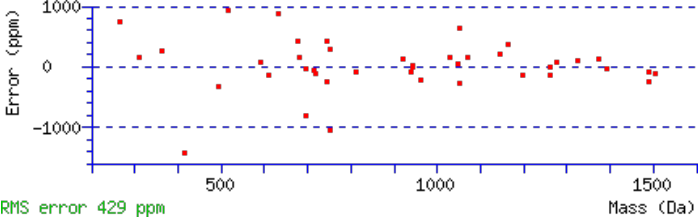
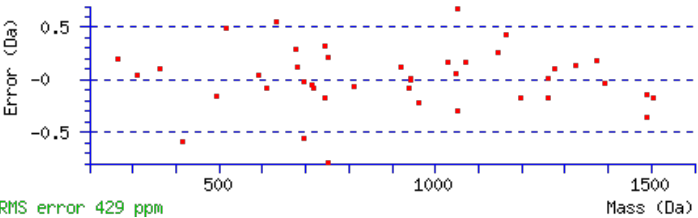
Match to Query 28119: 1654.620288 from(828.317420,2+)
Title: 091224LimSK_Exosome3_07.595.595.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1654.6152
Fixed modifications: Carbamidomethyl (C)
Ions Score: 43 Expect: 0.0056
Matches (**Bold Red**): 42/144 fragment ions using 68 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	130.0499	65.5286			112.0393	56.5233	E							14
2	217.0819	109.0446			199.0713	100.0393	S	1526.5799	763.7936	1509.5533	755.2803	1508.5693	754.7883	13
3	330.1660	165.5866			312.1554	156.5813	L	1439.5479	720.2776	1422.5213	711.7643	1421.5373	711.2723	12
4	458.2609	229.6341	441.2344	221.1208	440.2504	220.6288	K	1326.4638	663.7355	1309.4372	655.2223	1308.4532	654.7303	11
5	587.3035	294.1554	570.2770	285.6421	569.2930	285.1501	E	1198.3688	599.6881	1181.3423	591.1748	1180.3583	590.6828	10
6	716.3461	358.6767	699.3196	350.1634	698.3355	349.6714	E	1069.3262	535.1668	1052.2997	526.6535	1051.3157	526.1615	9

7	831.3731	416.1902	814.3465	407.6769	813.3625	407.1849	D	940.2836	470.6455	923.2571	462.1322	922.2731	461.6402	8
8	960.4156	480.7115	943.3891	472.1982	942.4051	471.7062	E	825.2567	413.1320	808.2302	404.6187	807.2461	404.1267	7
9	1047.4477	524.2275	1030.4211	515.7142	1029.4371	515.2222	S	696.2141	348.6107	679.1876	340.0974	678.2035	339.6054	6
10	1162.4746	581.7409	1145.4481	573.2277	1144.4641	572.7357	D	609.1821	305.0947	592.1555	296.5814	591.1715	296.0894	5
11	1277.5016	639.2544	1260.4750	630.7411	1259.4910	630.2491	D	494.1551	247.5812	477.1286	239.0679	476.1446	238.5759	4
12	1392.5285	696.7679	1375.5020	688.2546	1374.5179	687.7626	D	379.1282	190.0677	362.1016	181.5545	361.1176	181.0625	3
13	1506.5714	753.7894	1489.5449	745.2761	1488.5609	744.7841	N	264.1013	132.5543	247.0747	124.0410			2
14							M	150.0583	75.5328					1



All matches to this query

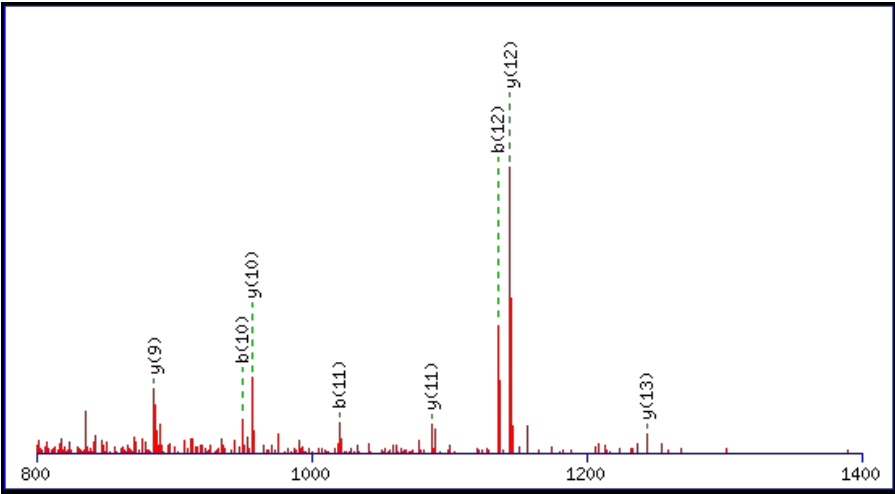
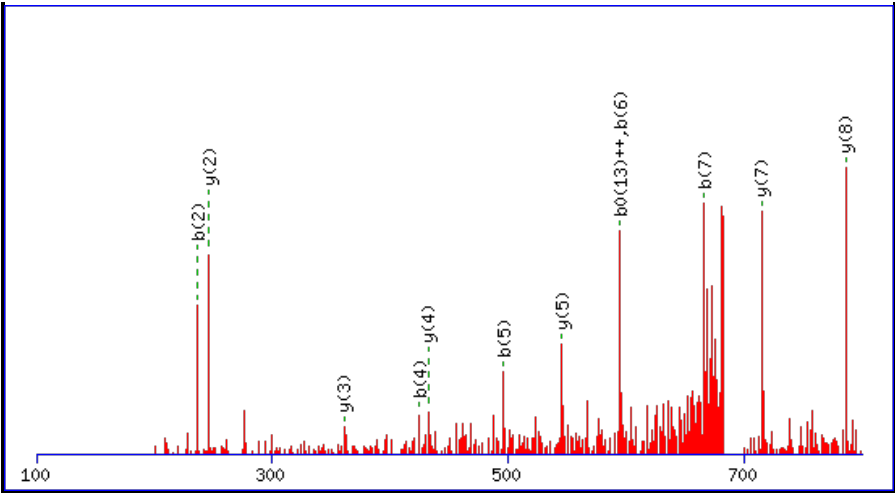
Score	Mr(calc):	Delta	Sequence
42.6	1654.6152	0.0051	ESLKEEDESDDDNM
5.1	1654.6117	0.0086	SNHVLAQMEQGDCS
4.1	1652.6155	2.0048	VTVGDTSCTGQGPSK
4.0	1652.5977	2.0226	MSGTKLEDSPPCR
4.0	1652.5977	2.0226	MSGTKLEDSPPCR
4.0	1652.6042	2.0161	LAQUESTMDIENDK
3.6	1652.6155	2.0048	VTVGDTSCTGQGPSK
2.9	1653.6284	0.9919	TEANAASISNNSTSK
2.2	1652.6155	2.0048	VTVGDTSCTGQGPSK

Spectrum No: 104; Query: 14250; Rank: 1

Peptide View

MS/MS Fragmentation of **HVGMAVAGLLADAR**
Found in **IPI00171199**, Tax_Id=9606 Gene_Symbol=PSMA3 Isoform 2 of Proteasome subunit alpha type-3

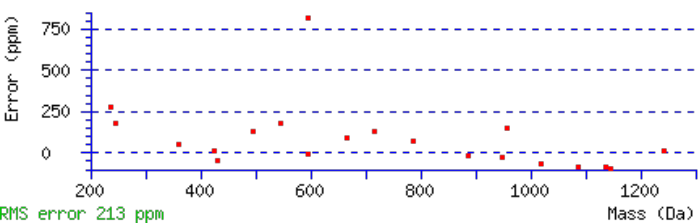
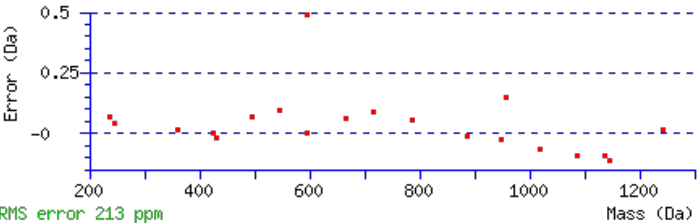
Match to Query 14250: 1379.745048 from(690.879800,2+)
Title: 091224LimSK_Exosome3_06.5159.5159.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1379.7343
Fixed modifications: Carbamidomethyl (C)
Ions Score: 102 Expect: 7.8e-009
Matches (**Red**): 20/104 fragment ions using 32 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	138.0662	69.5367			H							14
2	237.1346	119.0709			V	1243.6827	622.3450	1226.6562	613.8317	1225.6722	613.3397	13
3	294.1561	147.5817			G	1144.6143	572.8108	1127.5878	564.2975	1126.6037	563.8055	12
4	425.1966	213.1019			M	1087.5928	544.3001	1070.5663	535.7868	1069.5823	535.2948	11
5	496.2337	248.6205			A	956.5524	478.7798	939.5258	470.2665	938.5418	469.7745	10
6	595.3021	298.1547			V	885.5152	443.2613	868.4887	434.7480	867.5047	434.2560	9

7	666.3392	333.6732			A	786.4468	393.7271	769.4203	385.2138	768.4363	384.7218	8
8	723.3607	362.1840			G	715.4097	358.2085	698.3832	349.6952	697.3992	349.2032	7
9	836.4447	418.7260			L	658.3883	329.6978	641.3617	321.1845	640.3777	320.6925	6
10	949.5288	475.2680			L	545.3042	273.1557	528.2776	264.6425	527.2936	264.1504	5
11	1020.5659	510.7866			A	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	4
12	1135.5928	568.3001	1117.5823	559.2948	D	361.1830	181.0951	344.1565	172.5819	343.1724	172.0899	3
13	1206.6300	603.8186	1188.6194	594.8133	A	246.1561	123.5817	229.1295	115.0684			2
14					R	175.1190	88.0631	158.0924	79.5498			1



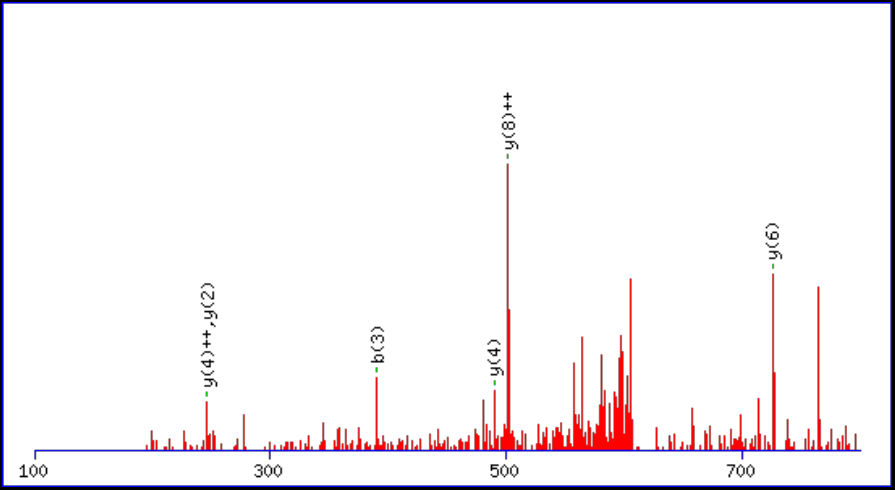
All matches to this query

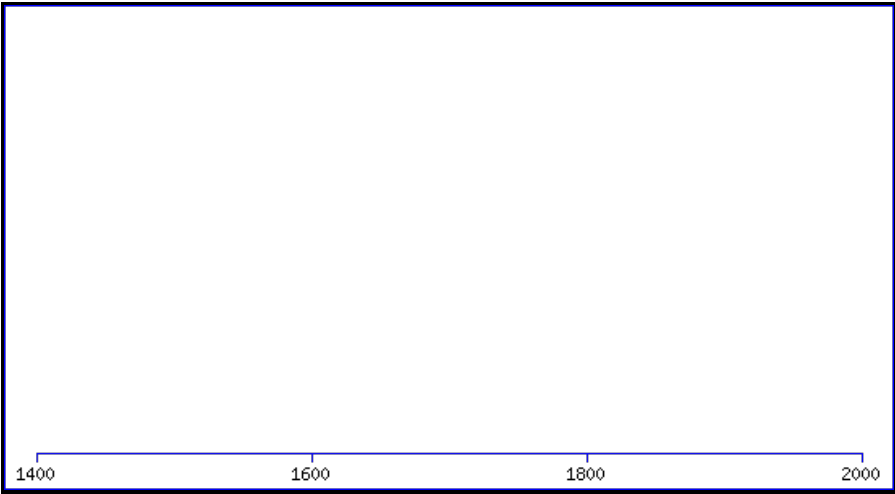
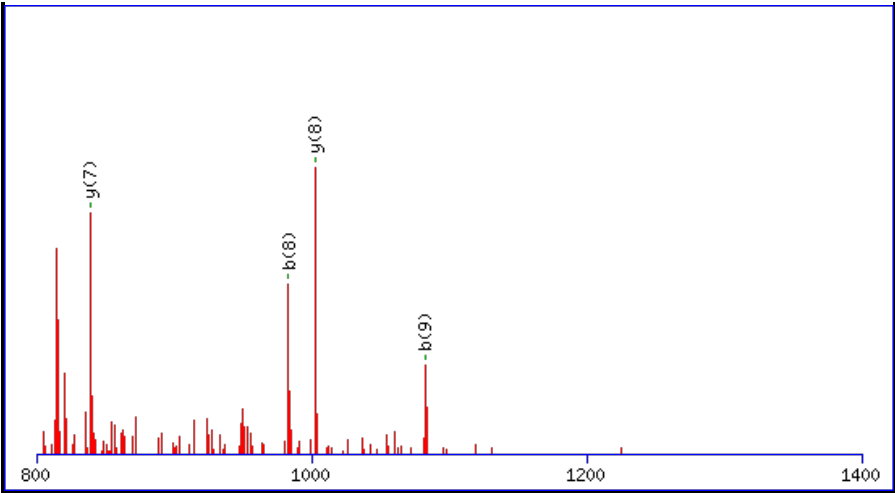
Score	Mr(calc):	Delta	Sequence
101.6	1379.7343	0.0107	HVGMVAVGLLADAR

Spectrum No: 105; Query: 8867; Rank: 1

Peptide View

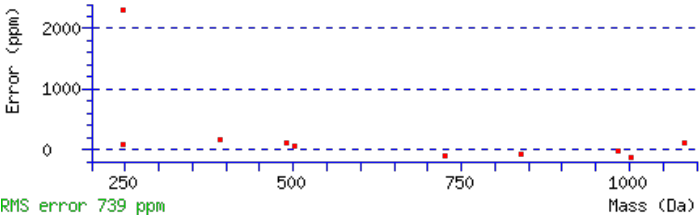
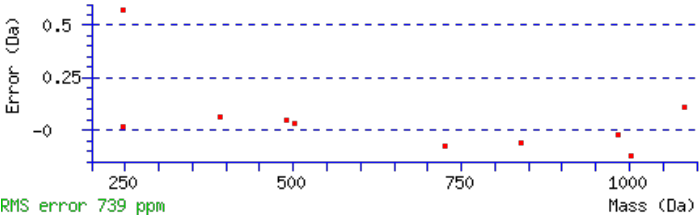
MS/MS Fragmentation of **IYYIVHDEVK**
Found in **IPI00171199**, Tax_Id=9606 Gene_Symbol=PSMA3 Isoform 2 of Proteasome subunit alpha type-3
Match to Query 8867: 1227.692468 from(614.853510,2+)
Title: 091224LimSK_Exosome3_06.1885.1885.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1227.6863
Fixed modifications: Carbamidomethyl (C)
Ions Score: 37 Expect: 0.019
Matches (**Bold Red**): 10/74 fragment ions using 23 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			I							10
2	227.1754	114.0913			I	1115.6095	558.3084	1098.5830	549.7951	1097.5990	549.3031	9
3	390.2387	195.6230			Y	1002.5255	501.7664	985.4989	493.2531	984.5149	492.7611	8
4	503.3228	252.1650			I	839.4621	420.2347	822.4356	411.7214	821.4516	411.2294	7
5	602.3912	301.6992			V	726.3781	363.6927	709.3515	355.1794	708.3675	354.6874	6
6	739.4501	370.2287			H	627.3097	314.1585	610.2831	305.6452	609.2991	305.1532	5
7	854.4771	427.7422	836.4665	418.7369	D	490.2508	245.6290	473.2242	237.1157	472.2402	236.6237	4
8	983.5197	492.2635	965.5091	483.2582	E	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
9	1082.5881	541.7977	1064.5775	532.7924	V	246.1812	123.5942	229.1547	115.0810			2
10					K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

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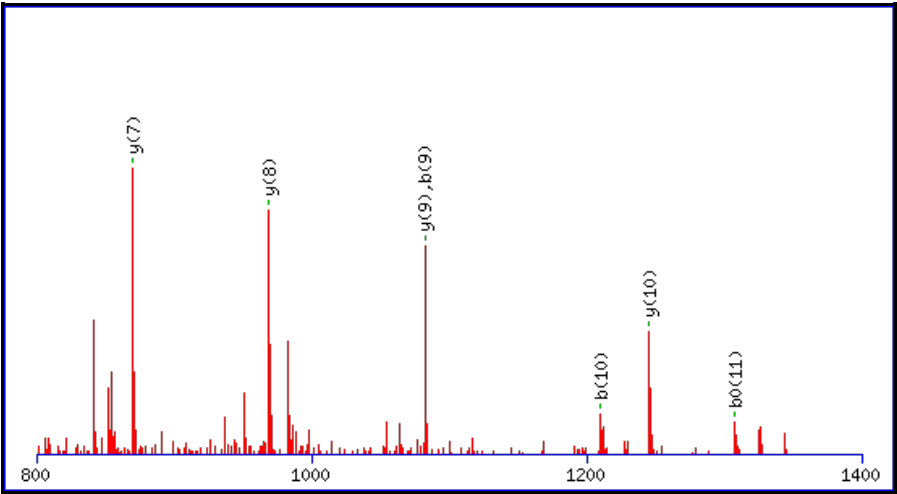
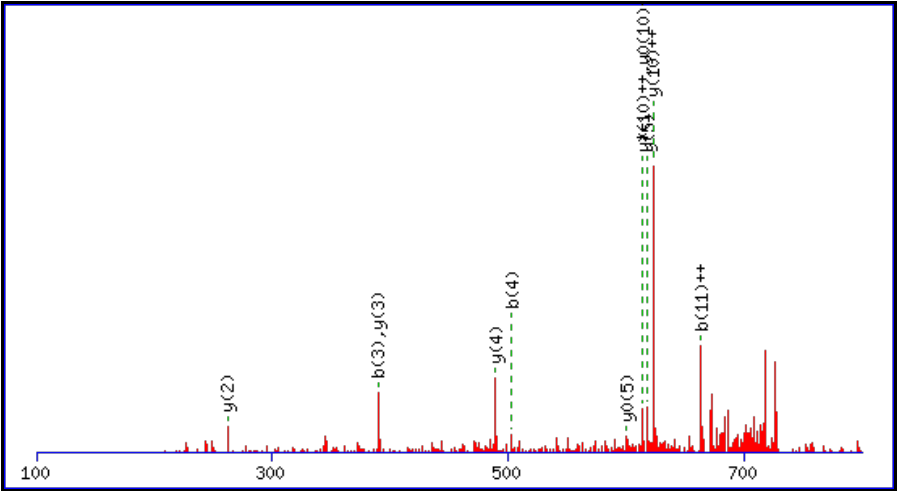
Score	Mr(calc):	Delta	Sequence
36.6	1227.6863	0.0062	IIYIVHDEVK
5.3	1227.6976	-0.0051	FIGPSPEVVRK
4.8	1227.6823	0.0102	IVAEAIEKAER
3.5	1227.6836	0.0088	EFVHGRLKSR
2.2	1227.6992	-0.0067	LLYKASVVKK
1.4	1227.6935	-0.0011	VRDDLQKQVK
0.1	1226.6996	0.9929	FRPAGPRATVR

Spectrum No: 106; Query: 19026; Rank: 1

Peptide View

MS/MS Fragmentation of **IIYIVHDEVKDK**
Found in **IP100171199**, Tax_Id=9606 Gene_Symbol=PSMA3 Isoform 2 of Proteasome subunit alpha type-3

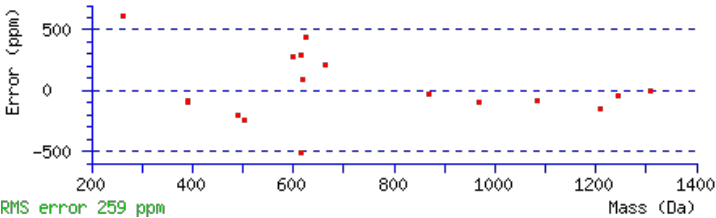
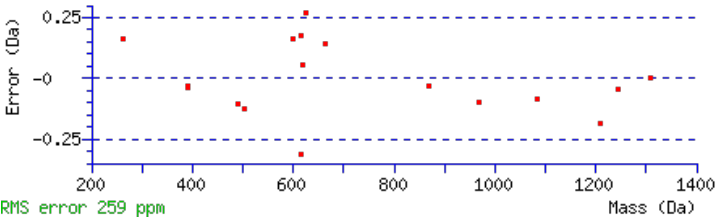
Match to Query 19026: 1470.816688 from(736.415620,2+)
Title: 091224LimSK_Exosome3_05.1438.1438.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1470.8082
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 **Expect:** 0.00032
Matches (Bold Red): 18/100 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	114.0913	57.5493					I							12
2	227.1754	114.0913					I	1358.7314	679.8694	1341.7049	671.3561	1340.7209	670.8641	11
3	390.2387	195.6230					Y	1245.6474	623.3273	1228.6208	614.8141	1227.6368	614.3220	10
4	503.3228	252.1650					I	1082.5841	541.7957	1065.5575	533.2824	1064.5735	532.7904	9
5	602.3912	301.6992					V	969.5000	485.2536	952.4734	476.7404	951.4894	476.2483	8
6	739.4501	370.2287					H	870.4316	435.7194	853.4050	427.2061	852.4210	426.7141	7
7	854.4771	427.7422			836.4665	418.7369	D	733.3727	367.1900	716.3461	358.6767	715.3621	358.1847	6
8	983.5197	492.2635			965.5091	483.2582	E	618.3457	309.6765	601.3192	301.1632	600.3352	300.6712	5
9	1082.5881	541.7977			1064.5775	532.7924	V	489.3031	245.1552	472.2766	236.6419	471.2926	236.1499	4
10	1210.6830	605.8452	1193.6565	597.3319	1192.6725	596.8399	K	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	3
11	1325.7100	663.3586	1308.6834	654.8454	1307.6994	654.3533	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
12							K	147.1128	74.0600	130.0863	65.5468			1



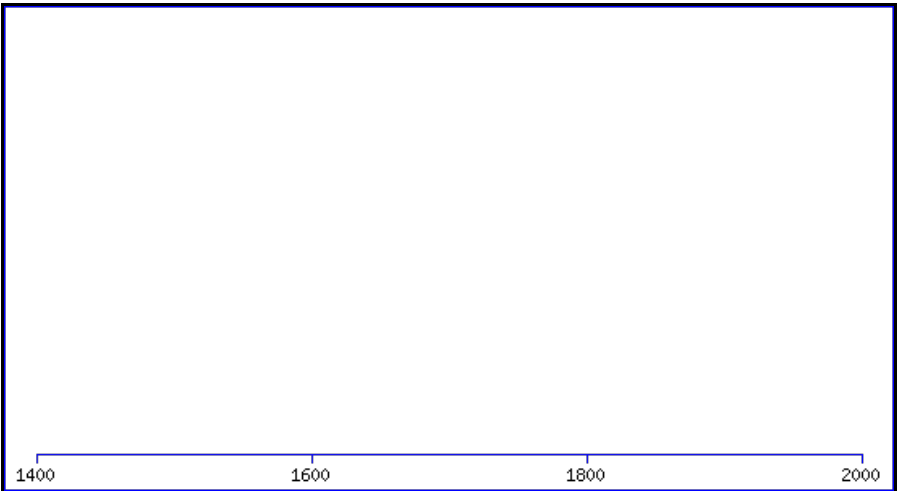
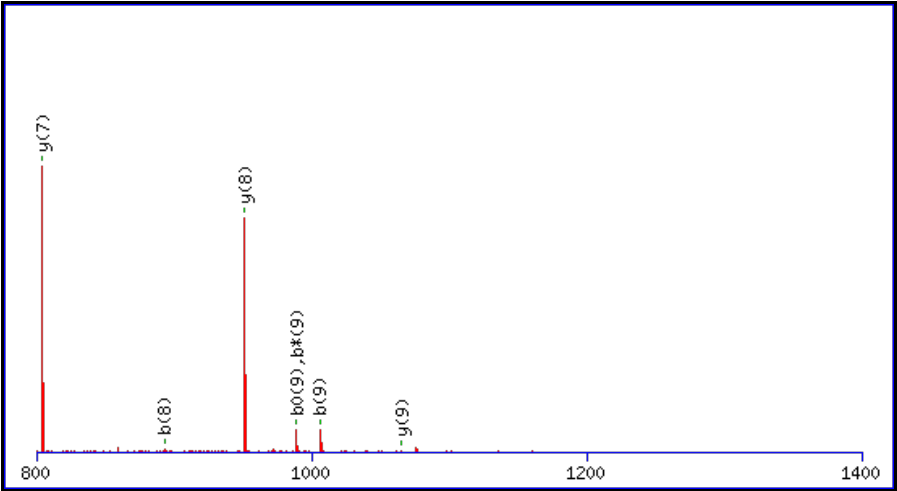
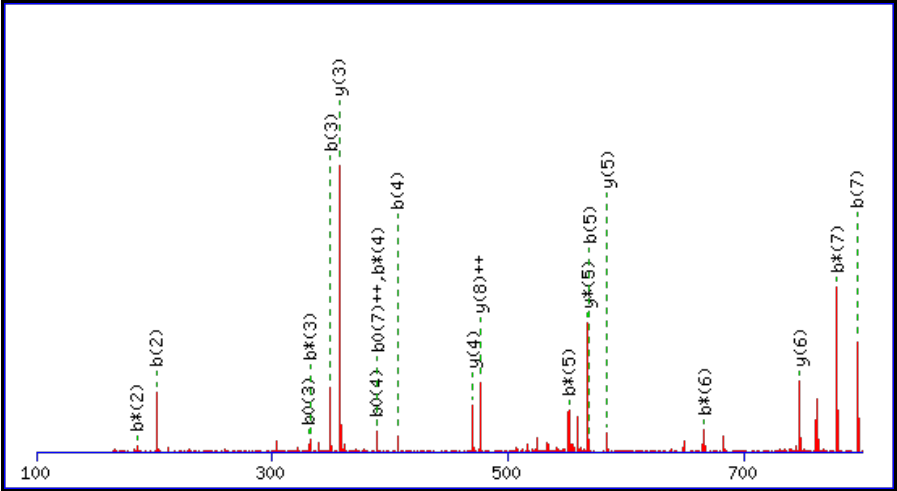
All matches to this query

Score	Mr(calc):	Delta	Sequence
54.2	1470.8082	0.0085	IIYIVHDEVKDK
16.4	1470.8042	0.0125	LLDKKQQENIDK
11.3	1470.8042	0.0125	KDQDQIIAGVEKK
10.7	1470.8099	0.0068	YTTILTPKTIHK
7.1	1470.8099	0.0068	YTTILTPKTIHK
5.8	1469.8143	1.0024	QPYSRFLRLRYK
5.6	1469.8201	0.9966	AKERQLENLIEK
5.2	1470.8154	0.0013	NITRGQSLDNLIK
4.9	1469.8089	1.0078	KEEKKPIETGSPK
4.7	1470.8129	0.0038	XSCRVAGWVAKLK

Spectrum No: 107; Query: 6296; Rank: 1

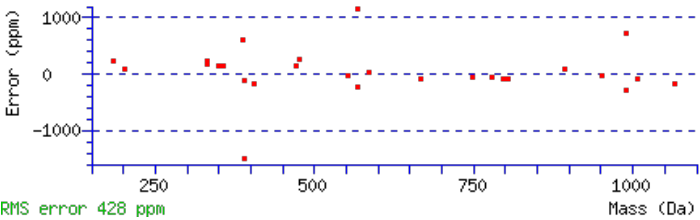
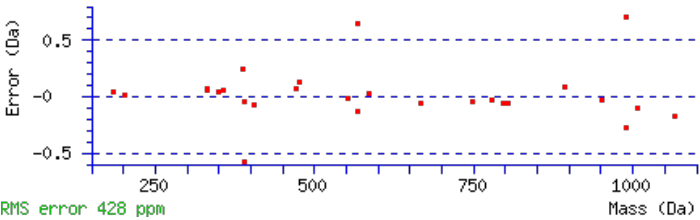
Peptide View

MS/MS Fragmentation of **SNFGYNIPLK**
Found in **IPI00171199**, Tax_Id=9606 Gene_Symbol=PSMA3 Isoform 2 of Proteasome subunit alpha type-3
Match to Query 6296: 1151.602728 from(576.808640,2+)
Title: 091224LimSK_Exosome3_06.3765.3765.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1151.5975
Fixed modifications: Carbamidomethyl (C)
Ions Score: 61 Expect: 0.00012
Matches (Bold Red): 27/88 fragment ions using 38 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S					10
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	N	1065.5728	533.2900	1048.5462	524.7767	9
3	349.1506	175.0790	332.1241	166.5657	331.1401	166.0737	F	951.5298	476.2686	934.5033	467.7553	8
4	406.1721	203.5897	389.1456	195.0764	388.1615	194.5844	G	804.4614	402.7343	787.4349	394.2211	7
5	569.2354	285.1214	552.2089	276.6081	551.2249	276.1161	Y	747.4400	374.2236	730.4134	365.7103	6
6	683.2784	342.1428	666.2518	333.6295	665.2678	333.1375	N	584.3766	292.6919	567.3501	284.1787	5
7	796.3624	398.6849	779.3359	390.1716	778.3519	389.6796	I	470.3337	235.6705	453.3071	227.1572	4
8	893.4152	447.2112	876.3886	438.6980	875.4046	438.2060	P	357.2496	179.1285	340.2231	170.6152	3
9	1006.4993	503.7533	989.4727	495.2400	988.4887	494.7480	L	260.1969	130.6021	243.1703	122.0888	2
10							K	147.1128	74.0600	130.0863	65.5468	1



All matches to this query

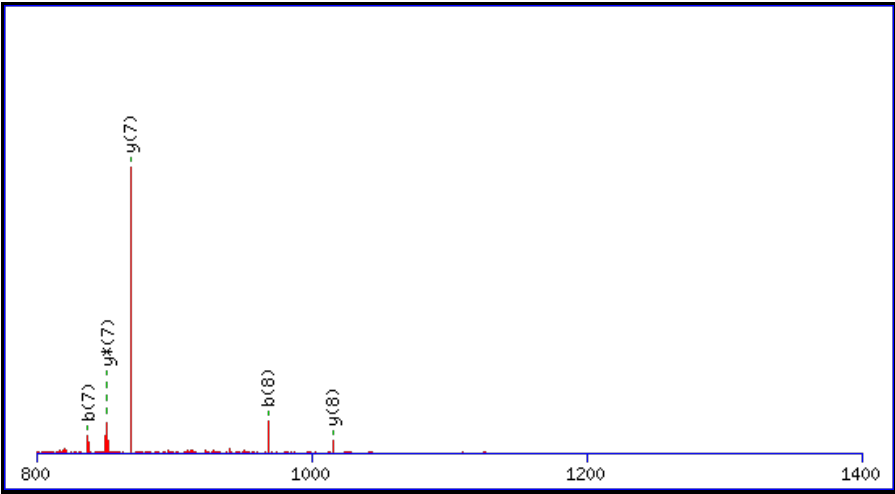
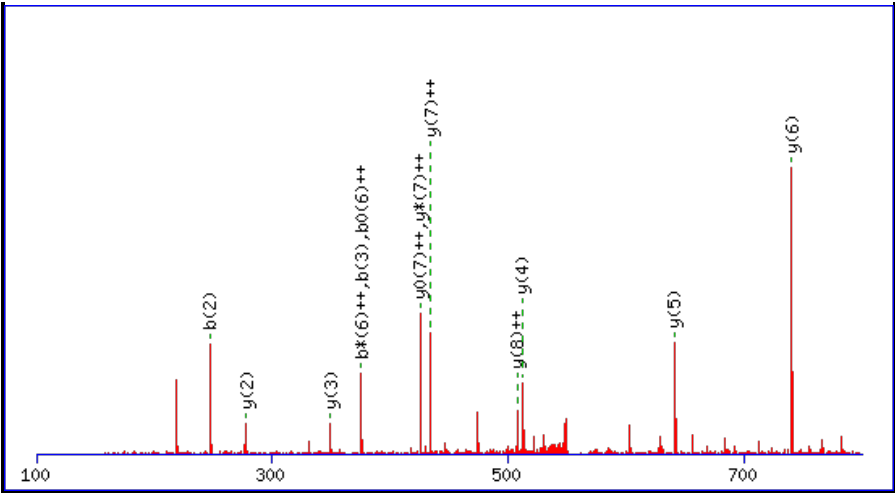
Score	Mr(calc):	Delta	Sequence
60.9	1151.5975	0.0052	SNFGYNIPLK
13.4	1151.5951	0.0076	SVLAVGTANIK
12.9	1151.6025	0.0002	SLTLGIPMLK
8.2	1151.6063	-0.0036	RGELOTKLK
7.9	1151.6063	-0.0036	SRLVLLSER
7.2	1151.6047	-0.0020	SLRDPASPPGR
6.9	1151.5951	0.0076	VLKEGGSLAAK
6.1	1151.6063	-0.0036	KLDQTIARK
6.0	1149.6046	1.9981	TSAELVLPK
4.8	1150.5999	1.0029	TSGKVLLPK

Spectrum No: 108; Query: 5157; Rank: 1

Peptide View

MS/MS Fragmentation of **VFQVEYAMK**
Found in **IPI00171199**, Tax_Id=9606 Gene_Symbol=PSMA3 Isoform 2 of Proteasome subunit alpha type-3

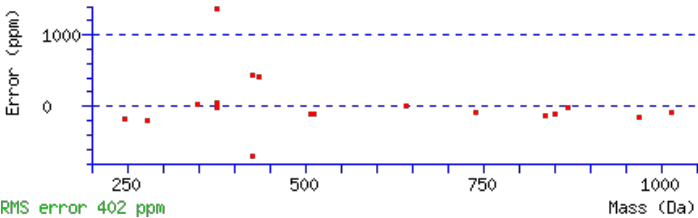
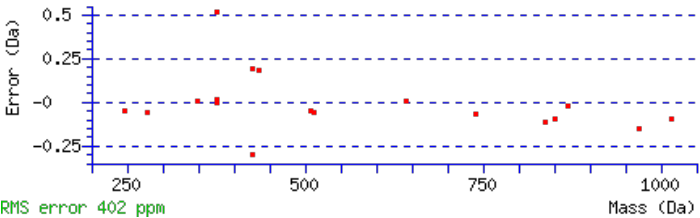
Match to Query 5157: 1113.558048 from(557.786300,2+)
Title: 091224LimSK_Exosome3_05.3026.3026.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1113.5529
Fixed modifications: Carbamidomethyl (C)
Ions Score: 57 Expect: 0.00026
Matches (Bold Red): 18/76 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	100.0757	50.5415					V							9
2	247.1441	124.0757					F	1015.4917	508.2495	998.4652	499.7362	997.4812	499.2442	8
3	375.2027	188.1050	358.1761	179.5917			Q	868.4233	434.7153	851.3968	426.2020	850.4128	425.7100	7
4	474.2711	237.6392	457.2445	229.1259			V	740.3647	370.6860	723.3382	362.1727	722.3542	361.6807	6
5	603.3137	302.1605	586.2871	293.6472	585.3031	293.1552	E	641.2963	321.1518	624.2698	312.6385	623.2858	312.1465	5
6	766.3770	383.6921	749.3505	375.1789	748.3665	374.6869	Y	512.2537	256.6305	495.2272	248.1172			4

7	837.4141	419.2107	820.3876	410.6974	819.4036	410.2054	A	349.1904	175.0988	332.1639	166.5856			3
8	968.4546	484.7309	951.4281	476.2177	950.4441	475.7257	M	278.1533	139.5803	261.1267	131.0670			2
9							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

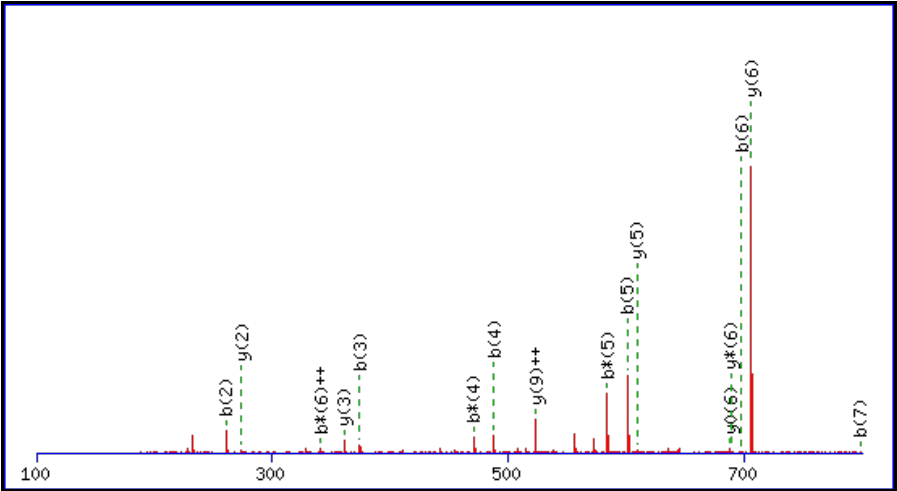
Score	Mr(calc):	Delta	Sequence
57.0	1113.5529	0.0052	VFQVEYAMK
23.1	1111.5526	2.0055	LLTDSLKK
14.6	1111.5526	2.0055	LLTDSLKK
13.9	1111.5526	2.0055	LITTEQVK
13.9	1111.5526	2.0055	LITTEQVK
13.9	1111.5526	2.0055	LITTEQVK
10.9	1112.5478	1.0102	VETLSQTKK
10.5	1111.5427	2.0154	SLNKEWKK
10.4	1111.5526	2.0055	LELDSLKK
10.4	1112.5631	0.9950	LIQAAYQVK

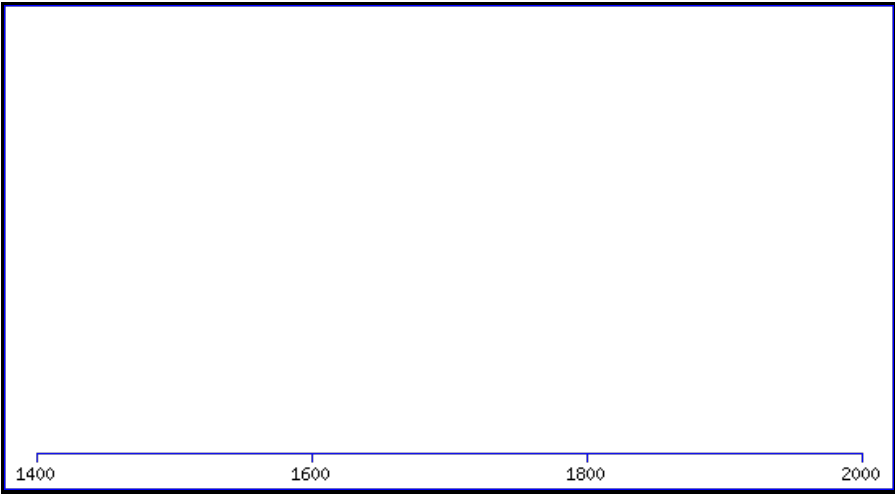
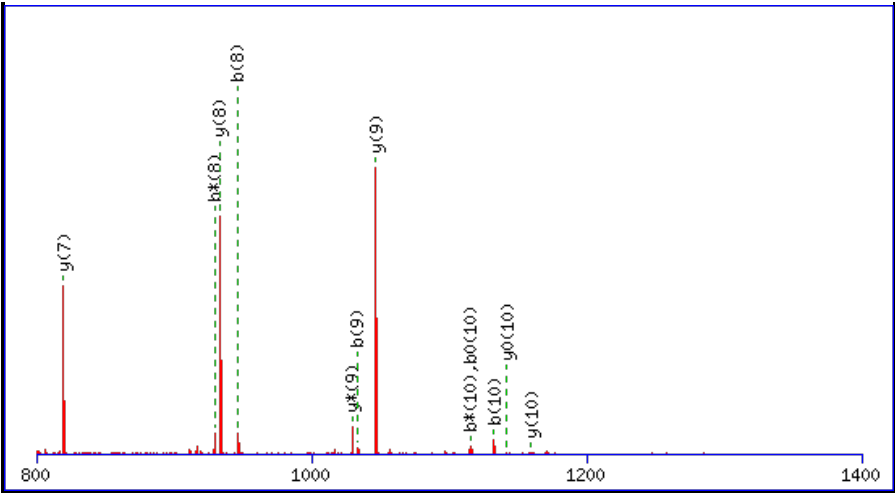
Spectrum No: 109; Query: 11548; Rank: 1

Peptide View

MS/MS Fragmentation of **FILNLPTFSVR**
Found in **IPI00028006**, Tax_Id=9606 Gene_Symbol=PSMB2 Proteasome subunit beta type-2

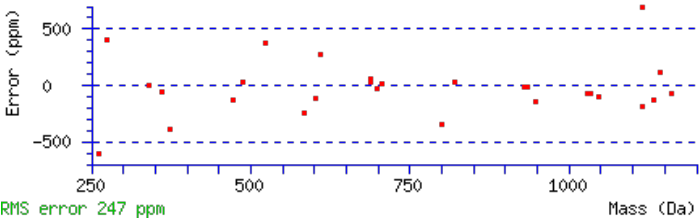
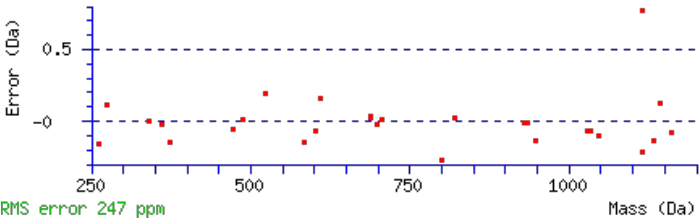
Match to Query 11548: 1305.751788 from(653.883170,2+)
Title: 091224LimSK_Exosome3_06.7754.7754.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1305.7445
Fixed modifications: Carbamidomethyl (C)
Ions Score: 55 Expect: 0.00019
Matches (Bold Red): 28/98 fragment ions using 62 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							11
2	261.1598	131.0835					I	1159.6834	580.3453	1142.6568	571.8320	1141.6728	571.3400	10
3	374.2438	187.6255					L	1046.5993	523.8033	1029.5728	515.2900	1028.5887	514.7980	9
4	488.2867	244.6470	471.2602	236.1337			N	933.5152	467.2613	916.4887	458.7480	915.5047	458.2560	8
5	601.3708	301.1890	584.3443	292.6758			L	819.4723	410.2398	802.4458	401.7265	801.4617	401.2345	7
6	698.4236	349.7154	681.3970	341.2022			P	706.3883	353.6978	689.3617	345.1845	688.3777	344.6925	6
7	799.4713	400.2393	782.4447	391.7260	781.4607	391.2340	T	609.3355	305.1714	592.3089	296.6581	591.3249	296.1661	5
8	946.5397	473.7735	929.5131	465.2602	928.5291	464.7682	F	508.2878	254.6475	491.2613	246.1343	490.2772	245.6423	4
9	1033.5717	517.2895	1016.5451	508.7762	1015.5611	508.2842	S	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
10	1132.6401	566.8237	1115.6136	558.3104	1114.6295	557.8184	V	274.1874	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

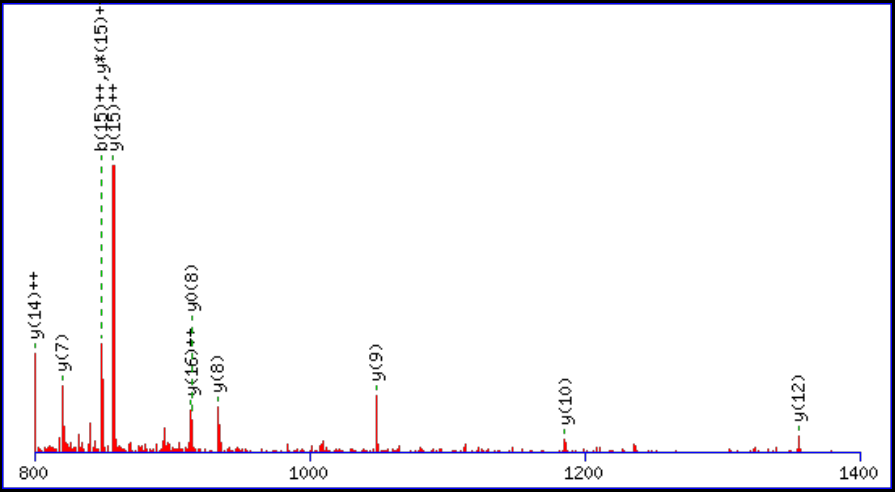
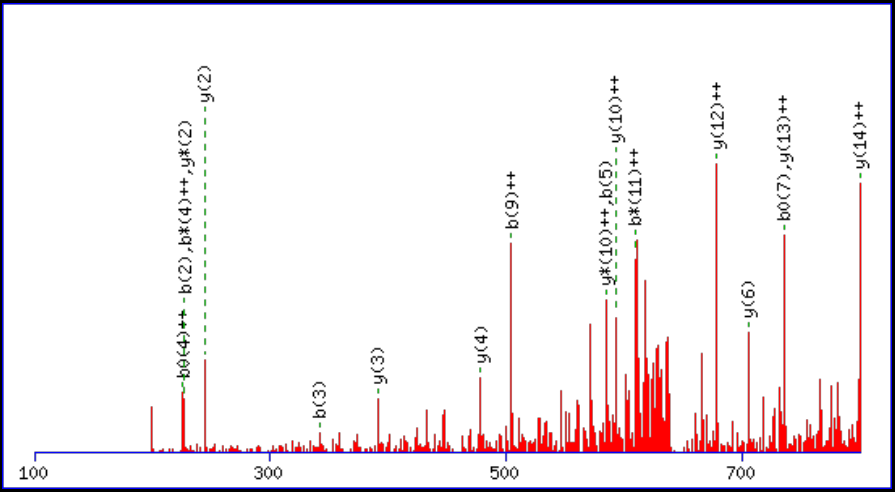
Score	Mr(calc):	Delta	Sequence
54.8	1305.7445	0.0073	FILNLPFSVR
9.7	1305.7517	0.0001	NAGQVVHLTLVR
7.0	1305.7478	0.0039	MLEFVSLARK
5.9	1305.7517	0.0001	HRAAEAINLK
5.1	1305.7478	0.0039	RIYLCDLLK
4.8	1304.7452	1.0066	IHETQPLLNLK
2.1	1305.7517	0.0001	QAPIPAELRGVR
0.8	1305.7405	0.0113	RFEVSSSLIR
0.5	1305.7421	0.0097	GLLSRVVLELK

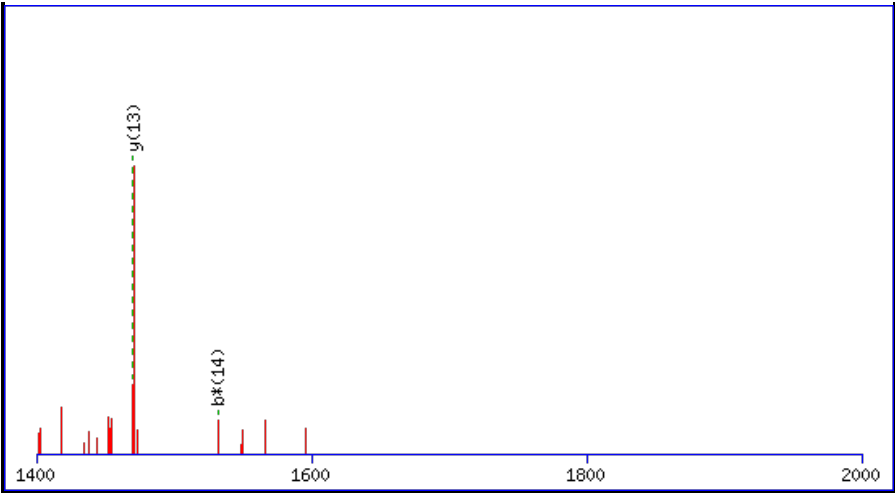
Spectrum No: 110; Query: 37606; Rank: 1

Peptide View

MS/MS Fragmentation of **IIDKNGIHDLNISFPK**
Found in **IPI0028006**, Tax_Id=9606 Gene_Symbol=PSMB2 Proteasome subunit beta type-2

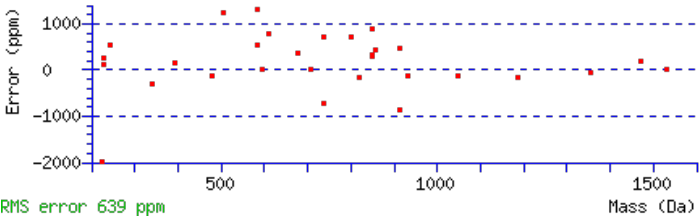
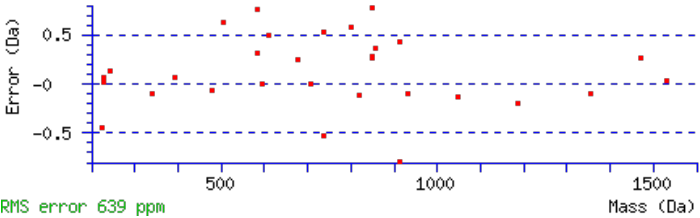
Match to Query 37606: 1939.015002 from(647.345610,3+)
Title: 091224LimSK_Exosome3_06.5301.5301.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1938.0211
Fixed modifications: Carbamidomethyl (C)
Ions Score: 46 Expect: 0.0031
Matches (Bold Red): 31/176 fragment ions using 46 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					I							17
2	227.1754	114.0913					I	1825.9443	913.4758	1808.9177	904.9625	1807.9337	904.4705	16
3	342.2023	171.6048			324.1918	162.5995	D	1712.8602	856.9338	1695.8337	848.4205	1694.8497	847.9285	15
4	470.2973	235.6523	453.2708	227.1390	452.2867	226.6470	K	1597.8333	799.4203	1580.8067	790.9070	1579.8227	790.4150	14
5	584.3402	292.6738	567.3137	284.1605	566.3297	283.6685	N	1469.7383	735.3728	1452.7118	726.8595	1451.7278	726.3675	13
6	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	G	1355.6954	678.3513	1338.6688	669.8381	1337.6848	669.3461	12
7	754.4458	377.7265	737.4192	369.2132	736.4352	368.7212	I	1298.6739	649.8406	1281.6474	641.3273	1280.6634	640.8353	11
8	891.5047	446.2560	874.4781	437.7427	873.4941	437.2507	H	1185.5899	593.2986	1168.5633	584.7853	1167.5793	584.2933	10
9	1006.5316	503.7694	989.5051	495.2562	988.5211	494.7642	D	1048.5310	524.7691	1031.5044	516.2558	1030.5204	515.7638	9
10	1119.6157	560.3115	1102.5891	551.7982	1101.6051	551.3062	L	933.5040	467.2556	916.4775	458.7424	915.4934	458.2504	8
11	1234.6426	617.8250	1217.6161	609.3117	1216.6321	608.8197	D	820.4199	410.7136	803.3934	402.2003	802.4094	401.7083	7
12	1348.6856	674.8464	1331.6590	666.3331	1330.6750	665.8411	N	705.3930	353.2001	688.3665	344.6869	687.3824	344.1949	6
13	1461.7696	731.3884	1444.7431	722.8752	1443.7591	722.3832	I	591.3501	296.1787	574.3235	287.6654	573.3395	287.1734	5
14	1548.8016	774.9045	1531.7751	766.3912	1530.7911	765.8992	S	478.2660	239.6366	461.2395	231.1234	460.2554	230.6314	4
15	1695.8701	848.4387	1678.8435	839.9254	1677.8595	839.4334	F	391.2340	196.1206	374.2074	187.6074			3
16	1792.9228	896.9651	1775.8963	888.4518	1774.9123	887.9598	P	244.1656	122.5864	227.1390	114.0731			2
17							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
46.5	1938.0211	0.9939	IIDKNGIHDLDNISFPK
4.0	1938.0210	0.9940	LLNLEDAQSPPSAFIAPR
3.6	1939.0309	-0.0159	AVGLEDOIVSQGIPMRAR
3.6	1938.9986	0.0164	NKTTTCVPVQLHPSSFPK
0.4	1937.9937	1.0213	MGSSPVIKLPLLYPSEK

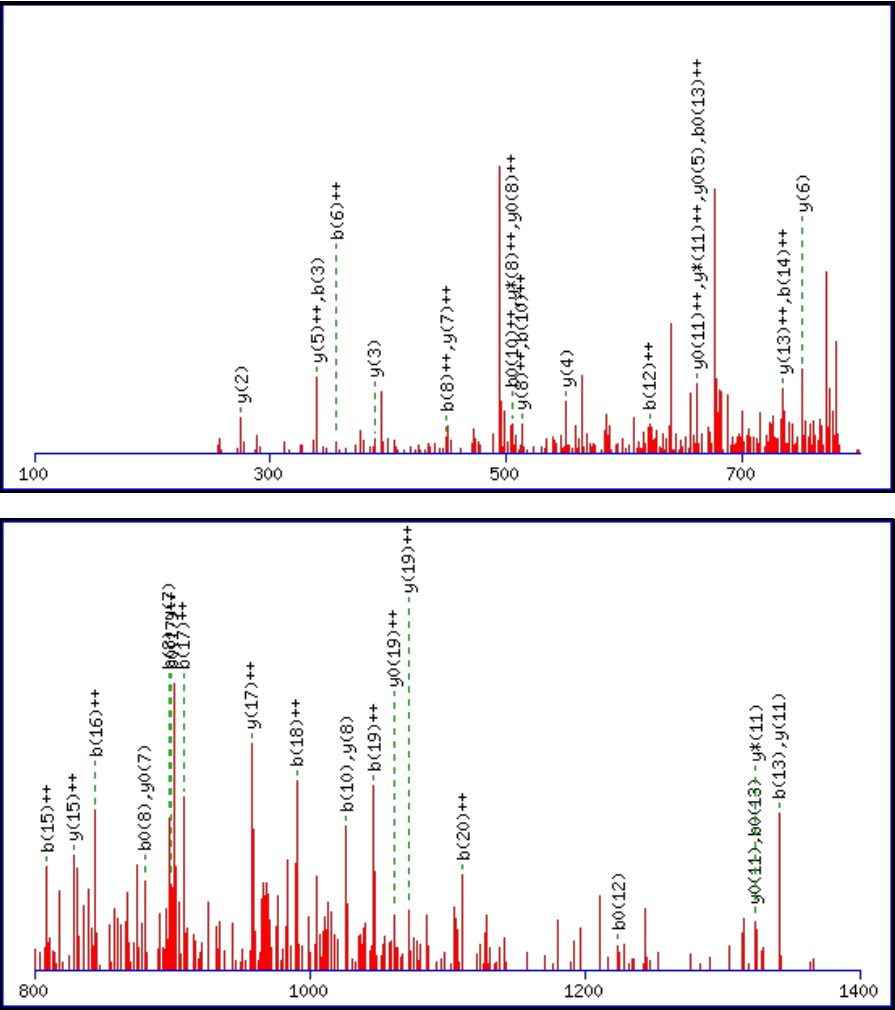
0.0	1939.0040	0.0110	KDSLVLGRVPAHPDSR
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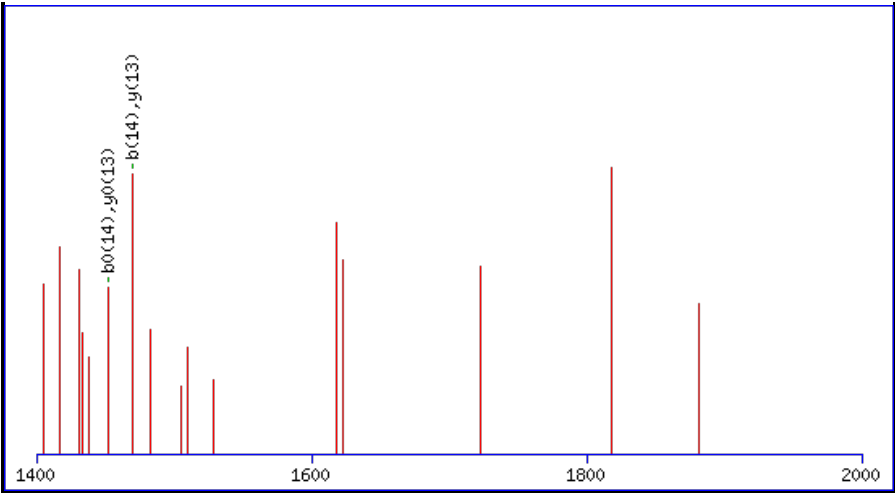
Spectrum No: 111; Query: 52854; Rank: 1

Peptide View

MS/MS Fragmentation of **ILLLCVGEAGDTVQFAEYIQK**
Found in **IP10028006**, Tax_Id=9606 Gene_Symbol=PSMB2 Proteasome subunit beta type-2

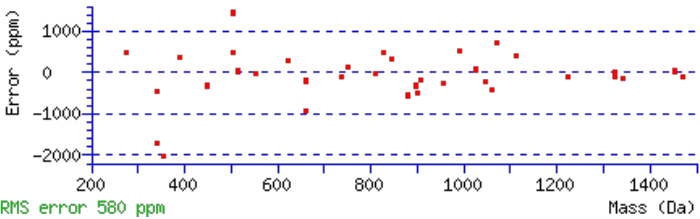
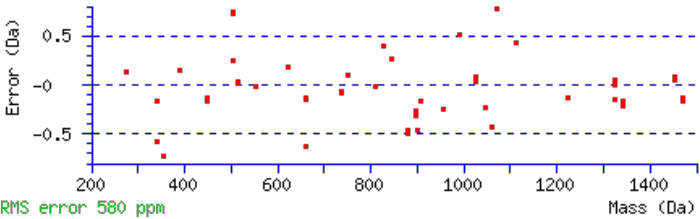
Match to Query 52854: 2367.239082 from(790.086970,3+)
Title: 091224LimSK_Exosome3_06.9656.9656.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2366.2192
Fixed modifications: Carbamidomethyl (C)
Ions Score: 33 Expect: 0.071
Matches (**Bold Red**): 48/192 fragment ions using 98 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					I							21
2	227.1754	114.0913					L	2254.1424	1127.5748	2237.1159	1119.0616	2236.1318	1118.5696	20
3	340.2595	170.6334					L	2141.0583	1071.0328	2124.0318	1062.5195	2123.0478	1062.0275	19
4	453.3435	227.1754					L	2027.9743	1014.4908	2010.9477	1005.9775	2009.9637	1005.4855	18
5	613.3742	307.1907					C	1914.8902	957.9487	1897.8637	949.4355	1896.8796	948.9435	17
6	712.4426	356.7249					V	1754.8596	877.9334	1737.8330	869.4201	1736.8490	868.9281	16
7	769.4641	385.2357					G	1655.7911	828.3992	1638.7646	819.8859	1637.7806	819.3939	15
8	898.5067	449.7570			880.4961	440.7517	E	1598.7697	799.8885	1581.7431	791.3752	1580.7591	790.8832	14
9	969.5438	485.2755			951.5332	476.2702	A	1469.7271	735.3672	1452.7005	726.8539	1451.7165	726.3619	13
10	1026.5652	513.7863			1008.5547	504.7810	G	1398.6900	699.8486	1381.6634	691.3354	1380.6794	690.8433	12
11	1141.5922	571.2997			1123.5816	562.2944	D	1341.6685	671.3379	1324.6420	662.8246	1323.6579	662.3326	11
12	1242.6399	621.8236			1224.6293	612.8183	T	1226.6416	613.8244	1209.6150	605.3111	1208.6310	604.8191	10
13	1341.7083	671.3578			1323.6977	662.3525	V	1125.5939	563.3006	1108.5673	554.7873	1107.5833	554.2953	9
14	1469.7668	735.3871	1452.7403	726.8738	1451.7563	726.3818	Q	1026.5255	513.7664	1009.4989	505.2531	1008.5149	504.7611	8
15	1616.8353	808.9213	1599.8087	800.4080	1598.8247	799.9160	F	898.4669	449.7371	881.4403	441.2238	880.4563	440.7318	7
16	1687.8724	844.4398	1670.8458	835.9265	1669.8618	835.4345	A	751.3985	376.2029	734.3719	367.6896	733.3879	367.1976	6
17	1816.9150	908.9611	1799.8884	900.4478	1798.9044	899.9558	E	680.3614	340.6843	663.3348	332.1710	662.3508	331.6790	5
18	1979.9783	990.4928	1962.9517	981.9795	1961.9677	981.4875	Y	551.3188	276.1630	534.2922	267.6498			4
19	2093.0624	1047.0348	2076.0358	1038.5215	2075.0518	1038.0295	I	388.2554	194.6314	371.2289	186.1181			3
20	2221.1209	1111.0641	2204.0944	1102.5508	2203.1104	1102.0588	Q	275.1714	138.0893	258.1448	129.5761			2
21							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

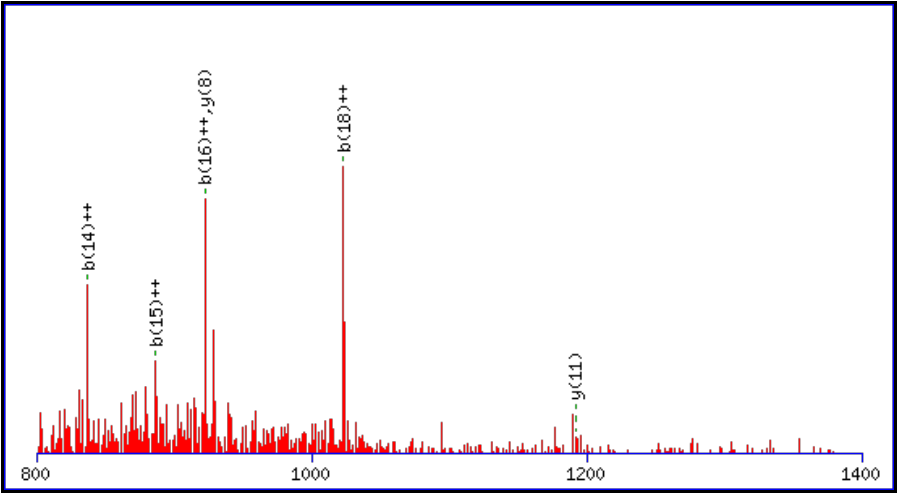
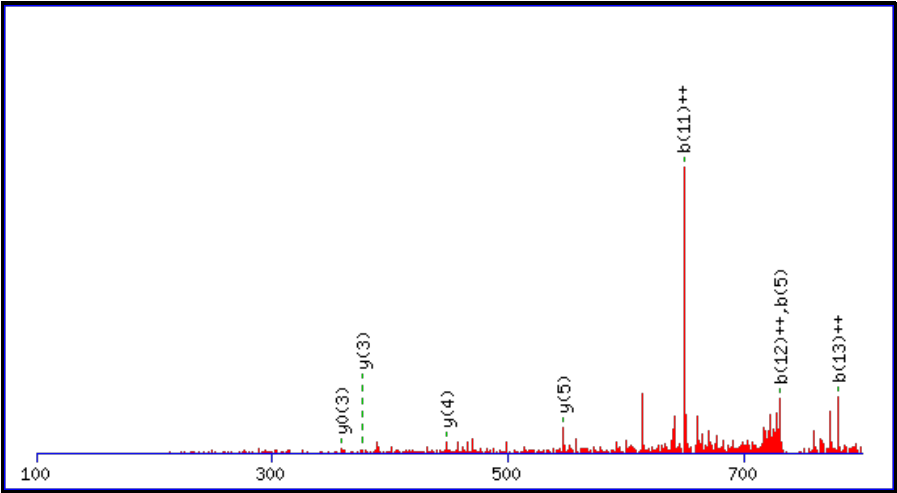
Score	Mr(calc):	Delta	Sequence
32.5	2366.2192	1.0199	ILLLCVGEAGDTVQFAEYIQK

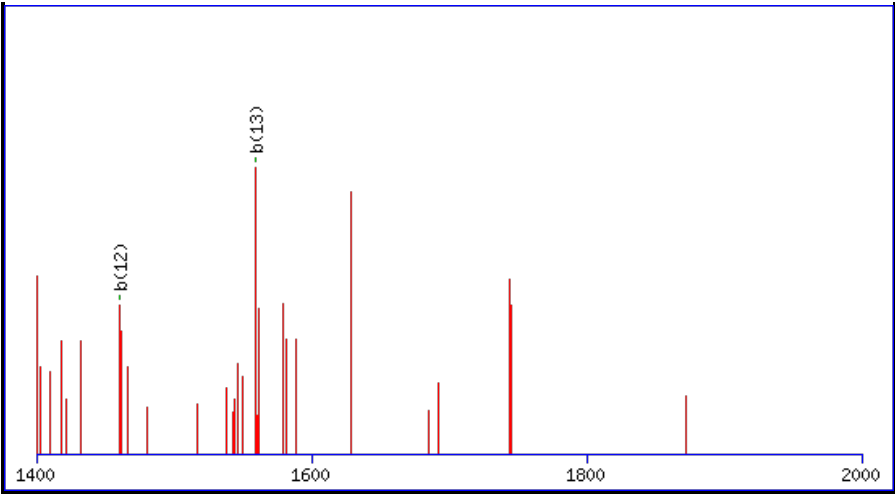
8.7	2367.2199	0.0192	KRDLQTSTHVETLLTFSALK
8.1	2367.2199	0.0192	KRDLQTSTHVETLLTFSALK
7.3	2366.2233	1.0158	RPAQPHRSPASSLQ RarefK
6.8	2365.2134	2.0257	SMLDTIKKGHITGLTGVMEFR
5.8	2366.2220	1.0171	RLSVEESGLGLGLGPGRSPHLR
5.0	2366.2233	1.0158	RPAQPHRSPASSLQ RarefK
4.7	2365.2112	2.0279	ETLITIMKTLIDFVKMMVK
4.7	2365.2112	2.0279	ETLITIMKTLIDFVKMMVK
4.3	2365.2112	2.0279	ETLITIMKTLIDFVKMMVK

Spectrum No: 112; Query: 47990; Rank: 1

Peptide View

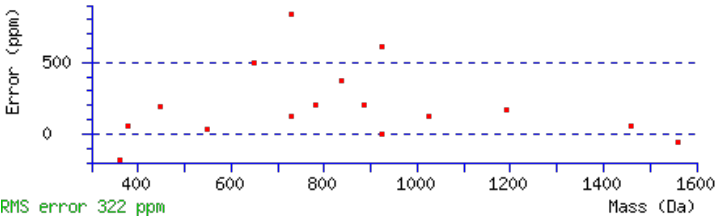
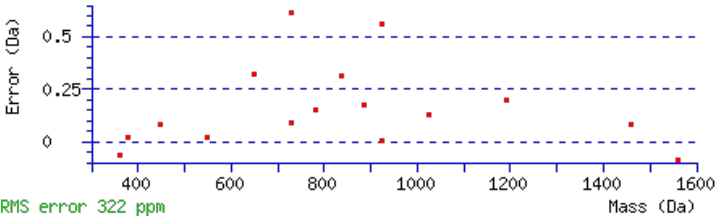
MS/MS Fragmentation of **MEYLIQGPDYVLVASDR**
Found in **IPI00028006**, Tax_Id=9606 Gene_Symbol=PSMB2 Proteasome subunit beta type-2
Match to Query 47990: 2218.044942 from(740.355590,3+)
Title: 091224LimSK_Exosome3_06.8914.8914.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2218.0381
Fixed modifications: Carbamidomethyl (C)
Variable modifications:
Y3 : Phospho (Y)
Ions Score: 22 Expect: 1.8
Matches (**Bold Red**): 16/198 fragment ions using 43 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	132.0478	66.5275					M							19
2	261.0904	131.0488			243.0798	122.0435	E	2088.0049	1044.5061	2070.9784	1035.9928	2069.9943	1035.5008	18
3	504.1200	252.5636			486.1094	243.5584	Y	1958.9623	979.9848	1941.9358	971.4715	1940.9518	970.9795	17
4	617.2041	309.1057			599.1935	300.1004	L	1715.9327	858.4700	1698.9061	849.9567	1697.9221	849.4647	16
5	730.2881	365.6477			712.2776	356.6424	I	1602.8486	801.9279	1585.8221	793.4147	1584.8380	792.9227	15
6	787.3096	394.1584			769.2990	385.1532	G	1489.7645	745.3859	1472.7380	736.8726	1471.7540	736.3806	14
7	900.3937	450.7005			882.3831	441.6952	I	1432.7431	716.8752	1415.7165	708.3619	1414.7325	707.8699	13
8	1028.4522	514.7298	1011.4257	506.2165	1010.4417	505.7245	Q	1319.6590	660.3331	1302.6325	651.8199	1301.6484	651.3279	12
9	1085.4737	543.2405	1068.4472	534.7272	1067.4631	534.2352	G	1191.6004	596.3039	1174.5739	587.7906	1173.5899	587.2986	11
10	1182.5265	591.7669	1165.4999	583.2536	1164.5159	582.7616	P	1134.5790	567.7931	1117.5524	559.2798	1116.5684	558.7878	10
11	1297.5534	649.2803	1280.5269	640.7671	1279.5428	640.2751	D	1037.5262	519.2667	1020.4997	510.7535	1019.5156	510.2615	9
12	1460.6167	730.8120	1443.5902	722.2987	1442.6062	721.8067	Y	922.4993	461.7533	905.4727	453.2400	904.4887	452.7480	8
13	1559.6852	780.3462	1542.6586	771.8329	1541.6746	771.3409	V	759.4359	380.2216	742.4094	371.7083	741.4254	371.2163	7
14	1672.7692	836.8882	1655.7427	828.3750	1654.7587	827.8830	L	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
15	1771.8376	886.4225	1754.8111	877.9092	1753.8271	877.4172	V	547.2835	274.1454	530.2569	265.6321	529.2729	265.1401	5
16	1842.8747	921.9410	1825.8482	913.4277	1824.8642	912.9357	A	448.2150	224.6112	431.1885	216.0979	430.2045	215.6059	4
17	1929.9068	965.4570	1912.8802	956.9438	1911.8962	956.4517	S	377.1779	189.0926	360.1514	180.5793	359.1674	180.0873	3
18	2044.9337	1022.9705	2027.9072	1014.4572	2026.9232	1013.9652	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
19							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
22.0	2218.0381	0.0068	MEYLIQIQGPDYVLVASDR
14.1	2218.0381	0.0068	MEYLIQIQGPDYVLVASDR

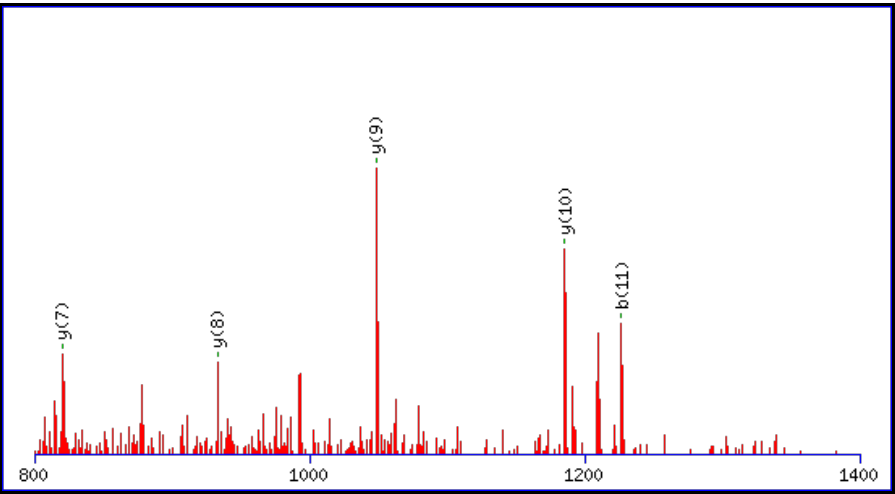
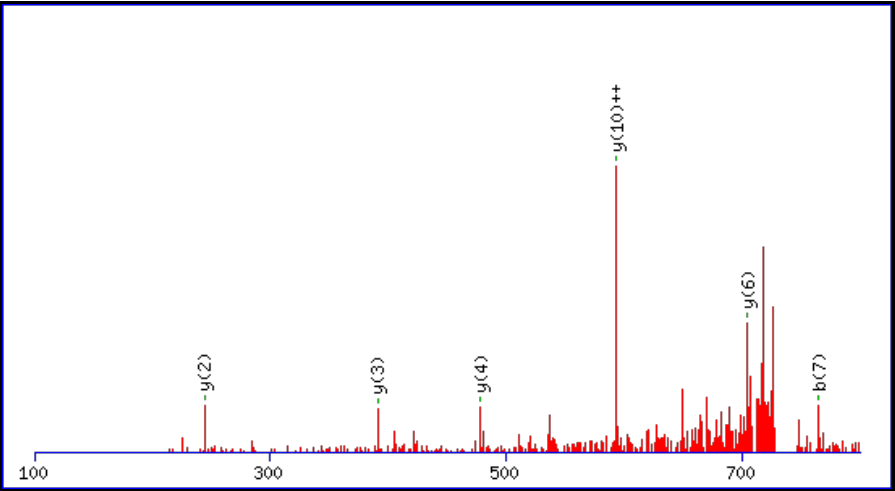
8.6	2217.0596	0.9854	ISSGDPKLPVLYQVERTR
8.6	2217.0596	0.9854	ISSGDPKLPVLYQVERTR
6.0	2218.0589	-0.0140	NTDMSPYPQRPAAQLVWSR
5.7	2216.0335	2.0115	EEHRLSATQQNSRGPAVEK
5.3	2216.0409	2.0040	DHCKVSKSAHSLQPSISQK
4.7	2218.0341	0.0109	DIMESSPGSSPPNLTPKPLR
4.5	2216.0409	2.0040	DHCKVSKSAHSLQPSISQK
4.4	2218.0314	0.0135	MGRLAGRGADPPTSLPDGAAGR

Spectrum No: 113; Query: 18907; Rank: 1

Peptide View

MS/MS Fragmentation of **NGIHDLDNISFPK**
Found in **IP100028006**, Tax_Id=9606 Gene_Symbol=PSMB2 Proteasome subunit beta type-2

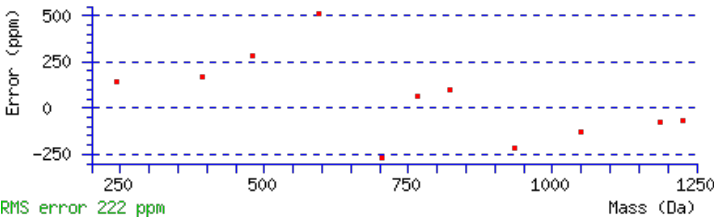
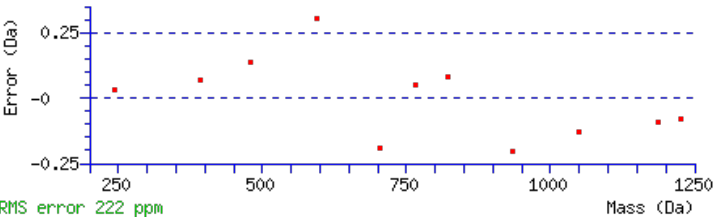
Match to Query 18907: 1468.741988 from(735.378270,2+)
Title: 091224LimSK_Exosome3_06.4581.4581.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1468.7310
Fixed modifications: Carbamidomethyl (C)
Ions Score: 61 Expect: 0.00013
Matches (Bold Red): 11/130 fragment ions using 21 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							13
2	172.0717	86.5395	155.0451	78.0262			G	1355.6954	678.3513	1338.6688	669.8381	1337.6848	669.3461	12
3	285.1557	143.0815	268.1292	134.5682			I	1298.6739	649.8406	1281.6474	641.3273	1280.6634	640.8353	11
4	422.2146	211.6110	405.1881	203.0977			H	1185.5899	593.2986	1168.5633	584.7853	1167.5793	584.2933	10
5	537.2416	269.1244	520.2150	260.6112	519.2310	260.1191	D	1048.5310	524.7691	1031.5044	516.2558	1030.5204	515.7638	9
6	650.3257	325.6665	633.2991	317.1532	632.3151	316.6612	L	933.5040	467.2556	916.4775	458.7424	915.4934	458.2504	8
7	765.3526	383.1799	748.3260	374.6667	747.3420	374.1747	D	820.4199	410.7136	803.3934	402.2003	802.4094	401.7083	7
8	879.3955	440.2014	862.3690	431.6881	861.3850	431.1961	N	705.3930	353.2001	688.3665	344.6869	687.3824	344.1949	6
9	992.4796	496.7434	975.4530	488.2302	974.4690	487.7381	I	591.3501	296.1787	574.3235	287.6654	573.3395	287.1734	5
10	1079.5116	540.2594	1062.4851	531.7462	1061.5010	531.2542	S	478.2660	239.6366	461.2395	231.1234	460.2554	230.6314	4
11	1226.5800	613.7937	1209.5535	605.2804	1208.5695	604.7884	F	391.2340	196.1206	374.2074	187.6074			3
12	1323.6328	662.3200	1306.6062	653.8068	1305.6222	653.3148	P	244.1656	122.5864	227.1390	114.0731			2
13							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

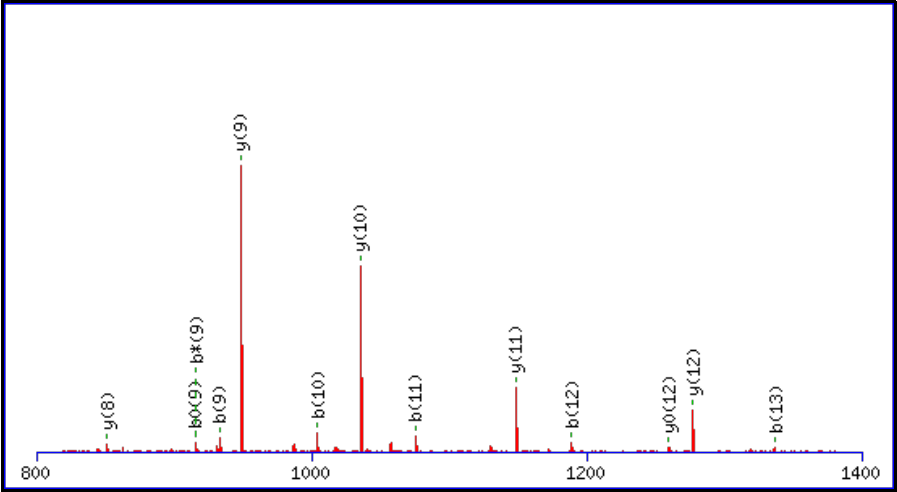
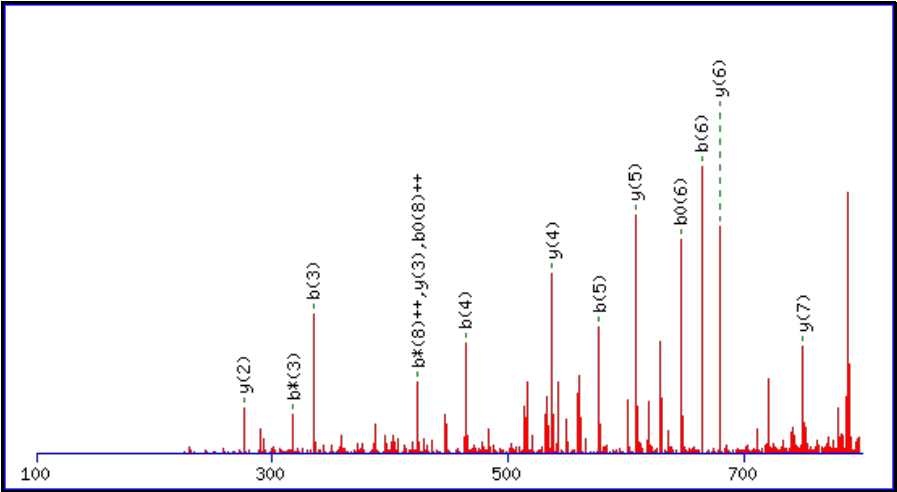
Score	Mr(calc):	Delta	Sequence
61.4	1468.7310	0.0110	NGIHDLDNISFPK
10.0	1466.7365	2.0055	KLNHQEVVEEDK
9.9	1467.7470	0.9950	RSFSIIGDFQNGK
7.6	1468.7286	0.0134	QDSVKSILERSK
7.1	1466.7287	2.0133	KIMGGSGTETTLEK
7.1	1468.7439	-0.0019	LLGKNGTGGLFQ GK
5.3	1468.7300	0.0120	RQHLAVSHEKGK
4.4	1468.7455	-0.0035	KKSLLLPA PSQK
3.7	1468.7286	0.0134	QDSVKSILERSK

3.1	1467.7392	1.0028	VPSTPVHLTNEMK
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Spectrum No: 114; Query: 26112; Rank: 1

Peptide View

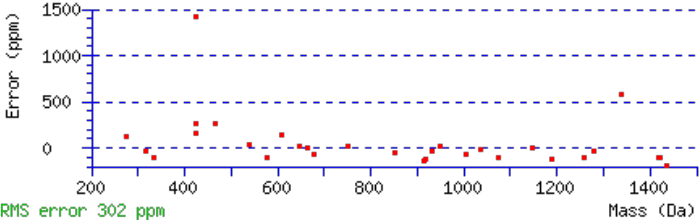
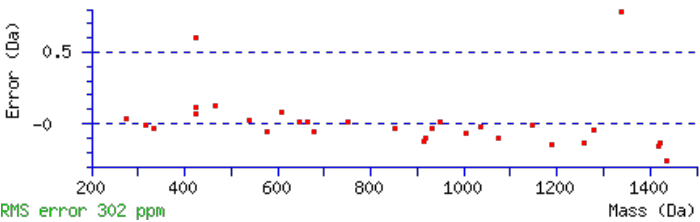
MS/MS Fragmentation of **NGYELSPTAAANFTR**
Found in **IPI00028006**, Tax_Id=9606 Gene_Symbol=PSMB2 Proteasome subunit beta type-2
Match to Query 26112: 1610.779388 from(806.396970,2+)
Title: 091224LimSK_Exosome3_06.3957.3957.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1610.7689
Fixed modifications: Carbamidomethyl (C)
Ions Score: 90 Expect: 1.9e-007
Matches (Bold Red): 30/160 fragment ions using 41 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							15
2	172.0717	86.5395	155.0451	78.0262			G	1497.7332	749.3703	1480.7067	740.8570	1479.7227	740.3650	14
3	335.1350	168.0711	318.1084	159.5579			Y	1440.7118	720.8595	1423.6852	712.3462	1422.7012	711.8542	13
4	464.1776	232.5924	447.1510	224.0792	446.1670	223.5872	E	1277.6484	639.3279	1260.6219	630.8146	1259.6379	630.3226	12
5	577.2617	289.1345	560.2351	280.6212	559.2511	280.1292	L	1148.6058	574.8066	1131.5793	566.2933	1130.5953	565.8013	11
6	664.2937	332.6505	647.2671	324.1372	646.2831	323.6452	S	1035.5218	518.2645	1018.4952	509.7513	1017.5112	509.2592	10
7	761.3464	381.1769	744.3199	372.6636	743.3359	372.1716	P	948.4898	474.7485	931.4632	466.2352	930.4792	465.7432	9
8	862.3941	431.7007	845.3676	423.1874	844.3836	422.6954	T	851.4370	426.2221	834.4104	417.7089	833.4264	417.2169	8
9	933.4312	467.2193	916.4047	458.7060	915.4207	458.2140	A	750.3893	375.6983	733.3628	367.1850	732.3787	366.6930	7
10	1004.4684	502.7378	987.4418	494.2245	986.4578	493.7325	A	679.3522	340.1797	662.3257	331.6665	661.3416	331.1745	6
11	1075.5055	538.2564	1058.4789	529.7431	1057.4949	529.2511	A	608.3151	304.6612	591.2885	296.1479	590.3045	295.6559	5
12	1189.5484	595.2778	1172.5218	586.7646	1171.5378	586.2726	N	537.2780	269.1426	520.2514	260.6293	519.2674	260.1373	4
13	1336.6168	668.8120	1319.5903	660.2988	1318.6062	659.8068	F	423.2350	212.1212	406.2085	203.6079	405.2245	203.1159	3
14	1437.6645	719.3359	1420.6379	710.8226	1419.6539	710.3306	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
15							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
90.3	1610.7689	0.0105	NGYELSPTAAANFTR
5.6	1610.7943	-0.0149	RAWHGARLPGSPAR
5.0	1610.7900	-0.0106	SSGSEESILDLRYR
4.5	1610.7818	-0.0024	TESEKATLTIHQR
3.6	1609.7709	1.0085	ANQNVNAVHSHYTR
3.3	1609.7882	0.9911	GFKIMSAGDGAGDRTK
1.9	1610.7851	-0.0057	LRKGGATALMDAAEK

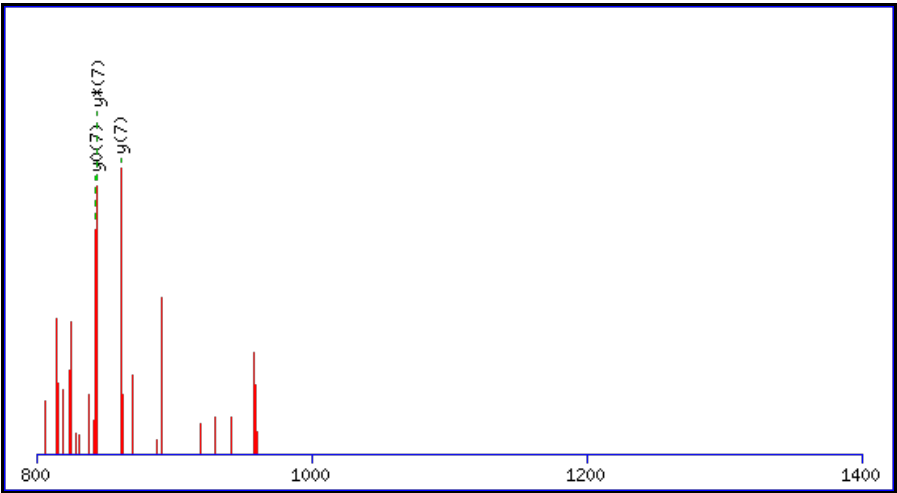
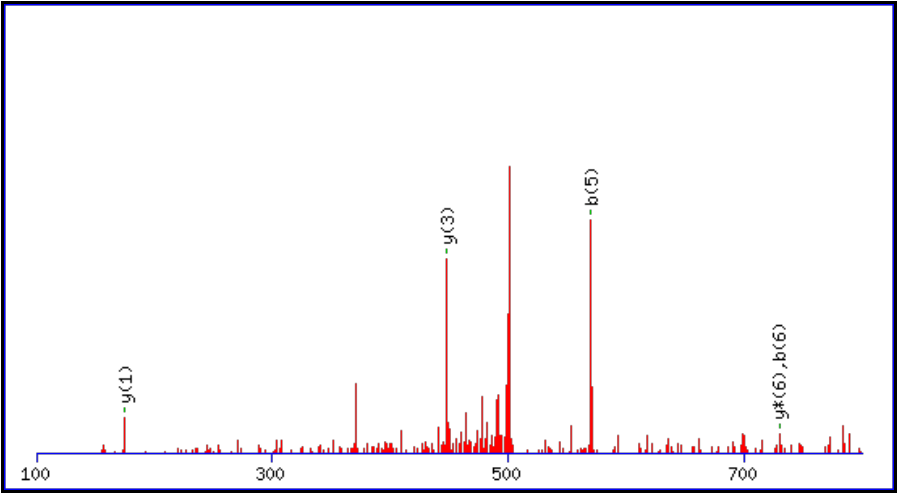
1.3	1608.7872	1.9922	EKRVTVLEQNGEK
0.9	1610.7657	0.0137	EFGKNREVMGLCR
0.7	1609.7899	0.9895	DPAPVKTMTISSKR

Spectrum No: 115; Query: 3033; Rank: 1

Peptide View

MS/MS Fragmentation of **RNLADCLR**
Found in **IP100028006**, Tax_Id=9606 Gene_Symbol=PSMB2 Proteasome subunit beta type-2

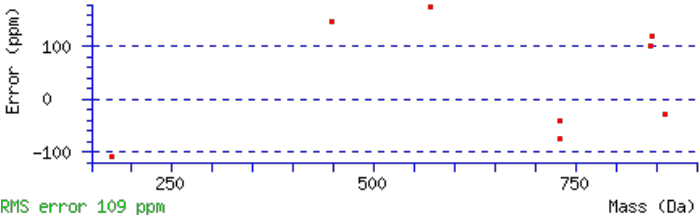
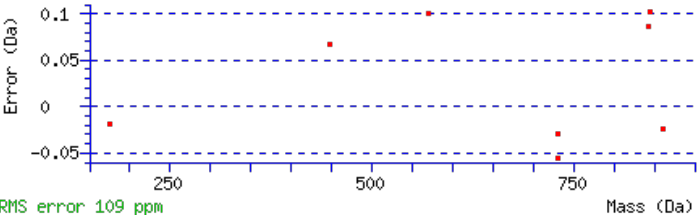
Match to Query 3033: 1016.522928 from(509.268740,2+)
Title: 091224LimSK_Exosome3_06.650.650.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1016.5185
Fixed modifications: Carbamidomethyl (C)
Ions Score: 20 Expect: 1.2
Matches (**Bold Red**): 9/70 fragment ions using 18 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							8
2	271.1513	136.0793	254.1248	127.5660			N	861.4247	431.2160	844.3982	422.7027	843.4141	422.2107	7
3	384.2354	192.6213	367.2088	184.1081			L	747.3818	374.1945	730.3552	365.6813	729.3712	365.1892	6
4	455.2725	228.1399	438.2459	219.6266			A	634.2977	317.6525	617.2712	309.1392	616.2872	308.6472	5
5	570.2994	285.6534	553.2729	277.1401	552.2889	276.6481	D	563.2606	282.1339	546.2341	273.6207	545.2500	273.1287	4
6	730.3301	365.6687	713.3035	357.1554	712.3195	356.6634	C	448.2337	224.6205	431.2071	216.1072			3
7	843.4141	422.2107	826.3876	413.6974	825.4036	413.2054	L	288.2030	144.6051	271.1765	136.0919			2
8							R	175.1190	88.0631	158.0924	79.5498			1



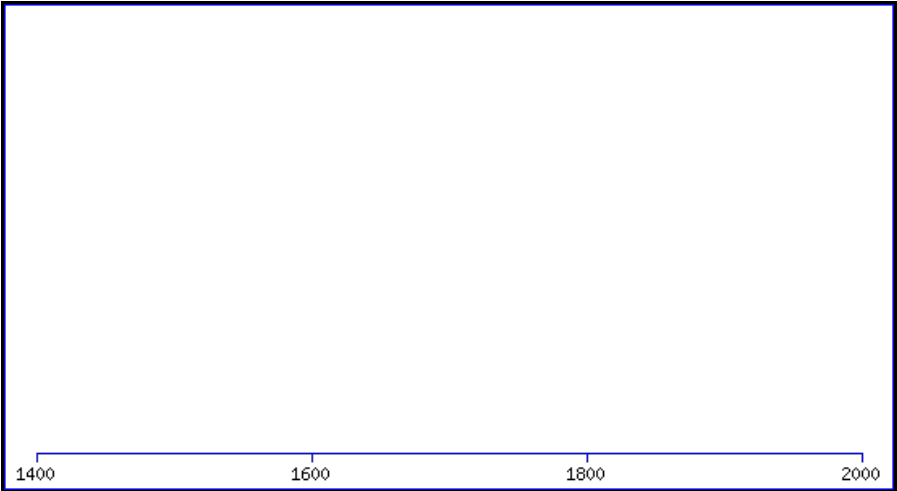
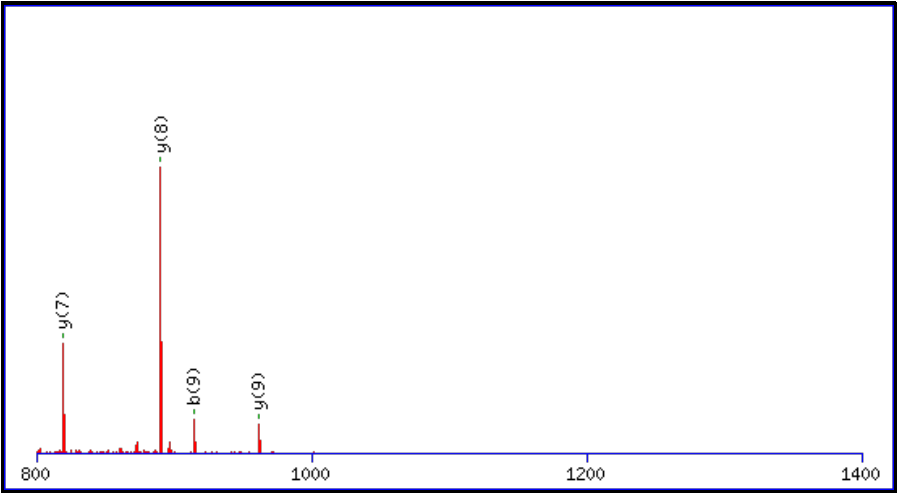
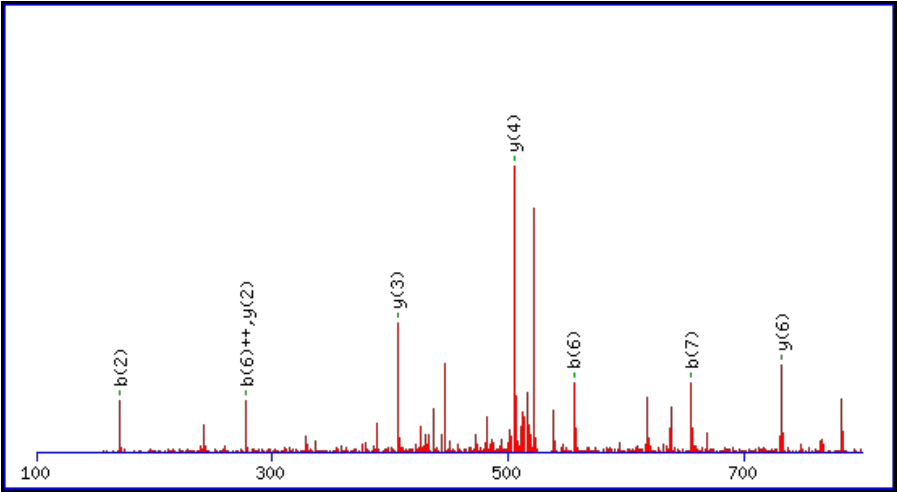
All matches to this query

Score	Mr(calc):	Delta	Sequence
20.1	1016.5185	0.0044	RNLADCLR
12.7	1016.5147	0.0082	MMPGAPLLR
11.2	1016.5297	-0.0068	RQMAARER
8.7	1015.5120	1.0109	GMKESISHK
8.2	1015.5271	0.9958	GROSQRER
7.9	1016.5325	-0.0095	GIMESPIVR
7.2	1016.5168	0.0061	HVAAASLIR
6.5	1016.5138	0.0091	STSLEPVER
6.3	1016.5251	-0.0021	EDQAGKTLR
5.9	1016.5251	-0.0021	RDLDLETR

Peptide View

MS/MS Fragmentation of **VAASNIVQMK**
Found in **IPI00028006**, Tax_Id=9606 Gene_Symbol=PSMB2 Proteasome subunit beta type-2

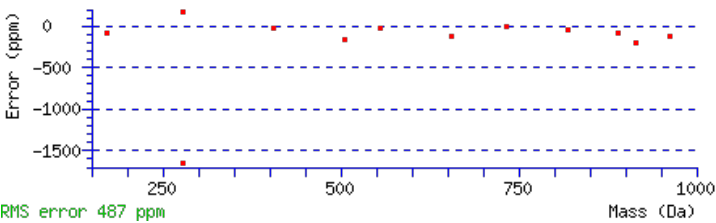
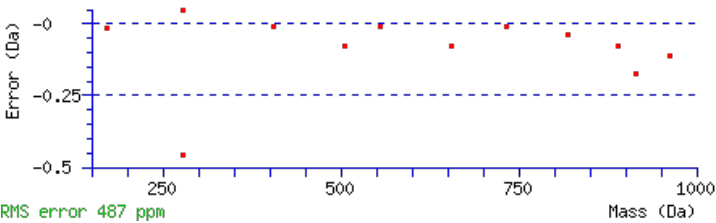
Match to Query 3868: 1059.579548 from(530.797050,2+)
Title: 091224LimSK_Exosome3_07.1303.1303.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide **Mr(calc):** 1059.5746
Fixed modifications: Carbamidomethyl (C)
Ions Score: 76 **Expect:** 3.4e-006
Matches (Bold Red): 12/82 fragment ions using 13 most intense peaks

		++		++	0	0++		++		++	0	0++	
--	--	----	--	----	---	-----	--	----	--	----	---	-----	--

#	b	b	b*	b*	b	b	Seq.	y	y	y*	y*	y	y	#
1	100.0757	50.5415					V							10
2	171.1128	86.0600					A	961.5135	481.2604	944.4870	472.7471	943.5030	472.2551	9
3	242.1499	121.5786					A	890.4764	445.7418	873.4499	437.2286	872.4658	436.7366	8
4	329.1819	165.0946			311.1714	156.0893	S	819.4393	410.2233	802.4128	401.7100	801.4287	401.2180	7
5	443.2249	222.1161	426.1983	213.6028	425.2143	213.1108	N	732.4073	366.7073	715.3807	358.1940			6
6	556.3089	278.6581	539.2824	270.1448	538.2984	269.6528	I	618.3643	309.6858	601.3378	301.1725			5
7	655.3774	328.1923	638.3508	319.6790	637.3668	319.1870	V	505.2803	253.1438	488.2537	244.6305			4
8	783.4359	392.2216	766.4094	383.7083	765.4254	383.2163	Q	406.2119	203.6096	389.1853	195.0963			3
9	914.4764	457.7418	897.4499	449.2286	896.4658	448.7366	M	278.1533	139.5803	261.1267	131.0670			2
10							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

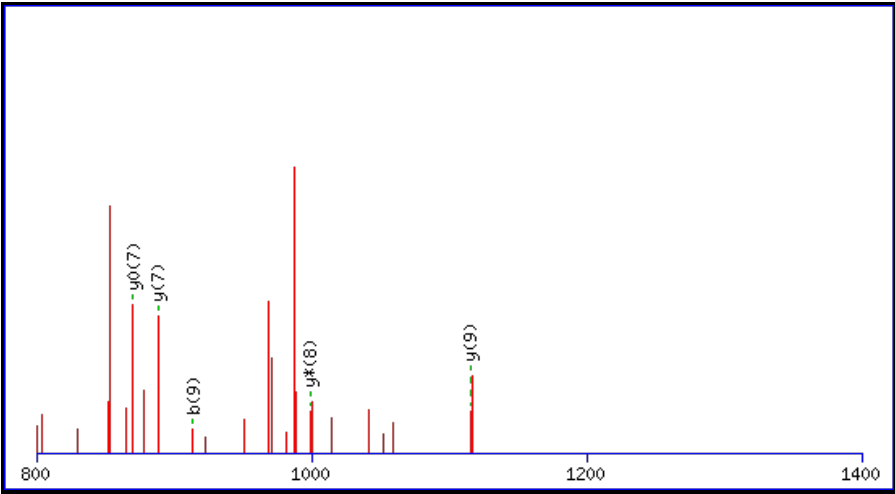
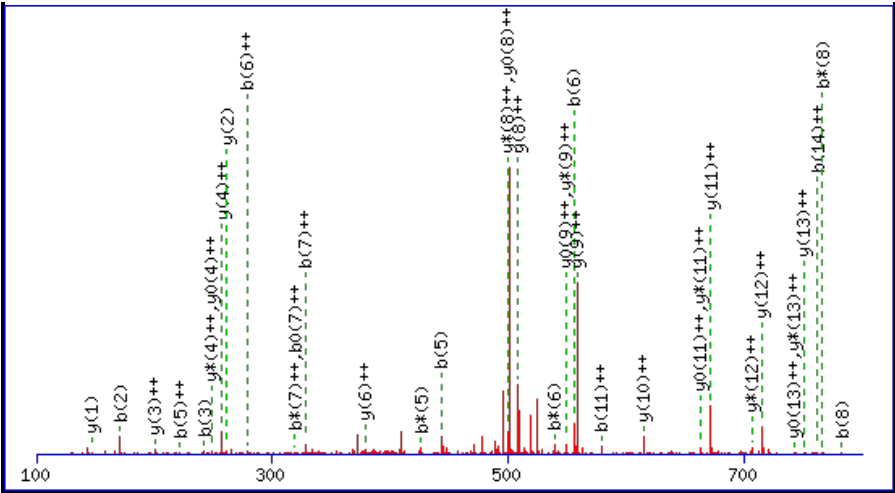
Score	Mr(calc):	Delta	Sequence
76.0	1059.5746	0.0049	VAASNIVQMK
2.4	1058.5720	1.0076	DAAEREKLK
1.5	1057.5628	2.0167	XSLSGARSAPR
1.3	1059.5785	0.0011	IQSSEGRRK
0.8	1059.5825	-0.0030	VTWRETIR
0.7	1057.5768	2.0028	QQIIATQEK

Spectrum No: 117; Query: 28688; Rank: 1

Peptide View

MS/MS Fragmentation of **VAASNIVQMKDDHDK**
Found in **IP100028006**, Tax_Id=9606 Gene_Symbol=PSMB2 Proteasome subunit beta type-2

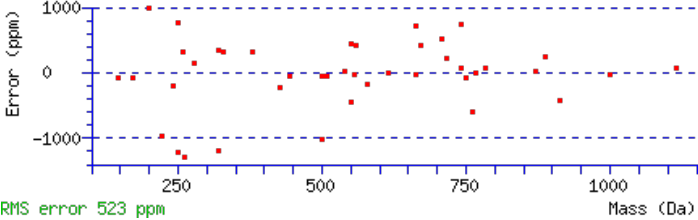
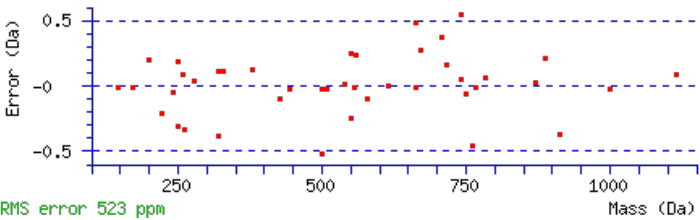
Match to Query 28688: 1669.815816 from(418.461230,4+)
Title: 091224LimSK_Exosome3_06.615.615.4.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1669.8094
Fixed modifications: Carbamidomethyl (C)
Ions Score: 36 Expect: 0.057
Matches (Bold Red): 42/152 fragment ions using 88 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							15
2	171.1128	86.0600					A	1571.7482	786.3778	1554.7217	777.8645	1553.7377	777.3725	14
3	242.1499	121.5786					A	1500.7111	750.8592	1483.6846	742.3459	1482.7006	741.8539	13
4	329.1819	165.0946			311.1714	156.0893	S	1429.6740	715.3406	1412.6475	706.8274	1411.6634	706.3354	12
5	443.2249	222.1161	426.1983	213.6028	425.2143	213.1108	N	1342.6420	671.8246	1325.6154	663.3114	1324.6314	662.8193	11
6	556.3089	278.6581	539.2824	270.1448	538.2984	269.6528	I	1228.5990	614.8032	1211.5725	606.2899	1210.5885	605.7979	10

7	655.3774	328.1923	638.3508	319.6790	637.3668	319.1870	V	1115.5150	558.2611	1098.4884	549.7479	1097.5044	549.2558	9
8	783.4359	392.2216	766.4094	383.7083	765.4254	383.2163	Q	1016.4466	508.7269	999.4200	500.2136	998.4360	499.7216	8
9	914.4764	457.7418	897.4499	449.2286	896.4658	448.7366	M	888.3880	444.6976	871.3614	436.1844	870.3774	435.6924	7
10	1042.5714	521.7893	1025.5448	513.2761	1024.5608	512.7840	K	757.3475	379.1774	740.3210	370.6641	739.3369	370.1721	6
11	1157.5983	579.3028	1140.5718	570.7895	1139.5878	570.2975	D	629.2525	315.1299	612.2260	306.6166	611.2420	306.1246	5
12	1272.6253	636.8163	1255.5987	628.3030	1254.6147	627.8110	D	514.2256	257.6164	497.1991	249.1032	496.2150	248.6112	4
13	1409.6842	705.3457	1392.6576	696.8325	1391.6736	696.3404	H	399.1987	200.1030	382.1721	191.5897	381.1881	191.0977	3
14	1524.7111	762.8592	1507.6846	754.3459	1506.7006	753.8539	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
15							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

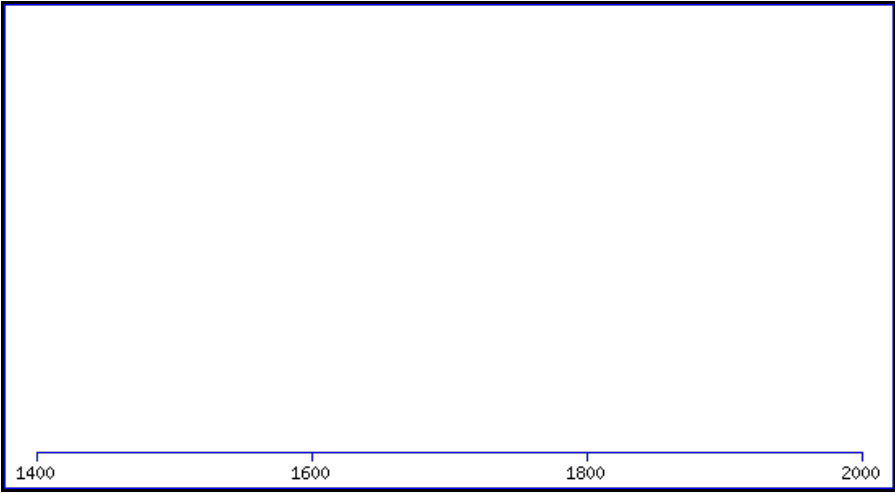
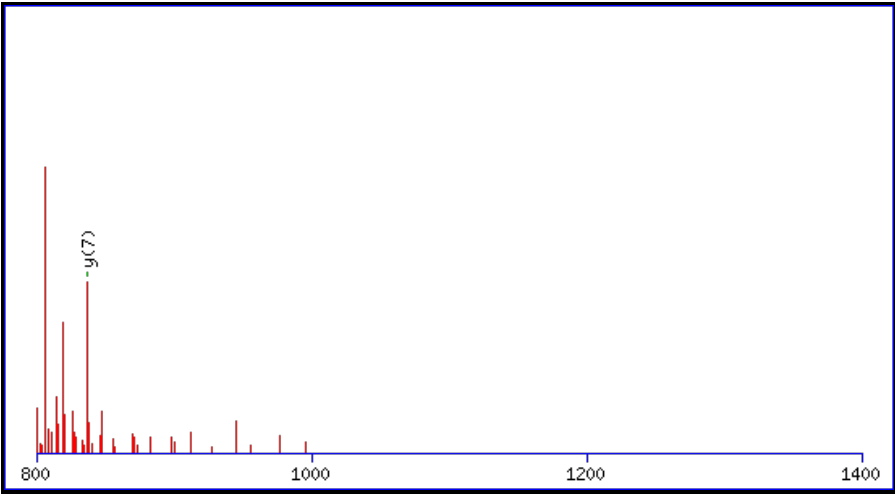
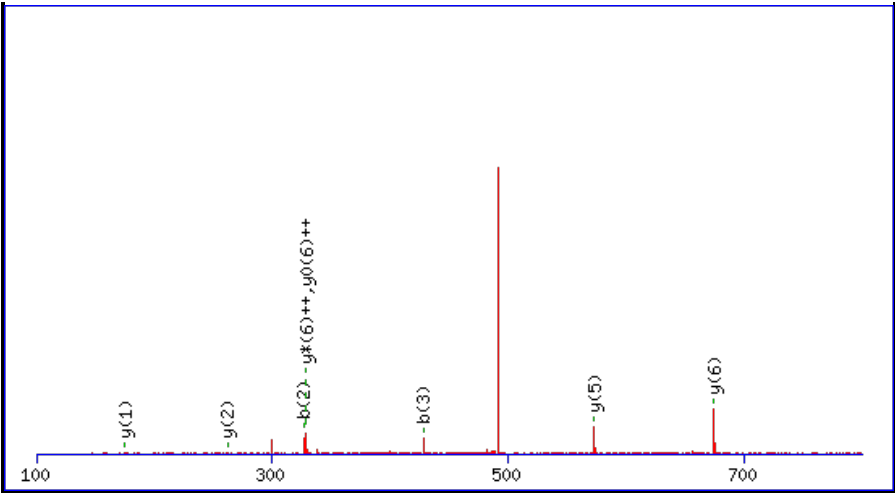
Score	Mr(calc):	Delta	Sequence
35.8	1669.8094	0.0065	VAASNIVQMKDDHDK
16.6	1668.8018	1.0140	LKMQNGSKGSGLQNK
14.3	1669.8157	0.0001	AARLCLSICSVKGR
14.1	1667.8079	2.0079	ASRCPPPPRGAAVPR
12.2	1668.8084	1.0075	DTLSKGSAAAATAVAAGK
11.9	1669.8172	-0.0014	QYDPPAESQVPRAGR
11.5	1667.8172	1.9987	GLGSLFSGSLLPTDPK
11.4	1667.8162	1.9996	GRAGADGARGMPGDPGVK
11.1	1667.8079	2.0079	ARARGSPCPPLPPGR
9.3	1667.8049	2.0109	VRSVILQSGVSPLP

Spectrum No: 118; Query: 2751; Rank: 1

Peptide View

MS/MS Fragmentation of **YYTPTISR**
Found in **IPI00028006**, Tax_Id=9606 Gene_Symbol=PSMB2 Proteasome subunit beta type-2

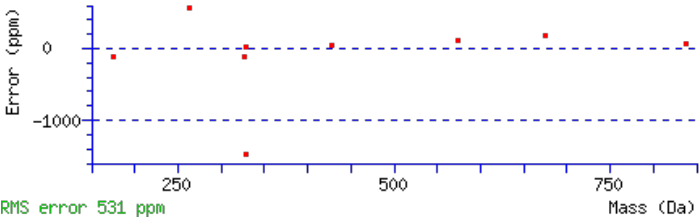
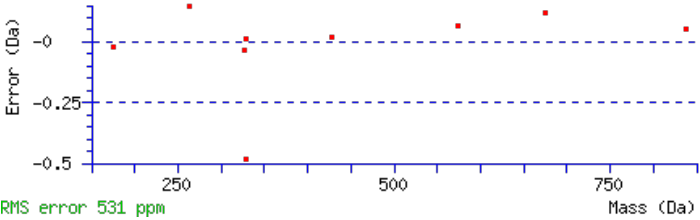
Match to Query 2751: 999.507288 from(500.760920,2+)
Title: 091224LimSK_Exosome3_06.1370.1370.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 999.5025
Fixed modifications: Carbamidomethyl (C)
Ions Score: 21 Expect: 0.84
Matches (**Bold Red**): 9/64 fragment ions using 23 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	164.0706	82.5389			Y							8
2	327.1339	164.0706			Y	837.4465	419.2269	820.4199	410.7136	819.4359	410.2216	7
3	428.1816	214.5944	410.1710	205.5892	T	674.3832	337.6952	657.3566	329.1819	656.3726	328.6899	6
4	525.2344	263.1208	507.2238	254.1155	P	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	5
5	626.2821	313.6447	608.2715	304.6394	T	476.2827	238.6450	459.2562	230.1317	458.2722	229.6397	4
6	739.3661	370.1867	721.3556	361.1814	I	375.2350	188.1212	358.2085	179.6079	357.2245	179.1159	3

7	826.3981	413.7027	808.3876	404.6974	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
8					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

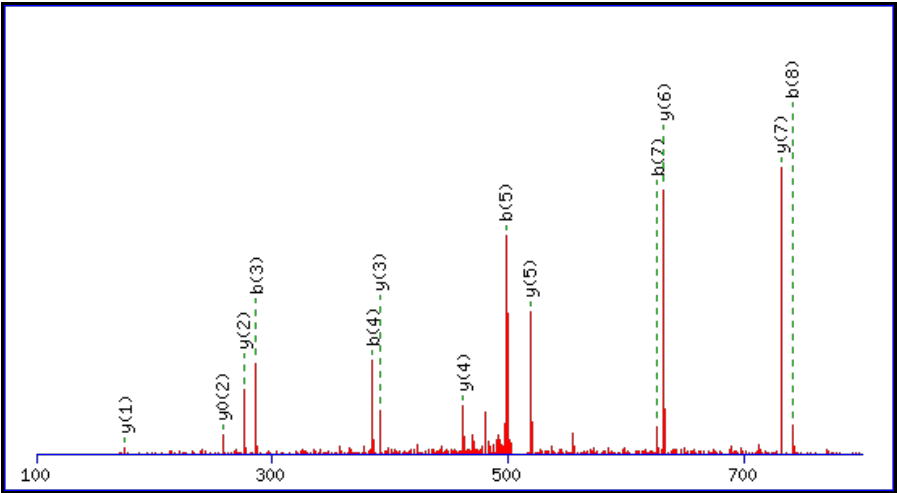
Score	Mr(calc):	Delta	Sequence
21.1	999.5025	0.0048	YYTPTISR
15.1	998.4950	1.0122	GAVVTGFLR
12.3	997.4957	2.0116	SLQKLSSR
11.5	997.4957	2.0116	KALSGLSSR
9.9	998.4950	1.0123	KPVLGSYR
9.9	998.4950	1.0123	KPVLGSYR
9.9	998.4968	1.0105	KPVQDCPR
9.4	999.5025	0.0048	YYSLGEIR
8.4	997.4941	2.0132	SPREEAGPR
7.1	997.4957	2.0116	KALSGLSSR

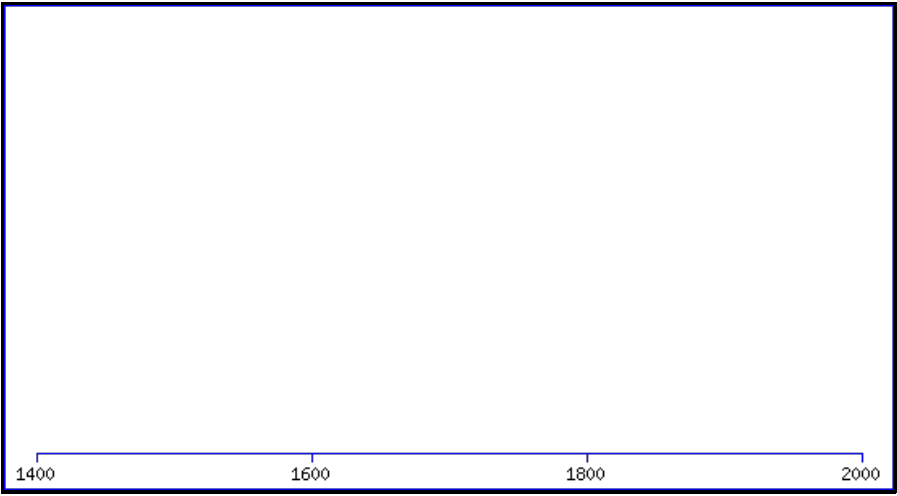
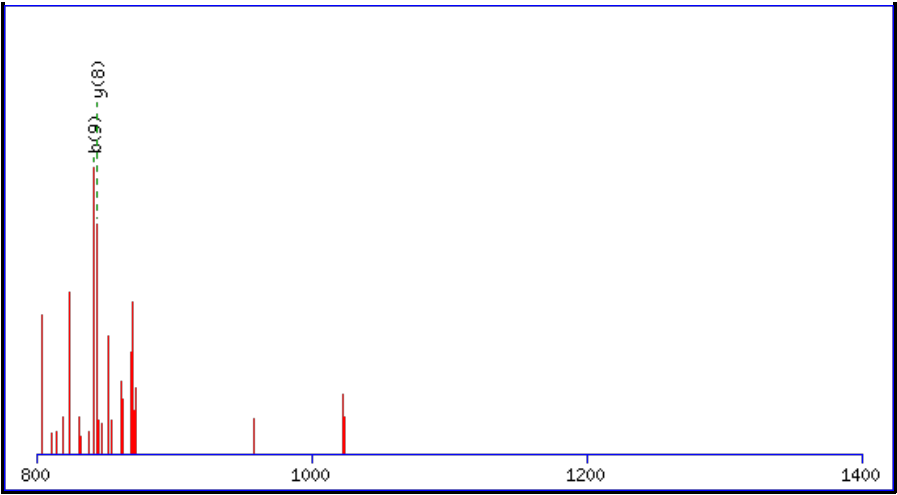
Spectrum No: 119; Query: 3022; Rank: 1

Peptide View

MS/MS Fragmentation of **DGIVLGADTR**
Found in **IPI00003217**, Tax_Id=9606 Gene_Symbol=PSMB7 Proteasome subunit beta type-7

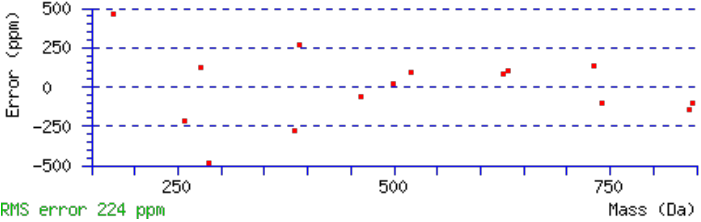
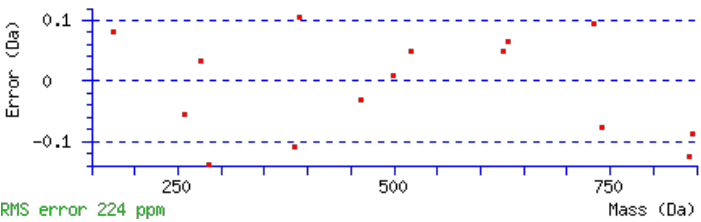
Match to Query 3022: 1015.535168 from(508.774860,2+)
Title: 091224LimSK_Exosome3_06.1359.1359.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1015.5298
Fixed modifications: Carbamidomethyl (C)
Ions Score: 69 Expect: 1.4e-005
Matches (**Bold Red**): 15/88 fragment ions using 26 most intense peaks

#	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							10
2	173.0557	87.0315	155.0451	78.0262	G	901.5102	451.2587	884.4836	442.7454	883.4996	442.2534	9
3	286.1397	143.5735	268.1292	134.5682	I	844.4887	422.7480	827.4621	414.2347	826.4781	413.7427	8
4	385.2082	193.1077	367.1976	184.1024	V	731.4046	366.2060	714.3781	357.6927	713.3941	357.2007	7
5	498.2922	249.6498	480.2817	240.6445	L	632.3362	316.6717	615.3097	308.1585	614.3257	307.6665	6
6	555.3137	278.1605	537.3031	269.1552	G	519.2522	260.1297	502.2256	251.6164	501.2416	251.1244	5
7	626.3508	313.6790	608.3402	304.6738	A	462.2307	231.6190	445.2041	223.1057	444.2201	222.6137	4
8	741.3777	371.1925	723.3672	362.1872	D	391.1936	196.1004	374.1670	187.5872	373.1830	187.0951	3
9	842.4254	421.7164	824.4149	412.7111	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
10					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query



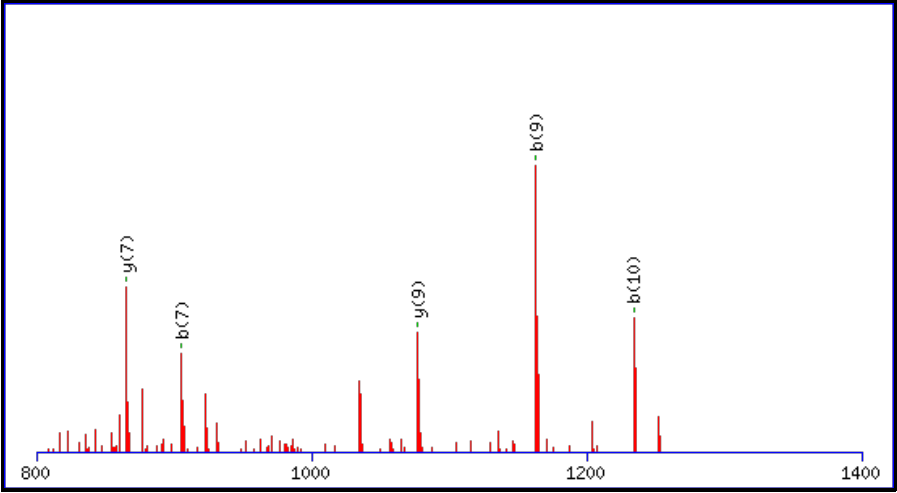
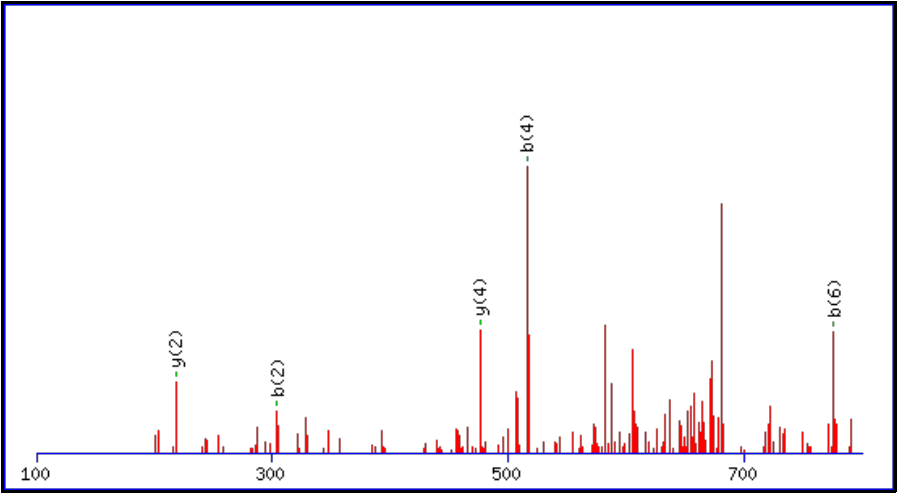
Score	Mr(calc):	Delta	Sequence
69.2	1015.5298	0.0053	DGIVLGADTR
20.8	1014.5319	1.0033	AGRVGGQSGAR
18.3	1015.5298	0.0054	LATVVNDER
16.8	1015.5410	-0.0059	GQQALGSSLR
12.2	1014.5263	1.0088	GIIFTKTR
11.8	1015.5410	-0.0058	RLNLSEER
10.7	1015.5298	0.0054	LRDEINEK
9.3	1014.5263	1.0088	GIIFTKTR
8.9	1013.5310	2.0041	ILRLYEK
7.2	1013.5310	2.0041	IRLLYEK

Spectrum No: 120; Query: 14207; Rank: 1

Peptide View

MS/MS Fragmentation of **FRPDMEEEEAK**
Found in **IPI00003217**, Tax_Id=9606 Gene_Symbol=PSMB7 Proteasome subunit beta type-7

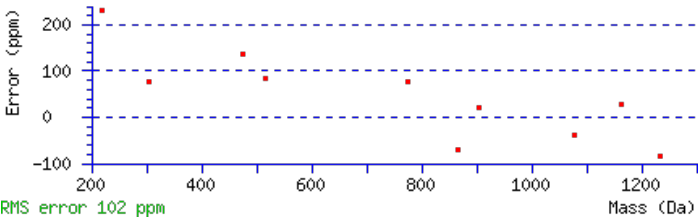
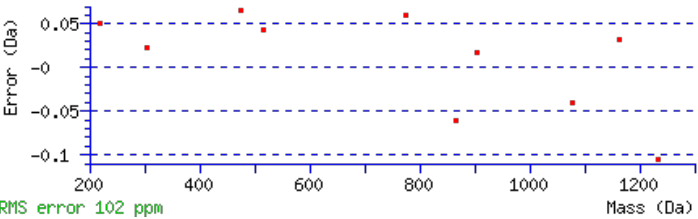
Match to Query 14207: 1379.609568 from(690.812060,2+)
Title: 091224LimSK_Exosome3_06.573.573.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1379.6027
Fixed modifications: Carbamidomethyl (C)
Ions Score: 57 Expect: 0.00033
Matches (**Bold Red**): 10/108 fragment ions using 12 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							11
2	304.1768	152.5920	287.1503	144.0788			R	1233.5416	617.2744	1216.5150	608.7612	1215.5310	608.2692	10
3	401.2296	201.1184	384.2030	192.6051			P	1077.4405	539.2239	1060.4139	530.7106	1059.4299	530.2186	9
4	516.2565	258.6319	499.2300	250.1186	498.2459	249.6266	D	980.3877	490.6975	963.3612	482.1842	962.3772	481.6922	8
5	647.2970	324.1521	630.2704	315.6389	629.2864	315.1469	M	865.3608	433.1840	848.3342	424.6708	847.3502	424.1787	7
6	776.3396	388.6734	759.3130	380.1602	758.3290	379.6681	E	734.3203	367.6638	717.2937	359.1505	716.3097	358.6585	6
7	905.3822	453.1947	888.3556	444.6815	887.3716	444.1894	E	605.2777	303.1425	588.2511	294.6292	587.2671	294.1372	5
8	1034.4248	517.7160	1017.3982	509.2027	1016.4142	508.7107	E	476.2351	238.6212	459.2086	230.1079	458.2245	229.6159	4
9	1163.4674	582.2373	1146.4408	573.7240	1145.4568	573.2320	E	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
10	1234.5045	617.7559	1217.4779	609.2426	1216.4939	608.7506	A	218.1499	109.5786	201.1234	101.0653			2
11							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

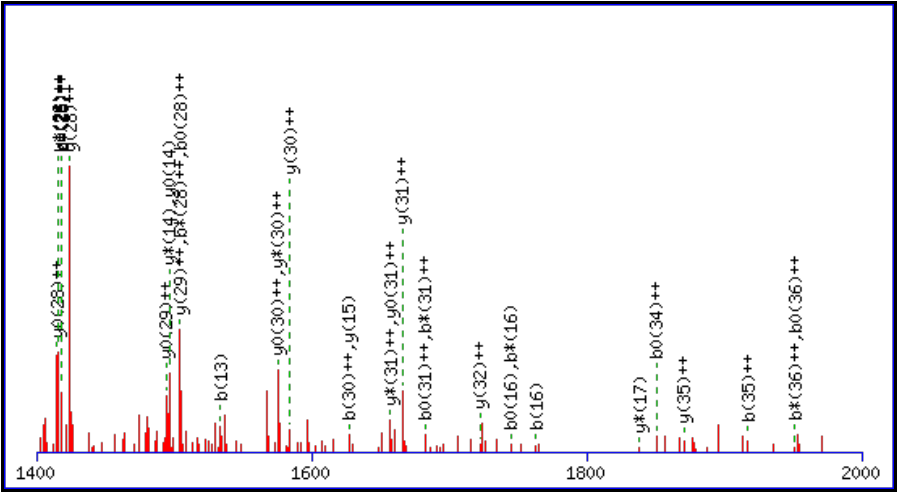
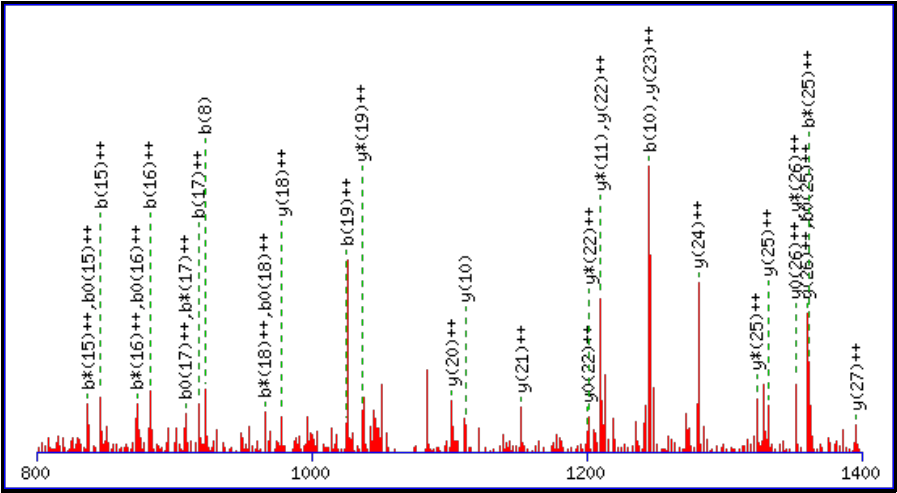
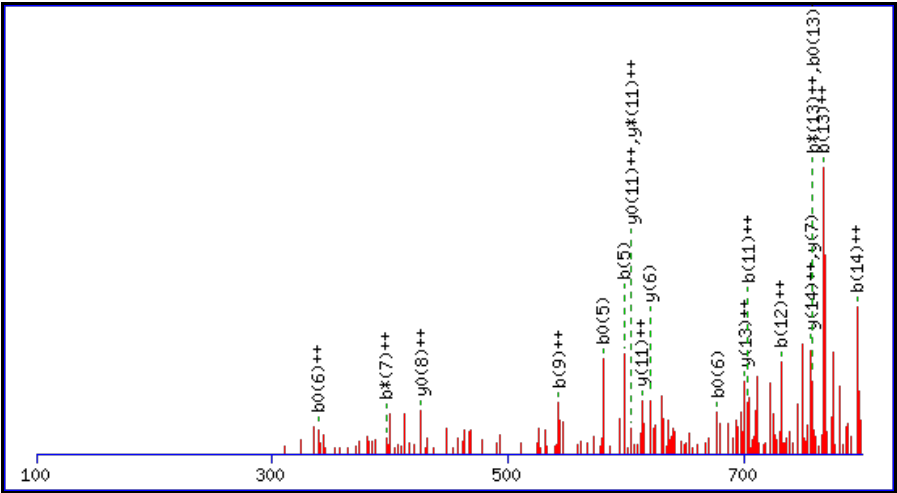
Score	Mr(calc):	Delta	Sequence
57.2	1379.6027	0.0069	FRPDMEEEEAK
19.9	1379.6213	-0.0118	CWEKIMPDSAK
9.6	1379.6061	0.0035	DGVMGMNSIEPAK
9.6	1379.5985	0.0111	MYTWEKPFAK
9.6	1379.5985	0.0111	MYTWEKPFAK
7.1	1379.6156	-0.0060	MTPGLSPSLPER
3.5	1379.5970	0.0126	EQEEAVPTIER
2.9	1379.6172	-0.0077	ITTEKMLLQK
2.8	1379.6194	-0.0098	RPSASSPNNTAAK
2.5	1379.6082	0.0014	AKSSSRFTDSK

Spectrum No: 121; Query: 74371; Rank: 1

Peptide View

MS/MS Fragmentation of **IHFISPNIYCCGAGTAADTDMTTQLISSNLELHSLSTGR**
Found in **IPI00003217**, Tax_Id=9606 Gene_Symbol=PSMB7 Proteasome subunit beta type-7

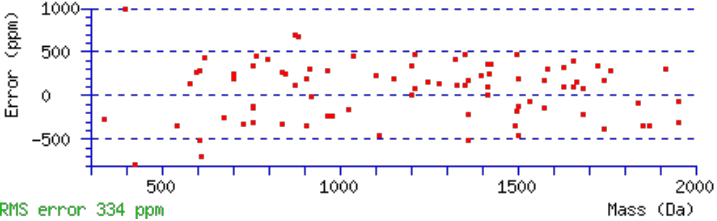
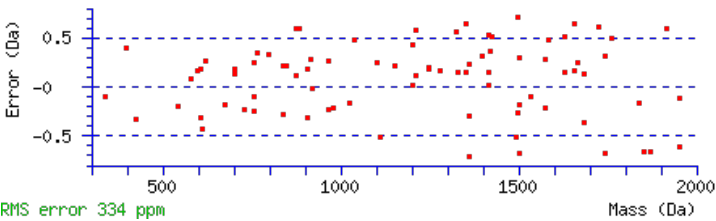
Match to Query 74371: 4252.036296 from(1064.016350,4+)
Title: 091224LimSK_Exosome3_06.7965.7965.4.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 4251.0035

Fixed modifications: Carbamidomethyl (C)
Ions Score: 48 Expect: 0.0038
Matches (**Bold Red**): 85/432 fragment ions using 151 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					I							39
2	251.1503	126.0788					H	4138.9267	2069.9670	4121.9001	2061.4537	4120.9161	2060.9617	38
3	398.2187	199.6130					F	4001.8678	2001.4375	3984.8412	1992.9243	3983.8572	1992.4322	37
4	511.3027	256.1550					I	3854.7994	1927.9033	3837.7728	1919.3900	3836.7888	1918.8980	36
5	598.3348	299.6710			580.3242	290.6657	S	3741.7153	1871.3613	3724.6888	1862.8480	3723.7047	1862.3560	35
6	695.3875	348.1974			677.3770	339.1921	P	3654.6833	1827.8453	3637.6567	1819.3320	3636.6727	1818.8400	34
7	809.4304	405.2189	792.4039	396.7056	791.4199	396.2136	N	3557.6305	1779.3189	3540.6040	1770.8056	3539.6199	1770.3136	33
8	922.5145	461.7609	905.4880	453.2476	904.5039	452.7556	I	3443.5876	1722.2974	3426.5610	1713.7842	3425.5770	1713.2921	32
9	1085.5778	543.2926	1068.5513	534.7793	1067.5673	534.2873	Y	3330.5035	1665.7554	3313.4770	1657.2421	3312.4930	1656.7501	31
10	1245.6085	623.3079	1228.5819	614.7946	1227.5979	614.3026	C	3167.4402	1584.2237	3150.4136	1575.7105	3149.4296	1575.2185	30
11	1405.6391	703.3232	1388.6126	694.8099	1387.6286	694.3179	C	3007.4095	1504.2084	2990.3830	1495.6951	2989.3990	1495.2031	29
12	1462.6606	731.8339	1445.6341	723.3207	1444.6500	722.8287	G	2847.3789	1424.1931	2830.3523	1415.6798	2829.3683	1415.1878	28
13	1533.6977	767.3525	1516.6712	758.8392	1515.6872	758.3472	A	2790.3574	1395.6824	2773.3309	1387.1691	2772.3469	1386.6771	27
14	1590.7192	795.8632	1573.6926	787.3500	1572.7086	786.8579	G	2719.3203	1360.1638	2702.2938	1351.6505	2701.3098	1351.1585	26
15	1691.7669	846.3871	1674.7403	837.8738	1673.7563	837.3818	T	2662.2989	1331.6531	2645.2723	1323.1398	2644.2883	1322.6478	25
16	1762.8040	881.9056	1745.7774	873.3924	1744.7934	872.9003	A	2561.2512	1281.1292	2544.2246	1272.6159	2543.2406	1272.1239	24
17	1833.8411	917.4242	1816.8145	908.9109	1815.8305	908.4189	A	2490.2141	1245.6107	2473.1875	1237.0974	2472.2035	1236.6054	23
18	1948.8680	974.9377	1931.8415	966.4244	1930.8575	965.9324	D	2419.1769	1210.0921	2402.1504	1201.5788	2401.1664	1201.0868	22
19	2049.9157	1025.4615	2032.8892	1016.9482	2031.9051	1016.4562	T	2304.1500	1152.5786	2287.1235	1144.0654	2286.1394	1143.5734	21
20	2164.9427	1082.9750	2147.9161	1074.4617	2146.9321	1073.9697	D	2203.1023	1102.0548	2186.0758	1093.5415	2185.0918	1093.0495	20
21	2295.9831	1148.4952	2278.9566	1139.9819	2277.9726	1139.4899	M	2088.0754	1044.5413	2071.0488	1036.0281	2070.0648	1035.5360	19
22	2397.0308	1199.0190	2380.0043	1190.5058	2379.0203	1190.0138	T	1957.0349	979.0211	1940.0083	970.5078	1939.0243	970.0158	18
23	2498.0785	1249.5429	2481.0519	1241.0296	2480.0679	1240.5376	T	1855.9872	928.4972	1838.9607	919.9840	1837.9767	919.4920	17
24	2626.1371	1313.5722	2609.1105	1305.0589	2608.1265	1304.5669	Q	1754.9395	877.9734	1737.9130	869.4601	1736.9290	868.9681	16
25	2739.2211	1370.1142	2722.1946	1361.6009	2721.2106	1361.1089	L	1626.8810	813.9441	1609.8544	805.4308	1608.8704	804.9388	15
26	2852.3052	1426.6562	2835.2787	1418.1430	2834.2946	1417.6510	I	1513.7969	757.4021	1496.7703	748.8888	1495.7863	748.3968	14
27	2939.3372	1470.1723	2922.3107	1461.6590	2921.3267	1461.1670	S	1400.7128	700.8601	1383.6863	692.3468	1382.7023	691.8548	13
28	3026.3693	1513.6883	3009.3427	1505.1750	3008.3587	1504.6830	S	1313.6808	657.3440	1296.6543	648.8308	1295.6702	648.3388	12
29	3140.4122	1570.7097	3123.3856	1562.1965	3122.4016	1561.7044	N	1226.6488	613.8280	1209.6222	605.3148	1208.6382	604.8227	11
30	3253.4962	1627.2518	3236.4697	1618.7385	3235.4857	1618.2465	L	1112.6058	556.8066	1095.5793	548.2933	1094.5953	547.8013	10
31	3382.5388	1691.7731	3365.5123	1683.2598	3364.5283	1682.7678	E	999.5218	500.2645	982.4952	491.7513	981.5112	491.2592	9
32	3495.6229	1748.3151	3478.5964	1739.8018	3477.6123	1739.3098	L	870.4792	435.7432	853.4526	427.2300	852.4686	426.7380	8
33	3632.6818	1816.8445	3615.6553	1808.3313	3614.6713	1807.8393	H	757.3951	379.2012	740.3686	370.6879	739.3846	370.1959	7
34	3719.7138	1860.3606	3702.6873	1851.8473	3701.7033	1851.3553	S	620.3362	310.6717	603.3097	302.1585	602.3257	301.6665	6
35	3832.7979	1916.9026	3815.7714	1908.3893	3814.7873	1907.8973	L	533.3042	267.1557	516.2776	258.6425	515.2936	258.1504	5
36	3919.8299	1960.4186	3902.8034	1951.9053	3901.8194	1951.4133	S	420.2201	210.6137	403.1936	202.1004	402.2096	201.6084	4
37	4020.8776	2010.9424	4003.8511	2002.4292	4002.8671	2001.9372	T	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
38	4077.8991	2039.4532	4060.8725	2030.9399	4059.8885	2030.4479	G	232.1404	116.5738	215.1139	108.0606			2
39							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

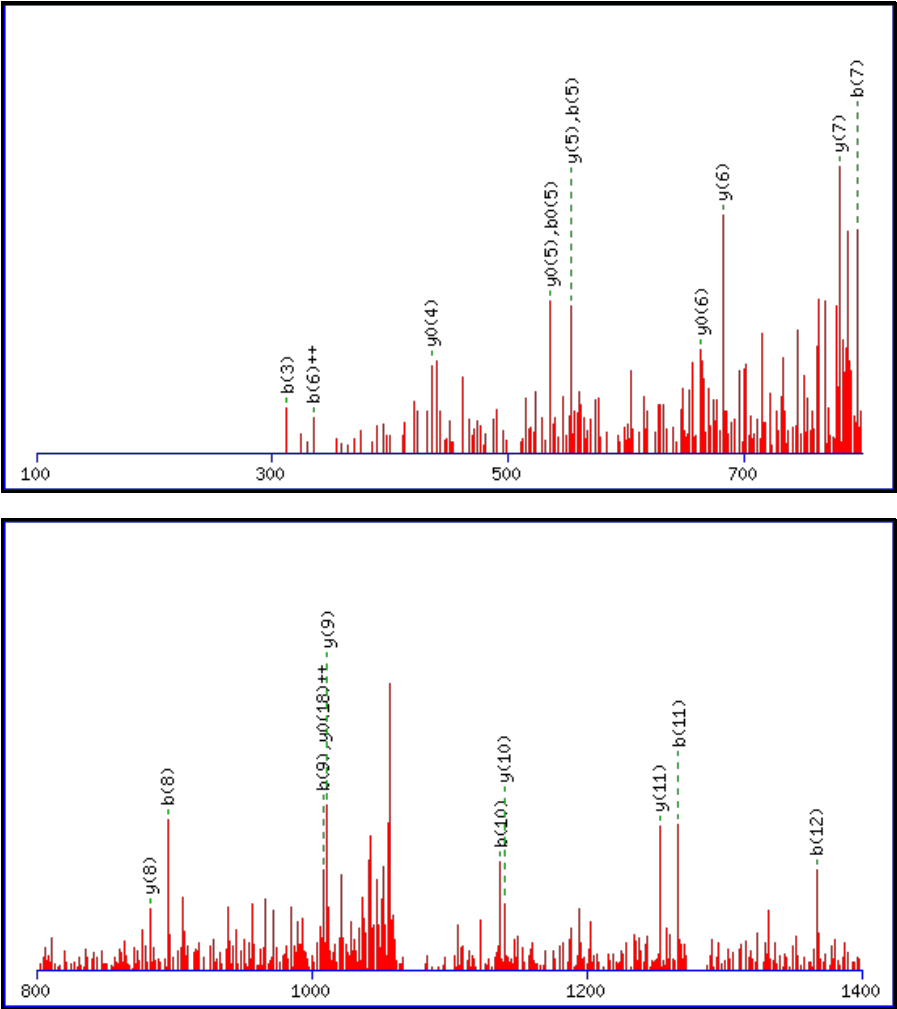
Score	Mr(calc):	Delta	Sequence
48.5	4251.0035	1.0328	IHFISPNIYCCGAGTAADTDMTTQLISSNLELHSLSTGR
10.7	4252.0055	0.0308	GTIAVGLVPQYYSLDHQPGWLPDSVAYHADDGKLYNGR
9.4	4250.0357	2.0006	GWLSAIGFFQYSPGAADVVMLLPAIMFSVSAAMMAIAIMK
9.4	4250.0357	2.0006	GWLSAIGFFQYSPGAADVVMLLPAIMFSVSAAMMAIAIMK
8.1	4252.0055	0.0308	GTIAVGLVPQYYSLDHQPGWLPDSVAYHADDGKLYNGR
7.5	4250.9975	1.0388	GPSHDGVAEFHMSLTVSCPDPTSTDPQGRHNREPILGR
7.2	4252.0518	-0.0155	LRELSTLAHCSRELQTQVPDASAHS LAVTLSELHSCR
7.2	4252.0518	-0.0155	LRELSTLAHCSRELQTQVPDASAHS LAVTLSELHSCR
7.2	4252.0007	0.0356	QITNFQLSIENLDQSLAHYGRPKIDGELKITSVER
7.1	4251.0128	1.0235	MPHPQLFSGESVVSWSDLNIIISVPWYLG LMFRT R

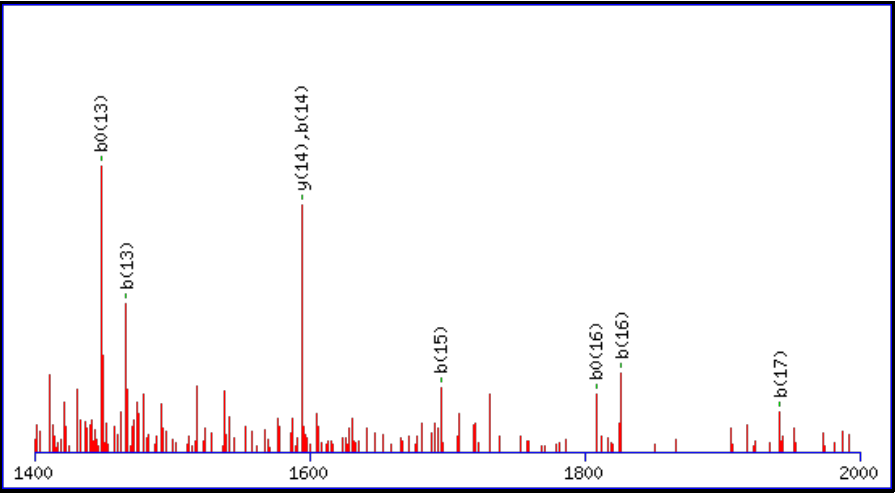
Spectrum No: 122; Query: 45016; Rank: 1

Peptide View

MS/MS Fragmentation of **ITPLEIEVLEETVQTMDTS**
Found in **IPI00003217**, Tax_Id=9606 Gene_Symbol=PSMB7 Proteasome subunit beta type-7

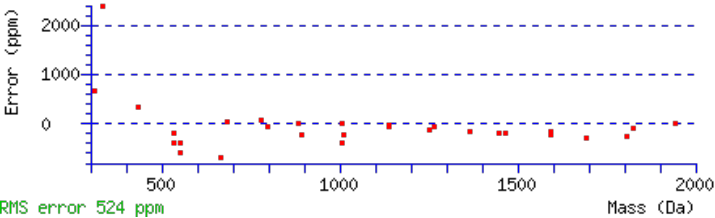
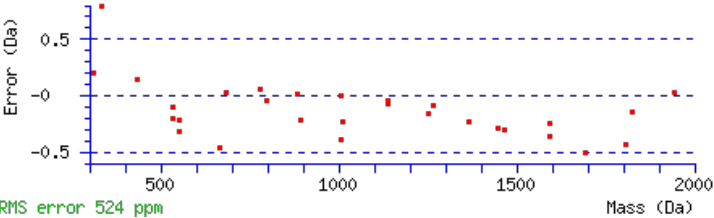
Match to Query 45016: 2147.069128 from(1074.541840,2+)
Title: 091224LimSK_Exosome3_07.9078.9078.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2147.0555
Fixed modifications: Carbamidomethyl (C)
Ions Score: 100 Expect: 2.4e-008
Matches (Bold Red): 29/178 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	114.0913	57.5493					I							19
2	215.1390	108.0731			197.1285	99.0679	T	2034.9787	1017.9930	2017.9522	1009.4797	2016.9682	1008.9877	18
3	312.1918	156.5995			294.1812	147.5942	P	1933.9311	967.4692	1916.9045	958.9559	1915.9205	958.4639	17
4	425.2758	213.1416			407.2653	204.1363	L	1836.8783	918.9428	1819.8518	910.4295	1818.8677	909.9375	16
5	554.3184	277.6629			536.3079	268.6576	E	1723.7942	862.4008	1706.7677	853.8875	1705.7837	853.3955	15
6	667.4025	334.2049			649.3919	325.1996	I	1594.7516	797.8795	1577.7251	789.3662	1576.7411	788.8742	14
7	796.4451	398.7262			778.4345	389.7209	E	1481.6676	741.3374	1464.6410	732.8242	1463.6570	732.3321	13
8	895.5135	448.2604			877.5029	439.2551	V	1352.6250	676.8161	1335.5984	668.3029	1334.6144	667.8109	12
9	1008.5976	504.8024			990.5870	495.7971	L	1253.5566	627.2819	1236.5300	618.7687	1235.5460	618.2766	11
10	1137.6402	569.3237			1119.6296	560.3184	E	1140.4725	570.7399	1123.4460	562.2266	1122.4619	561.7346	10
11	1266.6828	633.8450			1248.6722	624.8397	E	1011.4299	506.2186	994.4034	497.7053	993.4194	497.2133	9
12	1367.7304	684.3689			1349.7199	675.3636	T	882.3873	441.6973	865.3608	433.1840	864.3768	432.6920	8
13	1466.7989	733.9031			1448.7883	724.8978	V	781.3396	391.1735	764.3131	382.6602	763.3291	382.1682	7
14	1594.8574	797.9324	1577.8309	789.4191	1576.8469	788.9271	Q	682.2712	341.6393	665.2447	333.1260	664.2607	332.6340	6
15	1695.9051	848.4562	1678.8786	839.9429	1677.8945	839.4509	T	554.2127	277.6100			536.2021	268.6047	5
16	1826.9456	913.9764	1809.9190	905.4632	1808.9350	904.9712	M	453.1650	227.0861			435.1544	218.0808	4
17	1941.9725	971.4899	1924.9460	962.9766	1923.9620	962.4846	D	322.1245	161.5659			304.1139	152.5606	3
18	2043.0202	1022.0137	2025.9937	1013.5005	2025.0097	1013.0085	T	207.0975	104.0524			189.0870	95.0471	2
19							S	106.0499	53.5286			88.0393	44.5233	1



All matches to this query

Score	Mr(calc):	Delta	Sequence
99.9	2147.0555	0.0136	ITPLEIEVLEETVQTMDS
9.7	2147.0872	-0.0181	DSHLTQHTRIHTGEKPYK
6.5	2146.0558	1.0133	LKLTEDTSEKAGFASTLOK

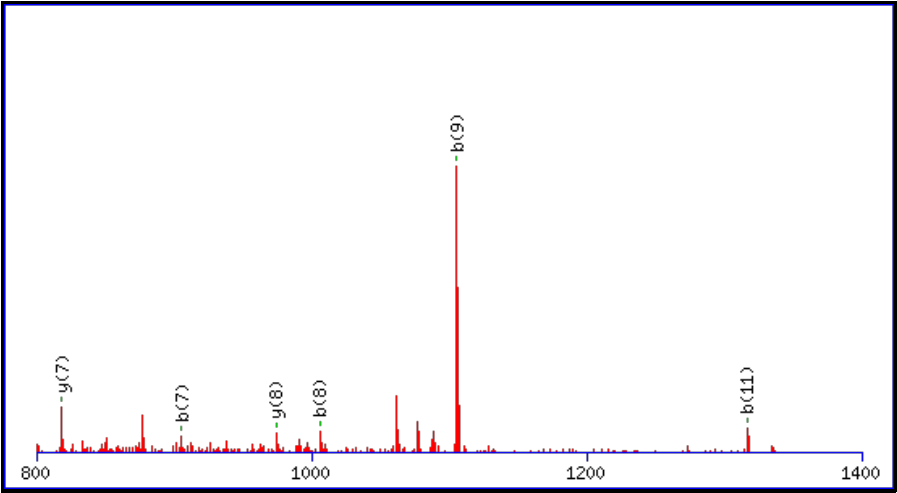
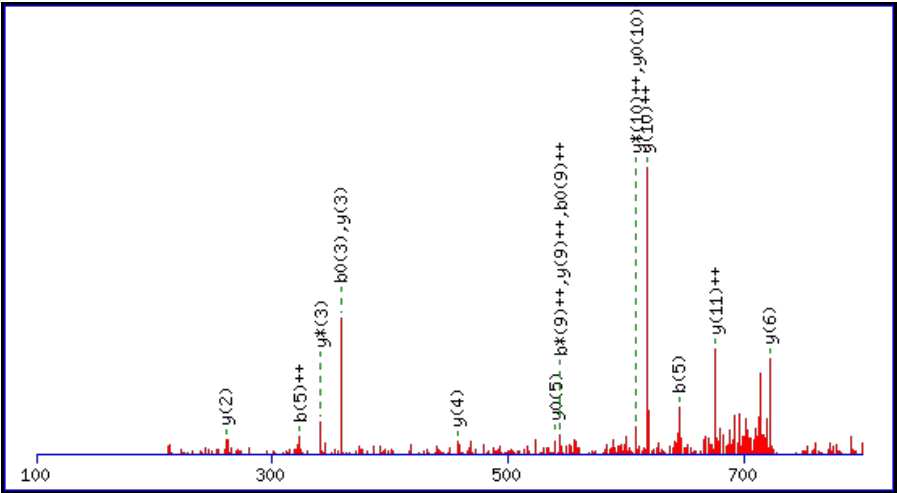
5.6	2146.0558	1.0133	LKLTEDTSEKAGFASTLOK
4.0	2146.0534	1.0158	MPTSGLIPLQAFLDADIHK
3.7	2146.0534	1.0158	MPTSGLIPLQAFLDADIHK
3.5	2147.0881	-0.0189	LAGPPSCIVPLMRQYRHH
2.8	2146.0493	1.0198	LEAKGTGGTDLMNFLKTVR
2.7	2145.0483	2.0208	LEIDINKITVKTNESIR
0.2	2145.0507	2.0184	QALKLQIEGSDPSFNYKK

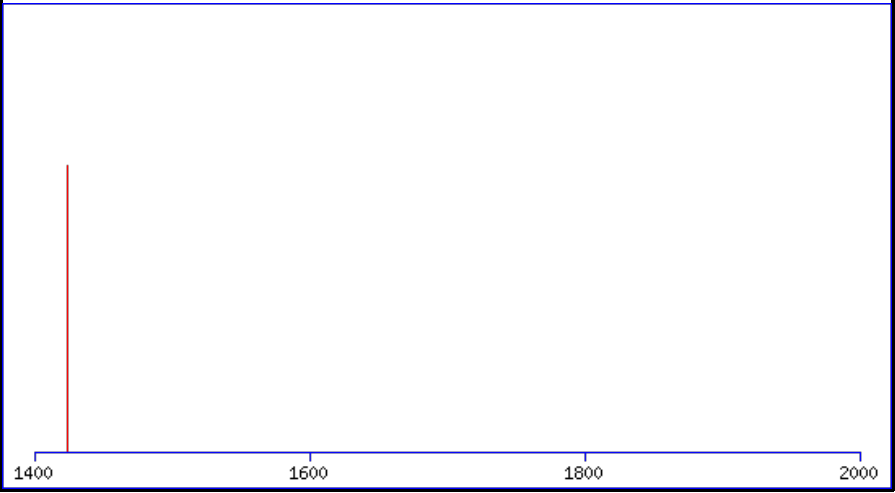
Spectrum No: 123; Query: 18591; Rank: 1

Peptide View

MS/MS Fragmentation of **LDFLRPYTVPNK**
Found in **IPI00003217**, Tax_Id=9606 Gene_Symbol=PSMB7 Proteasome subunit beta type-7

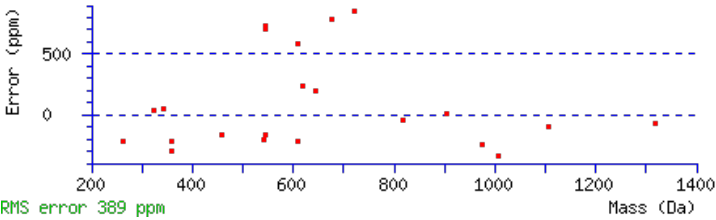
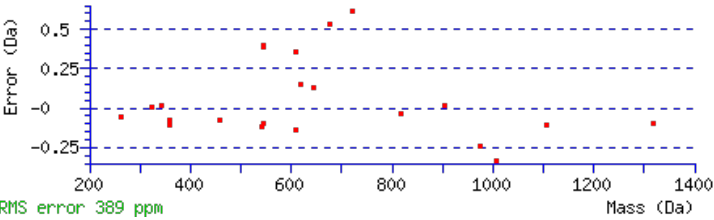
Match to Query 18591: 1461.807388 from(731.910970,2+)
Title: 091224LimSK_Exosome3_06.4674.4674.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1461.7980
Fixed modifications: Carbamidomethyl (C)
Ions Score: 33 **Expect:** 0.045
Matches (Bold Red): 22/114 fragment ions using 44 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							12
2	229.1183	115.0628			211.1077	106.0575	D	1349.7212	675.3642	1332.6947	666.8510	1331.7106	666.3590	11
3	376.1867	188.5970			358.1761	179.5917	F	1234.6943	617.8508	1217.6677	609.3375	1216.6837	608.8455	10
4	489.2708	245.1390			471.2602	236.1337	L	1087.6259	544.3166	1070.5993	535.8033	1069.6153	535.3113	9
5	645.3719	323.1896	628.3453	314.6763	627.3613	314.1843	R	974.5418	487.7745	957.5152	479.2613	956.5312	478.7693	8
6	742.4246	371.7160	725.3981	363.2027	724.4141	362.7107	P	818.4407	409.7240	801.4141	401.2107	800.4301	400.7187	7
7	905.4880	453.2476	888.4614	444.7343	887.4774	444.2423	Y	721.3879	361.1976	704.3614	352.6843	703.3774	352.1923	6
8	1006.5356	503.7715	989.5091	495.2582	988.5251	494.7662	T	558.3246	279.6659	541.2980	271.1527	540.3140	270.6606	5
9	1105.6041	553.3057	1088.5775	544.7924	1087.5935	544.3004	V	457.2769	229.1421	440.2504	220.6288			4
10	1202.6568	601.8320	1185.6303	593.3188	1184.6463	592.8268	P	358.2085	179.6079	341.1819	171.0946			3
11	1316.6997	658.8535	1299.6732	650.3402	1298.6892	649.8482	N	261.1557	131.0815	244.1292	122.5682			2
12							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

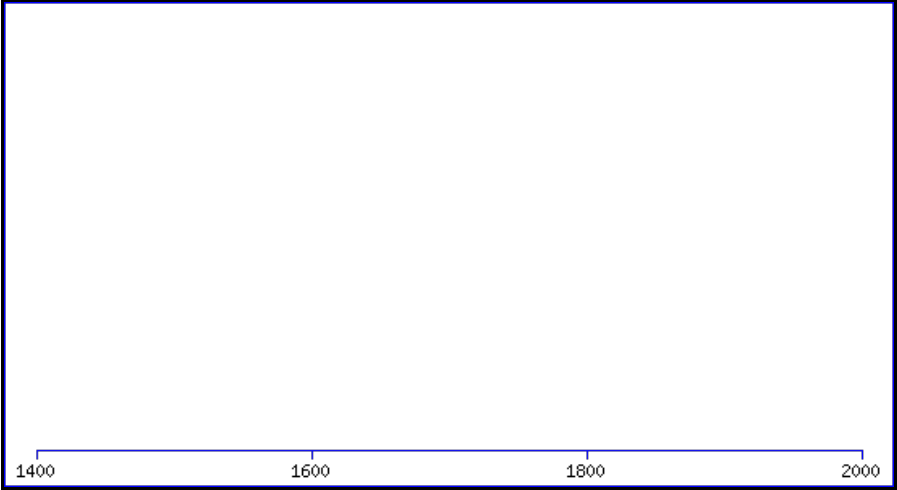
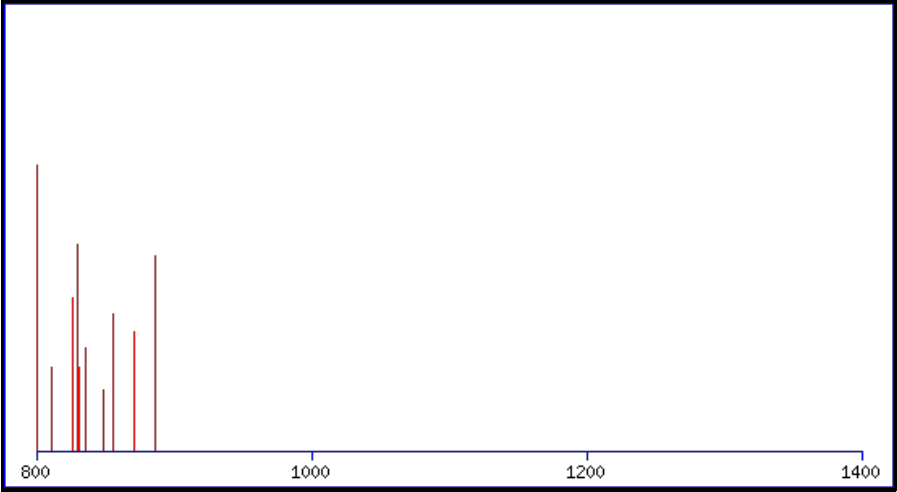
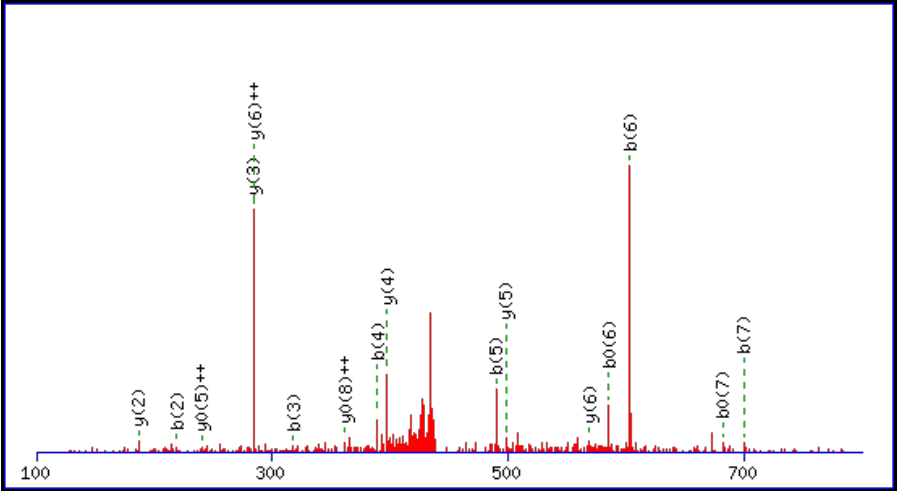
Score	Mr(calc):	Delta	Sequence
33.0	1461.7980	0.0094	LDFLRPYTVPNK
13.9	1460.8004	1.0070	ELDVVLRTVIPK
8.9	1461.7948	0.0126	MLLCYRHLKTK
7.3	1459.8109	1.9965	FLPVMTEILLER
5.8	1461.7969	0.0105	RAALLVPPRYAR
5.3	1461.7956	0.0118	INGALNITLNLVK
4.4	1461.7939	0.0135	ARIGQYEQLEK
1.2	1461.7940	0.0134	QGTGLOGQAVFKTK

Spectrum No: 124; Query: 1096; Rank: 1

Peptide View

MS/MS Fragmentation of **FAVATLPPA**
Found in **IPI00000811**, Tax_Id=9606 Gene_Symbol=PSMB6 Proteasome subunit beta type-6

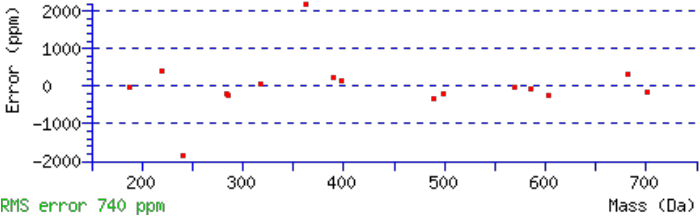
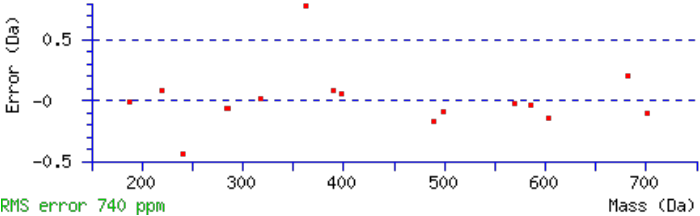
Match to Query 1096: 885.501608 from(443.758080,2+)
Title: 091224LimSK_Exosome3_06.3912.3912.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 885.4960
Fixed modifications: Carbamidomethyl (C)
Ions Score: 20 Expect: 0.66

Matches (Bold Red): 16/48 fragment ions using 70 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	148.0757	74.5415			F					9
2	219.1128	110.0600			A	739.4349	370.2211	721.4243	361.2158	8
3	318.1812	159.5942			V	668.3978	334.7025	650.3872	325.6972	7
4	389.2183	195.1128			A	569.3293	285.1683	551.3188	276.1630	6
5	490.2660	245.6366	472.2554	236.6314	T	498.2922	249.6498	480.2817	240.6445	5
6	603.3501	302.1787	585.3395	293.1734	L	397.2445	199.1259			4
7	700.4028	350.7051	682.3923	341.6998	P	284.1605	142.5839			3
8	797.4556	399.2314	779.4450	390.2262	P	187.1077	94.0575			2
9					A	90.0550	45.5311			1



All matches to this query

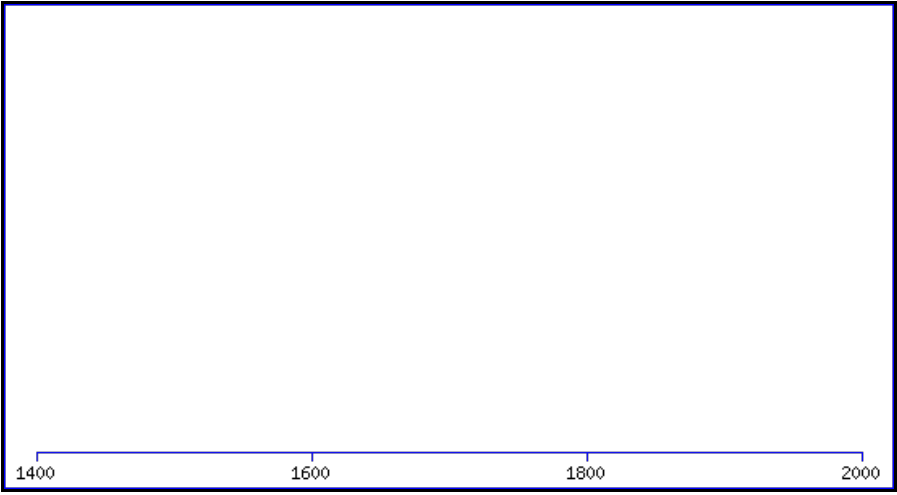
Score	Mr(calc):	Delta	Sequence
20.3	885.4960	0.0056	FAVATLPPA
10.0	883.5015	2.0001	LADPEVLK
4.5	885.5032	-0.0016	AAAAAAAKNK
4.3	883.5015	2.0001	ILEDGLPK
4.2	885.5032	-0.0016	GRALGAVDK
4.2	883.4949	2.0067	MLNLHK
2.6	885.5032	-0.0016	GLIKNGER
2.4	883.5015	2.0001	LLGPDLEK
2.3	884.4967	1.0049	XTPIGEIK
2.0	883.5015	2.0001	LVIDEPAK

Spectrum No: 125; Query: 5201; Rank: 1

Peptide View

MS/MS Fragmentation of **LAAIAESGVER**
Found in **IP100000811**, Tax_Id=9606 Gene_Symbol=PSMB6 Proteasome subunit beta type-6

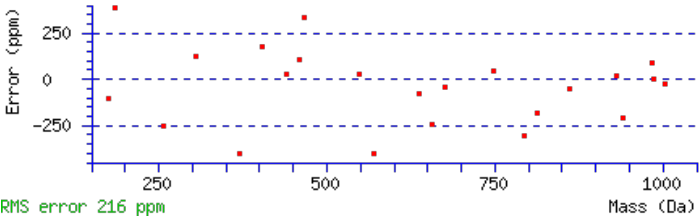
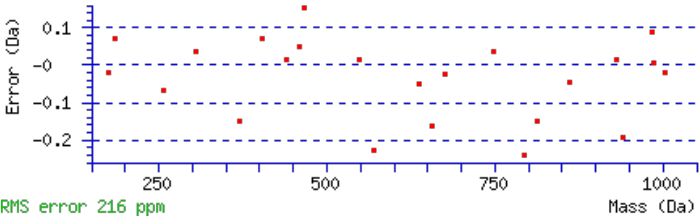
Match to Query 5201: 1114.601488 from(558.308020,2+)
Title: 091224LimSK_Exosome3_07.1136.1136.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1114.5982
 Fixed modifications: Carbamidomethyl (C)
 Ions Score: 80 Expect: 1.2e-006
 Matches (Bold Red): 24/88 fragment ions using 42 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y*	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	114.0913	57.5493			L							11
2	185.1285	93.0679			A	1002.5215	501.7644	985.4949	493.2511	984.5109	492.7591	10
3	256.1656	128.5864			A	931.4843	466.2458	914.4578	457.7325	913.4738	457.2405	9
4	369.2496	185.1285			I	860.4472	430.7272	843.4207	422.2140	842.4367	421.7220	8
5	440.2867	220.6470			A	747.3632	374.1852	730.3366	365.6719	729.3526	365.1799	7
6	569.3293	285.1683	551.3188	276.1630	E	676.3260	338.6667	659.2995	330.1534	658.3155	329.6614	6

7	656.3614	328.6843	638.3508	319.6790	S	547.2835	274.1454	530.2569	265.6321	529.2729	265.1401	5
8	713.3828	357.1951	695.3723	348.1898	G	460.2514	230.6293	443.2249	222.1161	442.2409	221.6241	4
9	812.4512	406.7293	794.4407	397.7240	V	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
10	941.4938	471.2506	923.4833	462.2453	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
11					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

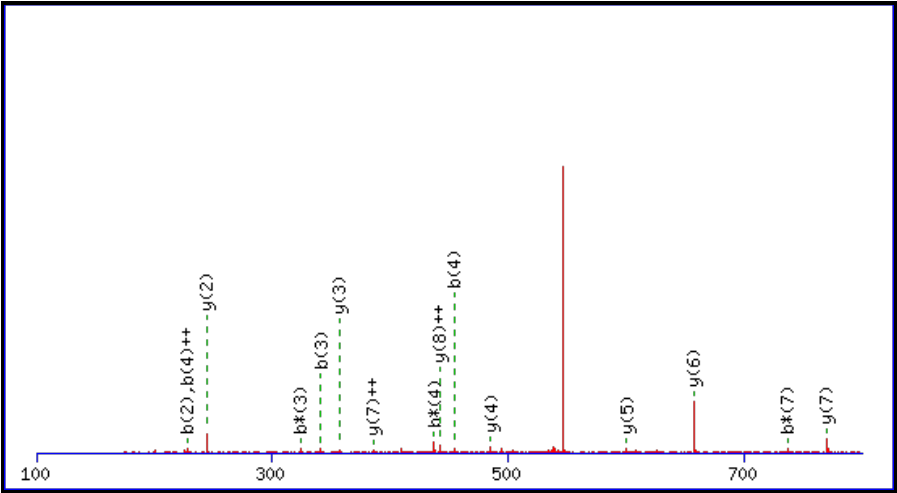
Score	Mr(calc):	Delta	Sequence
80.0	1114.5982	0.0033	LAAIAESGVER
7.7	1114.6095	-0.0080	LAPSSDLRTR
5.1	1114.6094	-0.0079	ALDEKVRER
4.3	1114.5982	0.0033	LAKQEELER
2.0	1112.5979	2.0036	TKAHVSSVVW
1.9	1114.5982	0.0033	TQEPSLGKQK
1.8	1114.6094	-0.0079	LDINLERSR
1.4	1114.5982	0.0033	ISTGPLGLDSR
0.6	1112.5938	2.0077	EARISPLGDR
0.6	1114.5957	0.0058	KMSIWTPPR

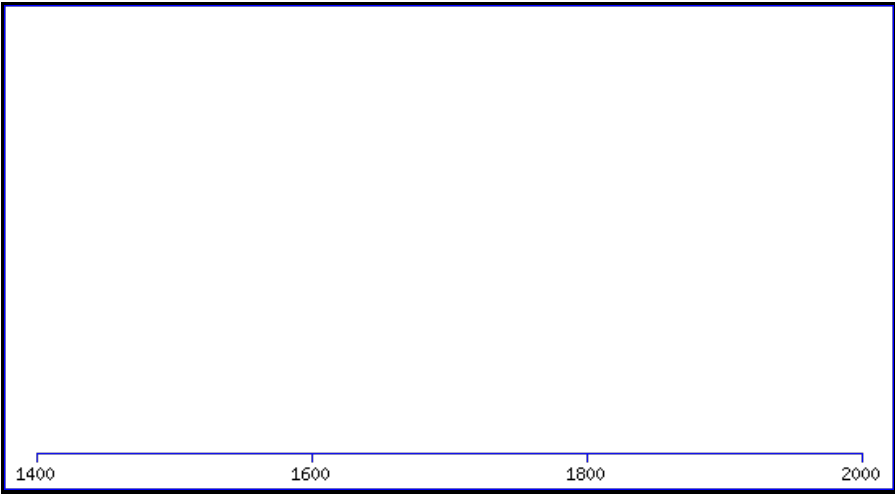
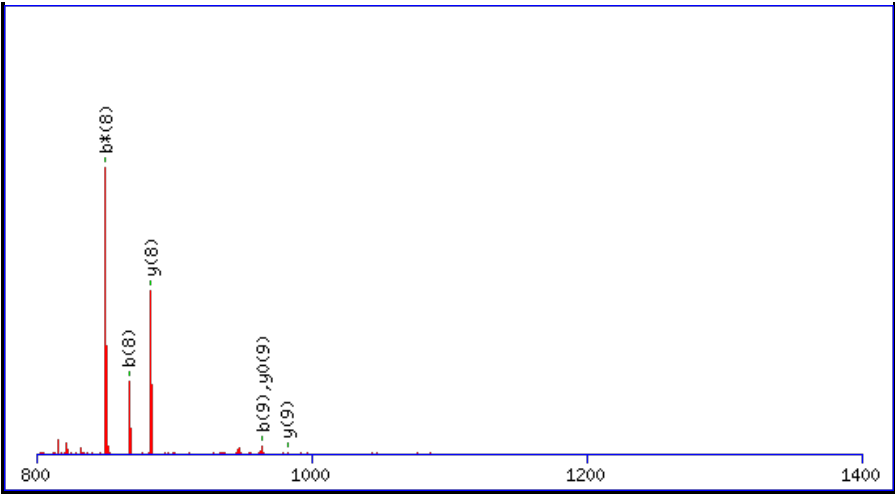
Spectrum No: 126; Query: 5045; Rank: 1

Peptide View

MS/MS Fragmentation of **QVLLGDQIPK**
Found in **IP100000811**, Tax_Id=9606 Gene_Symbol=PSMB6 Proteasome subunit beta type-6

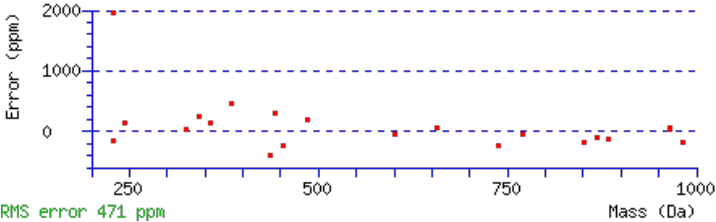
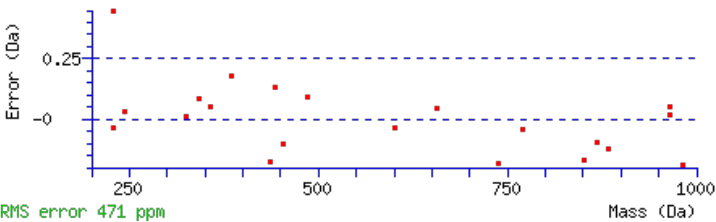
Match to Query 5045: 1109.649448 from(555.832000,2+)
Title: 091224LimSK_Exosome3_06.2638.2638.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1109.6445
Fixed modifications: Carbamidomethyl (C)
Ions Score: 65 Expect: 1.5e-005
Matches (Bold Red): 21/90 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	129.0659	65.0366	112.0393	56.5233			Q							10
2	228.1343	114.5708	211.1077	106.0575			V	982.5932	491.8002	965.5666	483.2869	964.5826	482.7949	9
3	341.2183	171.1128	324.1918	162.5995			L	883.5247	442.2660	866.4982	433.7527	865.5142	433.2607	8
4	454.3024	227.6548	437.2758	219.1416			L	770.4407	385.7240	753.4141	377.2107	752.4301	376.7187	7
5	511.3239	256.1656	494.2973	247.6523			G	657.3566	329.1819	640.3301	320.6687	639.3461	320.1767	6
6	626.3508	313.6790	609.3243	305.1658	608.3402	304.6738	D	600.3352	300.6712	583.3086	292.1579	582.3246	291.6659	5
7	754.4094	377.7083	737.3828	369.1951	736.3988	368.7030	Q	485.3082	243.1577	468.2817	234.6445			4
8	867.4934	434.2504	850.4669	425.7371	849.4829	425.2451	I	357.2496	179.1285	340.2231	170.6152			3
9	964.5462	482.7767	947.5197	474.2635	946.5356	473.7715	P	244.1656	122.5864	227.1390	114.0731			2
10							K	147.1128	74.0600	130.0863	65.5468			1

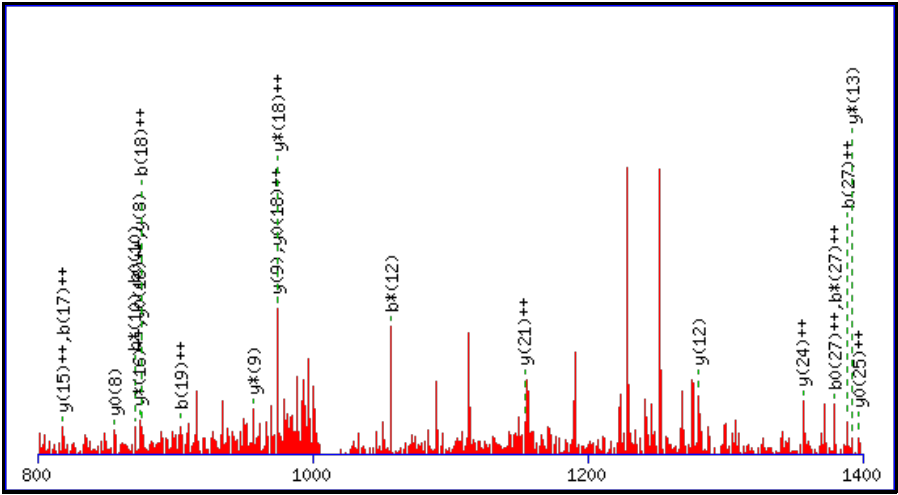
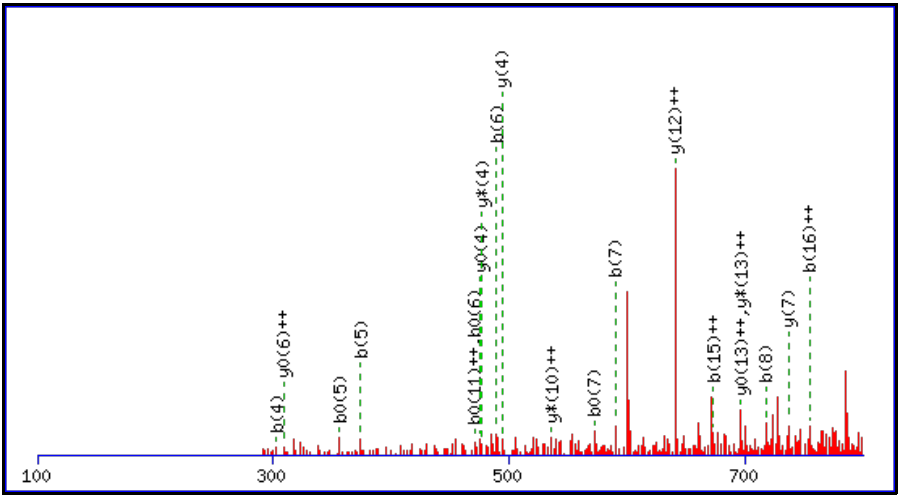


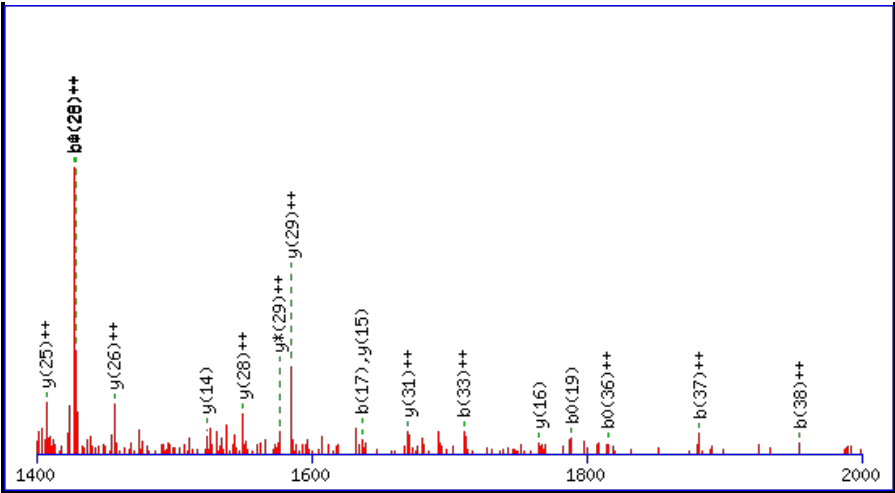
All matches to this query



Peptide View

Match to Query 74020: 4055.063336 from(1014.773110,4+)
Title: 091224LimSK_Exosome3_06.9066.9066.4.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf

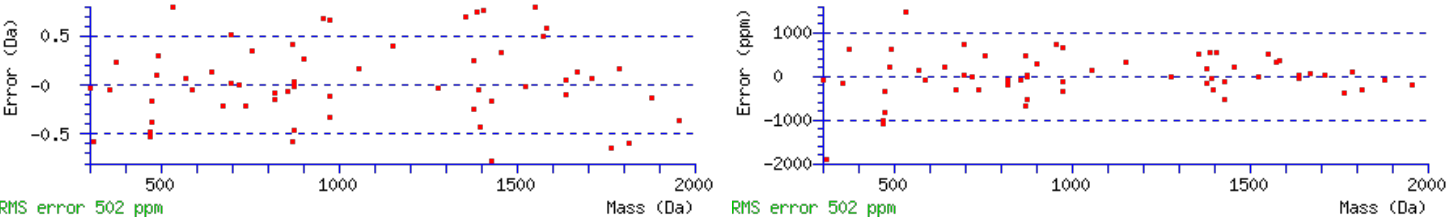




Monoisotopic mass of neutral peptide Mr(calc): 4055.0276
Fixed modifications: Carbamidomethyl (C)
Ions Score: 23 Expect: 0.62
Matches (**Bold Red**): 60/436 fragment ions using 145 most intense peaks

#	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							39
2	145.0608	73.0340			127.0502	64.0287	G	3969.0029	1985.0051	3951.9763	1976.4918	3950.9923	1975.9998	38
3	232.0928	116.5500			214.0822	107.5448	S	3911.9814	1956.4943	3894.9549	1947.9811	3893.9708	1947.4891	37
4	303.1299	152.0686			285.1193	143.0633	A	3824.9494	1912.9783	3807.9228	1904.4651	3806.9388	1903.9730	36
5	374.1670	187.5872			356.1565	178.5819	A	3753.9123	1877.4598	3736.8857	1868.9465	3735.9017	1868.4545	35
6	489.1940	245.1006			471.1834	236.0953	D	3682.8752	1841.9412	3665.8486	1833.4279	3664.8646	1832.9359	34
7	590.2416	295.6245			572.2311	286.6192	T	3567.8482	1784.4277	3550.8217	1775.9145	3549.8376	1775.4225	33
8	718.3002	359.6538	701.2737	351.1405	700.2897	350.6485	Q	3466.8005	1733.9039	3449.7740	1725.3906	3448.7900	1724.8986	32
9	789.3373	395.1723	772.3108	386.6590	771.3268	386.1670	A	3338.7420	1669.8746	3321.7154	1661.3613	3320.7314	1660.8693	31
10	888.4058	444.7065	871.3792	436.1932	870.3952	435.7012	V	3267.7048	1634.3561	3250.6783	1625.8428	3249.6943	1625.3508	30
11	959.4429	480.2251	942.4163	471.7118	941.4323	471.2198	A	3168.6364	1584.8219	3151.6099	1576.3086	3150.6259	1575.8166	29
12	1074.4698	537.7385	1057.4433	529.2253	1056.4592	528.7333	D	3097.5993	1549.3033	3080.5728	1540.7900	3079.5887	1540.2980	28
13	1145.5069	573.2571	1128.4804	564.7438	1127.4964	564.2518	A	2982.5724	1491.7898	2965.5458	1483.2765	2964.5618	1482.7845	27
14	1244.5753	622.7913	1227.5488	614.2780	1226.5648	613.7860	V	2911.5353	1456.2713	2894.5087	1447.7580	2893.5247	1447.2660	26
15	1345.6230	673.3151	1328.5965	664.8019	1327.6125	664.3099	T	2812.4668	1406.7371	2795.4403	1398.2238	2794.4563	1397.7318	25
16	1508.6863	754.8468	1491.6598	746.3335	1490.6758	745.8415	Y	2711.4192	1356.2132	2694.3926	1347.6999	2693.4086	1347.2079	24
17	1636.7449	818.8761	1619.7184	810.3628	1618.7344	809.8708	Q	2548.3558	1274.6816	2531.3293	1266.1683	2530.3453	1265.6763	23
18	1749.8290	875.4181	1732.8024	866.9049	1731.8184	866.4128	L	2420.2973	1210.6523	2403.2707	1202.1390	2402.2867	1201.6470	22
19	1806.8505	903.9289	1789.8239	895.4156	1788.8399	894.9236	G	2307.2132	1154.1102	2290.1866	1145.5970	2289.2026	1145.1050	21
20	1953.9189	977.4631	1936.8923	968.9498	1935.9083	968.4578	F	2250.1917	1125.5995	2233.1652	1117.0862	2232.1812	1116.5942	20
21	2090.9778	1045.9925	2073.9512	1037.4793	2072.9672	1036.9872	H	2103.1233	1052.0653	2086.0968	1043.5520	2085.1128	1043.0600	19
22	2178.0098	1089.5085	2160.9833	1080.9953	2159.9992	1080.5033	S	1966.0644	983.5358	1949.0379	975.0226	1948.0538	974.5306	18
23	2291.0939	1146.0506	2274.0673	1137.5373	2273.0833	1137.0453	I	1879.0324	940.0198	1862.0058	931.5066	1861.0218	931.0145	17
24	2420.1365	1210.5719	2403.1099	1202.0586	2402.1259	1201.5666	E	1765.9483	883.4778	1748.9218	874.9645	1747.9377	874.4725	16
25	2533.2205	1267.1139	2516.1940	1258.6006	2515.2100	1258.1086	L	1636.9057	818.9565	1619.8792	810.4432	1618.8952	809.9512	15
26	2647.2635	1324.1354	2630.2369	1315.6221	2629.2529	1315.1301	N	1523.8217	762.4145	1506.7951	753.9012	1505.8111	753.4092	14
27	2776.3060	1388.6567	2759.2795	1380.1434	2758.2955	1379.6514	E	1409.7787	705.3930	1392.7522	696.8797	1391.7682	696.3877	13
28	2873.3588	1437.1830	2856.3323	1428.6698	2855.3482	1428.1778	P	1280.7361	640.8717	1263.7096	632.3584	1262.7256	631.8664	12
29	2970.4116	1485.7094	2953.3850	1477.1962	2952.4010	1476.7041	P	1183.6834	592.3453	1166.6568	583.8320	1165.6728	583.3400	11
30	3083.4956	1542.2515	3066.4691	1533.7382	3065.4851	1533.2462	L	1086.6306	543.8189	1069.6041	535.3057	1068.6200	534.8137	10
31	3182.5641	1591.7857	3165.5375	1583.2724	3164.5535	1582.7804	V	973.5465	487.2769	956.5200	478.7636	955.5360	478.2716	9
32	3319.6230	1660.3151	3302.5964	1651.8018	3301.6124	1651.3098	H	874.4781	437.7427	857.4516	429.2294	856.4676	428.7374	8
33	3420.6706	1710.8390	3403.6441	1702.3257	3402.6601	1701.8337	T	737.4192	369.2132	720.3927	360.7000	719.4087	360.2080	7

34	3491.7078	1746.3575	3474.6812	1737.8442	3473.6972	1737.3522	A	636.3715	318.6894	619.3450	310.1761	618.3610	309.6841	6
35	3562.7449	1781.8761	3545.7183	1773.3628	3544.7343	1772.8708	A	565.3344	283.1709	548.3079	274.6576	547.3239	274.1656	5
36	3649.7769	1825.3921	3632.7504	1816.8788	3631.7663	1816.3868	S	494.2973	247.6523	477.2708	239.1390	476.2867	238.6470	4
37	3762.8610	1881.9341	3745.8344	1873.4208	3744.8504	1872.9288	L	407.2653	204.1363	390.2387	195.6230			3
38	3909.9294	1955.4683	3892.9028	1946.9551	3891.9188	1946.4630	F	294.1812	147.5942	277.1547	139.0810			2
39							K	147.1128	74.0600	130.0863	65.5468			1



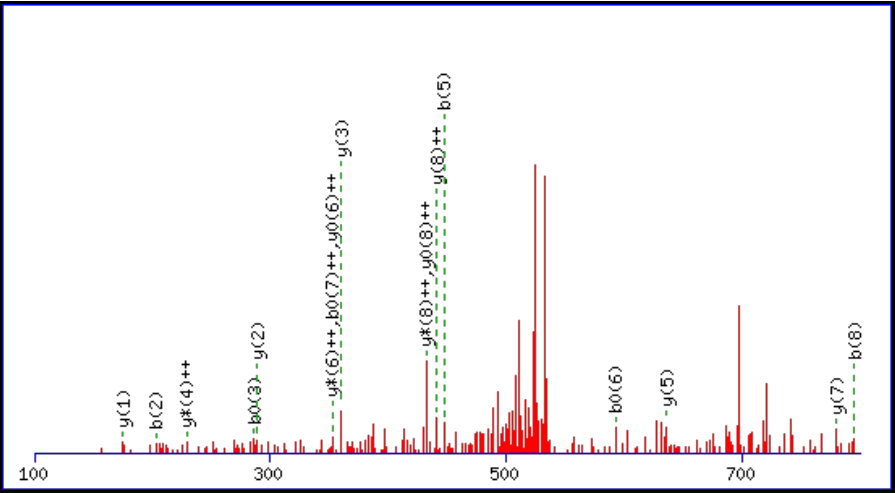
All matches to this query

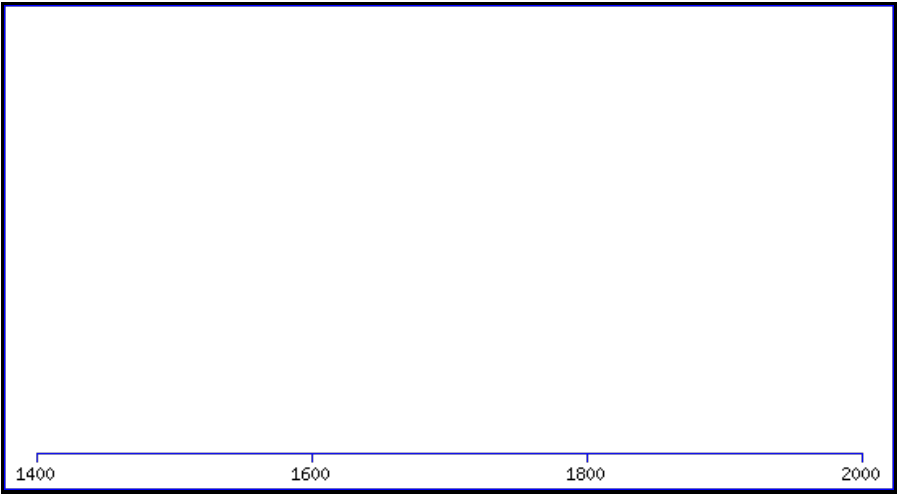
Score	Mr(calc):	Delta	Sequence
22.9	4055.0276	0.0357	SGSAADTQAVADAVTYQLGFHSIELNEPPLVHTAASLFK
11.9	4053.0322	2.0311	MAERGYSESLTTFESPSGKLVQIEYALA AAVAGGAPSVGIK
7.9	4055.0379	0.0254	LSIFIYEVVTL SLSLQIAQSGVLWFLSHSPARK
6.3	4053.0322	2.0311	MAERGYSESLTTFESPSGKLVQIEYALA AAVAGGAPSVGIK
5.5	4054.0947	0.9687	APMELLIGSLALADLLAGIGLITNFVFAYLLQSEATK
5.5	4053.0728	1.9905	GFTIVDVQRVLESINVQMDENTLHEILNEVDLNK
5.3	4054.0947	0.9687	APMELLIGSLALADLLAGIGLITNFVFAYLLQSEATK
5.2	4053.0322	2.0311	MAERGYSESLTTFESPSGKLVQIEYALA AAVAGGAPSVGIK
5.2	4053.0322	2.0311	MAERGYSESLTTFESPSGKLVQIEYALA AAVAGGAPSVGIK
5.2	4053.0322	2.0311	MAERGYSESLTTFESPSGKLVQIEYALA AAVAGGAPSVGIK

Spectrum No: 128; Query: 4307; Rank: 1

Peptide View

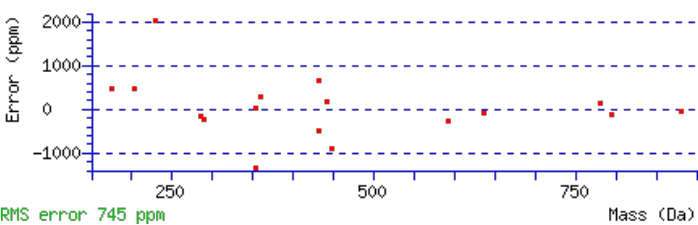
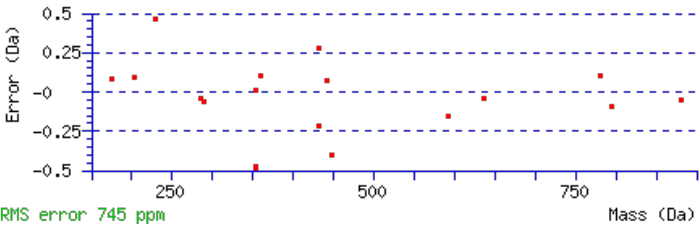
MS/MS Fragmentation of **TTTGSYIANR**
Found in **IPI00000811**, Tax_Id=9606 Gene_Symbol=PSMB6 Proteasome subunit beta type-6
Match to Query 4307: 1082.539168 from(542.276860,2+)
Title: 091224LimSK_Exosome3_07.361.361.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1082.5356
Fixed modifications: Carbamidomethyl (C)
Ions Score: 25 Expect: 0.45
Matches (**Bold Red**): 18/82 fragment ions using 55 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							10
2	203.1026	102.0550			185.0921	93.0497	T	982.4952	491.7513	965.4687	483.2380	964.4847	482.7460	9
3	304.1503	152.5788			286.1397	143.5735	T	881.4476	441.2274	864.4210	432.7141	863.4370	432.2221	8
4	361.1718	181.0895			343.1612	172.0842	G	780.3999	390.7036	763.3733	382.1903	762.3893	381.6983	7
5	448.2038	224.6055			430.1932	215.6003	S	723.3784	362.1928	706.3519	353.6796	705.3678	353.1876	6
6	611.2671	306.1372			593.2566	297.1319	Y	636.3464	318.6768	619.3198	310.1636			5
7	724.3512	362.6792			706.3406	353.6740	I	473.2831	237.1452	456.2565	228.6319			4
8	795.3883	398.1978			777.3777	389.1925	A	360.1990	180.6031	343.1724	172.0899			3
9	909.4312	455.2193	892.4047	446.7060	891.4207	446.2140	N	289.1619	145.0846	272.1353	136.5713			2
10							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

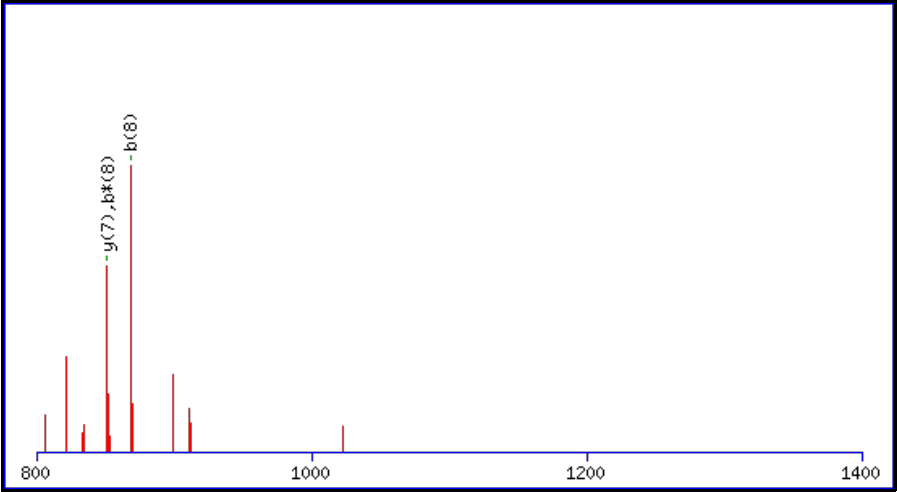
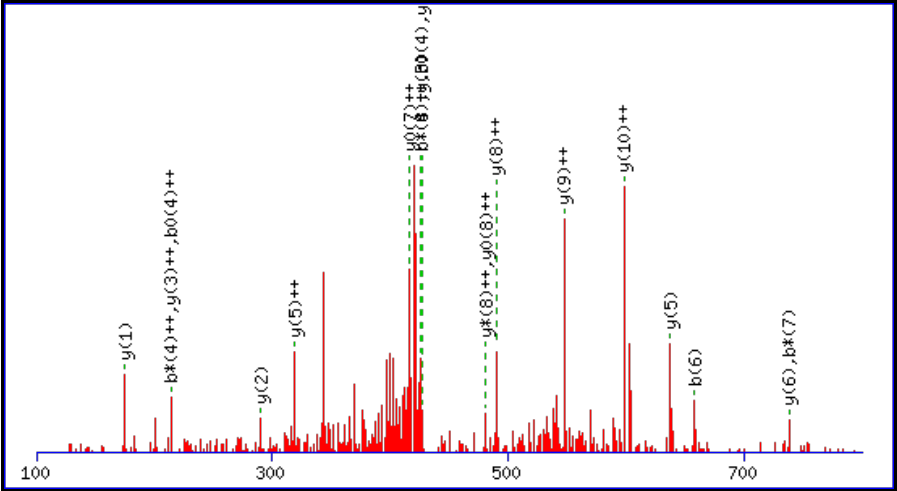
Score	Mr(calc):	Delta	Sequence
25.1	1082.5356	0.0035	TTTGSYIANR
13.0	1081.5451	0.9941	RLDAAPHMR
5.7	1080.5312	2.0080	EASGQPSLHR
5.1	1082.5468	-0.0077	NSSLIQHER
4.6	1080.5386	2.0006	EGLQMYGKR
4.3	1082.5403	-0.0011	AMYSGRRSR
4.1	1081.5281	1.0111	SISRPSSLR
4.1	1081.5281	1.0111	SISRPSSLR
3.9	1082.5485	-0.0093	TTIKKQER
3.9	1082.5485	-0.0093	TTIKKQER

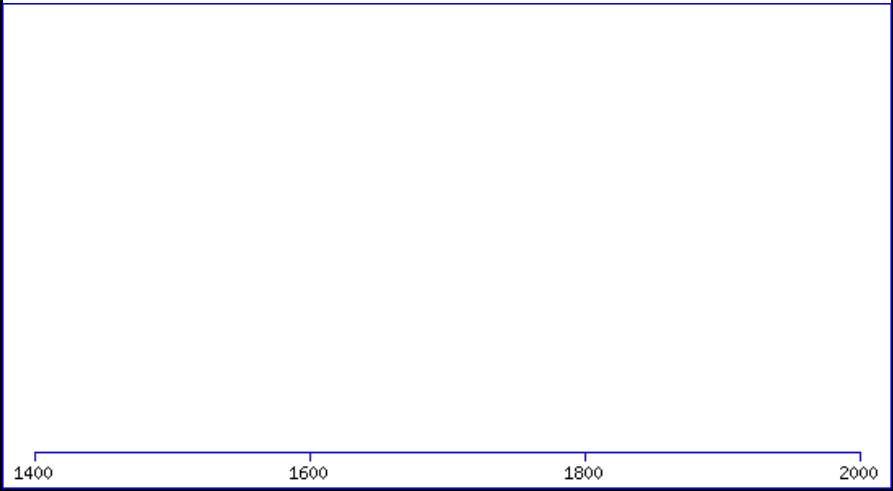
Spectrum No: 129; Query: 10994; Rank: 1

Peptide View

MS/MS Fragmentation of **VTDKLTPIHDR**
Found in **IP100000811**, Tax_Id=9606 Gene_Symbol=PSMB6 Proteasome subunit beta type-6

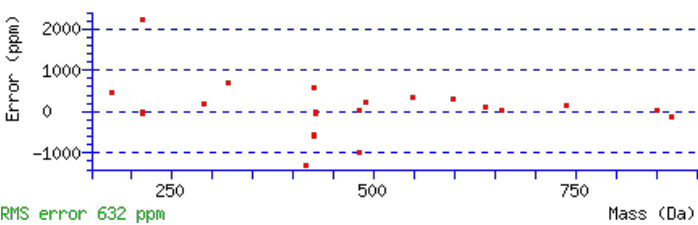
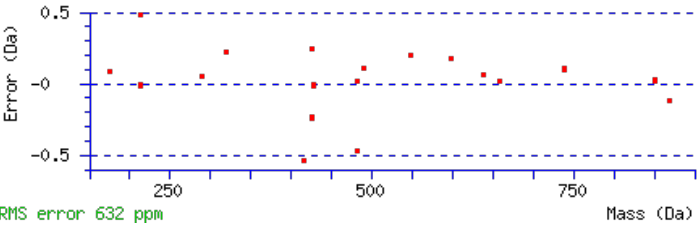
Match to Query 10994: 1293.709422 from(432.243750,3+)
Title: 091224LimSK_Exosome3_07.408.408.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1293.7041
Fixed modifications: Carbamidomethyl (C)
Ions Score: 52 **Expect:** 0.00074
Matches (Bold Red): 25/110 fragment ions using 29 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							11
2	201.1234	101.0653			183.1128	92.0600	T	1195.6430	598.3251	1178.6164	589.8118	1177.6324	589.3198	10
3	316.1503	158.5788			298.1397	149.5735	D	1094.5953	547.8013	1077.5687	539.2880	1076.5847	538.7960	9
4	444.2453	222.6263	427.2187	214.1130	426.2347	213.6210	K	979.5683	490.2878	962.5418	481.7745	961.5578	481.2825	8
5	557.3293	279.1683	540.3028	270.6550	539.3188	270.1630	L	851.4734	426.2403	834.4468	417.7271	833.4628	417.2350	7
6	658.3770	329.6921	641.3505	321.1789	640.3665	320.6869	T	738.3893	369.6983	721.3628	361.1850	720.3787	360.6930	6
7	755.4298	378.2185	738.4032	369.7053	737.4192	369.2132	P	637.3416	319.1745	620.3151	310.6612	619.3311	310.1692	5
8	868.5138	434.7606	851.4873	426.2473	850.5033	425.7553	I	540.2889	270.6481	523.2623	262.1348	522.2783	261.6428	4
9	1005.5728	503.2900	988.5462	494.7767	987.5622	494.2847	H	427.2048	214.1060	410.1783	205.5928	409.1942	205.1008	3
10	1120.5997	560.8035	1103.5732	552.2902	1102.5891	551.7982	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
11							R	175.1190	88.0631	158.0924	79.5498			1



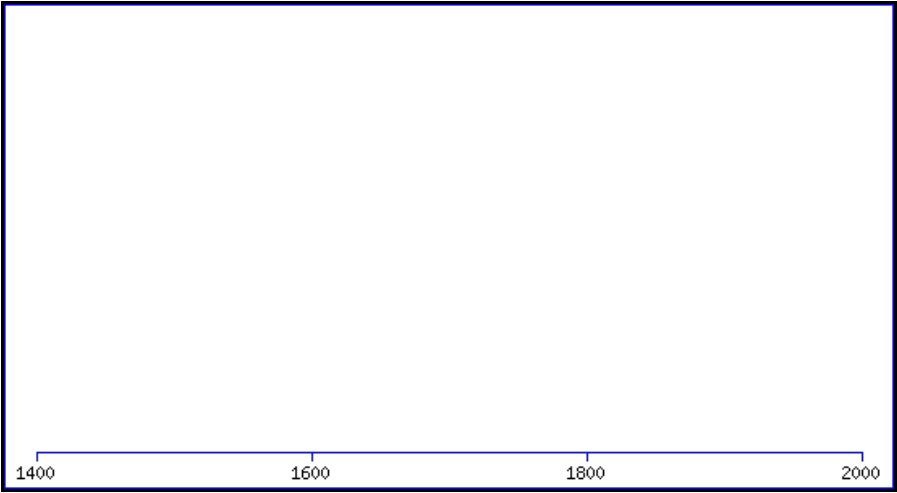
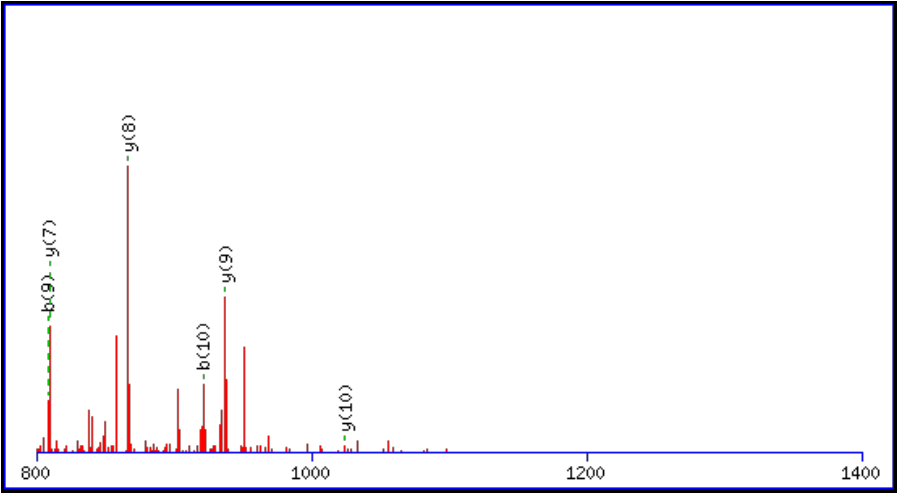
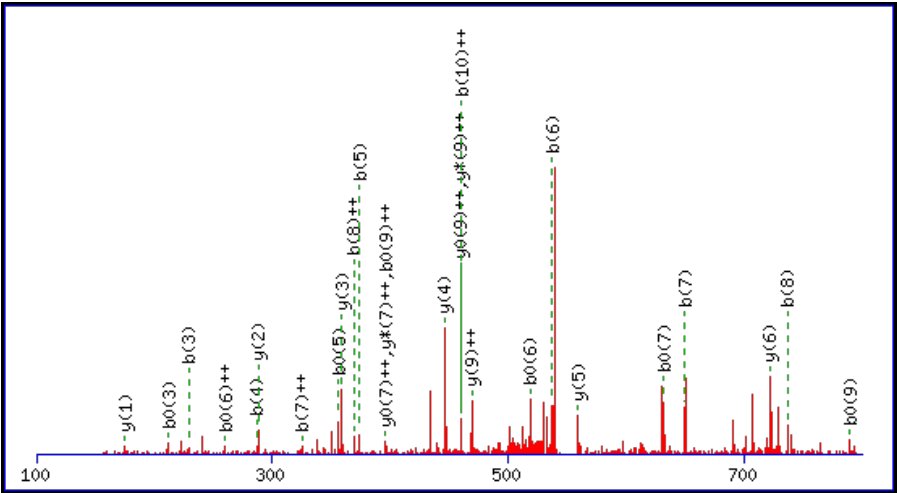
All matches to this query

Score	Mr(calc):	Delta	Sequence
51.8	1293.7041	0.0053	VTDKLTPIHDR
17.3	1293.7170	-0.0075	VIVISRSLTAR
14.1	1292.7078	1.0016	LRGVRLLSGSR
13.0	1293.7170	-0.0075	VIVISRSLTAR
8.6	1293.7153	-0.0059	SHALQLPKTSGR
8.4	1291.7013	2.0081	IRALTLQLER
7.3	1293.7071	0.0024	XWTLTLRR
6.7	1293.7041	0.0053	VLSTVHTHSSVK
6.4	1293.7170	-0.0075	VIVISRSLTAR
6.1	1291.7071	2.0024	KAIACLLFGGSR

Spectrum No: 130; Query: 4664; Rank: 1

Peptide View

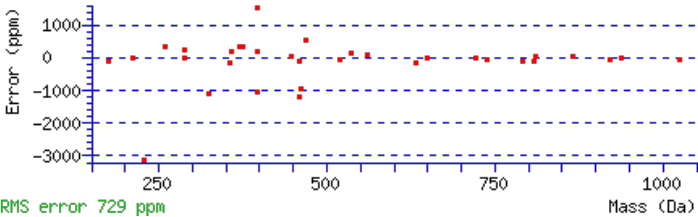
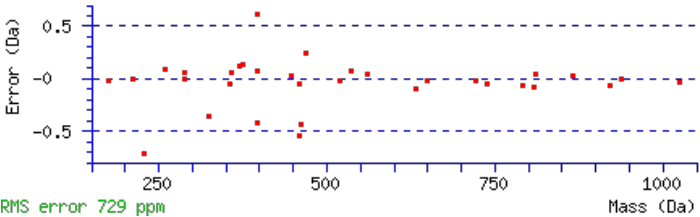
MS/MS Fragmentation of **ASAGSYISALR**
Found in **IP100000783**, Tax_Id=9606 Gene_Symbol=PSMB8 Isoform 1 of Proteasome subunit beta type-8
Match to Query 4664: 1094.577288 from(548.295920,2+)
Title: 091224LimSK_Exosome3_06.2748.2748.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1094.5720

Fixed modifications: Carbamidomethyl (C)
Ions Score: 59 Expect: 0.00015
Matches (Bold Red): 33/92 fragment ions using 70 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	72.0444	36.5258			A							11
2	159.0764	80.0418	141.0659	71.0366	S	1024.5422	512.7747	1007.5156	504.2615	1006.5316	503.7694	10
3	230.1135	115.5604	212.1030	106.5551	A	937.5102	469.2587	920.4836	460.7454	919.4996	460.2534	9
4	287.1350	144.0711	269.1244	135.0659	G	866.4730	433.7402	849.4465	425.2269	848.4625	424.7349	8
5	374.1670	187.5872	356.1565	178.5819	S	809.4516	405.2294	792.4250	396.7162	791.4410	396.2241	7
6	537.2304	269.1188	519.2198	260.1135	Y	722.4196	361.7134	705.3930	353.2001	704.4090	352.7081	6
7	650.3144	325.6608	632.3039	316.6556	I	559.3562	280.1817	542.3297	271.6685	541.3457	271.1765	5
8	737.3464	369.1769	719.3359	360.1716	S	446.2722	223.6397	429.2456	215.1264	428.2616	214.6344	4
9	808.3836	404.6954	790.3730	395.6901	A	359.2401	180.1237	342.2136	171.6104			3
10	921.4676	461.2374	903.4571	452.2322	L	288.2030	144.6051	271.1765	136.0919			2
11					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

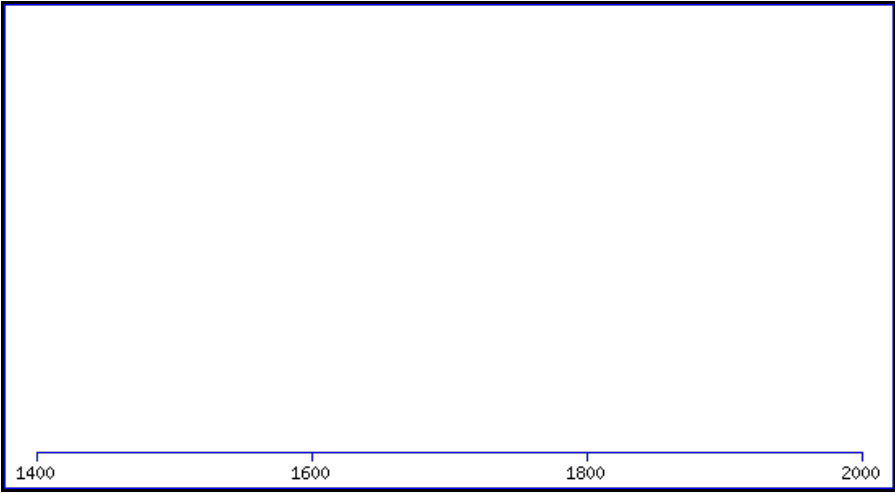
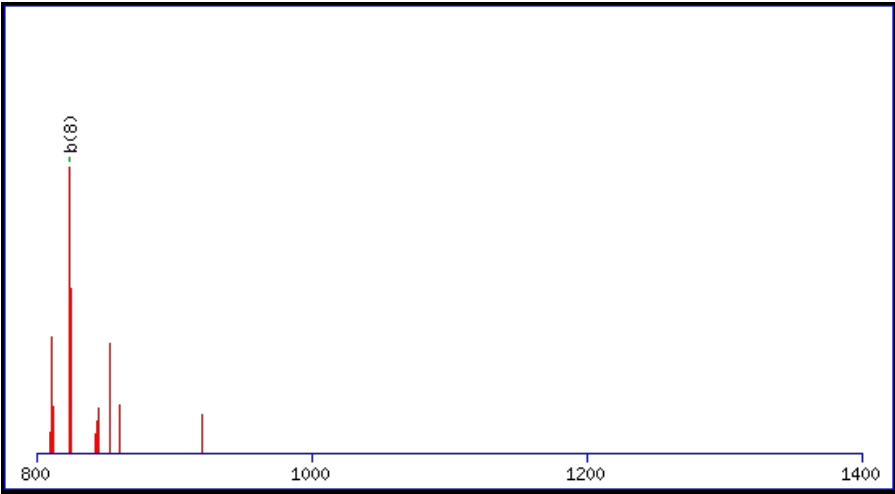
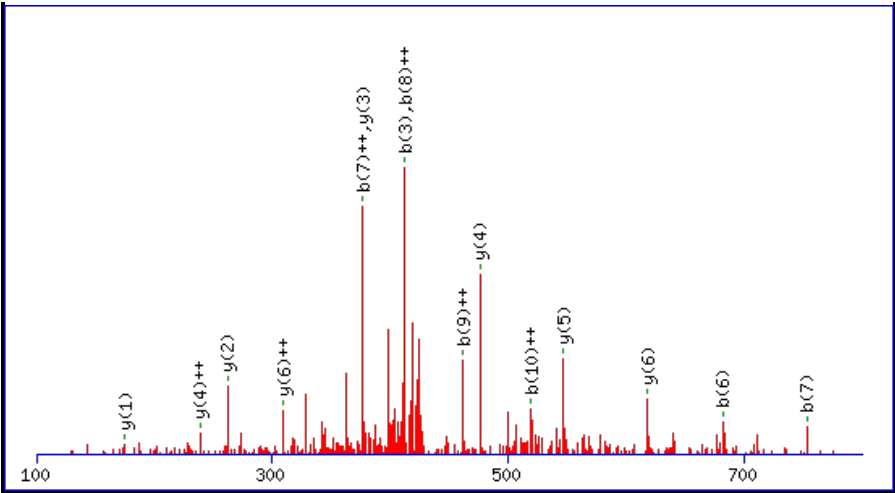
Score	Mr(calc):	Delta	Sequence
59.3	1094.5720	0.0053	ASAGSYISALR
13.3	1094.5720	0.0053	VFSQTSSLAR
9.9	1094.5832	-0.0059	LNQISHDIR
7.1	1094.5849	-0.0076	ASKLTQVLR
6.8	1094.5849	-0.0076	TGKLNLLTR
5.8	1094.5832	-0.0059	AESAALHAGLR
5.3	1094.5794	-0.0021	QMVSEKVK
5.0	1093.5698	1.0075	XIMMLSVLK
4.9	1093.5757	1.0016	RAVASGVKAR
4.8	1094.5832	-0.0059	AFSASTSLRR

Spectrum No: 131; Query: 11154; Rank: 1

Peptide View

MS/MS Fragmentation of **FQHGVIAAVDSR**
Found in **IP100000783**, Tax_Id=9606 Gene_Symbol=PSMB8 Isoform 1 of Proteasome subunit beta type-8

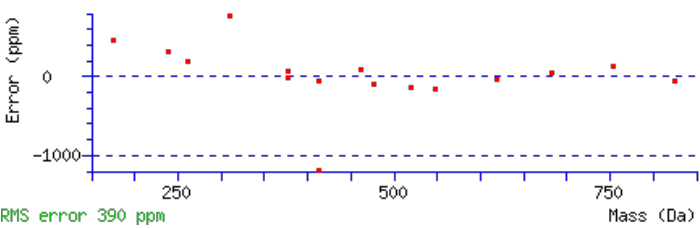
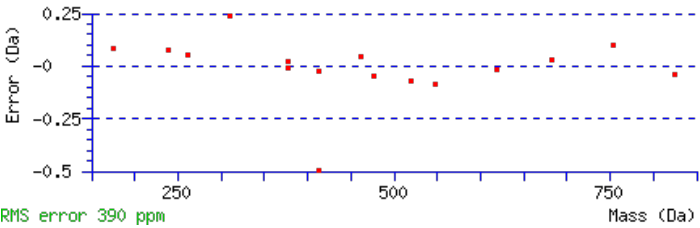
Match to Query 11154: 1298.680212 from(433.900680,3+)
Title: 091224LimSK_Exosome3_06.1172.1172.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1298.6731
Fixed modifications: Carbamidomethyl (C)
Ions Score: 31 Expect: 0.092
Matches (Bold Red): 16/110 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	148.0757	74.5415					F							12
2	276.1343	138.5708	259.1077	130.0575			Q	1152.6120	576.8096	1135.5854	568.2964	1134.6014	567.8044	11
3	413.1932	207.1002	396.1666	198.5870			H	1024.5534	512.7803	1007.5269	504.2671	1006.5429	503.7751	10
4	470.2146	235.6110	453.1881	227.0977			G	887.4945	444.2509	870.4680	435.7376	869.4839	435.2456	9
5	569.2831	285.1452	552.2565	276.6319			V	830.4730	415.7402	813.4465	407.2269	812.4625	406.7349	8
6	682.3671	341.6872	665.3406	333.1739			I	731.4046	366.2060	714.3781	357.6927	713.3941	357.2007	7

7	753.4042	377.2058	736.3777	368.6925			A	618.3206	309.6639	601.2940	301.1506	600.3100	300.6586	6
8	824.4413	412.7243	807.4148	404.2110			A	547.2835	274.1454	530.2569	265.6321	529.2729	265.1401	5
9	923.5098	462.2585	906.4832	453.7452			V	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
10	1038.5367	519.7720	1021.5102	511.2587	1020.5261	510.7667	D	377.1779	189.0926	360.1514	180.5793	359.1674	180.0873	3
11	1125.5687	563.2880	1108.5422	554.7747	1107.5582	554.2827	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
12							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

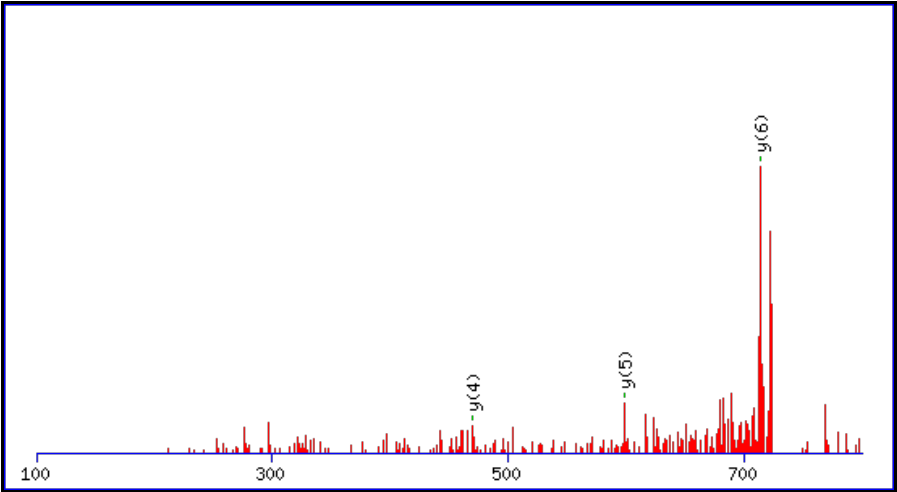
Score	Mr(calc):	Delta	Sequence
31.2	1298.6731	0.0071	FQHGVIAAVDSR
11.5	1298.6731	0.0071	RPWEPSALSTR
11.2	1297.6779	1.0023	NFSKFQATSLR
8.2	1296.6690	2.0112	KPISDTISCK
7.0	1298.6803	-0.0001	RALAQAGRGEDR
6.6	1297.6740	1.0062	LCFAVYAVLDK
6.2	1296.6690	2.0112	TIKTVKADVCK
6.2	1296.6690	2.0112	TIKTVKADVCK
5.8	1296.6690	2.0112	SSVLPKASTLSK
5.0	1296.6663	2.0139	RAVSTATLRSR

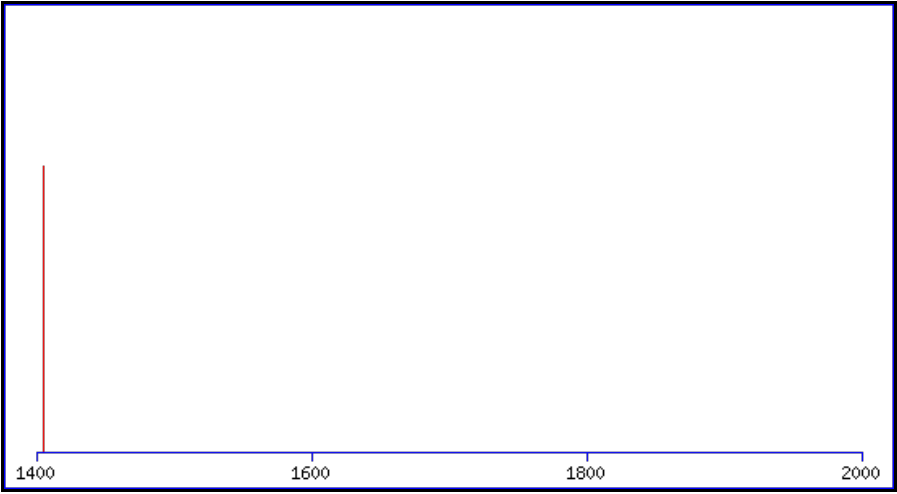
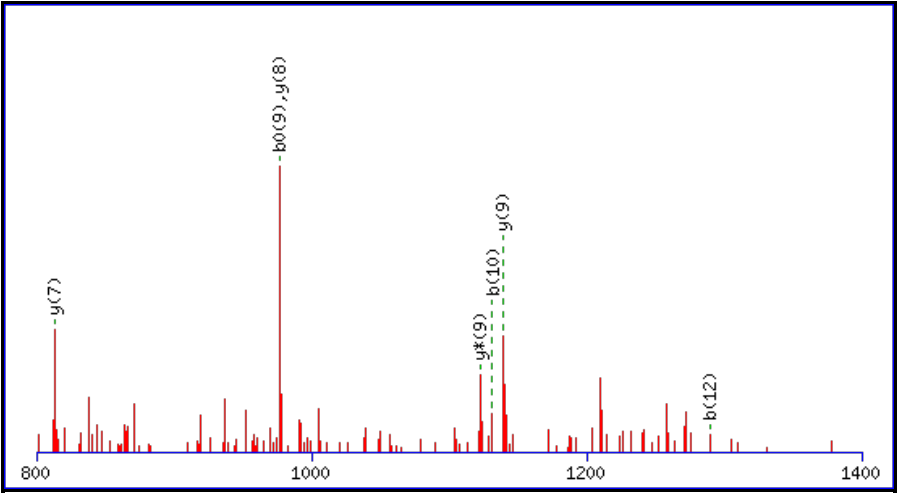
Spectrum No: 132; Query: 18625; Rank: 1

Peptide View

MS/MS Fragmentation of **GPGLYYVDEHGTR**
Found in **IPI00000783**, Tax_Id=9606 Gene_Symbol=PSMB8 Isoform 1 of Proteasome subunit beta type-8

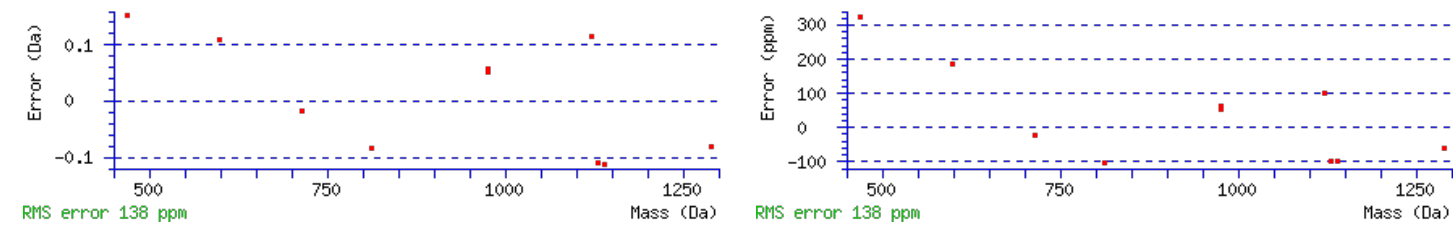
Match to Query 18625: 1462.690868 from(732.352710,2+)
Title: 091224LimSK_Exosome3_06.1477.1477.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1462.6841
Fixed modifications: Carbamidomethyl (C)
Ions Score: 31 Expect: 0.15
Matches (**Bold Red**): 10/104 fragment ions using 37 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			G							13
2	155.0815	78.0444			P	1406.6699	703.8386	1389.6434	695.3253	1388.6593	694.8333	12
3	212.1030	106.5551			G	1309.6171	655.3122	1292.5906	646.7989	1291.6066	646.3069	11
4	325.1870	163.0972			L	1252.5957	626.8015	1235.5691	618.2882	1234.5851	617.7962	10
5	488.2504	244.6288			Y	1139.5116	570.2594	1122.4851	561.7462	1121.5010	561.2542	9
6	651.3137	326.1605			Y	976.4483	488.7278	959.4217	480.2145	958.4377	479.7225	8
7	750.3821	375.6947			V	813.3850	407.1961	796.3584	398.6828	795.3744	398.1908	7
8	865.4090	433.2082	847.3985	424.2029	D	714.3165	357.6619	697.2900	349.1486	696.3060	348.6566	6
9	994.4516	497.7295	976.4411	488.7242	E	599.2896	300.1484	582.2631	291.6352	581.2790	291.1432	5
10	1131.5106	566.2589	1113.5000	557.2536	H	470.2470	235.6271	453.2205	227.1139	452.2364	226.6219	4
11	1188.5320	594.7696	1170.5215	585.7644	G	333.1881	167.0977	316.1615	158.5844	315.1775	158.0924	3
12	1289.5797	645.2935	1271.5691	636.2882	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
13					R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

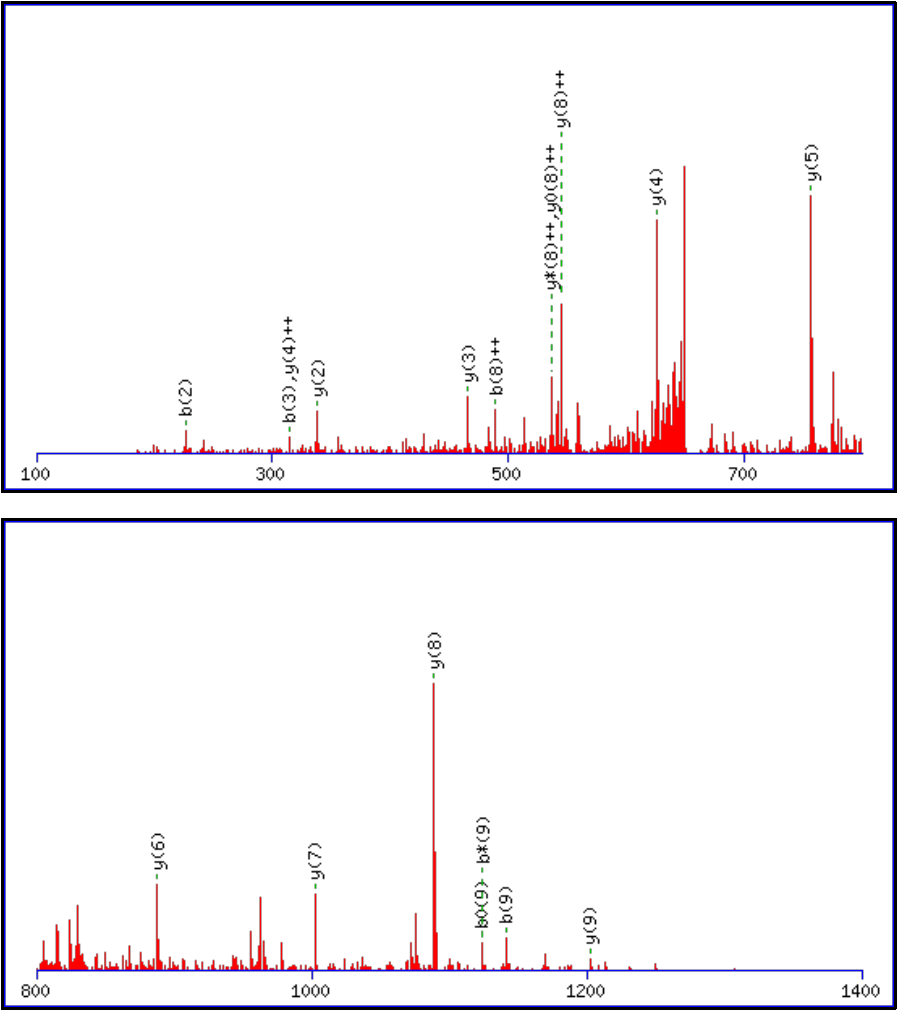
Score	Mr(calc):	Delta	Sequence
31.4	1462.6841	0.0068	GPGLYYVDEHGTR
1.3	1461.6881	1.0028	VSGIKSKVDELK
0.3	1462.6986	-0.0077	LLTPAQRTLYK

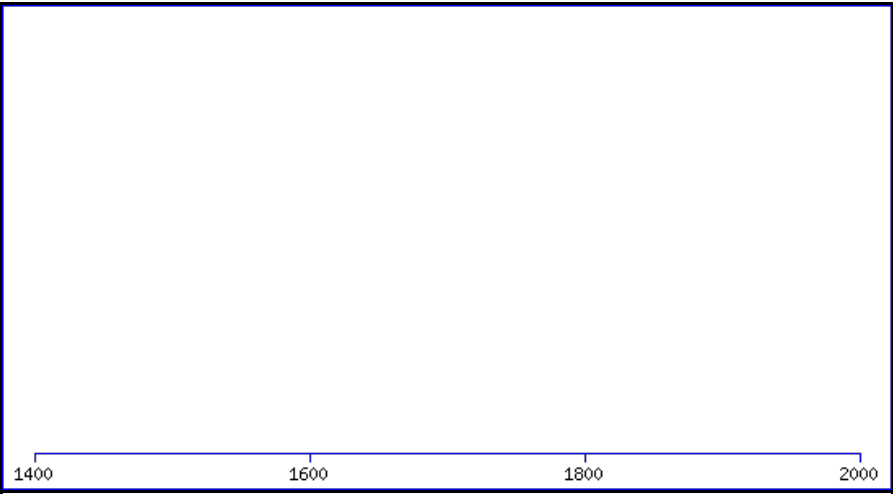
Spectrum No: 133; Query: 11817; Rank: 1

Peptide View

MS/MS Fragmentation of **LLSNMMCQYR**
Found in **IP100000783**, Tax_Id=9606 Gene_Symbol=PSMB8 Isoform 1 of Proteasome subunit beta type-8

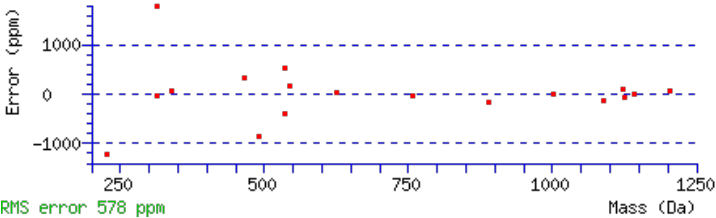
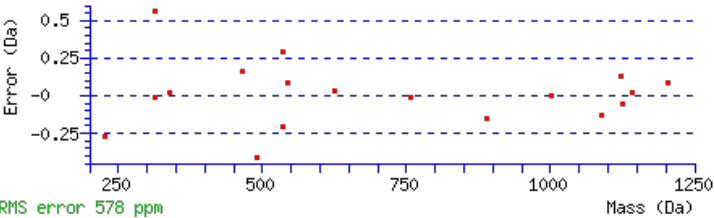
Match to Query 11817: 1314.596188 from(658.305370,2+)
Title: 091224LimSK_Exosome3_06.3302.3302.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1314.5883
Fixed modifications: Carbamidomethyl (C)
Ions Score: 54 Expect: 0.00073
Matches (**Bold Red**): 18/84 fragment ions using 37 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							10
2	227.1754	114.0913					L	1202.5115	601.7594	1185.4849	593.2461	1184.5009	592.7541	9
3	314.2074	157.6074			296.1969	148.6021	S	1089.4274	545.2174	1072.4009	536.7041	1071.4169	536.2121	8
4	428.2504	214.6288	411.2238	206.1155	410.2398	205.6235	N	1002.3954	501.7013	985.3689	493.1881			7
5	559.2908	280.1491	542.2643	271.6358	541.2803	271.1438	M	888.3525	444.6799	871.3259	436.1666			6
6	690.3313	345.6693	673.3048	337.1560	672.3208	336.6640	M	757.3120	379.1596	740.2854	370.6464			5
7	850.3620	425.6846	833.3354	417.1714	832.3514	416.6793	C	626.2715	313.6394	609.2450	305.1261			4
8	978.4206	489.7139	961.3940	481.2006	960.4100	480.7086	Q	466.2409	233.6241	449.2143	225.1108			3
9	1141.4839	571.2456	1124.4573	562.7323	1123.4733	562.2403	Y	338.1823	169.5948	321.1557	161.0815			2
10							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

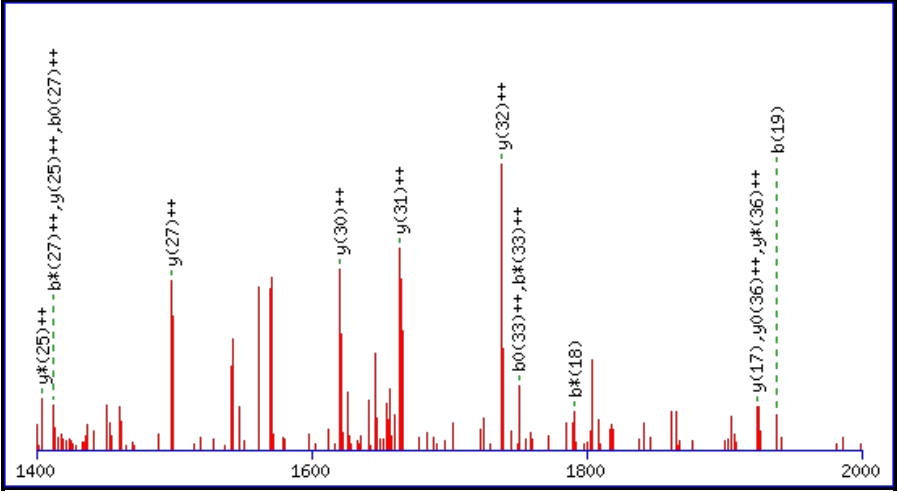
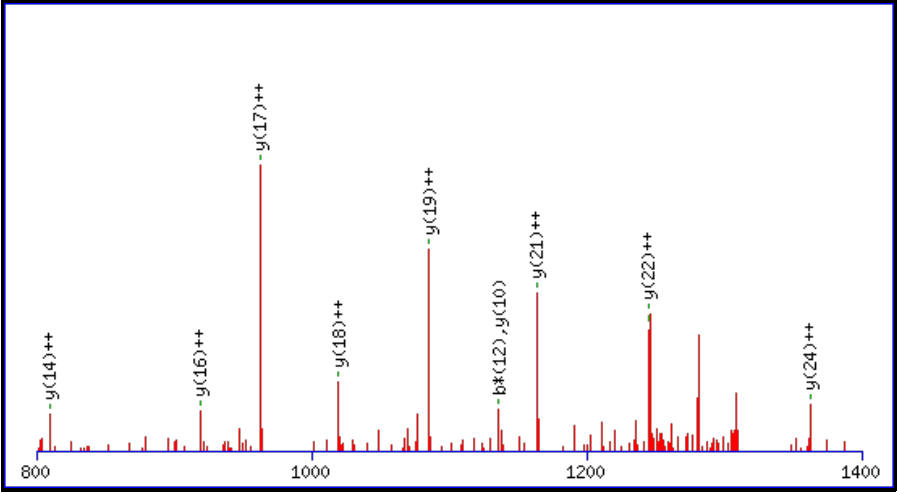
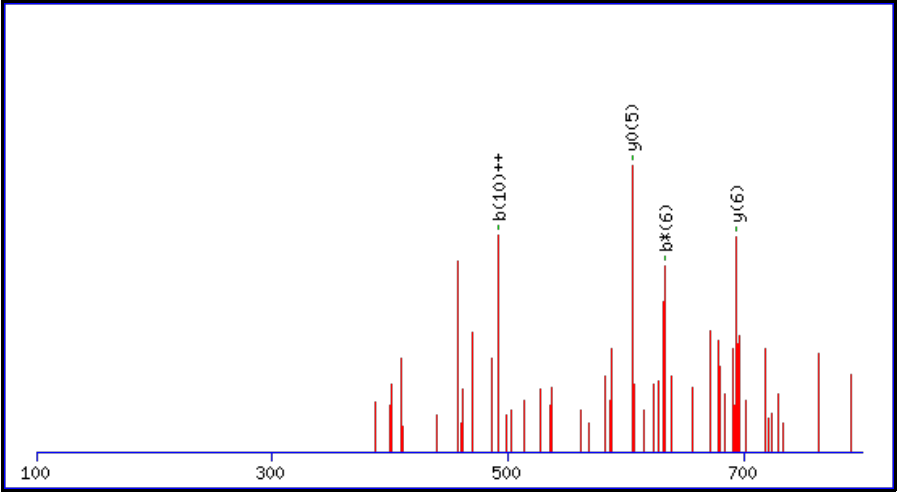
Score	Mr(calc):	Delta	Sequence
53.9	1314.5883	0.0079	LLSNMMCQYR
7.2	1314.6003	-0.0041	LLSLSCSVNSR
7.2	1314.6003	-0.0041	LLSLSCSVNSR
6.9	1314.6003	-0.0041	LLSLSCSVNSR
6.5	1314.5846	0.0115	LLSGPGATQRR
6.0	1314.6026	-0.0064	KLSYVIAFSK
5.8	1312.5942	2.0020	XSSNDKHVMSR
5.8	1314.5914	0.0048	EPLTTCEYR
4.8	1314.5891	0.0071	LLASCSADGTLK
4.8	1314.5891	0.0071	LLASCSADGTLK

Spectrum No: 134; Query: 73733; Rank: 1

Peptide View

MS/MS Fragmentation of **LSGNMFSTGSGNTYAYGVMDSGYRPNLSPEEAYDLGR**
Found in **IPI00000783**, Tax_Id=9606 Gene_Symbol=PSMB8 Isoform 1 of Proteasome subunit beta type-8

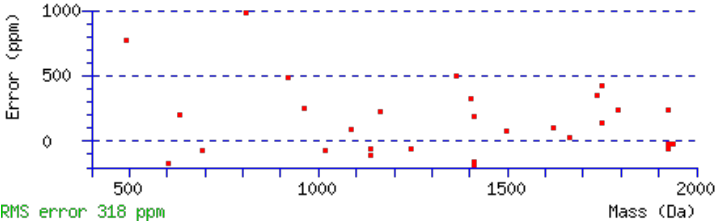
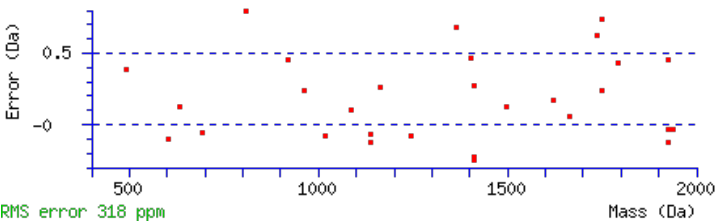
Match to Query 73733: 3976.801662 from(1326.607830,3+)
Title: 091224LimSK_Exosome3_06.7068.7068.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 3975.7680
Fixed modifications: Carbamidomethyl (C)
Ions Score: 67 Expect: 8.5e-005

Matches (Bold Red): 29/418 fragment ions using 43 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							37
2	201.1234	101.0653			183.1128	92.0600	S	3863.6912	1932.3492	3846.6646	1923.8360	3845.6806	1923.3440	36
3	258.1448	129.5761			240.1343	120.5708	G	3776.6592	1888.8332	3759.6326	1880.3199	3758.6486	1879.8279	35
4	372.1878	186.5975	355.1612	178.0842	354.1772	177.5922	N	3719.6377	1860.3225	3702.6112	1851.8092	3701.6271	1851.3172	34
5	503.2282	252.1178	486.2017	243.6045	485.2177	243.1125	M	3605.5948	1803.3010	3588.5682	1794.7878	3587.5842	1794.2957	33
6	650.2967	325.6520	633.2701	317.1387	632.2861	316.6467	F	3474.5543	1737.7808	3457.5277	1729.2675	3456.5437	1728.7755	32
7	737.3287	369.1680	720.3021	360.6547	719.3181	360.1627	S	3327.4859	1664.2466	3310.4593	1655.7333	3309.4753	1655.2413	31
8	838.3764	419.6918	821.3498	411.1785	820.3658	410.6865	T	3240.4538	1620.7306	3223.4273	1612.2173	3222.4433	1611.7253	30
9	895.3978	448.2026	878.3713	439.6893	877.3873	439.1973	G	3139.4062	1570.2067	3122.3796	1561.6934	3121.3956	1561.2014	29
10	982.4299	491.7186	965.4033	483.2053	964.4193	482.7133	S	3082.3847	1541.6960	3065.3582	1533.1827	3064.3741	1532.6907	28
11	1039.4513	520.2293	1022.4248	511.7160	1021.4408	511.2240	G	2995.3527	1498.1800	2978.3261	1489.6667	2977.3421	1489.1747	27
12	1153.4942	577.2508	1136.4677	568.7375	1135.4837	568.2455	N	2938.3312	1469.6692	2921.3047	1461.1560	2920.3206	1460.6640	26
13	1254.5419	627.7746	1237.5154	619.2613	1236.5314	618.7693	T	2824.2883	1412.6478	2807.2617	1404.1345	2806.2777	1403.6425	25
14	1417.6053	709.3063	1400.5787	700.7930	1399.5947	700.3010	Y	2723.2406	1362.1239	2706.2141	1353.6107	2705.2300	1353.1187	24
15	1488.6424	744.8248	1471.6158	736.3115	1470.6318	735.8195	A	2560.1773	1280.5923	2543.1507	1272.0790	2542.1667	1271.5870	23
16	1651.7057	826.3565	1634.6792	817.8432	1633.6951	817.3512	Y	2489.1402	1245.0737	2472.1136	1236.5604	2471.1296	1236.0684	22
17	1708.7272	854.8672	1691.7006	846.3539	1690.7166	845.8619	G	2326.0768	1163.5421	2309.0503	1155.0288	2308.0663	1154.5368	21
18	1807.7956	904.4014	1790.7690	895.8882	1789.7850	895.3961	V	2269.0554	1135.0313	2252.0288	1126.5180	2251.0448	1126.0260	20
19	1938.8361	969.9217	1921.8095	961.4084	1920.8255	960.9164	M	2169.9870	1085.4971	2152.9604	1076.9838	2151.9764	1076.4918	19
20	2053.8630	1027.4351	2036.8365	1018.9219	2035.8524	1018.4299	D	2038.9465	1019.9769	2021.9199	1011.4636	2020.9359	1010.9716	18
21	2140.8950	1070.9512	2123.8685	1062.4379	2122.8845	1061.9459	S	1923.9195	962.4634	1906.8930	953.9501	1905.9090	953.4581	17
22	2197.9165	1099.4619	2180.8899	1090.9486	2179.9059	1090.4566	G	1836.8875	918.9474	1819.8610	910.4341	1818.8769	909.9421	16
23	2360.9798	1180.9936	2343.9533	1172.4803	2342.9693	1171.9883	Y	1779.8660	890.4367	1762.8395	881.9234	1761.8555	881.4314	15
24	2517.0809	1259.0441	2500.0544	1250.5308	2499.0704	1250.0388	R	1616.8027	808.9050	1599.7762	800.3917	1598.7921	799.8997	14
25	2614.1337	1307.5705	2597.1072	1299.0572	2596.1231	1298.5652	P	1460.7016	730.8544	1443.6751	722.3412	1442.6910	721.8492	13
26	2728.1766	1364.5920	2711.1501	1356.0787	2710.1661	1355.5867	N	1363.6488	682.3281	1346.6223	673.8148	1345.6383	673.3228	12
27	2841.2607	1421.1340	2824.2341	1412.6207	2823.2501	1412.1287	L	1249.6059	625.3066	1232.5794	616.7933	1231.5953	616.3013	11
28	2928.2927	1464.6500	2911.2662	1456.1367	2910.2822	1455.6447	S	1136.5218	568.7646	1119.4953	560.2513	1118.5113	559.7593	10
29	3025.3455	1513.1764	3008.3189	1504.6631	3007.3349	1504.1711	P	1049.4898	525.2485	1032.4633	516.7353	1031.4793	516.2433	9
30	3154.3881	1577.6977	3137.3615	1569.1844	3136.3775	1568.6924	E	952.4371	476.7222	935.4105	468.2089	934.4265	467.7169	8
31	3283.4307	1642.2190	3266.4041	1633.7057	3265.4201	1633.2137	E	823.3945	412.2009	806.3679	403.6876	805.3839	403.1956	7
32	3354.4678	1677.7375	3337.4412	1669.2243	3336.4572	1668.7322	A	694.3519	347.6796	677.3253	339.1663	676.3413	338.6743	6
33	3517.5311	1759.2692	3500.5046	1750.7559	3499.5205	1750.2639	Y	623.3148	312.1610	606.2882	303.6477	605.3042	303.1557	5
34	3632.5581	1816.7827	3615.5315	1808.2694	3614.5475	1807.7774	D	460.2514	230.6293	443.2249	222.1161	442.2409	221.6241	4
35	3745.6421	1873.3247	3728.6156	1864.8114	3727.6316	1864.3194	L	345.2245	173.1159	328.1979	164.6026			3
36	3802.6636	1901.8354	3785.6370	1893.3222	3784.6530	1892.8301	G	232.1404	116.5738	215.1139	108.0606			2
37							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

Score	Mr(calc):	Delta	Sequence

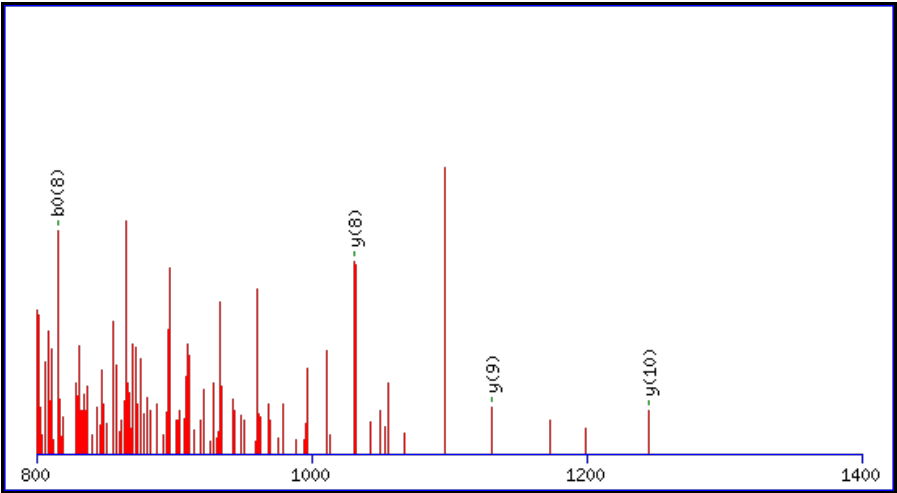
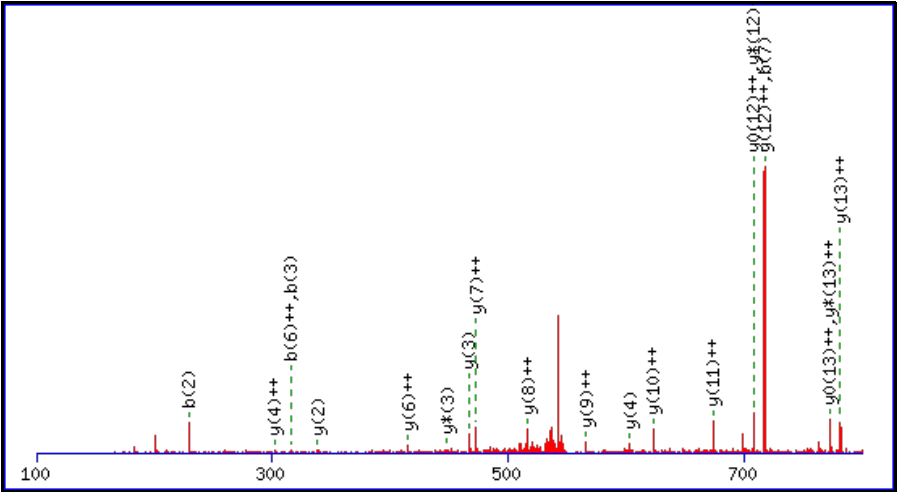
66.5	3975.7680	1.0337	LSGNMESTGSGNTYAYGVMDSGYRPNLSPEEAYDLGR
12.7	3975.7673	1.0343	STPYECGFDPMSPARVPFSMKFFLVAMPSYYLI
12.7	3975.7673	1.0343	STPYECGFDPMSPARVPFSMKFFLVAMPSYYLI
9.6	3975.7603	1.0413	MVAMQEAAQHLLGTHDFAFQSAGSPVPSPVRTLR
8.5	3976.8238	-0.0221	MSACHTQPSLGGGGSAGSGLGEAAWAGLPPDTGSFLLQVR
8.5	3976.8238	-0.0221	MSACHTQPSLGGGGSAGSGLGEAAWAGLPPDTGSFLLQVR
8.5	3976.8238	-0.0221	MSACHTQPSLGGGGSAGSGLGEAAWAGLPPDTGSFLLQVR
8.3	3975.7673	1.0343	STPYECGFDPMSPARVPFSMKFFLVAMPSYYLI
8.3	3974.7676	2.0341	GNVAGDSKNDPPMEAAGFTAQVIILNHPGQISQSK
7.9	3974.7679	2.0337	XPTIPAVANSSANSSPELADELPMITLDKISR

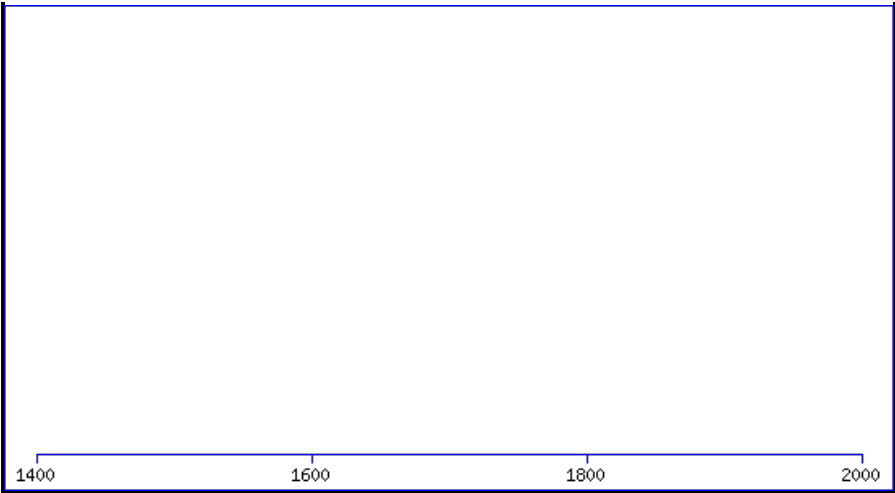
Spectrum No: 135; Query: 28355; Rank: 1

Peptide View

MS/MS Fragmentation of **VESTDVSDLLHQYR**
Found in **IP100000783**, Tax_Id=9606 Gene_Symbol=PSMB8 Isoform 1 of Proteasome subunit beta type-8

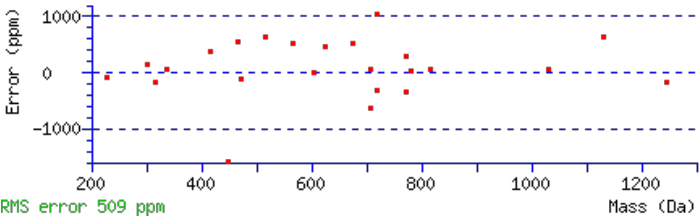
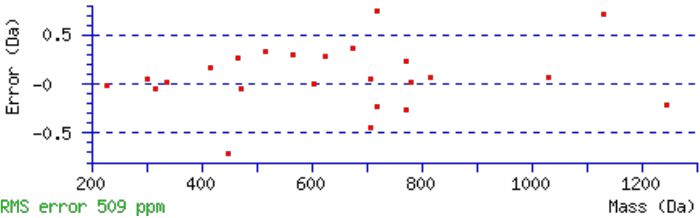
Match to Query 28355: 1660.813872 from(554.611900,3+)
Title: 091224LimSK_Exosome3_06.4600.4600.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1660.8057
Fixed modifications: Carbamidomethyl (C)
Ions Score: 50 Expect: 0.0024
Matches (**Bold Red**): 25/120 fragment ions using 57 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	100.0757	50.5415					V							14
2	229.1183	115.0628			211.1077	106.0575	E	1562.7445	781.8759	1545.7180	773.3626	1544.7340	772.8706	13
3	316.1503	158.5788			298.1397	149.5735	S	1433.7019	717.3546	1416.6754	708.8413	1415.6914	708.3493	12
4	417.1980	209.1026			399.1874	200.0974	T	1346.6699	673.8386	1329.6434	665.3253	1328.6593	664.8333	11
5	532.2249	266.6161			514.2144	257.6108	D	1245.6222	623.3148	1228.5957	614.8015	1227.6117	614.3095	10
6	631.2933	316.1503			613.2828	307.1450	V	1130.5953	565.8013	1113.5687	557.2880	1112.5847	556.7960	9
7	718.3254	359.6663			700.3148	350.6610	S	1031.5269	516.2671	1014.5003	507.7538	1013.5163	507.2618	8
8	833.3523	417.1798			815.3418	408.1745	D	944.4948	472.7511	927.4683	464.2378	926.4843	463.7458	7
9	946.4364	473.7218			928.4258	464.7165	L	829.4679	415.2376	812.4413	406.7243			6
10	1059.5204	530.2639			1041.5099	521.2586	L	716.3838	358.6956	699.3573	350.1823			5
11	1196.5794	598.7933			1178.5688	589.7880	H	603.2998	302.1535	586.2732	293.6402			4
12	1324.6379	662.8226	1307.6114	654.3093	1306.6274	653.8173	Q	466.2409	233.6241	449.2143	225.1108			3
13	1487.7013	744.3543	1470.6747	735.8410	1469.6907	735.3490	Y	338.1823	169.5948	321.1557	161.0815			2
14							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
49.6	1660.8057	0.0082	VESTDVSDLLHQYR
11.1	1658.8215	1.9924	QLFERLKMSLGNK
10.6	1659.8241	0.9897	KFTMLALRDLGMGK
10.3	1659.7981	1.0158	ENNTVSNIHPKLSK
10.3	1660.8298	-0.0159	EVSVRHSQTILNAK
8.9	1659.7981	1.0157	TRADSVANKLGSEFSK
8.9	1659.7981	1.0157	TRADSVANKLGSEFSK
8.6	1658.8103	2.0036	TGGMKLSATVIENPK

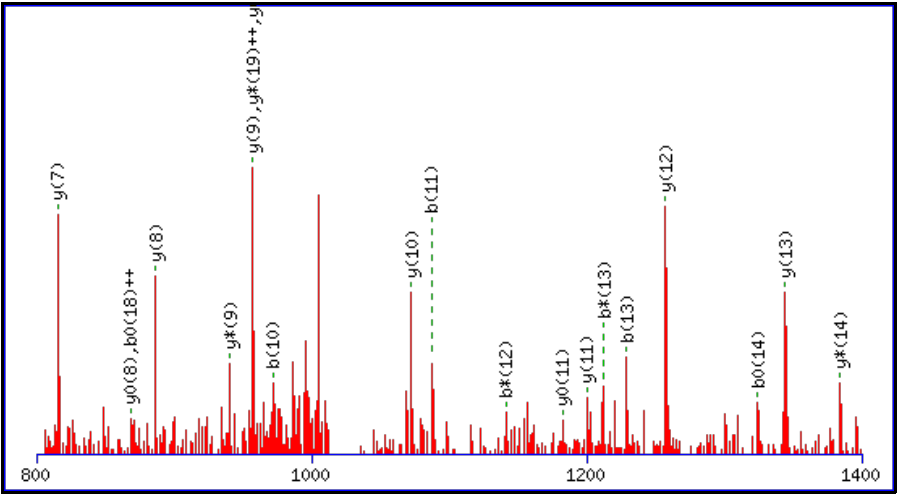
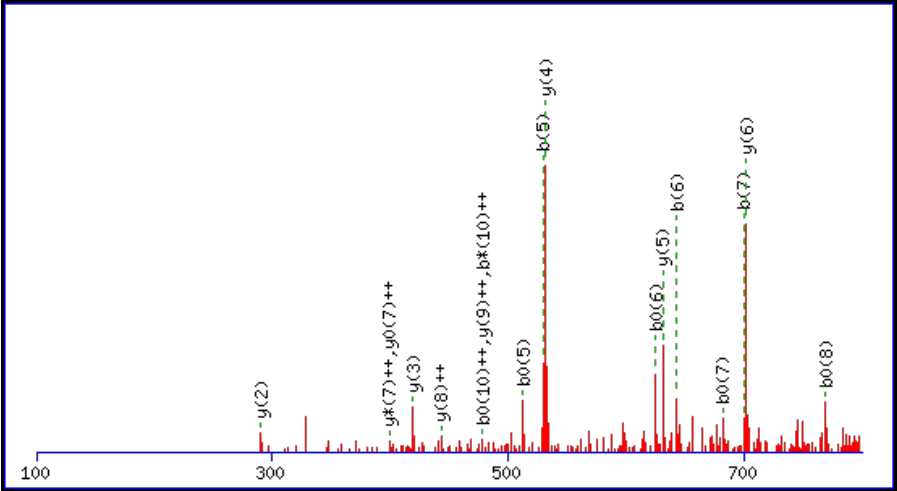
7.0	1660.8298	-0.0159	EVSVRHSQTILNAK
6.8	1658.7916	2.0222	KGSEQESVKEFLAK

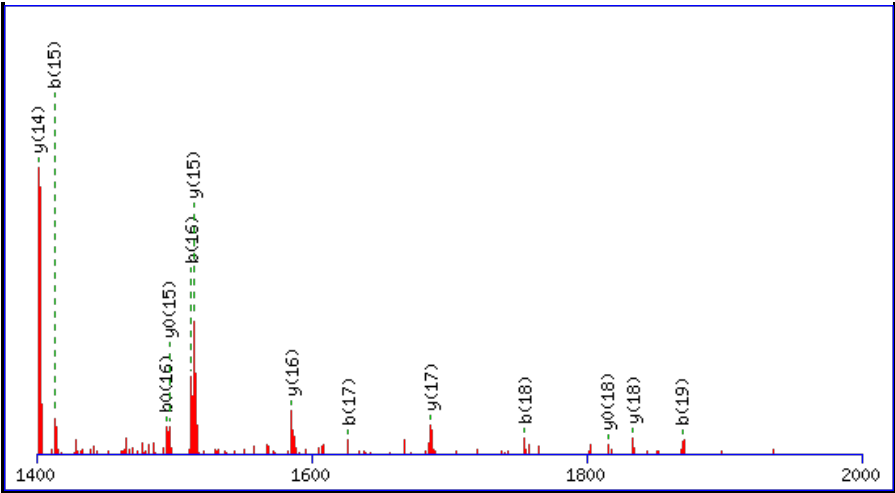
Spectrum No: 136; Query: 41347; Rank: 1

Peptide View

MS/MS Fragmentation of **LPFTALGSGQDAALAVLEDR**
Found in **IPI00027933**, Tax_Id=9606 Gene_Symbol=PSMB10 Proteasome subunit beta type-10

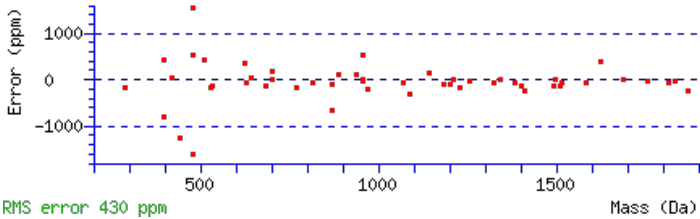
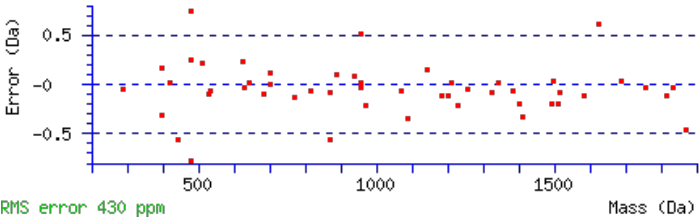
Match to Query 41347: 2043.080748 from(1022.547650,2+)
Title: 091224LimSK_Exosome3_06.7779.7779.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 2043.0637
Fixed modifications: Carbamidomethyl (C)
Ions Score: 113 Expect: 6e-010
Matches (Bold Red): 51/202 fragment ions using 92 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							20
2	211.1441	106.0757					P	1930.9869	965.9971	1913.9603	957.4838	1912.9763	956.9918	19
3	358.2125	179.6099					F	1833.9341	917.4707	1816.9076	908.9574	1815.9236	908.4654	18
4	459.2602	230.1337			441.2496	221.1285	T	1686.8657	843.9365	1669.8392	835.4232	1668.8551	834.9312	17
5	530.2973	265.6523			512.2867	256.6470	A	1585.8180	793.4127	1568.7915	784.8994	1567.8075	784.4074	16
6	643.3814	322.1943			625.3708	313.1890	L	1514.7809	757.8941	1497.7544	749.3808	1496.7703	748.8888	15
7	700.4028	350.7051			682.3923	341.6998	G	1401.6968	701.3521	1384.6703	692.8388	1383.6863	692.3468	14
8	787.4349	394.2211			769.4243	385.2158	S	1344.6754	672.8413	1327.6488	664.3281	1326.6648	663.8360	13
9	844.4563	422.7318			826.4458	413.7265	G	1257.6434	629.3253	1240.6168	620.8120	1239.6328	620.3200	12
10	972.5149	486.7611	955.4884	478.2478	954.5043	477.7558	Q	1200.6219	600.8146	1183.5953	592.3013	1182.6113	591.8093	11
11	1087.5419	544.2746	1070.5153	535.7613	1069.5313	535.2693	D	1072.5633	536.7853	1055.5368	528.2720	1054.5528	527.7800	10
12	1158.5790	579.7931	1141.5524	571.2798	1140.5684	570.7878	A	957.5364	479.2718	940.5098	470.7585	939.5258	470.2665	9
13	1229.6161	615.3117	1212.5895	606.7984	1211.6055	606.3064	A	886.4993	443.7533	869.4727	435.2400	868.4887	434.7480	8
14	1342.7001	671.8537	1325.6736	663.3404	1324.6896	662.8484	L	815.4621	408.2347	798.4356	399.7214	797.4516	399.2294	7
15	1413.7373	707.3723	1396.7107	698.8590	1395.7267	698.3670	A	702.3781	351.6927	685.3515	343.1794	684.3675	342.6874	6
16	1512.8057	756.9065	1495.7791	748.3932	1494.7951	747.9012	V	631.3410	316.1741	614.3144	307.6608	613.3304	307.1688	5
17	1625.8897	813.4485	1608.8632	804.9352	1607.8792	804.4432	L	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
18	1754.9323	877.9698	1737.9058	869.4565	1736.9218	868.9645	E	419.1885	210.0979	402.1619	201.5846	401.1779	201.0926	3
19	1869.9593	935.4833	1852.9327	926.9700	1851.9487	926.4780	D	290.1459	145.5766	273.1193	137.0633	272.1353	136.5713	2
20							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

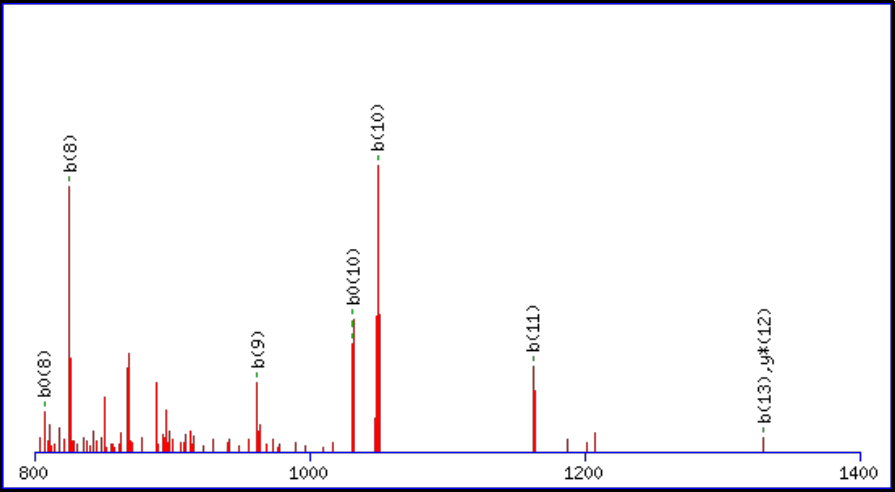
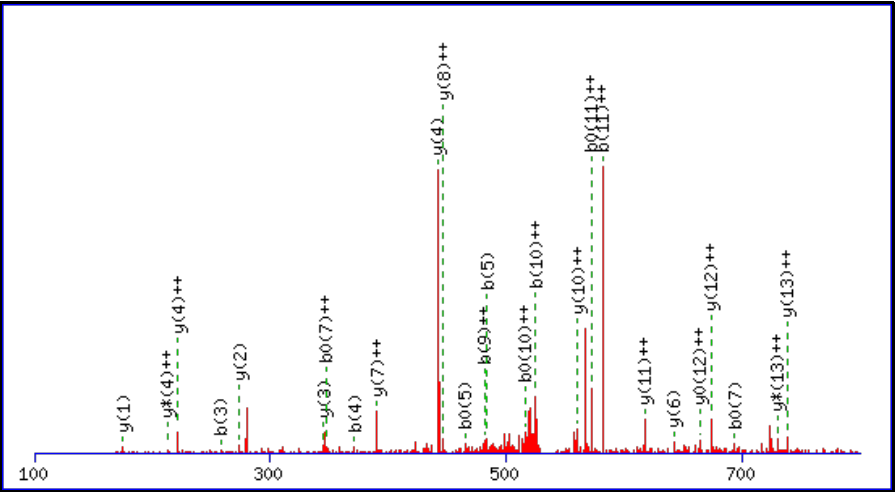
Score	Mr(calc):	Delta	Sequence
113.0	2043.0637	0.0171	LPFTALGSGQDAALAVLEDR
5.3	2043.0666	0.0141	LNAVYLNSSSKRVIEPR

0.8 | 2042.0579 | 1.0229 | [LEGVCERLDTVAGGLQGLR](#)

Spectrum No: 137; Query: 25774; Rank: 1

Peptide View

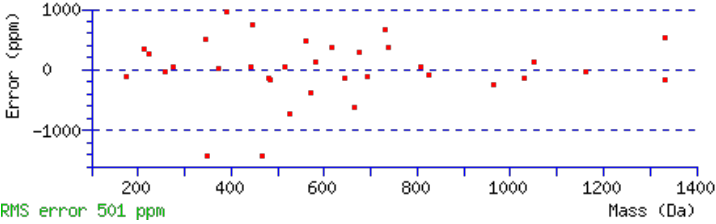
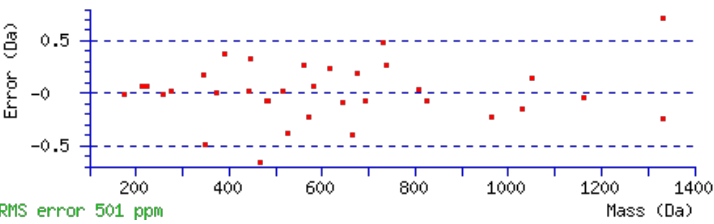
MS/MS Fragmentation of **GAEILEVLHSLPAVR**
Found in **IPI00014151**, Tax_Id=9606 Gene_Symbol=PSMD6 26S proteasome non-ATPase regulatory subunit 6
Match to Query 25774: 1602.918702 from(535.313510,3+)
Title: 091224LimSK_Exosome3_04.7281.7281.3.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide **Mr(calc):** 1602.9093
Fixed modifications: Carbamidomethyl (C)
Ions Score: 32 Expect: 0.026
Matches (**Bold Red**): 34/126 fragment ions using 81 most intense peaks

#	b	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180			G							15
2	129.0659	65.0366			A	1546.8952	773.9512	1529.8686	765.4379	1528.8846	764.9459	14
3	258.1084	129.5579	240.0979	120.5526	E	1475.8580	738.4327	1458.8315	729.9194	1457.8475	729.4274	13
4	371.1925	186.0999	353.1819	177.0946	I	1346.8154	673.9114	1329.7889	665.3981	1328.8049	664.9061	12
5	484.2766	242.6419	466.2660	233.6366	L	1233.7314	617.3693	1216.7048	608.8561	1215.7208	608.3640	11
6	613.3192	307.1632	595.3086	298.1579	E	1120.6473	560.8273	1103.6208	552.3140	1102.6368	551.8220	10
7	712.3876	356.6974	694.3770	347.6921	V	991.6047	496.3060	974.5782	487.7927	973.5942	487.3007	9
8	825.4716	413.2395	807.4611	404.2342	L	892.5363	446.7718	875.5098	438.2585	874.5257	437.7665	8
9	962.5306	481.7689	944.5200	472.7636	H	779.4522	390.2298	762.4257	381.7165	761.4417	381.2245	7
10	1049.5626	525.2849	1031.5520	516.2796	S	642.3933	321.7003	625.3668	313.1870	624.3828	312.6950	6
11	1162.6466	581.8270	1144.6361	572.8217	L	555.3613	278.1843	538.3348	269.6710			5
12	1259.6994	630.3533	1241.6888	621.3481	P	442.2772	221.6423	425.2507	213.1290			4
13	1330.7365	665.8719	1312.7260	656.8666	A	345.2245	173.1159	328.1979	164.6026			3
14	1429.8049	715.4061	1411.7944	706.4008	V	274.1874	137.5973	257.1608	129.0840			2
15					R	175.1190	88.0631	158.0924	79.5498			1



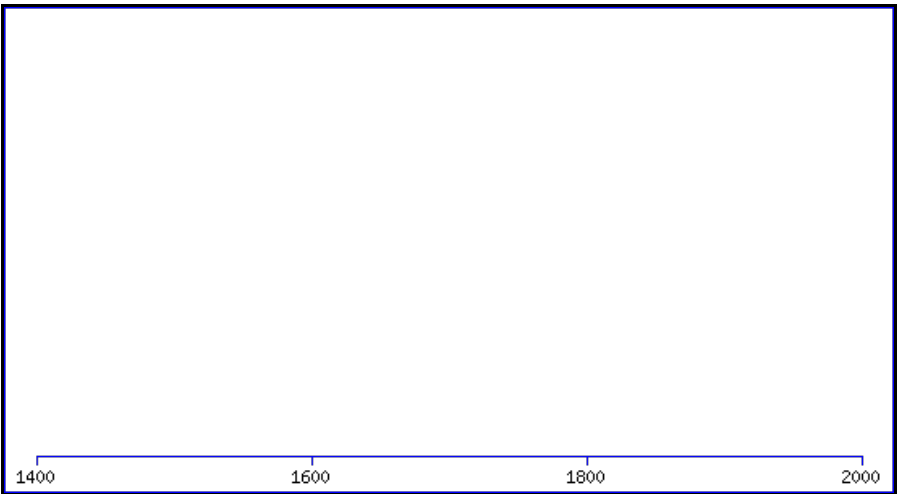
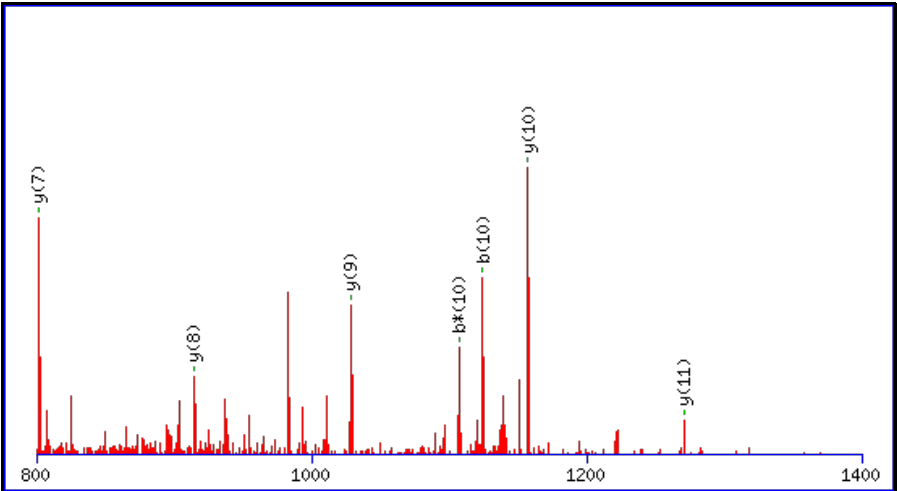
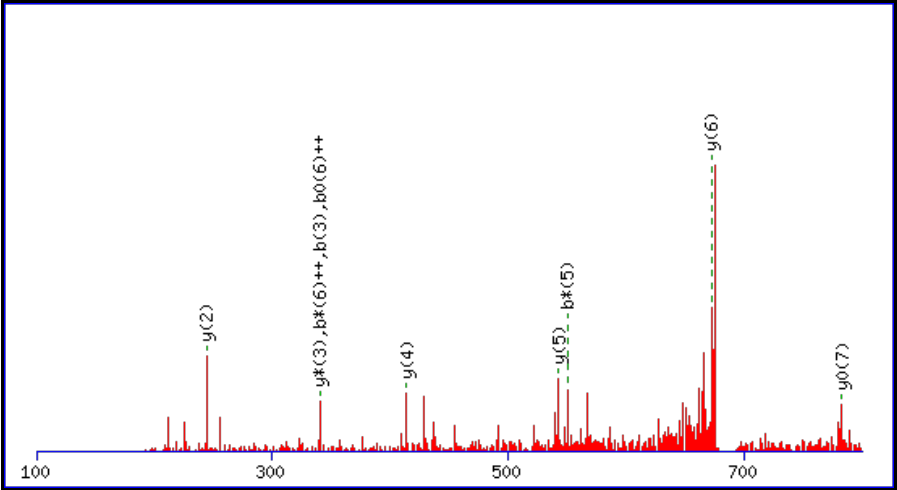
All matches to this query

Score	Mr(calc):	Delta	Sequence
32.2	1602.9093	0.0094	GAEILEVLHSLPAVR
5.8	1601.9242	0.9945	TLRALRPLRALSR
0.7	1601.9253	0.9934	RVVSVYQAALDLLR
0.5	1602.9205	-0.0018	GALLSYRRNDLYVK

Peptide View

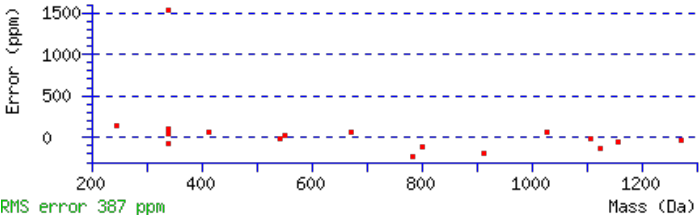
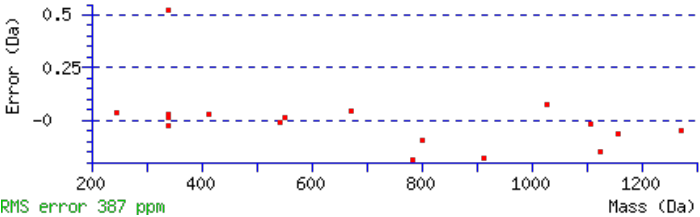
MS/MS Fragmentation of **PLENLEEEGLPK**
Found in **IPI00014151**, Tax_Id=9606 Gene_Symbol=PSMD6 26S proteasome non-ATPase regulatory subunit 6

Match to Query 13733: 1366.707948 from(684.361250,2+)
Title: 091224LimSK_Exosome3_04.3023.3023.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1366.6980
Fixed modifications: Carbamidomethyl (C)
Ions Score: 63 Expect: 6.5e-005
Matches (**Bold Red**): 17/114 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	98.0600	49.5337					P							12
2	211.1441	106.0757					L	1270.6525	635.8299	1253.6260	627.3166	1252.6420	626.8246	11
3	340.1867	170.5970			322.1761	161.5917	E	1157.5685	579.2879	1140.5419	570.7746	1139.5579	570.2826	10
4	454.2296	227.6185	437.2031	219.1052	436.2191	218.6132	N	1028.5259	514.7666	1011.4993	506.2533	1010.5153	505.7613	9
5	567.3137	284.1605	550.2871	275.6472	549.3031	275.1552	L	914.4829	457.7451	897.4564	449.2318	896.4724	448.7398	8
6	696.3563	348.6818	679.3297	340.1685	678.3457	339.6765	E	801.3989	401.2031	784.3723	392.6898	783.3883	392.1978	7
7	825.3989	413.2031	808.3723	404.6898	807.3883	404.1978	E	672.3563	336.6818	655.3297	328.1685	654.3457	327.6765	6
8	954.4415	477.7244	937.4149	469.2111	936.4309	468.7191	E	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	5
9	1011.4629	506.2351	994.4364	497.7218	993.4524	497.2298	G	414.2711	207.6392	397.2445	199.1259			4
10	1124.5470	562.7771	1107.5204	554.2639	1106.5364	553.7719	L	357.2496	179.1285	340.2231	170.6152			3
11	1221.5998	611.3035	1204.5732	602.7902	1203.5892	602.2982	P	244.1656	122.5864	227.1390	114.0731			2
12							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

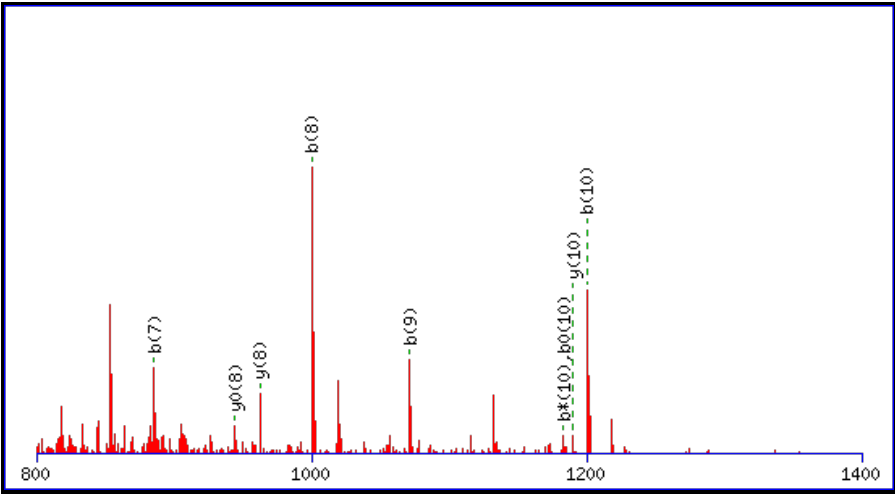
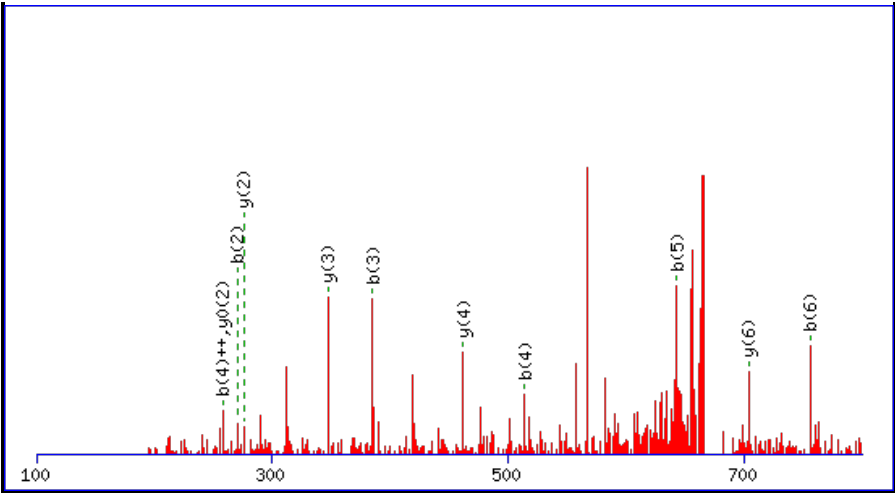
Score	Mr(calc):	Delta	Sequence
63.5	1366.6980	0.0100	PLENLEEEGLPK
4.5	1365.6929	1.0151	GSSYLGIPFNPSK
4.2	1365.7170	0.9910	RSPLLKSGPFGK
2.5	1366.7156	-0.0076	RSPVLIAKTMR
1.9	1365.7113	0.9966	GLADHVLQDRSR
1.4	1366.6969	0.0110	RASVTERLDLK
1.2	1366.7043	0.0036	ENILYMRLATK

Spectrum No: 139; Query: 12962; Rank: 1

Peptide View

MS/MS Fragmentation of **RLDEELEDAEK**
Found in **IPI00014151**, Tax_Id=9606 Gene_Symbol=PSMD6 26S proteasome non-ATPase regulatory subunit 6

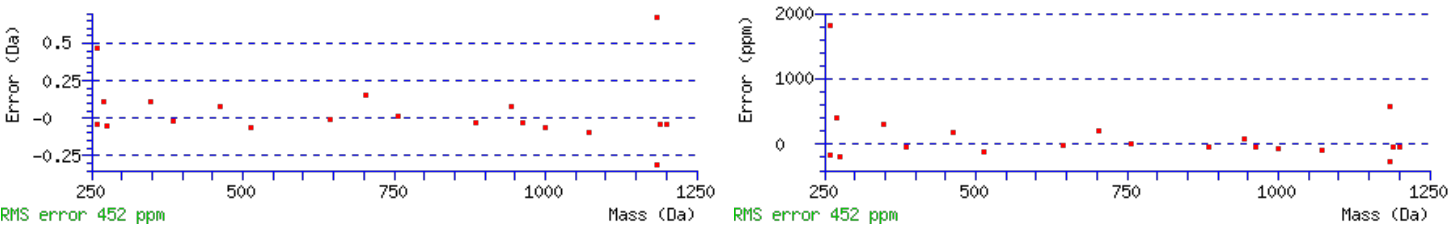
Match to Query 12962: 1345.643328 from(673.828940,2+)
Title: 091224LimSK_Exosome3_04.1124.1124.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf



Monoisotopic mass of neutral peptide Mr(calc): 1345.6361
Fixed modifications: Carbamidomethyl (C)
Ions Score: 41 Expect: 0.017
Matches (**Bold Red**): 20/114 fragment ions using 59 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺⁺	y ⁰	y ⁰⁺⁺	#
1	157.1084	79.0578	140.0818	70.5446			R							11
2	270.1925	135.5999	253.1659	127.0866			L	1190.5423	595.7748	1173.5158	587.2615	1172.5317	586.7695	10
3	385.2194	193.1133	368.1928	184.6001	367.2088	184.1081	D	1077.4582	539.2328	1060.4317	530.7195	1059.4477	530.2275	9
4	514.2620	257.6346	497.2354	249.1214	496.2514	248.6293	E	962.4313	481.7193	945.4047	473.2060	944.4207	472.7140	8
5	643.3046	322.1559	626.2780	313.6427	625.2940	313.1506	E	833.3887	417.1980	816.3622	408.6847	815.3781	408.1927	7
6	756.3886	378.6980	739.3621	370.1847	738.3781	369.6927	L	704.3461	352.6767	687.3196	344.1634	686.3355	343.6714	6

7	885.4312	443.2193	868.4047	434.7060	867.4207	434.2140	E	591.2620	296.1347	574.2355	287.6214	573.2515	287.1294	5
8	1000.4582	500.7327	983.4316	492.2195	982.4476	491.7274	D	462.2195	231.6134	445.1929	223.1001	444.2089	222.6081	4
9	1071.4953	536.2513	1054.4687	527.7380	1053.4847	527.2460	A	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
10	1200.5379	600.7726	1183.5113	592.2593	1182.5273	591.7673	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
11							K	147.1128	74.0600	130.0863	65.5468			1



All matches to this query

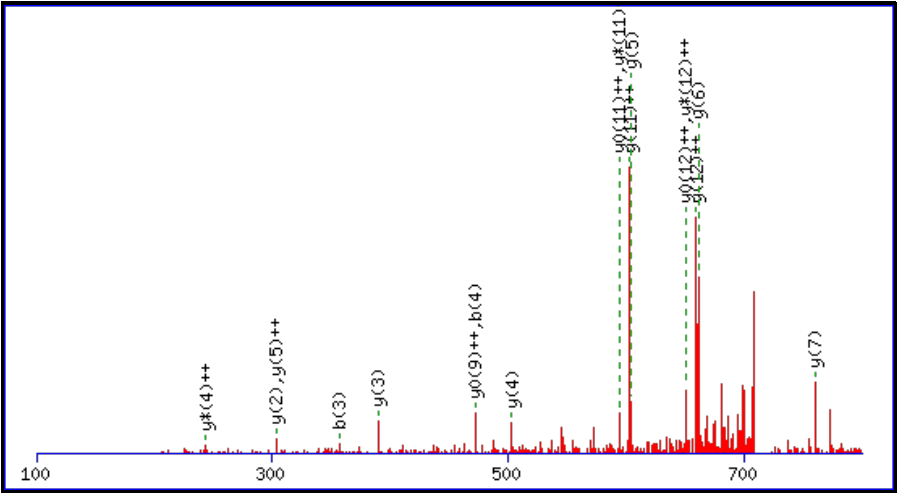
Score	Mr(calc):	Delta	Sequence
40.7	1345.6361	0.0072	RLDEELED AEK
8.2	1345.6520	-0.0087	IRSVIKQG GTK
8.1	1345.6337	0.0097	XIGLMYTFGDGR
5.4	1343.6470	1.9964	ATGDWAKVPEDR
4.2	1345.6449	-0.0016	AAGEPTASVCHTK
3.6	1345.6407	0.0026	LRLSIQDITK
2.5	1343.6486	1.9947	DLLRLSYGEAK
2.2	1343.6486	1.9947	SSVEEALFVKR
2.2	1343.6486	1.9947	SSVEEALFVKR
1.7	1345.6530	-0.0097	LKLSYEGEVTK

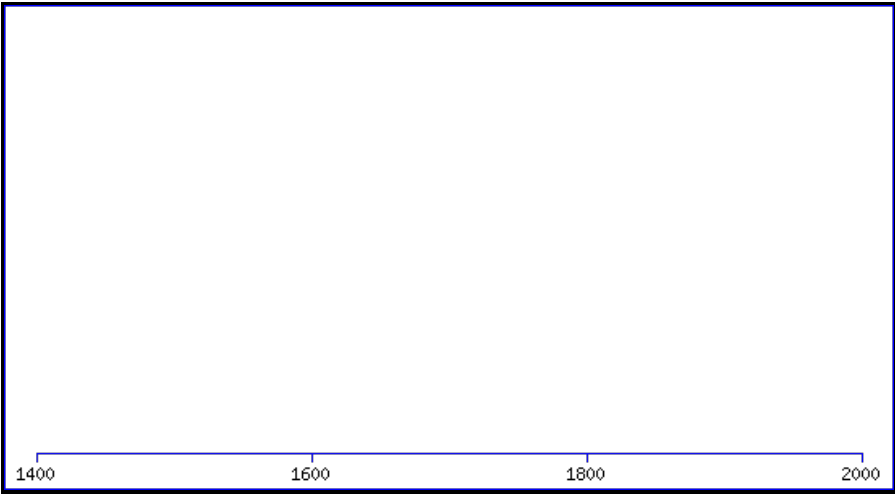
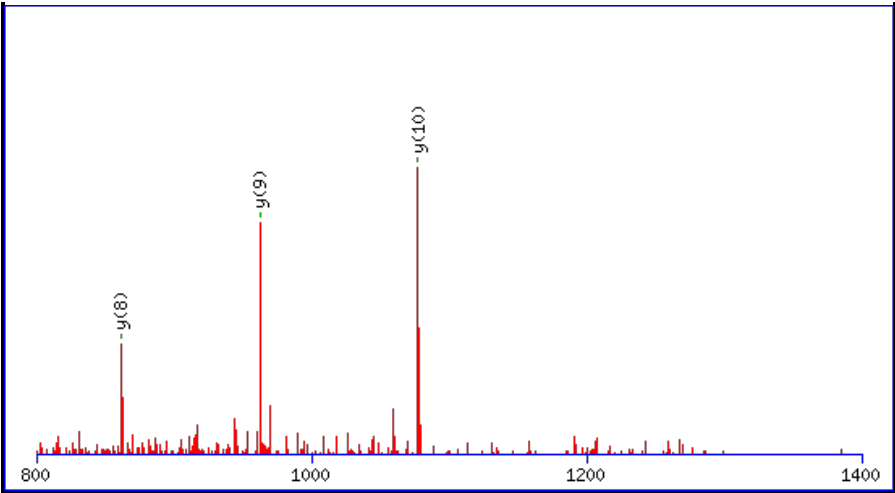
Spectrum No: 140; Query: 16923; Rank: 1

Peptide View

MS/MS Fragmentation of **DIKDTTVGTL SQ R**
Found in **IP100019927**, Tax_Id=9606 Gene_Symbol=PSMD7 26S proteasome non-ATPase regulatory subunit 7

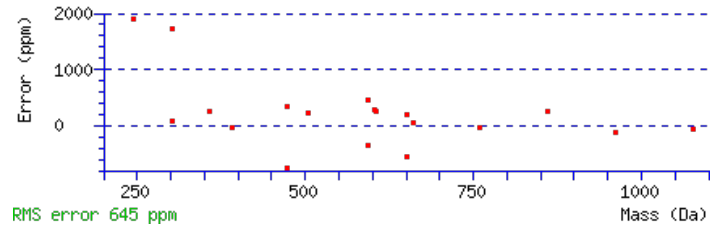
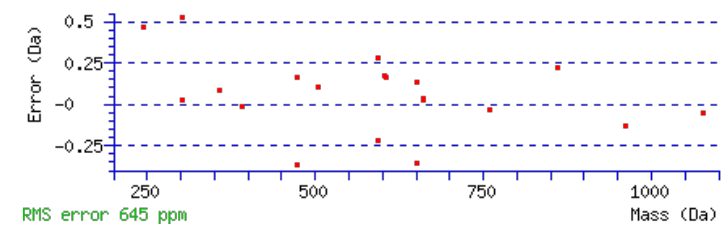
Match to Query 16923: 1432.761048 from(717.387800,2+)
Title: 091224LimSK_Exosome3_05.1608.1608.2.dta
Data file C:\Temp\Mascoti\LSK_2D\091224LimSK_Exosome3_01_2D.mgf





Monoisotopic mass of neutral peptide Mr(calc): 1432.7522
Fixed modifications: Carbamidomethyl (C)
Ions Score: 70 Expect: 1.5e-005
Matches (**Bold Red**): 20/136 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	116.0342	58.5207			98.0237	49.5155	D							13
2	229.1183	115.0628			211.1077	106.0575	I	1318.7325	659.8699	1301.7060	651.3566	1300.7219	650.8646	12
3	357.2132	179.1103	340.1867	170.5970	339.2027	170.1050	K	1205.6484	603.3279	1188.6219	594.8146	1187.6379	594.3226	11
4	472.2402	236.6237	455.2136	228.1105	454.2296	227.6185	D	1077.5535	539.2804	1060.5269	530.7671	1059.5429	530.2751	10
5	573.2879	287.1476	556.2613	278.6343	555.2773	278.1423	T	962.5265	481.7669	945.5000	473.2536	944.5160	472.7616	9
6	674.3355	337.6714	657.3090	329.1581	656.3250	328.6661	T	861.4789	431.2431	844.4523	422.7298	843.4683	422.2378	8
7	773.4040	387.2056	756.3774	378.6923	755.3934	378.2003	V	760.4312	380.7192	743.4046	372.2060	742.4206	371.7139	7
8	830.4254	415.7164	813.3989	407.2031	812.4149	406.7111	G	661.3628	331.1850	644.3362	322.6717	643.3522	322.1797	6
9	931.4731	466.2402	914.4466	457.7269	913.4625	457.2349	T	604.3413	302.6743	587.3148	294.1610	586.3307	293.6690	5
10	1044.5572	522.7822	1027.5306	514.2689	1026.5466	513.7769	L	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	4
11	1131.5892	566.2982	1114.5626	557.7850	1113.5786	557.2930	S	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
12	1259.6478	630.3275	1242.6212	621.8143	1241.6372	621.3222	Q	303.1775	152.0924	286.1510	143.5791			2
13							R	175.1190	88.0631	158.0924	79.5498			1



All matches to this query

Score	Mr(calc):	Delta	Sequence
69.5	1432.7522	0.0089	DIKDTTVGTLSQLR
12.1	1431.7504	1.0107	MNOIVGLGISTQR
9.0	1432.7596	0.0015	NLTLMATTSQLPK
6.7	1430.7477	2.0133	LLAGEDGTSERRK
6.1	1432.7674	-0.0063	EYRLTPALDSLRL
6.1	1430.7551	2.0059	LLGMLPSENSSKR
4.8	1431.7527	1.0084	LKLVDASVAFYK
4.5	1432.7634	-0.0023	LELRQLSTGSSSR
4.3	1432.7748	-0.0137	LMKDISQNEPIK
3.6	1430.7405	2.0205	DKIIFPDENVK

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