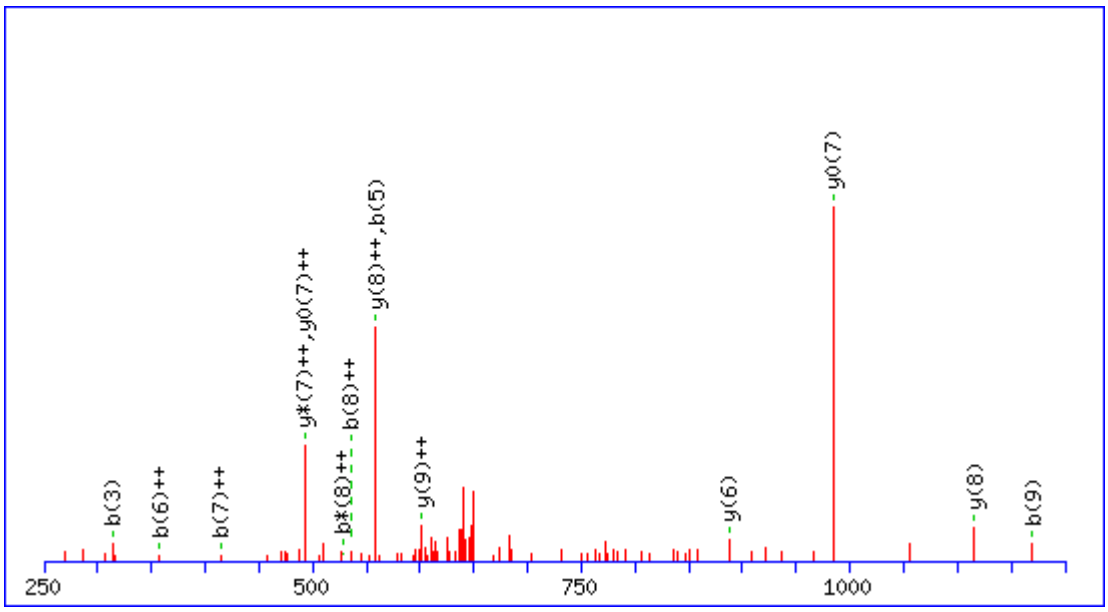
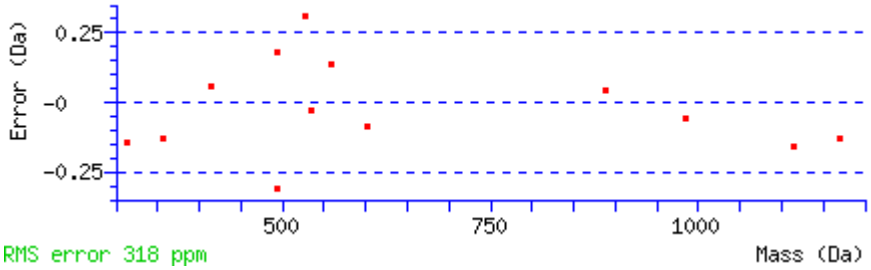
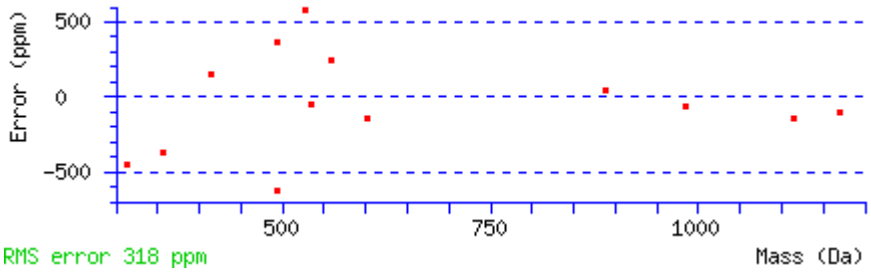
IDENTIFICATION 1
MS/MS Fragmentation of LSLDERIYVK
Found in IPI00230388



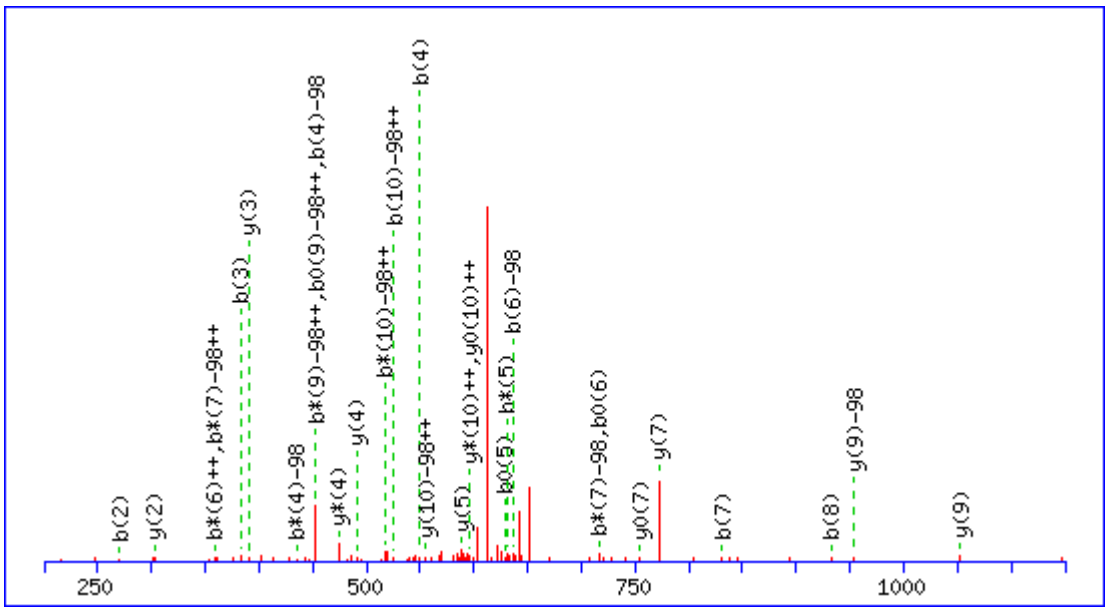
Monoisotopic mass of neutral peptide Mr(calc): 1314.6584
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y8 : Phospho (Y)
Ions Score: 21 Expect: 0.67 (help)

#	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	201.1234	101.0653			183.1128	92.0600	S	1202.5817	601.7945	1185.5551	593.2812	1184.5711	592.7892	9
3	314.2074	157.6074			296.1969	148.6021	L	1115.5497	558.2785	1098.5231	549.7652	1097.5391	549.2732	8
4	429.2344	215.1208			411.2238	206.1155	D	1002.4656	501.7364	985.4390	493.2232	984.4550	492.7312	7
5	558.2770	279.6421			540.2664	270.6368	E	887.4386	444.2230	870.4121	435.7097	869.4281	435.2177	6
6	714.3781	357.6927	697.3515	349.1794	696.3675	348.6874	R	758.3961	379.7017	741.3695	371.1884			5
7	827.4621	414.2347	810.4356	405.7214	809.4516	405.2294	I	602.2949	301.6511	585.2684	293.1378			4
8	1070.4918	535.7495	1053.4653	527.2363	1052.4812	526.7443	Y	489.2109	245.1091	472.1843	236.5958			3
9	1169.5602	585.2837	1152.5337	576.7705	1151.5497	576.2785	V	246.1812	123.5942	229.1547	115.0810			2
10							K	147.1128	74.0600	130.0863	65.5468			1



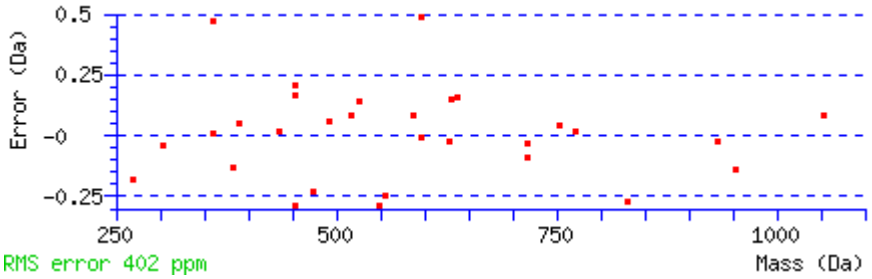


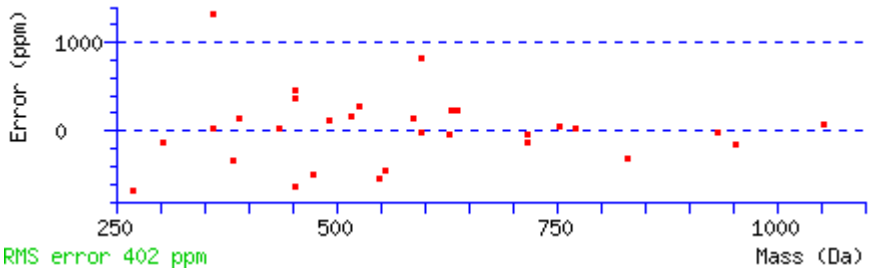
IDENTIFICATION 2
MS/MS Fragmentation of LRLSPSPTSQR
Found in IPI00230435



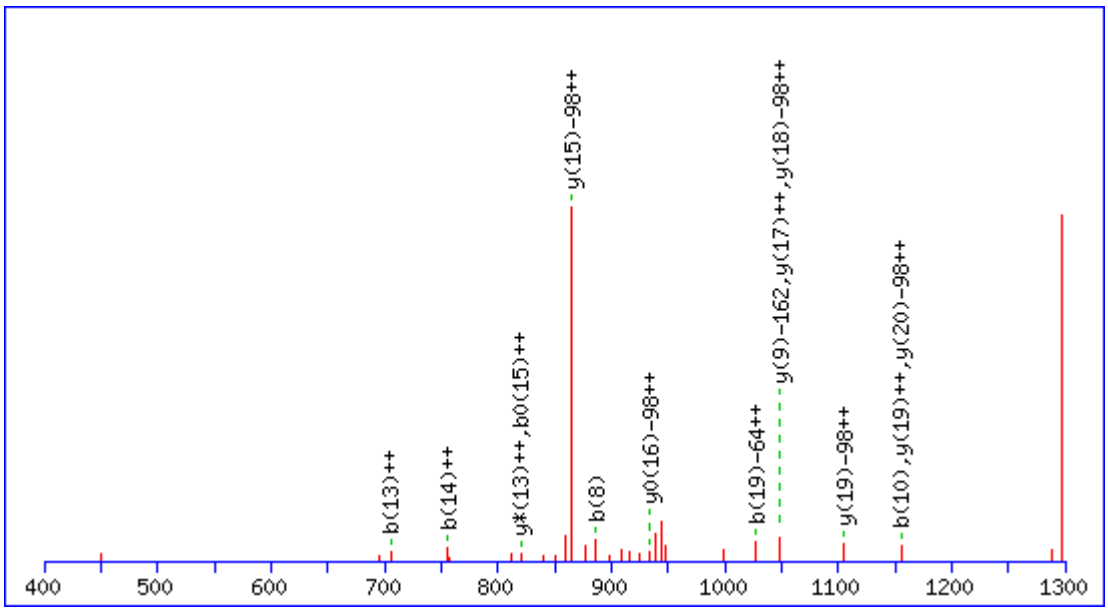
Monoisotopic mass of neutral peptide Mr(calc): 1320.6551
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 22 Expect: 0.77 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	270.1925	135.5999	253.1659	127.0866			R	1110.6014	555.8044	1093.5749	547.2911	1092.5909	546.7991	10
3	383.2765	192.1419	366.2500	183.6286			L	954.5003	477.7538	937.4738	469.2405	936.4898	468.7485	9
4	452.2980	226.6526	435.2714	218.1394	434.2874	217.6473	S	841.4163	421.2118	824.3897	412.6985	823.4057	412.2065	8
5	549.3507	275.1790	532.3242	266.6657	531.3402	266.1737	P	772.3948	386.7010	755.3682	378.1878	754.3842	377.6958	7
6	636.3828	318.6950	619.3562	310.1817	618.3722	309.6897	S	675.3420	338.1747	658.3155	329.6614	657.3315	329.1694	6
7	733.4355	367.2214	716.4090	358.7081	715.4250	358.2161	P	588.3100	294.6586	571.2835	286.1454	570.2994	285.6534	5
8	834.4832	417.7452	817.4567	409.2320	816.4726	408.7400	T	491.2572	246.1323	474.2307	237.6190	473.2467	237.1270	4
9	921.5152	461.2613	904.4887	452.7480	903.5047	452.2560	S	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
10	1049.5738	525.2905	1032.5473	516.7773	1031.5633	516.2853	Q	303.1775	152.0924	286.1510	143.5791			2
11							R	175.1190	88.0631	158.0924	79.5498			1



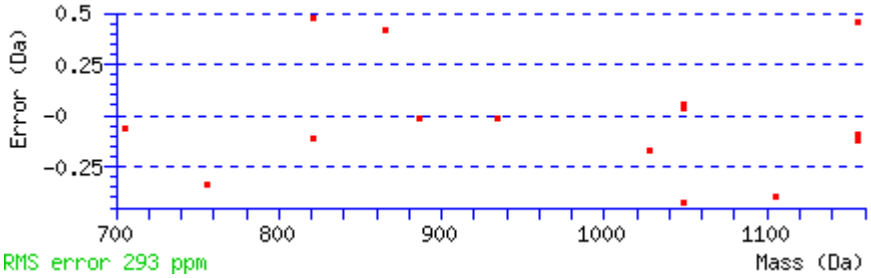


IDENTIFICATION 3
MS/MS Fragmentation of IMSIVDPNRLGVVTFQAFIDFMSR
Found in IPI00380436

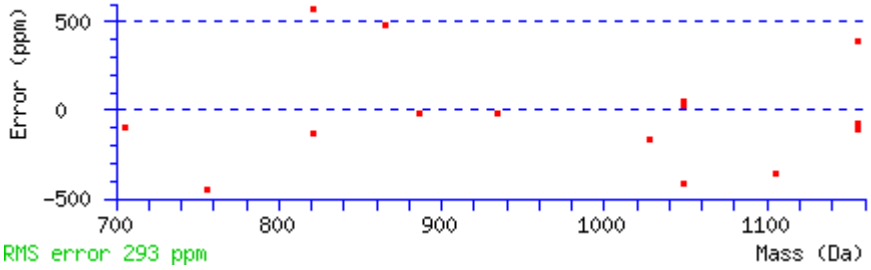


Monoisotopic mass of neutral peptide Mr(calc): 2867.3751
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M22 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
S23 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 23 Expect: 0.74 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							24
2	261.1267	131.0670					M	2657.3214	1329.1644	2640.2949	1320.6511	2639.3109	1320.1591	23
3	348.1588	174.5830			330.1482	165.5777	S	2510.2860	1255.6467	2493.2595	1247.1334	2492.2755	1246.6414	22
4	461.2428	231.1251			443.2323	222.1198	I	2423.2540	1212.1306	2406.2275	1203.6174	2405.2434	1203.1254	21
5	560.3112	280.6593			542.3007	271.6540	V	2310.1699	1155.5886	2293.1434	1147.0753	2292.1594	1146.5833	20
6	675.3382	338.1727			657.3276	329.1674	D	2211.1015	1106.0544	2194.0750	1097.5411	2193.0910	1097.0491	19
7	772.3910	386.6991			754.3804	377.6938	P	2096.0746	1048.5409	2079.0480	1040.0277	2078.0640	1039.5357	18
8	886.4339	443.7206	869.4073	435.2073	868.4233	434.7153	N	1999.0218	1000.0146	1981.9953	991.5013	1981.0113	991.0093	17
9	1042.5350	521.7711	1025.5084	513.2579	1024.5244	512.7659	R	1884.9789	942.9931	1867.9524	934.4798	1866.9683	933.9878	16
10	1155.6191	578.3132	1138.5925	569.7999	1137.6085	569.3079	L	1728.8778	864.9425	1711.8512	856.4293	1710.8672	855.9373	15
11	1212.6405	606.8239	1195.6140	598.3106	1194.6300	597.8186	G	1615.7937	808.4005	1598.7672	799.8872	1597.7832	799.3952	14
12	1311.7089	656.3581	1294.6824	647.8448	1293.6984	647.3528	V	1558.7723	779.8898	1541.7457	771.3765	1540.7617	770.8845	13
13	1410.7773	705.8923	1393.7508	697.3790	1392.7668	696.8870	V	1459.7038	730.3556	1442.6773	721.8423	1441.6933	721.3503	12
14	1511.8250	756.4162	1494.7985	747.9029	1493.8145	747.4109	T	1360.6354	680.8214	1343.6089	672.3081	1342.6249	671.8161	11
15	1658.8934	829.9504	1641.8669	821.4371	1640.8829	820.9451	F	1259.5878	630.2975	1242.5612	621.7842	1241.5772	621.2922	10
16	1786.9520	893.9796	1769.9255	885.4664	1768.9415	884.9744	Q	1112.5193	556.7633	1095.4928	548.2500	1094.5088	547.7580	9
17	1857.9891	929.4982	1840.9626	920.9849	1839.9786	920.4929	A	984.4608	492.7340	967.4342	484.2207	966.4502	483.7287	8
18	2005.0575	1003.0324	1988.0310	994.5191	1987.0470	994.0271	F	913.4237	457.2155	896.3971	448.7022	895.4131	448.2102	7
19	2118.1416	1059.5744	2101.1151	1051.0612	2100.1310	1050.5692	I	766.3552	383.6813	749.3287	375.1680	748.3447	374.6760	6
20	2233.1686	1117.0879	2216.1420	1108.5746	2215.1580	1108.0826	D	653.2712	327.1392	636.2446	318.6259	635.2606	318.1339	5
21	2380.2370	1190.6221	2363.2104	1182.1088	2362.2264	1181.6168	F	538.2442	269.6258	521.2177	261.1125	520.2337	260.6205	4
22	2527.2724	1264.1398	2510.2458	1255.6265	2509.2618	1255.1345	M	391.1758	196.0915	374.1493	187.5783	373.1653	187.0863	3
23	2596.2938	1298.6506	2579.2673	1290.1373	2578.2833	1289.6453	S	244.1404	122.5738	227.1139	114.0606	226.1299	113.5686	2
24							R	175.1190	88.0631	158.0924	79.5498			1

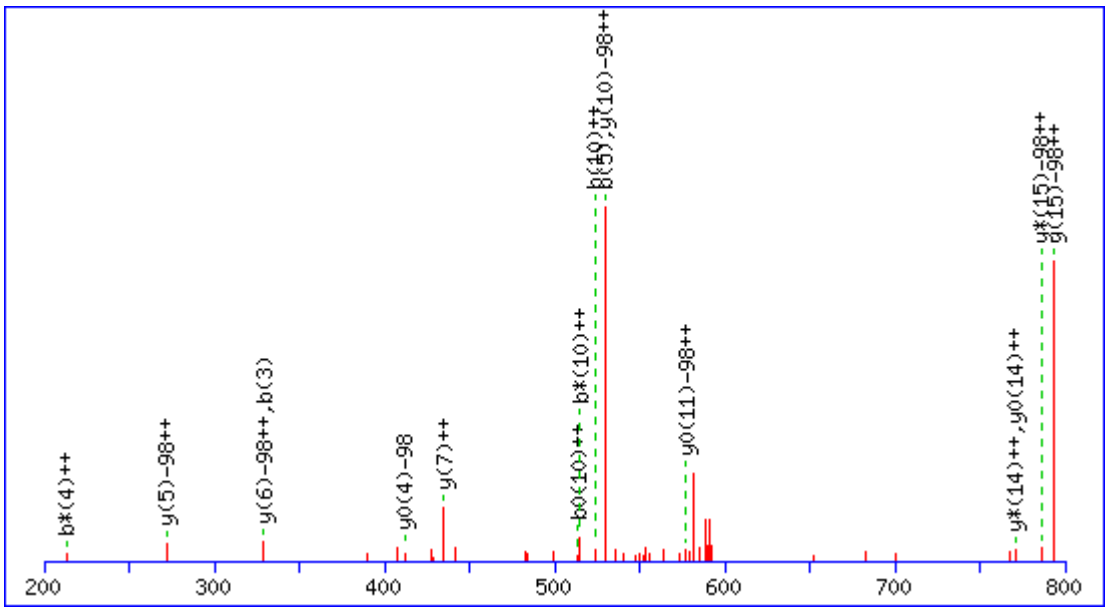


RMS error 293 ppm



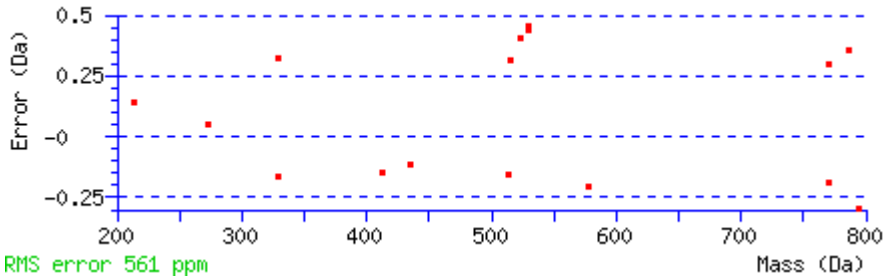
RMS error 293 ppm

IDENTIFICATION 4
MS/MS Fragmentation of IQSISNSKADLIDTGR
Found in IPI00124283

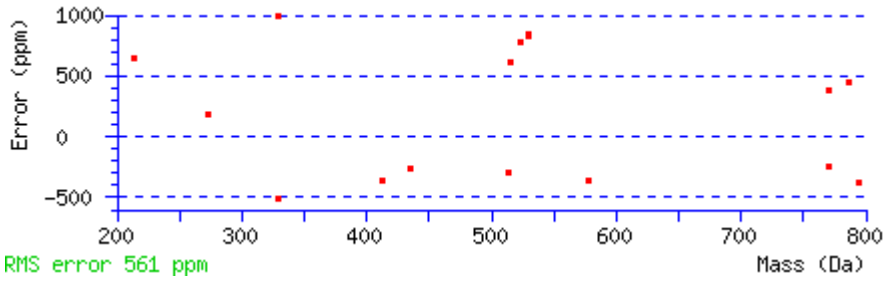


Monoisotopic mass of neutral peptide Mr(calc): 1797.8509
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N6 : Deamidated (NQ)
T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.38 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							16
2	242.1499	121.5786	225.1234	113.0653			Q	1587.7973	794.4023	1570.7707	785.8890	1569.7867	785.3970	15
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	S	1459.7387	730.3730	1442.7122	721.8597	1441.7281	721.3677	14
4	442.2660	221.6366	425.2395	213.1234	424.2554	212.6314	I	1372.7067	686.8570	1355.6801	678.3437	1354.6961	677.8517	13
5	529.2980	265.1527	512.2715	256.6394	511.2875	256.1474	S	1259.6226	630.3149	1242.5961	621.8017	1241.6121	621.3097	12
6	644.3250	322.6661	627.2984	314.1529	626.3144	313.6608	N	1172.5906	586.7989	1155.5640	578.2857	1154.5800	577.7937	11
7	731.3570	366.1821	714.3305	357.6689	713.3464	357.1769	S	1057.5636	529.2855	1040.5371	520.7722	1039.5531	520.2802	10
8	859.4520	430.2296	842.4254	421.7163	841.4414	421.2243	K	970.5316	485.7694	953.5051	477.2562	952.5211	476.7642	9
9	930.4891	465.7482	913.4625	457.2349	912.4785	456.7429	A	842.4367	421.7220	825.4101	413.2087	824.4261	412.7167	8
10	1045.5160	523.2617	1028.4895	514.7484	1027.5055	514.2564	D	771.3995	386.2034	754.3730	377.6901	753.3890	377.1981	7
11	1158.6001	579.8037	1141.5735	571.2904	1140.5895	570.7984	L	656.3726	328.6899	639.3461	320.1767	638.3620	319.6847	6
12	1271.6842	636.3457	1254.6576	627.8324	1253.6736	627.3404	I	543.2885	272.1479	526.2620	263.6346	525.2780	263.1426	5
13	1386.7111	693.8592	1369.6846	685.3459	1368.7005	684.8539	D	430.2045	215.6059	413.1779	207.0926	412.1939	206.6006	4
14	1469.7482	735.3777	1452.7217	726.8645	1451.7376	726.3725	T	315.1775	158.0924	298.1510	149.5791	297.1670	149.0871	3
15	1526.7697	763.8885	1509.7431	755.3752	1508.7591	754.8832	G	232.1404	116.5738	215.1139	108.0606			2
16							R	175.1190	88.0631	158.0924	79.5498			1

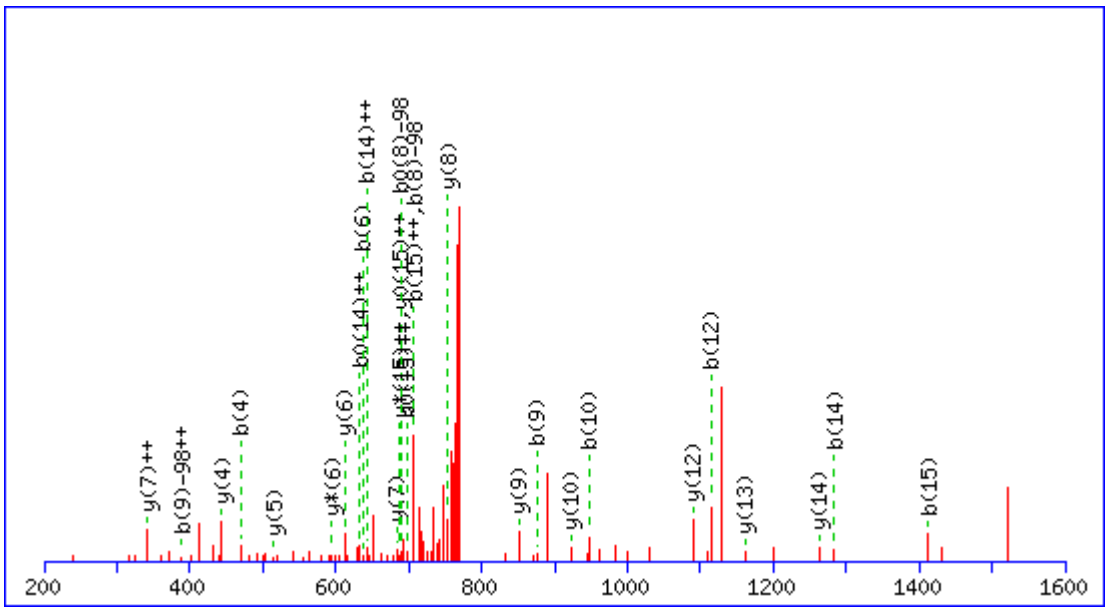


RMS error 561 ppm



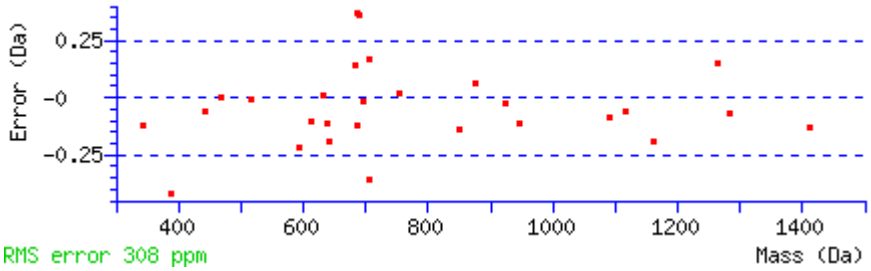
RMS error 561 ppm

IDENTIFICATION 5
MS/MS Fragmentation of SETAPAAPAAPAPAEK
Found in IPI00223714

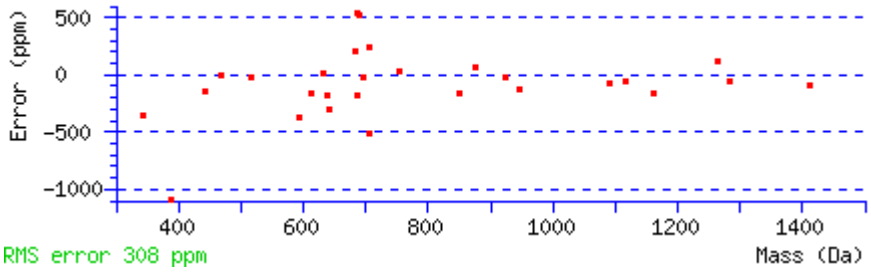


Monoisotopic mass of neutral peptide Mr(calc): 1557.7076
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 Expect: 0.17 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	168.0056	84.5065	149.9951	75.5012	S							16
2	297.0482	149.0278	279.0377	140.0225	E	1391.7165	696.3619	1374.6900	687.8486	1373.7060	687.3566	15
3	398.0959	199.5516	380.0853	190.5463	T	1262.6739	631.8406	1245.6474	623.3273	1244.6634	622.8353	14
4	469.1330	235.0701	451.1225	226.0649	A	1161.6263	581.3168	1144.5997	572.8035	1143.6157	572.3115	13
5	566.1858	283.5965	548.1752	274.5912	P	1090.5891	545.7982	1073.5626	537.2849	1072.5786	536.7929	12
6	637.2229	319.1151	619.2123	310.1098	A	993.5364	497.2718	976.5098	488.7585	975.5258	488.2665	11
7	708.2600	354.6336	690.2494	345.6284	A	922.4993	461.7533	905.4727	453.2400	904.4887	452.7480	10
8	805.3128	403.1600	787.3022	394.1547	P	851.4621	426.2347	834.4356	417.7214	833.4516	417.2294	9
9	876.3499	438.6786	858.3393	429.6733	A	754.4094	377.7083	737.3828	369.1951	736.3988	368.7030	8
10	947.3870	474.1971	929.3764	465.1919	A	683.3723	342.1898	666.3457	333.6765	665.3617	333.1845	7
11	1044.4398	522.7235	1026.4292	513.7182	P	612.3352	306.6712	595.3086	298.1579	594.3246	297.6659	6
12	1115.4769	558.2421	1097.4663	549.2368	A	515.2824	258.1448	498.2558	249.6316	497.2718	249.1395	5
13	1212.5296	606.7685	1194.5191	597.7632	P	444.2453	222.6263	427.2187	214.1130	426.2347	213.6210	4
14	1283.5668	642.2870	1265.5562	633.2817	A	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
15	1412.6094	706.8083	1394.5988	697.8030	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
16					K	147.1128	74.0600	130.0863	65.5468			1

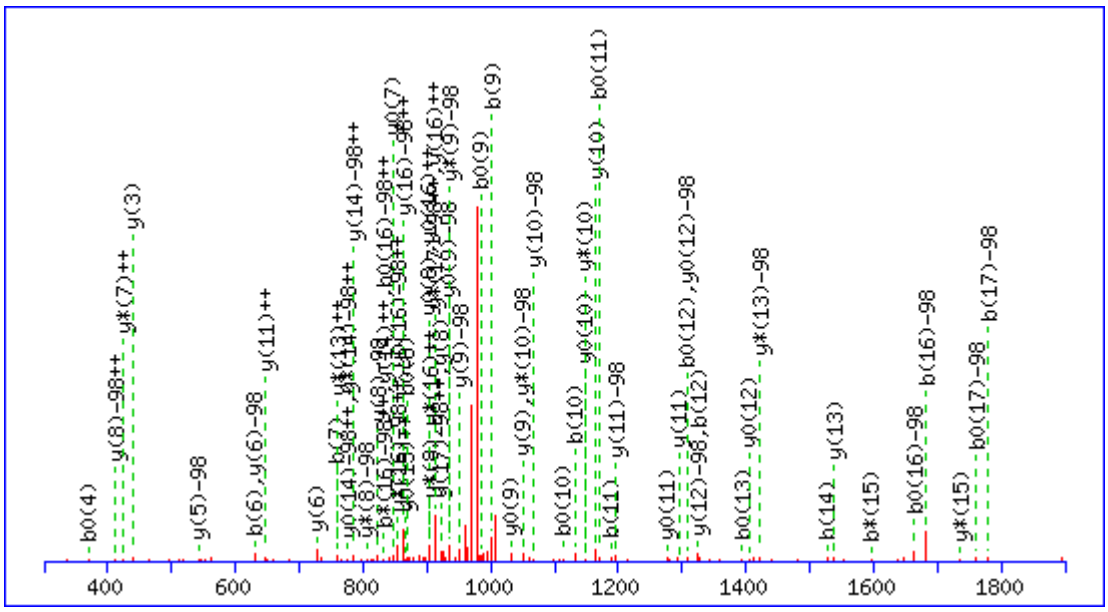


RMS error 308 ppm



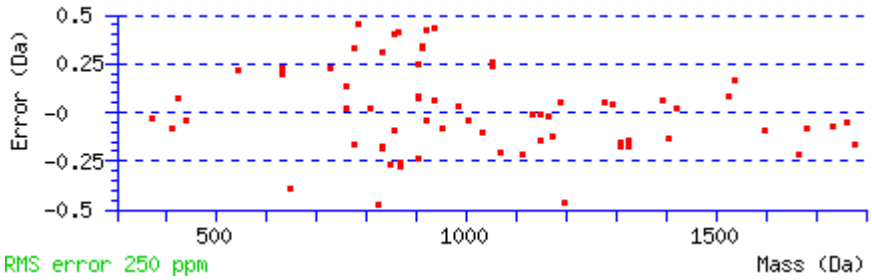
RMS error 308 ppm

IDENTIFICATION 6
MS/MS Fragmentation of IDASKNEEDEGHSNSSPR
Found in IPI00330958



Monoisotopic mass of neutral peptide Mr(calc): 2050.8229
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 44 Expect: 0.0069 (help)

#	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	229.1183	115.0628			211.1077	106.0575	D	1840.7692	920.8883	1823.7427	912.3750	1822.7587	911.8830	17
3	300.1554	150.5813			282.1448	141.5761	A	1725.7423	863.3748	1708.7157	854.8615	1707.7317	854.3695	16
4	387.1874	194.0974			369.1769	185.0921	S	1654.7052	827.8562	1637.6786	819.3430	1636.6946	818.8509	15
5	515.2824	258.1448	498.2558	249.6316	497.2718	249.1395	K	1567.6732	784.3402	1550.6466	775.8269	1549.6626	775.3349	14
6	629.3253	315.1663	612.2988	306.6530	611.3148	306.1610	N	1439.5782	720.2927	1422.5516	711.7795	1421.5676	711.2874	13
7	758.3679	379.6876	741.3414	371.1743	740.3573	370.6823	E	1325.5353	663.2713	1308.5087	654.7580	1307.5247	654.2660	12
8	887.4105	444.2089	870.3840	435.6956	869.3999	435.2036	E	1196.4927	598.7500	1179.4661	590.2367	1178.4821	589.7447	11
9	1002.4374	501.7224	985.4109	493.2091	984.4269	492.7171	D	1067.4501	534.2287	1050.4235	525.7154	1049.4395	525.2234	10
10	1131.4800	566.2437	1114.4535	557.7304	1113.4695	557.2384	E	952.4231	476.7152	935.3966	468.2019	934.4126	467.7099	9
11	1188.5015	594.7544	1171.4750	586.2411	1170.4909	585.7491	G	823.3805	412.1939	806.3540	403.6806	805.3700	403.1886	8
12	1325.5604	663.2838	1308.5339	654.7706	1307.5498	654.2786	H	766.3591	383.6832	749.3325	375.1699	748.3485	374.6779	7
13	1412.5924	706.7999	1395.5659	698.2866	1394.5819	697.7946	S	629.3002	315.1537	612.2736	306.6404	611.2896	306.1484	6
14	1526.6354	763.8213	1509.6088	755.3080	1508.6248	754.8160	N	542.2681	271.6377	525.2416	263.1244	524.2576	262.6324	5
15	1613.6674	807.3373	1596.6408	798.8241	1595.6568	798.3321	S	428.2252	214.6162	411.1987	206.1030	410.2146	205.6110	4
16	1682.6889	841.8481	1665.6623	833.3348	1664.6783	832.8428	S	341.1932	171.1002	324.1666	162.5870	323.1826	162.0949	3
17	1779.7416	890.3744	1762.7151	881.8612	1761.7311	881.3692	P	272.1717	136.5895	255.1452	128.0762			2
18							R	175.1190	88.0631	158.0924	79.5498			1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0.25
-0
-0.25
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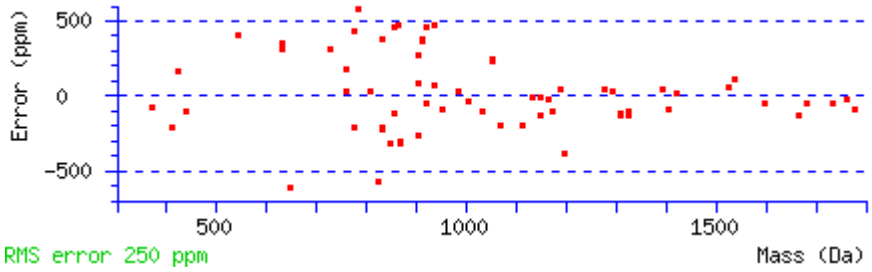
1000
1500
RMS error 250 ppm
Mass (Da)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Error (ppm)
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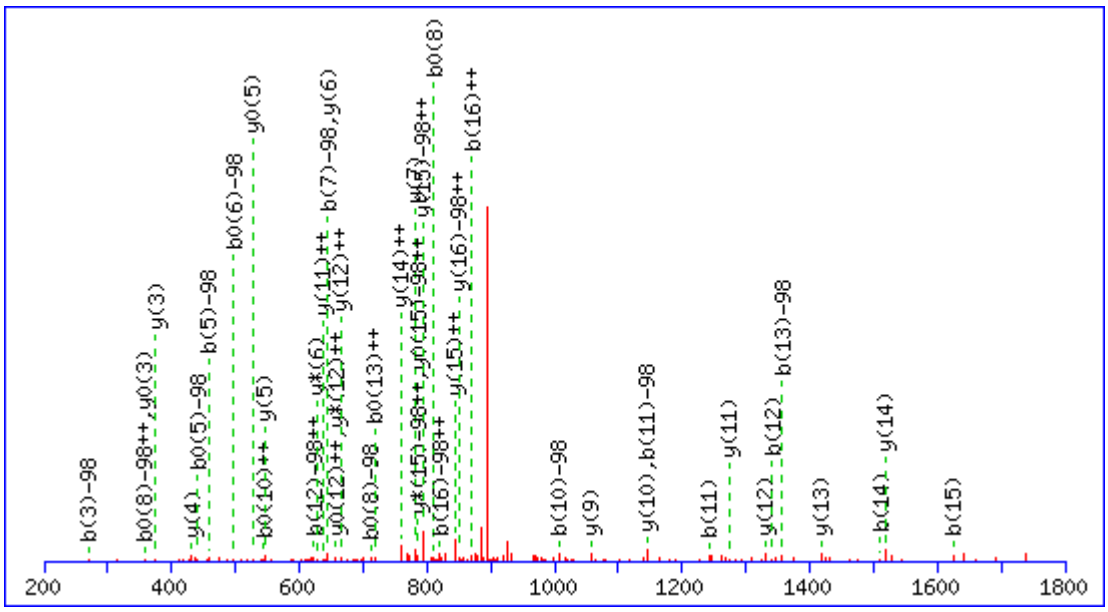
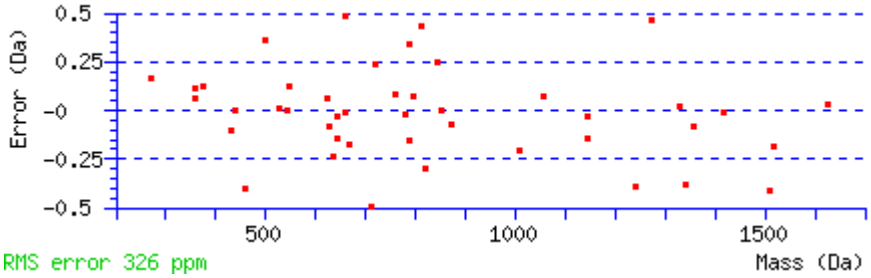
RMS error 250 ppm
Mass (Da)

IDENTIFICATION 7
MS/MS Fragmentation of SLSTSGESLYHVLGLDK
Found in IPI00132206

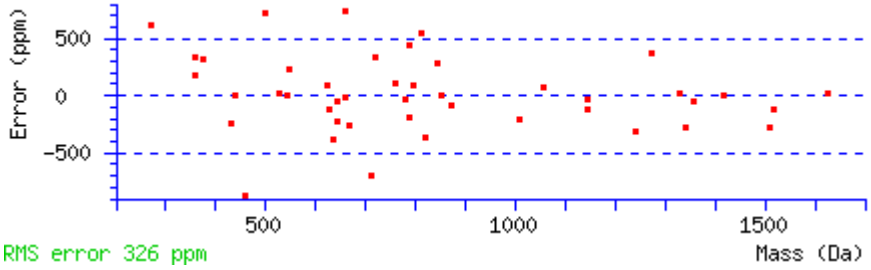


Monoisotopic mass of neutral peptide Mr(calc): 1884.8870
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 55 Expect: 0.00052 (help)

#	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							17
2	201.1234	101.0653	183.1128	92.0600	L	1700.8854	850.9463	1683.8588	842.4331	1682.8748	841.9410	16
3	270.1448	135.5761	252.1343	126.5708	S	1587.8013	794.4043	1570.7748	785.8910	1569.7907	785.3990	15
4	371.1925	186.0999	353.1819	177.0946	T	1518.7798	759.8936	1501.7533	751.3803	1500.7693	750.8883	14
5	458.2245	229.6159	440.2140	220.6106	S	1417.7322	709.3697	1400.7056	700.8564	1399.7216	700.3644	13
6	515.2460	258.1266	497.2354	249.1214	G	1330.7001	665.8537	1313.6736	657.3404	1312.6896	656.8484	12
7	644.2886	322.6479	626.2780	313.6427	E	1273.6787	637.3430	1256.6521	628.8297	1255.6681	628.3377	11
8	731.3206	366.1639	713.3101	357.1587	S	1144.6361	572.8217	1127.6095	564.3084	1126.6255	563.8164	10
9	844.4047	422.7060	826.3941	413.7007	L	1057.6041	529.3057	1040.5775	520.7924	1039.5935	520.3004	9
10	1007.4680	504.2376	989.4575	495.2324	Y	944.5200	472.7636	927.4934	464.2504	926.5094	463.7584	8
11	1144.5269	572.7671	1126.5164	563.7618	H	781.4567	391.2320	764.4301	382.7187	763.4461	382.2267	7
12	1243.5953	622.3013	1225.5848	613.2960	V	644.3978	322.7025	627.3712	314.1892	626.3872	313.6972	6
13	1356.6794	678.8433	1338.6688	669.8381	L	545.3293	273.1683	528.3028	264.6550	527.3188	264.1630	5
14	1413.7009	707.3541	1395.6903	698.3488	G	432.2453	216.6263	415.2187	208.1130	414.2347	207.6210	4
15	1526.7849	763.8961	1508.7744	754.8908	L	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
16	1641.8119	821.4096	1623.8013	812.4043	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



RMS error 326 ppm

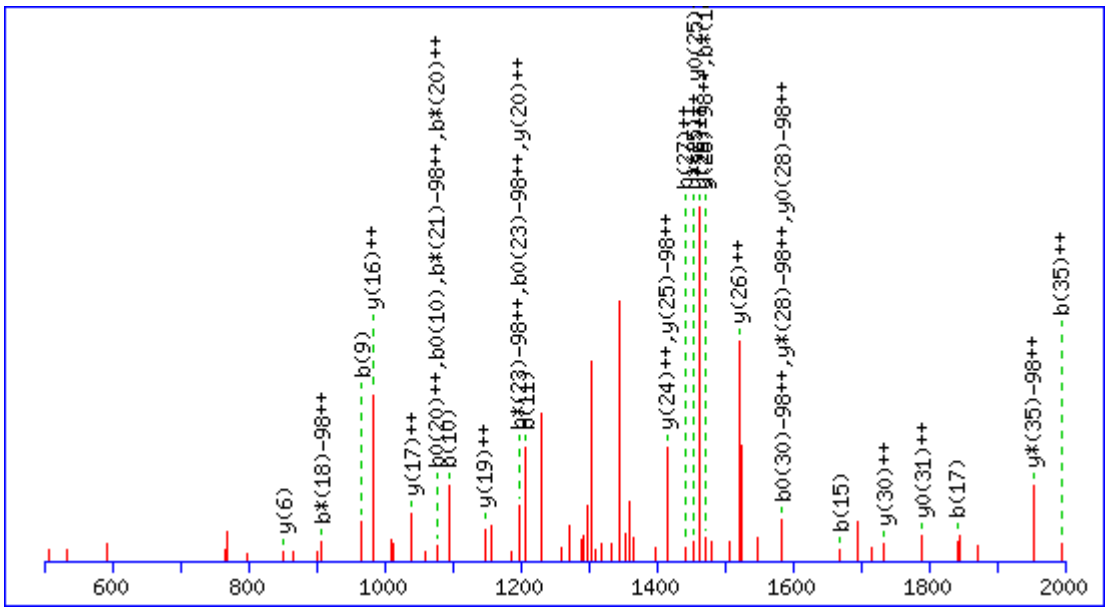


RMS error 326 ppm

IDENTIFICATION 8

MS/MS Fragmentation of IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK

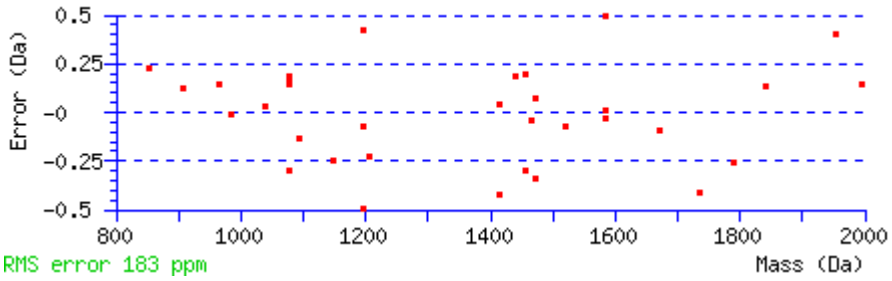
Found in IPI00223253

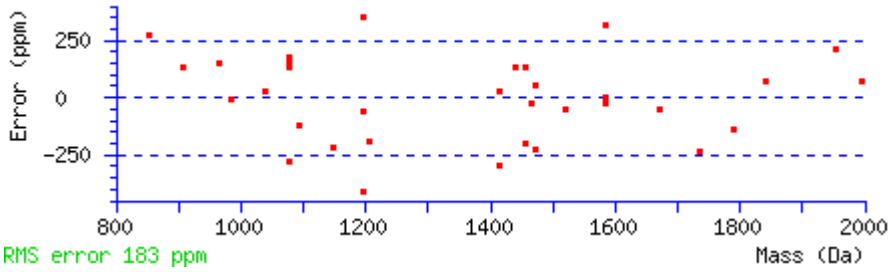


Monoisotopic mass of neutral peptide Mr(calc): 4133.9908
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T15 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.29 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							36
2	227.1754	114.0913					I	4021.9141	2011.4607	4004.8875	2002.9474	4003.9035	2002.4554	35
3	324.2282	162.6177					P	3908.8300	1954.9186	3891.8034	1946.4054	3890.8194	1945.9134	34
4	425.2758	213.1416			407.2653	204.1363	T	3811.7772	1906.3923	3794.7507	1897.8790	3793.7667	1897.3870	33
5	538.3599	269.6836			520.3493	260.6783	L	3710.7296	1855.8684	3693.7030	1847.3551	3692.7190	1846.8631	32
6	667.4025	334.2049			649.3919	325.1996	E	3597.6455	1799.3264	3580.6189	1790.8131	3579.6349	1790.3211	31
7	796.4451	398.7262			778.4345	389.7209	E	3468.6029	1734.8051	3451.5763	1726.2918	3450.5923	1725.7998	30
8	853.4666	427.2369			835.4560	418.2316	G	3339.5603	1670.2838	3322.5338	1661.7705	3321.5497	1661.2785	29
9	966.5506	483.7790			948.5401	474.7737	L	3282.5388	1641.7731	3265.5123	1633.2598	3264.5283	1632.7678	28
10	1094.6092	547.8082	1077.5827	539.2950	1076.5986	538.8030	Q	3169.4548	1585.2310	3152.4282	1576.7178	3151.4442	1576.2257	27
11	1207.6933	604.3503	1190.6667	595.8370	1189.6827	595.3450	L	3041.3962	1521.2017	3024.3696	1512.6885	3023.3856	1512.1965	26
12	1304.7460	652.8767	1287.7195	644.3634	1286.7355	643.8714	P	2928.3121	1464.6597	2911.2856	1456.1464	2910.3016	1455.6544	25
13	1391.7781	696.3927	1374.7515	687.8794	1373.7675	687.3874	S	2831.2594	1416.1333	2814.2328	1407.6200	2813.2488	1407.1280	24
14	1488.8308	744.9190	1471.8043	736.4058	1470.8203	735.9138	P	2744.2273	1372.6173	2727.2008	1364.1040	2726.2168	1363.6120	23
15	1669.8448	835.4261	1652.8183	826.9128	1651.8343	826.4208	T	2647.1746	1324.0909	2630.1480	1315.5777	2629.1640	1315.0856	22
16	1740.8819	870.9446	1723.8554	862.4313	1722.8714	861.9393	A	2466.1606	1233.5839	2449.1340	1225.0706	2448.1500	1224.5786	21
17	1841.9296	921.4685	1824.9031	912.9552	1823.9191	912.4632	T	2395.1235	1198.0654	2378.0969	1189.5521	2377.1129	1189.0601	20
18	1928.9617	964.9845	1911.9351	956.4712	1910.9511	955.9792	S	2294.0758	1147.5415	2277.0492	1139.0283	2276.0652	1138.5362	19
19	2057.0202	1029.0138	2039.9937	1020.5005	2039.0097	1020.0085	Q	2207.0437	1104.0255	2190.0172	1095.5122	2189.0332	1095.0202	18
20	2170.1043	1085.5558	2153.0777	1077.0425	2152.0937	1076.5505	L	2078.9852	1039.9962	2061.9586	1031.4829	2060.9746	1030.9909	17
21	2267.1571	1134.0822	2250.1305	1125.5689	2249.1465	1125.0769	P	1965.9011	983.4542	1948.8746	974.9409	1947.8905	974.4489	16
22	2380.2411	1190.6242	2363.2146	1182.1109	2362.2306	1181.6189	L	1868.8483	934.9278	1851.8218	926.4145	1850.8378	925.9225	15
23	2509.2837	1255.1455	2492.2572	1246.6322	2491.2732	1246.1402	E	1755.7643	878.3858	1738.7377	869.8725	1737.7537	869.3805	14
24	2596.3157	1298.6615	2579.2892	1290.1482	2578.3052	1289.6562	S	1626.7217	813.8645	1609.6951	805.3512	1608.7111	804.8592	13
25	2711.3427	1356.1750	2694.3161	1347.6617	2693.3321	1347.1697	D	1539.6897	770.3485	1522.6631	761.8352	1521.6791	761.3432	12
26	2782.3798	1391.6935	2765.3533	1383.1803	2764.3692	1382.6883	A	1424.6627	712.8350	1407.6362	704.3217	1406.6521	703.8297	11
27	2881.4482	1441.2277	2864.4217	1432.7145	2863.4377	1432.2225	V	1353.6256	677.3164	1336.5991	668.8032	1335.6150	668.3112	10

28	3010.4908	1505.7490	2993.4643	1497.2358	2992.4802	1496.7438	E	1254.5572	627.7822	1237.5306	619.2690	1236.5466	618.7769	9
29	3170.5215	1585.7644	3153.4949	1577.2511	3152.5109	1576.7591	C	1125.5146	563.2609	1108.4880	554.7477			8
30	3283.6055	1642.3064	3266.5790	1633.7931	3265.5950	1633.3011	L	965.4839	483.2456	948.4574	474.7323			7
31	3397.6484	1699.3279	3380.6219	1690.8146	3379.6379	1690.3226	N	852.3999	426.7036	835.3733	418.1903			6
32	3560.7118	1780.8595	3543.6852	1772.3463	3542.7012	1771.8542	Y	738.3570	369.6821	721.3304	361.1688			5
33	3688.7704	1844.8888	3671.7438	1836.3755	3670.7598	1835.8835	Q	575.2936	288.1504	558.2671	279.6372			4
34	3825.8293	1913.4183	3808.8027	1904.9050	3807.8187	1904.4130	H	447.2350	224.1212	430.2085	215.6079			3
35	3988.8926	1994.9499	3971.8660	1986.4367	3970.8820	1985.9447	Y	310.1761	155.5917	293.1496	147.0784			2
36							K	147.1128	74.0600	130.0863	65.5468			1

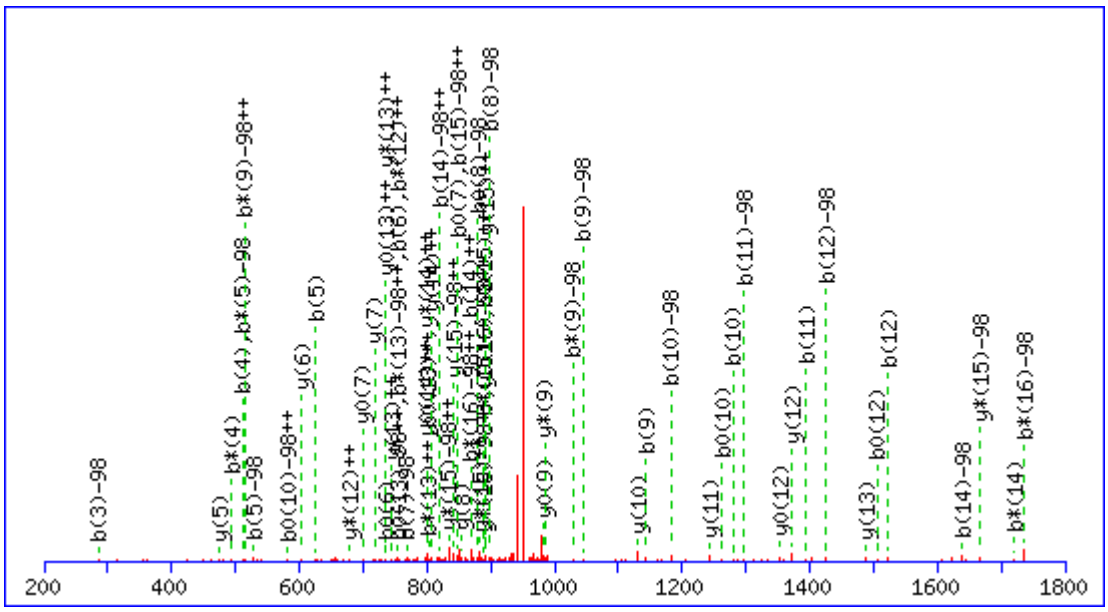




IDENTIFICATION 9

MS/MS Fragmentation of TNSQDKIEFHNEVDGGK

Found in IPI00126092



Monoisotopic mass of neutral peptide Mr(calc): 1996.8528

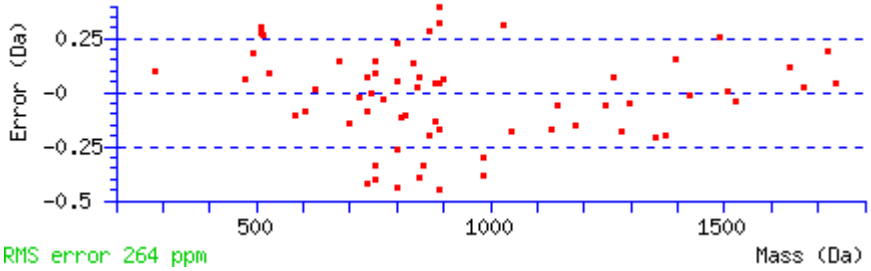
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

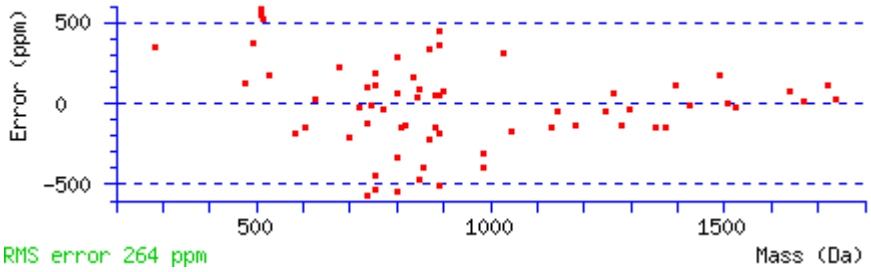
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 48 Expect: 0.003 (help)

#	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							17
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	N	1798.8355	899.9214	1781.8089	891.4081	1780.8249	890.9161	16
3	285.1193	143.0633	268.0928	134.5500	267.1088	134.0580	S	1684.7925	842.8999	1667.7660	834.3866	1666.7820	833.8946	15
4	413.1779	207.0926	396.1514	198.5793	395.1674	198.0873	Q	1615.7711	808.3892	1598.7445	799.8759	1597.7605	799.3839	14
5	528.2049	264.6061	511.1783	256.0928	510.1943	255.6008	D	1487.7125	744.3599	1470.6859	735.8466	1469.7019	735.3546	13
6	656.2998	328.6536	639.2733	320.1403	638.2893	319.6483	K	1372.6856	686.8464	1355.6590	678.3331	1354.6750	677.8411	12
7	769.3839	385.1956	752.3573	376.6823	751.3733	376.1903	I	1244.5906	622.7989	1227.5640	614.2857	1226.5800	613.7937	11
8	898.4265	449.7169	881.3999	441.2036	880.4159	440.7116	E	1131.5065	566.2569	1114.4800	557.7436	1113.4960	557.2516	10
9	1045.4949	523.2511	1028.4684	514.7378	1027.4843	514.2458	F	1002.4639	501.7356	985.4374	493.2223	984.4534	492.7303	9
10	1182.5538	591.7805	1165.5273	583.2673	1164.5432	582.7753	H	855.3955	428.2014	838.3690	419.6881	837.3850	419.1961	8
11	1296.5967	648.8020	1279.5702	640.2887	1278.5862	639.7967	N	718.3366	359.6719	701.3101	351.1587	700.3260	350.6667	7
12	1425.6393	713.3233	1408.6128	704.8100	1407.6288	704.3180	E	604.2937	302.6505	587.2671	294.1372	586.2831	293.6452	6
13	1524.7077	762.8575	1507.6812	754.3442	1506.6972	753.8522	V	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	5
14	1639.7347	820.3710	1622.7081	811.8577	1621.7241	811.3657	D	376.1827	188.5950	359.1561	180.0817	358.1721	179.5897	4
15	1696.7562	848.8817	1679.7296	840.3684	1678.7456	839.8764	G	261.1557	131.0815	244.1292	122.5682			3
16	1753.7776	877.3924	1736.7511	868.8792	1735.7671	868.3872	G	204.1343	102.5708	187.1077	94.0575			2
17							K	147.1128	74.0600	130.0863	65.5468			1

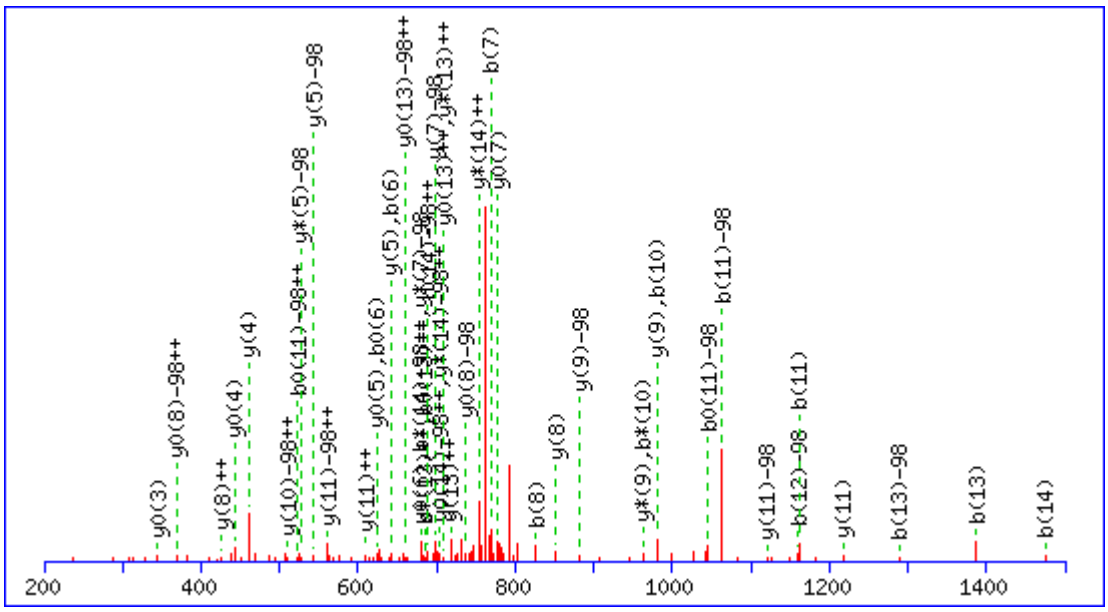


RMS error 264 ppm



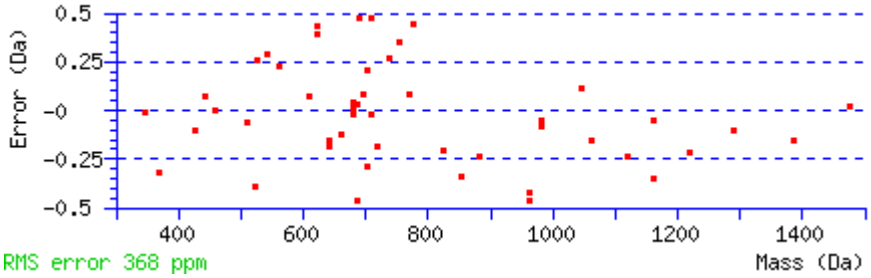
RMS error 264 ppm

IDENTIFICATION 10
MS/MS Fragmentation of VSSETHQGPGTPESK
Found in IPI00263048

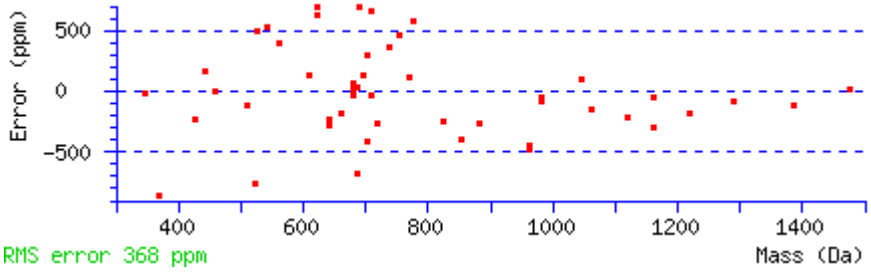


Monoisotopic mass of neutral peptide Mr(calc): 1619.6828
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 28 Expect: 0.25 (help)

#	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	187.1077	94.0575			169.0972	85.0522	S	1423.6448	712.3260	1406.6183	703.8128	1405.6342	703.3208	14
3	274.1397	137.5735			256.1292	128.5682	S	1336.6128	668.8100	1319.5862	660.2968	1318.6022	659.8047	13
4	403.1823	202.0948			385.1718	193.0895	E	1249.5808	625.2940	1232.5542	616.7807	1231.5702	616.2887	12
5	504.2300	252.6186			486.2195	243.6134	T	1120.5382	560.7727	1103.5116	552.2594	1102.5276	551.7674	11
6	641.2889	321.1481			623.2784	312.1428	H	1019.4905	510.2489	1002.4639	501.7356	1001.4799	501.2436	10
7	769.3475	385.1774	752.3210	376.6641	751.3369	376.1721	Q	882.4316	441.7194	865.4050	433.2062	864.4210	432.7141	9
8	826.3690	413.6881	809.3424	405.1748	808.3584	404.6828	G	754.3730	377.6901	737.3464	369.1769	736.3624	368.6849	8
9	923.4217	462.2145	906.3952	453.7012	905.4112	453.2092	P	697.3515	349.1794	680.3250	340.6661	679.3410	340.1741	7
10	980.4432	490.7252	963.4167	482.2120	962.4326	481.7200	G	600.2988	300.6530	583.2722	292.1397	582.2882	291.6477	6
11	1063.4803	532.2438	1046.4538	523.7305	1045.4697	523.2385	T	543.2773	272.1423	526.2508	263.6290	525.2667	263.1370	5
12	1160.5331	580.7702	1143.5065	572.2569	1142.5225	571.7649	P	460.2402	230.6237	443.2136	222.1105	442.2296	221.6185	4
13	1289.5757	645.2915	1272.5491	636.7782	1271.5651	636.2862	E	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
14	1376.6077	688.8075	1359.5812	680.2942	1358.5971	679.8022	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
15							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 368 ppm

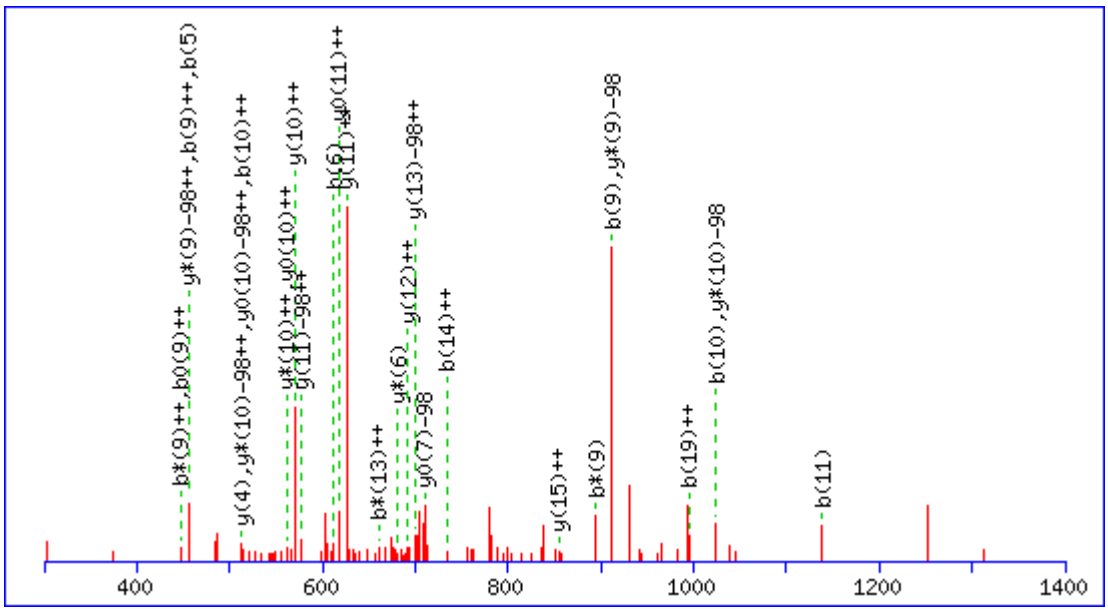


RMS error 368 ppm

IDENTIFICATION 11

MS/MS Fragmentation of LAAISRGLELLTVQGQLSGR

Found in IPI00117801



Monoisotopic mass of neutral peptide Mr(calc): 2162.1460

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

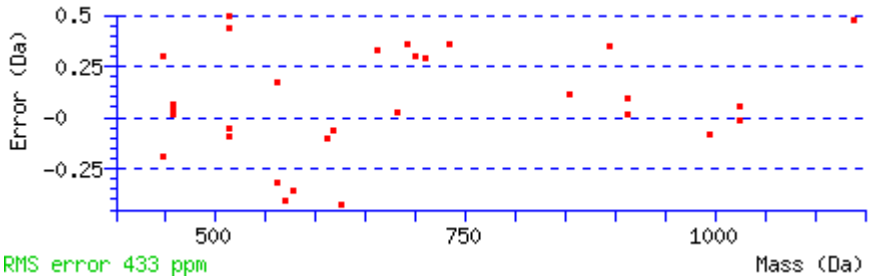
Variable modifications:

Q16 : Deamidated (NQ)

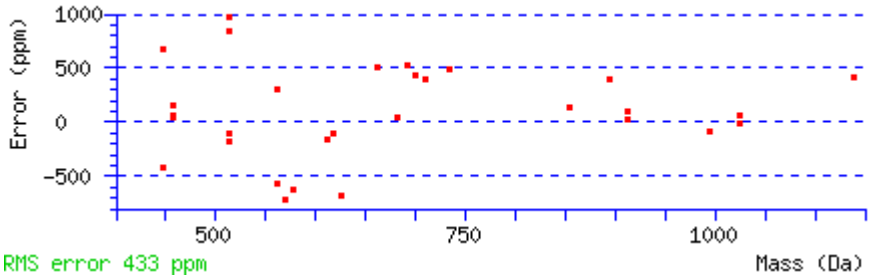
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 20 Expect: 0.54 (help)

#	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	185.1285	93.0679					A	2050.0692	1025.5383	2033.0427	1017.0250	2032.0587	1016.5330	19
3	256.1656	128.5864					A	1979.0321	990.0197	1962.0056	981.5064	1961.0216	981.0144	18
4	369.2496	185.1285					I	1907.9950	954.5011	1890.9685	945.9879	1889.9845	945.4959	17
5	456.2817	228.6445			438.2711	219.6392	S	1794.9110	897.9591	1777.8844	889.4458	1776.9004	888.9538	16
6	612.3828	306.6950	595.3562	298.1817	594.3722	297.6897	R	1707.8789	854.4431	1690.8524	845.9298	1689.8684	845.4378	15
7	669.4042	335.2058	652.3777	326.6925	651.3937	326.2005	G	1551.7778	776.3925	1534.7513	767.8793	1533.7673	767.3873	14
8	782.4883	391.7478	765.4618	383.2345	764.4777	382.7425	L	1494.7564	747.8818	1477.7298	739.3685	1476.7458	738.8765	13
9	911.5309	456.2691	894.5043	447.7558	893.5203	447.2638	E	1381.6723	691.3398	1364.6457	682.8265	1363.6617	682.3345	12
10	1024.6150	512.8111	1007.5884	504.2978	1006.6044	503.8058	L	1252.6297	626.8185	1235.6031	618.3052	1234.6191	617.8132	11
11	1137.6990	569.3531	1120.6725	560.8399	1119.6885	560.3479	L	1139.5456	570.2765	1122.5191	561.7632	1121.5351	561.2712	10
12	1238.7467	619.8770	1221.7202	611.3637	1220.7361	610.8717	T	1026.4616	513.7344	1009.4350	505.2211	1008.4510	504.7291	9
13	1337.8151	669.4112	1320.7886	660.8979	1319.8045	660.4059	V	925.4139	463.2106	908.3873	454.6973	907.4033	454.2053	8
14	1465.8737	733.4405	1448.8471	724.9272	1447.8631	724.4352	Q	826.3455	413.6764	809.3189	405.1631	808.3349	404.6711	7
15	1522.8952	761.9512	1505.8686	753.4379	1504.8846	752.9459	G	698.2869	349.6471	681.2603	341.1338	680.2763	340.6418	6
16	1651.9377	826.4725	1634.9112	817.9592	1633.9272	817.4672	Q	641.2654	321.1364	624.2389	312.6231	623.2549	312.1311	5
17	1765.0218	883.0145	1747.9953	874.5013	1747.0112	874.0093	L	512.2228	256.6151	495.1963	248.1018	494.2123	247.6098	4
18	1932.0202	966.5137	1914.9936	958.0004	1914.0096	957.5084	S	399.1388	200.0730	382.1122	191.5598	381.1282	191.0677	3
19	1989.0416	995.0245	1972.0151	986.5112	1971.0311	986.0192	G	232.1404	116.5738	215.1139	108.0606			2
20							R	175.1190	88.0631	158.0924	79.5498			1

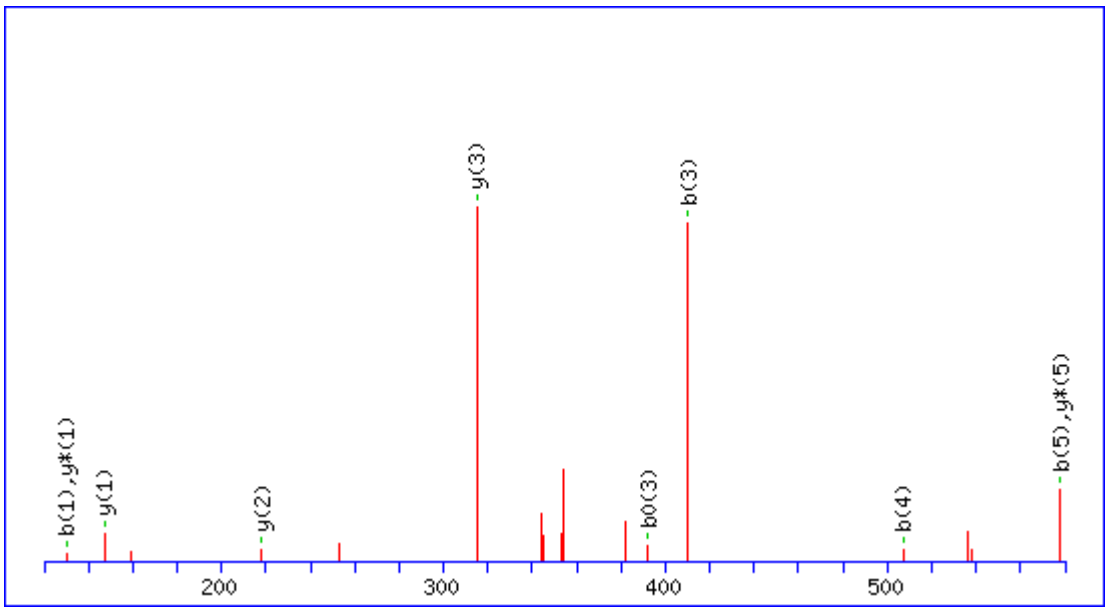


RMS error 433 ppm



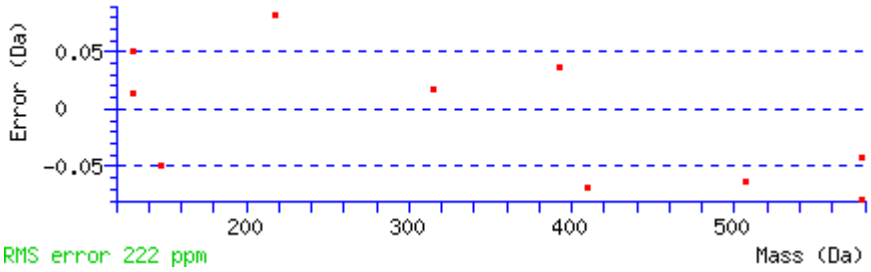
RMS error 433 ppm

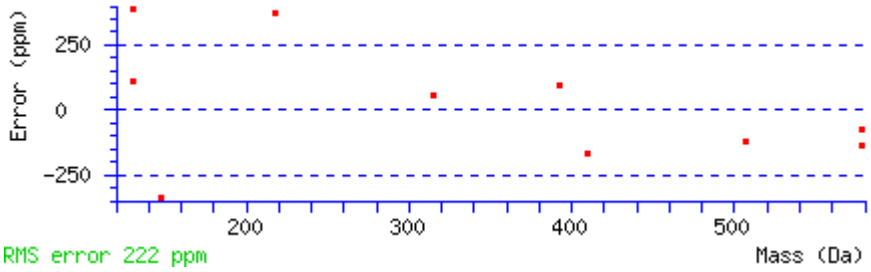
IDENTIFICATION 12
MS/MS Fragmentation of ESIPAK
Found in IPI00274795



Monoisotopic mass of neutral peptide Mr(calc): 723.3204
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 30 **Expect:** 0.057 (**help**)

#	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							6
2	297.0482	149.0278	279.0377	140.0225	S	595.2851	298.1462	578.2586	289.6329	577.2745	289.1409	5
3	410.1323	205.5698	392.1217	196.5645	I	428.2867	214.6470	411.2602	206.1337			4
4	507.1851	254.0962	489.1745	245.0909	P	315.2027	158.1050	298.1761	149.5917			3
5	578.2222	289.6147	560.2116	280.6094	A	218.1499	109.5786	201.1234	101.0653			2
6					K	147.1128	74.0600	130.0863	65.5468			1

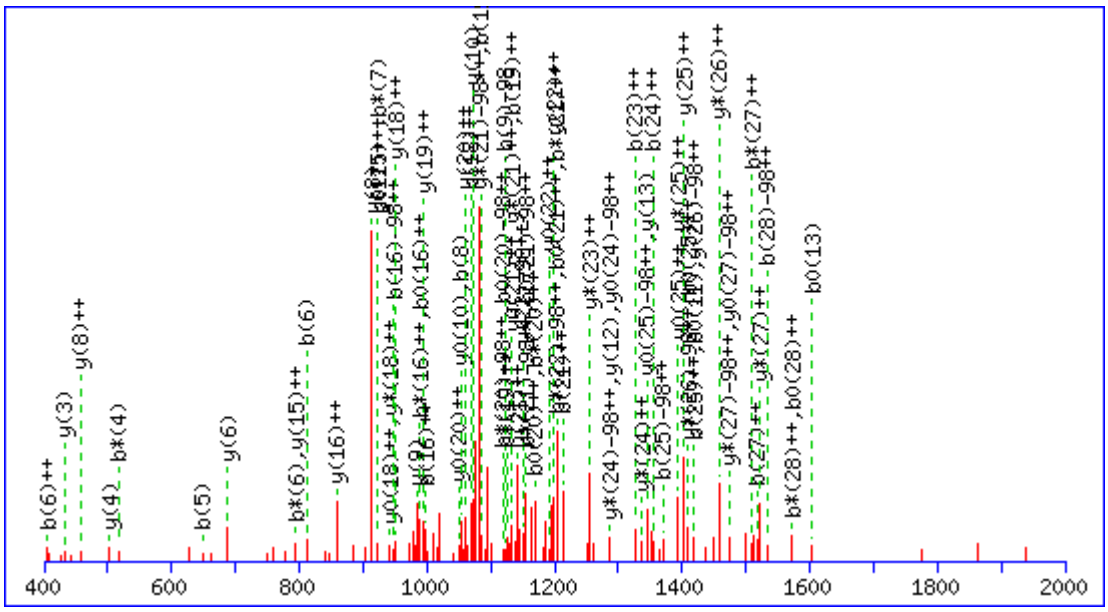




IDENTIFICATION 13

MS/MS Fragmentation of NYQQNYQNSESGEKNEGSESAPEGQAQQR

Found in IPI00120886



Monoisotopic mass of neutral peptide Mr(calc): 3336.3552

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

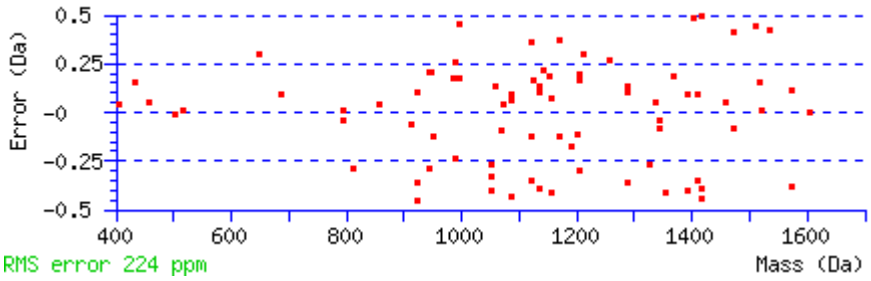
Variable modifications:

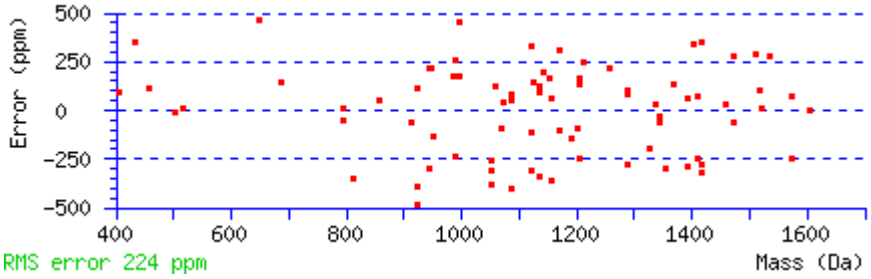
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 52 Expect: 0.0016 (help)

#	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							29
2	278.1135	139.5604	261.0870	131.0471			Y	3223.3196	1612.1634	3206.2931	1603.6502	3205.3090	1603.1582	28
3	406.1721	203.5897	389.1456	195.0764			Q	3060.2563	1530.6318	3043.2297	1522.1185	3042.2457	1521.6265	27
4	534.2307	267.6190	517.2041	259.1057			Q	2932.1977	1466.6025	2915.1712	1458.0892	2914.1871	1457.5972	26
5	648.2736	324.6404	631.2471	316.1272			N	2804.1391	1402.5732	2787.1126	1394.0599	2786.1286	1393.5679	25
6	811.3369	406.1721	794.3104	397.6588			Y	2690.0962	1345.5517	2673.0697	1337.0385	2672.0856	1336.5465	24
7	939.3955	470.2014	922.3690	461.6881			Q	2527.0329	1264.0201	2510.0063	1255.5068	2509.0223	1255.0148	23
8	1053.4384	527.2229	1036.4119	518.7096			N	2398.9743	1199.9908	2381.9477	1191.4775	2380.9637	1190.9855	22
9	1220.4368	610.7220	1203.4103	602.2088	1202.4262	601.7168	S	2284.9314	1142.9693	2267.9048	1134.4560	2266.9208	1133.9640	21
10	1349.4794	675.2433	1332.4529	666.7301	1331.4688	666.2381	E	2117.9330	1059.4701	2100.9065	1050.9569	2099.9224	1050.4649	20
11	1436.5114	718.7594	1419.4849	710.2461	1418.5009	709.7541	S	1988.8904	994.9488	1971.8639	986.4356	1970.8799	985.9436	19
12	1493.5329	747.2701	1476.5063	738.7568	1475.5223	738.2648	G	1901.8584	951.4328	1884.8318	942.9196	1883.8478	942.4275	18
13	1622.5755	811.7914	1605.5489	803.2781	1604.5649	802.7861	E	1844.8369	922.9221	1827.8104	914.4088	1826.8264	913.9168	17
14	1750.6704	875.8389	1733.6439	867.3256	1732.6599	866.8336	K	1715.7943	858.4008	1698.7678	849.8875	1697.7838	849.3955	16
15	1864.7134	932.8603	1847.6868	924.3471	1846.7028	923.8550	N	1587.6994	794.3533	1570.6728	785.8400	1569.6888	785.3480	15
16	1993.7560	997.3816	1976.7294	988.8683	1975.7454	988.3763	E	1473.6564	737.3319	1456.6299	728.8186	1455.6459	728.3266	14
17	2050.7774	1025.8924	2033.7509	1017.3791	2032.7669	1016.8871	G	1344.6138	672.8106	1327.5873	664.2973	1326.6033	663.8053	13
18	2137.8095	1069.4084	2120.7829	1060.8951	2119.7989	1060.4031	S	1287.5924	644.2998	1270.5658	635.7866	1269.5818	635.2945	12
19	2266.8521	1133.9297	2249.8255	1125.4164	2248.8415	1124.9244	E	1200.5604	600.7838	1183.5338	592.2705	1182.5498	591.7785	11
20	2353.8841	1177.4457	2336.8575	1168.9324	2335.8735	1168.4404	S	1071.5178	536.2625	1054.4912	527.7492	1053.5072	527.2572	10
21	2424.9212	1212.9642	2407.8946	1204.4510	2406.9106	1203.9590	A	984.4857	492.7465	967.4592	484.2332	966.4752	483.7412	9
22	2521.9740	1261.4906	2504.9474	1252.9773	2503.9634	1252.4853	P	913.4486	457.2279	896.4221	448.7147	895.4381	448.2227	8
23	2651.0166	1326.0119	2633.9900	1317.4986	2633.0060	1317.0066	E	816.3959	408.7016	799.3693	400.1883	798.3853	399.6963	7
24	2708.0380	1354.5226	2691.0115	1346.0094	2690.0275	1345.5174	G	687.3533	344.1803	670.3267	335.6670			6
25	2836.0966	1418.5519	2819.0700	1410.0387	2818.0860	1409.5467	Q	630.3318	315.6695	613.3053	307.1563			5
26	2907.1337	1454.0705	2890.1072	1445.5572	2889.1231	1445.0652	A	502.2732	251.6402	485.2467	243.1270			4
27	3035.1923	1518.0998	3018.1657	1509.5865	3017.1817	1509.0945	Q	431.2361	216.1217	414.2096	207.6084			3

28	3163.2509	1582.1291	3146.2243	1573.6158	3145.2403	1573.1238	Q	303.1775	152.0924	286.1510	143.5791			2
29							R	175.1190	88.0631	158.0924	79.5498			1

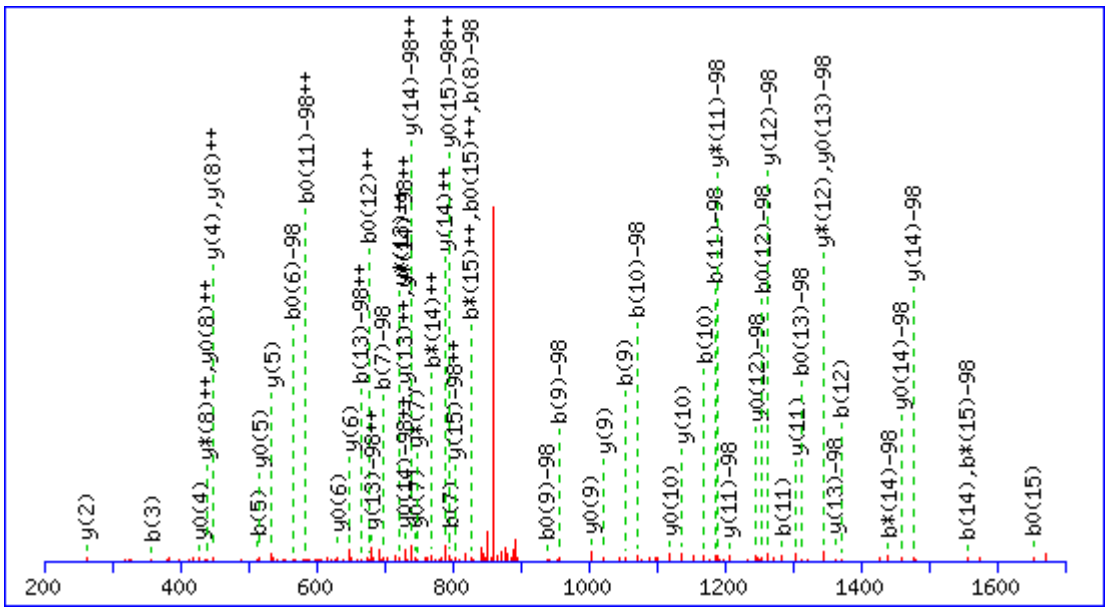




IDENTIFICATION 14

MS/MS Fragmentation of IEDVGSDEEDDSGKDK

Found in IPI00229080



Monoisotopic mass of neutral peptide Mr(calc): 1816.6888

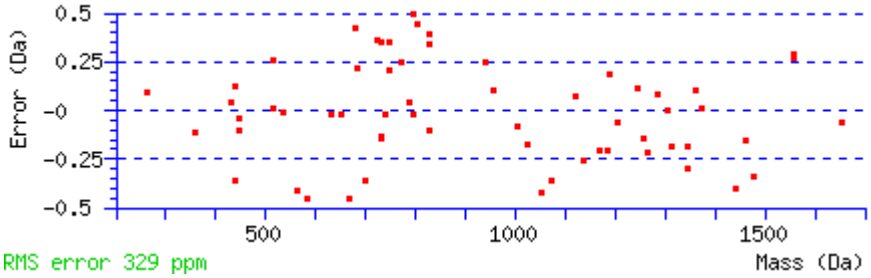
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

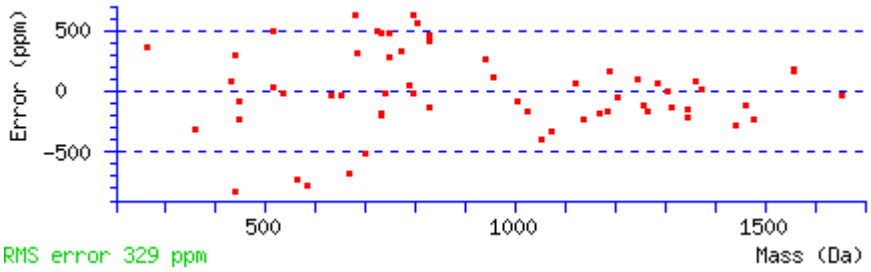
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 55 Expect: 0.00035 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							16
2	243.1339	122.0706			225.1234	113.0653	E	1606.6351	803.8212	1589.6085	795.3079	1588.6245	794.8159	15
3	358.1609	179.5841			340.1503	170.5788	D	1477.5925	739.2999	1460.5660	730.7866	1459.5819	730.2946	14
4	457.2293	229.1183			439.2187	220.1130	V	1362.5656	681.7864	1345.5390	673.2731	1344.5550	672.7811	13
5	514.2508	257.6290			496.2402	248.6237	G	1263.4971	632.2522	1246.4706	623.7389	1245.4866	623.2469	12
6	583.2722	292.1397			565.2617	283.1345	S	1206.4757	603.7415	1189.4491	595.2282	1188.4651	594.7362	11
7	698.2992	349.6532			680.2886	340.6479	D	1137.4542	569.2307	1120.4277	560.7175	1119.4437	560.2255	10
8	827.3418	414.1745			809.3312	405.1692	E	1022.4273	511.7173	1005.4007	503.2040	1004.4167	502.7120	9
9	956.3843	478.6958			938.3738	469.6905	E	893.3847	447.1960	876.3581	438.6827	875.3741	438.1907	8
10	1071.4113	536.2093			1053.4007	527.2040	D	764.3421	382.6747	747.3155	374.1614	746.3315	373.6694	7
11	1186.4382	593.7228			1168.4277	584.7175	D	649.3151	325.1612	632.2886	316.6479	631.3046	316.1559	6
12	1273.4703	637.2388			1255.4597	628.2335	S	534.2882	267.6477	517.2617	259.1345	516.2776	258.6425	5
13	1330.4917	665.7495			1312.4812	656.7442	G	447.2562	224.1317	430.2296	215.6185	429.2456	215.1264	4
14	1458.5867	729.7970	1441.5601	721.2837	1440.5761	720.7917	K	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	3
15	1573.6136	787.3105	1556.5871	778.7972	1555.6031	778.3052	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
16							K	147.1128	74.0600	130.0863	65.5468			1

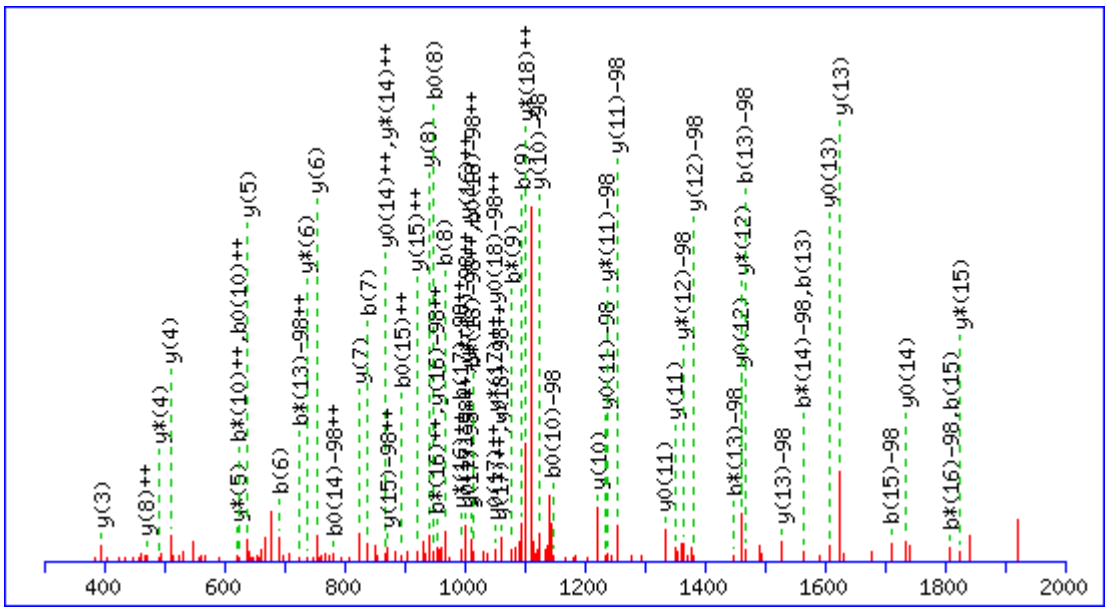


RMS error 329 ppm



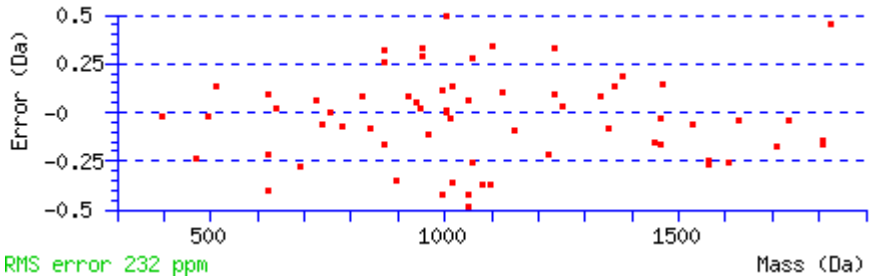
RMS error 329 ppm

IDENTIFICATION 15
MS/MS Fragmentation of VVDYSQFQESDDADEDYGR
Found in IPI00341869



Monoisotopic mass of neutral peptide Mr(calc): 2316.8696
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.029 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							19
2	199.1441	100.0757					V	2120.8316	1060.9194	2103.8050	1052.4061	2102.8210	1051.9141	18
3	314.1710	157.5892			296.1605	148.5839	D	2021.7631	1011.3852	2004.7366	1002.8719	2003.7526	1002.3799	17
4	477.2344	239.1208			459.2238	230.1155	Y	1906.7362	953.8717	1889.7097	945.3585	1888.7256	944.8665	16
5	564.2664	282.6368			546.2558	273.6316	S	1743.6729	872.3401	1726.6463	863.8268	1725.6623	863.3348	15
6	692.3250	346.6661	675.2984	338.1529	674.3144	337.6608	Q	1656.6409	828.8241	1639.6143	820.3108	1638.6303	819.8188	14
7	839.3934	420.2003	822.3668	411.6871	821.3828	411.1951	F	1528.5823	764.7948	1511.5557	756.2815	1510.5717	755.7895	13
8	967.4520	484.2296	950.4254	475.7164	949.4414	475.2243	Q	1381.5139	691.2606	1364.4873	682.7473	1363.5033	682.2553	12
9	1096.4946	548.7509	1079.4680	540.2376	1078.4840	539.7456	E	1253.4553	627.2313	1236.4287	618.7180	1235.4447	618.2260	11
10	1165.5160	583.2617	1148.4895	574.7484	1147.5055	574.2564	S	1124.4127	562.7100	1107.3861	554.1967	1106.4021	553.7047	10
11	1280.5430	640.7751	1263.5164	632.2619	1262.5324	631.7698	D	1055.3912	528.1993	1038.3647	519.6860	1037.3807	519.1940	9
12	1395.5699	698.2886	1378.5434	689.7753	1377.5594	689.2833	D	940.3643	470.6858	923.3377	462.1725	922.3537	461.6805	8
13	1466.6070	733.8072	1449.5805	725.2939	1448.5965	724.8019	A	825.3373	413.1723	808.3108	404.6590	807.3268	404.1670	7
14	1581.6340	791.3206	1564.6074	782.8074	1563.6234	782.3153	D	754.3002	377.6538	737.2737	369.1405	736.2897	368.6485	6
15	1710.6766	855.8419	1693.6500	847.3286	1692.6660	846.8366	E	639.2733	320.1403	622.2467	311.6270	621.2627	311.1350	5
16	1825.7035	913.3554	1808.6770	904.8421	1807.6929	904.3501	D	510.2307	255.6190	493.2041	247.1057	492.2201	246.6137	4
17	1988.7668	994.8871	1971.7403	986.3738	1970.7563	985.8818	Y	395.2037	198.1055	378.1772	189.5922			3
18	2045.7883	1023.3978	2028.7618	1014.8845	2027.7777	1014.3925	G	232.1404	116.5738	215.1139	108.0606			2
19							R	175.1190	88.0631	158.0924	79.5498			1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0.25
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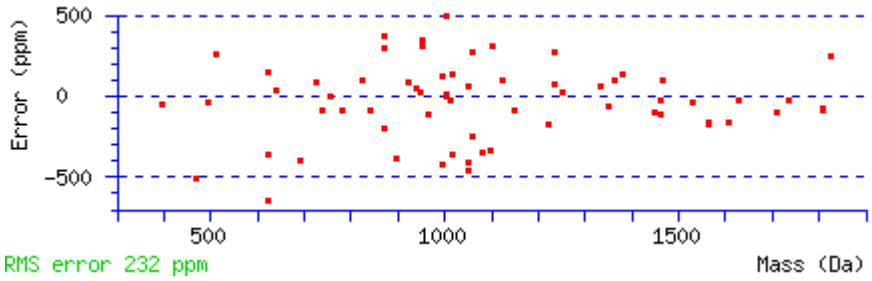
1000
1500
RMS error 232 ppm
Mass (Da)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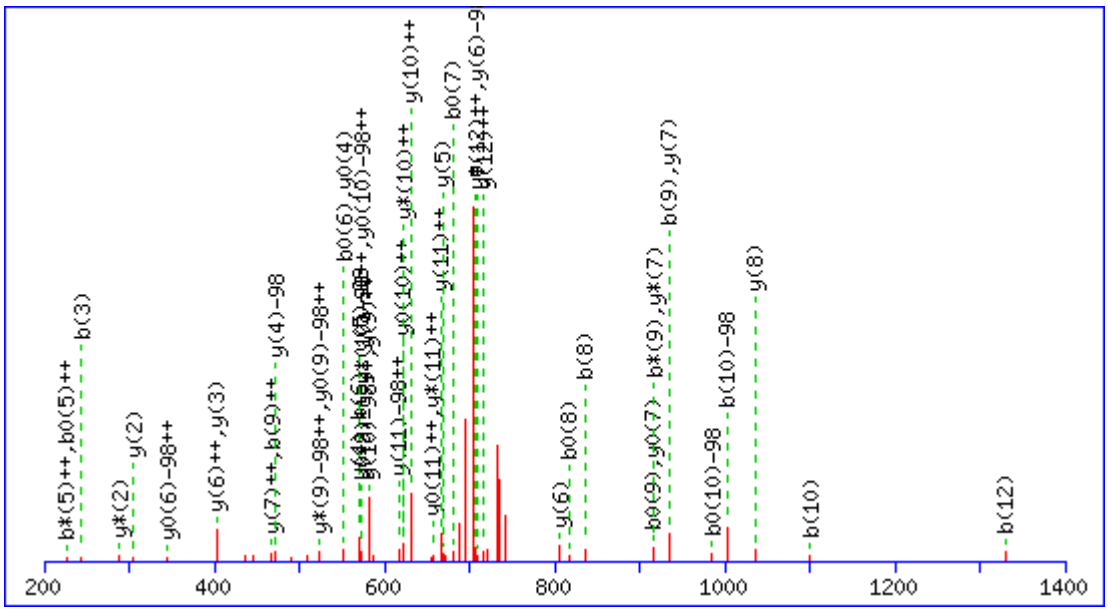
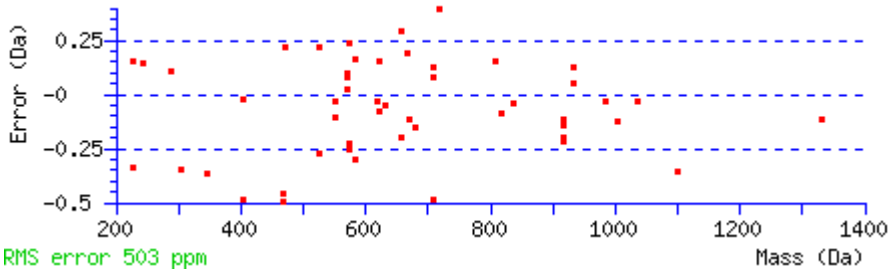
1000
1500
RMS error 232 ppm
Mass (Da)

IDENTIFICATION 16
MS/MS Fragmentation of ATAPQTQHVSPMR
Found in IPI00118875



Monoisotopic mass of neutral peptide Mr(calc): 1502.6701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 45 Expect: 0.0049 (help)

#	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	1432.6403	716.8238	1415.6137	708.3105	1414.6297	707.8185	12
3	244.1292	122.5682			226.1186	113.5629	A	1331.5926	666.2999	1314.5661	657.7867	1313.5820	657.2947	11
4	341.1819	171.0946			323.1714	162.0893	P	1260.5555	630.7814	1243.5289	622.2681	1242.5449	621.7761	10
5	469.2405	235.1239	452.2140	226.6106	451.2300	226.1186	Q	1163.5027	582.2550	1146.4762	573.7417	1145.4922	573.2497	9
6	570.2882	285.6477	553.2617	277.1345	552.2776	276.6425	T	1035.4441	518.2257	1018.4176	509.7124	1017.4336	509.2204	8
7	698.3468	349.6770	681.3202	341.1638	680.3362	340.6717	Q	934.3965	467.7019	917.3699	459.1886	916.3859	458.6966	7
8	835.4057	418.2065	818.3791	409.6932	817.3951	409.2012	H	806.3379	403.6726	789.3113	395.1593	788.3273	394.6673	6
9	934.4741	467.7407	917.4476	459.2274	916.4635	458.7354	V	669.2790	335.1431	652.2524	326.6299	651.2684	326.1378	5
10	1101.4725	551.2399	1084.4459	542.7266	1083.4619	542.2346	S	570.2106	285.6089	553.1840	277.0956	552.2000	276.6036	4
11	1198.5252	599.7663	1181.4987	591.2530	1180.5147	590.7610	P	403.2122	202.1097	386.1857	193.5965			3
12	1329.5657	665.2865	1312.5392	656.7732	1311.5552	656.2812	M	306.1594	153.5834	289.1329	145.0701			2
13							R	175.1190	88.0631	158.0924	79.5498			1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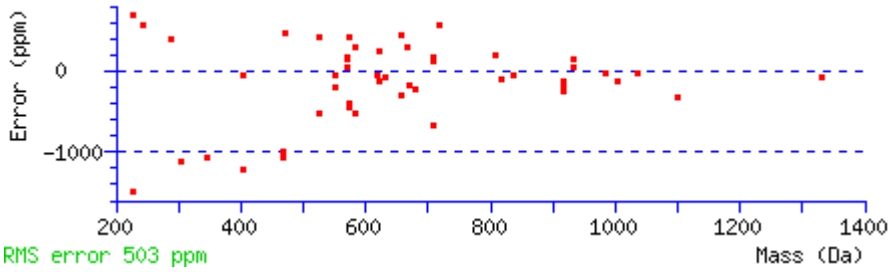
600
800
1000
1200
1400
Mass (Da)
RMS error 503 ppm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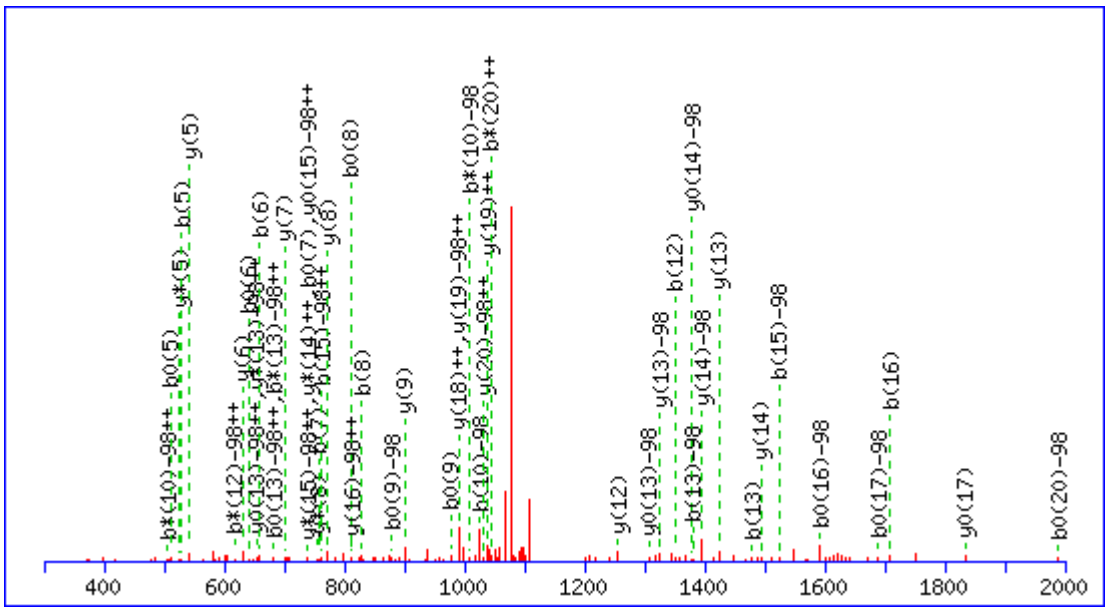
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 503 ppm

IDENTIFICATION 17

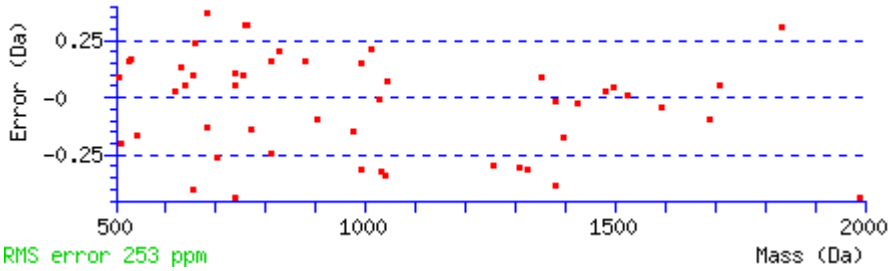
MS/MS Fragmentation of SSPKEEVASEPEEAASPTTPK

Found in IPI00318048



Monoisotopic mass of neutral peptide Mr(calc): 2249.9940 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 34 Expect: 0.08 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							21
2	175.0713	88.0393			157.0608	79.0340	S	2065.9924	1033.4998	2048.9659	1024.9866	2047.9819	1024.4946	20
3	272.1241	136.5657			254.1135	127.5604	P	1978.9604	989.9838	1961.9338	981.4706	1960.9498	980.9786	19
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	K	1881.9076	941.4575	1864.8811	932.9442	1863.8971	932.4522	18
5	529.2617	265.1345	512.2351	256.6212	511.2511	256.1292	E	1753.8127	877.4100	1736.7861	868.8967	1735.8021	868.4047	17
6	658.3042	329.6558	641.2777	321.1425	640.2937	320.6505	E	1624.7701	812.8887	1607.7435	804.3754	1606.7595	803.8834	16
7	757.3727	379.1900	740.3461	370.6767	739.3621	370.1847	V	1495.7275	748.3674	1478.7009	739.8541	1477.7169	739.3621	15
8	828.4098	414.7085	811.3832	406.1952	810.3992	405.7032	A	1396.6591	698.8332	1379.6325	690.3199	1378.6485	689.8279	14
9	897.4312	449.2193	880.4047	440.7060	879.4207	440.2140	S	1325.6220	663.3146	1308.5954	654.8013	1307.6114	654.3093	13
10	1026.4738	513.7406	1009.4473	505.2273	1008.4633	504.7353	E	1256.6005	628.8039	1239.5739	620.2906	1238.5899	619.7986	12
11	1123.5266	562.2669	1106.5000	553.7537	1105.5160	553.2617	P	1127.5579	564.2826	1110.5313	555.7693	1109.5473	555.2773	11
12	1252.5692	626.7882	1235.5426	618.2750	1234.5586	617.7829	E	1030.5051	515.7562	1013.4786	507.2429	1012.4946	506.7509	10
13	1381.6118	691.3095	1364.5852	682.7963	1363.6012	682.3042	E	901.4625	451.2349	884.4360	442.7216	883.4520	442.2296	9
14	1452.6489	726.8281	1435.6223	718.3148	1434.6383	717.8228	A	772.4199	386.7136	755.3934	378.2003	754.4094	377.7083	8
15	1523.6860	762.3466	1506.6595	753.8334	1505.6754	753.3414	A	701.3828	351.1951	684.3563	342.6818	683.3723	342.1898	7
16	1610.7180	805.8627	1593.6915	797.3494	1592.7075	796.8574	S	630.3457	315.6765	613.3192	307.1632	612.3352	306.6712	6
17	1707.7708	854.3890	1690.7443	845.8758	1689.7602	845.3838	P	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	5
18	1808.8185	904.9129	1791.7919	896.3996	1790.8079	895.9076	T	446.2609	223.6341	429.2344	215.1208	428.2504	214.6288	4
19	1909.8662	955.4367	1892.8396	946.9234	1891.8556	946.4314	T	345.2132	173.1103	328.1867	164.5970	327.2027	164.1050	3
20	2006.9189	1003.9631	1989.8924	995.4498	1988.9084	994.9578	P	244.1656	122.5864	227.1390	114.0731			2
21							K	147.1128	74.0600	130.0863	65.5468			1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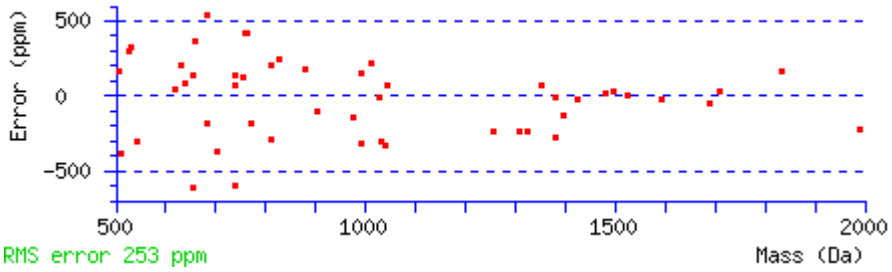
1000
1500
2000
RMS error 253 ppm
Mass (Da)


Error (ppm)
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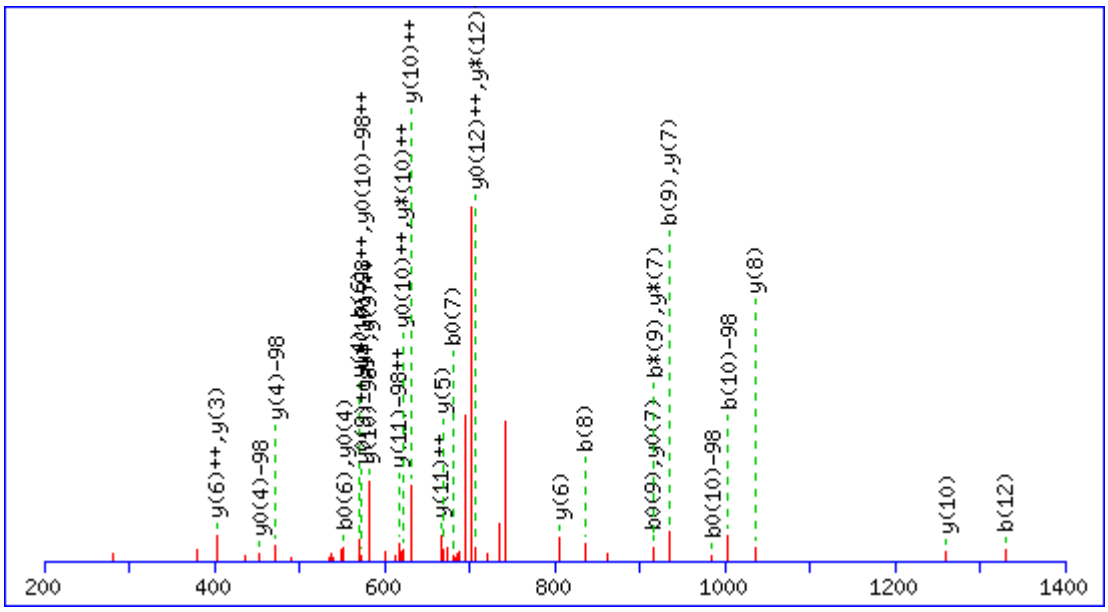
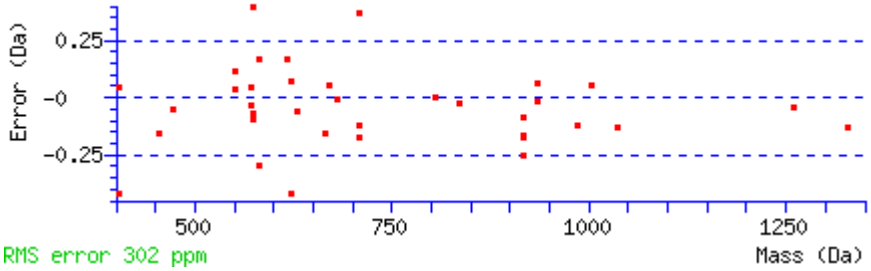
500
1000
1500
2000
RMS error 253 ppm
Mass (Da)

IDENTIFICATION 18
MS/MS Fragmentation of ATAPQTQHVSPMR
Found in IPI00118875



Monoisotopic mass of neutral peptide Mr(calc): 1502.6701
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.018 (help)

#	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	1432.6403	716.8238	1415.6137	708.3105	1414.6297	707.8185	12
3	244.1292	122.5682			226.1186	113.5629	A	1331.5926	666.2999	1314.5661	657.7867	1313.5820	657.2947	11
4	341.1819	171.0946			323.1714	162.0893	P	1260.5555	630.7814	1243.5289	622.2681	1242.5449	621.7761	10
5	469.2405	235.1239	452.2140	226.6106	451.2300	226.1186	Q	1163.5027	582.2550	1146.4762	573.7417	1145.4922	573.2497	9
6	570.2882	285.6477	553.2617	277.1345	552.2776	276.6425	T	1035.4441	518.2257	1018.4176	509.7124	1017.4336	509.2204	8
7	698.3468	349.6770	681.3202	341.1638	680.3362	340.6717	Q	934.3965	467.7019	917.3699	459.1886	916.3859	458.6966	7
8	835.4057	418.2065	818.3791	409.6932	817.3951	409.2012	H	806.3379	403.6726	789.3113	395.1593	788.3273	394.6673	6
9	934.4741	467.7407	917.4476	459.2274	916.4635	458.7354	V	669.2790	335.1431	652.2524	326.6299	651.2684	326.1378	5
10	1101.4725	551.2399	1084.4459	542.7266	1083.4619	542.2346	S	570.2106	285.6089	553.1840	277.0956	552.2000	276.6036	4
11	1198.5252	599.7663	1181.4987	591.2530	1180.5147	590.7610	P	403.2122	202.1097	386.1857	193.5965			3
12	1329.5657	665.2865	1312.5392	656.7732	1311.5552	656.2812	M	306.1594	153.5834	289.1329	145.0701			2
13							R	175.1190	88.0631	158.0924	79.5498			1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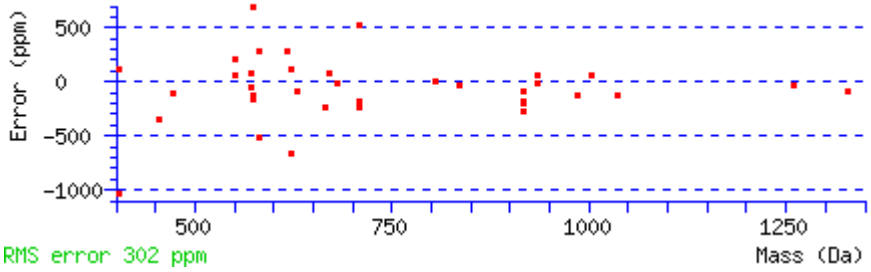
Mass (Da)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1000
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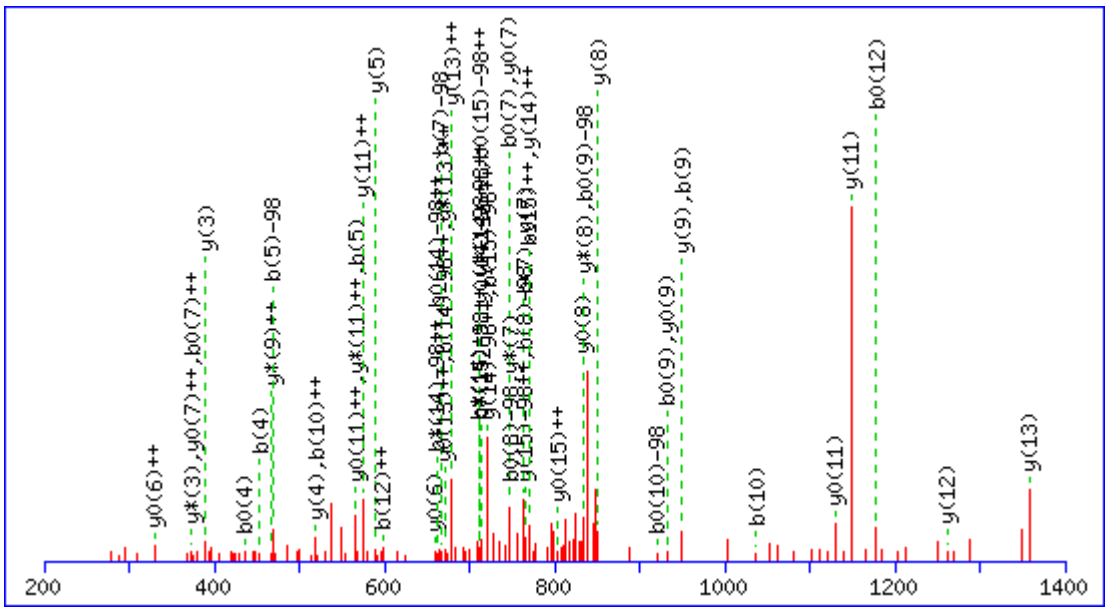
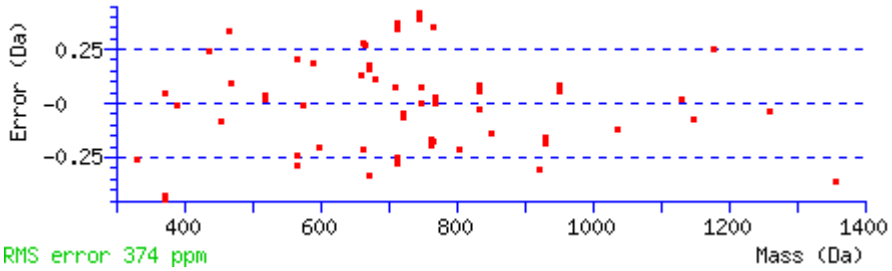
Mass (Da)

IDENTIFICATION 19
MS/MS Fragmentation of SSTPLPTVSSSAENTR
Found in IPI00126338



Monoisotopic mass of neutral peptide Mr(calc): 1712.7618
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.05 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							16
2	175.0713	88.0393			157.0608	79.0340	S	1626.7371	813.8722	1609.7105	805.3589	1608.7265	804.8669	15
3	356.0853	178.5463			338.0748	169.5410	T	1539.7050	770.3562	1522.6785	761.8429	1521.6945	761.3509	14
4	453.1381	227.0727			435.1275	218.0674	P	1358.6910	679.8492	1341.6645	671.3359	1340.6805	670.8439	13
5	566.2222	283.6147			548.2116	274.6094	L	1261.6383	631.3228	1244.6117	622.8095	1243.6277	622.3175	12
6	663.2749	332.1411			645.2644	323.1358	P	1148.5542	574.7807	1131.5277	566.2675	1130.5436	565.7755	11
7	764.3226	382.6649			746.3120	373.6597	T	1051.5014	526.2544	1034.4749	517.7411	1033.4909	517.2491	10
8	863.3910	432.1992			845.3805	423.1939	V	950.4538	475.7305	933.4272	467.2172	932.4432	466.7252	9
9	950.4231	475.7152			932.4125	466.7099	S	851.3853	426.1963	834.3588	417.6830	833.3748	417.1910	8
10	1037.4551	519.2312			1019.4445	510.2259	S	764.3533	382.6803	747.3268	374.1670	746.3428	373.6750	7
11	1124.4871	562.7472			1106.4765	553.7419	S	677.3213	339.1643	660.2947	330.6510	659.3107	330.1590	6
12	1195.5242	598.2658			1177.5137	589.2605	A	590.2893	295.6483	573.2627	287.1350	572.2787	286.6430	5
13	1324.5668	662.7870			1306.5563	653.7818	E	519.2522	260.1297	502.2256	251.6164	501.2416	251.1244	4
14	1438.6097	719.8085	1421.5832	711.2952	1420.5992	710.8032	N	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
15	1539.6574	770.3324	1522.6309	761.8191	1521.6469	761.3271	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
16							R	175.1190	88.0631	158.0924	79.5498			1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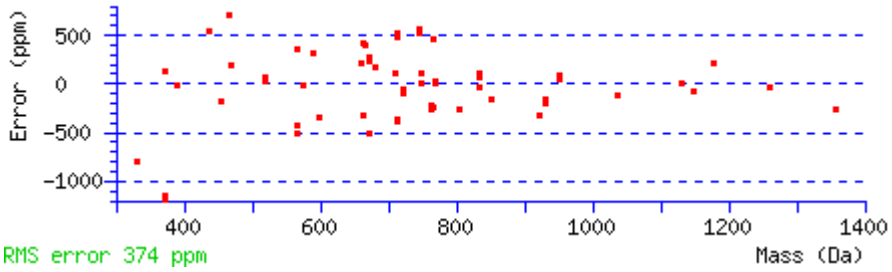
800
1000
1200
1400
RMS error 374 ppm
Mass (Da)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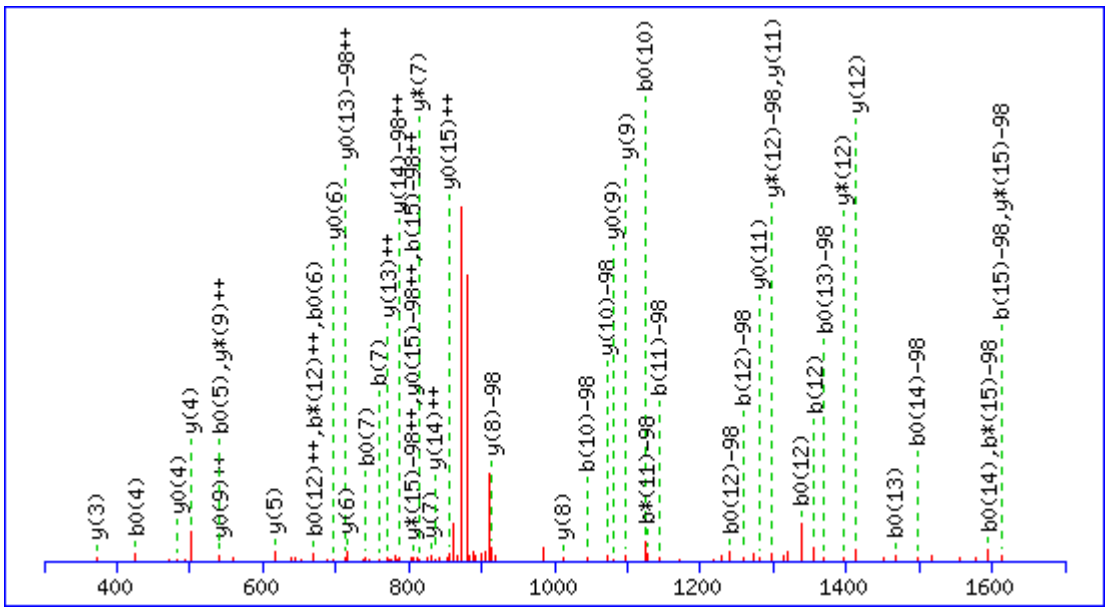
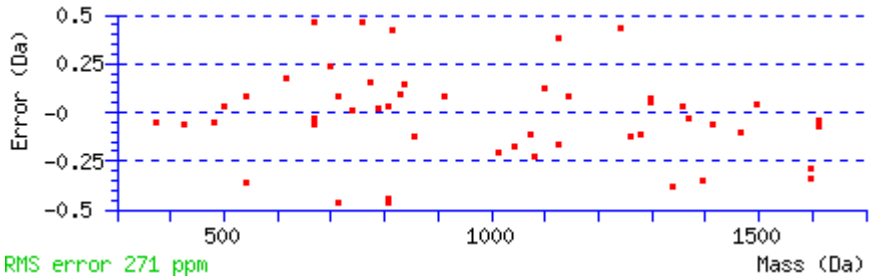
-500
-1000
400
600
800
1000
1200
1400
RMS error 374 ppm
Mass (Da)

IDENTIFICATION 20
MS/MS Fragmentation of EGKEDEASTDVDEKPK
Found in IPI00137194

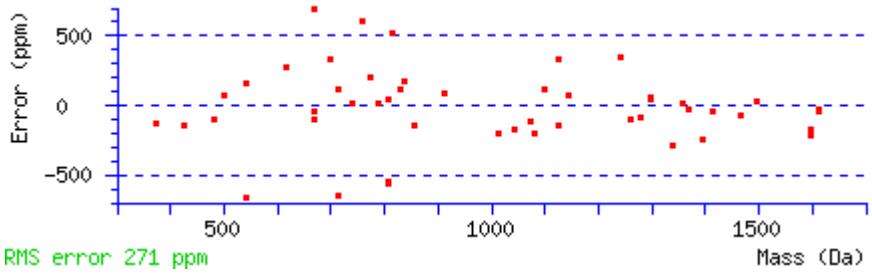


Monoisotopic mass of neutral peptide Mr(calc): 1855.7724
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.23 (help)

#	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							16
2	187.0713	94.0393			169.0608	85.0340	G	1629.7602	815.3838	1612.7337	806.8705	1611.7497	806.3785	15
3	315.1663	158.0868	298.1397	149.5735	297.1557	149.0815	K	1572.7388	786.8730	1555.7122	778.3597	1554.7282	777.8677	14
4	444.2089	222.6081	427.1823	214.0948	426.1983	213.6028	E	1444.6438	722.8255	1427.6173	714.3123	1426.6332	713.8203	13
5	559.2358	280.1216	542.2093	271.6083	541.2253	271.1163	D	1315.6012	658.3042	1298.5747	649.7910	1297.5907	649.2990	12
6	688.2784	344.6429	671.2519	336.1296	670.2679	335.6376	E	1200.5743	600.7908	1183.5477	592.2775	1182.5637	591.7855	11
7	759.3155	380.1614	742.2890	371.6481	741.3050	371.1561	A	1071.5317	536.2695	1054.5051	527.7562	1053.5211	527.2642	10
8	846.3476	423.6774	829.3210	415.1641	828.3370	414.6721	S	1000.4946	500.7509	983.4680	492.2376	982.4840	491.7456	9
9	929.3847	465.1960	912.3581	456.6827	911.3741	456.1907	T	913.4625	457.2349	896.4360	448.7216	895.4520	448.2296	8
10	1044.4116	522.7095	1027.3851	514.1962	1026.4011	513.7042	D	830.4254	415.7164	813.3989	407.2031	812.4149	406.7111	7
11	1143.4800	572.2437	1126.4535	563.7304	1125.4695	563.2384	V	715.3985	358.2029	698.3719	349.6896	697.3879	349.1976	6
12	1258.5070	629.7571	1241.4804	621.2439	1240.4964	620.7518	D	616.3301	308.6687	599.3035	300.1554	598.3195	299.6634	5
13	1387.5496	694.2784	1370.5230	685.7652	1369.5390	685.2731	E	501.3031	251.1552	484.2766	242.6419	483.2926	242.1499	4
14	1515.6445	758.3259	1498.6180	749.8126	1497.6340	749.3206	K	372.2605	186.6339	355.2340	178.1206			3
15	1612.6973	806.8523	1595.6708	798.3390	1594.6867	797.8470	P	244.1656	122.5864	227.1390	114.0731			2
16							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 271 ppm

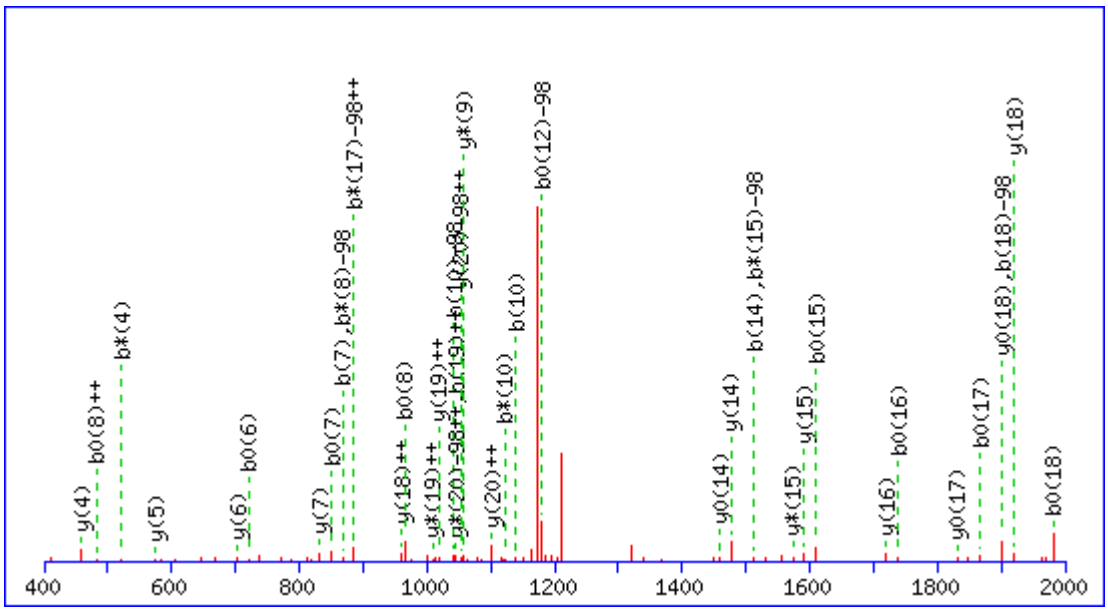


RMS error 271 ppm

IDENTIFICATION 21

MS/MS Fragmentation of QKSDAEEDGVTGSQDEEDSKPK

Found in IPI00119618



Monoisotopic mass of neutral peptide Mr(calc): 2458.0020

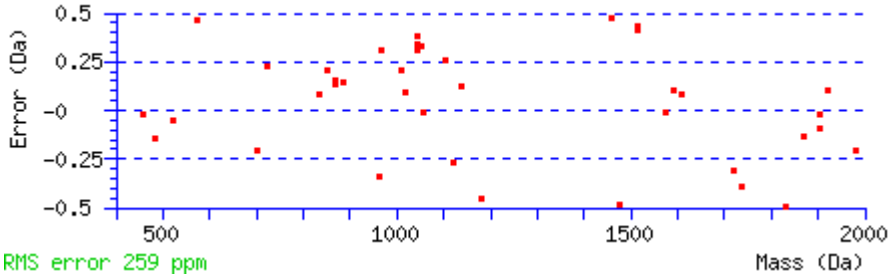
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

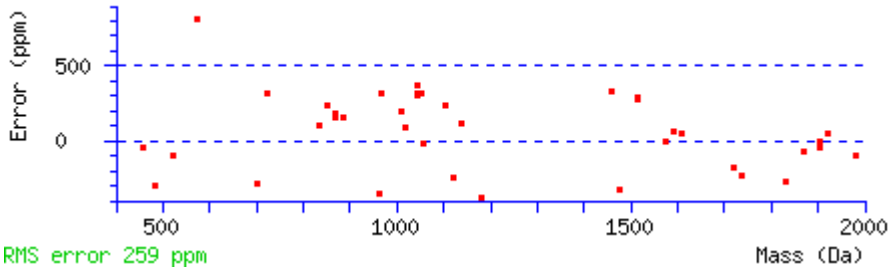
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 30 Expect: 0.21 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							22
2	257.1608	129.0840	240.1343	120.5708			K	2232.9739	1116.9906	2215.9473	1108.4773	2214.9633	1107.9853	21
3	326.1823	163.5948	309.1557	155.0815	308.1717	154.5895	S	2104.8789	1052.9431	2087.8524	1044.4298	2086.8683	1043.9378	20
4	441.2092	221.1082	424.1827	212.5950	423.1987	212.1030	D	2035.8574	1018.4324	2018.8309	1009.9191	2017.8469	1009.4271	19
5	512.2463	256.6268	495.2198	248.1135	494.2358	247.6215	A	1920.8305	960.9189	1903.8040	952.4056	1902.8199	951.9136	18
6	641.2889	321.1481	624.2624	312.6348	623.2784	312.1428	E	1849.7934	925.4003	1832.7668	916.8871	1831.7828	916.3950	17
7	770.3315	385.6694	753.3050	377.1561	752.3210	376.6641	E	1720.7508	860.8790	1703.7242	852.3658	1702.7402	851.8738	16
8	885.3585	443.1829	868.3319	434.6696	867.3479	434.1776	D	1591.7082	796.3577	1574.6817	787.8445	1573.6976	787.3525	15
9	942.3799	471.6936	925.3534	463.1803	924.3694	462.6883	G	1476.6813	738.8443	1459.6547	730.3310	1458.6707	729.8390	14
10	1041.4483	521.2278	1024.4218	512.7145	1023.4378	512.2225	V	1419.6598	710.3335	1402.6332	701.8203	1401.6492	701.3283	13
11	1142.4960	571.7516	1125.4695	563.2384	1124.4855	562.7464	T	1320.5914	660.7993	1303.5648	652.2861	1302.5808	651.7940	12
12	1199.5175	600.2624	1182.4909	591.7491	1181.5069	591.2571	G	1219.5437	610.2755	1202.5172	601.7622	1201.5331	601.2702	11
13	1286.5495	643.7784	1269.5230	635.2651	1268.5390	634.7731	S	1162.5222	581.7648	1145.4957	573.2515	1144.5117	572.7595	10
14	1414.6081	707.8077	1397.5815	699.2944	1396.5975	698.8024	Q	1075.4902	538.2487	1058.4637	529.7355	1057.4796	529.2435	9
15	1529.6350	765.3212	1512.6085	756.8079	1511.6245	756.3159	D	947.4316	474.2195	930.4051	465.7062	929.4211	465.2142	8
16	1658.6776	829.8425	1641.6511	821.3292	1640.6671	820.8372	E	832.4047	416.7060	815.3781	408.1927	814.3941	407.7007	7
17	1787.7202	894.3637	1770.6937	885.8505	1769.7097	885.3585	E	703.3621	352.1847	686.3355	343.6714	685.3515	343.1794	6
18	1902.7472	951.8772	1885.7206	943.3639	1884.7366	942.8719	D	574.3195	287.6634	557.2930	279.1501	556.3089	278.6581	5
19	1989.7792	995.3932	1972.7526	986.8800	1971.7686	986.3880	S	459.2926	230.1499	442.2660	221.6366	441.2820	221.1446	4
20	2117.8742	1059.4407	2100.8476	1050.9274	2099.8636	1050.4354	K	372.2605	186.6339	355.2340	178.1206			3
21	2214.9269	1107.9671	2197.9004	1099.4538	2196.9164	1098.9618	P	244.1656	122.5864	227.1390	114.0731			2
22							K	147.1128	74.0600	130.0863	65.5468			1

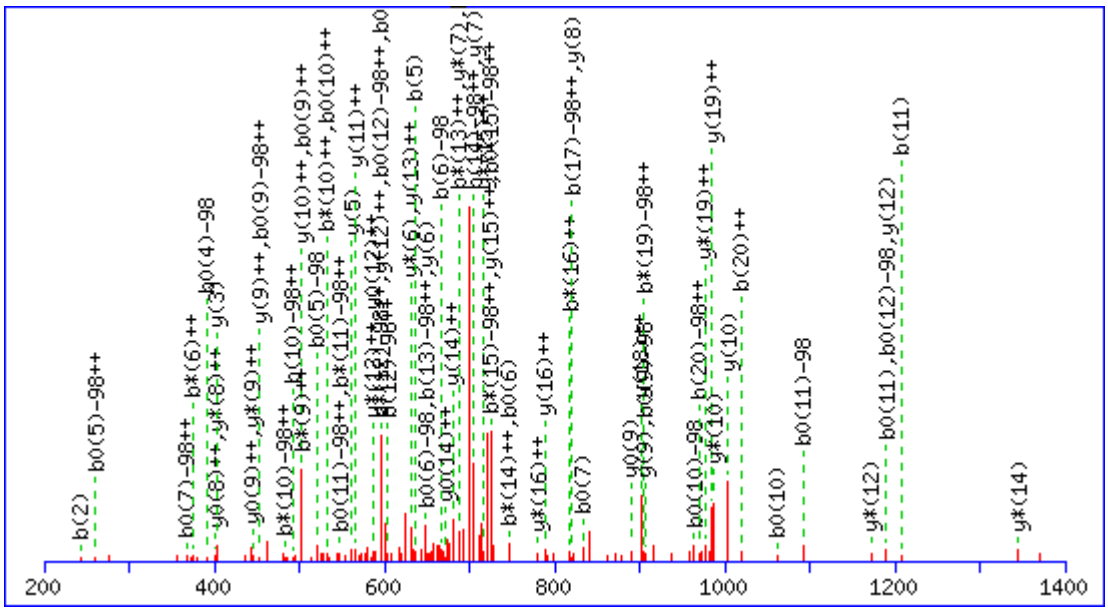


RMS error 259 ppm



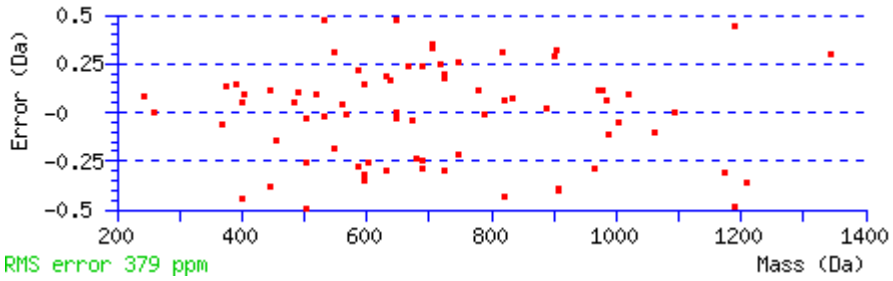
RMS error 259 ppm

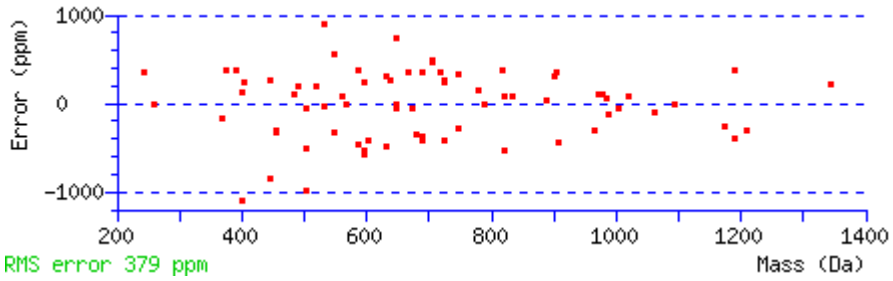
IDENTIFICATION 22
MS/MS Fragmentation of ELSPEQSTAGKPSDGSSALDR
Found in IPI00222461



Monoisotopic mass of neutral peptide Mr(calc): 2210.9692
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.024 (help)

#	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							21
2	243.1339	122.0706			225.1234	113.0653	L	2082.9339	1041.9706	2065.9074	1033.4573	2064.9234	1032.9653	20
3	410.1323	205.5698			392.1217	196.5645	S	1969.8499	985.4286	1952.8233	976.9153	1951.8393	976.4233	19
4	507.1851	254.0962			489.1745	245.0909	P	1802.8515	901.9294	1785.8250	893.4161	1784.8409	892.9241	18
5	636.2276	318.6175			618.2171	309.6122	E	1705.7987	853.4030	1688.7722	844.8897	1687.7882	844.3977	17
6	764.2862	382.6468	747.2597	374.1335	746.2757	373.6415	Q	1576.7562	788.8817	1559.7296	780.3684	1558.7456	779.8764	16
7	851.3183	426.1628	834.2917	417.6495	833.3077	417.1575	S	1448.6976	724.8524	1431.6710	716.3392	1430.6870	715.8471	15
8	952.3659	476.6866	935.3394	468.1733	934.3554	467.6813	T	1361.6655	681.3364	1344.6390	672.8231	1343.6550	672.3311	14
9	1023.4030	512.2052	1006.3765	503.6919	1005.3925	503.1999	A	1260.6179	630.8126	1243.5913	622.2993	1242.6073	621.8073	13
10	1080.4245	540.7159	1063.3980	532.2026	1062.4139	531.7106	G	1189.5808	595.2940	1172.5542	586.7807	1171.5702	586.2887	12
11	1208.5195	604.7634	1191.4929	596.2501	1190.5089	595.7581	K	1132.5593	566.7833	1115.5327	558.2700	1114.5487	557.7780	11
12	1305.5722	653.2898	1288.5457	644.7765	1287.5617	644.2845	P	1004.4643	502.7358	987.4378	494.2225	986.4538	493.7305	10
13	1392.6043	696.8058	1375.5777	688.2925	1374.5937	687.8005	S	907.4116	454.2094	890.3850	445.6961	889.4010	445.2041	9
14	1507.6312	754.3192	1490.6047	745.8060	1489.6206	745.3140	D	820.3795	410.6934	803.3530	402.1801	802.3690	401.6881	8
15	1564.6527	782.8300	1547.6261	774.3167	1546.6421	773.8247	G	705.3526	353.1799	688.3260	344.6667	687.3420	344.1747	7
16	1651.6847	826.3460	1634.6582	817.8327	1633.6741	817.3407	S	648.3311	324.6692	631.3046	316.1559	630.3206	315.6639	6
17	1738.7167	869.8620	1721.6902	861.3487	1720.7062	860.8567	S	561.2991	281.1532	544.2726	272.6399	543.2885	272.1479	5
18	1809.7538	905.3806	1792.7273	896.8673	1791.7433	896.3753	A	474.2671	237.6372	457.2405	229.1239	456.2565	228.6319	4
19	1922.8379	961.9226	1905.8114	953.4093	1904.8273	952.9173	L	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
20	2037.8649	1019.4361	2020.8383	1010.9228	2019.8543	1010.4308	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

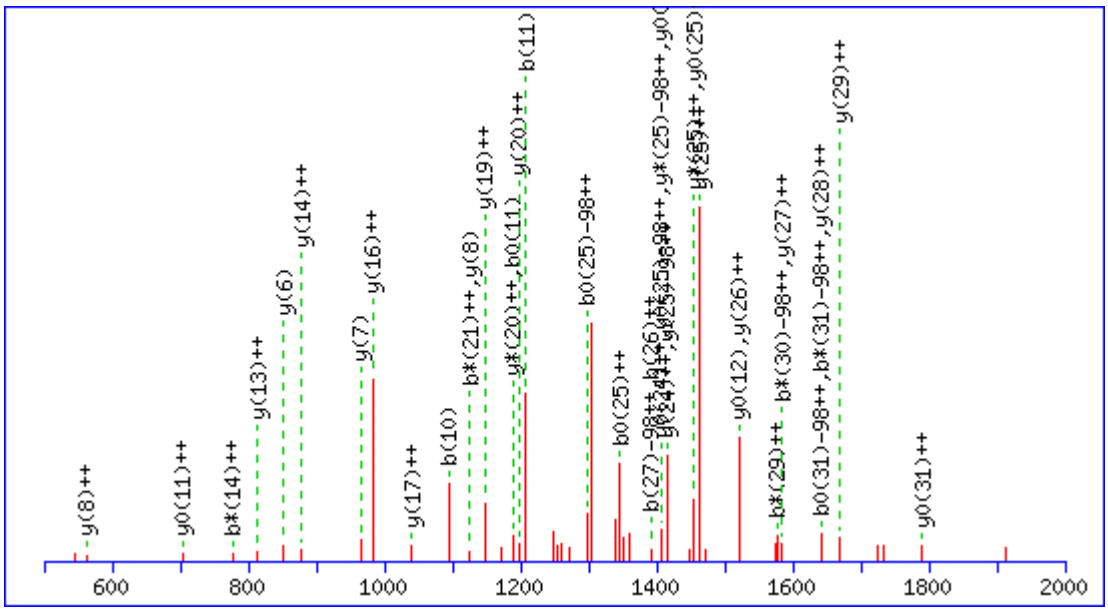

0.5
0.25
-0
-0.25
-0.5
Error (Da)
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 379 ppm


1000
0
-1000
Error (ppm)
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 379 ppm

IDENTIFICATION 23

MS/MS Fragmentation of IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK

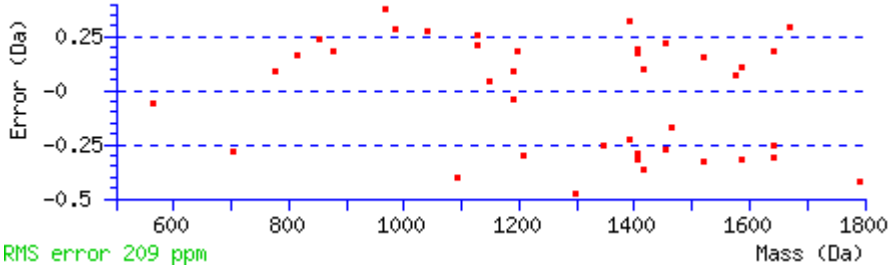
Found in IPI00223253

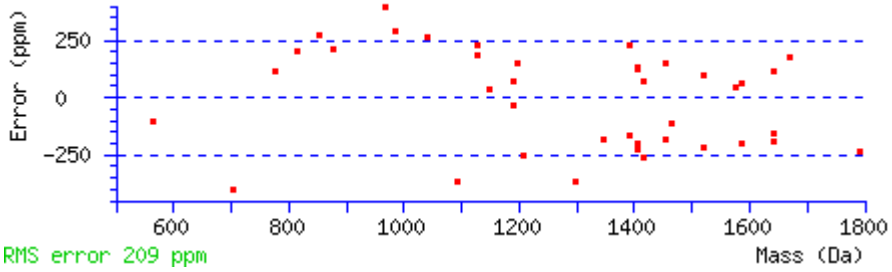


Monoisotopic mass of neutral peptide Mr(calc): 4133.9908
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 82 Expect: 1e-06 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							36
2	227.1754	114.0913					I	4021.9141	2011.4607	4004.8875	2002.9474	4003.9035	2002.4554	35
3	324.2282	162.6177					P	3908.8300	1954.9186	3891.8034	1946.4054	3890.8194	1945.9134	34
4	425.2758	213.1416			407.2653	204.1363	T	3811.7772	1906.3923	3794.7507	1897.8790	3793.7667	1897.3870	33
5	538.3599	269.6836			520.3493	260.6783	L	3710.7296	1855.8684	3693.7030	1847.3551	3692.7190	1846.8631	32
6	667.4025	334.2049			649.3919	325.1996	E	3597.6455	1799.3264	3580.6189	1790.8131	3579.6349	1790.3211	31
7	796.4451	398.7262			778.4345	389.7209	E	3468.6029	1734.8051	3451.5763	1726.2918	3450.5923	1725.7998	30
8	853.4666	427.2369			835.4560	418.2316	G	3339.5603	1670.2838	3322.5338	1661.7705	3321.5497	1661.2785	29
9	966.5506	483.7790			948.5401	474.7737	L	3282.5388	1641.7731	3265.5123	1633.2598	3264.5283	1632.7678	28
10	1094.6092	547.8082	1077.5827	539.2950	1076.5986	538.8030	Q	3169.4548	1585.2310	3152.4282	1576.7178	3151.4442	1576.2257	27
11	1207.6933	604.3503	1190.6667	595.8370	1189.6827	595.3450	L	3041.3962	1521.2017	3024.3696	1512.6885	3023.3856	1512.1965	26
12	1304.7460	652.8767	1287.7195	644.3634	1286.7355	643.8714	P	2928.3121	1464.6597	2911.2856	1456.1464	2910.3016	1455.6544	25
13	1471.7444	736.3758	1454.7178	727.8626	1453.7338	727.3706	S	2831.2594	1416.1333	2814.2328	1407.6200	2813.2488	1407.1280	24
14	1568.7972	784.9022	1551.7706	776.3889	1550.7866	775.8969	P	2664.2610	1332.6341	2647.2345	1324.1209	2646.2504	1323.6289	23
15	1669.8448	835.4261	1652.8183	826.9128	1651.8343	826.4208	T	2567.2082	1284.1078	2550.1817	1275.5945	2549.1977	1275.1025	22
16	1740.8819	870.9446	1723.8554	862.4313	1722.8714	861.9393	A	2466.1606	1233.5839	2449.1340	1225.0706	2448.1500	1224.5786	21
17	1841.9296	921.4685	1824.9031	912.9552	1823.9191	912.4632	T	2395.1235	1198.0654	2378.0969	1189.5521	2377.1129	1189.0601	20
18	1928.9617	964.9845	1911.9351	956.4712	1910.9511	955.9792	S	2294.0758	1147.5415	2277.0492	1139.0283	2276.0652	1138.5362	19
19	2057.0202	1029.0138	2039.9937	1020.5005	2039.0097	1020.0085	Q	2207.0437	1104.0255	2190.0172	1095.5122	2189.0332	1095.0202	18
20	2170.1043	1085.5558	2153.0777	1077.0425	2152.0937	1076.5505	L	2078.9852	1039.9962	2061.9586	1031.4829	2060.9746	1030.9909	17
21	2267.1571	1134.0822	2250.1305	1125.5689	2249.1465	1125.0769	P	1965.9011	983.4542	1948.8746	974.9409	1947.8905	974.4489	16
22	2380.2411	1190.6242	2363.2146	1182.1109	2362.2306	1181.6189	L	1868.8483	934.9278	1851.8218	926.4145	1850.8378	925.9225	15
23	2509.2837	1255.1455	2492.2572	1246.6322	2491.2732	1246.1402	E	1755.7643	878.3858	1738.7377	869.8725	1737.7537	869.3805	14
24	2596.3157	1298.6615	2579.2892	1290.1482	2578.3052	1289.6562	S	1626.7217	813.8645	1609.6951	805.3512	1608.7111	804.8592	13
25	2711.3427	1356.1750	2694.3161	1347.6617	2693.3321	1347.1697	D	1539.6897	770.3485	1522.6631	761.8352	1521.6791	761.3432	12
26	2782.3798	1391.6935	2765.3533	1383.1803	2764.3692	1382.6883	A	1424.6627	712.8350	1407.6362	704.3217	1406.6521	703.8297	11
27	2881.4482	1441.2277	2864.4217	1432.7145	2863.4377	1432.2225	V	1353.6256	677.3164	1336.5991	668.8032	1335.6150	668.3112	10

28	3010.4908	1505.7490	2993.4643	1497.2358	2992.4802	1496.7438	E	1254.5572	627.7822	1237.5306	619.2690	1236.5466	618.7769	9
29	3170.5215	1585.7644	3153.4949	1577.2511	3152.5109	1576.7591	C	1125.5146	563.2609	1108.4880	554.7477			8
30	3283.6055	1642.3064	3266.5790	1633.7931	3265.5950	1633.3011	L	965.4839	483.2456	948.4574	474.7323			7
31	3397.6484	1699.3279	3380.6219	1690.8146	3379.6379	1690.3226	N	852.3999	426.7036	835.3733	418.1903			6
32	3560.7118	1780.8595	3543.6852	1772.3463	3542.7012	1771.8542	Y	738.3570	369.6821	721.3304	361.1688			5
33	3688.7704	1844.8888	3671.7438	1836.3755	3670.7598	1835.8835	Q	575.2936	288.1504	558.2671	279.6372			4
34	3825.8293	1913.4183	3808.8027	1904.9050	3807.8187	1904.4130	H	447.2350	224.1212	430.2085	215.6079			3
35	3988.8926	1994.9499	3971.8660	1986.4367	3970.8820	1985.9447	Y	310.1761	155.5917	293.1496	147.0784			2
36							K	147.1128	74.0600	130.0863	65.5468			1

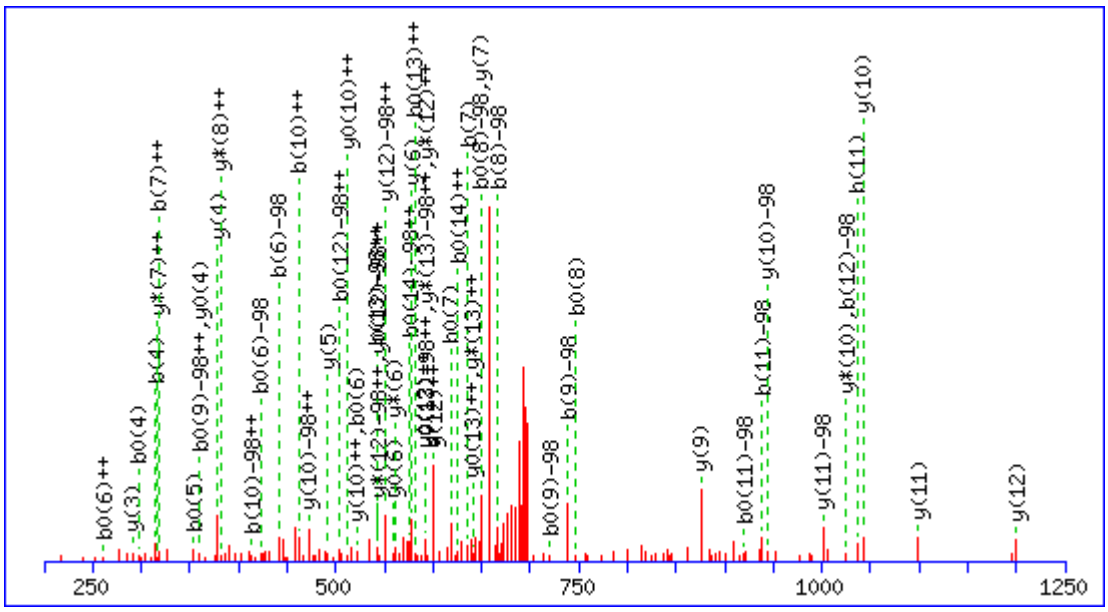




IDENTIFICATION 24

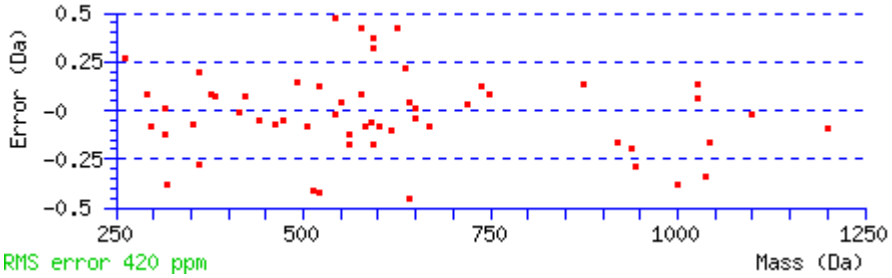
MS/MS Fragmentation of GGVTGSPEASISGSK

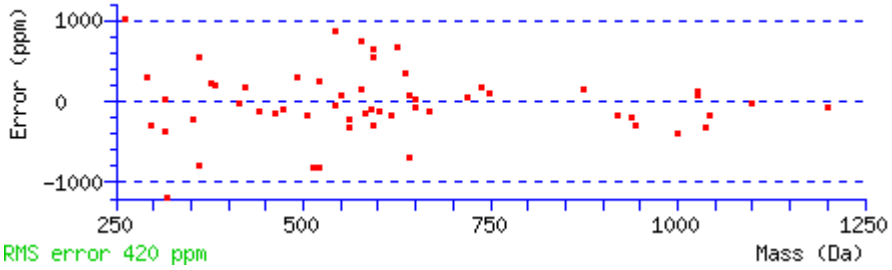
Found in IPI00553798



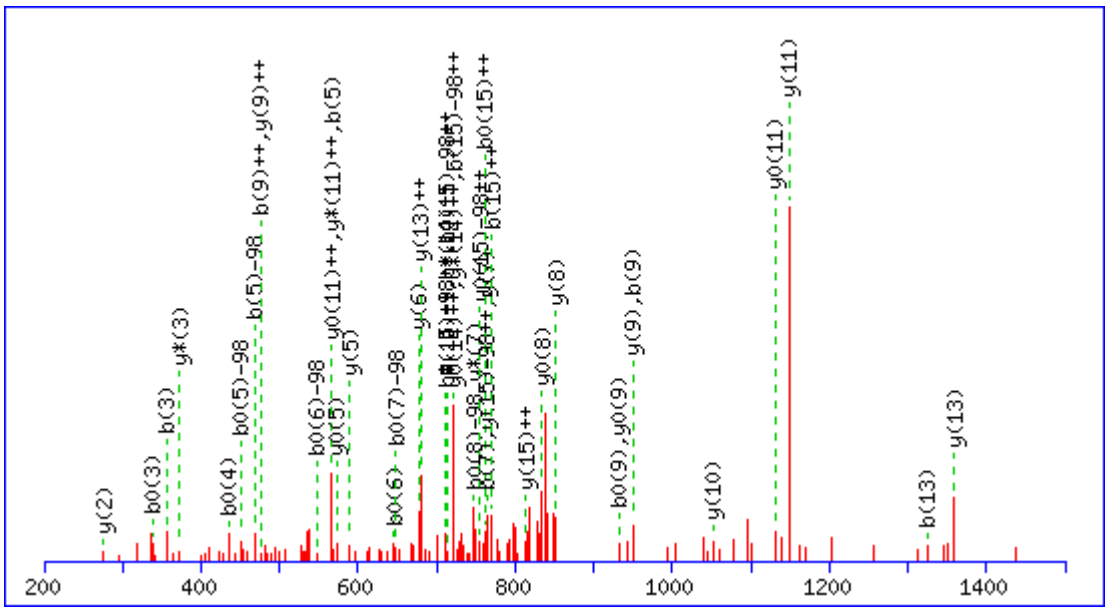
Monoisotopic mass of neutral peptide Mr(calc): 1412.6185
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 25 Expect: 0.42 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							15
2	115.0502	58.0287			G	1258.6274	629.8173	1241.6008	621.3040	1240.6168	620.8120	14
3	214.1186	107.5629			V	1201.6059	601.3066	1184.5794	592.7933	1183.5953	592.3013	13
4	315.1663	158.0868	297.1557	149.0815	T	1102.5375	551.7724	1085.5109	543.2591	1084.5269	542.7671	12
5	372.1878	186.5975	354.1772	177.5922	G	1001.4898	501.2485	984.4633	492.7353	983.4792	492.2433	11
6	441.2092	221.1082	423.1987	212.1030	S	944.4684	472.7378	927.4418	464.2245	926.4578	463.7325	10
7	538.2620	269.6346	520.2514	260.6293	P	875.4469	438.2271	858.4203	429.7138	857.4363	429.2218	9
8	667.3046	334.1559	649.2940	325.1506	E	778.3941	389.7007	761.3676	381.1874	760.3836	380.6954	8
9	738.3417	369.6745	720.3311	360.6692	A	649.3515	325.1794	632.3250	316.6661	631.3410	316.1741	7
10	825.3737	413.1905	807.3632	404.1852	S	578.3144	289.6608	561.2879	281.1476	560.3039	280.6556	6
11	938.4578	469.7325	920.4472	460.7272	I	491.2824	246.1448	474.2558	237.6316	473.2718	237.1395	5
12	1025.4898	513.2485	1007.4793	504.2433	S	378.1983	189.6028	361.1718	181.0895	360.1878	180.5975	4
13	1082.5113	541.7593	1064.5007	532.7540	G	291.1663	146.0868	274.1397	137.5735	273.1557	137.0815	3
14	1169.5433	585.2753	1151.5327	576.2700	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
15					K	147.1128	74.0600	130.0863	65.5468			1


0.5
0.25
-0
-0.25
-0.5
Error (Da)
250
500
750
1000
1250
Mass (Da)
RMS error 420 ppm

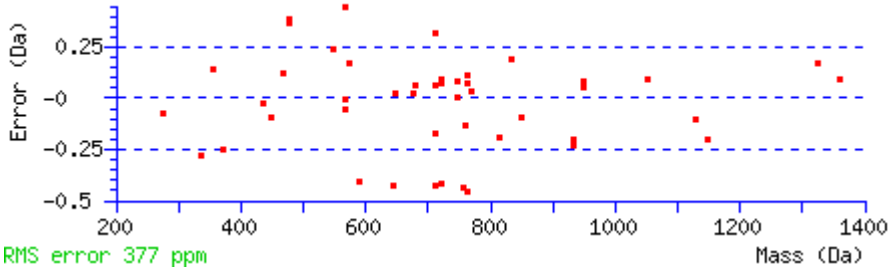

1000
0
-1000
Error (ppm)
250
500
750
1000
1250
Mass (Da)
RMS error 420 ppm

IDENTIFICATION 25
MS/MS Fragmentation of SSTPLPTVSSSAENTR
Found in IPI00126338



Monoisotopic mass of neutral peptide Mr(calc): 1712.7618
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 39 Expect: 0.021 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							16
2	255.0377	128.0225			237.0271	119.0172	S	1626.7371	813.8722	1609.7105	805.3589	1608.7265	804.8669	15
3	356.0853	178.5463			338.0748	169.5410	T	1459.7387	730.3730	1442.7122	721.8597	1441.7281	721.3677	14
4	453.1381	227.0727			435.1275	218.0674	P	1358.6910	679.8492	1341.6645	671.3359	1340.6805	670.8439	13
5	566.2222	283.6147			548.2116	274.6094	L	1261.6383	631.3228	1244.6117	622.8095	1243.6277	622.3175	12
6	663.2749	332.1411			645.2644	323.1358	P	1148.5542	574.7807	1131.5277	566.2675	1130.5436	565.7755	11
7	764.3226	382.6649			746.3120	373.6597	T	1051.5014	526.2544	1034.4749	517.7411	1033.4909	517.2491	10
8	863.3910	432.1992			845.3805	423.1939	V	950.4538	475.7305	933.4272	467.2172	932.4432	466.7252	9
9	950.4231	475.7152			932.4125	466.7099	S	851.3853	426.1963	834.3588	417.6830	833.3748	417.1910	8
10	1037.4551	519.2312			1019.4445	510.2259	S	764.3533	382.6803	747.3268	374.1670	746.3428	373.6750	7
11	1124.4871	562.7472			1106.4765	553.7419	S	677.3213	339.1643	660.2947	330.6510	659.3107	330.1590	6
12	1195.5242	598.2658			1177.5137	589.2605	A	590.2893	295.6483	573.2627	287.1350	572.2787	286.6430	5
13	1324.5668	662.7870			1306.5563	653.7818	E	519.2522	260.1297	502.2256	251.6164	501.2416	251.1244	4
14	1438.6097	719.8085	1421.5832	711.2952	1420.5992	710.8032	N	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
15	1539.6574	770.3324	1522.6309	761.8191	1521.6469	761.3271	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
16							R	175.1190	88.0631	158.0924	79.5498			1


Error (Da)
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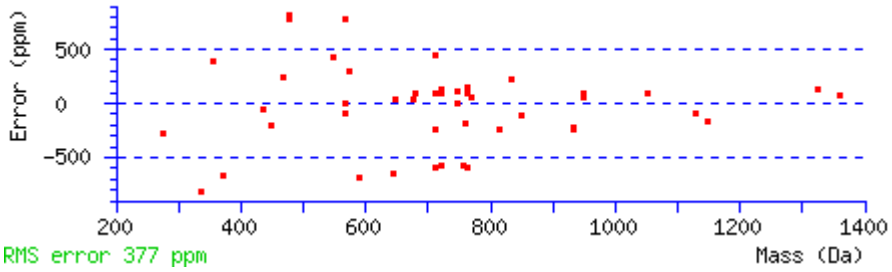
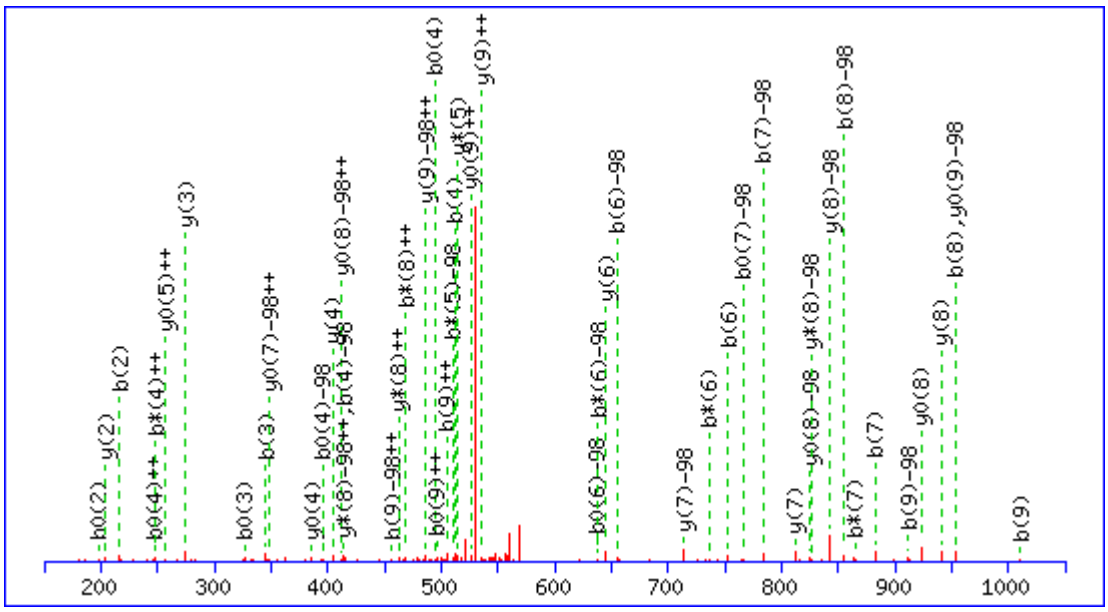
-0
-0.25
-0.5
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 377 ppm

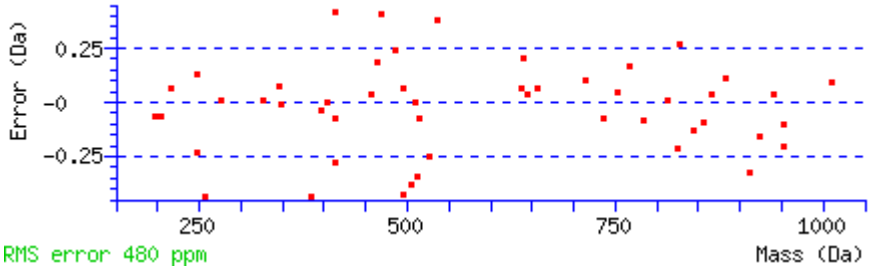

Error (ppm)
500
0
-500
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 377 ppm

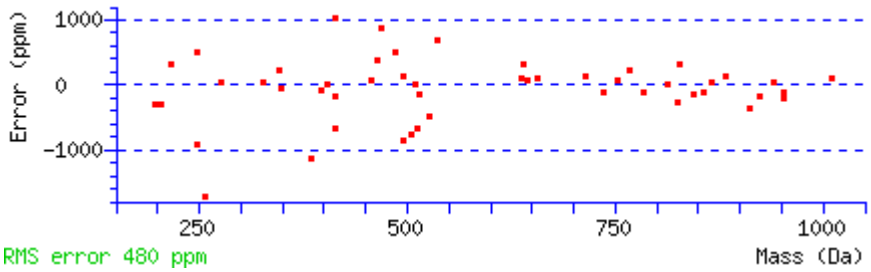
IDENTIFICATION 26
MS/MS Fragmentation of SKESLQEAGK
Found in IPI00137194



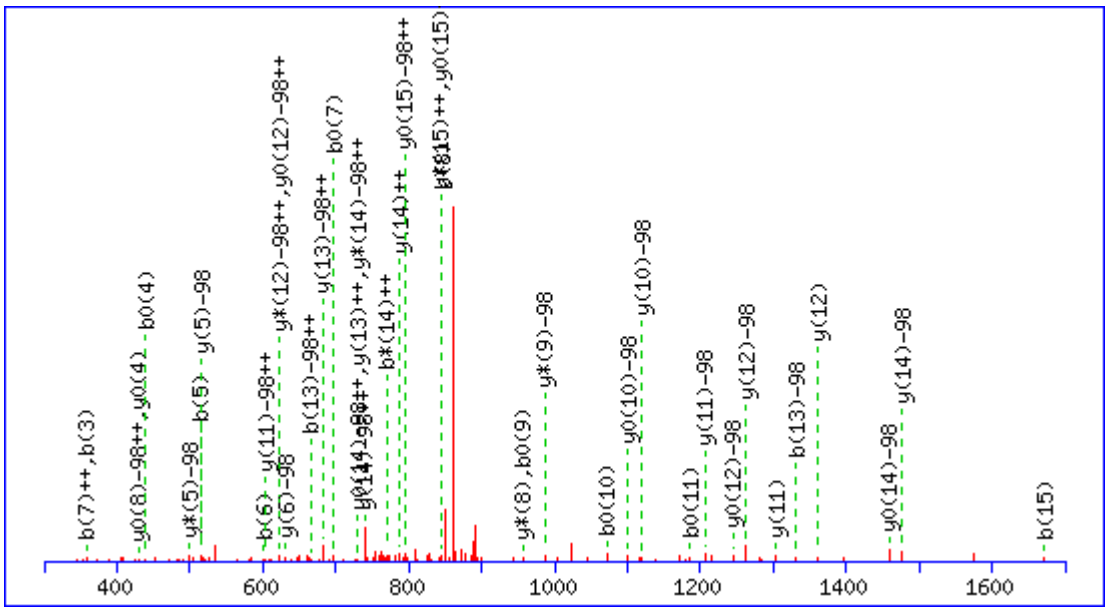
Monoisotopic mass of neutral peptide Mr(calc): 1155.5172
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 48 Expect: 0.0018 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							10
2	216.1343	108.5708	199.1077	100.0575	198.1237	99.5655	K	971.5156	486.2615	954.4891	477.7482	953.5051	477.2562	9
3	345.1769	173.0921	328.1503	164.5788	327.1663	164.0868	E	843.4207	422.2140	826.3941	413.7007	825.4101	413.2087	8
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	S	714.3781	357.6927	697.3515	349.1794	696.3675	348.6874	7
5	527.2824	264.1448	510.2558	255.6316	509.2718	255.1395	L	645.3566	323.1819	628.3301	314.6687	627.3461	314.1767	6
6	655.3410	328.1741	638.3144	319.6608	637.3304	319.1688	Q	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	5
7	784.3836	392.6954	767.3570	384.1821	766.3730	383.6901	E	404.2140	202.6106	387.1874	194.0974	386.2034	193.6053	4
8	855.4207	428.2140	838.3941	419.7007	837.4101	419.2087	A	275.1714	138.0893	258.1448	129.5761			3
9	912.4421	456.7247	895.4156	448.2114	894.4316	447.7194	G	204.1343	102.5708	187.1077	94.0575			2
10							K	147.1128	74.0600	130.0863	65.5468			1



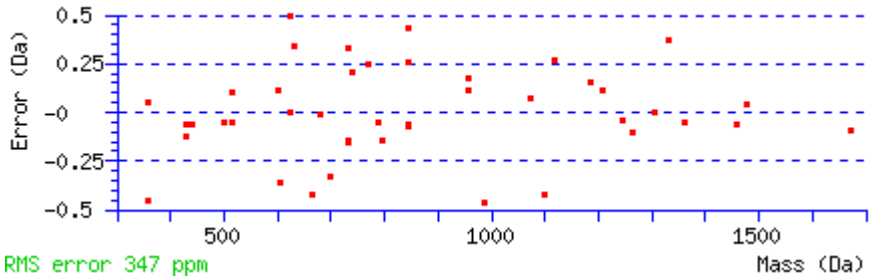


IDENTIFICATION 27
MS/MS Fragmentation of IEDVGSDEEDDSGKDK
Found in IPI00229080

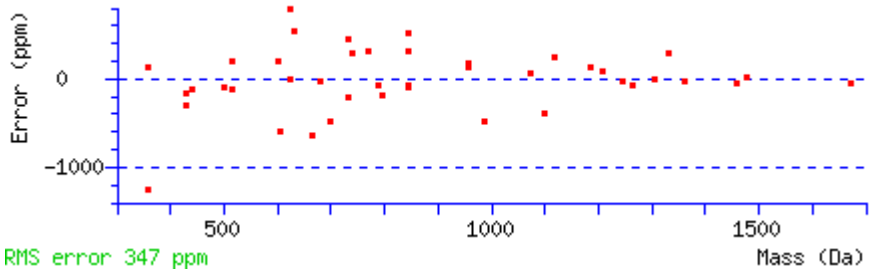


Monoisotopic mass of neutral peptide Mr(calc): 1816.6888
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.14 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							16
2	243.1339	122.0706			225.1234	113.0653	E	1606.6351	803.8212	1589.6085	795.3079	1588.6245	794.8159	15
3	358.1609	179.5841			340.1503	170.5788	D	1477.5925	739.2999	1460.5660	730.7866	1459.5819	730.2946	14
4	457.2293	229.1183			439.2187	220.1130	V	1362.5656	681.7864	1345.5390	673.2731	1344.5550	672.7811	13
5	514.2508	257.6290			496.2402	248.6237	G	1263.4971	632.2522	1246.4706	623.7389	1245.4866	623.2469	12
6	601.2828	301.1450			583.2722	292.1397	S	1206.4757	603.7415	1189.4491	595.2282	1188.4651	594.7362	11
7	716.3097	358.6585			698.2992	349.6532	D	1119.4437	560.2255	1102.4171	551.7122	1101.4331	551.2202	10
8	845.3523	423.1798			827.3418	414.1745	E	1004.4167	502.7120	987.3902	494.1987	986.4061	493.7067	9
9	974.3949	487.7011			956.3843	478.6958	E	875.3741	438.1907	858.3476	429.6774	857.3636	429.1854	8
10	1089.4219	545.2146			1071.4113	536.2093	D	746.3315	373.6694	729.3050	365.1561	728.3210	364.6641	7
11	1204.4488	602.7280			1186.4382	593.7228	D	631.3046	316.1559	614.2780	307.6427	613.2940	307.1506	6
12	1273.4703	637.2388			1255.4597	628.2335	S	516.2776	258.6425	499.2511	250.1292	498.2671	249.6372	5
13	1330.4917	665.7495			1312.4812	656.7442	G	447.2562	224.1317	430.2296	215.6185	429.2456	215.1264	4
14	1458.5867	729.7970	1441.5601	721.2837	1440.5761	720.7917	K	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	3
15	1573.6136	787.3105	1556.5871	778.7972	1555.6031	778.3052	D	262.1397	131.5735	245.1132	123.0602	244.1292	122.5682	2
16							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 347 ppm

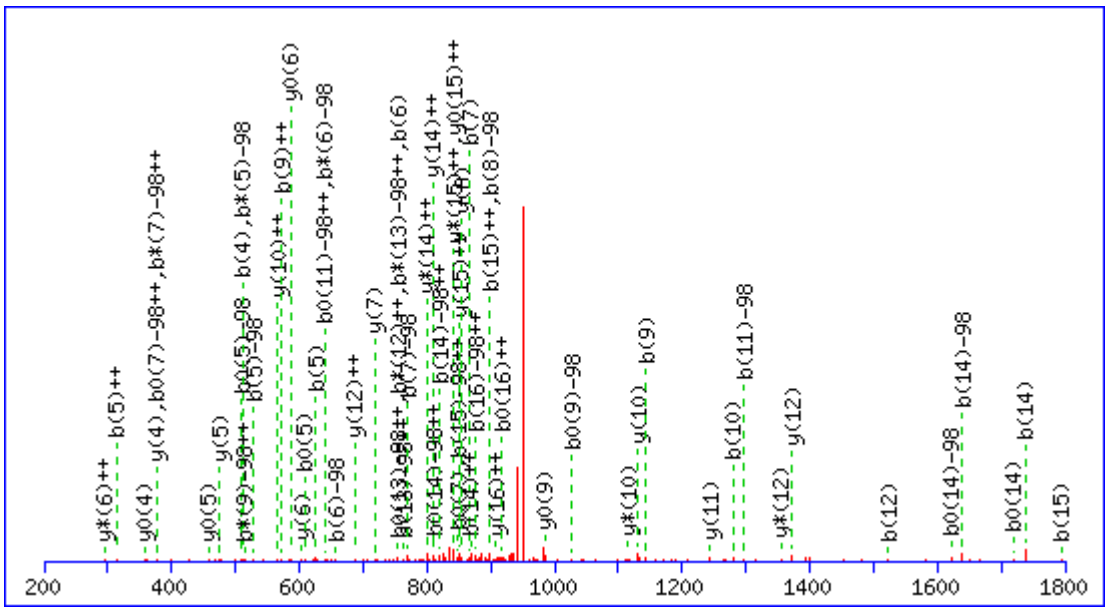


RMS error 347 ppm

IDENTIFICATION 28

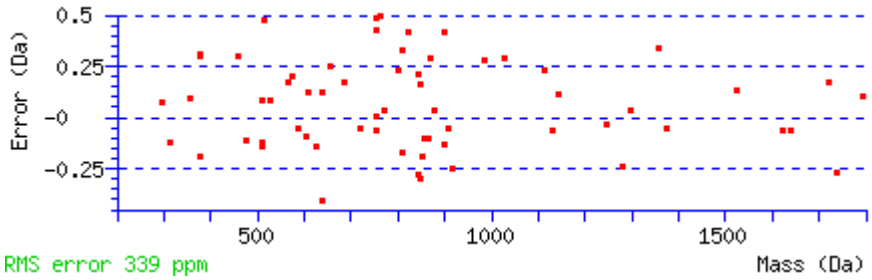
MS/MS Fragmentation of TNSQDKIEFHNEVDGGK

Found in IPI00126092

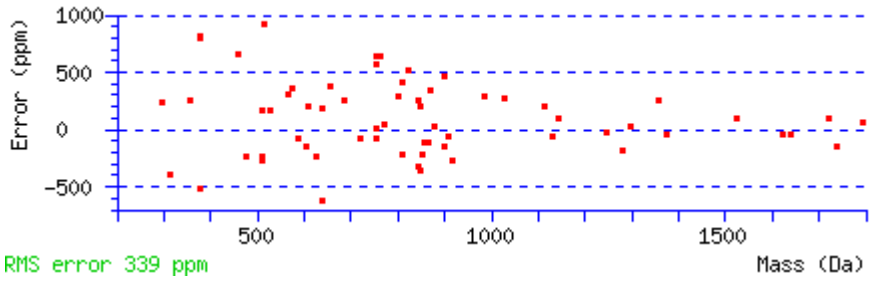


Monoisotopic mass of neutral peptide Mr(calc): 1996.8528
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.049 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	182.0213	91.5143			164.0107	82.5090	T							17
2	296.0642	148.5357	279.0377	140.0225	278.0536	139.5305	N	1816.8460	908.9267	1799.8195	900.4134	1798.8355	899.9214	16
3	383.0962	192.0518	366.0697	183.5385	365.0857	183.0465	S	1702.8031	851.9052	1685.7766	843.3919	1684.7925	842.8999	15
4	511.1548	256.0810	494.1283	247.5678	493.1443	247.0758	Q	1615.7711	808.3892	1598.7445	799.8759	1597.7605	799.3839	14
5	626.1818	313.5945	609.1552	305.0812	608.1712	304.5892	D	1487.7125	744.3599	1470.6859	735.8466	1469.7019	735.3546	13
6	754.2767	377.6420	737.2502	369.1287	736.2662	368.6367	K	1372.6856	686.8464	1355.6590	678.3331	1354.6750	677.8411	12
7	867.3608	434.1840	850.3342	425.6708	849.3502	425.1788	I	1244.5906	622.7989	1227.5640	614.2857	1226.5800	613.7937	11
8	996.4034	498.7053	979.3768	490.1921	978.3928	489.7000	E	1131.5065	566.2569	1114.4800	557.7436	1113.4960	557.2516	10
9	1143.4718	572.2395	1126.4452	563.7263	1125.4612	563.2343	F	1002.4639	501.7356	985.4374	493.2223	984.4534	492.7303	9
10	1280.5307	640.7690	1263.5042	632.2557	1262.5201	631.7637	H	855.3955	428.2014	838.3690	419.6881	837.3850	419.1961	8
11	1394.5736	697.7905	1377.5471	689.2772	1376.5631	688.7852	N	718.3366	359.6719	701.3101	351.1587	700.3260	350.6667	7
12	1523.6162	762.3118	1506.5897	753.7985	1505.6057	753.3065	E	604.2937	302.6505	587.2671	294.1372	586.2831	293.6452	6
13	1622.6846	811.8460	1605.6581	803.3327	1604.6741	802.8407	V	475.2511	238.1292	458.2245	229.6159	457.2405	229.1239	5
14	1737.7116	869.3594	1720.6850	860.8462	1719.7010	860.3541	D	376.1827	188.5950	359.1561	180.0817	358.1721	179.5897	4
15	1794.7330	897.8702	1777.7065	889.3569	1776.7225	888.8649	G	261.1557	131.0815	244.1292	122.5682			3
16	1851.7545	926.3809	1834.7280	917.8676	1833.7439	917.3756	G	204.1343	102.5708	187.1077	94.0575			2
17							K	147.1128	74.0600	130.0863	65.5468			1

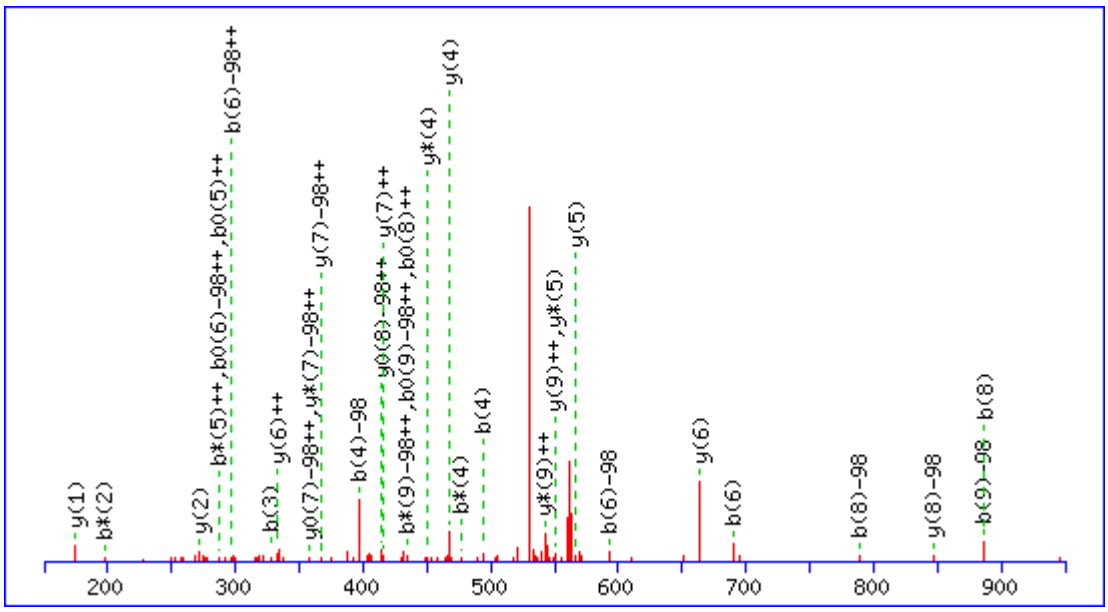


RMS error 339 ppm



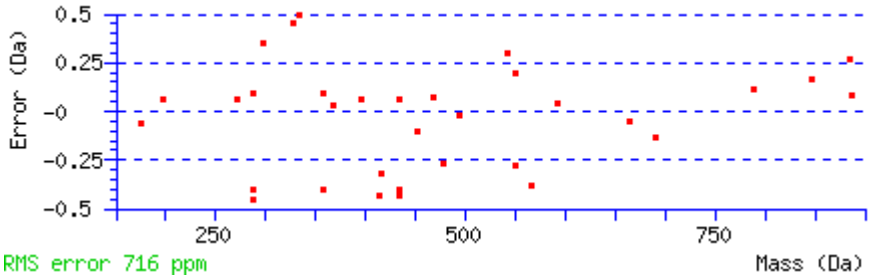
RMS error 339 ppm

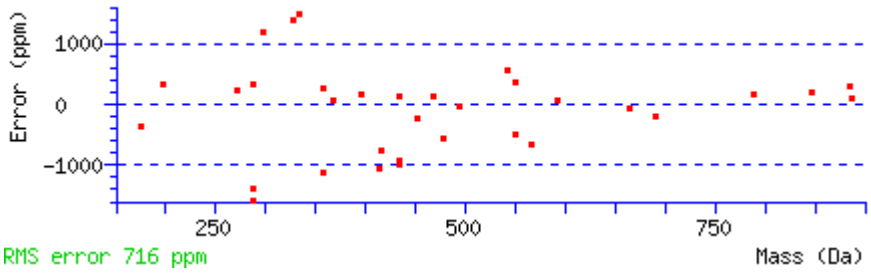
IDENTIFICATION 29
MS/MS Fragmentation of GRLSPVPVPR
Found in IPI00130147



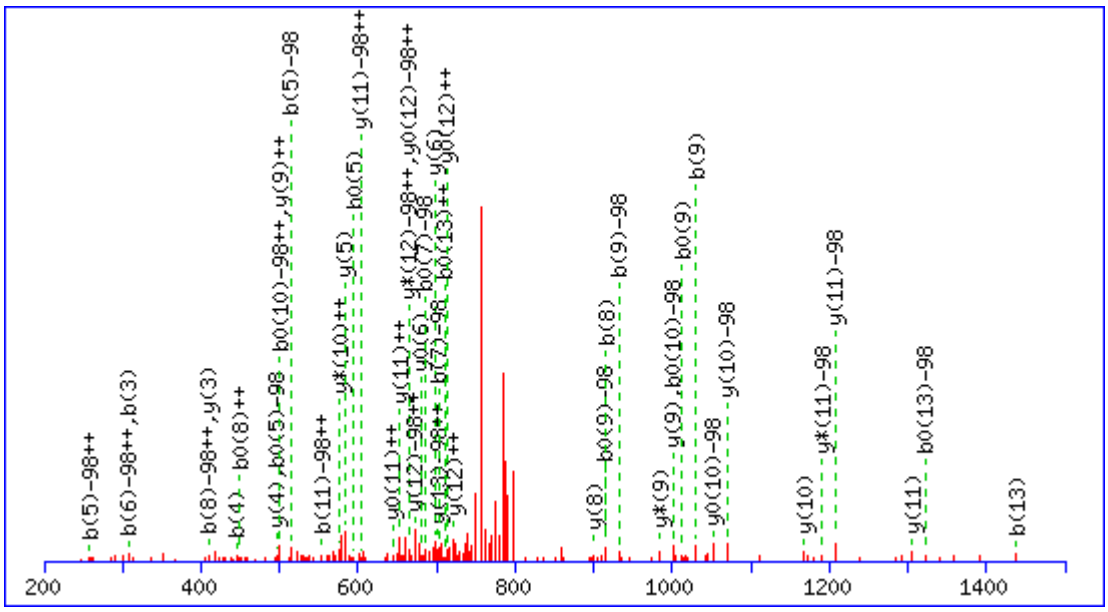
Monoisotopic mass of neutral peptide Mr(calc): 1156.6118
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.023 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							10
2	214.1299	107.5686	197.1033	99.0553			R	1002.6207	501.8140	985.5942	493.3007	984.6101	492.8087	9
3	327.2139	164.1106	310.1874	155.5973			L	846.5196	423.7634	829.4930	415.2502	828.5090	414.7582	8
4	396.2354	198.6213	379.2088	190.1081	378.2248	189.6160	S	733.4355	367.2214	716.4090	358.7081	715.4250	358.2161	7
5	493.2881	247.1477	476.2616	238.6344	475.2776	238.1424	P	664.4141	332.7107	647.3875	324.1974			6
6	592.3566	296.6819	575.3300	288.1686	574.3460	287.6766	V	567.3613	284.1843	550.3348	275.6710			5
7	689.4093	345.2083	672.3828	336.6950	671.3988	336.2030	P	468.2929	234.6501	451.2663	226.1368			4
8	788.4777	394.7425	771.4512	386.2292	770.4672	385.7372	V	371.2401	186.1237	354.2136	177.6104			3
9	885.5305	443.2689	868.5039	434.7556	867.5199	434.2636	P	272.1717	136.5895	255.1452	128.0762			2
10							R	175.1190	88.0631	158.0924	79.5498			1



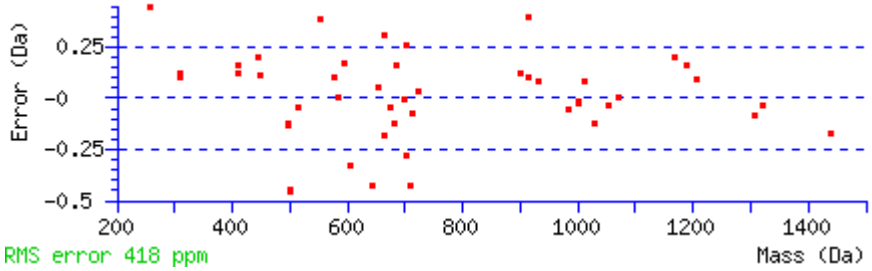


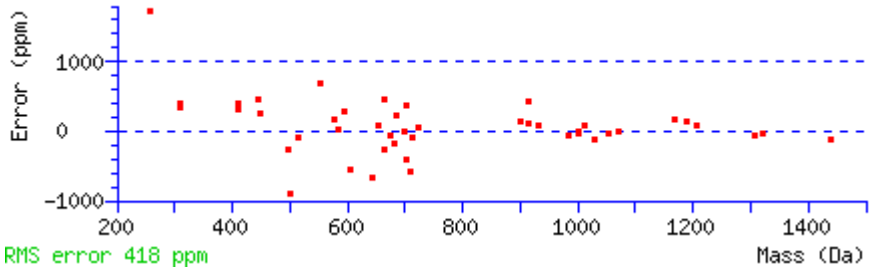
IDENTIFICATION 30
MS/MS Fragmentation of IGHHSTSDDSSAYR
Found in IPI00331555



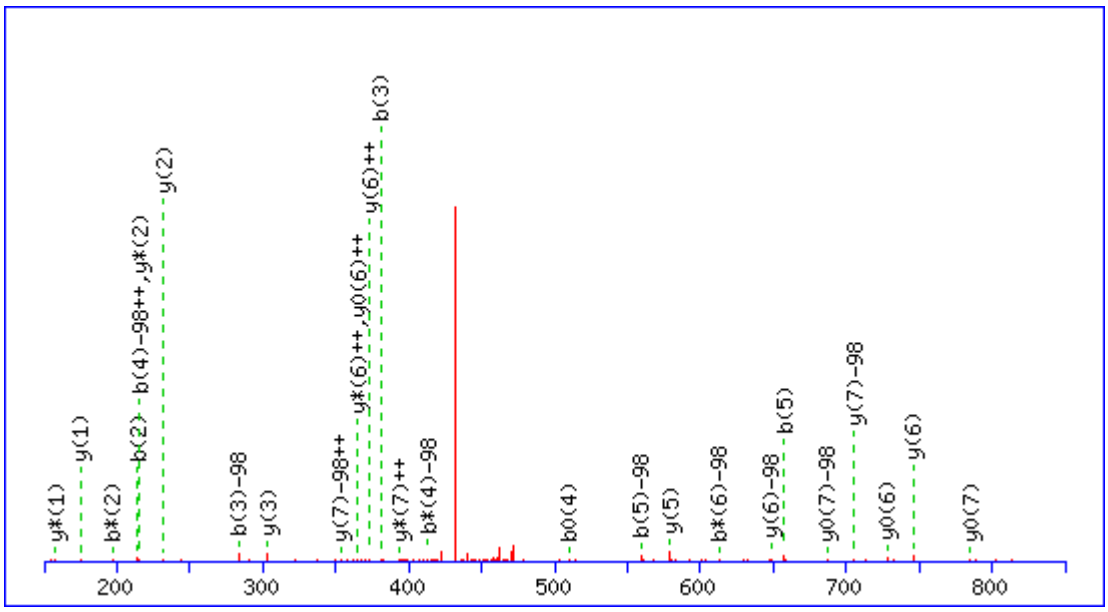
Monoisotopic mass of neutral peptide Mr(calc): 1611.6315
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.11 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			I							14
2	171.1128	86.0600			G	1401.5778	701.2925	1384.5512	692.7793	1383.5672	692.2873	13
3	308.1717	154.5895			H	1344.5563	672.7818	1327.5298	664.2685	1326.5458	663.7765	12
4	445.2306	223.1190			H	1207.4974	604.2523	1190.4709	595.7391	1189.4869	595.2471	11
5	514.2521	257.6297	496.2415	248.6244	S	1070.4385	535.7229	1053.4120	527.2096	1052.4279	526.7176	10
6	615.2998	308.1535	597.2892	299.1482	T	1001.4170	501.2122	984.3905	492.6989	983.4065	492.2069	9
7	702.3318	351.6695	684.3212	342.6643	S	900.3694	450.6883	883.3428	442.1750	882.3588	441.6830	8
8	817.3587	409.1830	799.3482	400.1777	D	813.3373	407.1723	796.3108	398.6590	795.3268	398.1670	7
9	932.3857	466.6965	914.3751	457.6912	D	698.3104	349.6588	681.2838	341.1456	680.2998	340.6536	6
10	1019.4177	510.2125	1001.4071	501.2072	S	583.2835	292.1454	566.2569	283.6321	565.2729	283.1401	5
11	1106.4497	553.7285	1088.4392	544.7232	S	496.2514	248.6293	479.2249	240.1161	478.2409	239.6241	4
12	1177.4869	589.2471	1159.4763	580.2418	A	409.2194	205.1133	392.1928	196.6001			3
13	1340.5502	670.7787	1322.5396	661.7734	Y	338.1823	169.5948	321.1557	161.0815			2
14					R	175.1190	88.0631	158.0924	79.5498			1


Error (Da)
0.25
-0
-0.25
-0.5
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 418 ppm

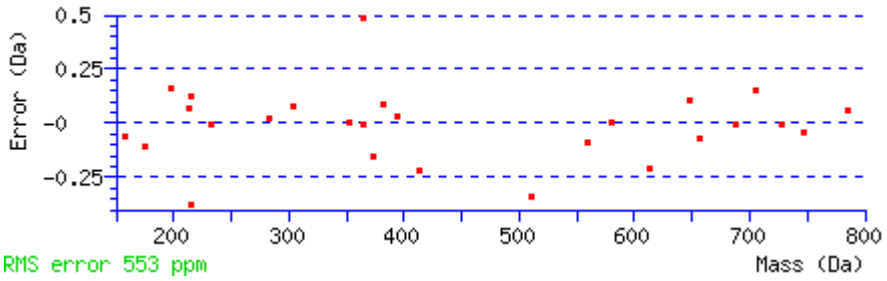

Error (ppm)
1000
0
-1000
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 418 ppm

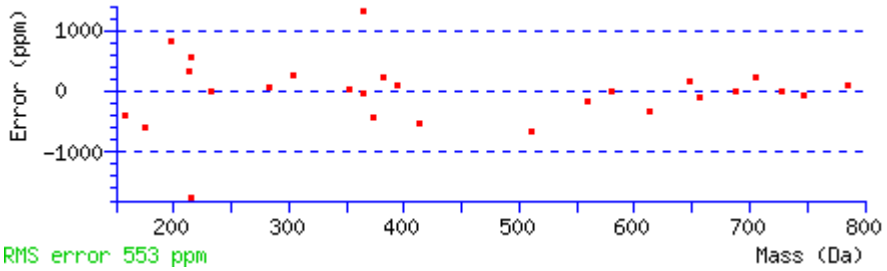
IDENTIFICATION 31
MS/MS Fragmentation of RGSFEAGR
Found in IPI00461575



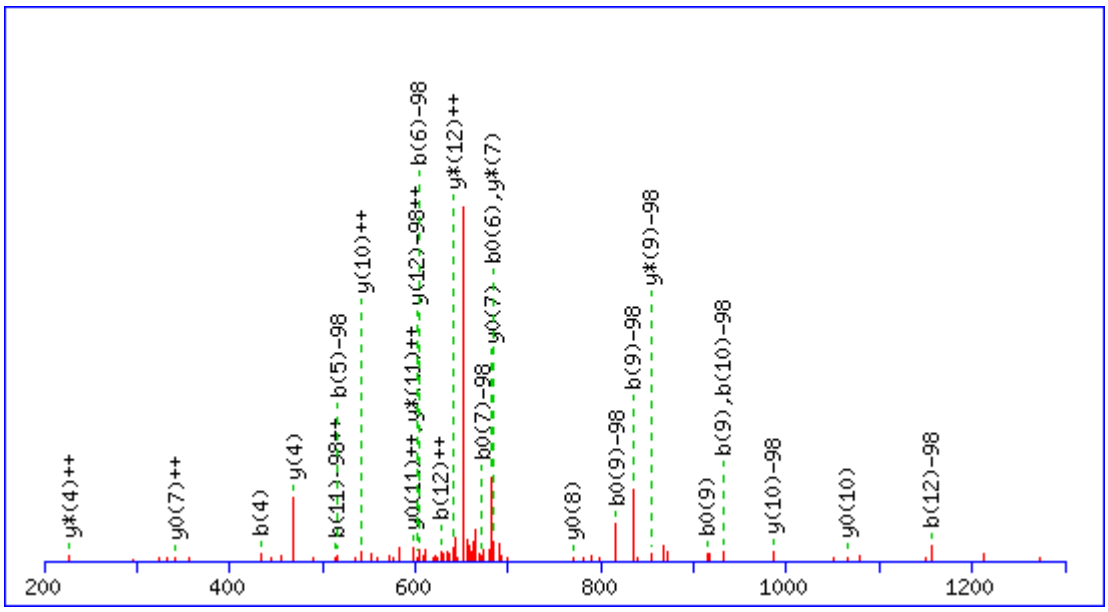
Monoisotopic mass of neutral peptide Mr(calc): 958.4022
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 36 Expect: 0.014 (help)

#	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	214.1299	107.5686	197.1033	99.0553			G	705.3315	353.1694	688.3049	344.6561	687.3209	344.1641	7
3	283.1513	142.0793	266.1248	133.5660	265.1407	133.0740	S	648.3100	324.6586	631.2835	316.1454	630.2994	315.6534	6
4	430.2197	215.6135	413.1932	207.1002	412.2092	206.6082	F	579.2885	290.1479	562.2620	281.6346	561.2780	281.1426	5
5	559.2623	280.1348	542.2358	271.6215	541.2518	271.1295	E	432.2201	216.6137	415.1936	208.1004	414.2096	207.6084	4
6	630.2994	315.6534	613.2729	307.1401	612.2889	306.6481	A	303.1775	152.0924	286.1510	143.5791			3
7	687.3209	344.1641	670.2944	335.6508	669.3103	335.1588	G	232.1404	116.5738	215.1139	108.0606			2
8							R	175.1190	88.0631	158.0924	79.5498			1



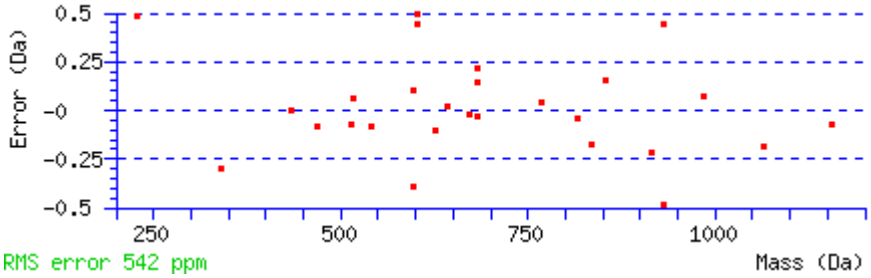


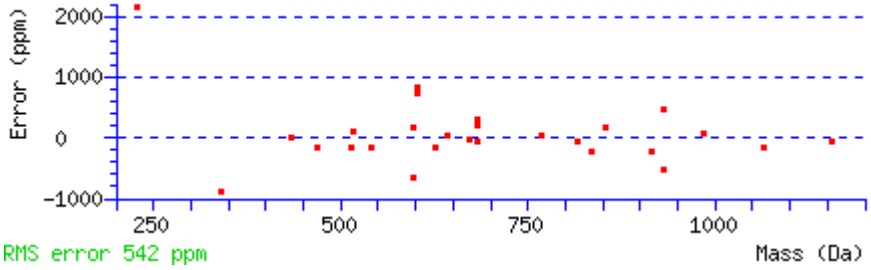
IDENTIFICATION 32
MS/MS Fragmentation of TSEDTSSGSPPKK
Found in IPI00399961



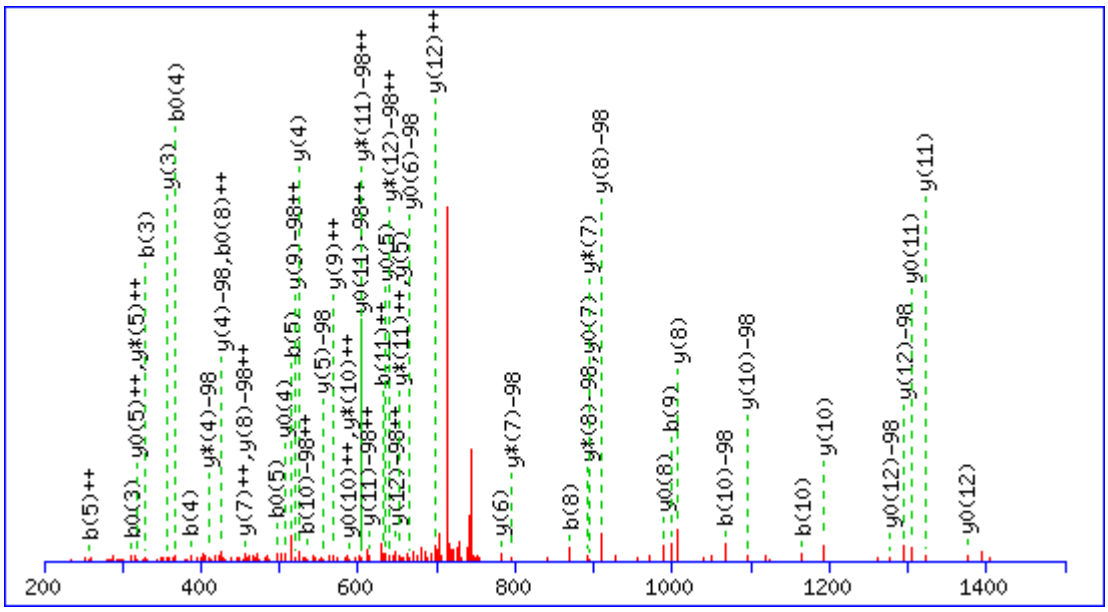
Monoisotopic mass of neutral peptide Mr(calc): 1399.5868
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.25 (help)

#	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							13
2	189.0870	95.0471			171.0764	86.0418	S	1201.5695	601.2884	1184.5430	592.7751	1183.5590	592.2831	12
3	318.1296	159.5684			300.1190	150.5631	E	1114.5375	557.7724	1097.5109	549.2591	1096.5269	548.7671	11
4	433.1565	217.0819			415.1460	208.0766	D	985.4949	493.2511	968.4684	484.7378	967.4843	484.2458	10
5	516.1936	258.6005			498.1831	249.5952	T	870.4680	435.7376	853.4414	427.2243	852.4574	426.7323	9
6	603.2257	302.1165			585.2151	293.1112	S	787.4308	394.2191	770.4043	385.7058	769.4203	385.2138	8
7	690.2577	345.6325			672.2471	336.6272	S	700.3988	350.7030	683.3723	342.1898	682.3883	341.6978	7
8	747.2792	374.1432			729.2686	365.1379	G	613.3668	307.1870	596.3402	298.6738	595.3562	298.1817	6
9	834.3112	417.6592			816.3006	408.6539	S	556.3453	278.6763	539.3188	270.1630	538.3348	269.6710	5
10	931.3639	466.1856			913.3534	457.1803	P	469.3133	235.1603	452.2867	226.6470			4
11	1028.4167	514.7120			1010.4061	505.7067	P	372.2605	186.6339	355.2340	178.1206			3
12	1156.5117	578.7595	1139.4851	570.2462	1138.5011	569.7542	K	275.2078	138.1075	258.1812	129.5942			2
13							K	147.1128	74.0600	130.0863	65.5468			1


0.5
0.25
-0
-0.25
-0.5
Error (Da)
250
500
750
1000
Mass (Da)
RMS error 542 ppm

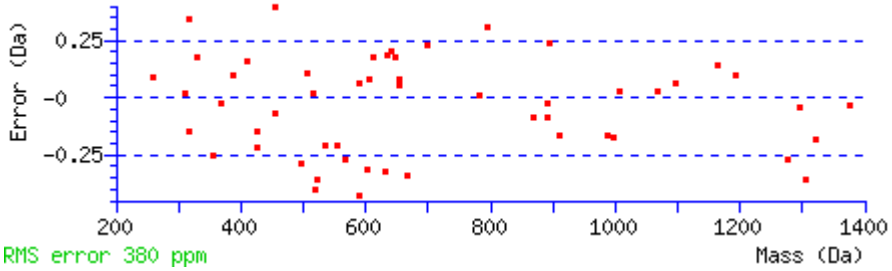

2000
1000
0
-1000
Error (ppm)
250
500
750
1000
Mass (Da)
RMS error 542 ppm

IDENTIFICATION 33
MS/MS Fragmentation of KAEGEPQEESPLK
Found in IPI00169477

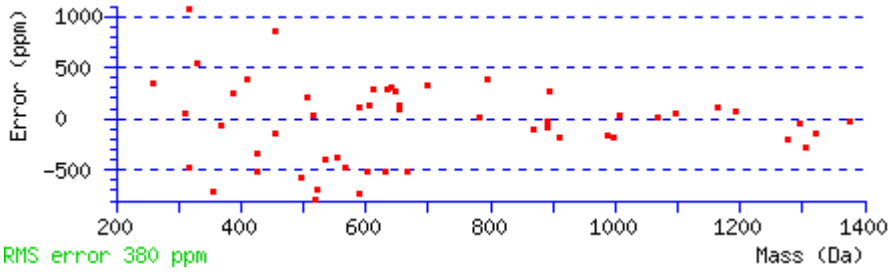


Monoisotopic mass of neutral peptide Mr(calc): 1520.6759
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 27 Expect: 0.26 (help)

#	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							13
2	200.1394	100.5733	183.1128	92.0600			A	1393.5883	697.2978	1376.5617	688.7845	1375.5777	688.2925	12
3	329.1819	165.0946	312.1554	156.5813	311.1714	156.0893	E	1322.5512	661.7792	1305.5246	653.2659	1304.5406	652.7739	11
4	386.2034	193.6053	369.1769	185.0921	368.1928	184.6001	G	1193.5086	597.2579	1176.4820	588.7447	1175.4980	588.2526	10
5	515.2460	258.1266	498.2195	249.6134	497.2354	249.1214	E	1136.4871	568.7472	1119.4606	560.2339	1118.4765	559.7419	9
6	612.2988	306.6530	595.2722	298.1397	594.2882	297.6477	P	1007.4445	504.2259	990.4180	495.7126	989.4340	495.2206	8
7	740.3573	370.6823	723.3308	362.1690	722.3468	361.6770	Q	910.3918	455.6995	893.3652	447.1862	892.3812	446.6942	7
8	869.3999	435.2036	852.3734	426.6903	851.3894	426.1983	E	782.3332	391.6702	765.3066	383.1570	764.3226	382.6649	6
9	998.4425	499.7249	981.4160	491.2116	980.4320	490.7196	E	653.2906	327.1489	636.2640	318.6357	635.2800	318.1436	5
10	1165.4409	583.2241	1148.4143	574.7108	1147.4303	574.2188	S	524.2480	262.6276	507.2214	254.1144	506.2374	253.6224	4
11	1262.4937	631.7505	1245.4671	623.2372	1244.4831	622.7452	P	357.2496	179.1285	340.2231	170.6152			3
12	1375.5777	688.2925	1358.5512	679.7792	1357.5672	679.2872	L	260.1969	130.6021	243.1703	122.0888			2
13							K	147.1128	74.0600	130.0863	65.5468			1

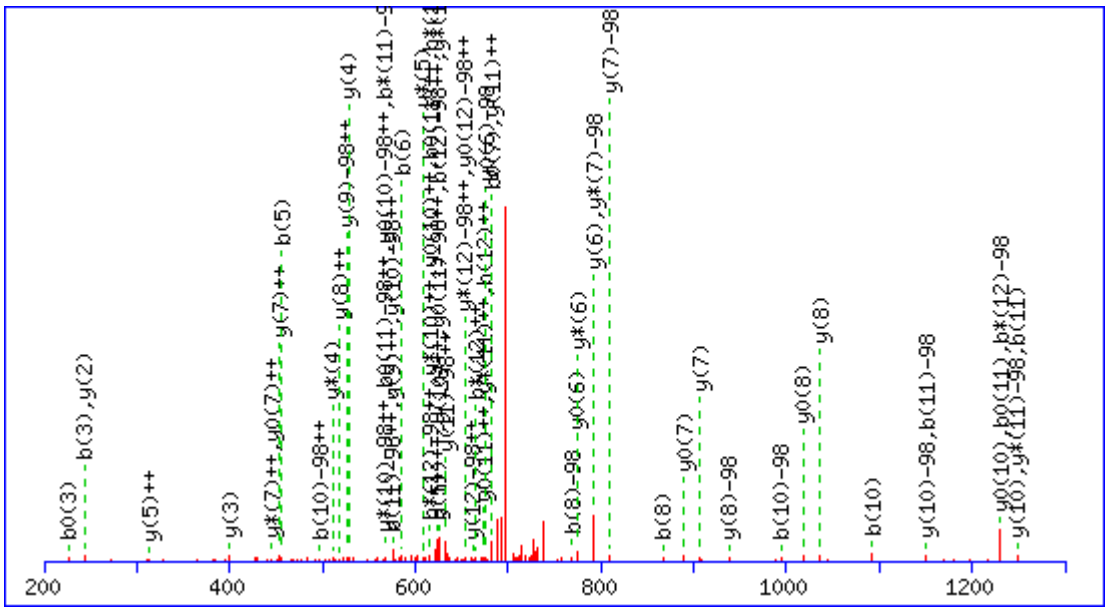


RMS error 380 ppm



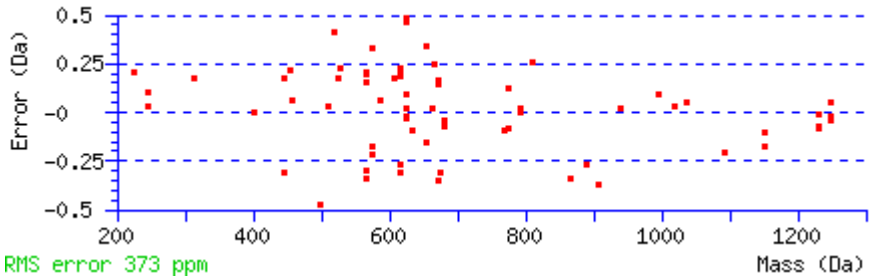
RMS error 380 ppm

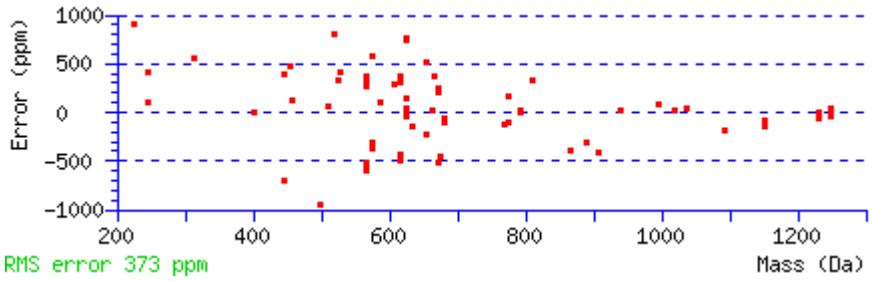
IDENTIFICATION 34
MS/MS Fragmentation of AGDVLEDSPKRPK
Found in IPI00313817



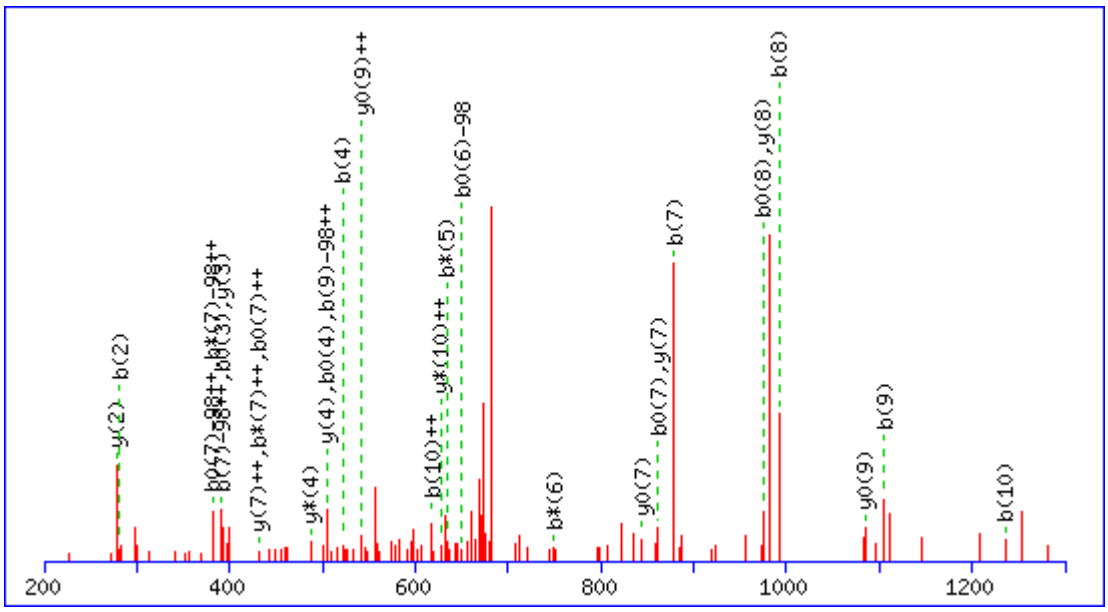
Monoisotopic mass of neutral peptide Mr(calc): 1490.7130
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 47 Expect: 0.0024 (help)

#	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	129.0659	65.0366					G	1420.6832	710.8452	1403.6566	702.3320	1402.6726	701.8399	12
3	244.0928	122.5500			226.0822	113.5448	D	1363.6617	682.3345	1346.6352	673.8212	1345.6512	673.3292	11
4	343.1612	172.0842			325.1506	163.0790	V	1248.6348	624.8210	1231.6082	616.3078	1230.6242	615.8157	10
5	456.2453	228.6263			438.2347	219.6210	L	1149.5664	575.2868	1132.5398	566.7735	1131.5558	566.2815	9
6	585.2879	293.1476			567.2773	284.1423	E	1036.4823	518.7448	1019.4558	510.2315	1018.4717	509.7395	8
7	700.3148	350.6610			682.3042	341.6558	D	907.4397	454.2235	890.4132	445.7102	889.4291	445.2182	7
8	867.3132	434.1602			849.3026	425.1549	S	792.4128	396.7100	775.3862	388.1967	774.4022	387.7047	6
9	964.3659	482.6866			946.3554	473.6813	P	625.4144	313.2108	608.3879	304.6976			5
10	1092.4609	546.7341	1075.4343	538.2208	1074.4503	537.7288	K	528.3616	264.6845	511.3351	256.1712			4
11	1248.5620	624.7846	1231.5355	616.2714	1230.5514	615.7794	R	400.2667	200.6370	383.2401	192.1237			3
12	1345.6148	673.3110	1328.5882	664.7977	1327.6042	664.3057	P	244.1656	122.5864	227.1390	114.0731			2
13							K	147.1128	74.0600	130.0863	65.5468			1


0.5
0.25
-0
-0.25
-0.5
Error (Da)
200
400
600
800
1000
1200
Mass (Da)
RMS error 373 ppm

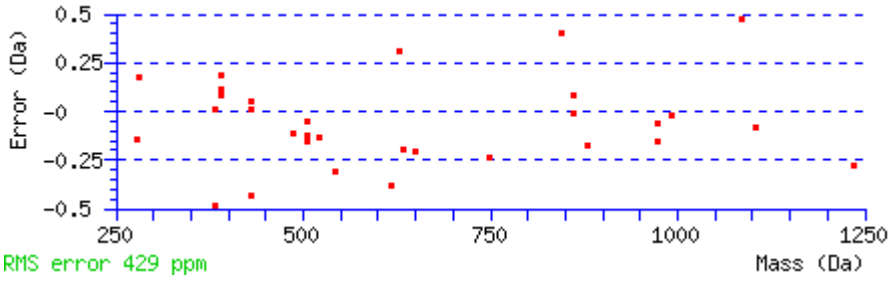

1000
500
0
-500
-1000
Error (ppm)
200
400
600
800
1000
1200
Mass (Da)
RMS error 373 ppm

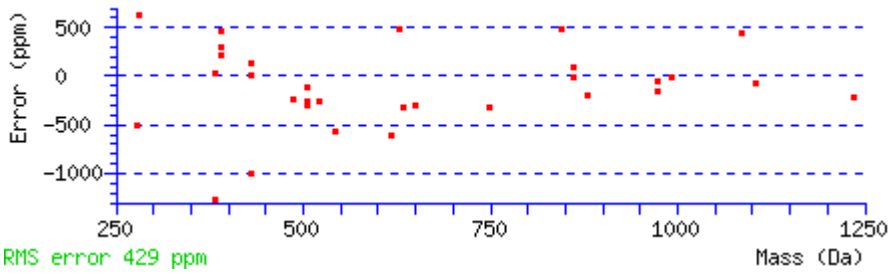
IDENTIFICATION 35
MS/MS Fragmentation of LSQIQDILLMK
Found in IPI00403993



Monoisotopic mass of neutral peptide Mr(calc): 1381.6928
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Q5 : Deamidated (NQ)
Ions Score: 21 Expect: 0.71 (help)

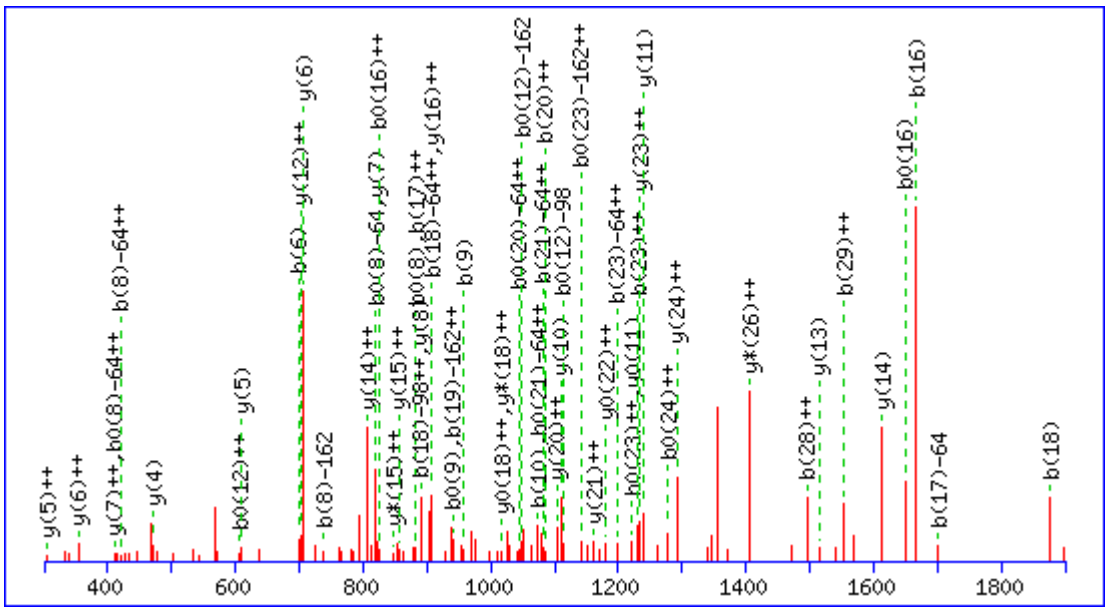
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							11
2	281.0897	141.0485			263.0791	132.0432	S	1269.6160	635.3116	1252.5895	626.7984	1251.6055	626.3064	10
3	409.1483	205.0778	392.1217	196.5645	391.1377	196.0725	Q	1102.6177	551.8125	1085.5911	543.2992	1084.6071	542.8072	9
4	522.2323	261.6198	505.2058	253.1065	504.2218	252.6145	I	974.5591	487.7832	957.5325	479.2699	956.5485	478.7779	8
5	651.2749	326.1411	634.2484	317.6278	633.2644	317.1358	Q	861.4750	431.2411	844.4485	422.7279	843.4645	422.2359	7
6	766.3019	383.6546	749.2753	375.1413	748.2913	374.6493	D	732.4324	366.7199	715.4059	358.2066	714.4219	357.7146	6
7	879.3859	440.1966	862.3594	431.6833	861.3754	431.1913	I	617.4055	309.2064	600.3789	300.6931			5
8	992.4700	496.7386	975.4435	488.2254	974.4594	487.7334	L	504.3214	252.6643	487.2949	244.1511			4
9	1105.5541	553.2807	1088.5275	544.7674	1087.5435	544.2754	L	391.2374	196.1223	374.2108	187.6090			3
10	1236.5946	618.8009	1219.5680	610.2876	1218.5840	609.7956	M	278.1533	139.5803	261.1267	131.0670			2
11							K	147.1128	74.0600	130.0863	65.5468			1





IDENTIFICATION 36

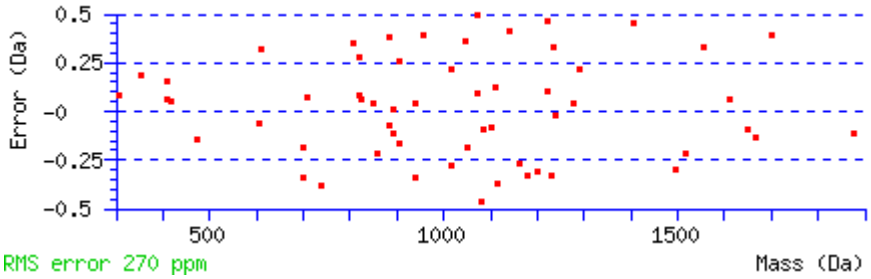
MS/MS Fragmentation of TTGIVMDSGDGVTHTVPIYEGYALPHAILR
Found in IPI00110850

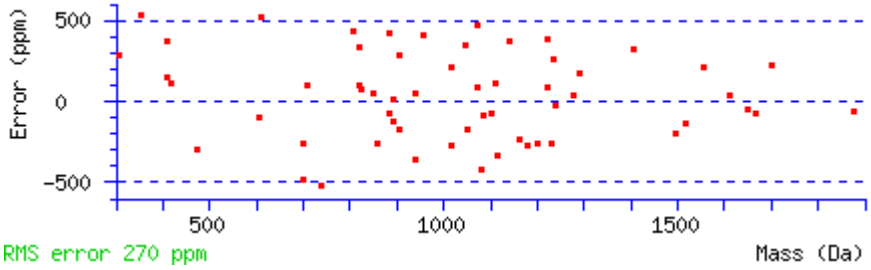


Monoisotopic mass of neutral peptide Mr(calc): 3278.5683
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
M6 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 55 Expect: 0.00038 (help)

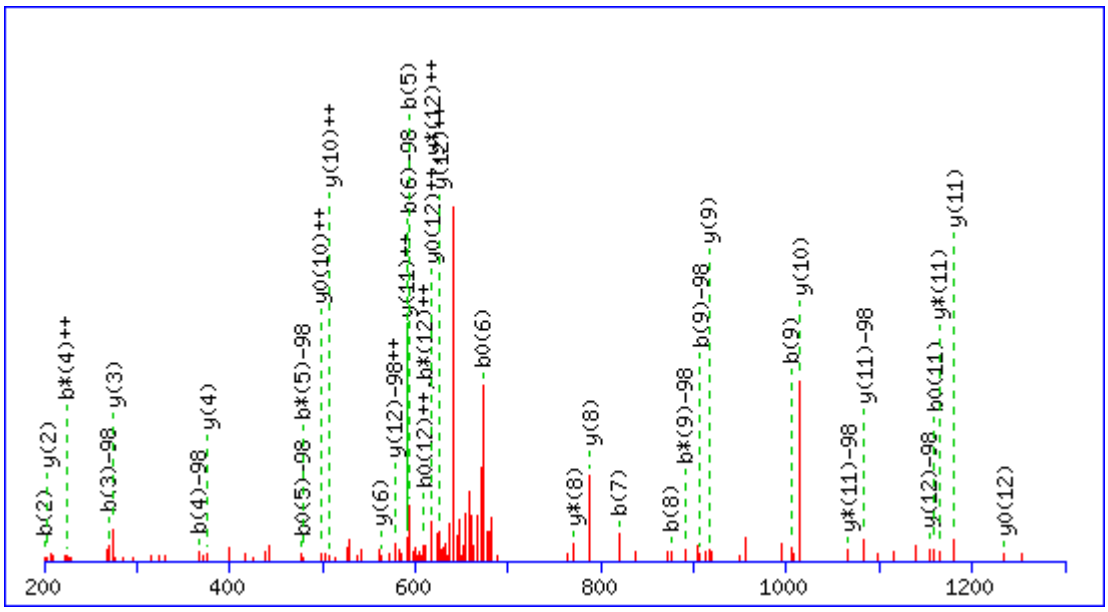
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	102.0550	51.5311	84.0444	42.5258	T							30
2	283.0690	142.0381	265.0584	133.0328	T	3178.5279	1589.7676	3161.5013	1581.2543	3160.5173	1580.7623	29
3	340.0904	170.5489	322.0799	161.5436	G	2997.5139	1499.2606	2980.4873	1490.7473	2979.5033	1490.2553	28
4	453.1745	227.0909	435.1639	218.0856	I	2940.4924	1470.7498	2923.4659	1462.2366	2922.4818	1461.7446	27
5	552.2429	276.6251	534.2323	267.6198	V	2827.4083	1414.2078	2810.3818	1405.6945	2809.3978	1405.2025	26
6	699.2783	350.1428	681.2677	341.1375	M	2728.3399	1364.6736	2711.3134	1356.1603	2710.3294	1355.6683	25
7	814.3053	407.6563	796.2947	398.6510	D	2581.3045	1291.1559	2564.2780	1282.6426	2563.2940	1282.1506	24
8	901.3373	451.1723	883.3267	442.1670	S	2466.2776	1233.6424	2449.2510	1225.1292	2448.2670	1224.6371	23
9	958.3587	479.6830	940.3482	470.6777	G	2379.2456	1190.1264	2362.2190	1181.6131	2361.2350	1181.1211	22
10	1073.3857	537.1965	1055.3751	528.1912	D	2322.2241	1161.6157	2305.1975	1153.1024	2304.2135	1152.6104	21
11	1130.4071	565.7072	1112.3966	556.7019	G	2207.1972	1104.1022	2190.1706	1095.5889	2189.1866	1095.0969	20
12	1229.4756	615.2414	1211.4650	606.2361	V	2150.1757	1075.5915	2133.1491	1067.0782	2132.1651	1066.5862	19
13	1330.5232	665.7653	1312.5127	656.7600	T	2051.1073	1026.0573	2034.0807	1017.5440	2033.0967	1017.0520	18
14	1467.5822	734.2947	1449.5716	725.2894	H	1950.0596	975.5334	1933.0330	967.0202	1932.0490	966.5282	17
15	1568.6298	784.8186	1550.6193	775.8133	T	1813.0007	907.0040	1795.9741	898.4907	1794.9901	897.9987	16
16	1667.6982	834.3528	1649.6877	825.3475	V	1711.9530	856.4801	1694.9265	847.9669	1693.9424	847.4749	15
17	1764.7510	882.8791	1746.7404	873.8739	P	1612.8846	806.9459	1595.8580	798.4327	1594.8740	797.9407	14
18	1877.8351	939.4212	1859.8245	930.4159	I	1515.8318	758.4196	1498.8053	749.9063	1497.8213	749.4143	13
19	2040.8984	1020.9528	2022.8878	1011.9476	Y	1402.7478	701.8775	1385.7212	693.3642	1384.7372	692.8722	12
20	2169.9410	1085.4741	2151.9304	1076.4689	E	1239.6844	620.3459	1222.6579	611.8326	1221.6739	611.3406	11
21	2226.9625	1113.9849	2208.9519	1104.9796	G	1110.6418	555.8246	1093.6153	547.3113			10
22	2390.0258	1195.5165	2372.0152	1186.5113	Y	1053.6204	527.3138	1036.5938	518.8006			9
23	2461.0629	1231.0351	2443.0523	1222.0298	A	890.5570	445.7822	873.5305	437.2689			8
24	2574.1470	1287.5771	2556.1364	1278.5718	L	819.5199	410.2636	802.4934	401.7503			7
25	2671.1997	1336.1035	2653.1892	1327.0982	P	706.4359	353.7216	689.4093	345.2083			6
26	2808.2586	1404.6330	2790.2481	1395.6277	H	609.3831	305.1952	592.3566	296.6819			5

27	2879.2958	1440.1515	2861.2852	1431.1462	A	472.3242	236.6657	455.2976	228.1525			4
28	2992.3798	1496.6935	2974.3693	1487.6883	I	401.2871	201.1472	384.2605	192.6339			3
29	3105.4639	1553.2356	3087.4533	1544.2303	L	288.2030	144.6051	271.1765	136.0919			2
30					R	175.1190	88.0631	158.0924	79.5498			1



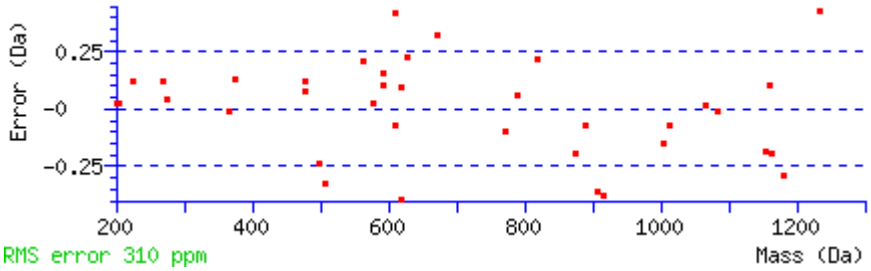


IDENTIFICATION 37
MS/MS Fragmentation of KASPEPEGETAGK
Found in IPI00453578

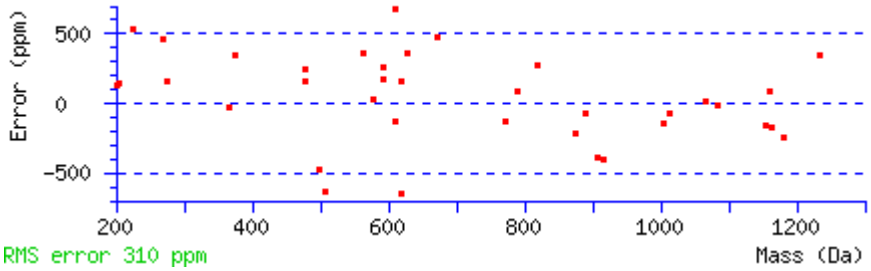


Monoisotopic mass of neutral peptide Mr(calc): 1379.5970
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.035 (help)

#	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							13
2	200.1394	100.5733	183.1128	92.0600			A	1154.5324	577.7698	1137.5059	569.2566	1136.5218	568.7646	12
3	269.1608	135.0840	252.1343	126.5708	251.1503	126.0788	S	1083.4953	542.2513	1066.4687	533.7380	1065.4847	533.2460	11
4	366.2136	183.6104	349.1870	175.0972	348.2030	174.6051	P	1014.4738	507.7406	997.4473	499.2273	996.4633	498.7353	10
5	495.2562	248.1317	478.2296	239.6185	477.2456	239.1264	E	917.4211	459.2142	900.3945	450.7009	899.4105	450.2089	9
6	592.3089	296.6581	575.2824	288.1448	574.2984	287.6528	P	788.3785	394.6929	771.3519	386.1796	770.3679	385.6876	8
7	721.3515	361.1794	704.3250	352.6661	703.3410	352.1741	E	691.3257	346.1665	674.2992	337.6532	673.3151	337.1612	7
8	778.3730	389.6901	761.3464	381.1769	760.3624	380.6849	G	562.2831	281.6452	545.2566	273.1319	544.2726	272.6399	6
9	907.4156	454.2114	890.3890	445.6982	889.4050	445.2061	E	505.2617	253.1345	488.2351	244.6212	487.2511	244.1292	5
10	1008.4633	504.7353	991.4367	496.2220	990.4527	495.7300	T	376.2191	188.6132	359.1925	180.0999	358.2085	179.6079	4
11	1079.5004	540.2538	1062.4738	531.7406	1061.4898	531.2485	A	275.1714	138.0893	258.1448	129.5761			3
12	1136.5218	568.7646	1119.4953	560.2513	1118.5113	559.7593	G	204.1343	102.5708	187.1077	94.0575			2
13							K	147.1128	74.0600	130.0863	65.5468			1

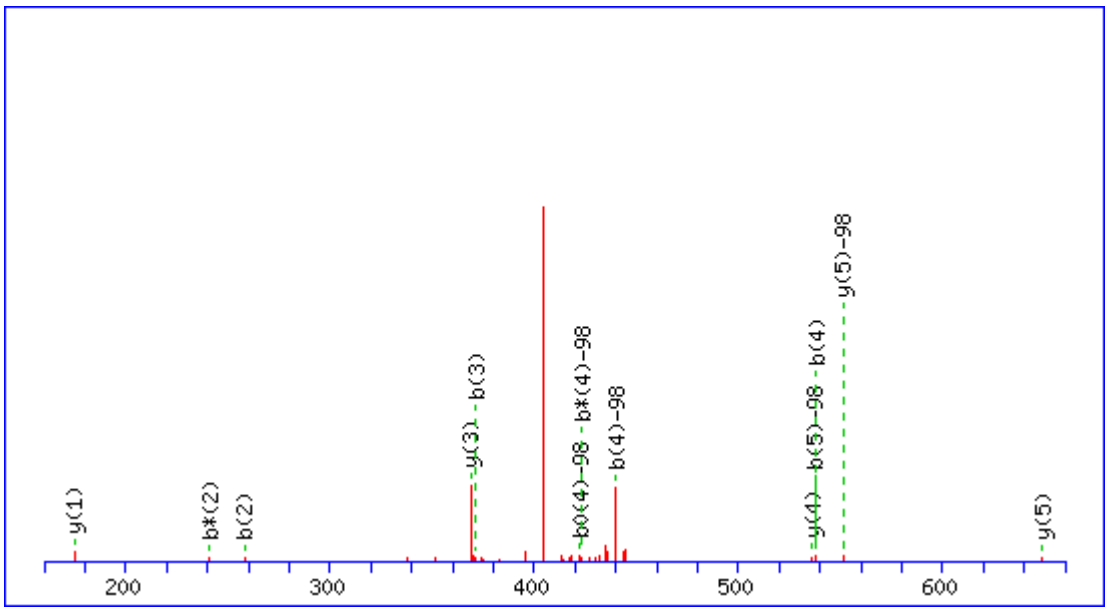


RMS error 310 ppm



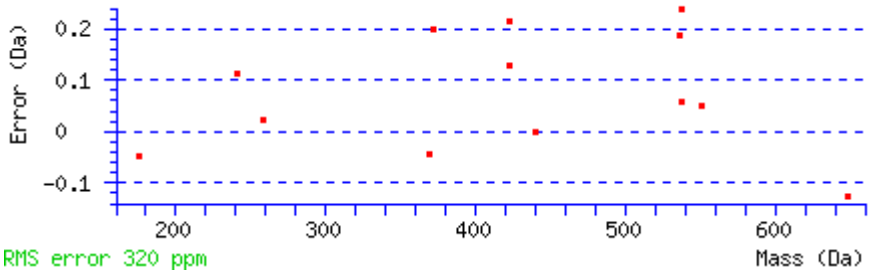
RMS error 310 ppm

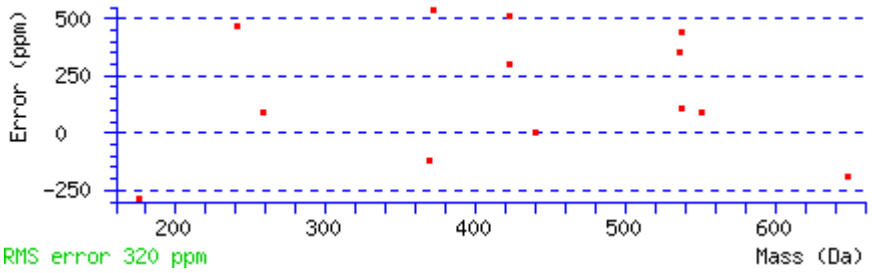
IDENTIFICATION 38
MS/MS Fragmentation of TRLSPPR
Found in IPI00404707



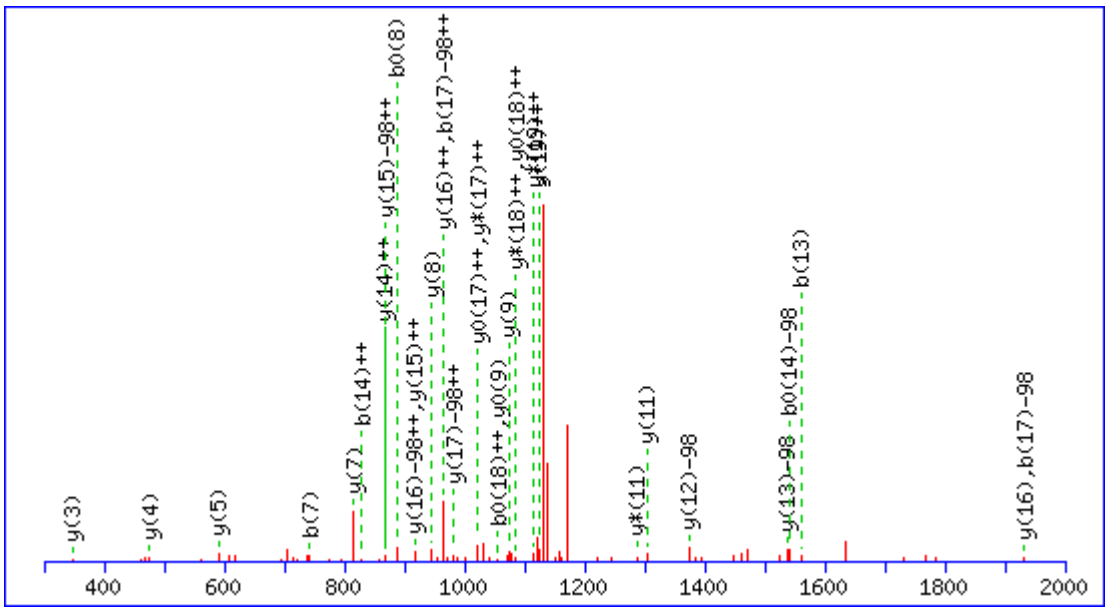
Monoisotopic mass of neutral peptide Mr(calc): 905.4484
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 32 Expect: 0.043 (help)

#	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							7
2	258.1561	129.5817	241.1295	121.0684	240.1455	120.5764	R	707.4311	354.2192	690.4046	345.7059	689.4206	345.2139	6
3	371.2401	186.1237	354.2136	177.6104	353.2296	177.1184	L	551.3300	276.1686	534.3035	267.6554	533.3194	267.1634	5
4	440.2616	220.6344	423.2350	212.1212	422.2510	211.6292	S	438.2459	219.6266	421.2194	211.1133	420.2354	210.6213	4
5	537.3144	269.1608	520.2878	260.6475	519.3038	260.1555	P	369.2245	185.1159	352.1979	176.6026			3
6	634.3671	317.6872	617.3406	309.1739	616.3566	308.6819	P	272.1717	136.5895	255.1452	128.0762			2
7							R	175.1190	88.0631	158.0924	79.5498			1



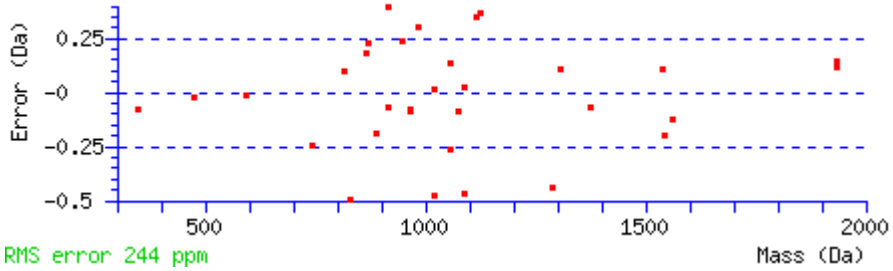


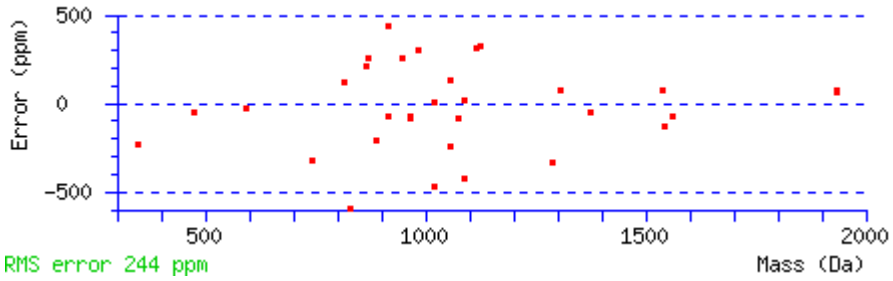
IDENTIFICATION 39
MS/MS Fragmentation of EGEEPTVYSDDEEPKDETAR
Found in IPI00319973



Monoisotopic mass of neutral peptide Mr(calc): 2374.9326
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.015 (help)

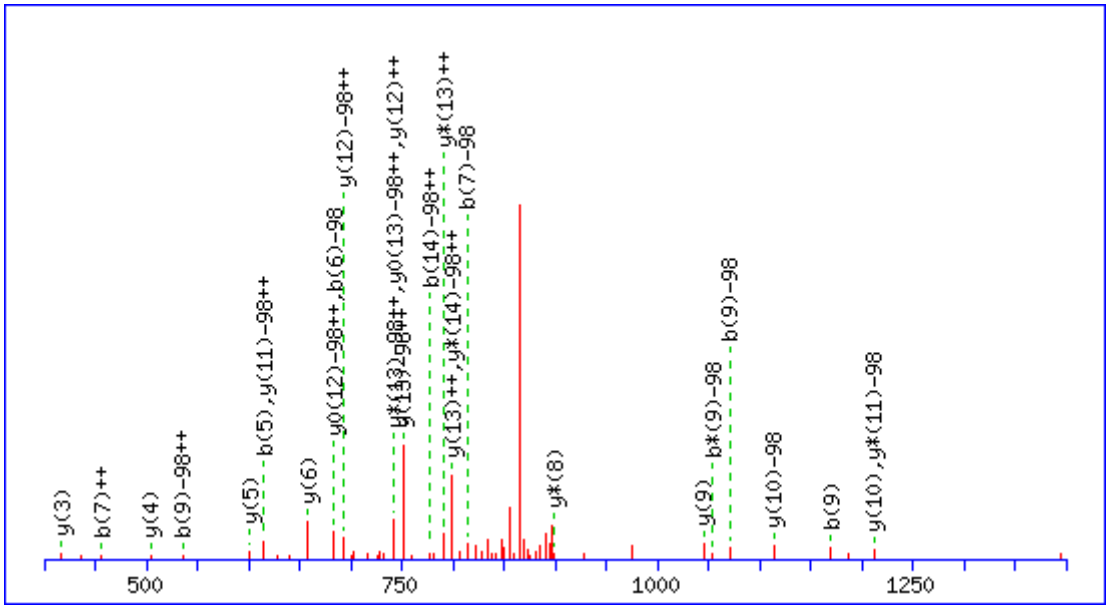
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286			112.0393	56.5233	E							20
2	187.0713	94.0393			169.0608	85.0340	G	2148.9204	1074.9638	2131.8938	1066.4506	2130.9098	1065.9585	19
3	316.1139	158.5606			298.1034	149.5553	E	2091.8989	1046.4531	2074.8724	1037.9398	2073.8883	1037.4478	18
4	445.1565	223.0819			427.1460	214.0766	E	1962.8563	981.9318	1945.8298	973.4185	1944.8458	972.9265	17
5	542.2093	271.6083			524.1987	262.6030	P	1833.8137	917.4105	1816.7872	908.8972	1815.8032	908.4052	16
6	643.2570	322.1321			625.2464	313.1268	T	1736.7610	868.8841	1719.7344	860.3708	1718.7504	859.8788	15
7	742.3254	371.6663			724.3148	362.6610	V	1635.7133	818.3603	1618.6867	809.8470	1617.7027	809.3550	14
8	905.3887	453.1980			887.3781	444.1927	Y	1536.6449	768.8261	1519.6183	760.3128	1518.6343	759.8208	13
9	974.4102	487.7087			956.3996	478.7034	S	1373.5815	687.2944	1356.5550	678.7811	1355.5710	678.2891	12
10	1089.4371	545.2222			1071.4265	536.2169	D	1304.5601	652.7837	1287.5335	644.2704	1286.5495	643.7784	11
11	1204.4641	602.7357			1186.4535	593.7304	D	1189.5331	595.2702	1172.5066	586.7569	1171.5226	586.2649	10
12	1333.5066	667.2570			1315.4961	658.2517	E	1074.5062	537.7567	1057.4796	529.2435	1056.4956	528.7515	9
13	1462.5492	731.7783			1444.5387	722.7730	E	945.4636	473.2354	928.4371	464.7222	927.4530	464.2302	8
14	1559.6020	780.3046			1541.5914	771.2994	P	816.4210	408.7141	799.3945	400.2009	798.4104	399.7089	7
15	1687.6970	844.3521	1670.6704	835.8388	1669.6864	835.3468	K	719.3682	360.1878	702.3417	351.6745	701.3577	351.1825	6
16	1802.7239	901.8656	1785.6974	893.3523	1784.7133	892.8603	D	591.2733	296.1403	574.2467	287.6270	573.2627	287.1350	5
17	1931.7665	966.3869	1914.7400	957.8736	1913.7559	957.3816	E	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
18	2032.8142	1016.9107	2015.7876	1008.3975	2014.8036	1007.9054	T	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
19	2103.8513	1052.4293	2086.8247	1043.9160	2085.8407	1043.4240	A	246.1561	123.5817	229.1295	115.0684			2
20							R	175.1190	88.0631	158.0924	79.5498			1


Error (Da)
0.25
-0
-0.25
-0.5
500
1000
1500
2000
RMS error 244 ppm
Mass (Da)


Error (ppm)
500
0
-500
500
1000
1500
2000
RMS error 244 ppm
Mass (Da)

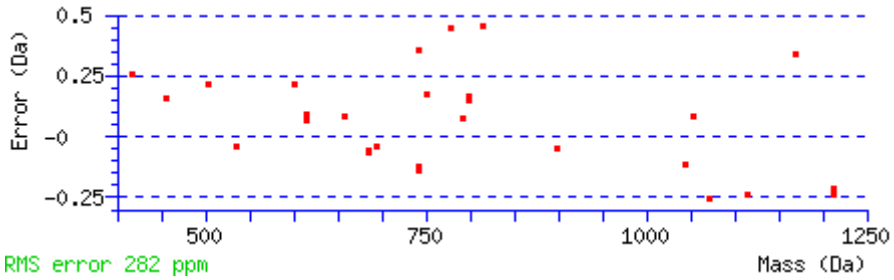
IDENTIFICATION 40

MS/MS Fragmentation of IDDRDSEEEGPSNQR
Found in IPI00474721

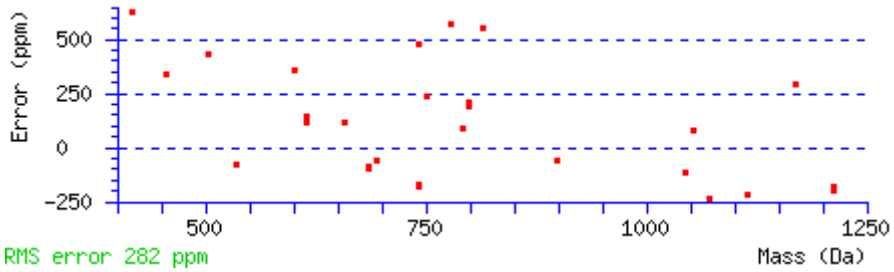


Monoisotopic mass of neutral peptide Mr(calc): 1825.7115 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 43 Expect: 0.0067 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							15
2	229.1183	115.0628			211.1077	106.0575	D	1615.6579	808.3326	1598.6313	799.8193	1597.6473	799.3273	14
3	344.1452	172.5763			326.1347	163.5710	D	1500.6310	750.8191	1483.6044	742.3058	1482.6204	741.8138	13
4	500.2463	250.6268	483.2198	242.1135	482.2358	241.6215	R	1385.6040	693.3056	1368.5775	684.7924	1367.5934	684.3004	12
5	615.2733	308.1403	598.2467	299.6270	597.2627	299.1350	D	1229.5029	615.2551	1212.4763	606.7418	1211.4923	606.2498	11
6	684.2947	342.6510	667.2682	334.1377	666.2842	333.6457	S	1114.4760	557.7416	1097.4494	549.2283	1096.4654	548.7363	10
7	813.3373	407.1723	796.3108	398.6590	795.3268	398.1670	E	1045.4545	523.2309	1028.4279	514.7176	1027.4439	514.2256	9
8	942.3799	471.6936	925.3534	463.1803	924.3694	462.6883	E	916.4119	458.7096	899.3854	450.1963	898.4013	449.7043	8
9	1071.4225	536.2149	1054.3960	527.7016	1053.4120	527.2096	E	787.3693	394.1883	770.3428	385.6750	769.3587	385.1830	7
10	1128.4440	564.7256	1111.4174	556.2124	1110.4334	555.7203	G	658.3267	329.6670	641.3002	321.1537	640.3161	320.6617	6
11	1225.4968	613.2520	1208.4702	604.7387	1207.4862	604.2467	P	601.3052	301.1563	584.2787	292.6430	583.2947	292.1510	5
12	1312.5288	656.7680	1295.5022	648.2548	1294.5182	647.7627	S	504.2525	252.6299	487.2259	244.1166	486.2419	243.6246	4
13	1426.5717	713.7895	1409.5452	705.2762	1408.5611	704.7842	N	417.2205	209.1139	400.1939	200.6006			3
14	1554.6303	777.8188	1537.6037	769.3055	1536.6197	768.8135	Q	303.1775	152.0924	286.1510	143.5791			2
15							R	175.1190	88.0631	158.0924	79.5498			1

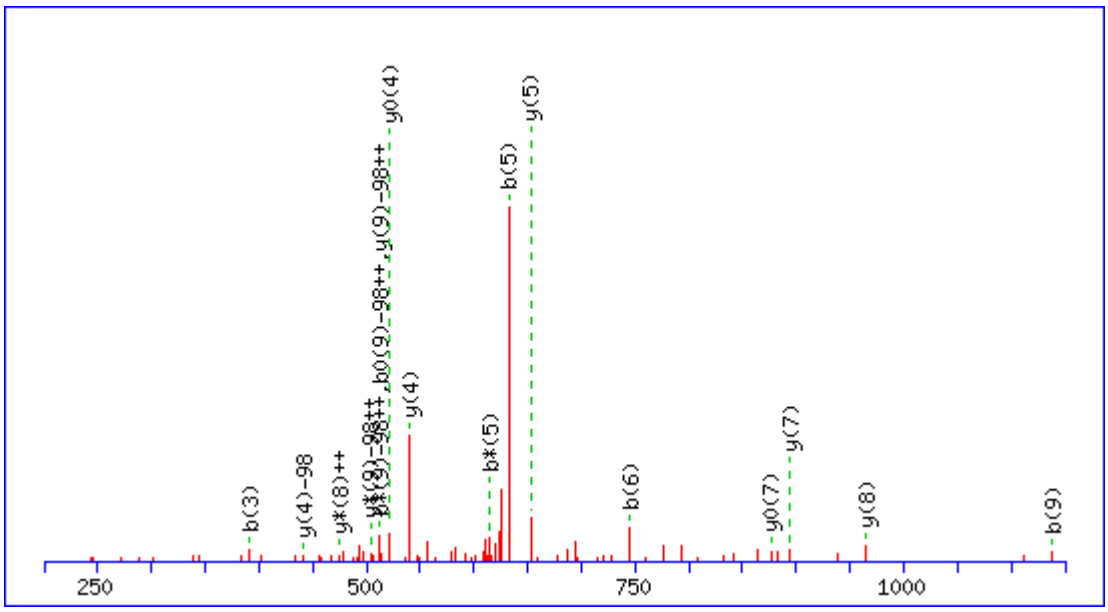


RMS error 282 ppm



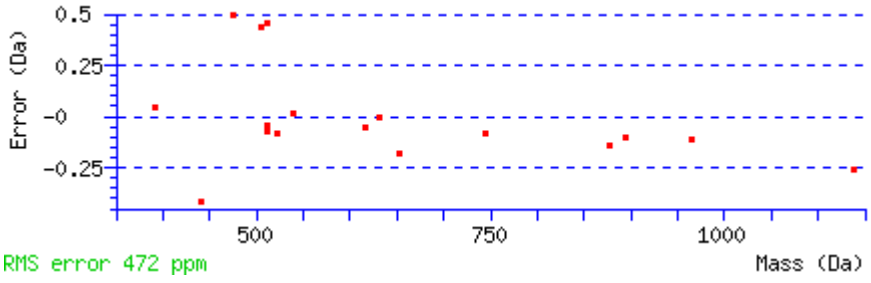
RMS error 282 ppm

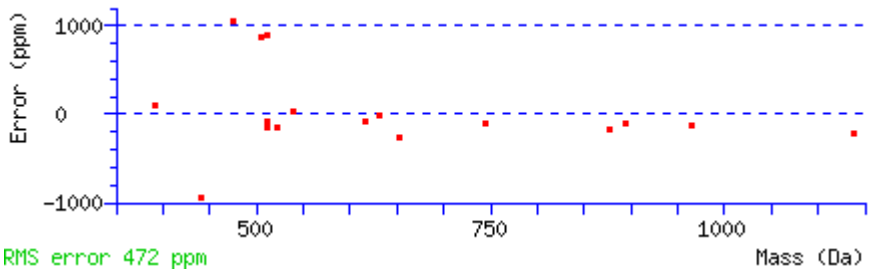
IDENTIFICATION 41
MS/MS Fragmentation of YRAQLLEPSK
Found in IPI00134820



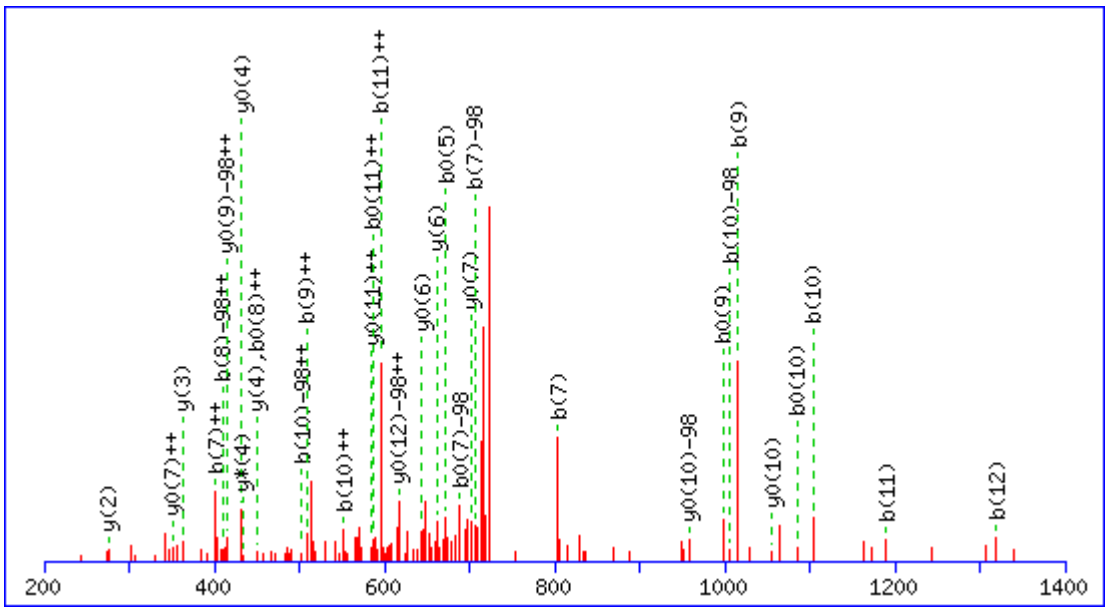
Monoisotopic mass of neutral peptide Mr(calc): 1283.6275 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 31 Expect: 0.076 (help)

#	b	b^{++}	b*	b^{*++}	b_0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	164.0706	82.5389					Y							10
2	320.1717	160.5895	303.1452	152.0762			R	1121.5715	561.2894	1104.5449	552.7761	1103.5609	552.2841	9
3	391.2088	196.1081	374.1823	187.5948			A	965.4703	483.2388	948.4438	474.7255	947.4598	474.2335	8
4	519.2674	260.1373	502.2409	251.6241			Q	894.4332	447.7203	877.4067	439.2070	876.4227	438.7150	7
5	632.3515	316.6794	615.3249	308.1661			L	766.3746	383.6910	749.3481	375.1777	748.3641	374.6857	6
6	745.4355	373.2214	728.4090	364.7081			L	653.2906	327.1489	636.2640	318.6357	635.2800	318.1436	5
7	874.4781	437.7427	857.4516	429.2294	856.4676	428.7374	E	540.2065	270.6069	523.1800	262.0936	522.1960	261.6016	4
8	971.5309	486.2691	954.5043	477.7558	953.5203	477.2638	P	411.1639	206.0856	394.1374	197.5723	393.1534	197.0803	3
9	1138.5293	569.7683	1121.5027	561.2550	1120.5187	560.7630	S	314.1112	157.5592	297.0846	149.0459	296.1006	148.5539	2
10							K	147.1128	74.0600	130.0863	65.5468			1



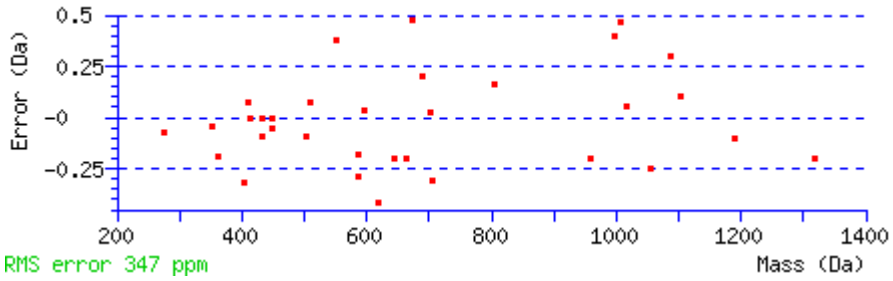


IDENTIFICATION 42
MS/MS Fragmentation of DYIMSGGLVSSEK
Found in IPI00330560

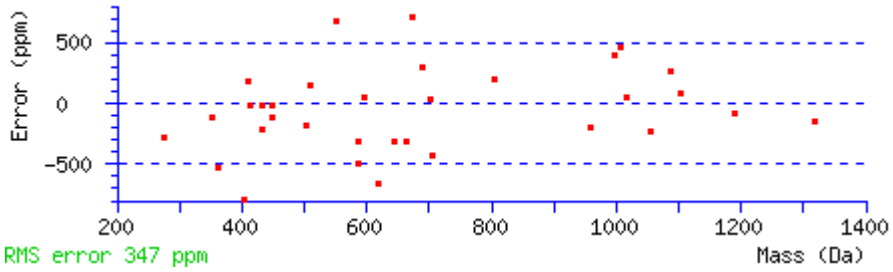


Monoisotopic mass of neutral peptide Mr(calc): 1464.6207
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.057 (help)

#	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	279.0975	140.0524	261.0870	131.0471	Y	1350.6011	675.8042	1333.5745	667.2909	1332.5905	666.7989	12
3	392.1816	196.5944	374.1710	187.5892	I	1187.5378	594.2725	1170.5112	585.7592	1169.5272	585.2672	11
4	523.2221	262.1147	505.2115	253.1094	M	1074.4537	537.7305	1057.4272	529.2172	1056.4431	528.7252	10
5	690.2205	345.6139	672.2099	336.6086	S	943.4132	472.2102	926.3867	463.6970	925.4027	463.2050	9
6	747.2419	374.1246	729.2314	365.1193	G	776.4149	388.7111	759.3883	380.1978	758.4043	379.7058	8
7	804.2634	402.6353	786.2528	393.6300	G	719.3934	360.2003	702.3668	351.6871	701.3828	351.1951	7
8	917.3474	459.1774	899.3369	450.1721	L	662.3719	331.6896	645.3454	323.1763	644.3614	322.6843	6
9	1016.4159	508.7116	998.4053	499.7063	V	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
10	1103.4479	552.2276	1085.4373	543.2223	S	450.2195	225.6134	433.1929	217.1001	432.2089	216.6081	4
11	1190.4799	595.7436	1172.4694	586.7383	S	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
12	1319.5225	660.2649	1301.5119	651.2596	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

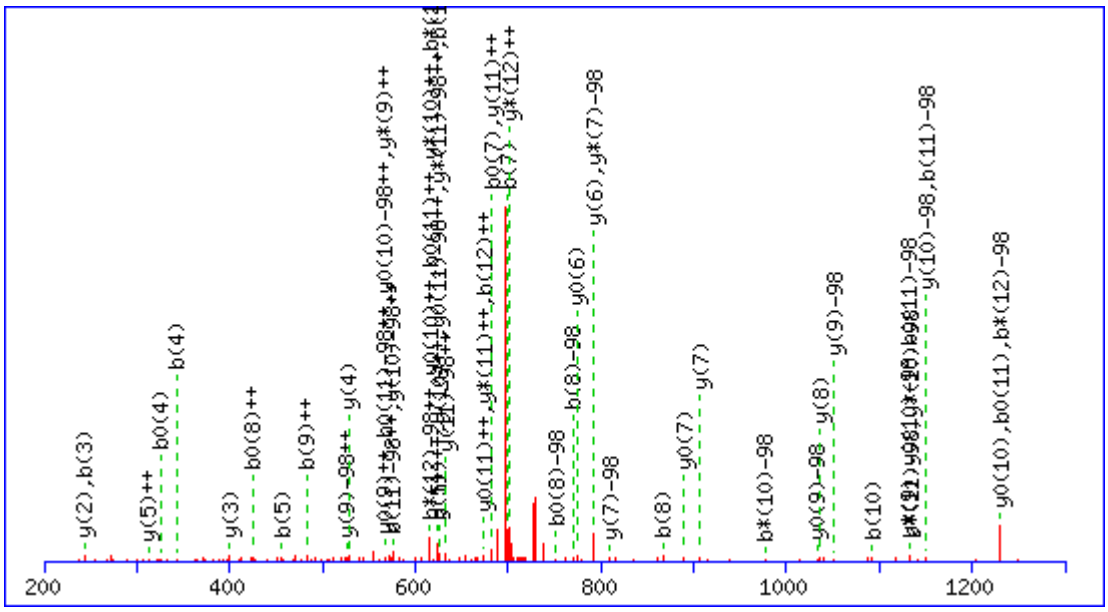


RMS error 347 ppm



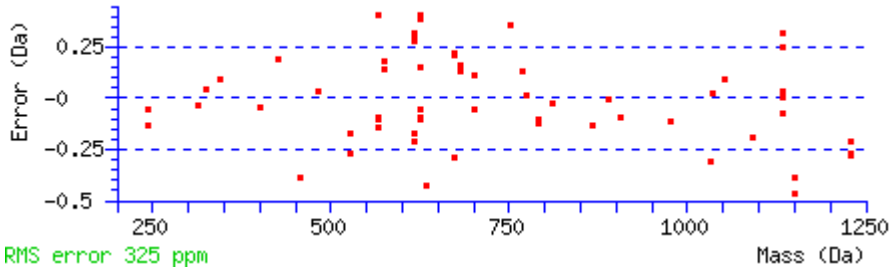
RMS error 347 ppm

IDENTIFICATION 43
MS/MS Fragmentation of AGDVLEDSPKRPK
Found in IPI00313817

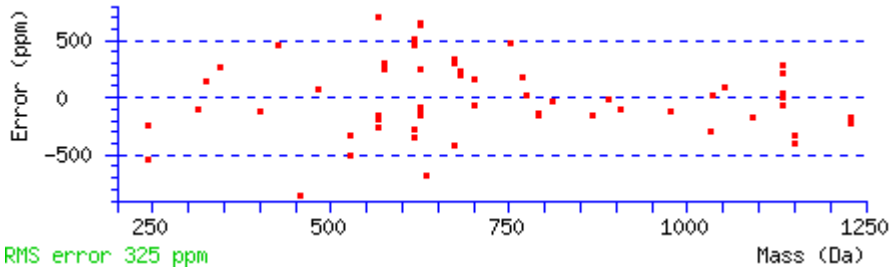


Monoisotopic mass of neutral peptide Mr(calc): 1490.7130
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.12 (help)

#	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	129.0659	65.0366					G	1322.7063	661.8568	1305.6797	653.3435	1304.6957	652.8515	12
3	244.0928	122.5500			226.0822	113.5448	D	1265.6848	633.3461	1248.6583	624.8328	1247.6743	624.3408	11
4	343.1612	172.0842			325.1506	163.0790	V	1150.6579	575.8326	1133.6313	567.3193	1132.6473	566.8273	10
5	456.2453	228.6263			438.2347	219.6210	L	1051.5895	526.2984	1034.5629	517.7851	1033.5789	517.2931	9
6	585.2879	293.1476			567.2773	284.1423	E	938.5054	469.7563	921.4789	461.2431	920.4948	460.7511	8
7	700.3148	350.6610			682.3042	341.6558	D	809.4628	405.2350	792.4363	396.7218	791.4522	396.2298	7
8	769.3363	385.1718			751.3257	376.1665	S	694.4359	347.7216	677.4093	339.2083	676.4253	338.7163	6
9	866.3890	433.6982			848.3785	424.6929	P	625.4144	313.2108	608.3879	304.6976			5
10	994.4840	497.7456	977.4575	489.2324	976.4734	488.7404	K	528.3616	264.6845	511.3351	256.1712			4
11	1150.5851	575.7962	1133.5586	567.2829	1132.5745	566.7909	R	400.2667	200.6370	383.2401	192.1237			3
12	1247.6379	624.3226	1230.6113	615.8093	1229.6273	615.3173	P	244.1656	122.5864	227.1390	114.0731			2
13							K	147.1128	74.0600	130.0863	65.5468			1



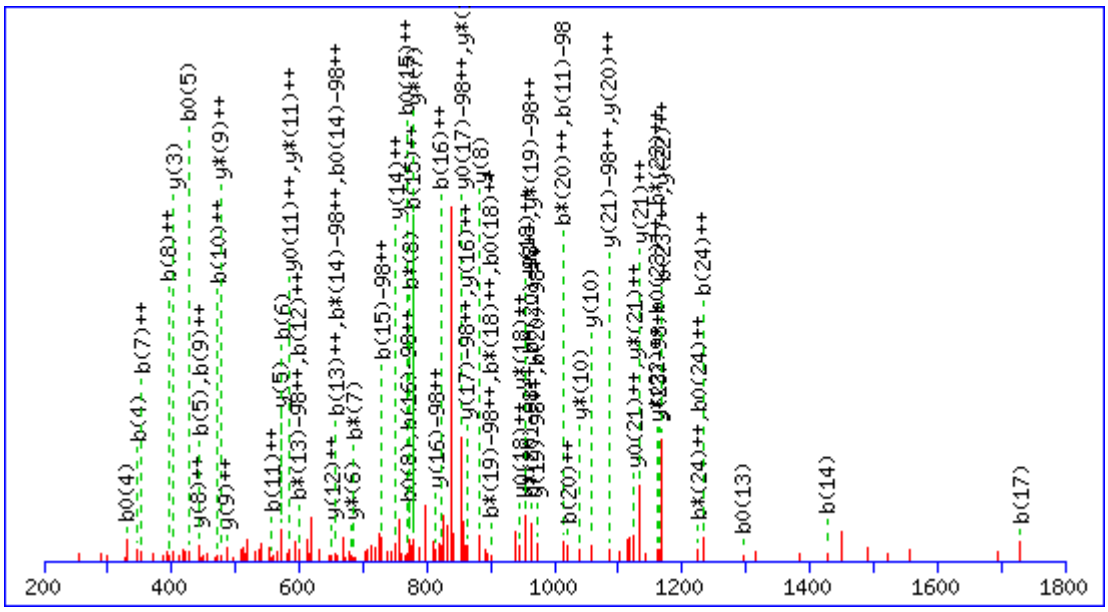
RMS error 325 ppm



RMS error 325 ppm

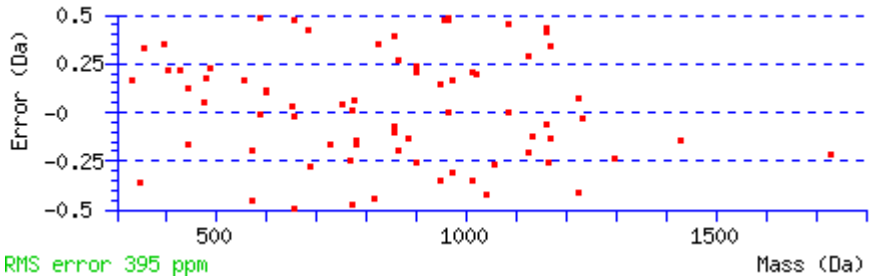
IDENTIFICATION 44

MS/MS Fragmentation of STSAPQMSPGSSDNQSSSPQPAQQK
Found in IPI00407835

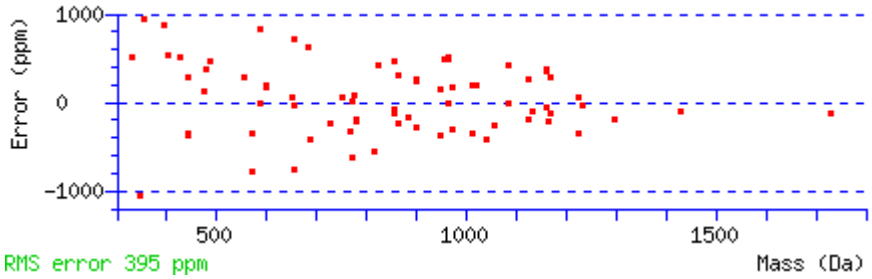


Monoisotopic mass of neutral peptide Mr(calc): 2611.0857
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 1.8 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							25
2	189.0870	95.0471			171.0764	86.0418	T	2525.0610	1263.0341	2508.0345	1254.5209	2507.0504	1254.0289	24
3	276.1190	138.5631			258.1084	129.5579	S	2424.0133	1212.5103	2406.9868	1203.9970	2406.0028	1203.5050	23
4	347.1561	174.0817			329.1456	165.0764	A	2336.9813	1168.9943	2319.9547	1160.4810	2318.9707	1159.9890	22
5	444.2089	222.6081			426.1983	213.6028	P	2265.9442	1133.4757	2248.9176	1124.9625	2247.9336	1124.4704	21
6	572.2675	286.6374	555.2409	278.1241	554.2569	277.6321	Q	2168.8914	1084.9493	2151.8649	1076.4361	2150.8809	1075.9441	20
7	703.3080	352.1576	686.2814	343.6443	685.2974	343.1523	M	2040.8328	1020.9201	2023.8063	1012.4068	2022.8223	1011.9148	19
8	790.3400	395.6736	773.3134	387.1604	772.3294	386.6683	S	1909.7924	955.3998	1892.7658	946.8865	1891.7818	946.3945	18
9	887.3927	444.2000	870.3662	435.6867	869.3822	435.1947	P	1822.7603	911.8838	1805.7338	903.3705	1804.7498	902.8785	17
10	944.4142	472.7107	927.3877	464.1975	926.4036	463.7055	G	1725.7076	863.3574	1708.6810	854.8441	1707.6970	854.3521	16
11	1111.4126	556.2099	1094.3860	547.6966	1093.4020	547.2046	S	1668.6861	834.8467	1651.6596	826.3334	1650.6755	825.8414	15
12	1198.4446	599.7259	1181.4180	591.2127	1180.4340	590.7207	S	1501.6877	751.3475	1484.6612	742.8342	1483.6772	742.3422	14
13	1313.4715	657.2394	1296.4450	648.7261	1295.4610	648.2341	D	1414.6557	707.8315	1397.6292	699.3182	1396.6451	698.8262	13
14	1427.5145	714.2609	1410.4879	705.7476	1409.5039	705.2556	N	1299.6288	650.3180	1282.6022	641.8047	1281.6182	641.3127	12
15	1555.5730	778.2902	1538.5465	769.7769	1537.5625	769.2849	Q	1185.5858	593.2966	1168.5593	584.7833	1167.5753	584.2913	11
16	1642.6051	821.8062	1625.5785	813.2929	1624.5945	812.8009	S	1057.5273	529.2673	1040.5007	520.7540	1039.5167	520.2620	10
17	1729.6371	865.3222	1712.6106	856.8089	1711.6265	856.3169	S	970.4952	485.7513	953.4687	477.2380	952.4847	476.7460	9
18	1816.6691	908.8382	1799.6426	900.3249	1798.6586	899.8329	S	883.4632	442.2352	866.4367	433.7220	865.4526	433.2300	8
19	1913.7219	957.3646	1896.6953	948.8513	1895.7113	948.3593	P	796.4312	398.7192	779.4046	390.2060			7
20	2041.7805	1021.3939	2024.7539	1012.8806	2023.7699	1012.3886	Q	699.3784	350.1928	682.3519	341.6796			6
21	2138.8332	1069.9203	2121.8067	1061.4070	2120.8227	1060.9150	P	571.3198	286.1636	554.2933	277.6503			5
22	2209.8703	1105.4388	2192.8438	1096.9255	2191.8598	1096.4335	A	474.2671	237.6372	457.2405	229.1239			4
23	2337.9289	1169.4681	2320.9024	1160.9548	2319.9184	1160.4628	Q	403.2300	202.1186	386.2034	193.6053			3
24	2465.9875	1233.4974	2448.9610	1224.9841	2447.9769	1224.4921	Q	275.1714	138.0893	258.1448	129.5761			2
25							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 395 ppm

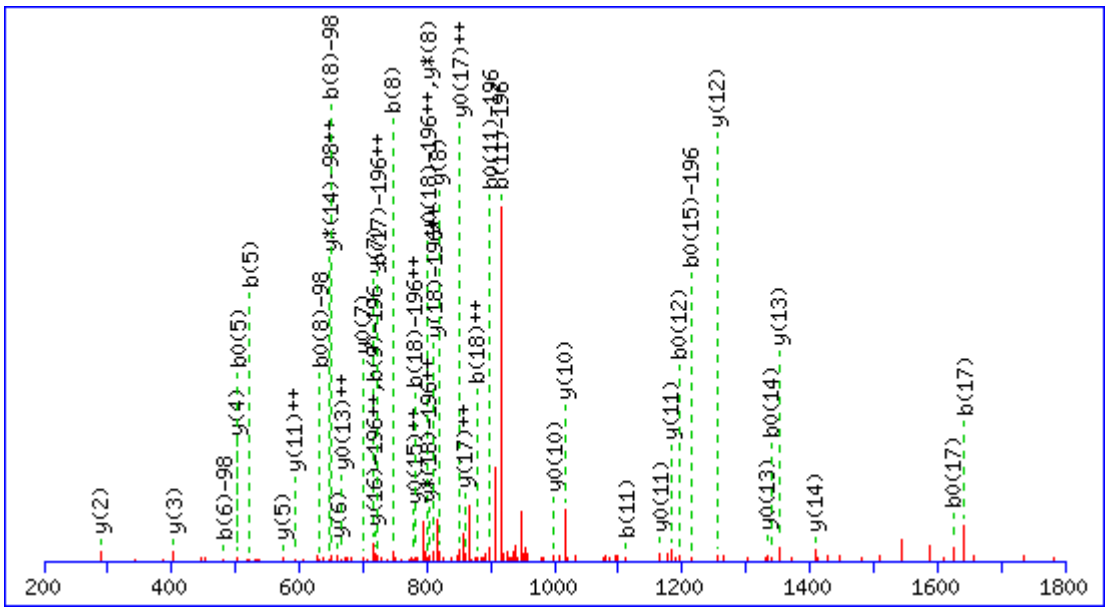


RMS error 395 ppm

IDENTIFICATION 45

MS/MS Fragmentation of LPSGSGPASPTTGSAVDIR

Found in IPI00553798



Monoisotopic mass of neutral peptide Mr(calc):

1928.8282

Fixed modifications:

Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S5 :

Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

S9 :

Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score:

68

Expect:

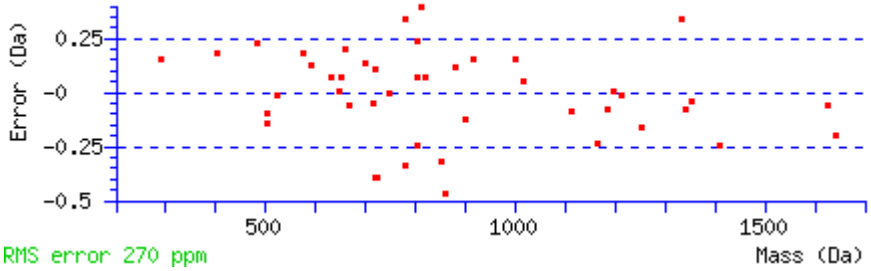
2.9e-05 (

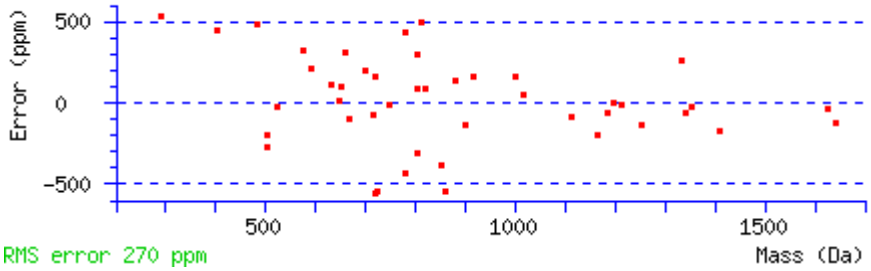
help

)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							19
2	211.1441	106.0757			P	1816.7514	908.8793	1799.7249	900.3661	1798.7409	899.8741	18
3	298.1761	149.5917	280.1656	140.5864	S	1719.6987	860.3530	1702.6721	851.8397	1701.6881	851.3477	17
4	355.1976	178.1024	337.1870	169.0972	G	1632.6666	816.8370	1615.6401	808.3237	1614.6561	807.8317	16
5	522.1960	261.6016	504.1854	252.5963	S	1575.6452	788.3262	1558.6186	779.8129	1557.6346	779.3209	15
6	579.2174	290.1123	561.2069	281.1071	G	1408.6468	704.8270	1391.6203	696.3138	1390.6362	695.8218	14
7	676.2702	338.6387	658.2596	329.6334	P	1351.6253	676.3163	1334.5988	667.8030	1333.6148	667.3110	13
8	747.3073	374.1573	729.2967	365.1520	A	1254.5726	627.7899	1237.5460	619.2767	1236.5620	618.7846	12
9	914.3057	457.6565	896.2951	448.6512	S	1183.5355	592.2714	1166.5089	583.7581	1165.5249	583.2661	11
10	1011.3584	506.1828	993.3479	497.1776	P	1016.5371	508.7722	999.5106	500.2589	998.5265	499.7669	10
11	1112.4061	556.7067	1094.3955	547.7014	T	919.4843	460.2458	902.4578	451.7325	901.4738	451.2405	9

12	1213.4538	607.2305	1195.4432	598.2252	T	818.4367	409.7220	801.4101	401.2087	800.4261	400.7167	8
13	1270.4752	635.7413	1252.4647	626.7360	G	717.3890	359.1981	700.3624	350.6849	699.3784	350.1928	7
14	1357.5073	679.2573	1339.4967	670.2520	S	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
15	1428.5444	714.7758	1410.5338	705.7705	A	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	5
16	1527.6128	764.3100	1509.6022	755.3048	V	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
17	1642.6397	821.8235	1624.6292	812.8182	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
18	1755.7238	878.3655	1737.7132	869.3603	I	288.2030	144.6051	271.1765	136.0919			2
19					R	175.1190	88.0631	158.0924	79.5498			1

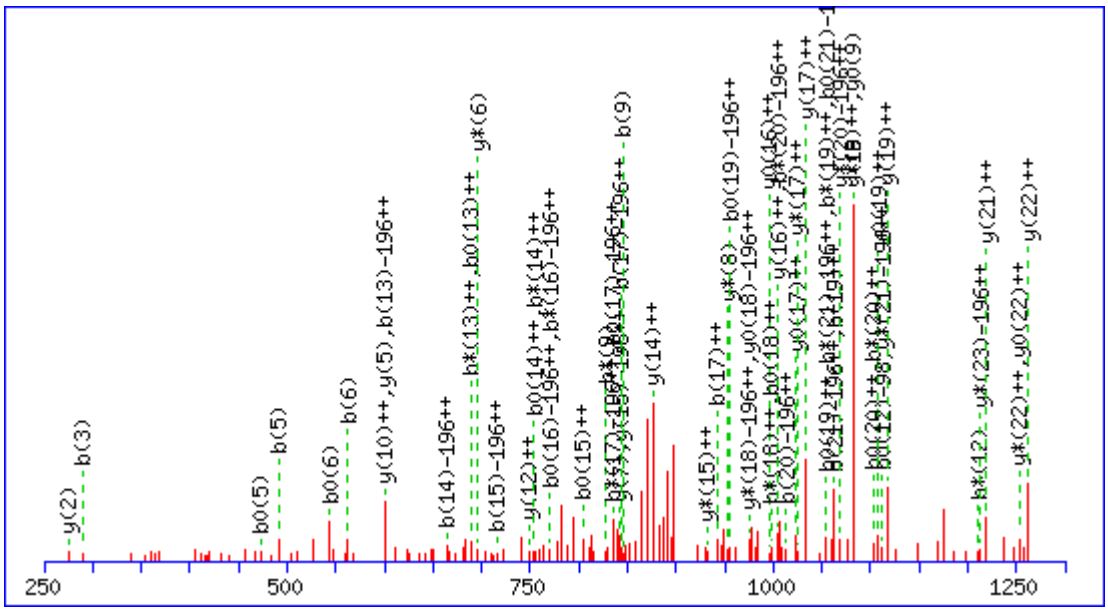




IDENTIFICATION 46

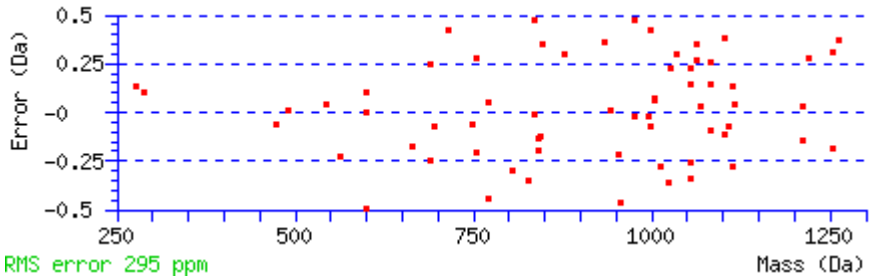
MS/MS Fragmentation of SNSSDAPGEESSSETEKEIPVEQK

Found in IPI00120691



Monoisotopic mass of neutral peptide Mr(calc): 2723.0735
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 23 Expect: 1.1 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							24
2	202.0822	101.5448	185.0557	93.0315	184.0717	92.5395	N	2637.0488	1319.0281	2620.0223	1310.5148	2619.0383	1310.0228	23
3	289.1143	145.0608	272.0877	136.5475	271.1037	136.0555	S	2523.0059	1262.0066	2505.9794	1253.4933	2504.9953	1253.0013	22
4	376.1463	188.5768	359.1197	180.0635	358.1357	179.5715	S	2435.9739	1218.4906	2418.9473	1209.9773	2417.9633	1209.4853	21
5	491.1732	246.0903	474.1467	237.5770	473.1627	237.0850	D	2348.9419	1174.9746	2331.9153	1166.4613	2330.9313	1165.9693	20
6	562.2103	281.6088	545.1838	273.0955	544.1998	272.6035	A	2233.9149	1117.4611	2216.8884	1108.9478	2215.9043	1108.4558	19
7	659.2631	330.1352	642.2366	321.6219	641.2525	321.1299	P	2162.8778	1081.9425	2145.8512	1073.4293	2144.8672	1072.9373	18
8	716.2846	358.6459	699.2580	350.1326	698.2740	349.6406	G	2065.8250	1033.4162	2048.7985	1024.9029	2047.8145	1024.4109	17
9	845.3272	423.1672	828.3006	414.6539	827.3166	414.1619	E	2008.8036	1004.9054	1991.7770	996.3921	1990.7930	995.9001	16
10	974.3698	487.6885	957.3432	479.1752	956.3592	478.6832	E	1879.7610	940.3841	1862.7344	931.8709	1861.7504	931.3788	15
11	1061.4018	531.2045	1044.3752	522.6913	1043.3912	522.1992	S	1750.7184	875.8628	1733.6918	867.3496	1732.7078	866.8575	14
12	1228.4001	614.7037	1211.3736	606.1904	1210.3896	605.6984	S	1663.6864	832.3468	1646.6598	823.8335	1645.6758	823.3415	13
13	1395.3985	698.2029	1378.3720	689.6896	1377.3879	689.1976	S	1496.6880	748.8476	1479.6614	740.3344	1478.6774	739.8424	12
14	1524.4411	762.7242	1507.4145	754.2109	1506.4305	753.7189	E	1329.6896	665.3485	1312.6631	656.8352	1311.6791	656.3432	11
15	1625.4888	813.2480	1608.4622	804.7348	1607.4782	804.2427	T	1200.6470	600.8272	1183.6205	592.3139	1182.6365	591.8219	10
16	1754.5314	877.7693	1737.5048	869.2560	1736.5208	868.7640	E	1099.5994	550.3033	1082.5728	541.7900	1081.5888	541.2980	9
17	1882.6263	941.8168	1865.5998	933.3035	1864.6158	932.8115	K	970.5568	485.7820	953.5302	477.2688	952.5462	476.7767	8
18	2011.6689	1006.3381	1994.6424	997.8248	1993.6584	997.3328	E	842.4618	421.7345	825.4353	413.2213	824.4512	412.7293	7
19	2124.7530	1062.8801	2107.7264	1054.3669	2106.7424	1053.8749	I	713.4192	357.2132	696.3927	348.7000	695.4087	348.2080	6
20	2221.8058	1111.4065	2204.7792	1102.8932	2203.7952	1102.4012	P	600.3352	300.6712	583.3086	292.1579	582.3246	291.6659	5
21	2320.8742	1160.9407	2303.8476	1152.4274	2302.8636	1151.9354	V	503.2824	252.1448	486.2558	243.6316	485.2718	243.1396	4
22	2449.9168	1225.4620	2432.8902	1216.9487	2431.9062	1216.4567	E	404.2140	202.6106	387.1874	194.0974	386.2034	193.6053	3
23	2577.9753	1289.4913	2560.9488	1280.9780	2559.9648	1280.4860	Q	275.1714	138.0893	258.1448	129.5761			2
24							K	147.1128	74.0600	130.0863	65.5468			1


0.5
0.25
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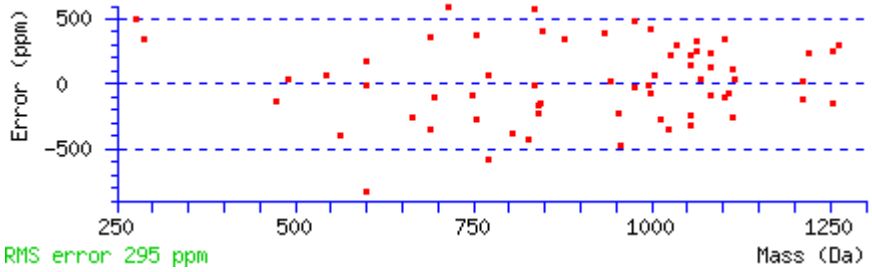
Error (Da)
250
500
750
1000
1250
Mass (Da)
RMS error 295 ppm


500
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-500
Error (ppm)
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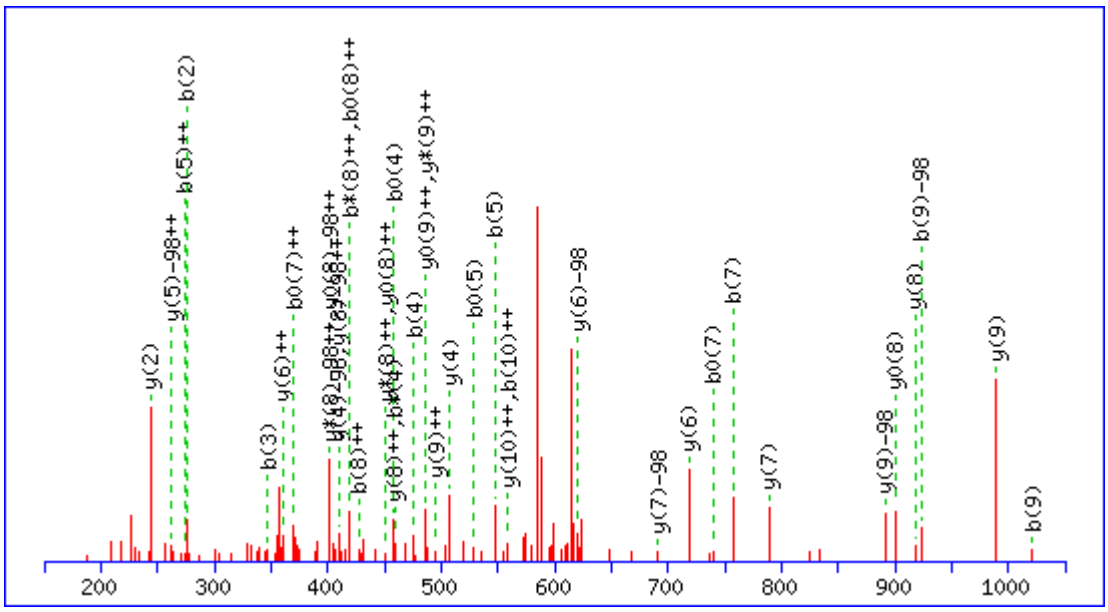
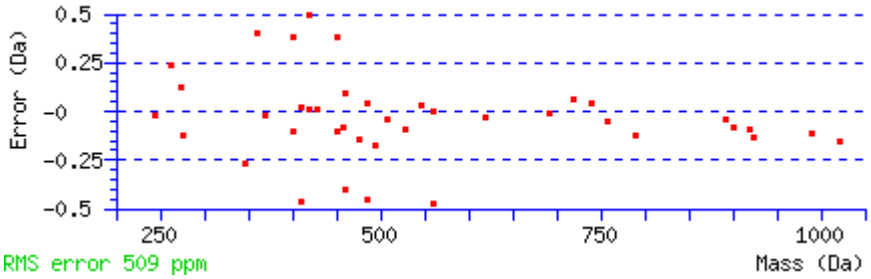
500
750
1000
1250
Mass (Da)
RMS error 295 ppm

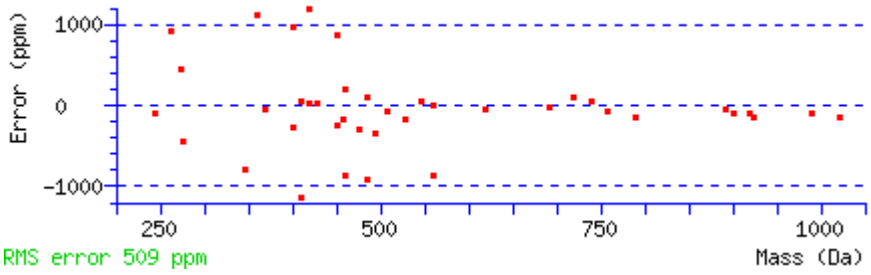
IDENTIFICATION 47
MS/MS Fragmentation of FKAEAPLPSPK
Found in IPI00553798



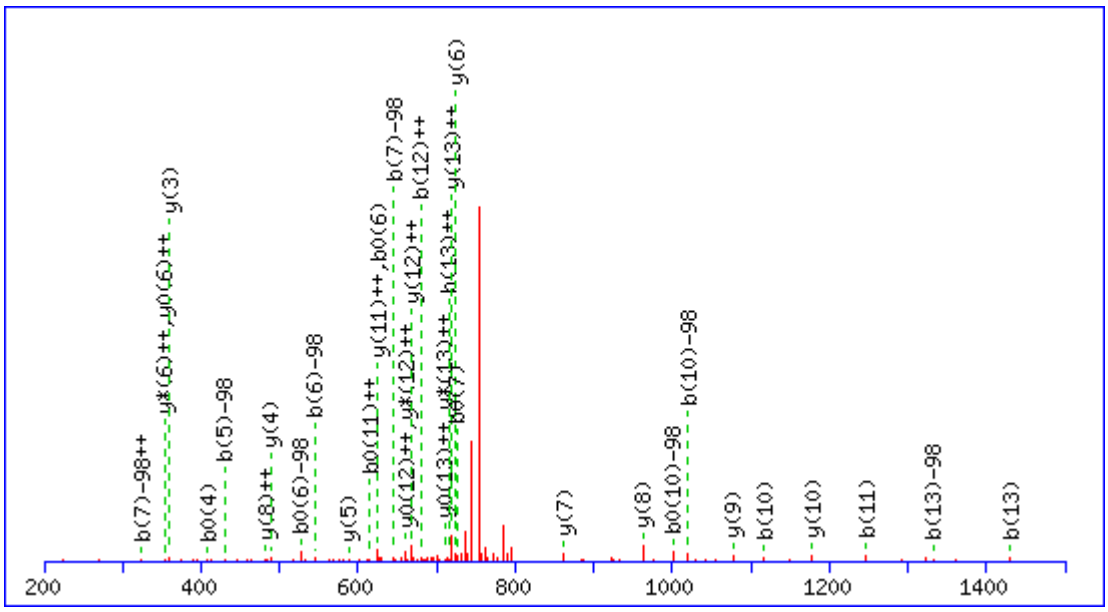
Monoisotopic mass of neutral peptide Mr(calc): 1263.6264 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 34 Expect: 0.041 (help)

#	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	276.1707	138.5890	259.1441	130.0757			K	1117.5653	559.2863	1100.5388	550.7730	1099.5547	550.2810	10
3	347.2078	174.1075	330.1812	165.5942			A	989.4703	495.2388	972.4438	486.7255	971.4598	486.2335	9
4	476.2504	238.6288	459.2238	230.1155	458.2398	229.6235	E	918.4332	459.7203	901.4067	451.2070	900.4227	450.7150	8
5	547.2875	274.1474	530.2609	265.6341	529.2769	265.1421	A	789.3906	395.1990	772.3641	386.6857	771.3801	386.1937	7
6	644.3402	322.6738	627.3137	314.1605	626.3297	313.6685	P	718.3535	359.6804	701.3270	351.1671	700.3430	350.6751	6
7	757.4243	379.2158	740.3978	370.7025	739.4137	370.2105	L	621.3008	311.1540	604.2742	302.6407	603.2902	302.1487	5
8	854.4771	427.7422	837.4505	419.2289	836.4665	418.7369	P	508.2167	254.6120	491.1901	246.0987	490.2061	245.6067	4
9	1021.4754	511.2414	1004.4489	502.7281	1003.4649	502.2361	S	411.1639	206.0856	394.1374	197.5723	393.1534	197.0803	3
10	1118.5282	559.7677	1101.5016	551.2545	1100.5176	550.7624	P	244.1656	122.5864	227.1390	114.0731			2
11							K	147.1128	74.0600	130.0863	65.5468			1



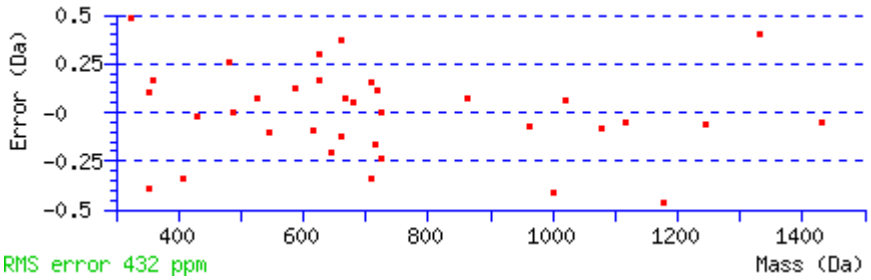


IDENTIFICATION 48
MS/MS Fragmentation of STSATDTHHVELAR
Found in IPI00115094

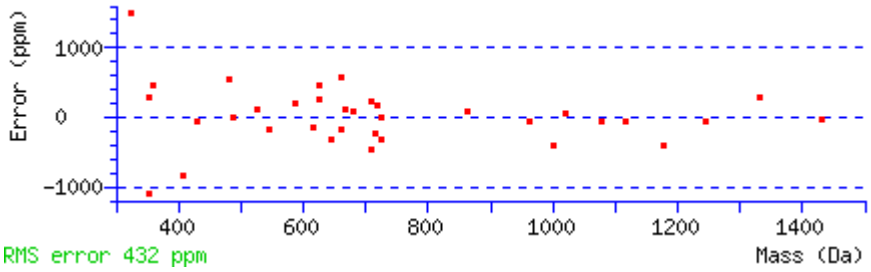


Monoisotopic mass of neutral peptide Mr(calc): 1603.6992
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S1 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 41 Expect: 0.011 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	70.0287	35.5180	52.0182	26.5127	S							14
2	171.0764	86.0418	153.0659	77.0366	T	1437.7081	**719.3577**	1420.6815	**710.8444**	1419.6975	**710.3524**	13
3	258.1084	129.5579	240.0979	120.5526	S	1336.6604	**668.8338**	1319.6339	**660.3206**	1318.6498	**659.8286**	12
4	329.1456	165.0764	311.1350	156.0711	A	1249.6284	**625.3178**	1232.6018	616.8046	1231.6178	616.3125	11
5	**430.1932**	215.6003	412.1827	206.5950	T	**1178.5913**	589.7993	1161.5647	581.2860	1160.5807	580.7940	10
6	**545.2202**	273.1137	**527.2096**	264.1084	D	**1077.5436**	539.2754	1060.5170	530.7622	1059.5330	530.2701	9
7	**646.2679**	323.6376	628.2573	314.6323	T	**962.5166**	**481.7620**	945.4901	473.2487	944.5061	472.7567	8
8	783.3268	392.1670	765.3162	383.1617	H	**861.4690**	431.2381	844.4424	422.7248	843.4584	422.2328	7
9	920.3857	460.6965	902.3751	451.6912	H	**724.4100**	362.7087	707.3835	**354.1954**	706.3995	**353.7034**	6
10	**1019.4541**	510.2307	**1001.4435**	501.2254	V	**587.3511**	294.1792	570.3246	285.6659	569.3406	285.1739	5
11	1148.4967	574.7520	1130.4861	565.7467	E	**488.2827**	244.6450	471.2562	236.1317	470.2722	235.6397	4
12	1261.5808	631.2940	1243.5702	622.2887	L	**359.2401**	180.1237	342.2136	171.6104			3
13	**1332.6179**	666.8126	1314.6073	657.8073	A	246.1561	123.5817	229.1295	115.0684			2
14					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 432 ppm

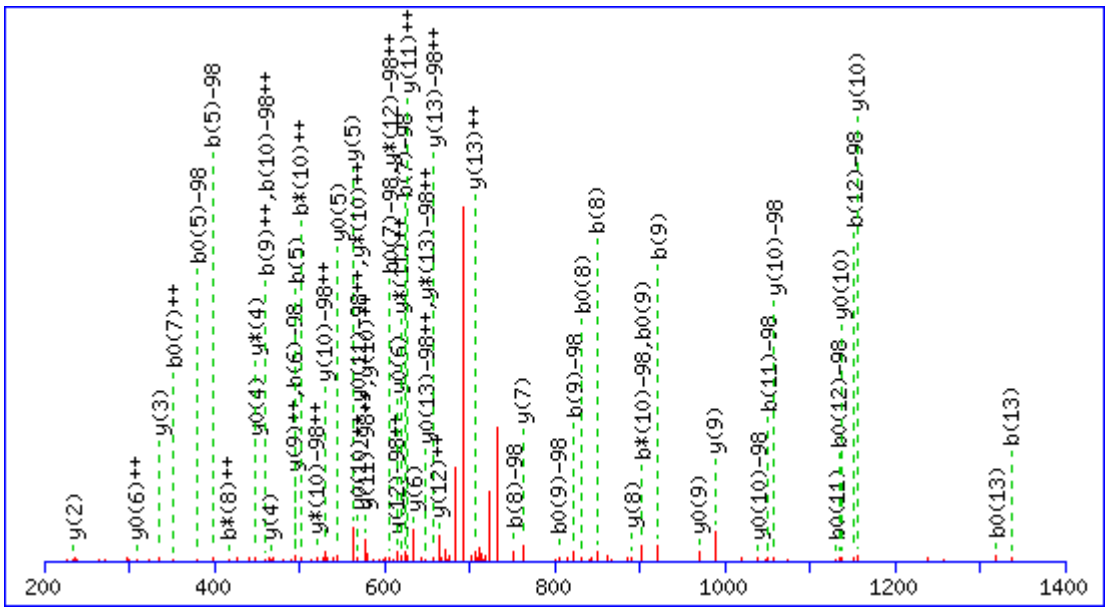


RMS error 432 ppm

IDENTIFICATION 49

MS/MS Fragmentation of ASAVSPEKAPMTSK

Found in IPI00115660



Monoisotopic mass of neutral peptide Mr(calc): 1482.6789

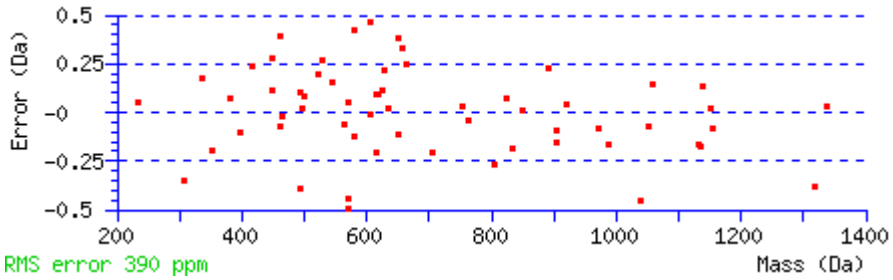
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 43 Expect: 0.007 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							14
2	159.0764	80.0418			141.0659	71.0366	S	1314.6722	657.8397	1297.6457	649.3265	1296.6616	648.8345	13
3	230.1135	115.5604			212.1030	106.5551	A	1227.6402	614.3237	1210.6136	605.8105	1209.6296	605.3184	12
4	329.1819	165.0946			311.1714	156.0893	V	1156.6031	578.8052	1139.5765	570.2919	1138.5925	569.7999	11
5	398.2034	199.6053			380.1928	190.6001	S	1057.5347	529.2710	1040.5081	520.7577	1039.5241	520.2657	10
6	495.2562	248.1317			477.2456	239.1264	P	988.5132	494.7602	971.4866	486.2470	970.5026	485.7550	9
7	624.2988	312.6530			606.2882	303.6477	E	891.4604	446.2339	874.4339	437.7206	873.4499	437.2286	8
8	752.3937	376.7005	735.3672	368.1872	734.3832	367.6952	K	762.4178	381.7126	745.3913	373.1993	744.4073	372.7073	7
9	823.4308	412.2191	806.4043	403.7058	805.4203	403.2138	A	634.3229	317.6651	617.2963	309.1518	616.3123	308.6598	6
10	920.4836	460.7454	903.4571	452.2322	902.4730	451.7402	P	563.2858	282.1465	546.2592	273.6332	545.2752	273.1412	5
11	1051.5241	526.2657	1034.4975	517.7524	1033.5135	517.2604	M	466.2330	233.6201	449.2064	225.1069	448.2224	224.6149	4
12	1152.5718	576.7895	1135.5452	568.2762	1134.5612	567.7842	T	335.1925	168.0999	318.1660	159.5866	317.1819	159.0946	3
13	1239.6038	620.3055	1222.5773	611.7923	1221.5932	611.3003	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
14							K	147.1128	74.0600	130.0863	65.5468			1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-0.5
Error (Da)
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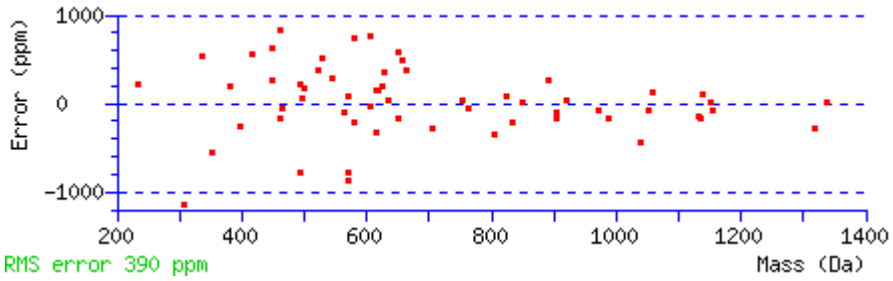
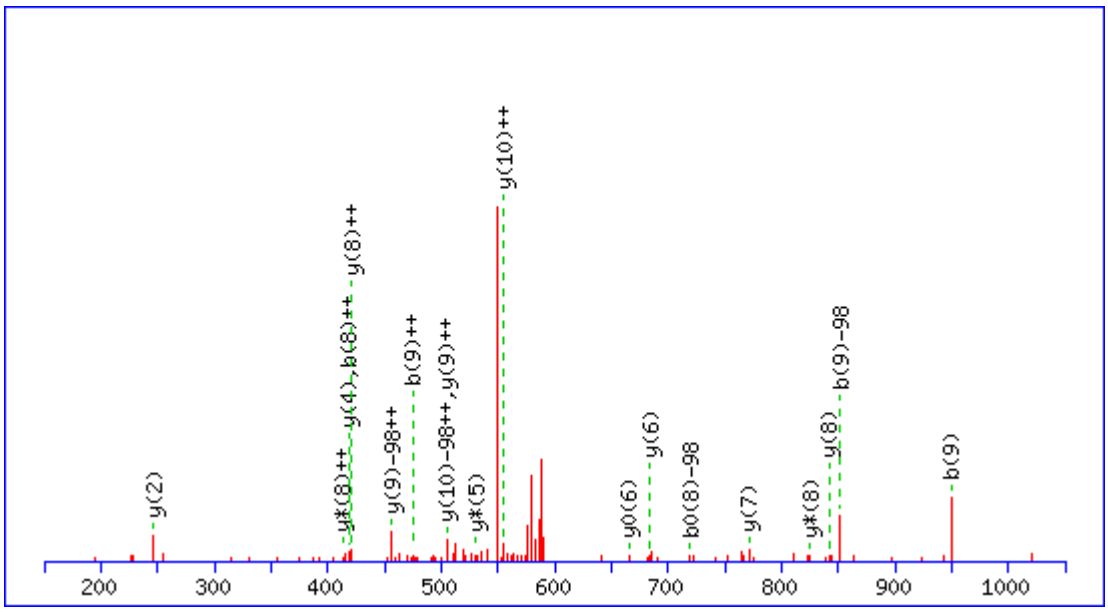
400
600
800
1000
1200
1400
Mass (Da)
RMS error 390 ppm

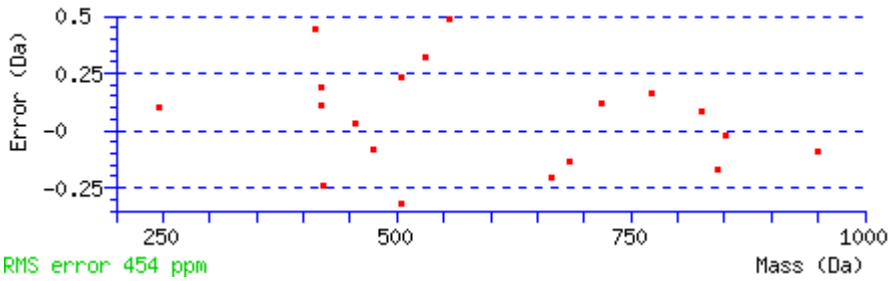

1000
0
-1000
Error (ppm)
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 390 ppm

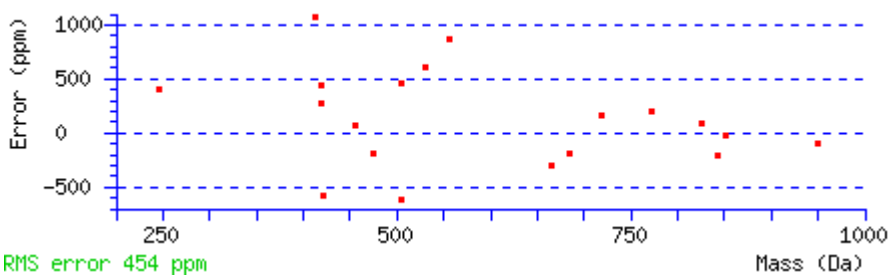
IDENTIFICATION 50
MS/MS Fragmentation of SVSASHEGDVK
Found in IPI00331173



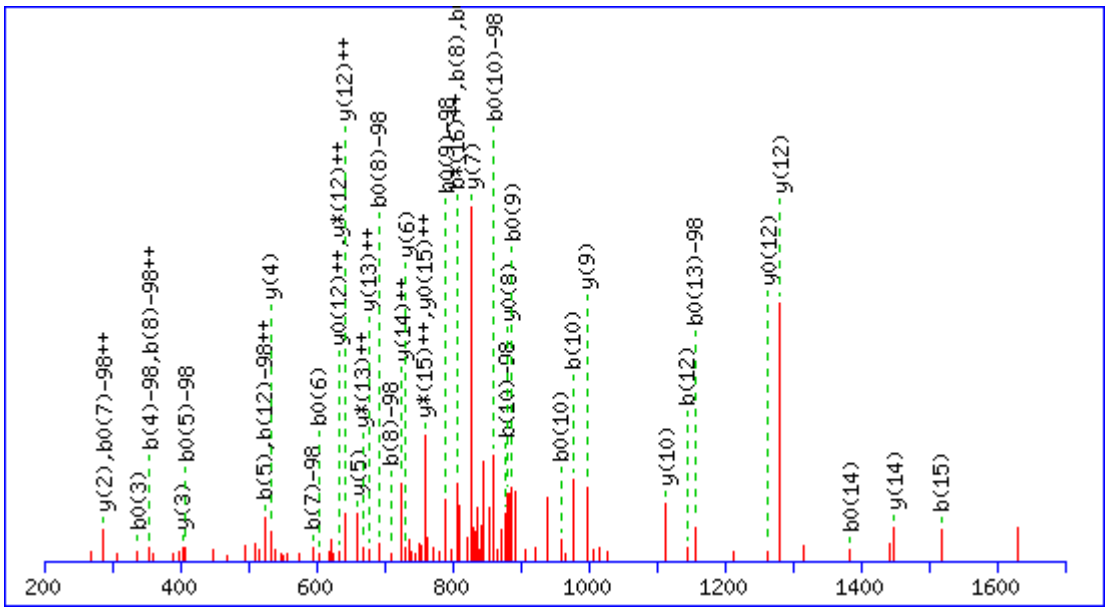
Monoisotopic mass of neutral peptide Mr(calc): 1194.4918
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 19 Expect: 1 (help)

#	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							11
2	187.1077	94.0575	169.0972	85.0522	V	1010.4901	505.7487	993.4636	497.2354	992.4796	496.7434	10
3	256.1292	128.5682	238.1186	119.5629	S	911.4217	456.2145	894.3952	447.7012	893.4112	447.2092	9
4	327.1663	164.0868	309.1557	155.0815	A	842.4003	421.7038	825.3737	413.1905	824.3897	412.6985	8
5	414.1983	207.6028	396.1878	198.5975	S	771.3632	386.1852	754.3366	377.6719	753.3526	377.1799	7
6	551.2572	276.1323	533.2467	267.1270	H	684.3311	342.6692	667.3046	334.1559	666.3206	333.6639	6
7	680.2998	340.6536	662.2893	331.6483	E	547.2722	274.1397	530.2457	265.6265	529.2617	265.1345	5
8	737.3213	369.1643	719.3107	360.1590	G	418.2296	209.6185	401.2031	201.1052	400.2191	200.6132	4
9	852.3482	426.6778	834.3377	417.6725	D	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
10	951.4166	476.2120	933.4061	467.2067	V	246.1812	123.5942	229.1547	115.0810			2
11					K	147.1128	74.0600	130.0863	65.5468			1



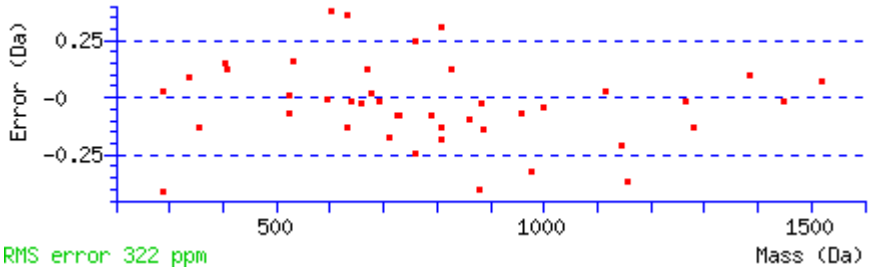


IDENTIFICATION 51
MS/MS Fragmentation of STSPAPADVAPAQEDLR
Found in IPI00130095

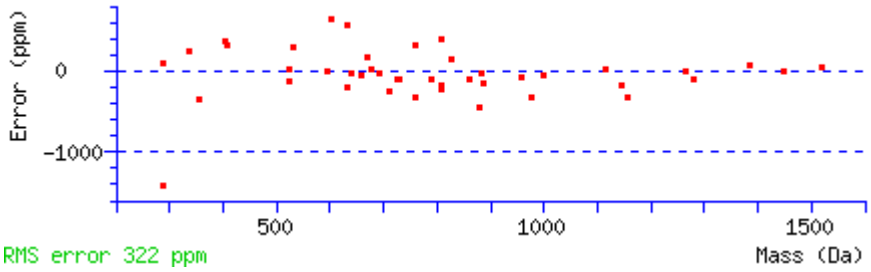


Monoisotopic mass of neutral peptide Mr(calc): 1803.8040
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 6.1e-05 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							17
2	269.0533	135.0303			251.0427	126.0250	T	1717.7793	859.3933	1700.7527	850.8800	1699.7687	850.3880	16
3	356.0853	178.5463			338.0748	169.5410	S	1536.7653	768.8863	1519.7387	760.3730	1518.7547	759.8810	15
4	453.1381	227.0727			435.1275	218.0674	P	1449.7332	725.3703	1432.7067	716.8570	1431.7227	716.3650	14
5	524.1752	262.5912			506.1647	253.5860	A	1352.6805	676.8439	1335.6539	668.3306	1334.6699	667.8386	13
6	621.2280	311.1176			603.2174	302.1123	P	1281.6434	641.3253	1264.6168	632.8120	1263.6328	632.3200	12
7	692.2651	346.6362			674.2545	337.6309	A	1184.5906	592.7989	1167.5640	584.2857	1166.5800	583.7937	11
8	807.2920	404.1497			789.2815	395.1444	D	1113.5535	557.2804	1096.5269	548.7671	1095.5429	548.2751	10
9	906.3605	453.6839			888.3499	444.6786	V	998.5265	499.7669	981.5000	491.2536	980.5160	490.7616	9
10	977.3976	489.2024			959.3870	480.1971	A	899.4581	450.2327	882.4316	441.7194	881.4476	441.2274	8
11	1074.4503	537.7288			1056.4398	528.7235	P	828.4210	414.7141	811.3945	406.2009	810.4104	405.7089	7
12	1145.4874	573.2474			1127.4769	564.2421	A	731.3682	366.1878	714.3417	357.6745	713.3577	357.1825	6
13	1273.5460	637.2767	1256.5195	628.7634	1255.5355	628.2714	Q	660.3311	330.6692	643.3046	322.1559	642.3206	321.6639	5
14	1402.5886	701.7979	1385.5621	693.2847	1384.5781	692.7927	E	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
15	1517.6156	759.3114	1500.5890	750.7981	1499.6050	750.3061	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
16	1630.6996	815.8535	1613.6731	807.3402	1612.6891	806.8482	L	288.2030	144.6051	271.1765	136.0919			2
17							R	175.1190	88.0631	158.0924	79.5498			1

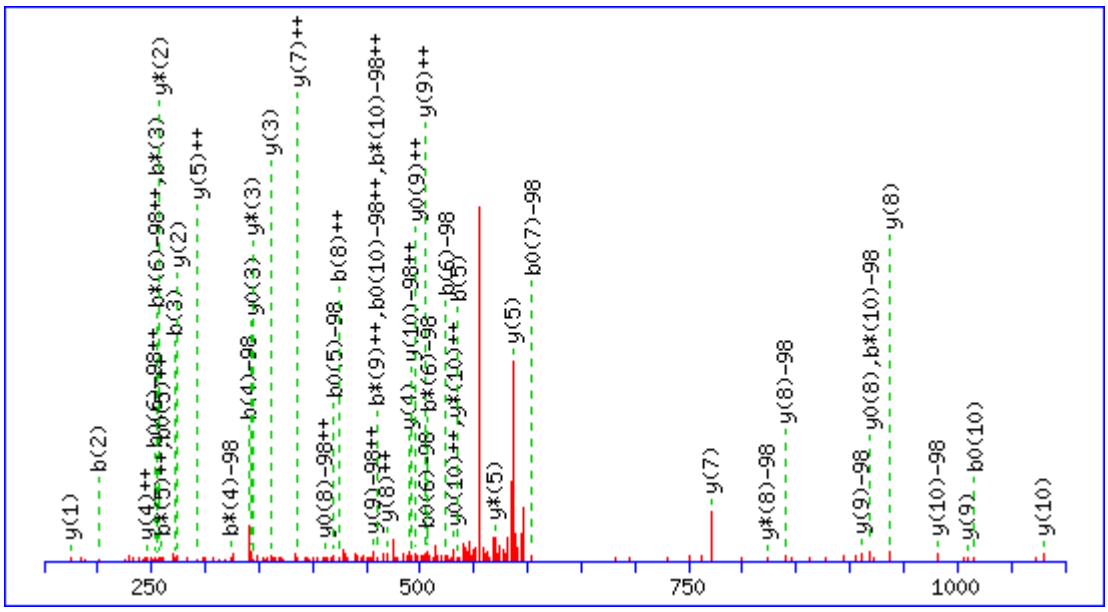


RMS error 322 ppm



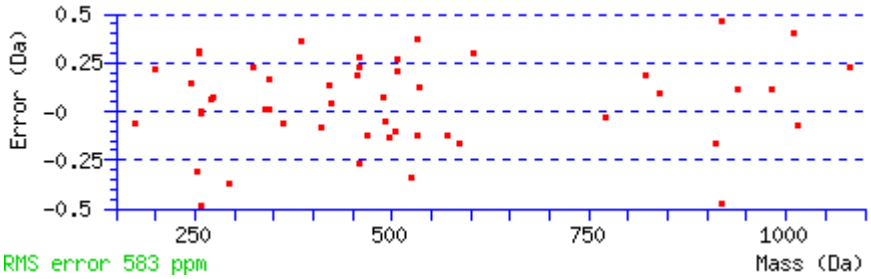
RMS error 322 ppm

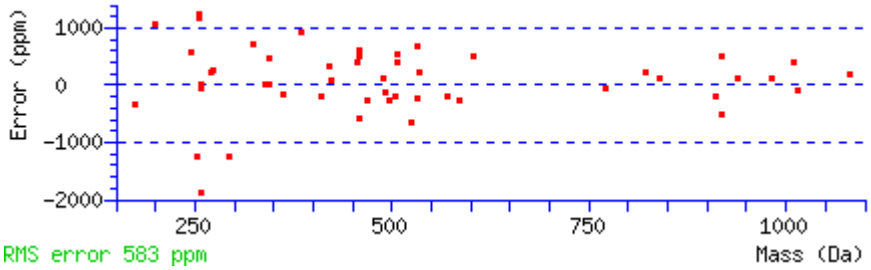
IDENTIFICATION 52
MS/MS Fragmentation of KAASPSPQSVR
Found in IPI00118438



Monoisotopic mass of neutral peptide Mr(calc): 1206.5758
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 30 Expect: 0.11 (help)

#	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							11
2	200.1394	100.5733	183.1128	92.0600			A	981.5112	491.2592	964.4847	482.7460	963.5007	482.2540	10
3	271.1765	136.0919	254.1499	127.5786			A	910.4741	455.7407	893.4476	447.2274	892.4635	446.7354	9
4	340.1979	170.6026	323.1714	162.0893	322.1874	161.5973	S	839.4370	420.2221	822.4104	411.7089	821.4264	411.2169	8
5	437.2507	219.1290	420.2241	210.6157	419.2401	210.1237	P	770.4155	385.7114	753.3890	377.1981	752.4050	376.7061	7
6	524.2827	262.6450	507.2562	254.1317	506.2722	253.6397	S	673.3628	337.1850	656.3362	328.6717	655.3522	328.1797	6
7	621.3355	311.1714	604.3089	302.6581	603.3249	302.1661	P	586.3307	293.6690	569.3042	285.1557	568.3202	284.6637	5
8	749.3941	375.2007	732.3675	366.6874	731.3835	366.1954	Q	489.2780	245.1426	472.2514	236.6293	471.2674	236.1373	4
9	836.4261	418.7167	819.3995	410.2034	818.4155	409.7114	S	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
10	935.4945	468.2509	918.4680	459.7376	917.4839	459.2456	V	274.1874	137.5973	257.1608	129.0840			2
11							R	175.1190	88.0631	158.0924	79.5498			1

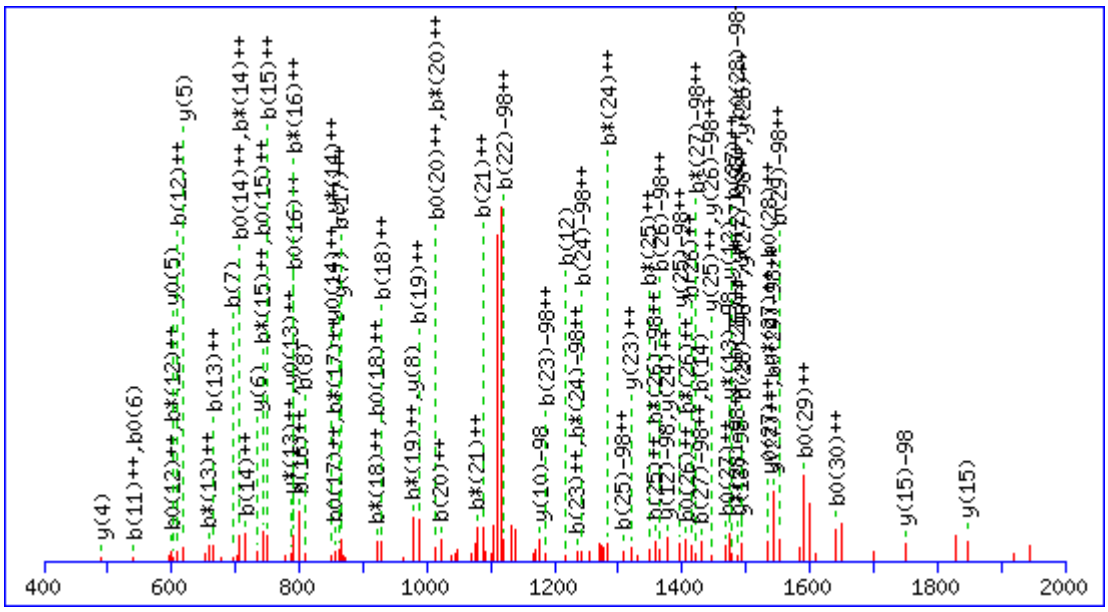




IDENTIFICATION 53

MS/MS Fragmentation of CGSGPVHISGQHLVAVEEDAESEDEDEEDVK

Found in IPI00127415



Monoisotopic mass of neutral peptide Mr(calc): 3445.4141

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

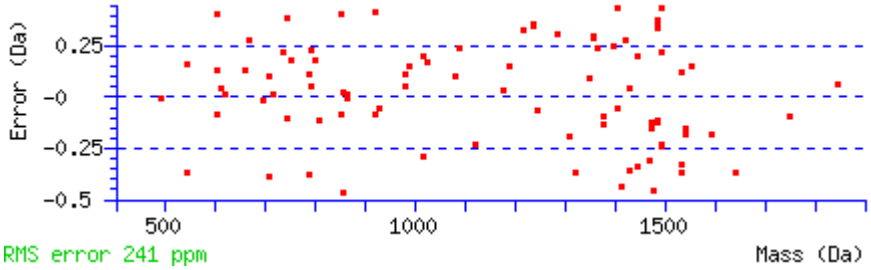
Variable modifications:

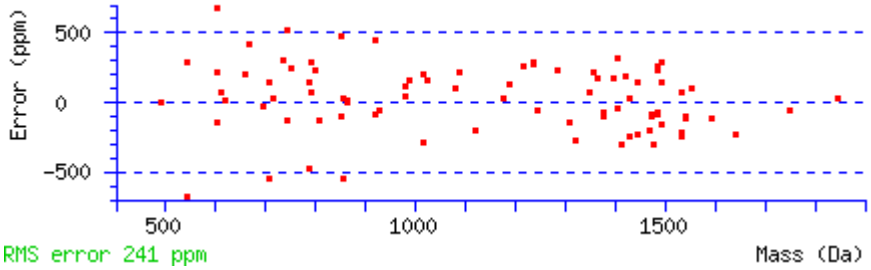
S22 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 97 Expect: 5.4e-08 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	161.0379	81.0226					C							31
2	218.0594	109.5333					G	3188.4138	1594.7105	3171.3873	1586.1973	3170.4033	1585.7053	30
3	305.0914	153.0493			287.0809	144.0441	S	3131.3924	1566.1998	3114.3658	1557.6865	3113.3818	1557.1945	29
4	362.1129	181.5601			344.1023	172.5548	G	3044.3603	1522.6838	3027.3338	1514.1705	3026.3498	1513.6785	28
5	459.1656	230.0865			441.1551	221.0812	P	2987.3389	1494.1731	2970.3123	1485.6598	2969.3283	1485.1678	27
6	558.2341	279.6207			540.2235	270.6154	V	2890.2861	1445.6467	2873.2595	1437.1334	2872.2755	1436.6414	26
7	695.2930	348.1501			677.2824	339.1448	H	2791.2177	1396.1125	2774.1911	1387.5992	2773.2071	1387.1072	25
8	808.3770	404.6922			790.3665	395.6869	I	2654.1588	1327.5830	2637.1322	1319.0697	2636.1482	1318.5777	24
9	895.4091	448.2082			877.3985	439.2029	S	2541.0747	1271.0410	2524.0482	1262.5277	2523.0641	1262.0357	23
10	952.4305	476.7189			934.4200	467.7136	G	2454.0427	1227.5250	2437.0161	1219.0117	2436.0321	1218.5197	22
11	1080.4891	540.7482	1063.4626	532.2349	1062.4785	531.7429	Q	2397.0212	1199.0142	2379.9947	1190.5010	2379.0106	1190.0090	21
12	1217.5480	609.2776	1200.5215	600.7644	1199.5375	600.2724	H	2268.9626	1134.9850	2251.9361	1126.4717	2250.9521	1125.9797	20
13	1330.6321	665.8197	1313.6055	657.3064	1312.6215	656.8144	L	2131.9037	1066.4555	2114.8772	1057.9422	2113.8932	1057.4502	19
14	1429.7005	715.3539	1412.6739	706.8406	1411.6899	706.3486	V	2018.8197	1009.9135	2001.7931	1001.4002	2000.8091	1000.9082	18
15	1500.7376	750.8724	1483.7111	742.3592	1482.7270	741.8672	A	1919.7512	960.3793	1902.7247	951.8660	1901.7407	951.3740	17
16	1599.8060	800.4066	1582.7795	791.8934	1581.7955	791.4014	V	1848.7141	924.8607	1831.6876	916.3474	1830.7036	915.8554	16
17	1728.8486	864.9279	1711.8221	856.4147	1710.8381	855.9227	E	1749.6457	875.3265	1732.6192	866.8132	1731.6352	866.3212	15
18	1857.8912	929.4492	1840.8647	920.9360	1839.8806	920.4440	E	1620.6031	810.8052	1603.5766	802.2919	1602.5926	801.7999	14
19	1972.9182	986.9627	1955.8916	978.4494	1954.9076	977.9574	D	1491.5605	746.2839	1474.5340	737.7706	1473.5500	737.2786	13
20	2043.9553	1022.4813	2026.9287	1013.9680	2025.9447	1013.4760	A	1376.5336	688.7704	1359.5070	680.2572	1358.5230	679.7652	12
21	2172.9979	1087.0026	2155.9713	1078.4893	2154.9873	1077.9973	E	1305.4965	653.2519	1288.4699	644.7386	1287.4859	644.2466	11
22	2242.0193	1121.5133	2224.9928	1113.0000	2224.0088	1112.5080	S	1176.4539	588.7306	1159.4273	580.2173	1158.4433	579.7253	10
23	2371.0619	1186.0346	2354.0354	1177.5213	2353.0514	1177.0293	E	1107.4324	554.2198	1090.4059	545.7066	1089.4219	545.2146	9
24	2486.0889	1243.5481	2469.0623	1235.0348	2468.0783	1234.5428	D	978.3898	489.6986	961.3633	481.1853	960.3793	480.6933	8
25	2615.1315	1308.0694	2598.1049	1299.5561	2597.1209	1299.0641	E	863.3629	432.1851	846.3363	423.6718	845.3523	423.1798	7
26	2730.1584	1365.5828	2713.1318	1357.0696	2712.1478	1356.5776	D	734.3203	367.6638	717.2937	359.1505	716.3097	358.6585	6
27	2859.2010	1430.1041	2842.1744	1421.5909	2841.1904	1421.0988	E	619.2933	310.1503	602.2668	301.6370	601.2828	301.1450	5

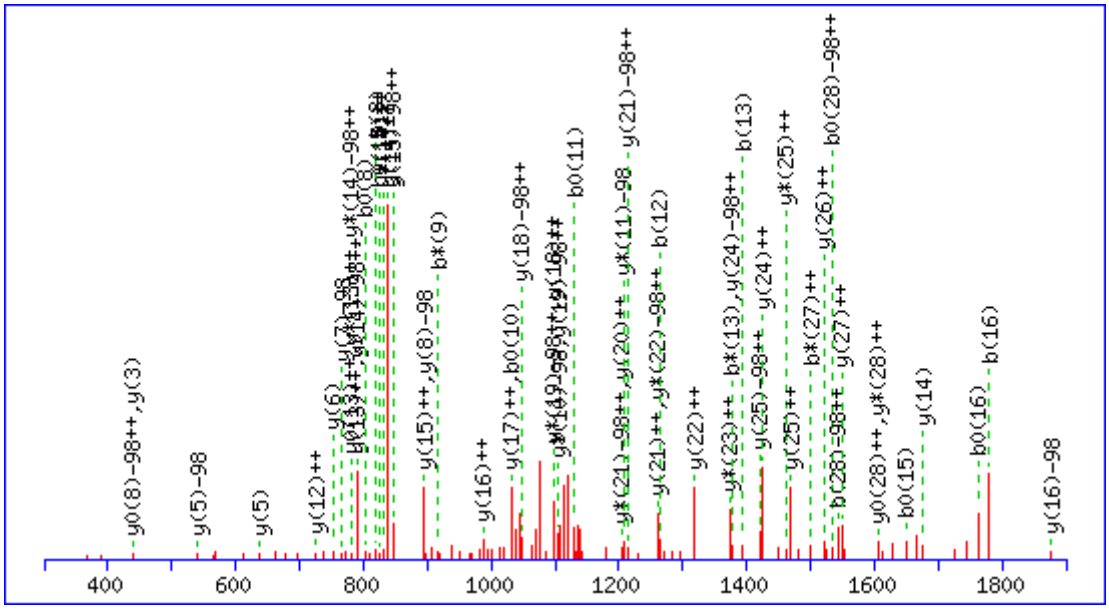
28	2988.2436	1494.6254	2971.2170	1486.1122	2970.2330	1485.6201	E	490.2508	245.6290	473.2242	237.1157	472.2402	236.6237	4
29	3103.2705	1552.1389	3086.2440	1543.6256	3085.2600	1543.1336	D	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
30	3202.3389	1601.6731	3185.3124	1593.1598	3184.3284	1592.6678	V	246.1812	123.5942	229.1547	115.0810			2
31							K	147.1128	74.0600	130.0863	65.5468			1





IDENTIFICATION 54

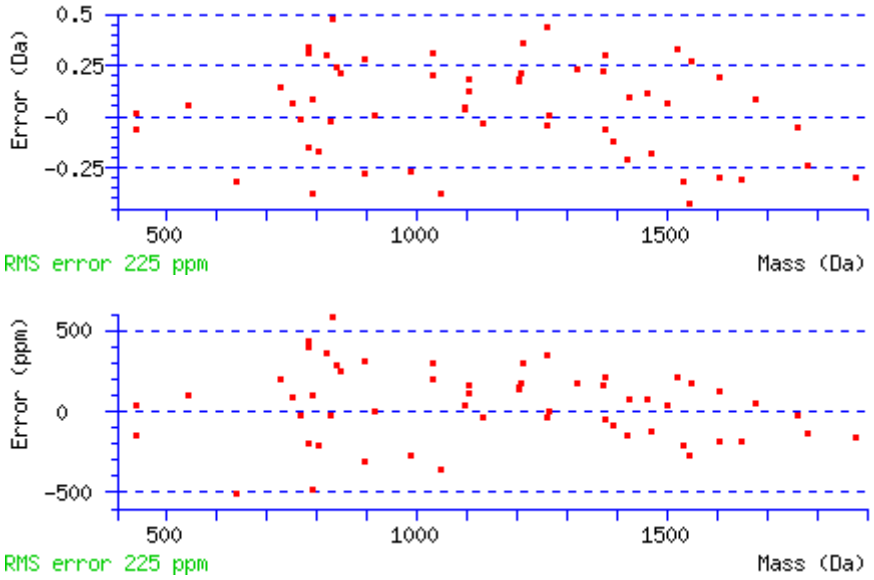
MS/MS Fragmentation of VEMGTSSQNDVDMSWIPQETLNQINKASPR
Found in IPI00755329



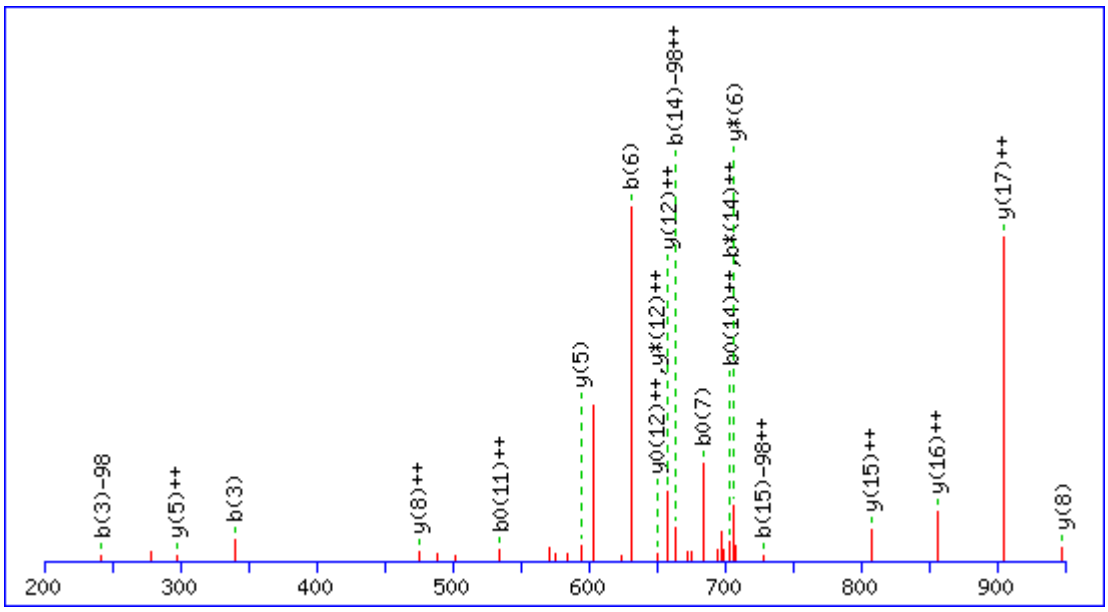
Monoisotopic mass of neutral peptide Mr(calc): 3454.5534
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S28 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 62 Expect: 0.00015 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							30
2	229.1183	115.0628			211.1077	106.0575	E	3356.4923	1678.7498	3339.4657	1670.2365	3338.4817	1669.7445	29
3	360.1588	180.5830			342.1482	171.5777	M	3227.4497	1614.2285	3210.4232	1605.7152	3209.4391	1605.2232	28
4	417.1802	209.0938			399.1697	200.0885	G	3096.4092	1548.7082	3079.3827	1540.1950	3078.3987	1539.7030	27
5	518.2279	259.6176			500.2173	250.6123	T	3039.3878	1520.1975	3022.3612	1511.6842	3021.3772	1511.1922	26
6	605.2599	303.1336			587.2494	294.1283	S	2938.3401	1469.6737	2921.3135	1461.1604	2920.3295	1460.6684	25
7	692.2920	346.6496			674.2814	337.6443	S	2851.3080	1426.1577	2834.2815	1417.6444	2833.2975	1417.1524	24
8	820.3505	410.6789	803.3240	402.1656	802.3400	401.6736	Q	2764.2760	1382.6416	2747.2495	1374.1284	2746.2655	1373.6364	23
9	934.3935	467.7004	917.3669	459.1871	916.3829	458.6951	N	2636.2174	1318.6124	2619.1909	1310.0991	2618.2069	1309.6071	22
10	1049.4204	525.2138	1032.3939	516.7006	1031.4099	516.2086	D	2522.1745	1261.5909	2505.1480	1253.0776	2504.1640	1252.5856	21
11	1148.4888	574.7481	1131.4623	566.2348	1130.4783	565.7428	V	2407.1476	1204.0774	2390.1210	1195.5641	2389.1370	1195.0721	20
12	1263.5158	632.2615	1246.4892	623.7482	1245.5052	623.2562	D	2308.0792	1154.5432	2291.0526	1146.0299	2290.0686	1145.5379	19
13	1394.5563	697.7818	1377.5297	689.2685	1376.5457	688.7765	M	2193.0522	1097.0297	2176.0257	1088.5165	2175.0417	1088.0245	18
14	1481.5883	741.2978	1464.5617	732.7845	1463.5777	732.2925	S	2062.0117	1031.5095	2044.9852	1022.9962	2044.0012	1022.5042	17
15	1667.6676	834.3374	1650.6410	825.8242	1649.6570	825.3322	W	1974.9797	987.9935	1957.9532	979.4802	1956.9691	978.9882	16
16	1780.7517	890.8795	1763.7251	882.3662	1762.7411	881.8742	I	1788.9004	894.9538	1771.8738	886.4406	1770.8898	885.9486	15
17	1877.8044	939.4059	1860.7779	930.8926	1859.7939	930.4006	P	1675.8163	838.4118	1658.7898	829.8985	1657.8058	829.4065	14
18	2005.8630	1003.4351	1988.8365	994.9219	1987.8524	994.4299	Q	1578.7636	789.8854	1561.7370	781.3721	1560.7530	780.8801	13
19	2134.9056	1067.9564	2117.8790	1059.4432	2116.8950	1058.9512	E	1450.7050	725.8561	1433.6784	717.3429	1432.6944	716.8508	12
20	2235.9533	1118.4803	2218.9267	1109.9670	2217.9427	1109.4750	T	1321.6624	661.3348	1304.6358	652.8216	1303.6518	652.3296	11
21	2349.0373	1175.0223	2332.0108	1166.5090	2331.0268	1166.0170	L	1220.6147	610.8110	1203.5882	602.2977	1202.6041	601.8057	10
22	2463.0803	1232.0438	2446.0537	1223.5305	2445.0697	1223.0385	N	1107.5306	554.2690	1090.5041	545.7557	1089.5201	545.2637	9
23	2591.1388	1296.0731	2574.1123	1287.5598	2573.1283	1287.0678	Q	993.4877	497.2475	976.4612	488.7342	975.4772	488.2422	8
24	2704.2229	1352.6151	2687.1964	1344.1018	2686.2123	1343.6098	I	865.4291	433.2182	848.4026	424.7049	847.4186	424.2129	7
25	2818.2658	1409.6366	2801.2393	1401.1233	2800.2553	1400.6313	N	752.3451	376.6762	735.3185	368.1629	734.3345	367.6709	6
26	2946.3608	1473.6840	2929.3342	1465.1708	2928.3502	1464.6788	K	638.3022	319.6547	621.2756	311.1414	620.2916	310.6494	5

27	3017.3979	1509.2026	3000.3714	1500.6893	2999.3873	1500.1973	A	510.2072	255.6072	493.1806	247.0940	492.1966	246.6020	4
28	3184.3963	1592.7018	3167.3697	1584.1885	3166.3857	1583.6965	S	439.1701	220.0887	422.1435	211.5754	421.1595	211.0834	3
29	3281.4490	1641.2282	3264.4225	1632.7149	3263.4385	1632.2229	P	272.1717	136.5895	255.1452	128.0762			2
30							R	175.1190	88.0631	158.0924	79.5498			1

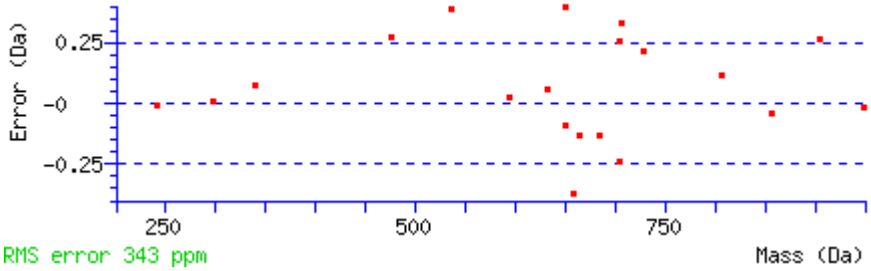


IDENTIFICATION 55
MS/MS Fragmentation of SATPPPAEPASLPQEPPKPR
Found in IPI00331295



Monoisotopic mass of neutral peptide Mr(calc): 2146.0459 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 38 Expect: 0.019 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							20
2	159.0764	80.0418			141.0659	71.0366	A	2060.0212	1030.5143	2042.9947	1022.0010	2042.0107	1021.5090	19
3	340.0904	170.5489			322.0799	161.5436	T	1988.9841	994.9957	1971.9576	986.4824	1970.9736	985.9904	18
4	437.1432	219.0752			419.1326	210.0700	P	1807.9701	904.4887	1790.9436	895.9754	1789.9595	895.4834	17
5	534.1960	267.6016			516.1854	258.5963	P	1710.9173	855.9623	1693.8908	847.4490	1692.9068	846.9570	16
6	631.2487	316.1280			613.2382	307.1227	P	1613.8646	807.4359	1596.8380	798.9227	1595.8540	798.4306	15
7	702.2858	351.6466			684.2753	342.6413	A	1516.8118	758.9095	1499.7853	750.3963	1498.8013	749.9043	14
8	831.3284	416.1679			813.3179	407.1626	E	1445.7747	723.3910	1428.7482	714.8777	1427.7641	714.3857	13
9	928.3812	464.6942			910.3706	455.6890	P	1316.7321	658.8697	1299.7056	650.3564	1298.7215	649.8644	12
10	999.4183	500.2128			981.4077	491.2075	A	1219.6793	610.3433	1202.6528	601.8300	1201.6688	601.3380	11
11	1086.4503	543.7288			1068.4398	534.7235	S	1148.6422	574.8248	1131.6157	566.3115	1130.6317	565.8195	10
12	1199.5344	600.2708			1181.5238	591.2656	L	1061.6102	531.3087	1044.5837	522.7955	1043.5996	522.3035	9
13	1296.5872	648.7972			1278.5766	639.7919	P	948.5261	474.7667	931.4996	466.2534	930.5156	465.7614	8
14	1424.6457	712.8265	1407.6192	704.3132	1406.6352	703.8212	Q	851.4734	426.2403	834.4468	417.7271	833.4628	417.2350	7
15	1553.6883	777.3478	1536.6618	768.8345	1535.6778	768.3425	E	723.4148	362.2110	706.3883	353.6978	705.4042	353.2058	6
16	1650.7411	825.8742	1633.7145	817.3609	1632.7305	816.8689	P	594.3722	297.6897	577.3457	289.1765			5
17	1747.7939	874.4006	1730.7673	865.8873	1729.7833	865.3953	P	497.3194	249.1634	480.2929	240.6501			4
18	1875.8888	938.4480	1858.8623	929.9348	1857.8783	929.4428	K	400.2667	200.6370	383.2401	192.1237			3
19	1972.9416	986.9744	1955.9150	978.4612	1954.9310	977.9691	P	272.1717	136.5895	255.1452	128.0762			2
20							R	175.1190	88.0631	158.0924	79.5498			1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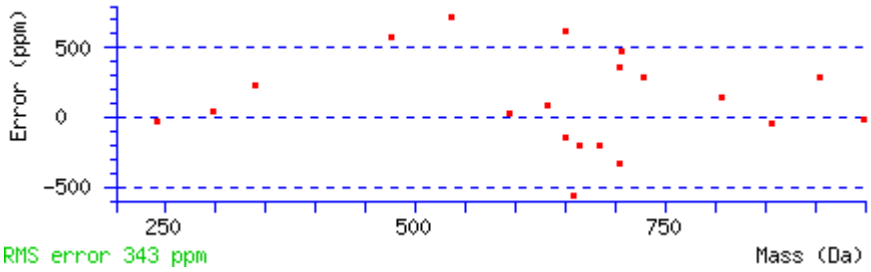
750
RMS error 343 ppm
Mass (Da)


Error (ppm)
500
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250
500
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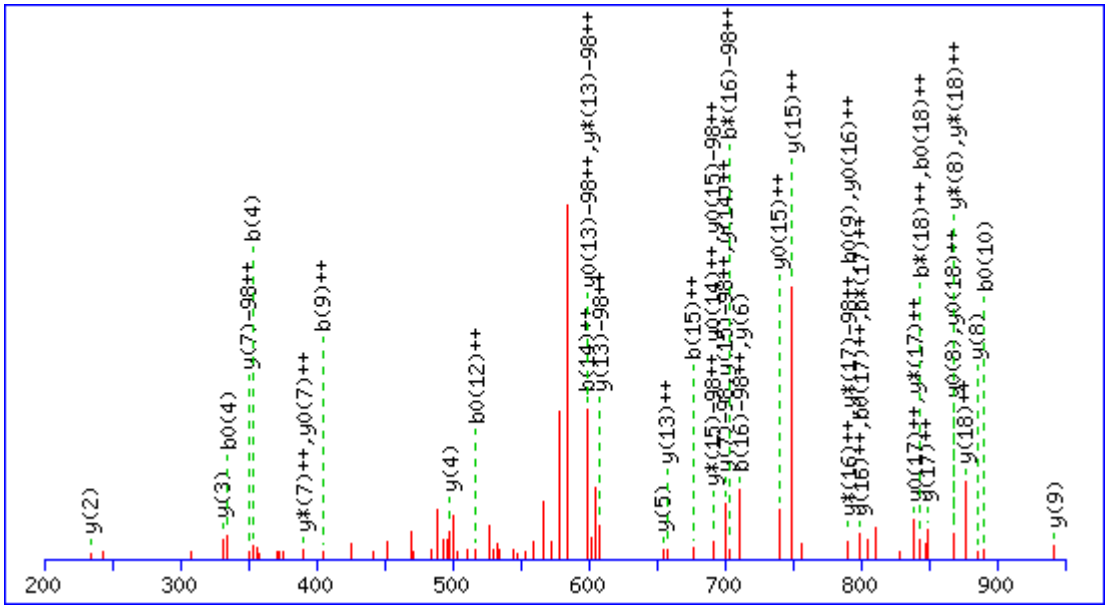
RMS error 343 ppm
Mass (Da)

IDENTIFICATION 56
MS/MS Fragmentation of

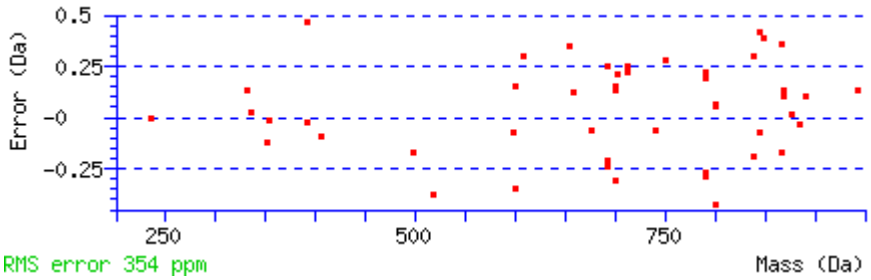
PGPTPSGTNVGSSGRSPSK

Found in IPI00133030

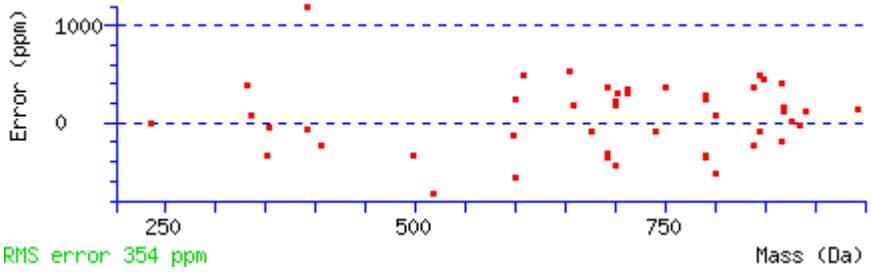


Monoisotopic mass of neutral peptide Mr(calc): 1848.8367 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 38 Expect: 0.028 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	98.0600	49.5337					P							19
2	155.0815	78.0444					G	1752.7912	876.8993	1735.7647	868.3860	1734.7807	867.8940	18
3	252.1343	126.5708					P	1695.7698	848.3885	1678.7432	839.8752	1677.7592	839.3832	17
4	353.1819	177.0946			335.1714	168.0893	T	1598.7170	799.8621	1581.6905	791.3489	1580.7064	790.8569	16
5	450.2347	225.6210			432.2241	216.6157	P	1497.6693	749.3383	1480.6428	740.8250	1479.6588	740.3330	15
6	537.2667	269.1370			519.2562	260.1317	S	1400.6166	700.8119	1383.5900	692.2986	1382.6060	691.8066	14
7	594.2882	297.6477			576.2776	288.6425	G	1313.5845	657.2959	1296.5580	648.7826	1295.5740	648.2906	13
8	695.3359	348.1716			677.3253	339.1663	T	1256.5631	628.7852	1239.5365	620.2719	1238.5525	619.7799	12
9	809.3788	405.1930	792.3523	396.6798	791.3682	396.1878	N	1155.5154	578.2613	1138.4888	569.7481	1137.5048	569.2561	11
10	908.4472	454.7272	891.4207	446.2140	890.4367	445.7220	V	1041.4725	521.2399	1024.4459	512.7266	1023.4619	512.2346	10
11	965.4687	483.2380	948.4421	474.7247	947.4581	474.2327	G	942.4041	471.7057	925.3775	463.1924	924.3935	462.7004	9
12	1052.5007	526.7540	1035.4742	518.2407	1034.4902	517.7487	S	885.3826	443.1949	868.3560	434.6817	867.3720	434.1896	8
13	1139.5327	570.2700	1122.5062	561.7567	1121.5222	561.2647	S	798.3506	399.6789	781.3240	391.1656	780.3400	390.6736	7
14	1196.5542	598.7807	1179.5277	590.2675	1178.5436	589.7755	G	711.3185	356.1629	694.2920	347.6496	693.3080	347.1576	6
15	1352.6553	676.8313	1335.6288	668.3180	1334.6448	667.8260	R	654.2971	327.6522	637.2705	319.1389	636.2865	318.6469	5
16	1519.6537	760.3305	1502.6271	751.8172	1501.6431	751.3252	S	498.1960	249.6016	481.1694	241.0883	480.1854	240.5963	4
17	1616.7064	808.8569	1599.6799	800.3436	1598.6959	799.8516	P	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	3
18	1703.7385	852.3729	1686.7119	843.8596	1685.7279	843.3676	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
19							K	147.1128	74.0600	130.0863	65.5468			1

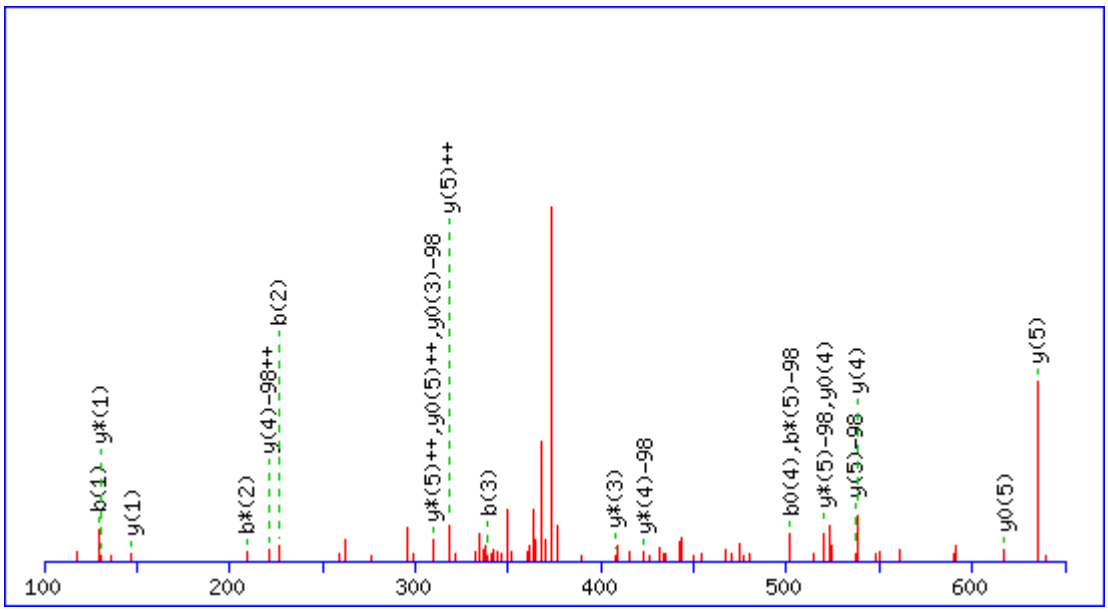


RMS error 354 ppm



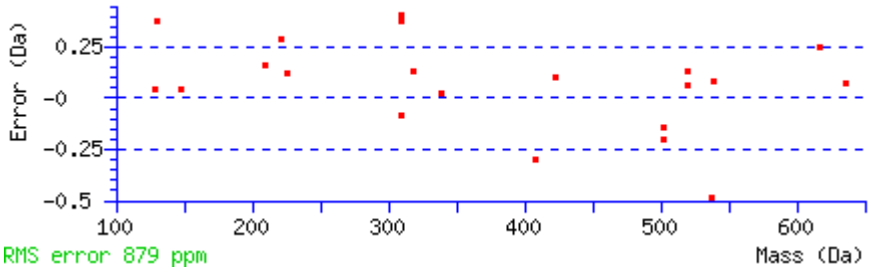
RMS error 354 ppm

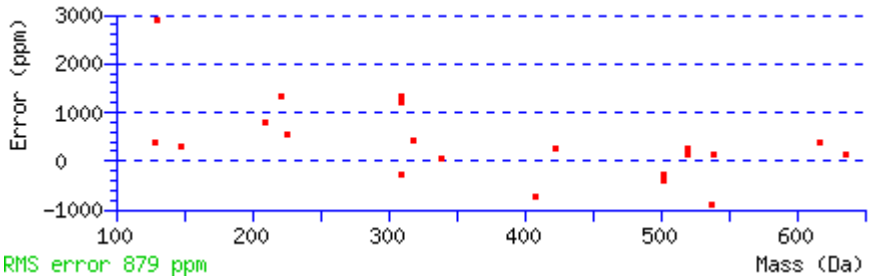
IDENTIFICATION 57
MS/MS Fragmentation of KPLTPK
Found in IPI00122273



Monoisotopic mass of neutral peptide Mr(calc): 762.4041
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 19 Expect: 0.87 (help)

#	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							6
2	226.1550	113.5811	209.1285	105.0679			P	635.3164	318.1618	618.2899	309.6486	617.3058	309.1566	5
3	339.2391	170.1232	322.2125	161.6099			L	538.2636	269.6355	521.2371	261.1222	520.2531	260.6302	4
4	520.2531	260.6302	503.2265	252.1169	502.2425	251.6249	T	425.1796	213.0934	408.1530	204.5802	407.1690	204.0881	3
5	617.3058	309.1566	600.2793	300.6433	599.2953	300.1513	P	244.1656	122.5864	227.1390	114.0731			2
6							K	147.1128	74.0600	130.0863	65.5468			1

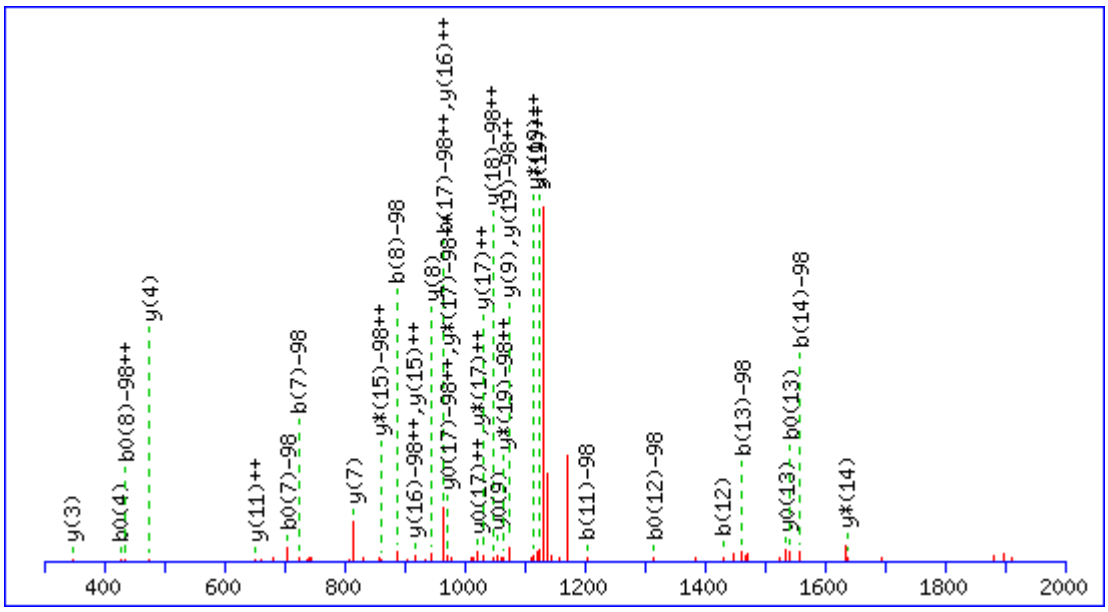




IDENTIFICATION 58

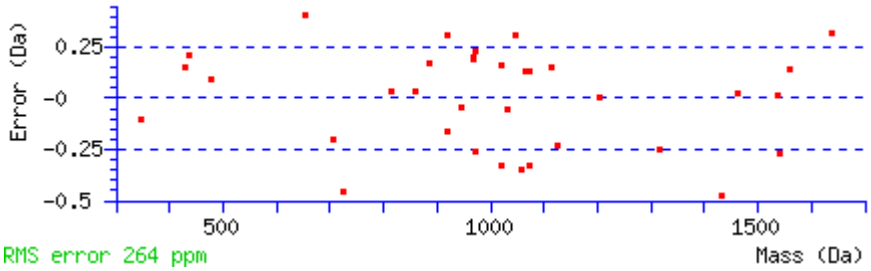
MS/MS Fragmentation of EGEEPTVYSDDEEPKDETAR

Found in IPI00319973



Monoisotopic mass of neutral peptide Mr(calc): 2374.9326 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: T6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 30 Expect: 0.19 (help)

#	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							20
2	187.0713	94.0393			169.0608	85.0340	G	2148.9204	1074.9638	2131.8938	1066.4506	2130.9098	1065.9585	19
3	316.1139	158.5606			298.1034	149.5553	E	2091.8989	1046.4531	2074.8724	1037.9398	2073.8883	1037.4478	18
4	445.1565	223.0819			427.1460	214.0766	E	1962.8563	981.9318	1945.8298	973.4185	1944.8458	972.9265	17
5	542.2093	271.6083			524.1987	262.6030	P	1833.8137	917.4105	1816.7872	908.8972	1815.8032	908.4052	16
6	625.2464	313.1268			607.2358	304.1216	T	1736.7610	868.8841	1719.7344	860.3708	1718.7504	859.8788	15
7	724.3148	362.6610			706.3042	353.6558	V	1653.7239	827.3656	1636.6973	818.8523	1635.7133	818.3603	14
8	887.3781	444.1927			869.3676	435.1874	Y	1554.6554	777.8314	1537.6289	769.3181	1536.6449	768.8261	13
9	974.4102	487.7087			956.3996	478.7034	S	1391.5921	696.2997	1374.5656	687.7864	1373.5815	687.2944	12
10	1089.4371	545.2222			1071.4265	536.2169	D	1304.5601	652.7837	1287.5335	644.2704	1286.5495	643.7784	11
11	1204.4641	602.7357			1186.4535	593.7304	D	1189.5331	595.2702	1172.5066	586.7569	1171.5226	586.2649	10
12	1333.5066	667.2570			1315.4961	658.2517	E	1074.5062	537.7567	1057.4796	529.2435	1056.4956	528.7515	9
13	1462.5492	731.7783			1444.5387	722.7730	E	945.4636	473.2354	928.4371	464.7222	927.4530	464.2302	8
14	1559.6020	780.3046			1541.5914	771.2994	P	816.4210	408.7141	799.3945	400.2009	798.4104	399.7089	7
15	1687.6970	844.3521	1670.6704	835.8388	1669.6864	835.3468	K	719.3682	360.1878	702.3417	351.6745	701.3577	351.1825	6
16	1802.7239	901.8656	1785.6974	893.3523	1784.7133	892.8603	D	591.2733	296.1403	574.2467	287.6270	573.2627	287.1350	5
17	1931.7665	966.3869	1914.7400	957.8736	1913.7559	957.3816	E	476.2463	238.6268	459.2198	230.1135	458.2358	229.6215	4
18	2032.8142	1016.9107	2015.7876	1008.3975	2014.8036	1007.9054	T	347.2037	174.1055	330.1772	165.5922	329.1932	165.1002	3
19	2103.8513	1052.4293	2086.8247	1043.9160	2085.8407	1043.4240	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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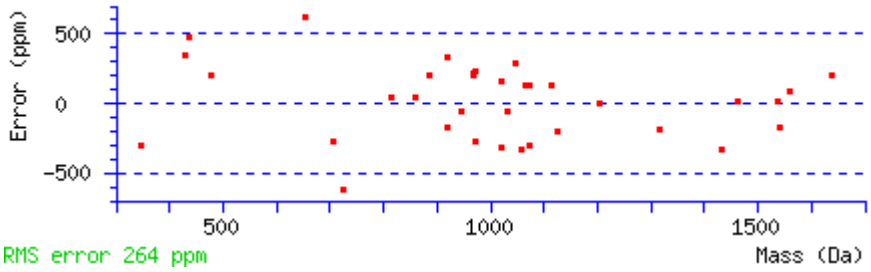
Mass (Da)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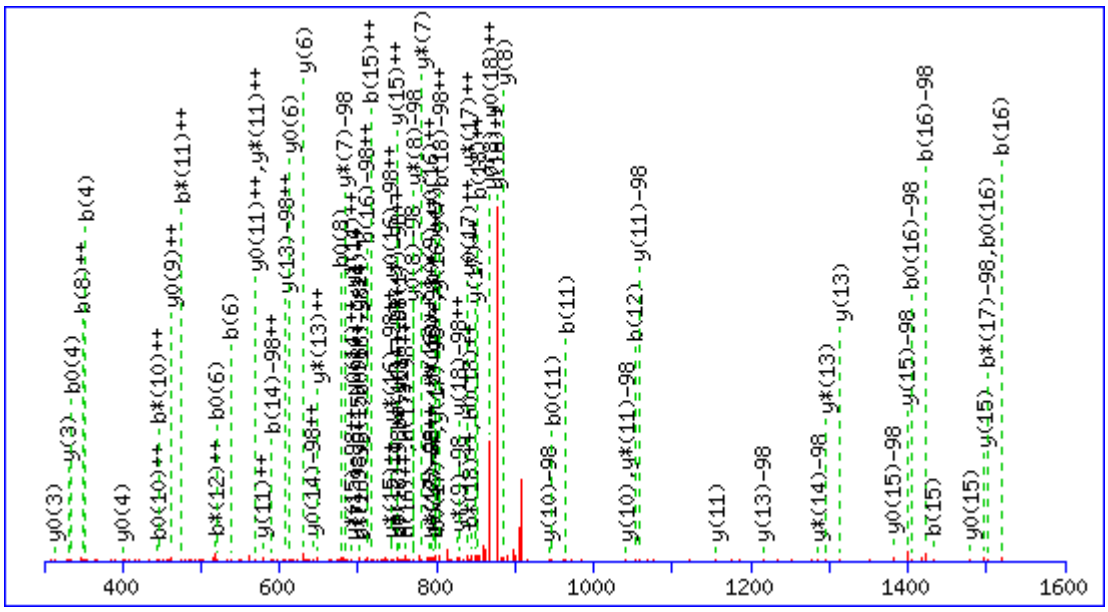
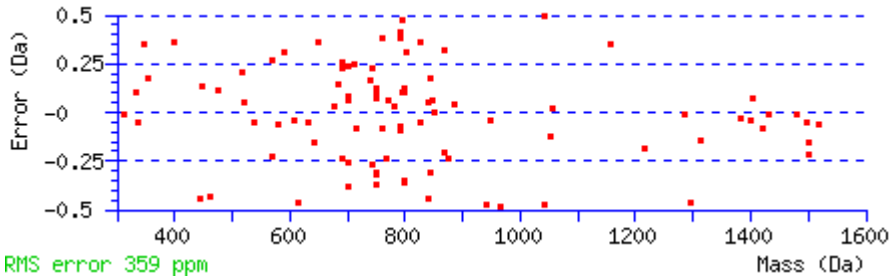
RMS error 264 ppm
Mass (Da)

IDENTIFICATION 59
MS/MS Fragmentation of PGPTPSGTNVGSSGRSPSK
Found in IPI00133030



Monoisotopic mass of neutral peptide Mr(calc): 1848.8367
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.062 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	98.0600	49.5337					P							19
2	155.0815	78.0444					G	1654.8143	827.9108	1637.7878	819.3975	1636.8038	818.9055	18
3	252.1343	126.5708					P	1597.7929	799.4001	1580.7663	790.8868	1579.7823	790.3948	17
4	353.1819	177.0946			335.1714	168.0893	T	1500.7401	750.8737	1483.7136	742.3604	1482.7295	741.8684	16
5	450.2347	225.6210			432.2241	216.6157	P	1399.6924	700.3499	1382.6659	691.8366	1381.6819	691.3446	15
6	537.2667	269.1370			519.2562	260.1317	S	1302.6397	651.8235	1285.6131	643.3102	1284.6291	642.8182	14
7	594.2882	297.6477			576.2776	288.6425	G	1215.6076	608.3075	1198.5811	599.7942	1197.5971	599.3022	13
8	695.3359	348.1716			677.3253	339.1663	T	1158.5862	579.7967	1141.5596	571.2835	1140.5756	570.7914	12
9	809.3788	405.1930	792.3523	396.6798	791.3682	396.1878	N	1057.5385	529.2729	1040.5119	520.7596	1039.5279	520.2676	11
10	908.4472	454.7272	891.4207	446.2140	890.4367	445.7220	V	943.4956	472.2514	926.4690	463.7381	925.4850	463.2461	10
11	965.4687	483.2380	948.4421	474.7247	947.4581	474.2327	G	844.4272	422.7172	827.4006	414.2039	826.4166	413.7119	9
12	1052.5007	526.7540	1035.4742	518.2407	1034.4902	517.7487	S	787.4057	394.2065	770.3791	385.6932	769.3951	385.2012	8
13	1121.5222	561.2647	1104.4956	552.7515	1103.5116	552.2594	S	700.3737	350.6905	683.3471	342.1772	682.3631	341.6852	7
14	1178.5436	589.7755	1161.5171	581.2622	1160.5331	580.7702	G	631.3522	316.1797	614.3257	307.6665	613.3416	307.1745	6
15	1334.6448	667.8260	1317.6182	659.3127	1316.6342	658.8207	R	574.3307	287.6690	557.3042	279.1557	556.3202	278.6637	5
16	1421.6768	711.3420	1404.6502	702.8288	1403.6662	702.3367	S	418.2296	209.6185	401.2031	201.1052	400.2191	200.6132	4
17	1518.7295	759.8684	1501.7030	751.3551	1500.7190	750.8631	P	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	3
18	1605.7616	803.3844	1588.7350	794.8712	1587.7510	794.3791	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
19							K	147.1128	74.0600	130.0863	65.5468			1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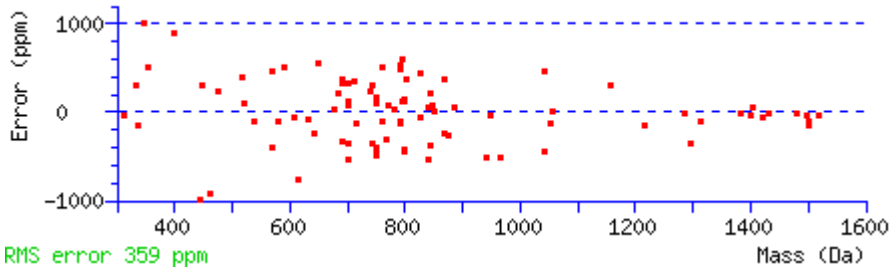
Mass (Da)
RMS error 359 ppm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Error (ppm)
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Mass (Da)
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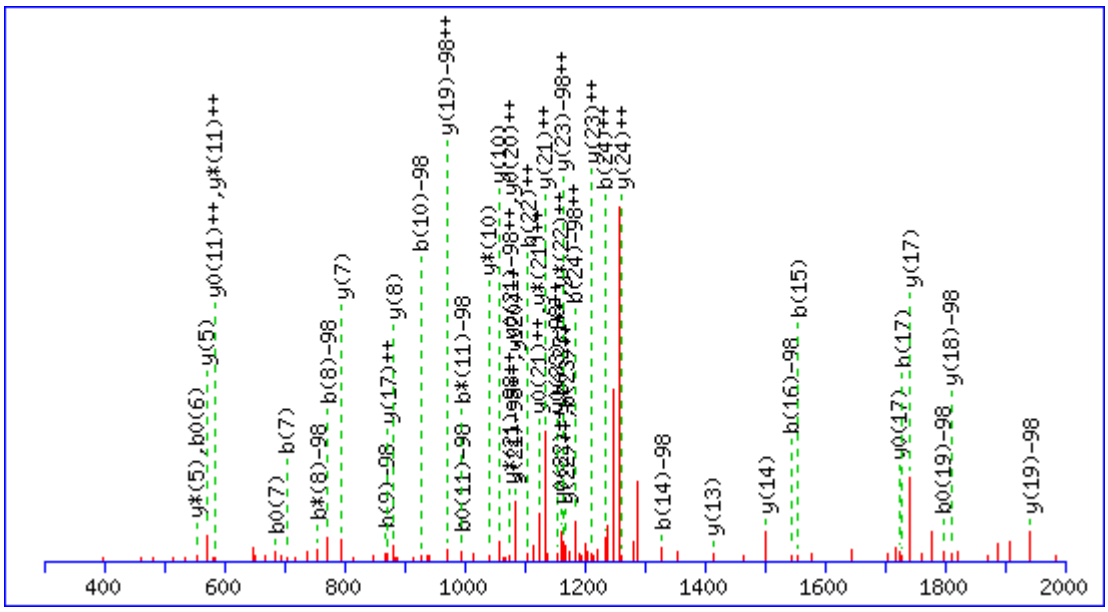
IDENTIFICATION 60

MS/MS Fragmentation of STSAPQMSPGSSDNQSSSPQPAQQK

Found in IPI00407835



Monoisotopic mass of neutral peptide Mr(calc): 2611.0857

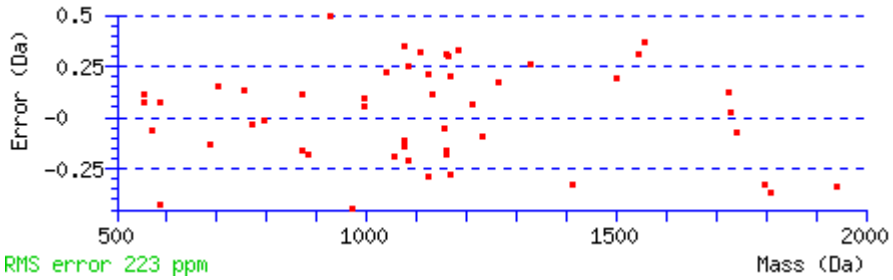
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

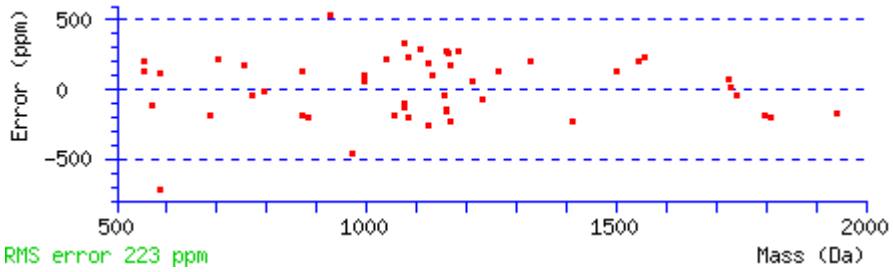
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 43 Expect: 0.01 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							25
2	189.0870	95.0471			171.0764	86.0418	T	2427.0841	1214.0457	2410.0576	1205.5324	2409.0735	1205.0404	24
3	276.1190	138.5631			258.1084	129.5579	S	2326.0364	1163.5219	2309.0099	1155.0086	2308.0259	1154.5166	23
4	347.1561	174.0817			329.1456	165.0764	A	2239.0044	1120.0058	2221.9779	1111.4926	2220.9938	1111.0006	22
5	444.2089	222.6081			426.1983	213.6028	P	2167.9673	1084.4873	2150.9407	1075.9740	2149.9567	1075.4820	21
6	572.2675	286.6374	555.2409	278.1241	554.2569	277.6321	Q	2070.9145	1035.9609	2053.8880	1027.4476	2052.9040	1026.9556	20
7	703.3080	352.1576	686.2814	343.6443	685.2974	343.1523	M	1942.8559	971.9316	1925.8294	963.4183	1924.8454	962.9263	19
8	772.3294	386.6683	755.3029	378.1551	754.3188	377.6631	S	1811.8155	906.4114	1794.7889	897.8981	1793.8049	897.4061	18
9	869.3822	435.1947	852.3556	426.6815	851.3716	426.1894	P	1742.7940	871.9006	1725.7674	863.3874	1724.7834	862.8954	17
10	926.4036	463.7055	909.3771	455.1922	908.3931	454.7002	G	1645.7412	823.3743	1628.7147	814.8610	1627.7307	814.3690	16
11	1013.4357	507.2215	996.4091	498.7082	995.4251	498.2162	S	1588.7198	794.8635	1571.6932	786.3502	1570.7092	785.8582	15
12	1100.4677	550.7375	1083.4412	542.2242	1082.4571	541.7322	S	1501.6877	751.3475	1484.6612	742.8342	1483.6772	742.3422	14
13	1215.4946	608.2510	1198.4681	599.7377	1197.4841	599.2457	D	1414.6557	707.8315	1397.6292	699.3182	1396.6451	698.8262	13
14	1329.5376	665.2724	1312.5110	656.7591	1311.5270	656.2671	N	1299.6288	650.3180	1282.6022	641.8047	1281.6182	641.3127	12
15	1457.5961	729.3017	1440.5696	720.7884	1439.5856	720.2964	Q	1185.5858	593.2966	1168.5593	584.7833	1167.5753	584.2913	11
16	1544.6282	772.8177	1527.6016	764.3045	1526.6176	763.8124	S	1057.5273	529.2673	1040.5007	520.7540	1039.5167	520.2620	10
17	1631.6602	816.3337	1614.6337	807.8205	1613.6496	807.3285	S	970.4952	485.7513	953.4687	477.2380	952.4847	476.7460	9
18	1718.6922	859.8498	1701.6657	851.3365	1700.6817	850.8445	S	883.4632	442.2352	866.4367	433.7220	865.4526	433.2300	8
19	1815.7450	908.3761	1798.7184	899.8629	1797.7344	899.3709	P	796.4312	398.7192	779.4046	390.2060			7
20	1943.8036	972.4054	1926.7770	963.8922	1925.7930	963.4001	Q	699.3784	350.1928	682.3519	341.6796			6
21	2040.8563	1020.9318	2023.8298	1012.4185	2022.8458	1011.9265	P	571.3198	286.1636	554.2933	277.6503			5
22	2111.8935	1056.4504	2094.8669	1047.9371	2093.8829	1047.4451	A	474.2671	237.6372	457.2405	229.1239			4
23	2239.9520	1120.4797	2222.9255	1111.9664	2221.9415	1111.4744	Q	403.2300	202.1186	386.2034	193.6053			3
24	2368.0106	1184.5089	2350.9841	1175.9957	2350.0000	1175.5037	Q	275.1714	138.0893	258.1448	129.5761			2
25							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 223 ppm



RMS error 223 ppm

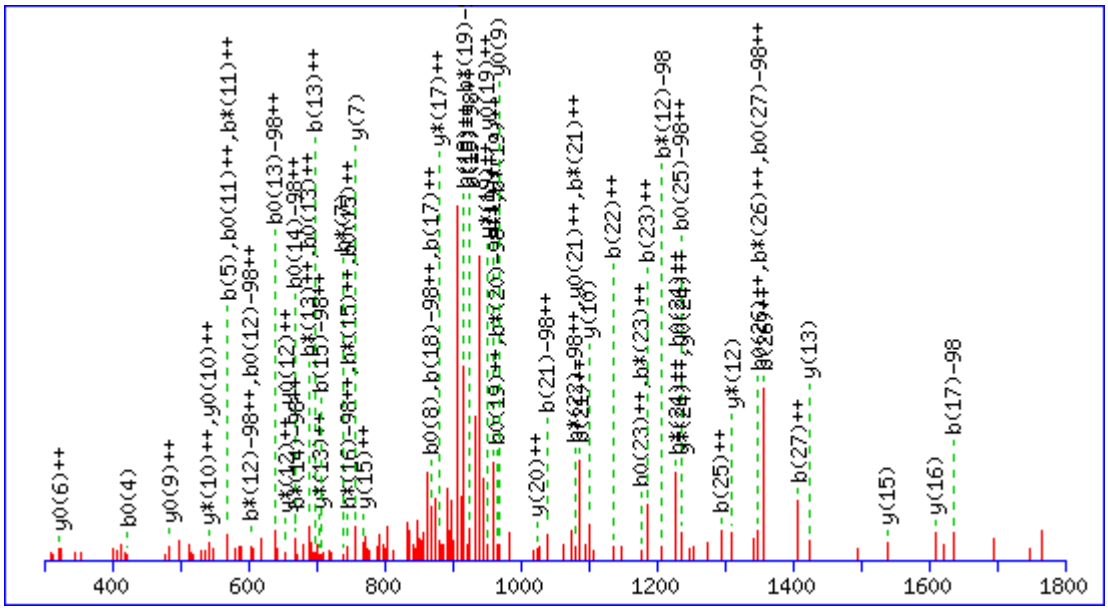
IDENTIFICATION 61

MS/MS Fragmentation of

KKPSEGEEEAASAGGPQVNPMPVTDEVV

Found in

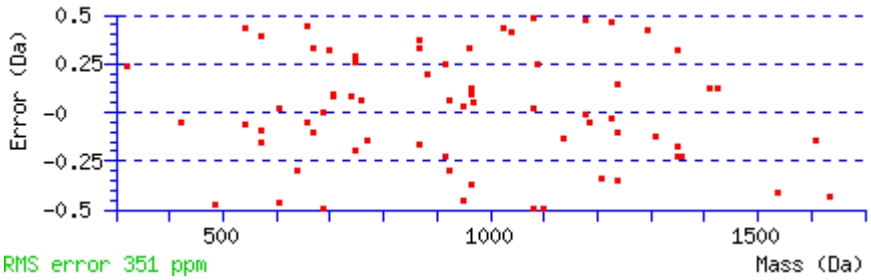
IPI00222418

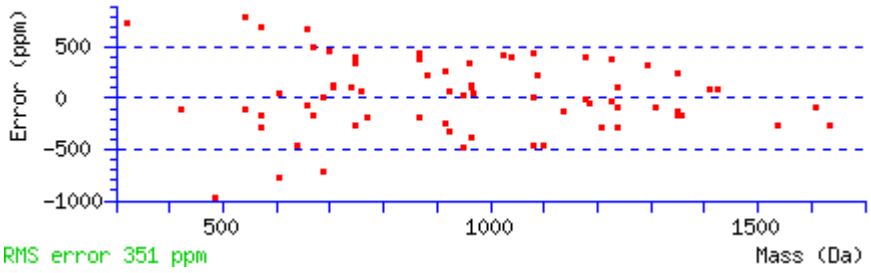


Monoisotopic mass of neutral peptide Mr(calc): 2931.3209
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S12 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.38 (help)

#	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							28
2	257.1972	129.1022	240.1707	120.5890			K	2804.2332	1402.6202	2787.2067	1394.1070	2786.2226	1393.6150	27
3	354.2500	177.6286	337.2234	169.1153			P	2676.1383	1338.5728	2659.1117	1330.0595	2658.1277	1329.5675	26
4	441.2820	221.1446	424.2554	212.6314	423.2714	212.1394	S	2579.0855	1290.0464	2562.0589	1281.5331	2561.0749	1281.0411	25
5	570.3246	285.6659	553.2980	277.1527	552.3140	276.6606	E	2492.0535	1246.5304	2475.0269	1238.0171	2474.0429	1237.5251	24
6	627.3461	314.1767	610.3195	305.6634	609.3355	305.1714	G	2363.0109	1182.0091	2345.9843	1173.4958	2345.0003	1173.0038	23
7	756.3886	378.6980	739.3621	370.1847	738.3781	369.6927	E	2305.9894	1153.4983	2288.9629	1144.9851	2287.9788	1144.4931	22
8	885.4312	443.2193	868.4047	434.7060	867.4207	434.2140	E	2176.9468	1088.9770	2159.9203	1080.4638	2158.9362	1079.9718	21
9	1014.4738	507.7406	997.4473	499.2273	996.4633	498.7353	E	2047.9042	1024.4557	2030.8777	1015.9425	2029.8937	1015.4505	20
10	1085.5109	543.2591	1068.4844	534.7458	1067.5004	534.2538	A	1918.8616	959.9344	1901.8351	951.4212	1900.8511	950.9292	19
11	1156.5481	578.7777	1139.5215	570.2644	1138.5375	569.7724	A	1847.8245	924.4159	1830.7980	915.9026	1829.8139	915.4106	18
12	1323.5464	662.2768	1306.5199	653.7636	1305.5359	653.2716	S	1776.7874	888.8973	1759.7608	880.3841	1758.7768	879.8921	17

13	1394.5835	697.7954	1377.5570	689.2821	1376.5730	688.7901	A	1609.7890	805.3982	1592.7625	796.8849	1591.7785	796.3929	16
14	1451.6050	726.3061	1434.5784	717.7929	1433.5944	717.3009	G	1538.7519	769.8796	1521.7254	761.3663	1520.7414	760.8743	15
15	1508.6265	754.8169	1491.5999	746.3036	1490.6159	745.8116	G	1481.7305	741.3689	1464.7039	732.8556	1463.7199	732.3636	14
16	1605.6792	803.3432	1588.6527	794.8300	1587.6687	794.3380	P	1424.7090	712.8581	1407.6824	704.3449	1406.6984	703.8529	13
17	1733.7378	867.3725	1716.7113	858.8593	1715.7272	858.3673	Q	1327.6562	664.3318	1310.6297	655.8185	1309.6457	655.3265	12
18	1832.8062	916.9067	1815.7797	908.3935	1814.7957	907.9015	V	1199.5977	600.3025	1182.5711	591.7892	1181.5871	591.2972	11
19	1946.8491	973.9282	1929.8226	965.4149	1928.8386	964.9229	N	1100.5292	550.7683	1083.5027	542.2550	1082.5187	541.7630	10
20	2043.9019	1022.4546	2026.8754	1013.9413	2025.8913	1013.4493	P	986.4863	493.7468			968.4757	484.7415	9
21	2174.9424	1087.9748	2157.9158	1079.4616	2156.9318	1078.9696	M	889.4335	445.2204			871.4230	436.2151	8
22	2271.9952	1136.5012	2254.9686	1127.9879	2253.9846	1127.4959	P	758.3931	379.7002			740.3825	370.6949	7
23	2371.0636	1186.0354	2354.0370	1177.5221	2353.0530	1177.0301	V	661.3403	331.1738			643.3297	322.1685	6
24	2472.1112	1236.5593	2455.0847	1228.0460	2454.1007	1227.5540	T	562.2719	281.6396			544.2613	272.6343	5
25	2587.1382	1294.0727	2570.1116	1285.5595	2569.1276	1285.0675	D	461.2242	231.1157			443.2136	222.1105	4
26	2716.1808	1358.5940	2699.1542	1350.0808	2698.1702	1349.5887	E	346.1973	173.6023			328.1867	164.5970	3
27	2815.2492	1408.1282	2798.2226	1399.6150	2797.2386	1399.1230	V	217.1547	109.0810					2
28							V	118.0863	59.5468					1

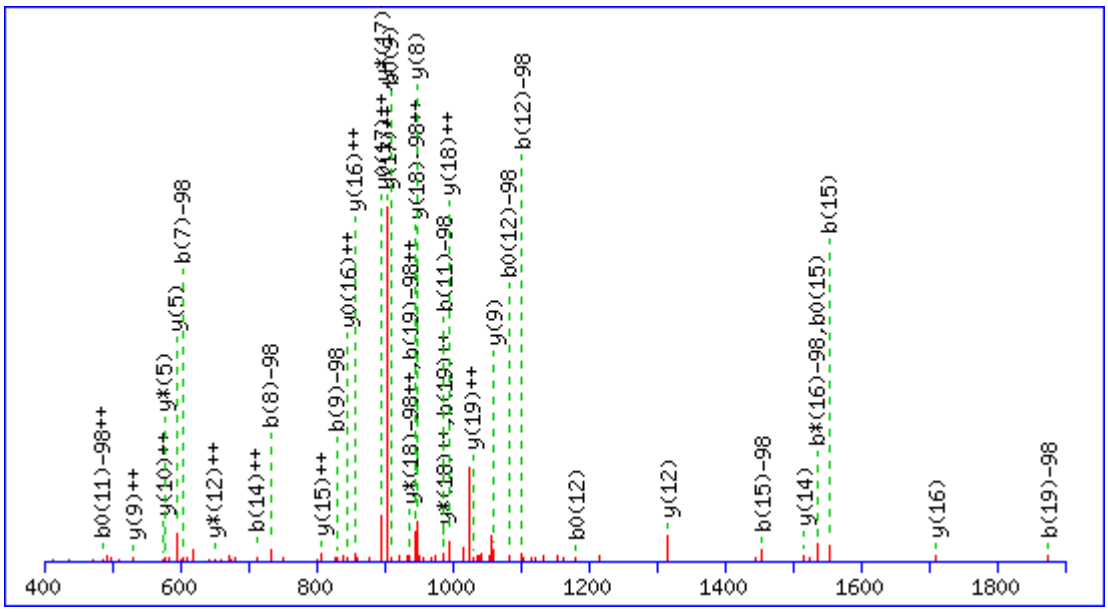




IDENTIFICATION 62

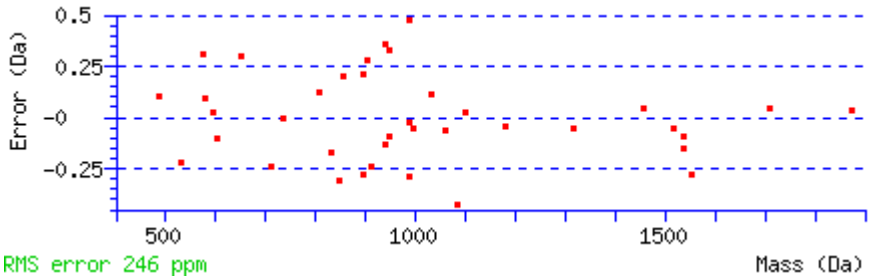
MS/MS Fragmentation of SATPPPAEPASLPQEPPKPR

Found in IPI00331295

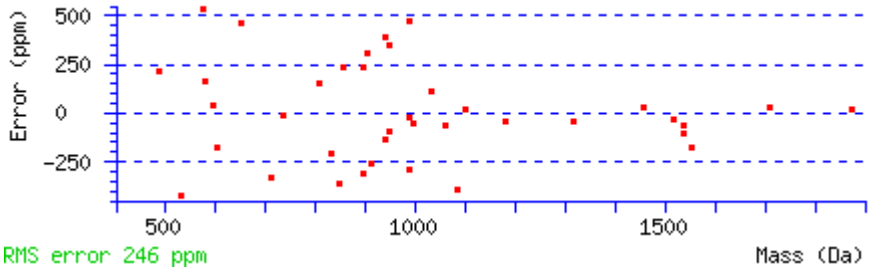


Monoisotopic mass of neutral peptide Mr(calc): 2146.0459 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 36 Expect: 0.028 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							20
2	159.0764	80.0418			141.0659	71.0366	A	1962.0443	981.5258	1945.0178	973.0125	1944.0338	972.5205	19
3	242.1135	121.5604			224.1030	112.5551	T	1891.0072	946.0073	1873.9807	937.4940	1872.9967	937.0020	18
4	339.1663	170.0868			321.1557	161.0815	P	1807.9701	904.4887	1790.9436	895.9754	1789.9595	895.4834	17
5	436.2191	218.6132			418.2085	209.6079	P	1710.9173	855.9623	1693.8908	847.4490	1692.9068	846.9570	16
6	533.2718	267.1396			515.2613	258.1343	P	1613.8646	807.4359	1596.8380	798.9227	1595.8540	798.4306	15
7	604.3089	302.6581			586.2984	293.6528	A	1516.8118	758.9095	1499.7853	750.3963	1498.8013	749.9043	14
8	733.3515	367.1794			715.3410	358.1741	E	1445.7747	723.3910	1428.7482	714.8777	1427.7641	714.3857	13
9	830.4043	415.7058			812.3937	406.7005	P	1316.7321	658.8697	1299.7056	650.3564	1298.7215	649.8644	12
10	901.4414	451.2243			883.4308	442.2191	A	1219.6793	610.3433	1202.6528	601.8300	1201.6688	601.3380	11
11	988.4734	494.7404			970.4629	485.7351	S	1148.6422	574.8248	1131.6157	566.3115	1130.6317	565.8195	10
12	1101.5575	551.2824			1083.5469	542.2771	L	1061.6102	531.3087	1044.5837	522.7955	1043.5996	522.3035	9
13	1198.6103	599.8088			1180.5997	590.8035	P	948.5261	474.7667	931.4996	466.2534	930.5156	465.7614	8
14	1326.6688	663.8381	1309.6423	655.3248	1308.6583	654.8328	Q	851.4734	426.2403	834.4468	417.7271	833.4628	417.2350	7
15	1455.7114	728.3594	1438.6849	719.8461	1437.7009	719.3541	E	723.4148	362.2110	706.3883	353.6978	705.4042	353.2058	6
16	1552.7642	776.8857	1535.7377	768.3725	1534.7536	767.8805	P	594.3722	297.6897	577.3457	289.1765			5
17	1649.8170	825.4121	1632.7904	816.8988	1631.8064	816.4068	P	497.3194	249.1634	480.2929	240.6501			4
18	1777.9119	889.4596	1760.8854	880.9463	1759.9014	880.4543	K	400.2667	200.6370	383.2401	192.1237			3
19	1874.9647	937.9860	1857.9381	929.4727	1856.9541	928.9807	P	272.1717	136.5895	255.1452	128.0762			2
20							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 246 ppm

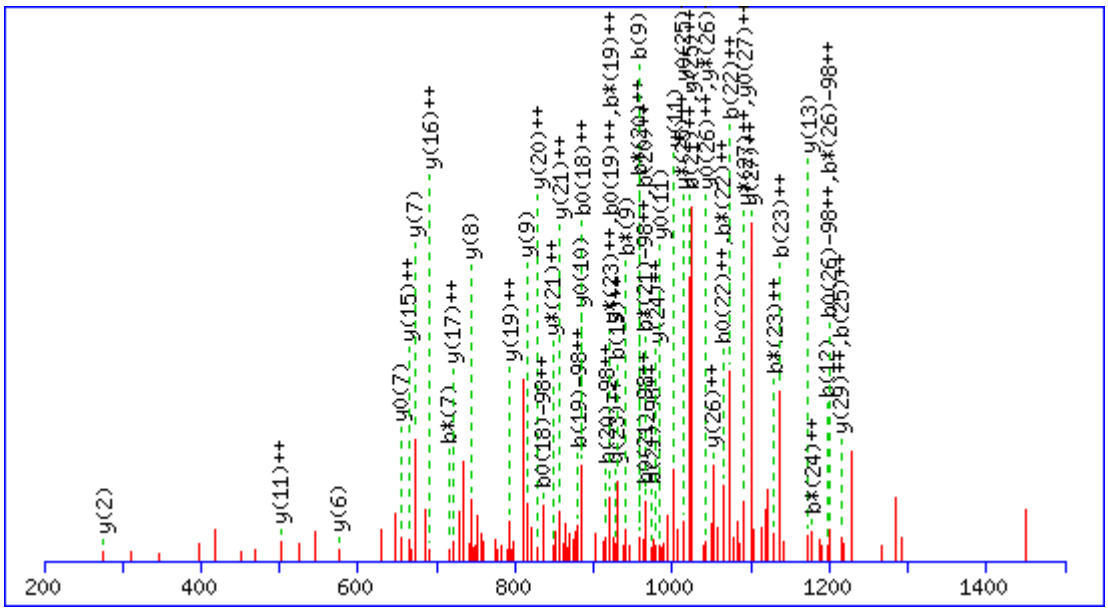


RMS error 246 ppm

IDENTIFICATION 63

MS/MS Fragmentation of SSEAETQQPPAAPAAALSAADTKPGSTGSGAGSGGPGGLTSAAPAGGDKK

Found in IPI00120886



Monoisotopic mass of neutral peptide Mr(calc): 4471.0776

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

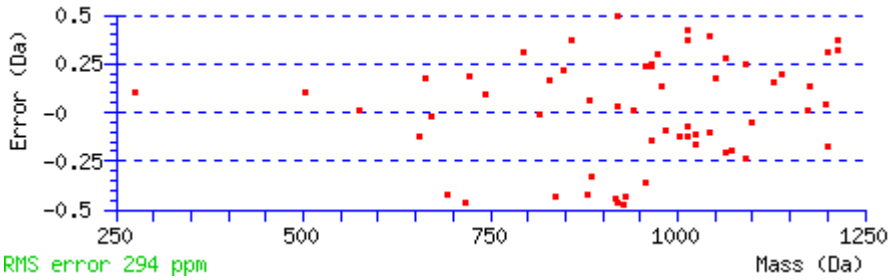
Variable modifications:

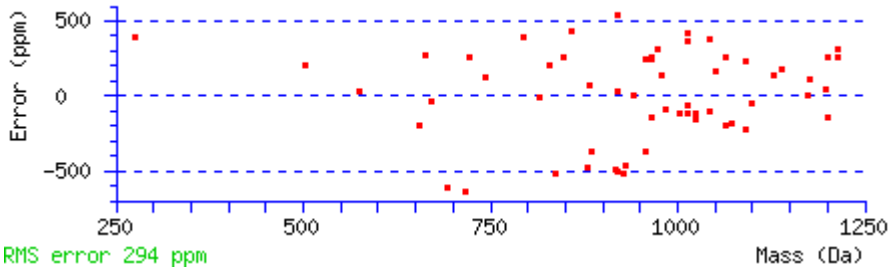
S18 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 23 Expect: 0.9 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							50
2	175.0713	88.0393			157.0608	79.0340	S	4385.0529	2193.0301	4368.0263	2184.5168	4367.0423	2184.0248	49
3	304.1139	152.5606			286.1034	143.5553	E	4298.0209	2149.5141	4280.9943	2141.0008	4280.0103	2140.5088	48
4	375.1510	188.0792			357.1405	179.0739	A	4168.9783	2084.9928	4151.9517	2076.4795	4150.9677	2075.9875	47
5	504.1936	252.6005			486.1831	243.5952	E	4097.9412	2049.4742	4080.9146	2040.9609	4079.9306	2040.4689	46
6	605.2413	303.1243			587.2307	294.1190	T	3968.8986	1984.9529	3951.8720	1976.4396	3950.8880	1975.9476	45
7	733.2999	367.1536	716.2733	358.6403	715.2893	358.1483	Q	3867.8509	1934.4291	3850.8243	1925.9158	3849.8403	1925.4238	44
8	861.3585	431.1829	844.3319	422.6696	843.3479	422.1776	Q	3739.7923	1870.3998	3722.7658	1861.8865	3721.7817	1861.3945	43
9	958.4112	479.7093	941.3847	471.1960	940.4007	470.7040	P	3611.7337	1806.3705	3594.7072	1797.8572	3593.7232	1797.3652	42
10	1055.4640	528.2356	1038.4374	519.7224	1037.4534	519.2304	P	3514.6810	1757.8441	3497.6544	1749.3308	3496.6704	1748.8388	41
11	1126.5011	563.7542	1109.4746	555.2409	1108.4905	554.7489	A	3417.6282	1709.3177	3400.6017	1700.8045	3399.6176	1700.3125	40
12	1197.5382	599.2727	1180.5117	590.7595	1179.5277	590.2675	A	3346.5911	1673.7992	3329.5645	1665.2859	3328.5805	1664.7939	39
13	1294.5910	647.7991	1277.5644	639.2859	1276.5804	638.7938	P	3275.5540	1638.2806	3258.5274	1629.7674	3257.5434	1629.2753	38
14	1365.6281	683.3177	1348.6016	674.8044	1347.6175	674.3124	A	3178.5012	1589.7542	3161.4747	1581.2410	3160.4906	1580.7490	37
15	1436.6652	718.8362	1419.6387	710.3230	1418.6546	709.8310	A	3107.4641	1554.2357	3090.4375	1545.7224	3089.4535	1545.2304	36
16	1507.7023	754.3548	1490.6758	745.8415	1489.6918	745.3495	A	3036.4270	1518.7171	3019.4004	1510.2039	3018.4164	1509.7118	35
17	1620.7864	810.8968	1603.7598	802.3836	1602.7758	801.8916	L	2965.3899	1483.1986	2948.3633	1474.6853	2947.3793	1474.1933	34
18	1787.7848	894.3960	1770.7582	885.8827	1769.7742	885.3907	S	2852.3058	1426.6565	2835.2793	1418.1433	2834.2952	1417.6513	33
19	1858.8219	929.9146	1841.7953	921.4013	1840.8113	920.9093	A	2685.3074	1343.1574	2668.2809	1334.6441	2667.2969	1334.1521	32
20	1929.8590	965.4331	1912.8324	956.9199	1911.8484	956.4278	A	2614.2703	1307.6388	2597.2438	1299.1255	2596.2598	1298.6335	31
21	2044.8859	1022.9466	2027.8594	1014.4333	2026.8754	1013.9413	D	2543.2332	1272.1202	2526.2067	1263.6070	2525.2227	1263.1150	30
22	2145.9336	1073.4704	2128.9071	1064.9572	2127.9230	1064.4652	T	2428.2063	1214.6068	2411.1797	1206.0935	2410.1957	1205.6015	29
23	2274.0286	1137.5179	2257.0020	1129.0046	2256.0180	1128.5126	K	2327.1586	1164.0829	2310.1320	1155.5697	2309.1480	1155.0777	28
24	2371.0813	1186.0443	2354.0548	1177.5310	2353.0708	1177.0390	P	2199.0636	1100.0355	2182.0371	1091.5222	2181.0531	1091.0302	27
25	2428.1028	1214.5550	2411.0762	1206.0418	2410.0922	1205.5498	G	2102.0109	1051.5091	2084.9843	1042.9958	2084.0003	1042.5038	26
26	2515.1348	1258.0710	2498.1083	1249.5578	2497.1243	1249.0658	S	2044.9894	1022.9983	2027.9629	1014.4851	2026.9788	1013.9931	25
27	2616.1825	1308.5949	2599.1560	1300.0816	2598.1719	1299.5896	T	1957.9574	979.4823	1940.9308	970.9691	1939.9468	970.4770	24

28	2673.2040	1337.1056	2656.1774	1328.5923	2655.1934	1328.1003	G	1856.9097	928.9585	1839.8831	920.4452	1838.8991	919.9532	23
29	2760.2360	1380.6216	2743.2094	1372.1084	2742.2254	1371.6164	S	1799.8882	900.4478	1782.8617	891.9345	1781.8777	891.4425	22
30	2817.2575	1409.1324	2800.2309	1400.6191	2799.2469	1400.1271	G	1712.8562	856.9317	1695.8297	848.4185	1694.8456	847.9265	21
31	2888.2946	1444.6509	2871.2680	1436.1376	2870.2840	1435.6456	A	1655.8347	828.4210	1638.8082	819.9077	1637.8242	819.4157	20
32	2945.3160	1473.1617	2928.2895	1464.6484	2927.3055	1464.1564	G	1584.7976	792.9025	1567.7711	784.3892	1566.7871	783.8972	19
33	3032.3481	1516.6777	3015.3215	1508.1644	3014.3375	1507.6724	S	1527.7762	764.3917	1510.7496	755.8784	1509.7656	755.3864	18
34	3089.3695	1545.1884	3072.3430	1536.6751	3071.3590	1536.1831	G	1440.7441	720.8757	1423.7176	712.3624	1422.7336	711.8704	17
35	3146.3910	1573.6991	3129.3644	1565.1859	3128.3804	1564.6939	G	1383.7227	692.3650	1366.6961	683.8517	1365.7121	683.3597	16
36	3243.4438	1622.2255	3226.4172	1613.7122	3225.4332	1613.2202	P	1326.7012	663.8542	1309.6747	655.3410	1308.6906	654.8490	15
37	3300.4652	1650.7362	3283.4387	1642.2230	3282.4547	1641.7310	G	1229.6484	615.3279	1212.6219	606.8146	1211.6379	606.3226	14
38	3357.4867	1679.2470	3340.4601	1670.7337	3339.4761	1670.2417	G	1172.6270	586.8171	1155.6004	578.3039	1154.6164	577.8118	13
39	3470.5707	1735.7890	3453.5442	1727.2757	3452.5602	1726.7837	L	1115.6055	558.3064	1098.5790	549.7931	1097.5949	549.3011	12
40	3571.6184	1786.3129	3554.5919	1777.7996	3553.6079	1777.3076	T	1002.5215	501.7644	985.4949	493.2511	984.5109	492.7591	11
41	3658.6505	1829.8289	3641.6239	1821.3156	3640.6399	1820.8236	S	901.4738	451.2405	884.4472	442.7272	883.4632	442.2352	10
42	3729.6876	1865.3474	3712.6610	1856.8341	3711.6770	1856.3421	A	814.4417	407.7245	797.4152	399.2112	796.4312	398.7192	9
43	3800.7247	1900.8660	3783.6981	1892.3527	3782.7141	1891.8607	A	743.4046	372.2060	726.3781	363.6927	725.3941	363.2007	8
44	3897.7774	1949.3924	3880.7509	1940.8791	3879.7669	1940.3871	P	672.3675	336.6874	655.3410	328.1741	654.3570	327.6821	7
45	3968.8146	1984.9109	3951.7880	1976.3976	3950.8040	1975.9056	A	575.3148	288.1610	558.2882	279.6477	557.3042	279.1557	6
46	4025.8360	2013.4216	4008.8095	2004.9084	4007.8255	2004.4164	G	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	5
47	4082.8575	2041.9324	4065.8309	2033.4191	4064.8469	2032.9271	G	447.2562	224.1317	430.2296	215.6185	429.2456	215.1264	4
48	4197.8844	2099.4459	4180.8579	2090.9326	4179.8739	2090.4406	D	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	3
49	4325.9794	2163.4933	4308.9528	2154.9801	4307.9688	2154.4881	K	275.2078	138.1075	258.1812	129.5942			2
50							K	147.1128	74.0600	130.0863	65.5468			1

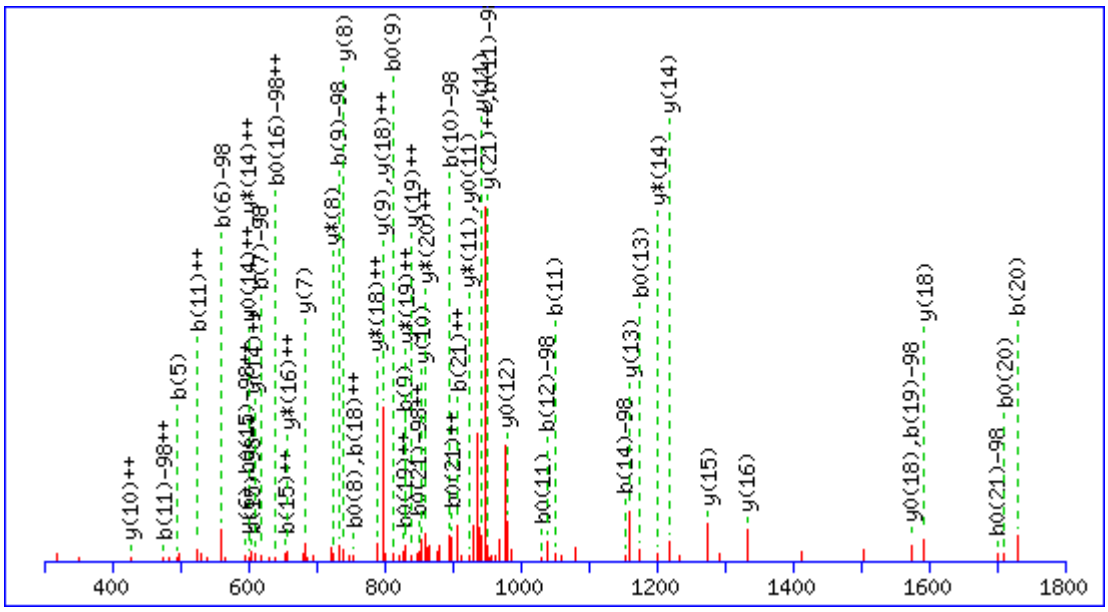




IDENTIFICATION 64

MS/MS Fragmentation of SSGSPYGGGYGSGGGSGGYGSR

Found in IPI00269661



Monoisotopic mass of neutral peptide Mr(calc): 1989.7491

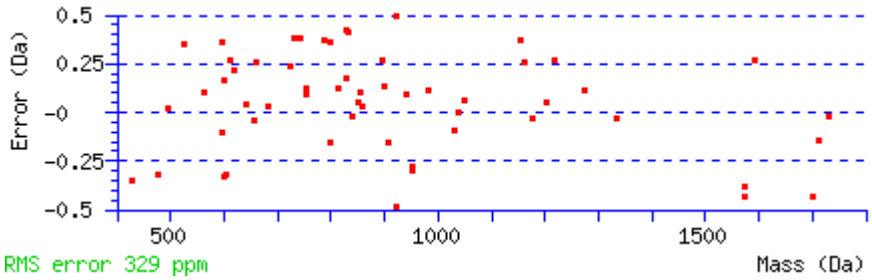
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

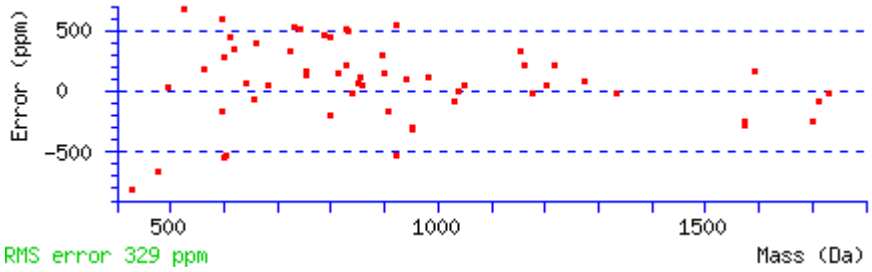
S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

Ions Score: 60 Expect: 0.00015 (help)

#	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							22
2	157.0608	79.0340	139.0502	70.0287	S	1805.7474	903.3773	1788.7208	894.8641	1787.7368	894.3720	21
3	214.0822	107.5448	196.0717	98.5395	G	1736.7259	868.8666	1719.6994	860.3533	1718.7154	859.8613	20
4	301.1143	151.0608	283.1037	142.0555	S	1679.7045	840.3559	1662.6779	831.8426	1661.6939	831.3506	19
5	398.1670	199.5871	380.1565	190.5819	P	1592.6724	796.8399	1575.6459	788.3266	1574.6619	787.8346	18
6	561.2304	281.1188	543.2198	272.1135	Y	1495.6197	748.3135	1478.5931	739.8002	1477.6091	739.3082	17
7	618.2518	309.6295	600.2413	300.6243	G	1332.5563	666.7818	1315.5298	658.2685	1314.5458	657.7765	16
8	675.2733	338.1403	657.2627	329.1350	G	1275.5349	638.2711	1258.5083	629.7578	1257.5243	629.2658	15
9	732.2947	366.6510	714.2842	357.6457	G	1218.5134	609.7603	1201.4869	601.2471	1200.5028	600.7551	14
10	895.3581	448.1827	877.3475	439.1774	Y	1161.4919	581.2496	1144.4654	572.7363	1143.4814	572.2443	13
11	952.3795	476.6934	934.3690	467.6881	G	998.4286	499.7179	981.4021	491.2047	980.4180	490.7127	12
12	1039.4116	520.2094	1021.4010	511.2041	S	941.4071	471.2072	924.3806	462.6939	923.3966	462.2019	11
13	1096.4330	548.7202	1078.4225	539.7149	G	854.3751	427.6912	837.3486	419.1779	836.3646	418.6859	10
14	1153.4545	577.2309	1135.4439	568.2256	G	797.3537	399.1805	780.3271	390.6672	779.3431	390.1752	9
15	1210.4760	605.7416	1192.4654	596.7363	G	740.3322	370.6697	723.3056	362.1565	722.3216	361.6645	8
16	1297.5080	649.2576	1279.4974	640.2523	S	683.3107	342.1590	666.2842	333.6457	665.3002	333.1537	7
17	1354.5294	677.7684	1336.5189	668.7631	G	596.2787	298.6430	579.2522	290.1297	578.2681	289.6377	6
18	1411.5509	706.2791	1393.5403	697.2738	G	539.2572	270.1323	522.2307	261.6190	521.2467	261.1270	5
19	1574.6142	787.8108	1556.6037	778.8055	Y	482.2358	241.6215	465.2092	233.1082	464.2252	232.6162	4
20	1631.6357	816.3215	1613.6251	807.3162	G	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
21	1718.6677	859.8375	1700.6572	850.8322	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
22					R	175.1190	88.0631	158.0924	79.5498			1

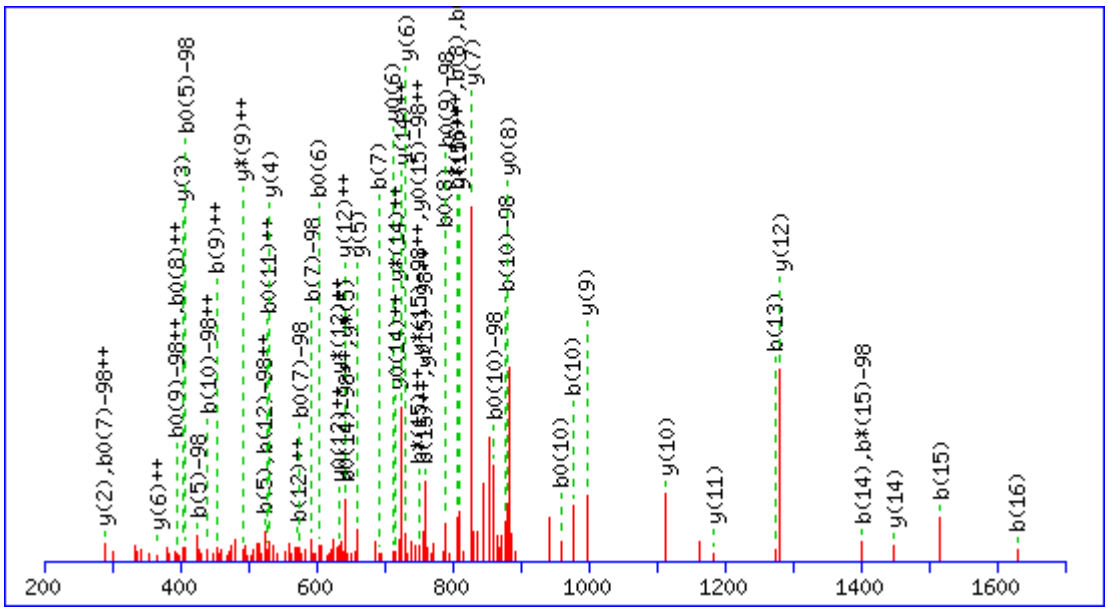


RMS error 329 ppm



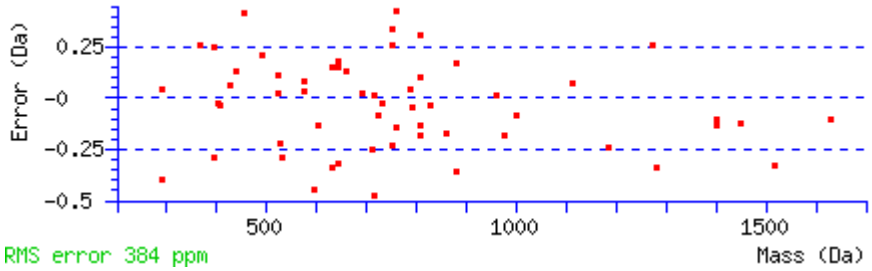
RMS error 329 ppm

IDENTIFICATION 65
MS/MS Fragmentation of STSPAPADVAPAQEDLR
Found in IPI00130095

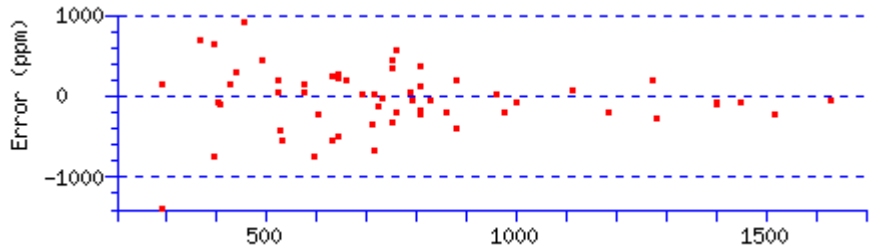


Monoisotopic mass of neutral peptide Mr(calc): 1803.8040
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 80 Expect: 1.7e-06 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							17
2	189.0870	95.0471			171.0764	86.0418	T	1619.8024	810.4048	1602.7758	801.8916	1601.7918	801.3995	16
3	258.1084	129.5579			240.0979	120.5526	S	1518.7547	759.8810	1501.7281	751.3677	1500.7441	750.8757	15
4	355.1612	178.0842			337.1506	169.0790	P	1449.7332	725.3703	1432.7067	716.8570	1431.7227	716.3650	14
5	426.1983	213.6028			408.1878	204.5975	A	1352.6805	676.8439	1335.6539	668.3306	1334.6699	667.8386	13
6	523.2511	262.1292			505.2405	253.1239	P	1281.6434	641.3253	1264.6168	632.8120	1263.6328	632.3200	12
7	594.2882	297.6477			576.2776	288.6425	A	1184.5906	592.7989	1167.5640	584.2857	1166.5800	583.7937	11
8	709.3151	355.1612			691.3046	346.1559	D	1113.5535	557.2804	1096.5269	548.7671	1095.5429	548.2751	10
9	808.3836	404.6954			790.3730	395.6901	V	998.5265	499.7669	981.5000	491.2536	980.5160	490.7616	9
10	879.4207	440.2140			861.4101	431.2087	A	899.4581	450.2327	882.4316	441.7194	881.4476	441.2274	8
11	976.4734	488.7404			958.4629	479.7351	P	828.4210	414.7141	811.3945	406.2009	810.4104	405.7089	7
12	1047.5106	524.2589			1029.5000	515.2536	A	731.3682	366.1878	714.3417	357.6745	713.3577	357.1825	6
13	1175.5691	588.2882	1158.5426	579.7749	1157.5586	579.2829	Q	660.3311	330.6692	643.3046	322.1559	642.3206	321.6639	5
14	1304.6117	652.8095	1287.5852	644.2962	1286.6012	643.8042	E	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
15	1419.6387	710.3230	1402.6121	701.8097	1401.6281	701.3177	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
16	1532.7227	766.8650	1515.6962	758.3517	1514.7122	757.8597	L	288.2030	144.6051	271.1765	136.0919			2
17							R	175.1190	88.0631	158.0924	79.5498			1



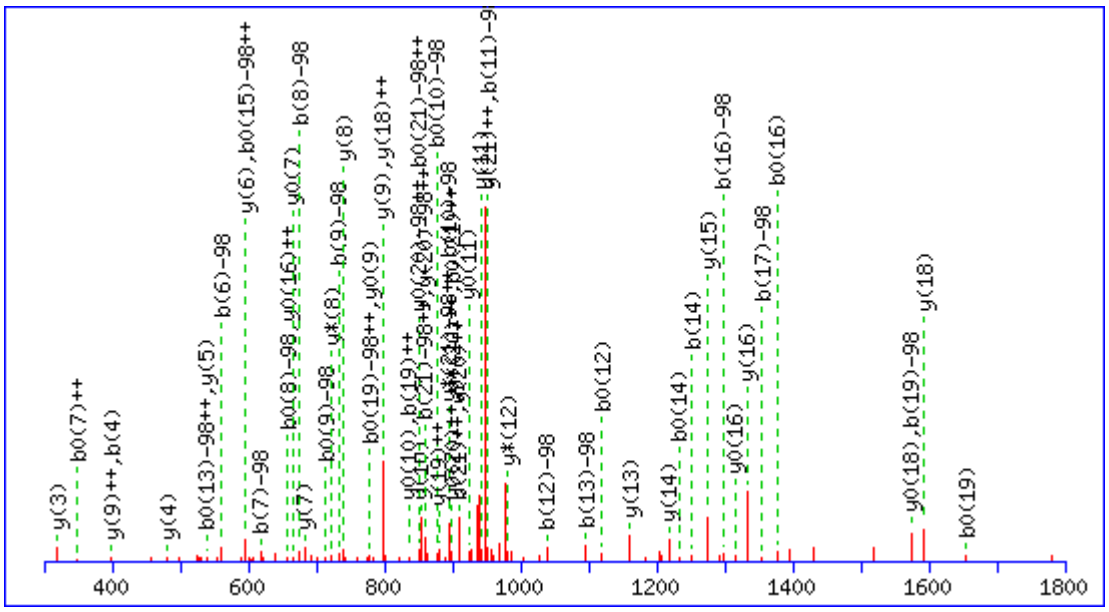
RMS error 384 ppm



RMS error 384 ppm

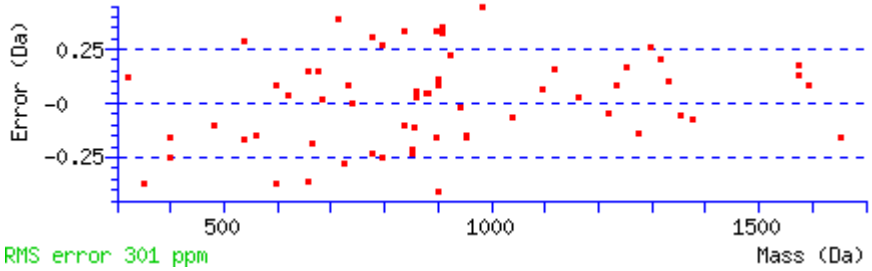
IDENTIFICATION 66

MS/MS Fragmentation of SSGSPYGGGYGSGGGSGGYGSR
Found in IPI00269661



Monoisotopic mass of neutral peptide Mr(calc): 1989.7491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 82 Expect: 9.6e-07 (help)

#	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							22
2	175.0713	88.0393	157.0608	79.0340	S	1805.7474	903.3773	1788.7208	894.8641	1787.7368	894.3720	21
3	232.0928	116.5500	214.0822	107.5448	G	1718.7154	859.8613	1701.6888	851.3480	1700.7048	850.8560	20
4	301.1143	151.0608	283.1037	142.0555	S	1661.6939	831.3506	1644.6673	822.8373	1643.6833	822.3453	19
5	398.1670	199.5871	380.1565	190.5819	P	1592.6724	796.8399	1575.6459	788.3266	1574.6619	787.8346	18
6	561.2304	281.1188	543.2198	272.1135	Y	1495.6197	748.3135	1478.5931	739.8002	1477.6091	739.3082	17
7	618.2518	309.6295	600.2413	300.6243	G	1332.5563	666.7818	1315.5298	658.2685	1314.5458	657.7765	16
8	675.2733	338.1403	657.2627	329.1350	G	1275.5349	638.2711	1258.5083	629.7578	1257.5243	629.2658	15
9	732.2947	366.6510	714.2842	357.6457	G	1218.5134	609.7603	1201.4869	601.2471	1200.5028	600.7551	14
10	895.3581	448.1827	877.3475	439.1774	Y	1161.4919	581.2496	1144.4654	572.7363	1143.4814	572.2443	13
11	952.3795	476.6934	934.3690	467.6881	G	998.4286	499.7179	981.4021	491.2047	980.4180	490.7127	12
12	1039.4116	520.2094	1021.4010	511.2041	S	941.4071	471.2072	924.3806	462.6939	923.3966	462.2019	11
13	1096.4330	548.7202	1078.4225	539.7149	G	854.3751	427.6912	837.3486	419.1779	836.3646	418.6859	10
14	1153.4545	577.2309	1135.4439	568.2256	G	797.3537	399.1805	780.3271	390.6672	779.3431	390.1752	9
15	1210.4760	605.7416	1192.4654	596.7363	G	740.3322	370.6697	723.3056	362.1565	722.3216	361.6645	8
16	1297.5080	649.2576	1279.4974	640.2523	S	683.3107	342.1590	666.2842	333.6457	665.3002	333.1537	7
17	1354.5294	677.7684	1336.5189	668.7631	G	596.2787	298.6430	579.2522	290.1297	578.2681	289.6377	6
18	1411.5509	706.2791	1393.5403	697.2738	G	539.2572	270.1323	522.2307	261.6190	521.2467	261.1270	5
19	1574.6142	787.8108	1556.6037	778.8055	Y	482.2358	241.6215	465.2092	233.1082	464.2252	232.6162	4
20	1631.6357	816.3215	1613.6251	807.3162	G	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
21	1718.6677	859.8375	1700.6572	850.8322	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
22					R	175.1190	88.0631	158.0924	79.5498			1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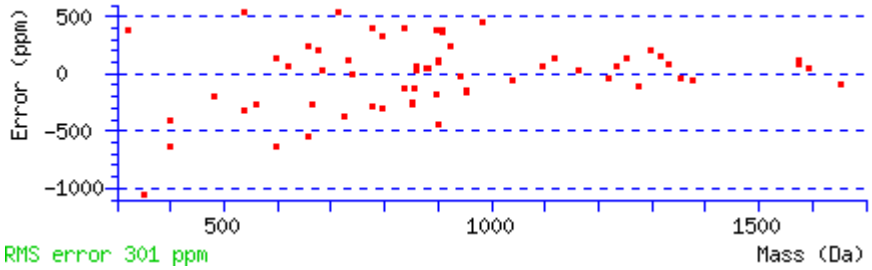
-0.25
500
1000
1500
RMS error 301 ppm
Mass (Da)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1000
1500
RMS error 301 ppm
Mass (Da)

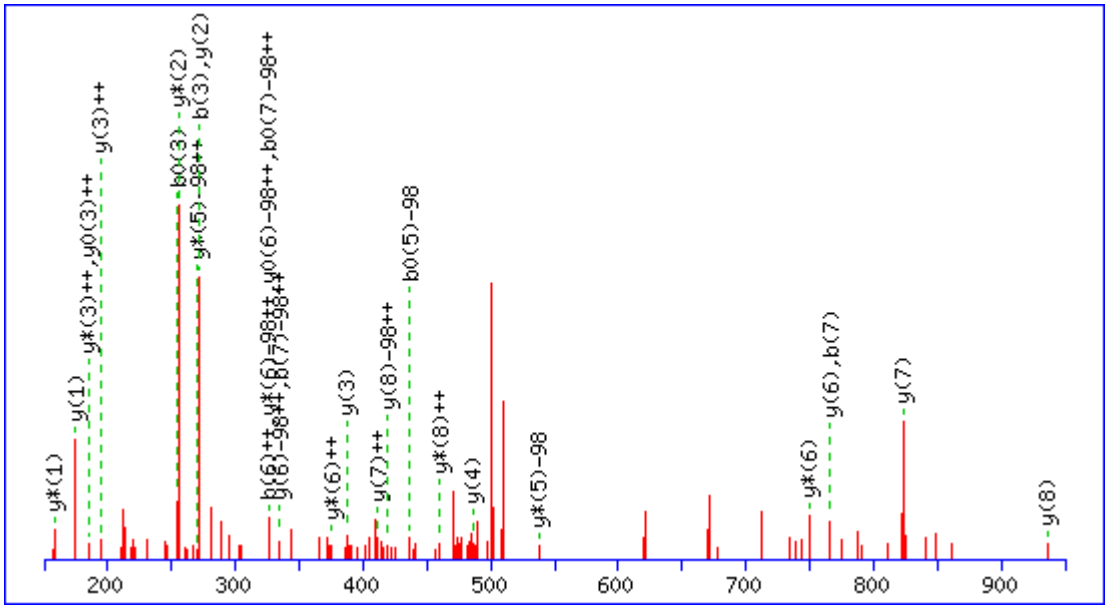
IDENTIFICATION 67

MS/MS Fragmentation of

TIGISVDPR

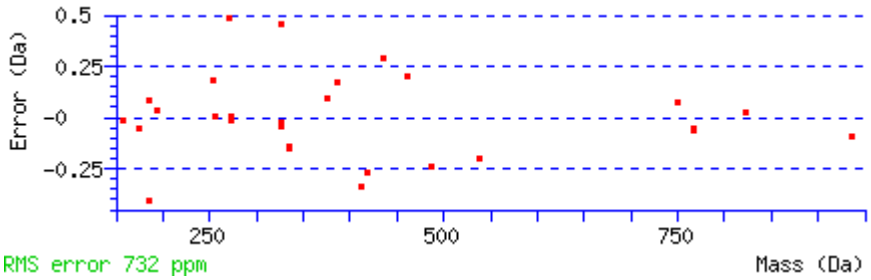
Found in

IPI00134097

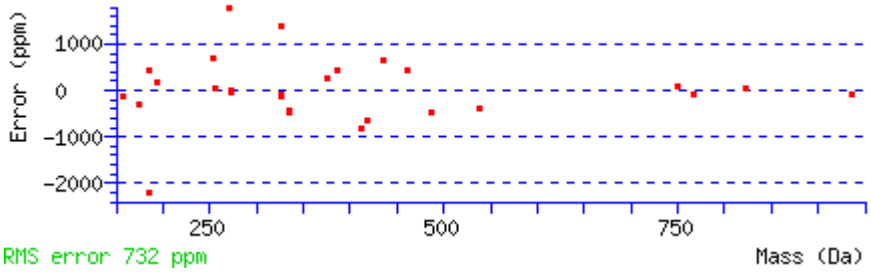


Monoisotopic mass of neutral peptide Mr(calc): 1036.4954
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 35 Expect: 0.024 (help)

#	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	215.1390	108.0731	197.1285	99.0679	I	936.4550	468.7312	919.4285	460.2179	918.4445	459.7259	8
3	272.1605	136.5839	254.1499	127.5786	G	823.3710	412.1891	806.3444	403.6758	805.3604	403.1838	7
4	385.2445	193.1259	367.2340	184.1206	I	766.3495	383.6784	749.3229	375.1651	748.3389	374.6731	6
5	552.2429	276.6251	534.2323	267.6198	S	653.2654	327.1364	636.2389	318.6231	635.2549	318.1311	5
6	651.3113	326.1593	633.3008	317.1540	V	486.2671	243.6372	469.2405	235.1239	468.2565	234.6319	4
7	766.3383	383.6728	748.3277	374.6675	D	387.1987	194.1030	370.1721	185.5897	369.1881	185.0977	3
8	863.3910	432.1992	845.3805	423.1939	P	272.1717	136.5895	255.1452	128.0762			2
9					R	175.1190	88.0631	158.0924	79.5498			1

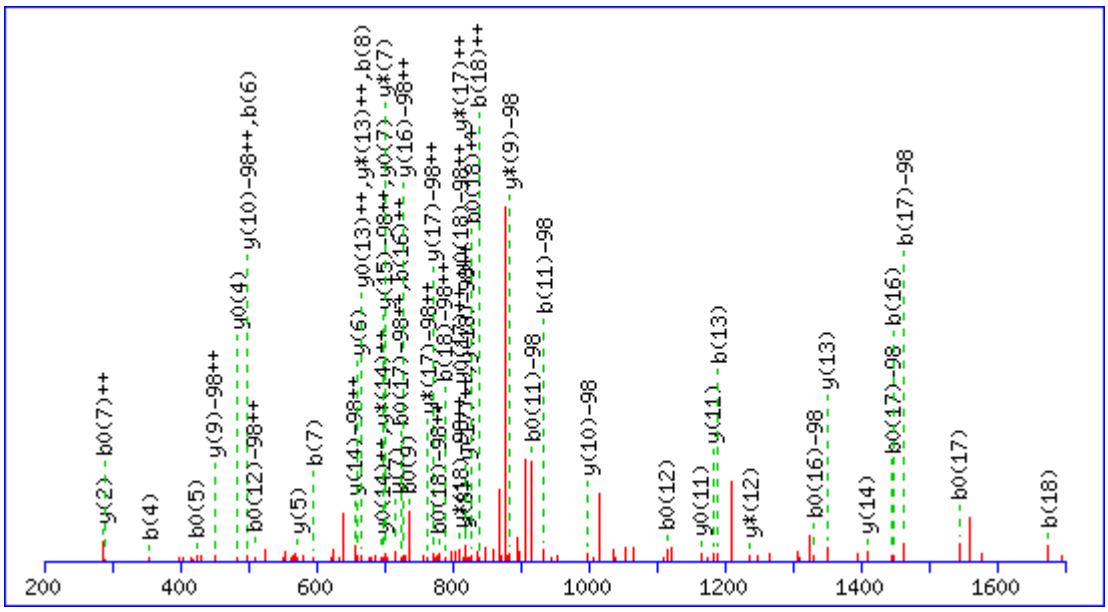


RMS error 732 ppm



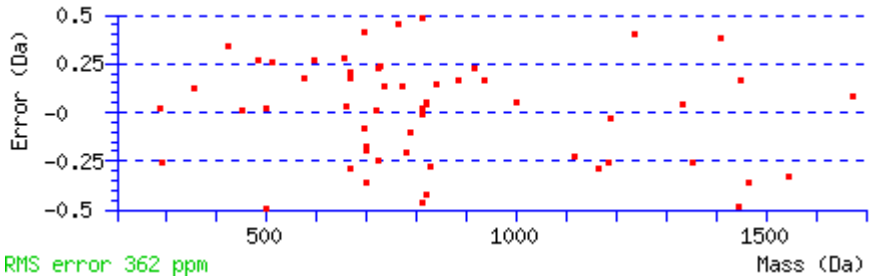
RMS error 732 ppm

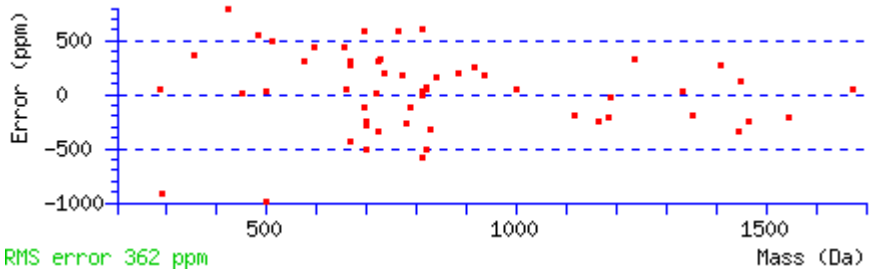
IDENTIFICATION 68
MS/MS Fragmentation of LPSGSGPASPTTGSAVDIR
Found in IPI00553798



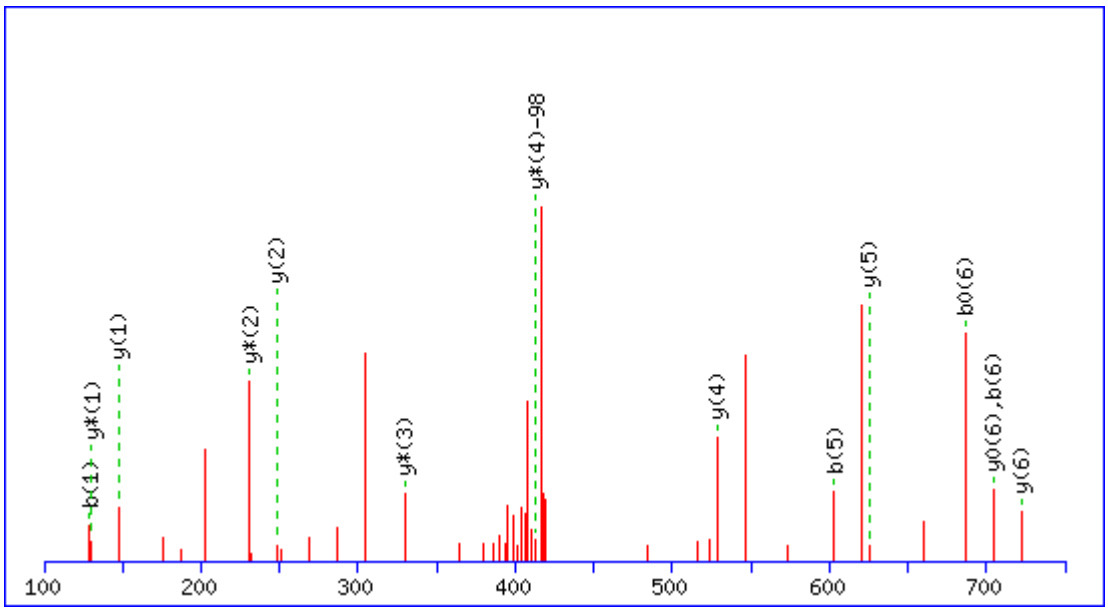
Monoisotopic mass of neutral peptide Mr(calc): 1848.8619
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 33 Expect: 0.09 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							19
2	211.1441	106.0757			P	1638.8082	819.9077	1621.7816	811.3945	1620.7976	810.9025	18
3	298.1761	149.5917	280.1656	140.5864	S	1541.7554	771.3814	1524.7289	762.8681	1523.7449	762.3761	17
4	355.1976	178.1024	337.1870	169.0972	G	1454.7234	727.8653	1437.6968	719.3521	1436.7128	718.8601	16
5	442.2296	221.6184	424.2191	212.6132	S	1397.7019	699.3546	1380.6754	690.8413	1379.6914	690.3493	15
6	499.2511	250.1292	481.2405	241.1239	G	1310.6699	655.8386	1293.6434	647.3253	1292.6593	646.8333	14
7	596.3039	298.6556	578.2933	289.6503	P	1253.6484	627.3279	1236.6219	618.8146	1235.6379	618.3226	13
8	667.3410	334.1741	649.3304	325.1688	A	1156.5957	578.8015	1139.5691	570.2882	1138.5851	569.7962	12
9	754.3730	377.6901	736.3624	368.6849	S	1085.5586	543.2829	1068.5320	534.7696	1067.5480	534.2776	11
10	851.4258	426.2165	833.4152	417.2112	P	998.5265	499.7669	981.5000	491.2536	980.5160	490.7616	10
11	934.4629	467.7351	916.4523	458.7298	T	901.4738	451.2405	884.4472	442.7272	883.4632	442.2352	9
12	1035.5106	518.2589	1017.5000	509.2536	T	818.4367	409.7220	801.4101	401.2087	800.4261	400.7167	8
13	1092.5320	546.7696	1074.5214	537.7644	G	717.3890	359.1981	700.3624	350.6849	699.3784	350.1928	7
14	1179.5640	590.2857	1161.5535	581.2804	S	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
15	1250.6012	625.8042	1232.5906	616.7989	A	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	5
16	1349.6696	675.3384	1331.6590	666.3331	V	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
17	1464.6965	732.8519	1446.6859	723.8466	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
18	1577.7806	789.3939	1559.7700	780.3886	I	288.2030	144.6051	271.1765	136.0919			2
19					R	175.1190	88.0631	158.0924	79.5498			1


0.5
0.25
-0
-0.25
-0.5
Error (Da)
500
1000
1500
Mass (Da)
RMS error 362 ppm

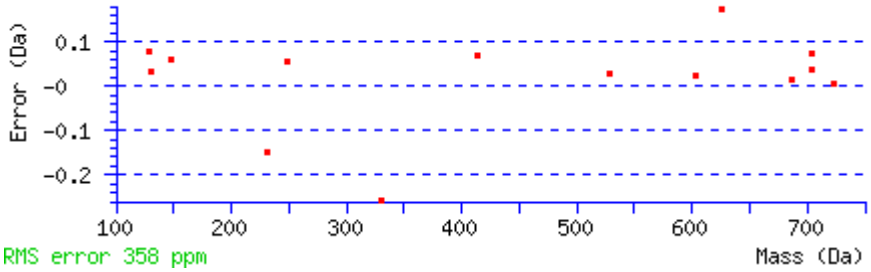

500
0
-500
-1000
Error (ppm)
500
1000
1500
Mass (Da)
RMS error 362 ppm

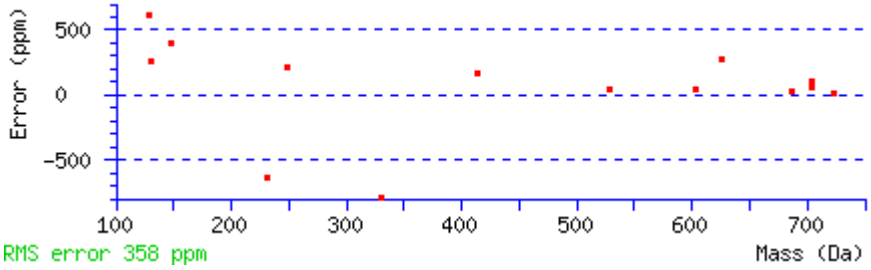
IDENTIFICATION 69
MS/MS Fragmentation of QPPTVTK
Found in IPI00416315



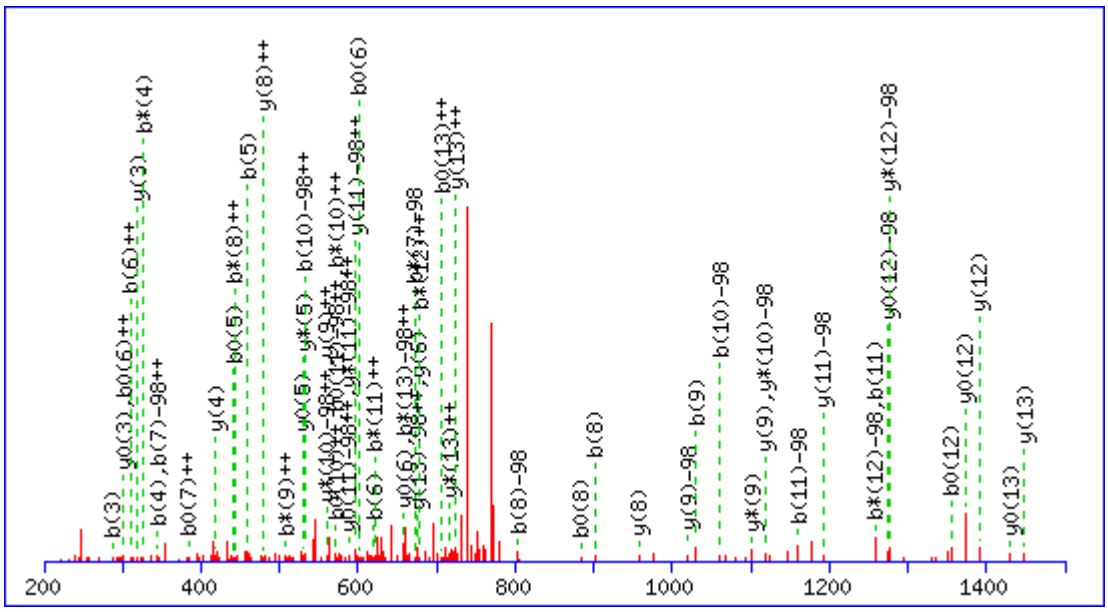
Monoisotopic mass of neutral peptide Mr(calc): 849.3997
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.11 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	129.0659	65.0366	112.0393	56.5233			Q							7
2	226.1186	113.5629	209.0921	105.0497			P	722.3484	361.6779	705.3219	353.1646	704.3379	352.6726	6
3	323.1714	162.0893	306.1448	153.5761			P	625.2957	313.1515	608.2691	304.6382	607.2851	304.1462	5
4	504.1854	252.5963	487.1588	244.0831	486.1748	243.5911	T	528.2429	264.6251	511.2164	256.1118	510.2323	255.6198	4
5	603.2538	302.1305	586.2273	293.6173	585.2432	293.1253	V	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
6	704.3015	352.6544	687.2749	344.1411	686.2909	343.6491	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
7							K	147.1128	74.0600	130.0863	65.5468			1



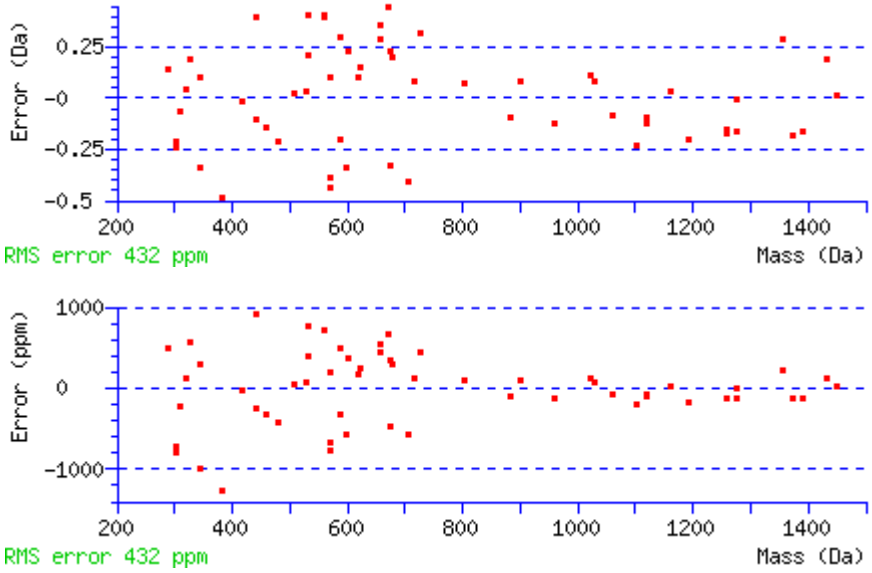


IDENTIFICATION 70
MS/MS Fragmentation of KGTGDCSDEEVDGK
Found in IPI00123181



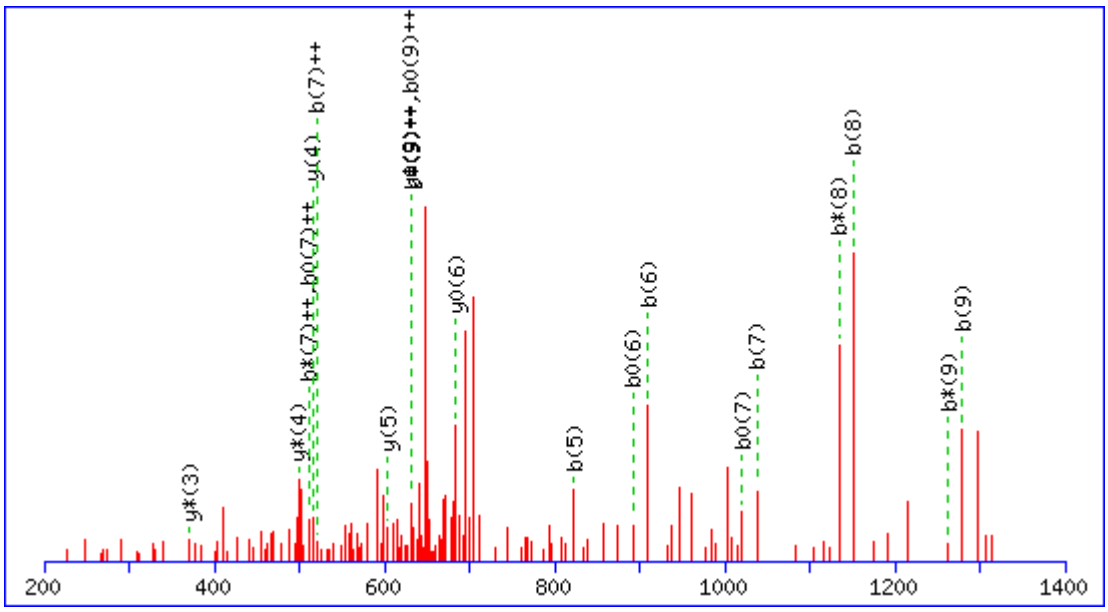
Monoisotopic mass of neutral peptide Mr(calc): 1575.5760
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 28 Expect: 0.13 (help)

#	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							14
2	186.1237	93.5655	169.0972	85.0522			G	1448.4883	724.7478	1431.4618	716.2345	1430.4777	715.7425	13
3	287.1714	144.0893	270.1448	135.5761	269.1608	135.0840	T	1391.4668	696.2371	1374.4403	687.7238	1373.4563	687.2318	12
4	344.1928	172.6001	327.1663	164.0868	326.1823	163.5948	G	1290.4192	645.7132	1273.3926	637.1999	1272.4086	636.7079	11
5	459.2198	230.1135	442.1932	221.6003	441.2092	221.1082	D	1233.3977	617.2025	1216.3712	608.6892	1215.3871	608.1972	10
6	619.2504	310.1289	602.2239	301.6156	601.2399	301.1236	C	1118.3708	559.6890	1101.3442	551.1757	1100.3602	550.6837	9
7	786.2488	393.6280	769.2222	385.1148	768.2382	384.6228	S	958.3401	479.6737	941.3136	471.1604	940.3295	470.6684	8
8	901.2757	451.1415	884.2492	442.6282	883.2652	442.1362	D	791.3418	396.1745	774.3152	387.6612	773.3312	387.1692	7
9	1030.3183	515.6628	1013.2918	507.1495	1012.3078	506.6575	E	676.3148	338.6610	659.2883	330.1478	658.3042	329.6558	6
10	1159.3609	580.1841	1142.3344	571.6708	1141.3504	571.1788	E	547.2722	274.1397	530.2457	265.6265	529.2617	265.1345	5
11	1258.4293	629.7183	1241.4028	621.2050	1240.4188	620.7130	V	418.2296	209.6185	401.2031	201.1052	400.2191	200.6132	4
12	1373.4563	687.2318	1356.4297	678.7185	1355.4457	678.2265	D	319.1612	160.0842	302.1347	151.5710	301.1506	151.0790	3
13	1430.4777	715.7425	1413.4512	707.2292	1412.4672	706.7372	G	204.1343	102.5708	187.1077	94.0575			2
14							K	147.1128	74.0600	130.0863	65.5468			1


Error (Da)
0.25
-0
-0.25
-0.5
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 432 ppm

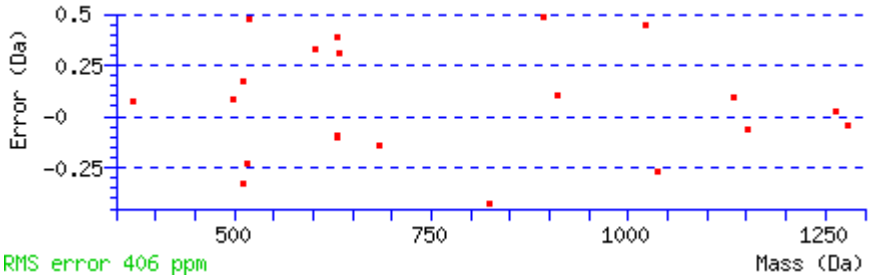
Error (ppm)
1000
0
-1000
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 432 ppm

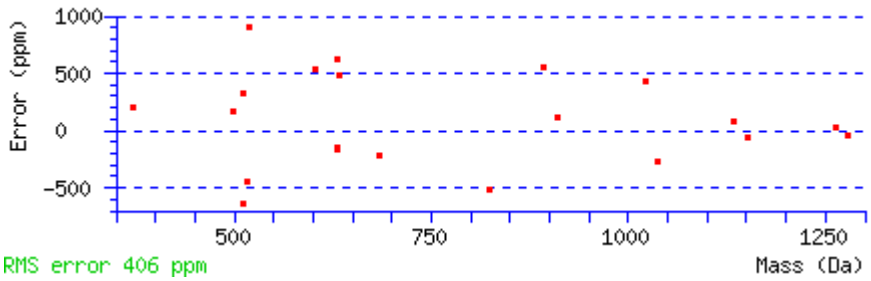
IDENTIFICATION 71
MS/MS Fragmentation of FWYFVSQLKK
Found in IPI00162790



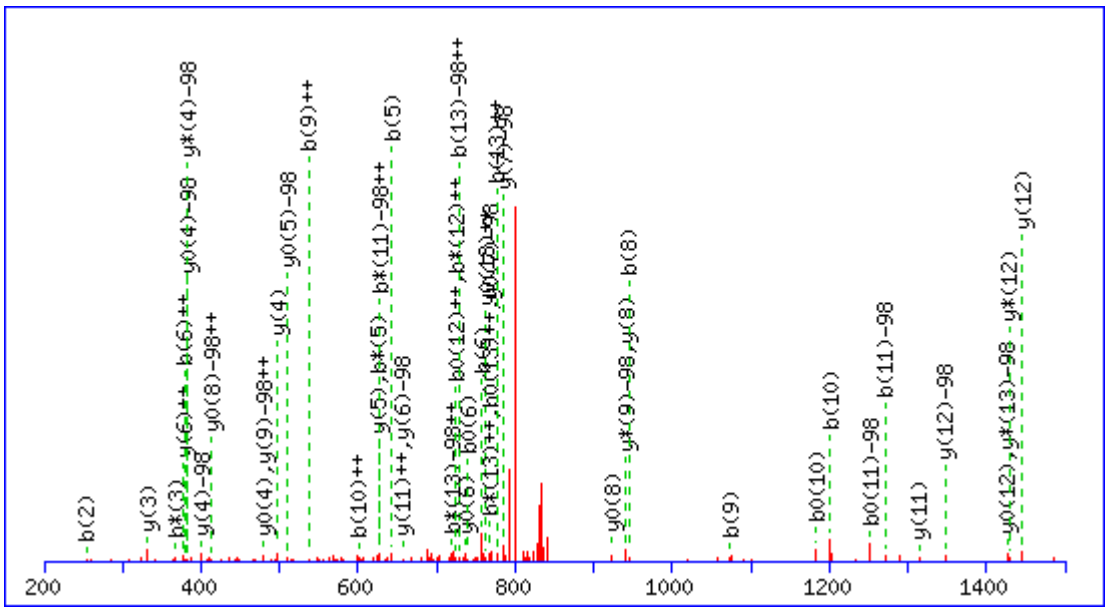
Monoisotopic mass of neutral peptide Mr(calc): 1424.6894
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y3 : Phospho (Y)
Ions Score: 22 Expect: 0.71 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							10
2	334.1550	167.5811					W	1278.6282	639.8178	1261.6017	631.3045	1260.6177	630.8125	9
3	577.1847	289.0960					Y	1092.5489	546.7781	1075.5224	538.2648	1074.5384	537.7728	8
4	724.2531	362.6302					F	849.5193	425.2633	832.4927	416.7500	831.5087	416.2580	7
5	823.3215	412.1644					V	702.4509	351.7291	685.4243	343.2158	684.4403	342.7238	6
6	910.3535	455.6804			892.3430	446.6751	S	603.3824	302.1949	586.3559	293.6816	585.3719	293.1896	5
7	1038.4121	519.7097	1021.3855	511.1964	1020.4015	510.7044	Q	516.3504	258.6788	499.3239	250.1656			4
8	1151.4962	576.2517	1134.4696	567.7384	1133.4856	567.2464	L	388.2918	194.6496	371.2653	186.1363			3
9	1279.5911	640.2992	1262.5646	631.7859	1261.5806	631.2939	K	275.2078	138.1075	258.1812	129.5942			2
10							K	147.1128	74.0600	130.0863	65.5468			1



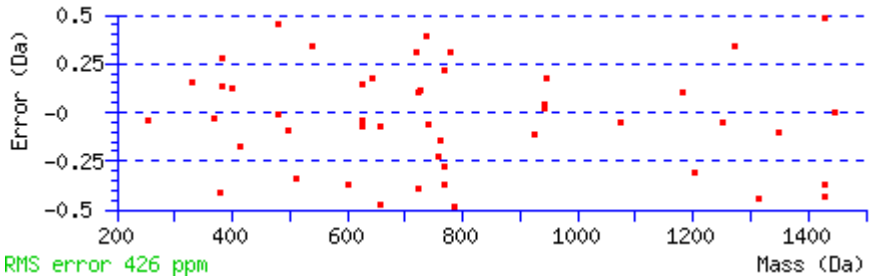


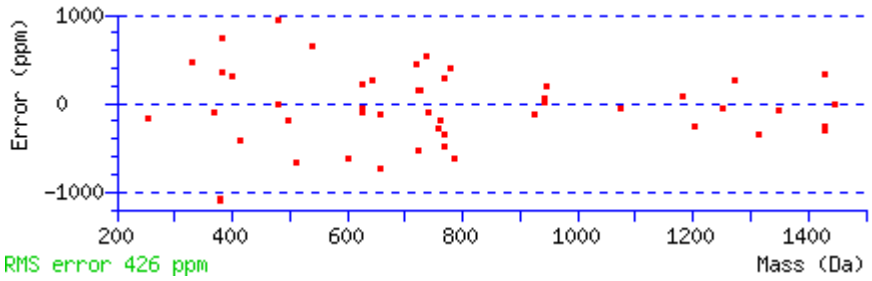
IDENTIFICATION 72
MS/MS Fragmentation of RPMEEDGEEKSPSK
Found in IPI00130591



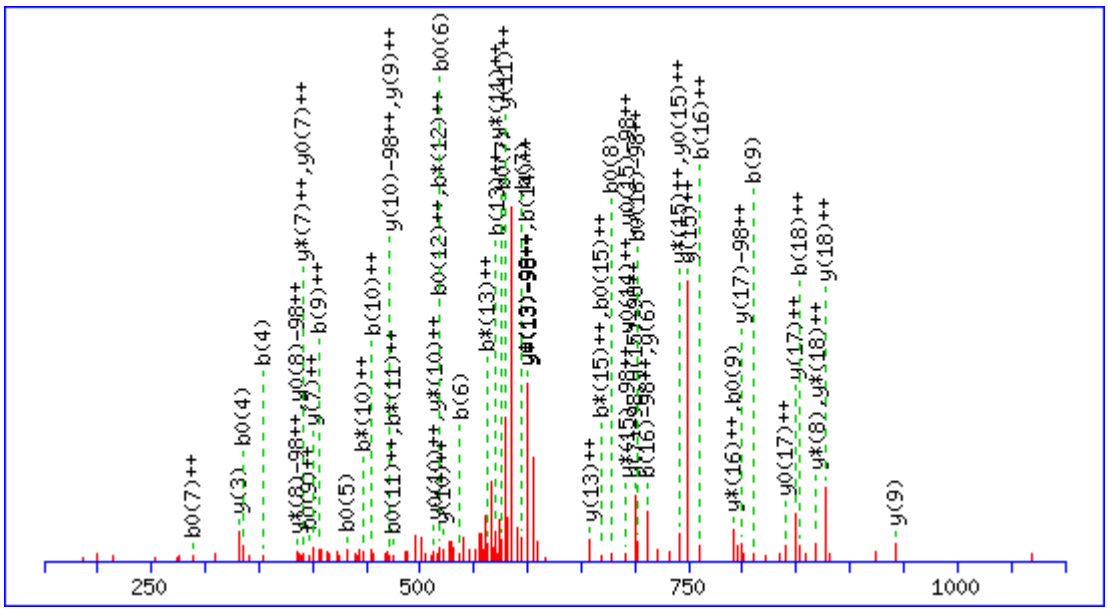
Monoisotopic mass of neutral peptide Mr(calc): 1697.6967
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.32 (help)

#	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	254.1612	127.5842	237.1346	119.0709			P	1444.6261	722.8167	1427.5995	714.3034	1426.6155	713.8114	13
3	385.2016	193.1045	368.1751	184.5912			M	1347.5733	674.2903	1330.5467	665.7770	1329.5627	665.2850	12
4	514.2442	257.6258	497.2177	249.1125	496.2337	248.6205	E	1216.5328	608.7700	1199.5063	600.2568	1198.5222	599.7648	11
5	643.2868	322.1470	626.2603	313.6338	625.2763	313.1418	E	1087.4902	544.2487	1070.4637	535.7355	1069.4796	535.2435	10
6	758.3138	379.6605	741.2872	371.1472	740.3032	370.6552	D	958.4476	479.7274	941.4211	471.2142	940.4371	470.7222	9
7	815.3352	408.1713	798.3087	399.6580	797.3247	399.1660	G	843.4207	422.2140	826.3941	413.7007	825.4101	413.2087	8
8	944.3778	472.6925	927.3513	464.1793	926.3673	463.6873	E	786.3992	393.7032	769.3727	385.1900	768.3886	384.6980	7
9	1073.4204	537.2138	1056.3939	528.7006	1055.4099	528.2086	E	657.3566	329.1819	640.3301	320.6687	639.3461	320.1767	6
10	1201.5154	601.2613	1184.4888	592.7481	1183.5048	592.2560	K	528.3140	264.6606	511.2875	256.1474	510.3035	255.6554	5
11	1270.5368	635.7721	1253.5103	627.2588	1252.5263	626.7668	S	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	4
12	1367.5896	684.2984	1350.5631	675.7852	1349.5790	675.2932	P	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	3
13	1454.6216	727.8145	1437.5951	719.3012	1436.6111	718.8092	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
14							K	147.1128	74.0600	130.0863	65.5468			1


0.5
0.25
-0
-0.25
-0.5
Error (Da)
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 426 ppm

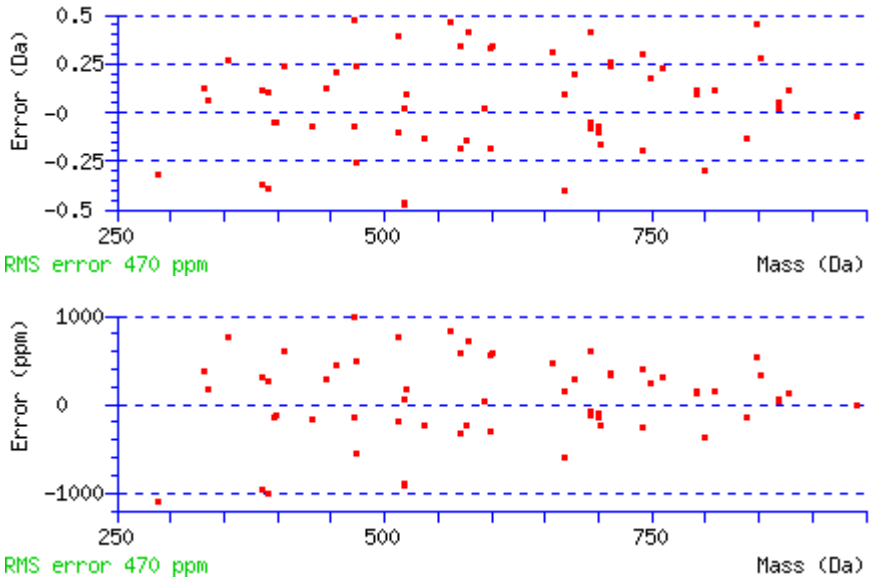

1000
0
-1000
Error (ppm)
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 426 ppm

IDENTIFICATION 73
MS/MS Fragmentation of PGPTPSGTNVGSSGRSPSK
Found in IPI00133030



Monoisotopic mass of neutral peptide Mr(calc): 1848.8367
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S16 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 31 Expect: 0.14 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y_{0}	y^{0++}	#
1	98.0600	49.5337					P							19
2	155.0815	78.0444					G	1752.7912	876.8993	1735.7647	868.3860	1734.7807	867.8940	18
3	252.1343	126.5708					P	1695.7698	848.3885	1678.7432	839.8752	1677.7592	839.3832	17
4	353.1819	177.0946			335.1714	168.0893	T	1598.7170	799.8621	1581.6905	791.3489	1580.7064	790.8569	16
5	450.2347	225.6210			432.2241	216.6157	P	1497.6693	749.3383	1480.6428	740.8250	1479.6588	740.3330	15
6	537.2667	269.1370			519.2562	260.1317	S	1400.6166	700.8119	1383.5900	692.2986	1382.6060	691.8066	14
7	594.2882	297.6477			576.2776	288.6425	G	1313.5845	657.2959	1296.5580	648.7826	1295.5740	648.2906	13
8	695.3359	348.1716			677.3253	339.1663	T	1256.5631	628.7852	1239.5365	620.2719	1238.5525	619.7799	12
9	809.3788	405.1930	792.3523	396.6798	791.3682	396.1878	N	1155.5154	578.2613	1138.4888	569.7481	1137.5048	569.2561	11
10	908.4472	454.7272	891.4207	446.2140	890.4367	445.7220	V	1041.4725	521.2399	1024.4459	512.7266	1023.4619	512.2346	10
11	965.4687	483.2380	948.4421	474.7247	947.4581	474.2327	G	942.4041	471.7057	925.3775	463.1924	924.3935	462.7004	9
12	1052.5007	526.7540	1035.4742	518.2407	1034.4902	517.7487	S	885.3826	443.1949	868.3560	434.6817	867.3720	434.1896	8
13	1139.5327	570.2700	1122.5062	561.7567	1121.5222	561.2647	S	798.3506	399.6789	781.3240	391.1656	780.3400	390.6736	7
14	1196.5542	598.7807	1179.5277	590.2675	1178.5436	589.7755	G	711.3185	356.1629	694.2920	347.6496	693.3080	347.1576	6
15	1352.6553	676.8313	1335.6288	668.3180	1334.6448	667.8260	R	654.2971	327.6522	637.2705	319.1389	636.2865	318.6469	5
16	1519.6537	760.3305	1502.6271	751.8172	1501.6431	751.3252	S	498.1960	249.6016	481.1694	241.0883	480.1854	240.5963	4
17	1616.7064	808.8569	1599.6799	800.3436	1598.6959	799.8516	P	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	3
18	1703.7385	852.3729	1686.7119	843.8596	1685.7279	843.3676	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
19							K	147.1128	74.0600	130.0863	65.5468			1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500
750
RMS error 470 ppm
Mass (Da)

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-1000
Error (ppm)
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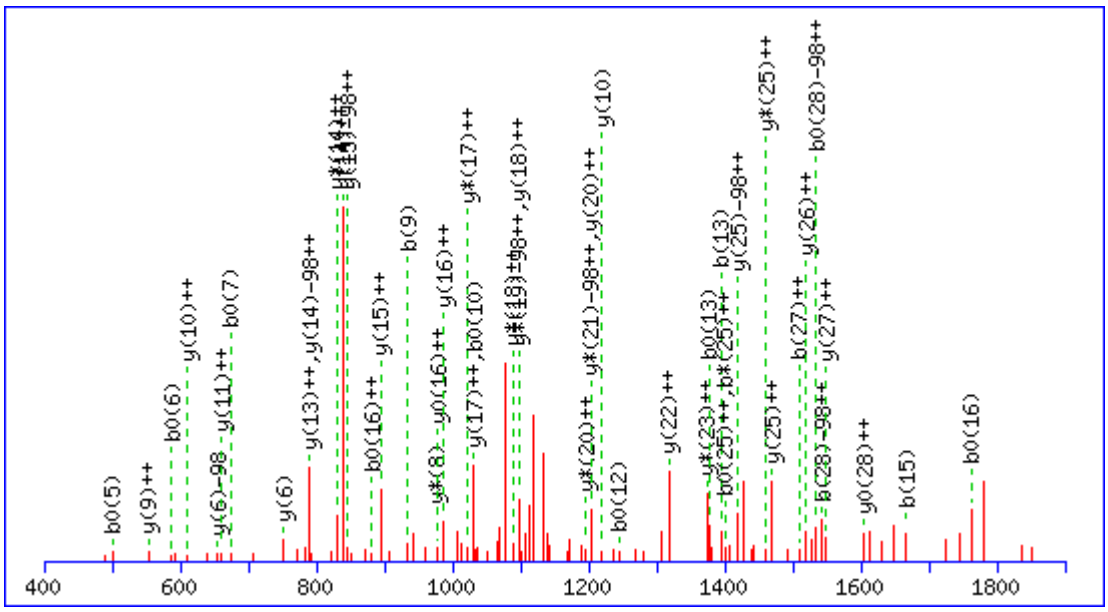
RMS error 470 ppm
Mass (Da)

IDENTIFICATION 74

MS/MS Fragmentation of VEMGTSSQNDVDMSWIPQETLNQINKASPR

Found in IPI00755329



Monoisotopic mass of neutral peptide Mr(calc): 3454.5534

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

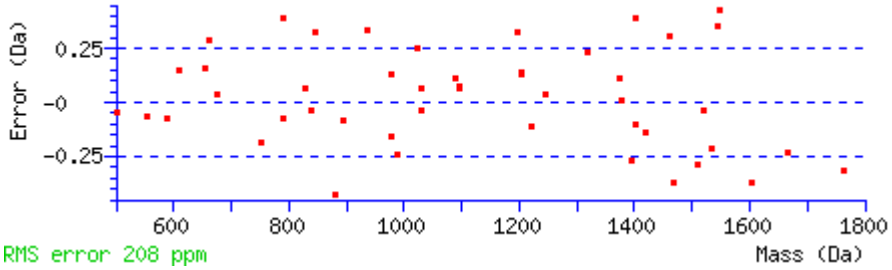
Variable modifications:

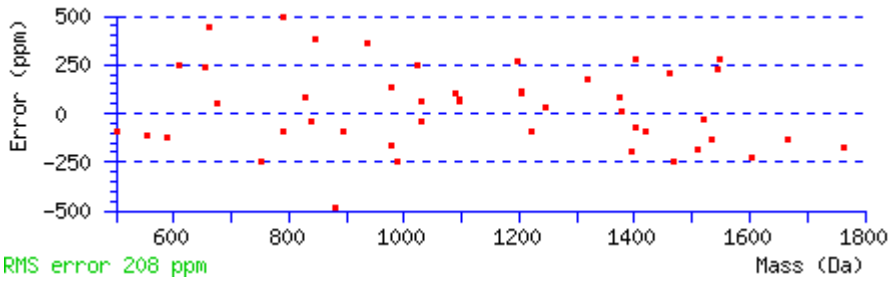
S28 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 49 Expect: 0.0031 (help)

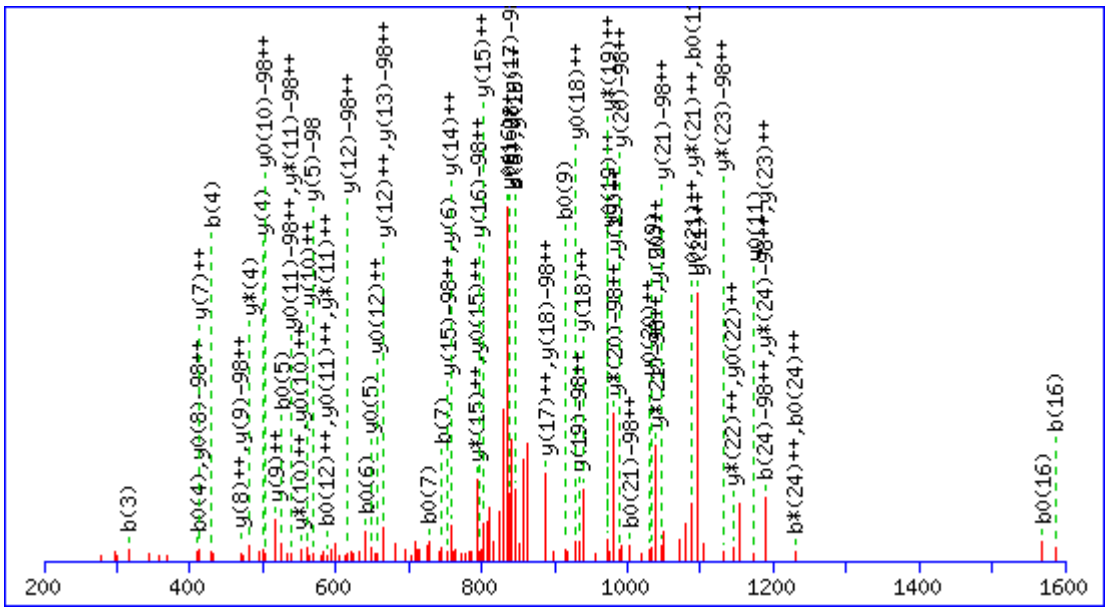
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	100.0757	50.5415					V							30
2	229.1183	115.0628			211.1077	106.0575	E	3356.4923	1678.7498	3339.4657	1670.2365	3338.4817	1669.7445	29
3	360.1588	180.5830			342.1482	171.5777	M	3227.4497	1614.2285	3210.4232	1605.7152	3209.4391	1605.2232	28
4	417.1802	209.0938			399.1697	200.0885	G	3096.4092	1548.7082	3079.3827	1540.1950	3078.3987	1539.7030	27
5	518.2279	259.6176			500.2173	250.6123	T	3039.3878	1520.1975	3022.3612	1511.6842	3021.3772	1511.1922	26
6	605.2599	303.1336			587.2494	294.1283	S	2938.3401	1469.6737	2921.3135	1461.1604	2920.3295	1460.6684	25
7	692.2920	346.6496			674.2814	337.6443	S	2851.3080	1426.1577	2834.2815	1417.6444	2833.2975	1417.1524	24
8	820.3505	410.6789	803.3240	402.1656	802.3400	401.6736	Q	2764.2760	1382.6416	2747.2495	1374.1284	2746.2655	1373.6364	23
9	934.3935	467.7004	917.3669	459.1871	916.3829	458.6951	N	2636.2174	1318.6124	2619.1909	1310.0991	2618.2069	1309.6071	22
10	1049.4204	525.2138	1032.3939	516.7006	1031.4099	516.2086	D	2522.1745	1261.5909	2505.1480	1253.0776	2504.1640	1252.5856	21
11	1148.4888	574.7481	1131.4623	566.2348	1130.4783	565.7428	V	2407.1476	1204.0774	2390.1210	1195.5641	2389.1370	1195.0721	20
12	1263.5158	632.2615	1246.4892	623.7482	1245.5052	623.2562	D	2308.0792	1154.5432	2291.0526	1146.0299	2290.0686	1145.5379	19
13	1394.5563	697.7818	1377.5297	689.2685	1376.5457	688.7765	M	2193.0522	1097.0297	2176.0257	1088.5165	2175.0417	1088.0245	18
14	1481.5883	741.2978	1464.5617	732.7845	1463.5777	732.2925	S	2062.0117	1031.5095	2044.9852	1022.9962	2044.0012	1022.5042	17
15	1667.6676	834.3374	1650.6410	825.8242	1649.6570	825.3322	W	1974.9797	987.9935	1957.9532	979.4802	1956.9691	978.9882	16
16	1780.7517	890.8795	1763.7251	882.3662	1762.7411	881.8742	I	1788.9004	894.9538	1771.8738	886.4406	1770.8898	885.9486	15
17	1877.8044	939.4059	1860.7779	930.8926	1859.7939	930.4006	P	1675.8163	838.4118	1658.7898	829.8985	1657.8058	829.4065	14
18	2005.8630	1003.4351	1988.8365	994.9219	1987.8524	994.4299	Q	1578.7636	789.8854	1561.7370	781.3721	1560.7530	780.8801	13
19	2134.9056	1067.9564	2117.8790	1059.4432	2116.8950	1058.9512	E	1450.7050	725.8561	1433.6784	717.3429	1432.6944	716.8508	12
20	2235.9533	1118.4803	2218.9267	1109.9670	2217.9427	1109.4750	T	1321.6624	661.3348	1304.6358	652.8216	1303.6518	652.3296	11
21	2349.0373	1175.0223	2332.0108	1166.5090	2331.0268	1166.0170	L	1220.6147	610.8110	1203.5882	602.2977	1202.6041	601.8057	10
22	2463.0803	1232.0438	2446.0537	1223.5305	2445.0697	1223.0385	N	1107.5306	554.2690	1090.5041	545.7557	1089.5201	545.2637	9
23	2591.1388	1296.0731	2574.1123	1287.5598	2573.1283	1287.0678	Q	993.4877	497.2475	976.4612	488.7342	975.4772	488.2422	8
24	2704.2229	1352.6151	2687.1964	1344.1018	2686.2123	1343.6098	I	865.4291	433.2182	848.4026	424.7049	847.4186	424.2129	7
25	2818.2658	1409.6366	2801.2393	1401.1233	2800.2553	1400.6313	N	752.3451	376.6762	735.3185	368.1629	734.3345	367.6709	6
26	2946.3608	1473.6840	2929.3342	1465.1708	2928.3502	1464.6788	K	638.3022	319.6547	621.2756	311.1414	620.2916	310.6494	5
27	3017.3979	1509.2026	3000.3714	1500.6893	2999.3873	1500.1973	A	510.2072	255.6072	493.1806	247.0940	492.1966	246.6020	4

28	3184.3963	1592.7018	3167.3697	1584.1885	3166.3857	1583.6965	S	439.1701	220.0887	422.1435	211.5754	421.1595	211.0834	3
29	3281.4490	1641.2282	3264.4225	1632.7149	3263.4385	1632.2229	P	272.1717	136.5895	255.1452	128.0762			2
30							R	175.1190	88.0631	158.0924	79.5498			1



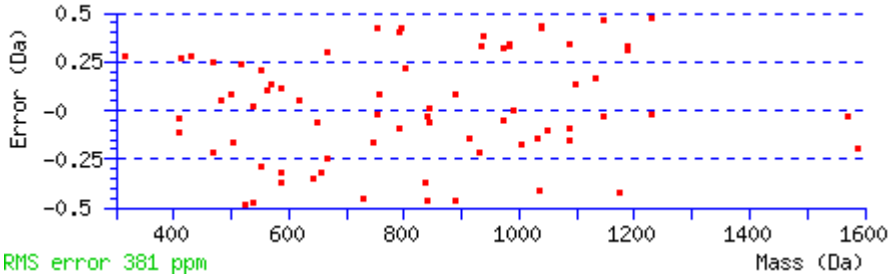


IDENTIFICATION 75
MS/MS Fragmentation of EDALDDSVSSSSVHASPLASSPVRK
Found in IPI00337844



Monoisotopic mass of neutral peptide Mr(calc): 2620.2018
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 79 Expect: 2.6e-06 (help)

#	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							25
2	245.0768	123.0420			227.0662	114.0368	D	2492.1665	1246.5869	2475.1399	1238.0736	2474.1559	1237.5816	24
3	316.1139	158.5606			298.1034	149.5553	A	2377.1395	1189.0734	2360.1130	1180.5601	2359.1289	1180.0681	23
4	429.1980	215.1026			411.1874	206.0974	L	2306.1024	1153.5548	2289.0758	1145.0416	2288.0918	1144.5496	22
5	544.2249	272.6161			526.2144	263.6108	D	2193.0183	1097.0128	2175.9918	1088.4995	2175.0078	1088.0075	21
6	659.2519	330.1296			641.2413	321.1243	D	2077.9914	1039.4993	2060.9648	1030.9861	2059.9808	1030.4940	20
7	746.2839	373.6456			728.2733	364.6403	S	1962.9644	981.9859	1945.9379	973.4726	1944.9539	972.9806	19
8	845.3523	423.1798			827.3418	414.1745	V	1875.9324	938.4698	1858.9059	929.9566	1857.9219	929.4646	18
9	932.3843	466.6958			914.3738	457.6905	S	1776.8640	888.9356	1759.8375	880.4224	1758.8534	879.9304	17
10	1019.4164	510.2118			1001.4058	501.2065	S	1689.8320	845.4196	1672.8054	836.9064	1671.8214	836.4143	16
11	1106.4484	553.7278			1088.4378	544.7226	S	1602.7999	801.9036	1585.7734	793.3903	1584.7894	792.8983	15
12	1193.4804	597.2439			1175.4699	588.2386	S	1515.7679	758.3876	1498.7414	749.8743	1497.7574	749.3823	14
13	1292.5488	646.7781			1274.5383	637.7728	V	1428.7359	714.8716	1411.7093	706.3583	1410.7253	705.8663	13
14	1429.6078	715.3075			1411.5972	706.3022	H	1329.6675	665.3374	1312.6409	656.8241	1311.6569	656.3321	12
15	1500.6449	750.8261			1482.6343	741.8208	A	1192.6086	596.8079	1175.5820	588.2946	1174.5980	587.8026	11
16	1587.6769	794.3421			1569.6663	785.3368	S	1121.5714	561.2894	1104.5449	552.7761	1103.5609	552.2841	10
17	1684.7297	842.8685			1666.7191	833.8632	P	1034.5394	517.7733	1017.5129	509.2601	1016.5289	508.7681	9
18	1797.8137	899.4105			1779.8032	890.4052	L	937.4867	469.2470	920.4601	460.7337	919.4761	460.2417	8
19	1868.8508	934.9291			1850.8403	925.9238	A	824.4026	412.7049	807.3760	404.1917	806.3920	403.6997	7
20	1955.8829	978.4451			1937.8723	969.4398	S	753.3655	377.1864	736.3389	368.6731	735.3549	368.1811	6
21	2122.8812	1061.9443			2104.8707	1052.9390	S	666.3335	333.6704	649.3069	325.1571	648.3229	324.6651	5
22	2219.9340	1110.4706			2201.9234	1101.4654	P	499.3351	250.1712	482.3085	241.6579			4
23	2319.0024	1160.0048			2300.9918	1150.9996	V	402.2823	201.6448	385.2558	193.1315			3
24	2475.1035	1238.0554	2458.0770	1229.5421	2457.0930	1229.0501	R	303.2139	152.1106	286.1874	143.5973			2
25							K	147.1128	74.0600	130.0863	65.5468			1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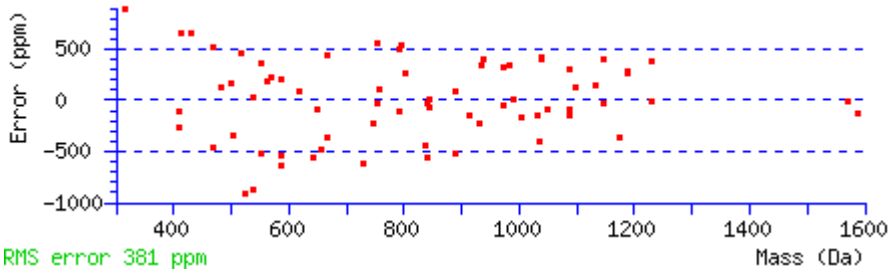
Mass (Da)
RMS error 381 ppm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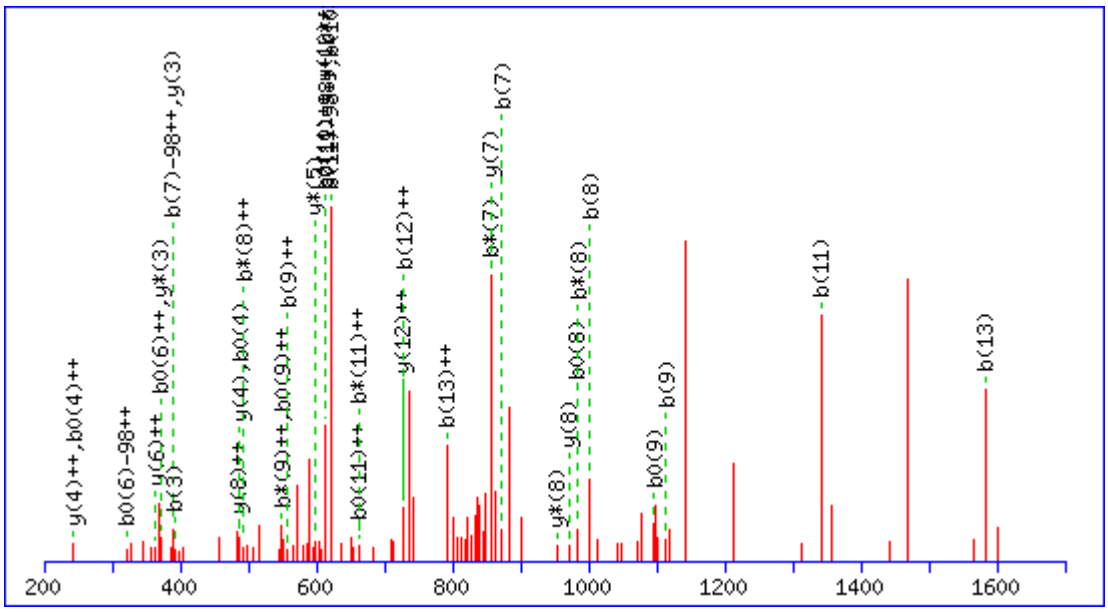
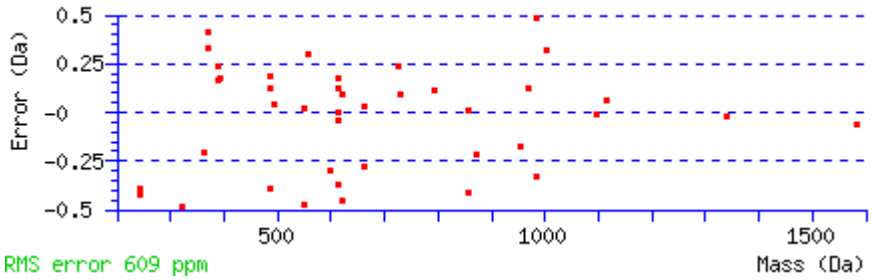
1400
1600
Mass (Da)
RMS error 381 ppm

IDENTIFICATION 76
MS/MS Fragmentation of YLDISSNKIQVIQK
Found in IPI00122181

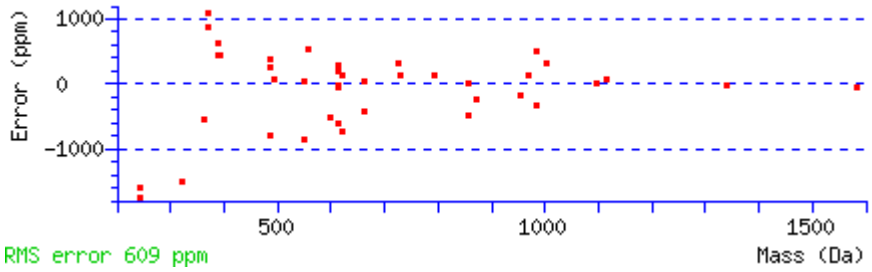


Monoisotopic mass of neutral peptide Mr(calc): 1727.8859
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 22 Expect: 0.64 (help)

#	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	277.1547	139.0810					L	1565.8298	783.4186	1548.8033	774.9053	1547.8193	774.4133	13
3	392.1816	196.5944			374.1710	187.5892	D	1452.7458	726.8765	1435.7192	718.3633	1434.7352	717.8712	12
4	505.2657	253.1365			487.2551	244.1312	I	1337.7188	669.3631	1320.6923	660.8498	1319.7083	660.3578	11
5	592.2977	296.6525			574.2871	287.6472	S	1224.6348	612.8210	1207.6082	604.3078	1206.6242	603.8157	10
6	759.2961	380.1517			741.2855	371.1464	S	1137.6028	569.3050	1120.5762	560.7917	1119.5922	560.2997	9
7	873.3390	437.1731	856.3124	428.6599	855.3284	428.1679	N	970.6044	485.8058	953.5778	477.2926			8
8	1001.4340	501.2206	984.4074	492.7073	983.4234	492.2153	K	856.5615	428.7844	839.5349	420.2711			7
9	1114.5180	557.7626	1097.4915	549.2494	1096.5075	548.7574	I	728.4665	364.7369	711.4400	356.2236			6
10	1242.5766	621.7919	1225.5500	613.2787	1224.5660	612.7867	Q	615.3824	308.1949	598.3559	299.6816			5
11	1341.6450	671.3261	1324.6185	662.8129	1323.6344	662.3209	V	487.3239	244.1656	470.2973	235.6523			4
12	1454.7291	727.8682	1437.7025	719.3549	1436.7185	718.8629	I	388.2554	194.6314	371.2289	186.1181			3
13	1582.7877	791.8975	1565.7611	783.3842	1564.7771	782.8922	Q	275.1714	138.0893	258.1448	129.5761			2
14							K	147.1128	74.0600	130.0863	65.5468			1

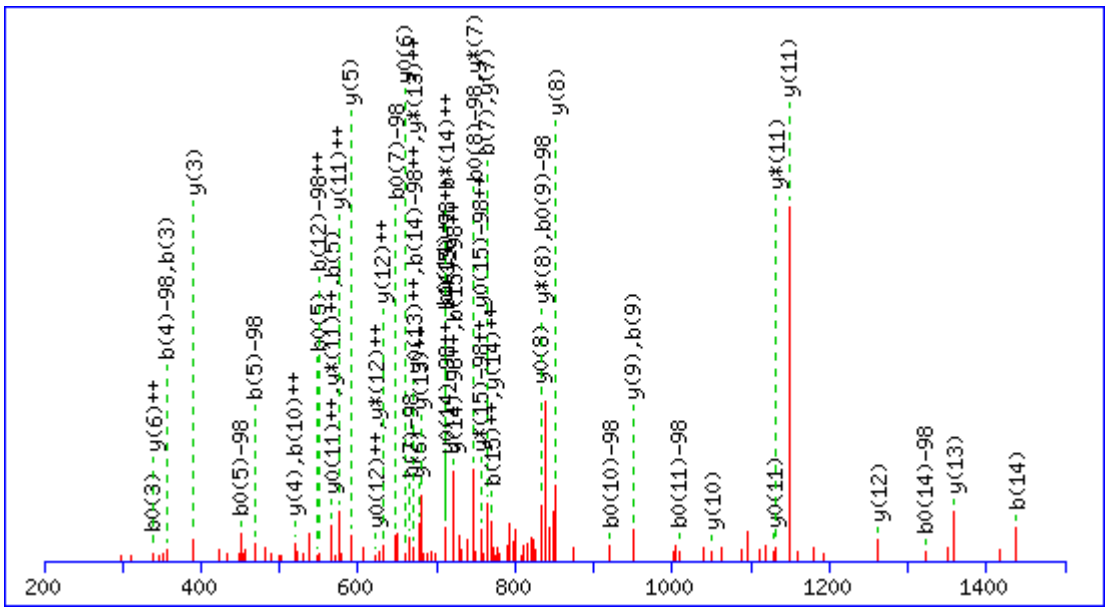


RMS error 609 ppm



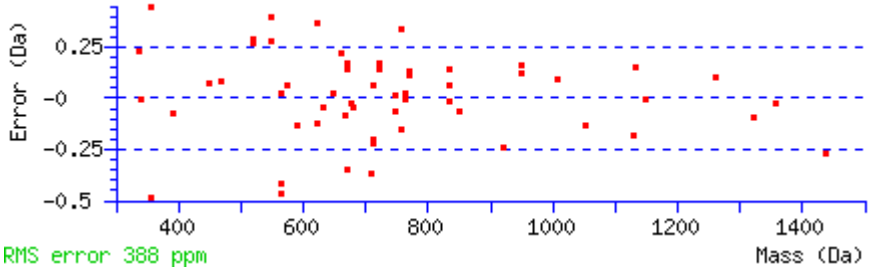
RMS error 609 ppm

IDENTIFICATION 77
MS/MS Fragmentation of SSTPLPTVSSSAENTR
Found in IPI00126338

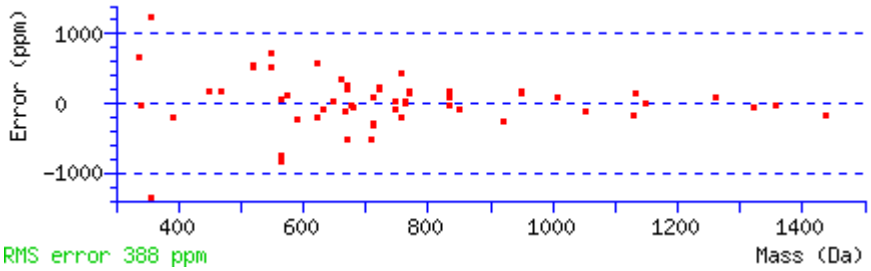


Monoisotopic mass of neutral peptide Mr(calc): 1712.7618
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 60 Expect: 0.00019 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							16
2	175.0713	88.0393			157.0608	79.0340	S	1528.7602	764.8837	1511.7336	756.3705	1510.7496	755.8784	15
3	258.1084	129.5579			240.0979	120.5526	T	1441.7281	721.3677	1424.7016	712.8544	1423.7176	712.3624	14
4	355.1612	178.0842			337.1506	169.0790	P	1358.6910	679.8492	1341.6645	671.3359	1340.6805	670.8439	13
5	468.2453	234.6263			450.2347	225.6210	L	1261.6383	631.3228	1244.6117	622.8095	1243.6277	622.3175	12
6	565.2980	283.1527			547.2875	274.1474	P	1148.5542	574.7807	1131.5277	566.2675	1130.5436	565.7755	11
7	666.3457	333.6765			648.3352	324.6712	T	1051.5014	526.2544	1034.4749	517.7411	1033.4909	517.2491	10
8	765.4141	383.2107			747.4036	374.2054	V	950.4538	475.7305	933.4272	467.2172	932.4432	466.7252	9
9	852.4462	426.7267			834.4356	417.7214	S	851.3853	426.1963	834.3588	417.6830	833.3748	417.1910	8
10	939.4782	470.2427			921.4676	461.2374	S	764.3533	382.6803	747.3268	374.1670	746.3428	373.6750	7
11	1026.5102	513.7587			1008.4997	504.7535	S	677.3213	339.1643	660.2947	330.6510	659.3107	330.1590	6
12	1097.5473	549.2773			1079.5368	540.2720	A	590.2893	295.6483	573.2627	287.1350	572.2787	286.6430	5
13	1226.5899	613.7986			1208.5794	604.7933	E	519.2522	260.1297	502.2256	251.6164	501.2416	251.1244	4
14	1340.6328	670.8201	1323.6063	662.3068	1322.6223	661.8148	N	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
15	1441.6805	721.3439	1424.6540	712.8306	1423.6700	712.3386	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
16							R	175.1190	88.0631	158.0924	79.5498			1

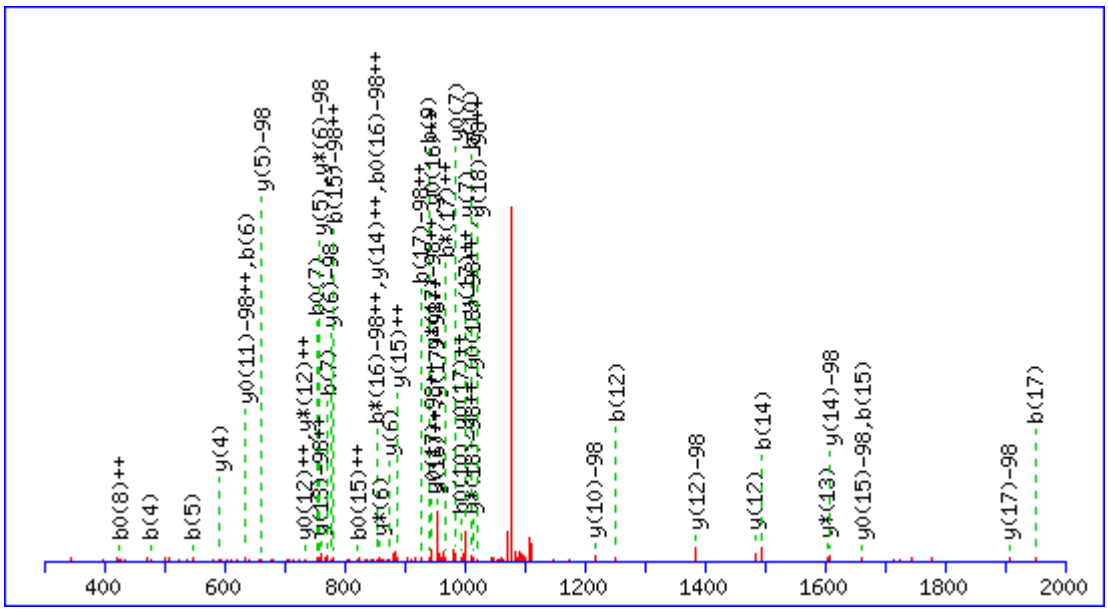


RMS error 388 ppm



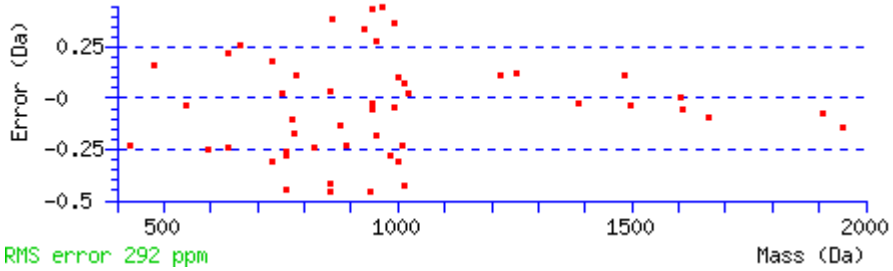
RMS error 388 ppm

IDENTIFICATION 78
MS/MS Fragmentation of IHPEASHPAAIQQDSCEER
Found in IPI00113389

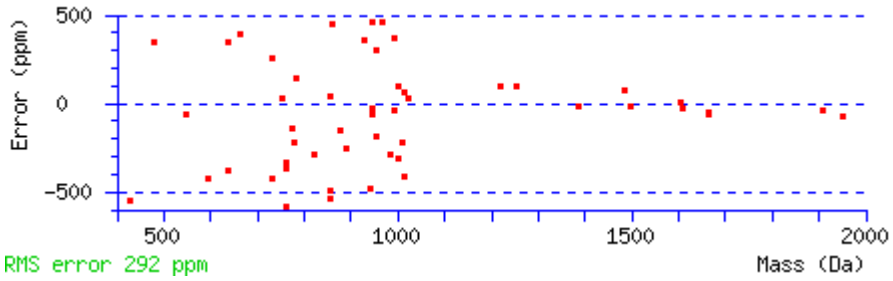


Monoisotopic mass of neutral peptide Mr(calc): 2253.9474
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 31 Expect: 0.19 (help)

#	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	251.1503	126.0788					H	2043.8937	1022.4505	2026.8672	1013.9372	2025.8832	1013.4452	18
3	348.2030	174.6051					P	1906.8348	953.9210	1889.8083	945.4078	1888.8243	944.9158	17
4	477.2456	239.1264			459.2350	230.1212	E	1809.7821	905.3947	1792.7555	896.8814	1791.7715	896.3894	16
5	548.2827	274.6450			530.2722	265.6397	A	1680.7395	840.8734	1663.7129	832.3601	1662.7289	831.8681	15
6	635.3148	318.1610			617.3042	309.1557	S	1609.7023	805.3548	1592.6758	796.8415	1591.6918	796.3495	14
7	772.3737	386.6905			754.3631	377.6852	H	1522.6703	761.8388	1505.6438	753.3255	1504.6598	752.8335	13
8	869.4264	435.2169			851.4159	426.2116	P	1385.6114	693.3093	1368.5849	684.7961	1367.6008	684.3041	12
9	940.4635	470.7354			922.4530	461.7301	A	1288.5586	644.7830	1271.5321	636.2697	1270.5481	635.7777	11
10	1011.5007	506.2540			993.4901	497.2487	A	1217.5215	609.2644	1200.4950	600.7511	1199.5110	600.2591	10
11	1124.5847	562.7960			1106.5742	553.7907	I	1146.4844	573.7458	1129.4579	565.2326	1128.4738	564.7406	9
12	1252.6433	626.8253	1235.6167	618.3120	1234.6327	617.8200	Q	1033.4003	517.2038	1016.3738	508.6905	1015.3898	508.1985	8
13	1380.7019	690.8546	1363.6753	682.3413	1362.6913	681.8493	Q	905.3418	453.1745	888.3152	444.6612	887.3312	444.1692	7
14	1495.7288	748.3680	1478.7023	739.8548	1477.7183	739.3628	D	777.2832	389.1452	760.2566	380.6320	759.2726	380.1400	6
15	1564.7503	782.8788	1547.7237	774.3655	1546.7397	773.8735	S	662.2563	331.6318	645.2297	323.1185	644.2457	322.6265	5
16	1724.7809	862.8941	1707.7544	854.3808	1706.7704	853.8888	C	593.2348	297.1210	576.2082	288.6078	575.2242	288.1157	4
17	1853.8235	927.4154	1836.7970	918.9021	1835.8130	918.4101	E	433.2041	217.1057	416.1776	208.5924	415.1936	208.1004	3
18	1982.8661	991.9367	1965.8396	983.4234	1964.8556	982.9314	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
19							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 292 ppm

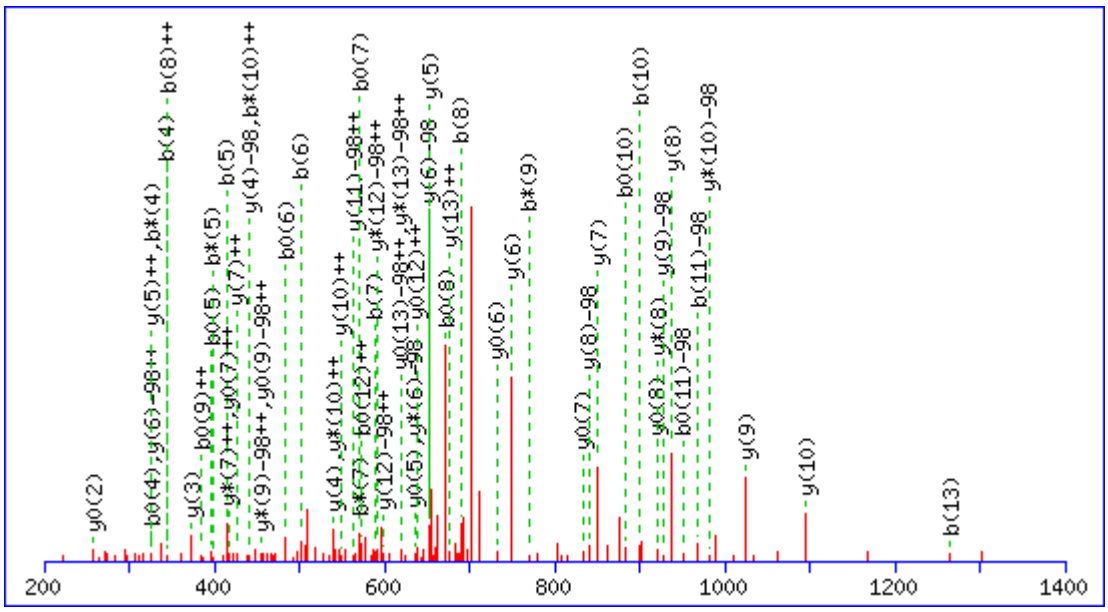


RMS error 292 ppm

IDENTIFICATION 79

MS/MS Fragmentation of SGAQASSTPLSPTR

Found in IPI00400300



Monoisotopic mass of neutral peptide Mr(calc): 1438.6453

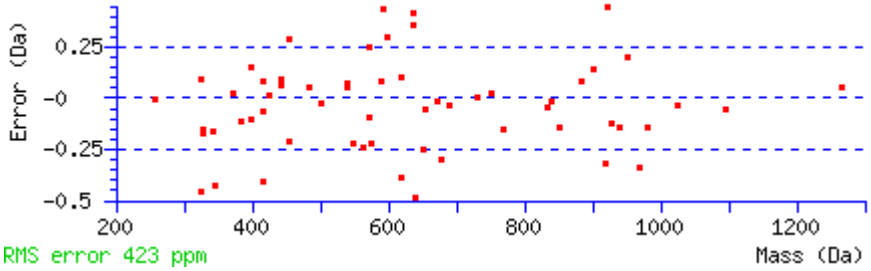
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

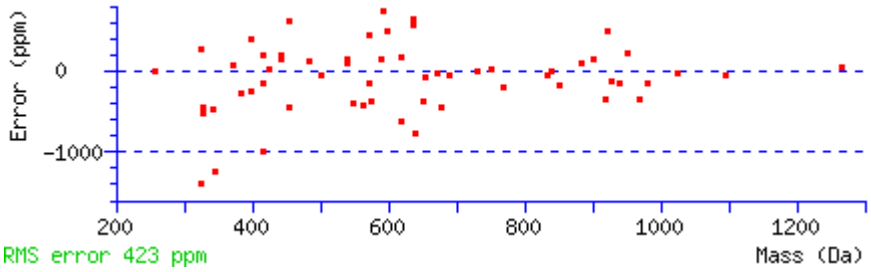
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 41 Expect: 0.012 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							14
2	145.0608	73.0340			127.0502	64.0287	G	1352.6206	676.8139	1335.5940	668.3007	1334.6100	667.8086	13
3	216.0979	108.5526			198.0873	99.5473	A	1295.5991	648.3032	1278.5726	639.7899	1277.5886	639.2979	12
4	344.1565	172.5819	327.1299	164.0686	326.1459	163.5766	Q	1224.5620	612.7846	1207.5355	604.2714	1206.5514	603.7794	11
5	415.1936	208.1004	398.1670	199.5872	397.1830	199.0951	A	1096.5034	548.7554	1079.4769	540.2421	1078.4929	539.7501	10
6	502.2256	251.6164	485.1991	243.1032	484.2150	242.6112	S	1025.4663	513.2368	1008.4398	504.7235	1007.4558	504.2315	9
7	589.2576	295.1325	572.2311	286.6192	571.2471	286.1272	S	938.4343	469.7208	921.4077	461.2075	920.4237	460.7155	8
8	690.3053	345.6563	673.2788	337.1430	672.2947	336.6510	T	851.4023	426.2048	834.3757	417.6915	833.3917	417.1995	7
9	787.3581	394.1827	770.3315	385.6694	769.3475	385.1774	P	750.3546	375.6809	733.3280	367.1677	732.3440	366.6756	6
10	900.4421	450.7247	883.4156	442.2114	882.4316	441.7194	L	653.3018	327.1545	636.2753	318.6413	635.2913	318.1493	5
11	1067.4405	534.2239	1050.4139	525.7106	1049.4299	525.2186	S	540.2178	270.6125	523.1912	262.0992	522.2072	261.6072	4
12	1164.4933	582.7503	1147.4667	574.2370	1146.4827	573.7450	P	373.2194	187.1133	356.1928	178.6001	355.2088	178.1081	3
13	1265.5409	633.2741	1248.5144	624.7608	1247.5304	624.2688	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

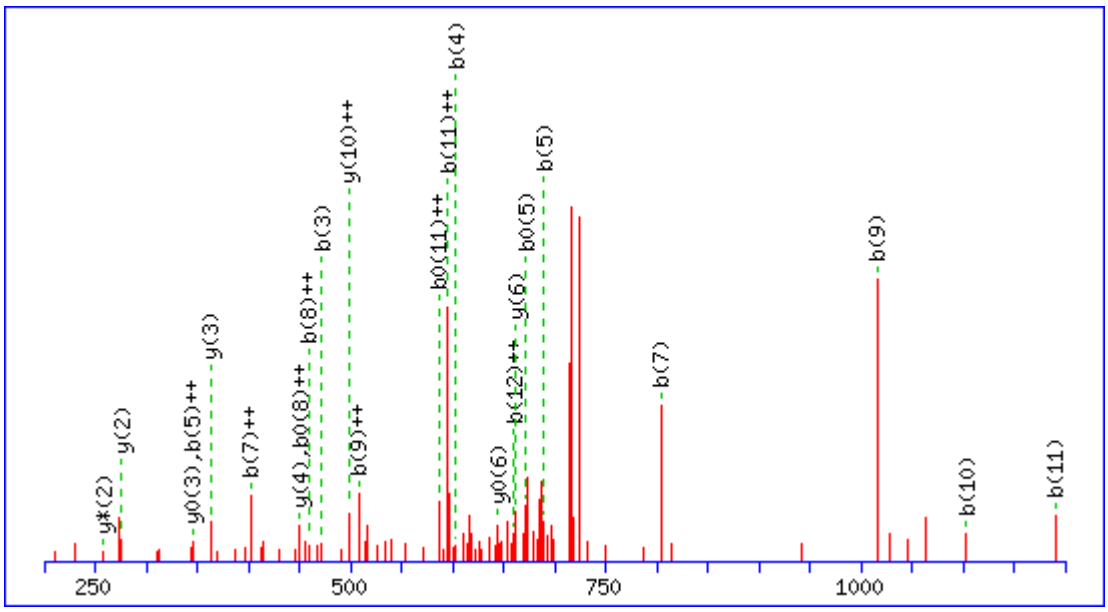


RMS error 423 ppm



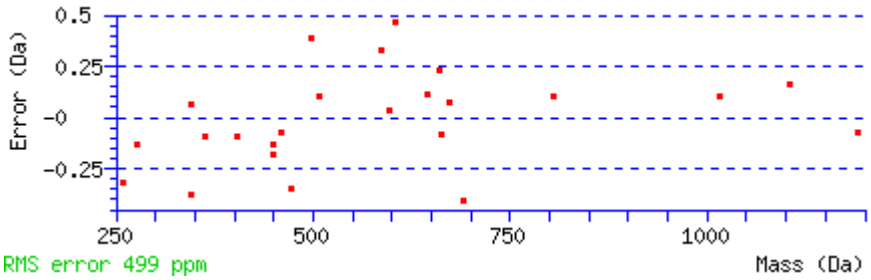
RMS error 423 ppm

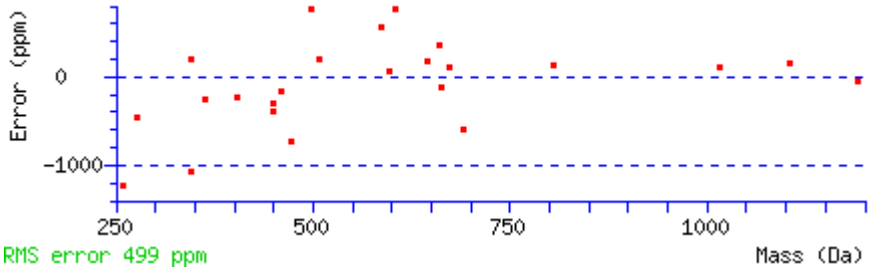
IDENTIFICATION 80
MS/MS Fragmentation of DYIMSGGLVSSEK
Found in IPI00330560



Monoisotopic mass of neutral peptide Mr(calc): 1464.6207
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
Y2 : Phospho (Y)
Ions Score: 23 Expect: 0.66 (help)

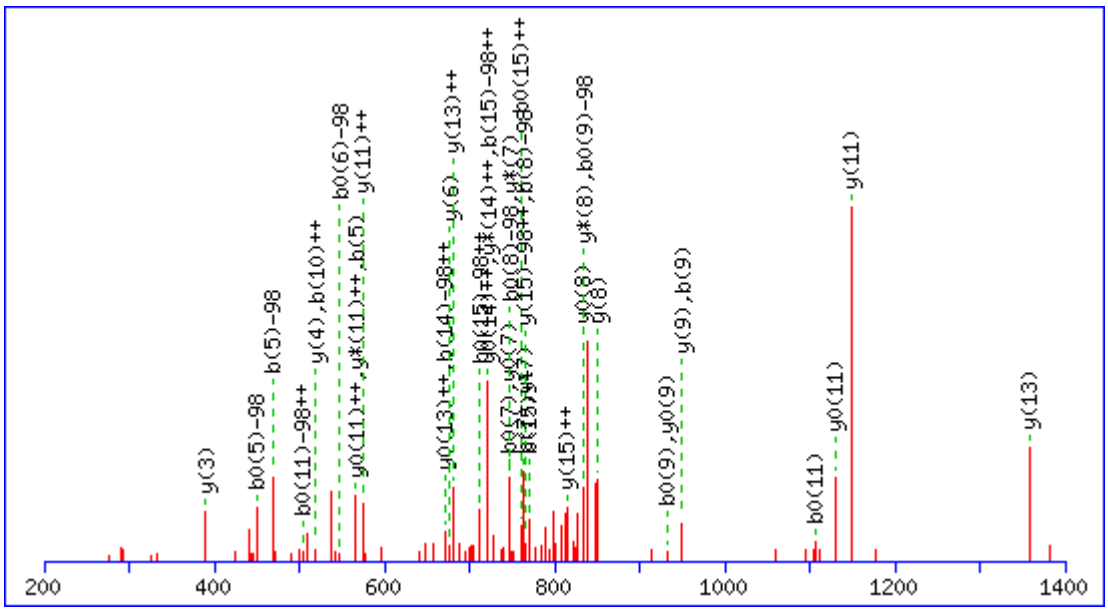
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207	98.0237	49.5155	D							13
2	359.0639	180.0356	341.0533	171.0303	Y	1350.6011	675.8042	1333.5745	667.2909	1332.5905	666.7989	12
3	472.1479	236.5776	454.1374	227.5723	I	1107.5714	554.2894	1090.5449	545.7761	1089.5609	545.2841	11
4	603.1884	302.0979	585.1779	293.0926	M	994.4874	497.7473	977.4608	489.2340	976.4768	488.7420	10
5	690.2205	345.6139	672.2099	336.6086	S	863.4469	432.2271	846.4203	423.7138	845.4363	423.2218	9
6	747.2419	374.1246	729.2314	365.1193	G	776.4149	388.7111	759.3883	380.1978	758.4043	379.7058	8
7	804.2634	402.6353	786.2528	393.6300	G	719.3934	360.2003	702.3668	351.6871	701.3828	351.1951	7
8	917.3474	459.1774	899.3369	450.1721	L	662.3719	331.6896	645.3454	323.1763	644.3614	322.6843	6
9	1016.4159	508.7116	998.4053	499.7063	V	549.2879	275.1476	532.2613	266.6343	531.2773	266.1423	5
10	1103.4479	552.2276	1085.4373	543.2223	S	450.2195	225.6134	433.1929	217.1001	432.2089	216.6081	4
11	1190.4799	595.7436	1172.4694	586.7383	S	363.1874	182.0974	346.1609	173.5841	345.1769	173.0921	3
12	1319.5225	660.2649	1301.5119	651.2596	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





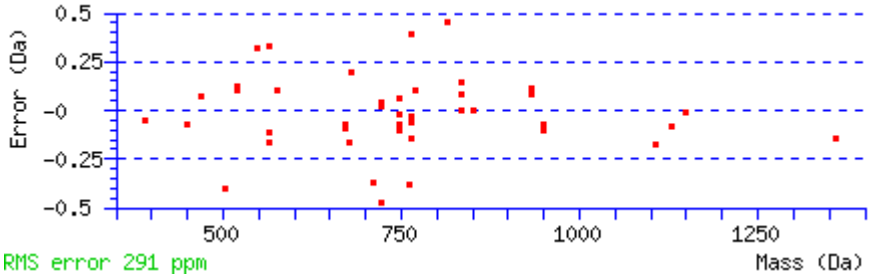
RMS error 499 ppm

IDENTIFICATION 81
MS/MS Fragmentation of SSTPLPTVSSSAENTR
Found in IPI00126338

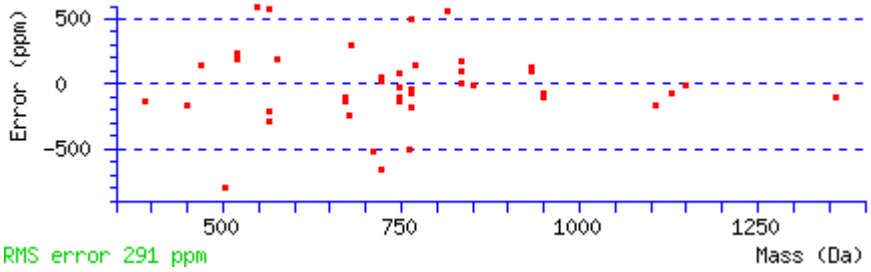


Monoisotopic mass of neutral peptide Mr(calc): 1712.7618
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 36 Expect: 0.038 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							16
2	255.0377	128.0225			237.0271	119.0172	S	1626.7371	813.8722	1609.7105	805.3589	1608.7265	804.8669	15
3	356.0853	178.5463			338.0748	169.5410	T	1459.7387	730.3730	1442.7122	721.8597	1441.7281	721.3677	14
4	453.1381	227.0727			435.1275	218.0674	P	1358.6910	679.8492	1341.6645	671.3359	1340.6805	670.8439	13
5	566.2222	283.6147			548.2116	274.6094	L	1261.6383	631.3228	1244.6117	622.8095	1243.6277	622.3175	12
6	663.2749	332.1411			645.2644	323.1358	P	1148.5542	574.7807	1131.5277	566.2675	1130.5436	565.7755	11
7	764.3226	382.6649			746.3120	373.6597	T	1051.5014	526.2544	1034.4749	517.7411	1033.4909	517.2491	10
8	863.3910	432.1992			845.3805	423.1939	V	950.4538	475.7305	933.4272	467.2172	932.4432	466.7252	9
9	950.4231	475.7152			932.4125	466.7099	S	851.3853	426.1963	834.3588	417.6830	833.3748	417.1910	8
10	1037.4551	519.2312			1019.4445	510.2259	S	764.3533	382.6803	747.3268	374.1670	746.3428	373.6750	7
11	1124.4871	562.7472			1106.4765	553.7419	S	677.3213	339.1643	660.2947	330.6510	659.3107	330.1590	6
12	1195.5242	598.2658			1177.5137	589.2605	A	590.2893	295.6483	573.2627	287.1350	572.2787	286.6430	5
13	1324.5668	662.7870			1306.5563	653.7818	E	519.2522	260.1297	502.2256	251.6164	501.2416	251.1244	4
14	1438.6097	719.8085	1421.5832	711.2952	1420.5992	710.8032	N	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
15	1539.6574	770.3324	1522.6309	761.8191	1521.6469	761.3271	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
16							R	175.1190	88.0631	158.0924	79.5498			1

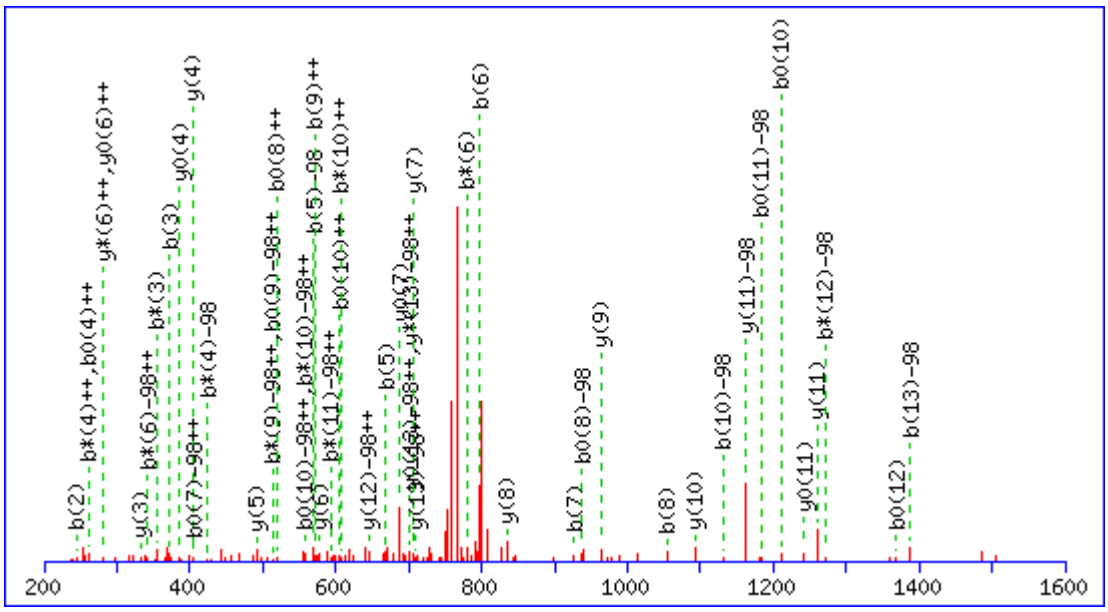


RMS error 291 ppm



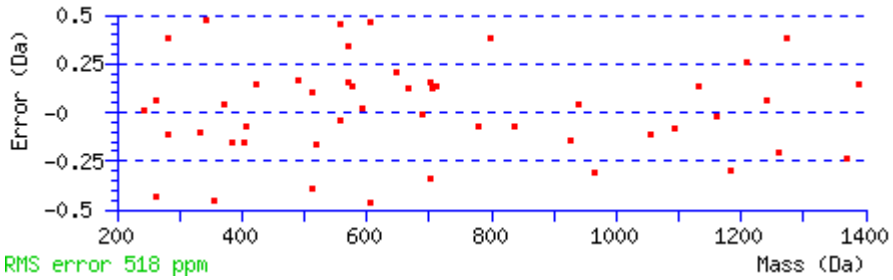
RMS error 291 ppm

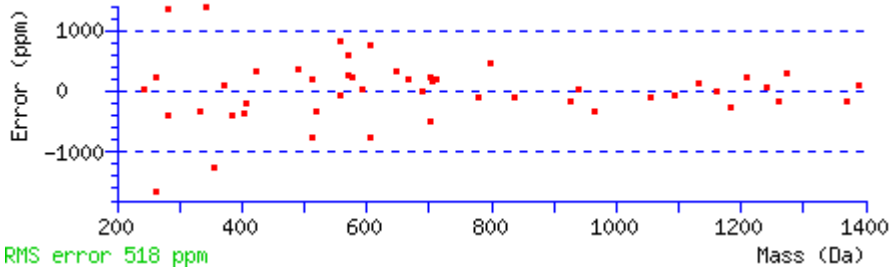
IDENTIFICATION 82
MS/MS Fragmentation of NEKSEEEQSSASVK
Found in IPI00130343



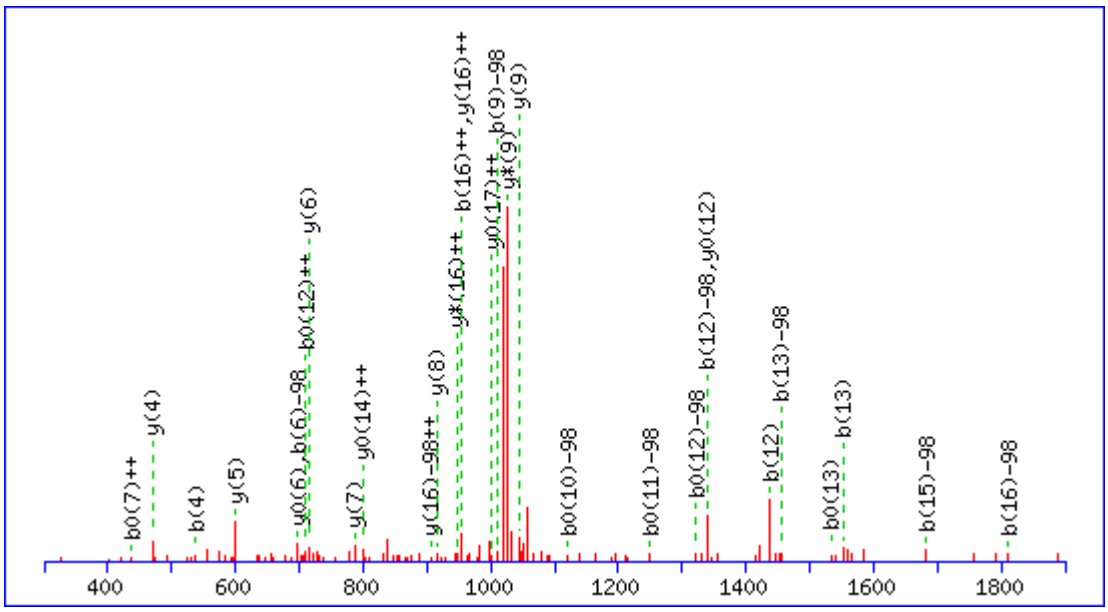
Monoisotopic mass of neutral peptide Mr(calc): 1630.6723
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 26 Expect: 0.37 (help)

#	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	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	E	1419.6598	710.3335	1402.6332	701.8203	1401.6492	701.3283	13
3	372.1878	186.5975	355.1612	178.0842	354.1772	177.5922	K	1290.6172	645.8122	1273.5907	637.2990	1272.6066	636.8070	12
4	441.2092	221.1082	424.1827	212.5950	423.1987	212.1030	S	1162.5222	581.7648	1145.4957	573.2515	1144.5117	572.7595	11
5	570.2518	285.6295	553.2253	277.1163	552.2413	276.6243	E	1093.5008	547.2540	1076.4742	538.7408	1075.4902	538.2487	10
6	699.2944	350.1508	682.2679	341.6376	681.2838	341.1456	E	964.4582	482.7327	947.4316	474.2195	946.4476	473.7274	9
7	828.3370	414.6721	811.3105	406.1589	810.3264	405.6669	E	835.4156	418.2114	818.3890	409.6982	817.4050	409.2061	8
8	956.3956	478.7014	939.3690	470.1882	938.3850	469.6961	Q	706.3730	353.6901	689.3464	345.1769	688.3624	344.6849	7
9	1043.4276	522.2174	1026.4011	513.7042	1025.4170	513.2122	S	578.3144	289.6608	561.2879	281.1476	560.3039	280.6556	6
10	1130.4596	565.7335	1113.4331	557.2202	1112.4491	556.7282	S	491.2824	246.1448	474.2558	237.6316	473.2718	237.1395	5
11	1201.4967	601.2520	1184.4702	592.7387	1183.4862	592.2467	A	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	4
12	1288.5288	644.7680	1271.5022	636.2548	1270.5182	635.7627	S	333.2132	167.1103	316.1867	158.5970	315.2027	158.1050	3
13	1387.5972	694.3022	1370.5706	685.7890	1369.5866	685.2970	V	246.1812	123.5942	229.1547	115.0810			2
14							K	147.1128	74.0600	130.0863	65.5468			1


0.5
0.25
-0
-0.25
-0.5
Error (Da)
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 518 ppm

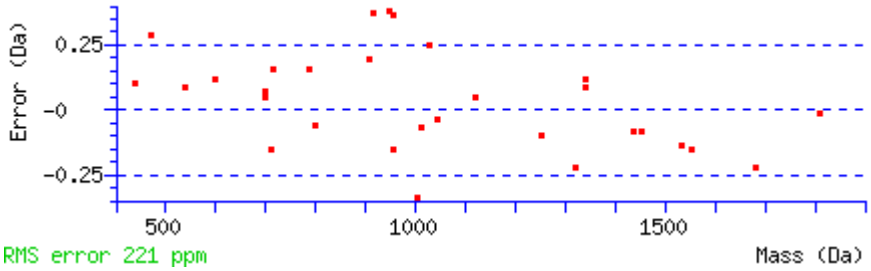

1000
0
-1000
Error (ppm)
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 518 ppm

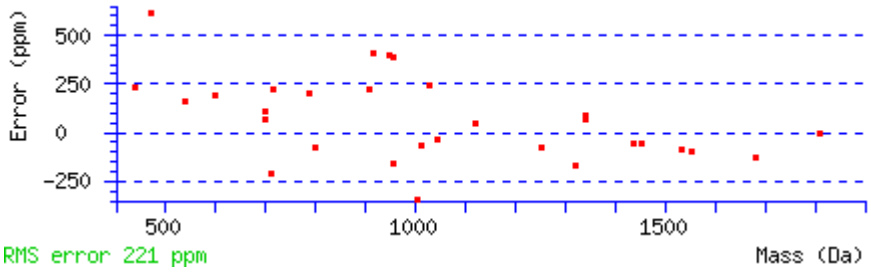
IDENTIFICATION 83
MS/MS Fragmentation of EIITEEPSEEEADMPKPK
Found in IPI00120691



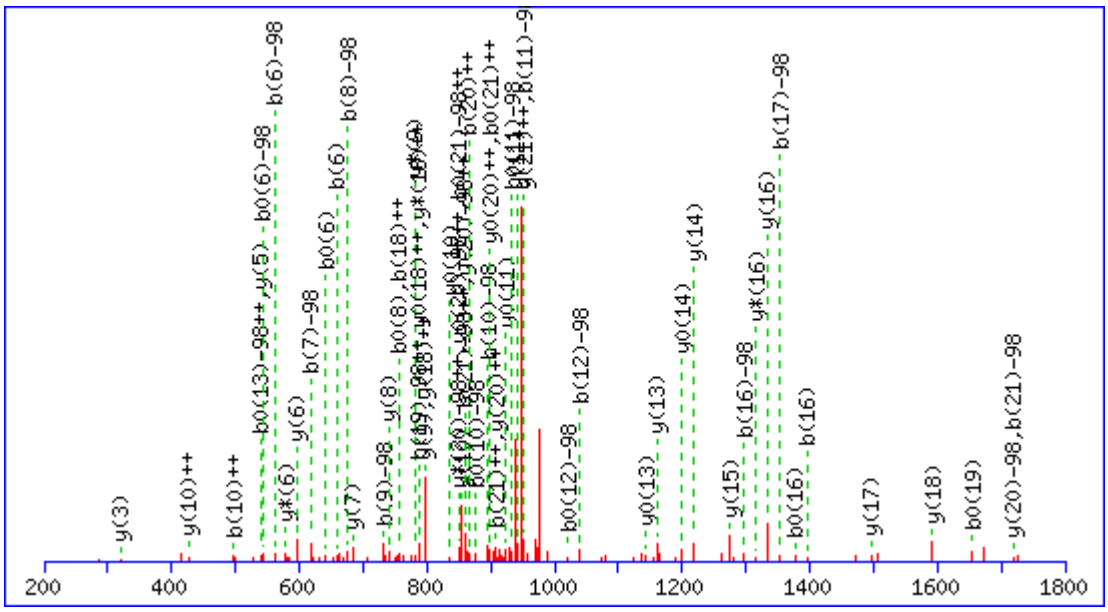
Monoisotopic mass of neutral peptide Mr(calc): 2150.9330
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 29 Expect: 0.23 (help)

#	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							18
2	243.1339	122.0706			225.1234	113.0653	I	1924.9208	962.9641	1907.8943	954.4508	1906.9103	953.9588	17
3	356.2180	178.6126			338.2074	169.6074	I	1811.8368	906.4220	1794.8102	897.9087	1793.8262	897.4167	16
4	439.2551	220.1312			421.2445	211.1259	T	1698.7527	849.8800	1681.7262	841.3667	1680.7421	840.8747	15
5	568.2977	284.6525			550.2871	275.6472	E	1615.7156	808.3614	1598.6890	799.8482	1597.7050	799.3562	14
6	697.3403	349.1738			679.3297	340.1685	E	1486.6730	743.8401	1469.6465	735.3269	1468.6624	734.8349	13
7	794.3931	397.7002			776.3825	388.6949	P	1357.6304	679.3188	1340.6039	670.8056	1339.6198	670.3136	12
8	881.4251	441.2162			863.4145	432.2109	S	1260.5776	630.7925	1243.5511	622.2792	1242.5671	621.7872	11
9	1010.4677	505.7375			992.4571	496.7322	E	1173.5456	587.2764	1156.5191	578.7632	1155.5351	578.2712	10
10	1139.5103	570.2588			1121.4997	561.2535	E	1044.5030	522.7551	1027.4765	514.2419	1026.4925	513.7499	9
11	1268.5529	634.7801			1250.5423	625.7748	E	915.4604	458.2339	898.4339	449.7206	897.4499	449.2286	8
12	1339.5900	670.2986			1321.5794	661.2933	A	786.4178	393.7126	769.3913	385.1993	768.4073	384.7073	7
13	1454.6169	727.8121			1436.6064	718.8068	D	715.3807	358.1940	698.3542	349.6807	697.3702	349.1887	6
14	1585.6574	793.3323			1567.6468	784.3271	M	600.3538	300.6805	583.3272	292.1673			5
15	1682.7102	841.8587			1664.6996	832.8534	P	469.3133	235.1603	452.2867	226.6470			4
16	1810.8051	905.9062	1793.7786	897.3929	1792.7946	896.9009	K	372.2605	186.6339	355.2340	178.1206			3
17	1907.8579	954.4326	1890.8314	945.9193	1889.8473	945.4273	P	244.1656	122.5864	227.1390	114.0731			2
18							K	147.1128	74.0600	130.0863	65.5468			1


Error (Da)
0.25
-0
-0.25
500
1000
1500
RMS error 221 ppm
Mass (Da)

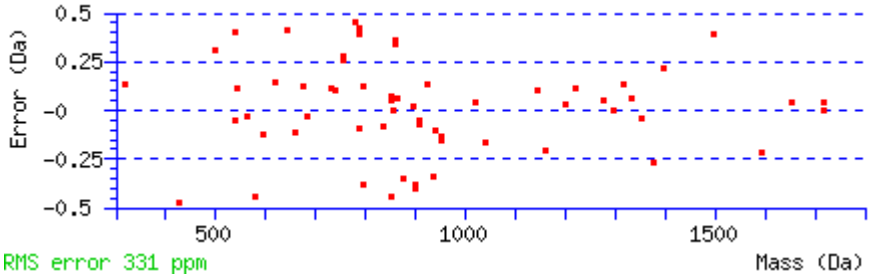

Error (ppm)
500
250
0
-250
500
1000
1500
RMS error 221 ppm
Mass (Da)

IDENTIFICATION 84
MS/MS Fragmentation of SSGSPYGGGYGSGGGSGGYGSR
Found in IPI00269661

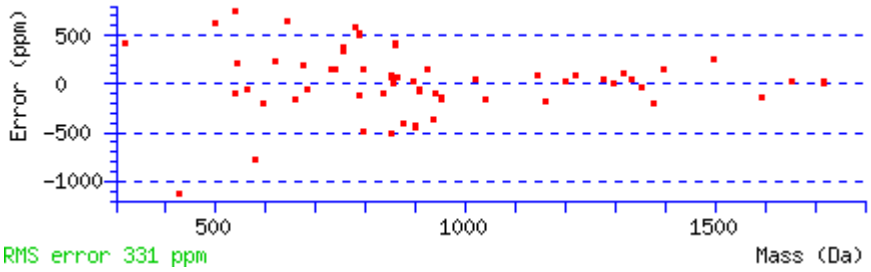


Monoisotopic mass of neutral peptide Mr(calc): 1989.7491
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 97 Expect: 2.8e-08 (help)

#	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							22
2	175.0713	88.0393	157.0608	79.0340	S	1805.7474	903.3773	1788.7208	894.8641	1787.7368	894.3720	21
3	232.0928	116.5500	214.0822	107.5448	G	1718.7154	859.8613	1701.6888	851.3480	1700.7048	850.8560	20
4	301.1143	151.0608	283.1037	142.0555	S	1661.6939	831.3506	1644.6673	822.8373	1643.6833	822.3453	19
5	398.1670	199.5871	380.1565	190.5819	P	1592.6724	796.8399	1575.6459	788.3266	1574.6619	787.8346	18
6	561.2304	281.1188	543.2198	272.1135	Y	1495.6197	748.3135	1478.5931	739.8002	1477.6091	739.3082	17
7	618.2518	309.6295	600.2413	300.6243	G	1332.5563	666.7818	1315.5298	658.2685	1314.5458	657.7765	16
8	675.2733	338.1403	657.2627	329.1350	G	1275.5349	638.2711	1258.5083	629.7578	1257.5243	629.2658	15
9	732.2947	366.6510	714.2842	357.6457	G	1218.5134	609.7603	1201.4869	601.2471	1200.5028	600.7551	14
10	895.3581	448.1827	877.3475	439.1774	Y	1161.4919	581.2496	1144.4654	572.7363	1143.4814	572.2443	13
11	952.3795	476.6934	934.3690	467.6881	G	998.4286	499.7179	981.4021	491.2047	980.4180	490.7127	12
12	1039.4116	520.2094	1021.4010	511.2041	S	941.4071	471.2072	924.3806	462.6939	923.3966	462.2019	11
13	1096.4330	548.7202	1078.4225	539.7149	G	854.3751	427.6912	837.3486	419.1779	836.3646	418.6859	10
14	1153.4545	577.2309	1135.4439	568.2256	G	797.3537	399.1805	780.3271	390.6672	779.3431	390.1752	9
15	1210.4760	605.7416	1192.4654	596.7363	G	740.3322	370.6697	723.3056	362.1565	722.3216	361.6645	8
16	1297.5080	649.2576	1279.4974	640.2523	S	683.3107	342.1590	666.2842	333.6457	665.3002	333.1537	7
17	1354.5294	677.7684	1336.5189	668.7631	G	596.2787	298.6430	579.2522	290.1297	578.2681	289.6377	6
18	1411.5509	706.2791	1393.5403	697.2738	G	539.2572	270.1323	522.2307	261.6190	521.2467	261.1270	5
19	1574.6142	787.8108	1556.6037	778.8055	Y	482.2358	241.6215	465.2092	233.1082	464.2252	232.6162	4
20	1631.6357	816.3215	1613.6251	807.3162	G	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
21	1718.6677	859.8375	1700.6572	850.8322	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
22					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 331 ppm



RMS error 331 ppm

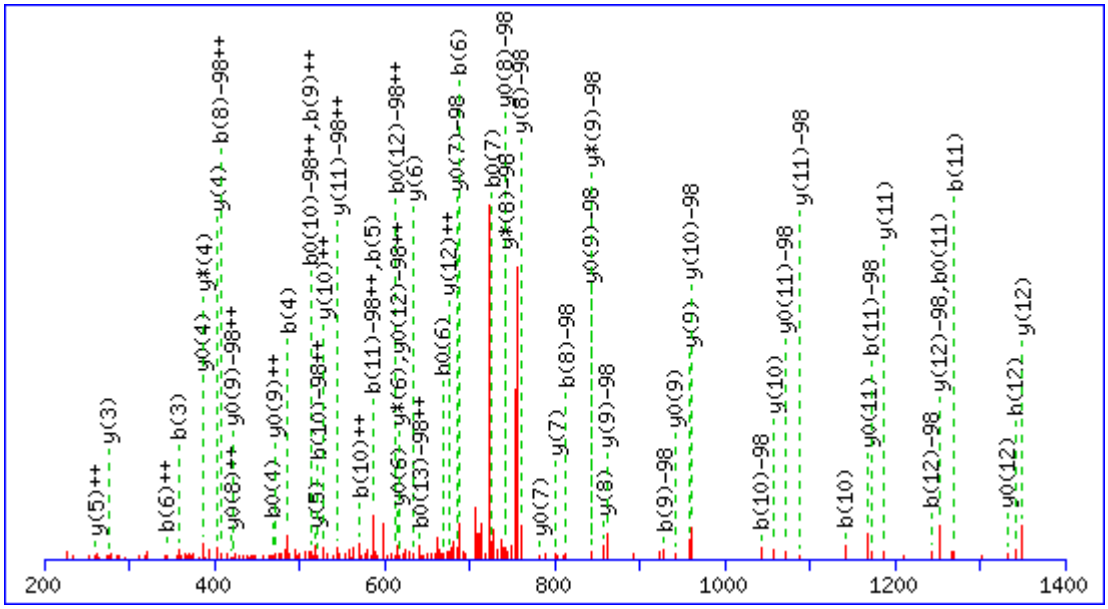
IDENTIFICATION 85

MS/MS Fragmentation of

GHYEVTGSDDEAGK

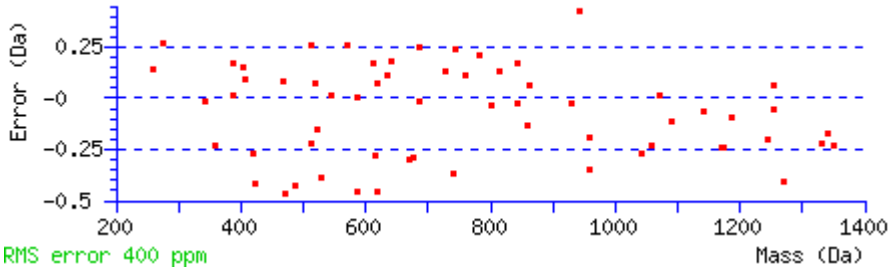
Found in

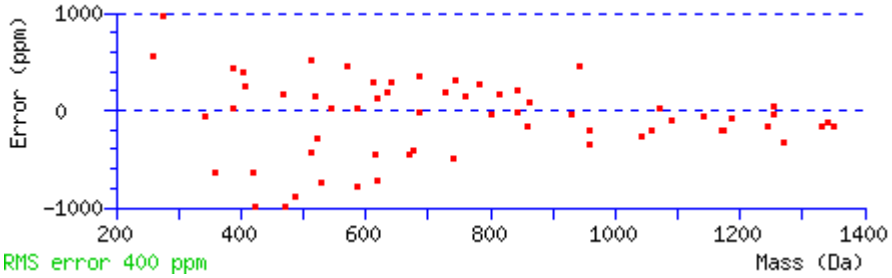
IPI00553798



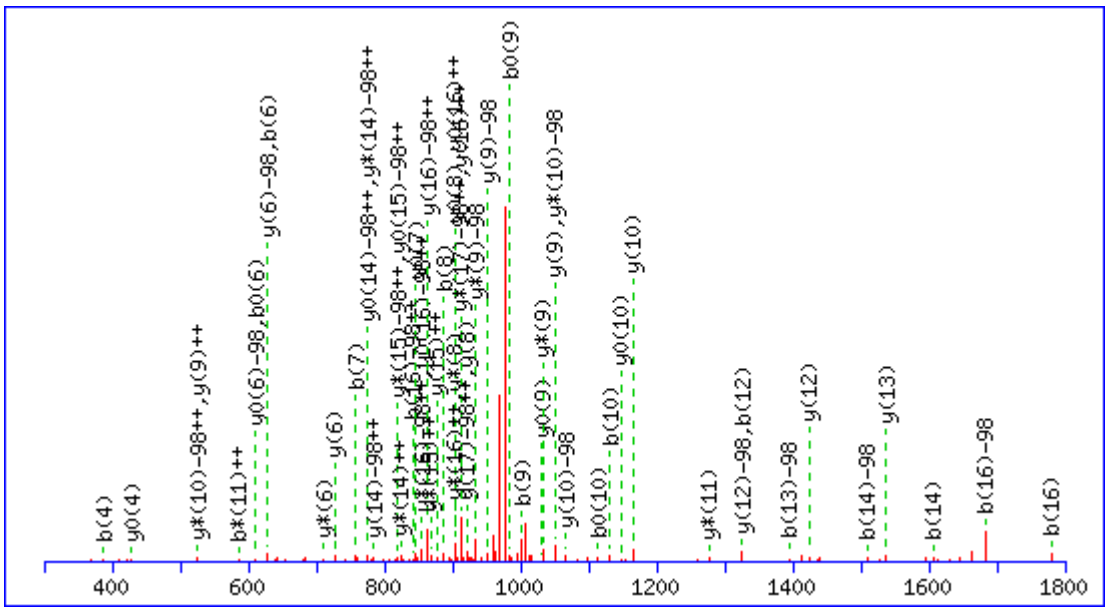
Monoisotopic mass of neutral peptide Mr(calc): 1543.5828
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 47 Expect: 0.002 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180			G							14
2	195.0877	98.0475			H	1389.5917	695.2995	1372.5652	686.7862	1371.5812	686.2942	13
3	358.1510	179.5791			Y	1252.5328	626.7700	1235.5063	618.2568	1234.5222	617.7648	12
4	487.1936	244.1004	469.1830	235.0951	E	1089.4695	545.2384	1072.4429	536.7251	1071.4589	536.2331	11
5	586.2620	293.6346	568.2514	284.6293	V	960.4269	480.7171	943.4003	472.2038	942.4163	471.7118	10
6	687.3097	344.1585	669.2991	335.1532	T	861.3585	431.1829	844.3319	422.6696	843.3479	422.1776	9
7	744.3311	372.6692	726.3206	363.6639	G	760.3108	380.6590	743.2842	372.1458	742.3002	371.6537	8
8	813.3526	407.1799	795.3420	398.1747	S	703.2893	352.1483	686.2628	343.6350	685.2788	343.1430	7
9	928.3795	464.6934	910.3690	455.6881	D	634.2679	317.6376	617.2413	309.1243	616.2573	308.6323	6
10	1043.4065	522.2069	1025.3959	513.2016	D	519.2409	260.1241	502.2144	251.6108	501.2304	251.1188	5
11	1172.4491	586.7282	1154.4385	577.7229	E	404.2140	202.6106	387.1874	194.0974	386.2034	193.6053	4
12	1243.4862	622.2467	1225.4756	613.2414	A	275.1714	138.0893	258.1448	129.5761			3
13	1300.5077	650.7575	1282.4971	641.7522	G	204.1343	102.5708	187.1077	94.0575			2
14					K	147.1128	74.0600	130.0863	65.5468			1


Error (Da)
0.25
-0
-0.25
-0.5
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 400 ppm

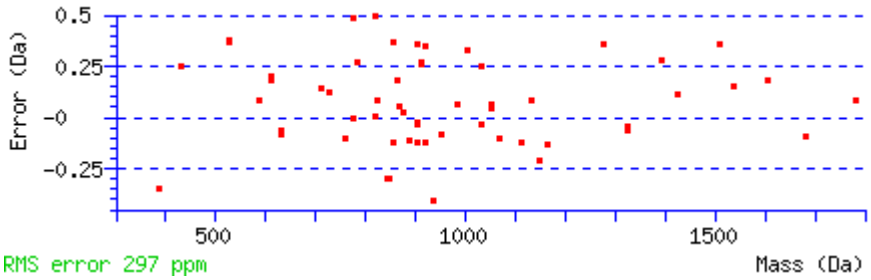

Error (ppm)
1000
0
-1000
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 400 ppm

IDENTIFICATION 86
MS/MS Fragmentation of IDASKNEEDEGHSNSSPR
Found in IPI00330958

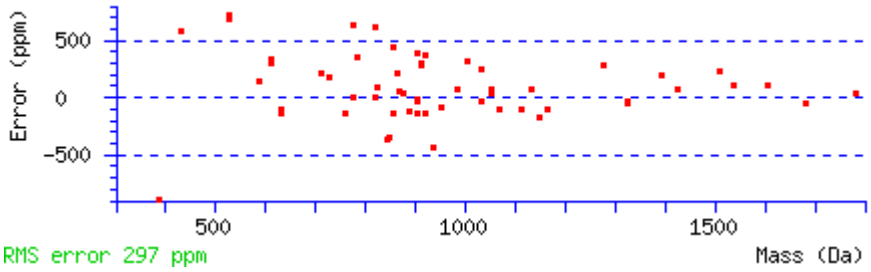


Monoisotopic mass of neutral peptide Mr(calc): 2050.8229
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 46 Expect: 0.0044 (help)

#	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	229.1183	115.0628			211.1077	106.0575	D	1840.7692	920.8883	1823.7427	912.3750	1822.7587	911.8830	17
3	300.1554	150.5813			282.1448	141.5761	A	1725.7423	863.3748	1708.7157	854.8615	1707.7317	854.3695	16
4	387.1874	194.0974			369.1769	185.0921	S	1654.7052	827.8562	1637.6786	819.3430	1636.6946	818.8509	15
5	515.2824	258.1448	498.2558	249.6316	497.2718	249.1395	K	1567.6732	784.3402	1550.6466	775.8269	1549.6626	775.3349	14
6	629.3253	315.1663	612.2988	306.6530	611.3148	306.1610	N	1439.5782	720.2927	1422.5516	711.7795	1421.5676	711.2874	13
7	758.3679	379.6876	741.3414	371.1743	740.3573	370.6823	E	1325.5353	663.2713	1308.5087	654.7580	1307.5247	654.2660	12
8	887.4105	444.2089	870.3840	435.6956	869.3999	435.2036	E	1196.4927	598.7500	1179.4661	590.2367	1178.4821	589.7447	11
9	1002.4374	501.7224	985.4109	493.2091	984.4269	492.7171	D	1067.4501	534.2287	1050.4235	525.7154	1049.4395	525.2234	10
10	1131.4800	566.2437	1114.4535	557.7304	1113.4695	557.2384	E	952.4231	476.7152	935.3966	468.2019	934.4126	467.7099	9
11	1188.5015	594.7544	1171.4750	586.2411	1170.4909	585.7491	G	823.3805	412.1939	806.3540	403.6806	805.3700	403.1886	8
12	1325.5604	663.2838	1308.5339	654.7706	1307.5498	654.2786	H	766.3591	383.6832	749.3325	375.1699	748.3485	374.6779	7
13	1394.5819	697.7946	1377.5553	689.2813	1376.5713	688.7893	S	629.3002	315.1537	612.2736	306.6404	611.2896	306.1484	6
14	1508.6248	754.8160	1491.5983	746.3028	1490.6142	745.8108	N	560.2787	280.6430	543.2522	272.1297	542.2681	271.6377	5
15	1595.6568	798.3321	1578.6303	789.8188	1577.6463	789.3268	S	446.2358	223.6215	429.2092	215.1082	428.2252	214.6162	4
16	1682.6889	841.8481	1665.6623	833.3348	1664.6783	832.8428	S	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
17	1779.7416	890.3744	1762.7151	881.8612	1761.7311	881.3692	P	272.1717	136.5895	255.1452	128.0762			2
18							R	175.1190	88.0631	158.0924	79.5498			1

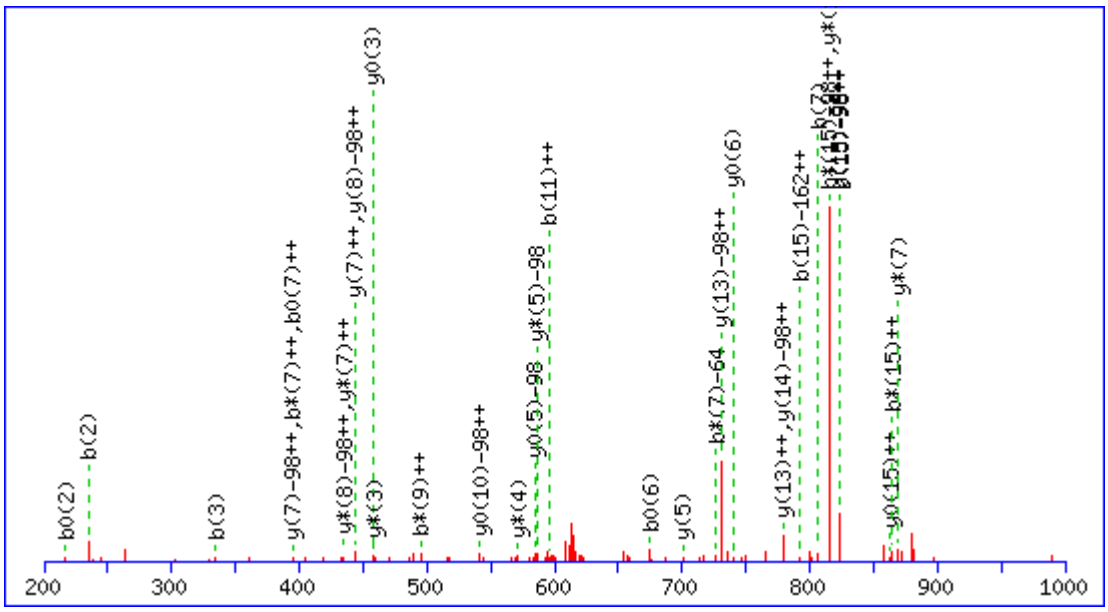


RMS error 297 ppm



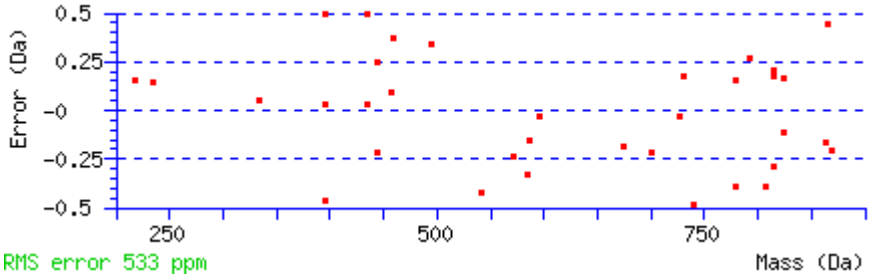
RMS error 297 ppm

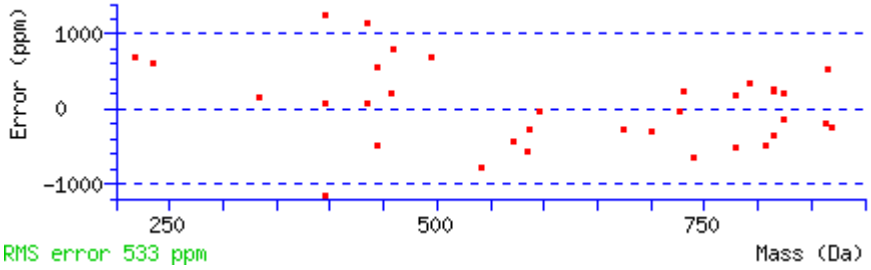
IDENTIFICATION 87
MS/MS Fragmentation of MSVFLVNTPQGLLTFK
Found in IPI00885690



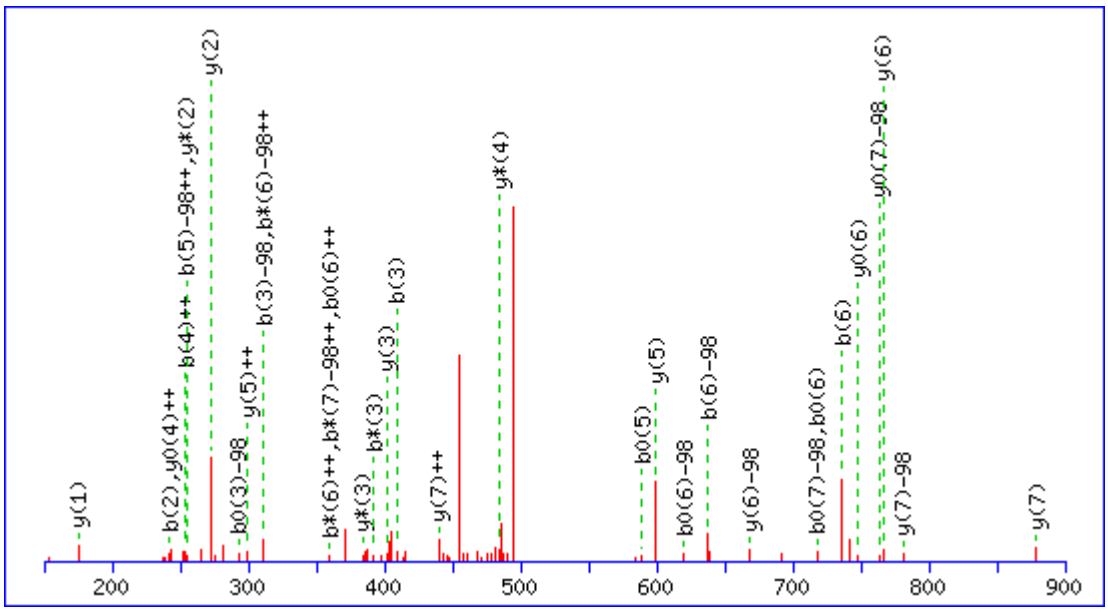
Monoisotopic mass of neutral peptide Mr(calc): 1889.9362
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
M1 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
T14 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 21 Expect: 0.86 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y_{0}	y^{0++}	#
1	148.0427	74.5250					M							16
2	235.0747	118.0410			217.0641	109.0357	S	1645.9312	823.4692	1628.9047	814.9560	1627.9206	814.4640	15
3	334.1431	167.5752			316.1326	158.5699	V	1558.8992	779.9532	1541.8726	771.4400	1540.8886	770.9479	14
4	481.2115	241.1094			463.2010	232.1041	F	1459.8308	730.4190	1442.8042	721.9057	1441.8202	721.4137	13
5	594.2956	297.6514			576.2850	288.6462	L	1312.7623	656.8848	1295.7358	648.3715	1294.7518	647.8795	12
6	693.3640	347.1856			675.3534	338.1804	V	1199.6783	600.3428	1182.6517	591.8295	1181.6677	591.3375	11
7	807.4069	404.2071	790.3804	395.6938	789.3964	395.2018	N	1100.6099	550.8086	1083.5833	542.2953	1082.5993	541.8033	10
8	908.4546	454.7309	891.4281	446.2177	890.4441	445.7257	T	986.5669	493.7871	969.5404	485.2738	968.5564	484.7818	9
9	1005.5074	503.2573	988.4808	494.7441	987.4968	494.2520	P	885.5193	443.2633	868.4927	434.7500	867.5087	434.2580	8
10	1133.5660	567.2866	1116.5394	558.7733	1115.5554	558.2813	Q	788.4665	394.7369	771.4400	386.2236	770.4559	385.7316	7
11	1190.5874	595.7973	1173.5609	587.2841	1172.5769	586.7921	G	660.4079	330.7076	643.3814	322.1943	642.3974	321.7023	6
12	1303.6715	652.3394	1286.6449	643.8261	1285.6609	643.3341	L	603.3865	302.1969	586.3599	293.6836	585.3759	293.1916	5
13	1416.7555	708.8814	1399.7290	700.3681	1398.7450	699.8761	L	490.3024	245.6548	473.2758	237.1416	472.2918	236.6496	4
14	1499.7927	750.4000	1482.7661	741.8867	1481.7821	741.3947	T	377.2183	189.1128	360.1918	180.5995	359.2078	180.1075	3
15	1646.8611	823.9342	1629.8345	815.4209	1628.8505	814.9289	F	294.1812	147.5942	277.1547	139.0810			2
16							K	147.1128	74.0600	130.0863	65.5468			1


0.5
0.25
-0
-0.25
-0.5
Error (Da)
250
500
750
RMS error 533 ppm
Mass (Da)

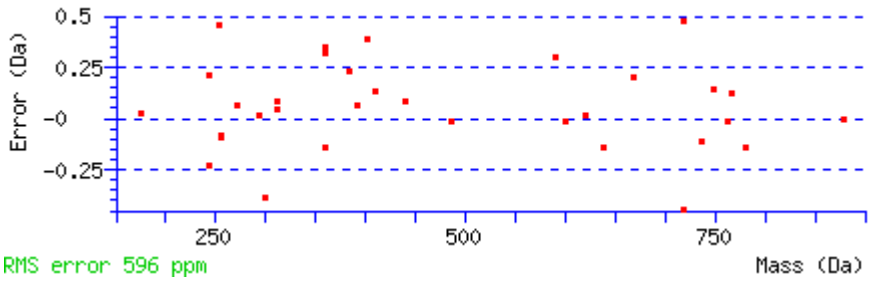

1000
0
-1000
Error (ppm)
250
500
750
RMS error 533 ppm
Mass (Da)

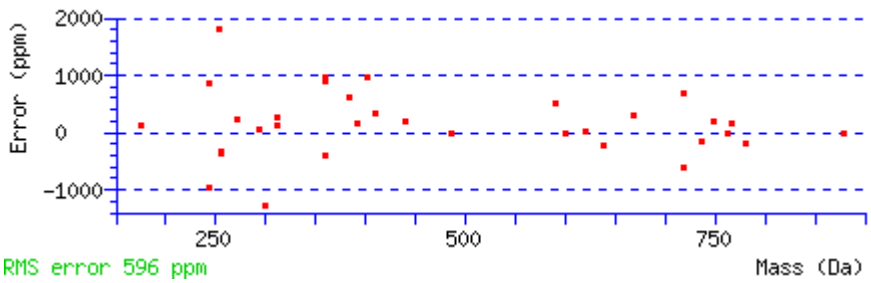
IDENTIFICATION 88
MS/MS Fragmentation of KLSPTEPR
Found in IPI00132604



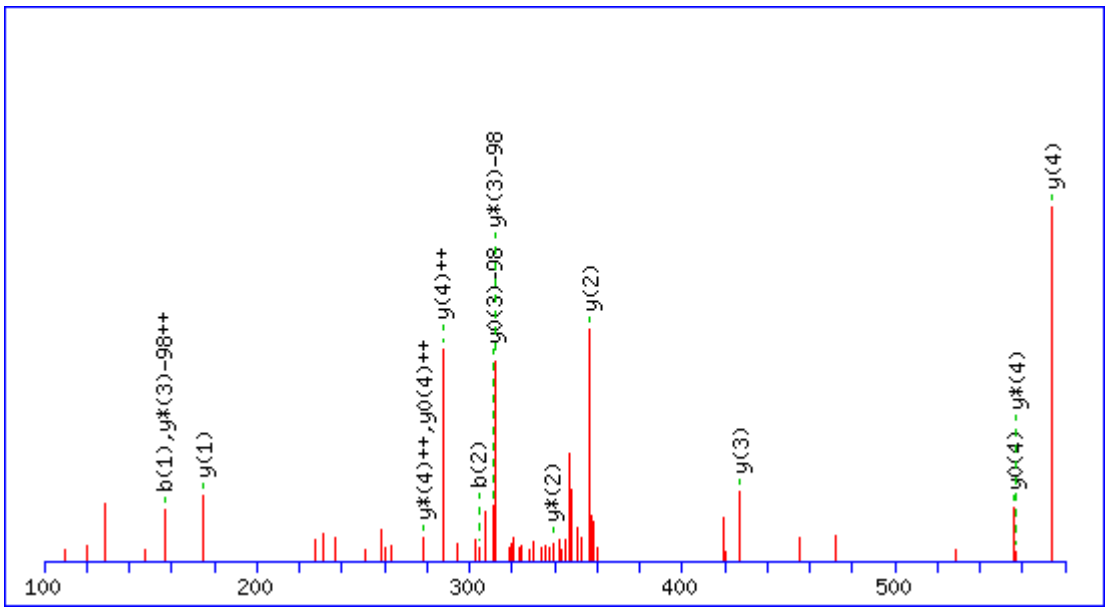
Monoisotopic mass of neutral peptide Mr(calc): 1006.4848 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 41 Expect: 0.0051 (help)

#	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							8
2	242.1863	121.5968	225.1598	113.0835			L	879.3972	440.2022	862.3706	431.6890	861.3866	431.1969	7
3	409.1847	205.0960	392.1581	196.5827	391.1741	196.0907	S	766.3131	383.6602	749.2866	375.1469	748.3025	374.6549	6
4	506.2374	253.6224	489.2109	245.1091	488.2269	244.6171	P	599.3148	300.1610	582.2882	291.6477	581.3042	291.1557	5
5	607.2851	304.1462	590.2586	295.6329	589.2745	295.1409	T	502.2620	251.6346	485.2354	243.1214	484.2514	242.6293	4
6	736.3277	368.6675	719.3011	360.1542	718.3171	359.6622	E	401.2143	201.1108	384.1878	192.5975	383.2037	192.1055	3
7	833.3805	417.1939	816.3539	408.6806	815.3699	408.1886	P	272.1717	136.5895	255.1452	128.0762			2
8							R	175.1190	88.0631	158.0924	79.5498			1



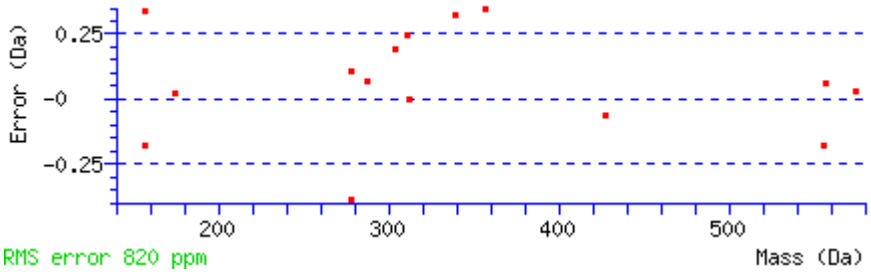


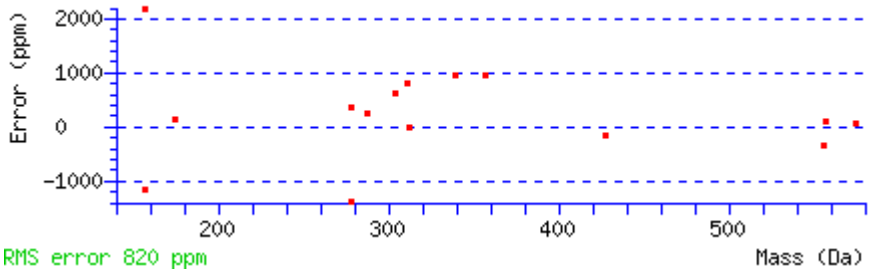
IDENTIFICATION 89
MS/MS Fragmentation of RFATR
Found in IPI00653851



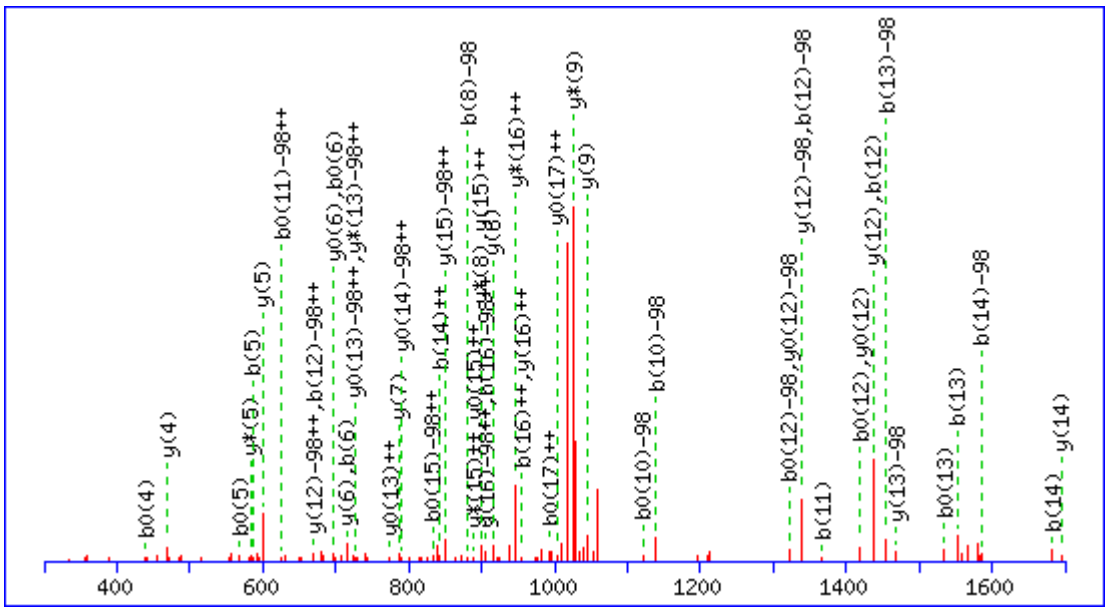
Monoisotopic mass of neutral peptide Mr(calc): 729.3323
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.0018 (help)

#	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							5
2	304.1768	152.5920	287.1503	144.0788			F	574.2385	287.6229	557.2119	279.1096	556.2279	278.6176	4
3	375.2139	188.1106	358.1874	179.5973			A	427.1701	214.0887	410.1435	205.5754	409.1595	205.0834	3
4	556.2279	278.6176	539.2014	270.1043	538.2174	269.6123	T	356.1330	178.5701	339.1064	170.0568	338.1224	169.5648	2
5							R	175.1190	88.0631	158.0924	79.5498			1



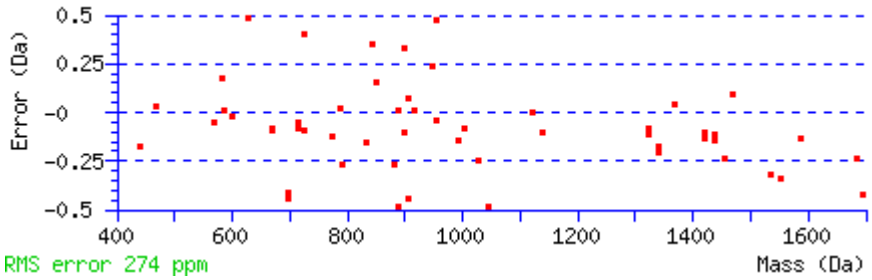


IDENTIFICATION 90
MS/MS Fragmentation of EIITEEPSEEEADMPKPK
Found in IPI00120691

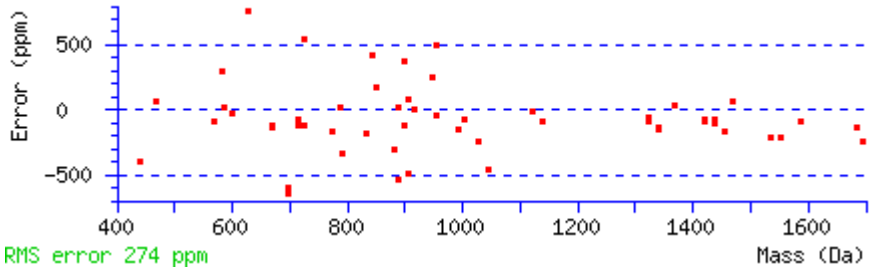


Monoisotopic mass of neutral peptide Mr(calc): 2150.9330
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 34 Expect: 0.085 (help)

#	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							18
2	243.1339	122.0706			225.1234	113.0653	I	1924.9208	962.9641	1907.8943	954.4508	1906.9103	953.9588	17
3	356.2180	178.6126			338.2074	169.6074	I	1811.8368	906.4220	1794.8102	897.9087	1793.8262	897.4167	16
4	457.2657	229.1365			439.2551	220.1312	T	1698.7527	849.8800	1681.7262	841.3667	1680.7421	840.8747	15
5	586.3083	293.6578			568.2977	284.6525	E	1597.7050	799.3562	1580.6785	790.8429	1579.6945	790.3509	14
6	715.3509	358.1791			697.3403	349.1738	E	1468.6624	734.8349	1451.6359	726.3216	1450.6519	725.8296	13
7	812.4036	406.7055			794.3931	397.7002	P	1339.6198	670.3136	1322.5933	661.8003	1321.6093	661.3083	12
8	881.4251	441.2162			863.4145	432.2109	S	1242.5671	621.7872	1225.5405	613.2739	1224.5565	612.7819	11
9	1010.4677	505.7375			992.4571	496.7322	E	1173.5456	587.2764	1156.5191	578.7632	1155.5351	578.2712	10
10	1139.5103	570.2588			1121.4997	561.2535	E	1044.5030	522.7551	1027.4765	514.2419	1026.4925	513.7499	9
11	1268.5529	634.7801			1250.5423	625.7748	E	915.4604	458.2339	898.4339	449.7206	897.4499	449.2286	8
12	1339.5900	670.2986			1321.5794	661.2933	A	786.4178	393.7126	769.3913	385.1993	768.4073	384.7073	7
13	1454.6169	727.8121			1436.6064	718.8068	D	715.3807	358.1940	698.3542	349.6807	697.3702	349.1887	6
14	1585.6574	793.3323			1567.6468	784.3271	M	600.3538	300.6805	583.3272	292.1673			5
15	1682.7102	841.8587			1664.6996	832.8534	P	469.3133	235.1603	452.2867	226.6470			4
16	1810.8051	905.9062	1793.7786	897.3929	1792.7946	896.9009	K	372.2605	186.6339	355.2340	178.1206			3
17	1907.8579	954.4326	1890.8314	945.9193	1889.8473	945.4273	P	244.1656	122.5864	227.1390	114.0731			2
18							K	147.1128	74.0600	130.0863	65.5468			1

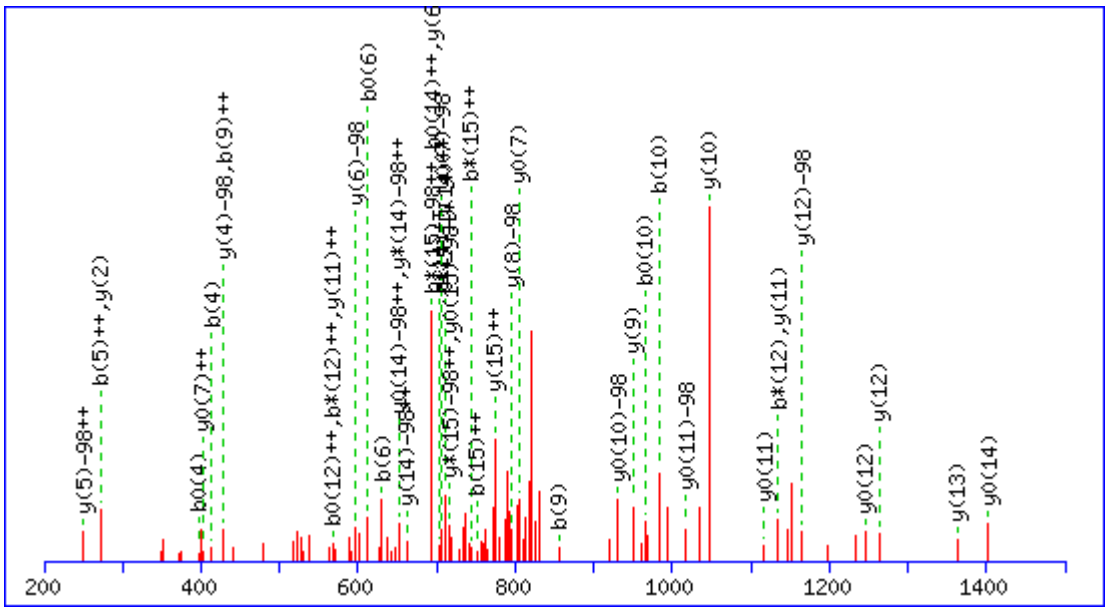


RMS error 274 ppm



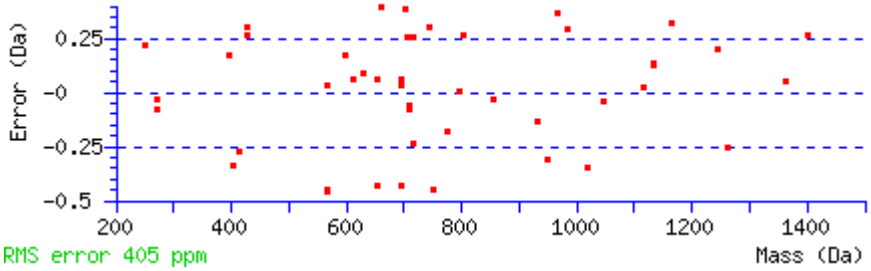
RMS error 274 ppm

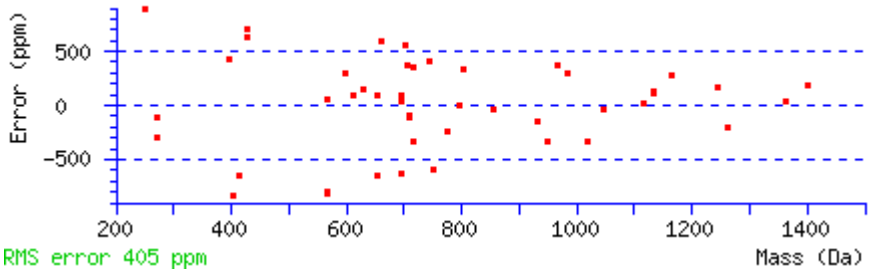
IDENTIFICATION 91
MS/MS Fragmentation of EQGVESPGAQPASSPR
Found in IPI00342749



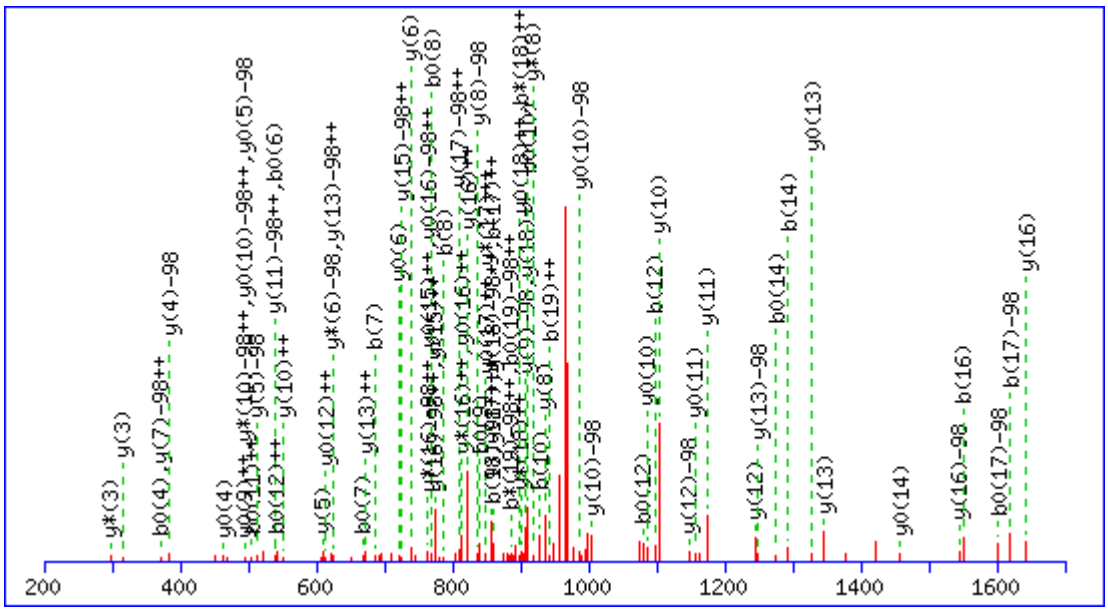
Monoisotopic mass of neutral peptide Mr(calc): 1675.7203
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 41 Expect: 0.011 (help)

#	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							16
2	258.1084	129.5579	241.0819	121.0446	240.0979	120.5526	Q	1547.6850	774.3461	1530.6584	765.8329	1529.6744	765.3408	15
3	315.1299	158.0686	298.1034	149.5553	297.1193	149.0633	G	1419.6264	710.3168	1402.5999	701.8036	1401.6158	701.3116	14
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	V	1362.6049	681.8061	1345.5784	673.2928	1344.5944	672.8008	13
5	543.2409	272.1241	526.2144	263.6108	525.2304	263.1188	E	1263.5365	632.2719	1246.5100	623.7586	1245.5260	623.2666	12
6	630.2729	315.6401	613.2464	307.1268	612.2624	306.6348	S	1134.4939	567.7506	1117.4674	559.2373	1116.4834	558.7453	11
7	727.3257	364.1665	710.2992	355.6532	709.3151	355.1612	P	1047.4619	524.2346	1030.4354	515.7213	1029.4513	515.2293	10
8	784.3472	392.6772	767.3206	384.1640	766.3366	383.6719	G	950.4091	475.7082	933.3826	467.1949	932.3986	466.7029	9
9	855.3843	428.1958	838.3577	419.6825	837.3737	419.1905	A	893.3877	447.1975	876.3611	438.6842	875.3771	438.1922	8
10	983.4429	492.2251	966.4163	483.7118	965.4323	483.2198	Q	822.3506	411.6789	805.3240	403.1656	804.3400	402.6736	7
11	1080.4956	540.7515	1063.4691	532.2382	1062.4851	531.7462	P	694.2920	347.6496	677.2654	339.1364	676.2814	338.6443	6
12	1151.5327	576.2700	1134.5062	567.7567	1133.5222	567.2647	A	597.2392	299.1232	580.2127	290.6100	579.2287	290.1180	5
13	1238.5648	619.7860	1221.5382	611.2727	1220.5542	610.7807	S	526.2021	263.6047	509.1756	255.0914	508.1915	254.5994	4
14	1405.5631	703.2852	1388.5366	694.7719	1387.5526	694.2799	S	439.1701	220.0887	422.1435	211.5754	421.1595	211.0834	3
15	1502.6159	751.8116	1485.5893	743.2983	1484.6053	742.8063	P	272.1717	136.5895	255.1452	128.0762			2
16							R	175.1190	88.0631	158.0924	79.5498			1


Error (Da)
0.25
-0
-0.25
-0.5
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 405 ppm

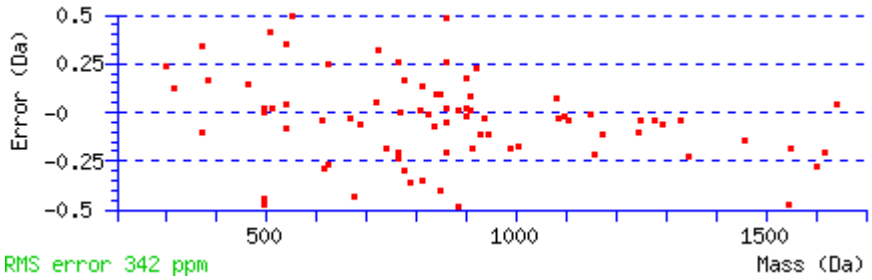

Error (ppm)
500
0
-500
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 405 ppm

IDENTIFICATION 92
MS/MS Fragmentation of SETAPAETAAPAPVEKSPAK
Found in IPI00230133

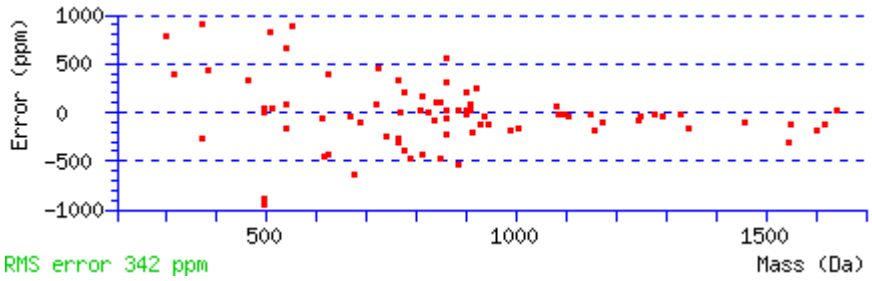


Monoisotopic mass of neutral peptide Mr(calc): 2030.9561
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 54 Expect: 0.00065 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							20
2	217.0819	109.0446			199.0713	100.0393	E	1846.9545	923.9809	1829.9280	915.4676	1828.9440	914.9756	19
3	318.1296	159.5684			300.1190	150.5631	T	1717.9119	859.4596	1700.8854	850.9463	1699.9014	850.4543	18
4	389.1667	195.0870			371.1561	186.0817	A	1616.8642	808.9358	1599.8377	800.4225	1598.8537	799.9305	17
5	486.2195	243.6134			468.2089	234.6081	P	1545.8271	773.4172	1528.8006	764.9039	1527.8166	764.4119	16
6	557.2566	279.1319			539.2460	270.1266	A	1448.7744	724.8908	1431.7478	716.3775	1430.7638	715.8855	15
7	686.2992	343.6532			668.2886	334.6479	E	1377.7373	689.3723	1360.7107	680.8590	1359.7267	680.3670	14
8	787.3468	394.1771			769.3363	385.1718	T	1248.6947	624.8510	1231.6681	616.3377	1230.6841	615.8457	13
9	858.3840	429.6956			840.3734	420.6903	A	1147.6470	574.3271	1130.6204	565.8139	1129.6364	565.3218	12
10	929.4211	465.2142			911.4105	456.2089	A	1076.6099	538.8086	1059.5833	530.2953	1058.5993	529.8033	11
11	1026.4738	513.7406			1008.4633	504.7353	P	1005.5728	503.2900	988.5462	494.7767	987.5622	494.2847	10
12	1097.5109	549.2591			1079.5004	540.2538	A	908.5200	454.7636	891.4934	446.2504	890.5094	445.7584	9
13	1194.5637	597.7855			1176.5531	588.7802	P	837.4829	419.2451	820.4563	410.7318	819.4723	410.2398	8
14	1293.6321	647.3197			1275.6216	638.3144	V	740.4301	370.7187	723.4036	362.2054	722.4196	361.7134	7
15	1422.6747	711.8410			1404.6642	702.8357	E	641.3617	321.1845	624.3352	312.6712	623.3511	312.1792	6
16	1550.7697	775.8885	1533.7431	767.3752	1532.7591	766.8832	K	512.3191	256.6632	495.2926	248.1499	494.3085	247.6579	5
17	1619.7911	810.3992	1602.7646	801.8859	1601.7806	801.3939	S	384.2241	192.6157	367.1976	184.1024	366.2136	183.6104	4
18	1716.8439	858.9256	1699.8174	850.4123	1698.8333	849.9203	P	315.2027	158.1050	298.1761	149.5917			3
19	1787.8810	894.4441	1770.8545	885.9309	1769.8705	885.4389	A	218.1499	109.5786	201.1234	101.0653			2
20							K	147.1128	74.0600	130.0863	65.5468			1

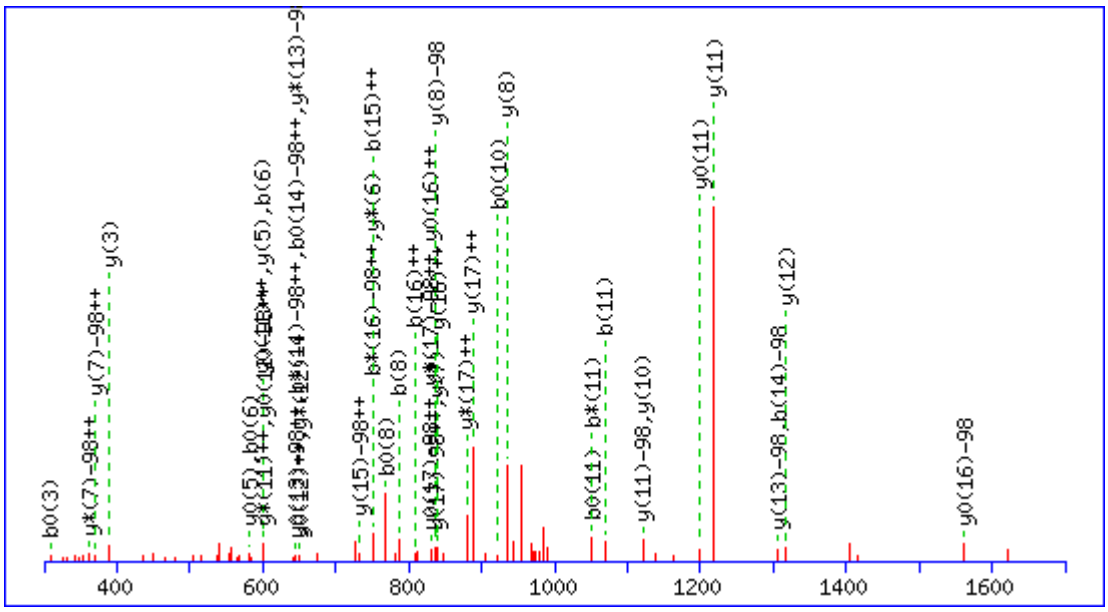


RMS error 342 ppm



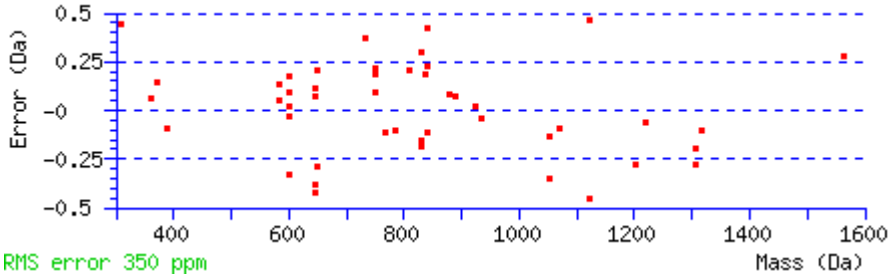
RMS error 342 ppm

IDENTIFICATION 93
MS/MS Fragmentation of TQPDGTSVPGEPASPISQR
Found in IPI00263048



Monoisotopic mass of neutral peptide Mr(calc): 2002.8997
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S14 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 29 Expect: 0.21 (help)

#	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							19
2	230.1135	115.5604	213.0870	107.0471	212.1030	106.5551	Q	1902.8593	951.9333	1885.8328	943.4200	1884.8487	942.9280	18
3	327.1663	164.0868	310.1397	155.5735	309.1557	155.0815	P	1774.8007	887.9040	1757.7742	879.3907	1756.7902	878.8987	17
4	442.1932	221.6003	425.1667	213.0870	424.1827	212.5950	D	1677.7480	839.3776	1660.7214	830.8643	1659.7374	830.3723	16
5	499.2147	250.1110	482.1882	241.5977	481.2041	241.1057	G	1562.7210	781.8642	1545.6945	773.3509	1544.7105	772.8589	15
6	600.2624	300.6348	583.2358	292.1216	582.2518	291.6295	T	1505.6996	753.3534	1488.6730	744.8401	1487.6890	744.3481	14
7	687.2944	344.1508	670.2679	335.6376	669.2838	335.1456	S	1404.6519	702.8296	1387.6253	694.3163	1386.6413	693.8243	13
8	786.3628	393.6851	769.3363	385.1718	768.3523	384.6798	V	1317.6199	659.3136	1300.5933	650.8003	1299.6093	650.3083	12
9	883.4156	442.2114	866.3890	433.6982	865.4050	433.2062	P	1218.5514	609.7794	1201.5249	601.2661	1200.5409	600.7741	11
10	940.4371	470.7222	923.4105	462.2089	922.4265	461.7169	G	1121.4987	561.2530	1104.4721	552.7397	1103.4881	552.2477	10
11	1069.4796	535.2435	1052.4531	526.7302	1051.4691	526.2382	E	1064.4772	532.7422	1047.4507	524.2290	1046.4667	523.7370	9
12	1166.5324	583.7698	1149.5059	575.2566	1148.5218	574.7646	P	935.4346	468.2209	918.4081	459.7077	917.4241	459.2157	8
13	1237.5695	619.2884	1220.5430	610.7751	1219.5590	610.2831	A	838.3819	419.6946	821.3553	411.1813	820.3713	410.6893	7
14	1404.5679	702.7876	1387.5413	694.2743	1386.5573	693.7823	S	767.3447	384.1760	750.3182	375.6627	749.3342	375.1707	6
15	1501.6206	751.3140	1484.5941	742.8007	1483.6101	742.3087	P	600.3464	300.6768	583.3198	292.1636	582.3358	291.6715	5
16	1614.7047	807.8560	1597.6782	799.3427	1596.6941	798.8507	I	503.2936	252.1504	486.2671	243.6372	485.2831	243.1452	4
17	1701.7367	851.3720	1684.7102	842.8587	1683.7262	842.3667	S	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
18	1829.7953	915.4013	1812.7688	906.8880	1811.7848	906.3960	Q	303.1775	152.0924	286.1510	143.5791			2
19							R	175.1190	88.0631	158.0924	79.5498			1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-0.5
Error (Da)
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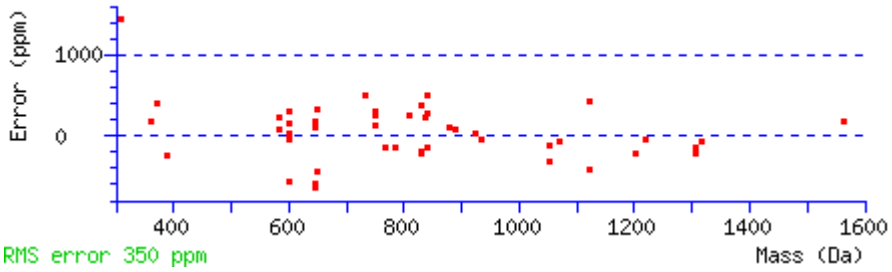
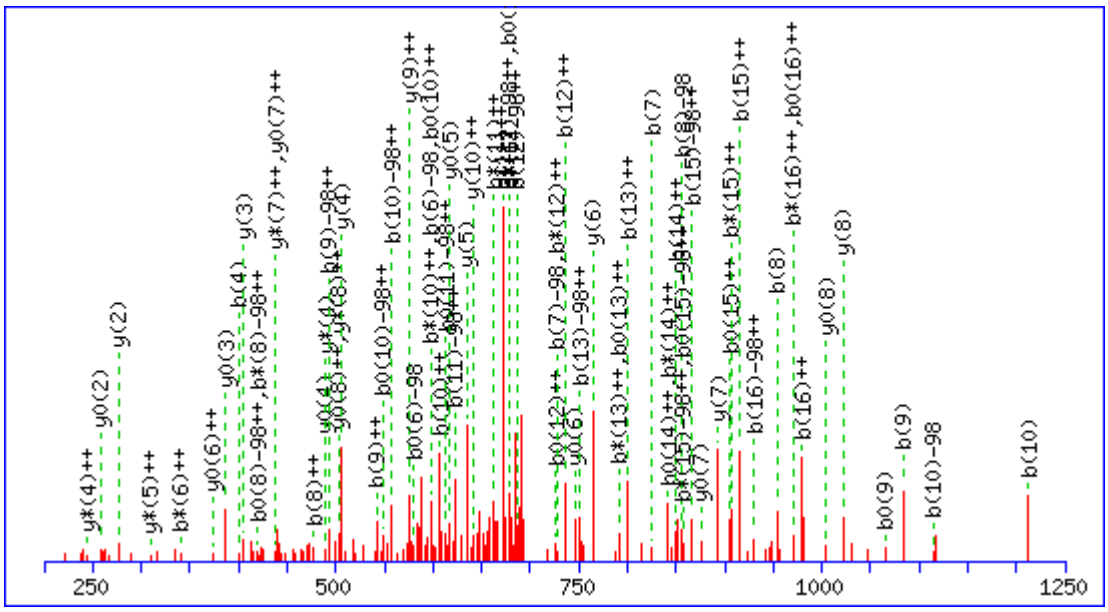
600
800
1000
1200
1400
1600
Mass (Da)
RMS error 350 ppm


1000
0
Error (ppm)
400
600
800
1000
1200
1400
1600
Mass (Da)
RMS error 350 ppm

IDENTIFICATION 94

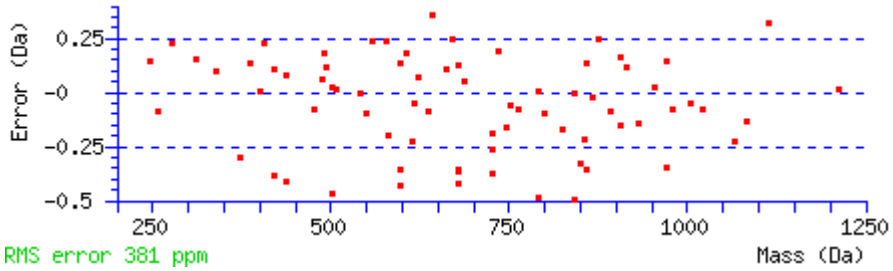
MS/MS Fragmentation of AAKESEEEEEEEETEEK

Found in IPI00719871

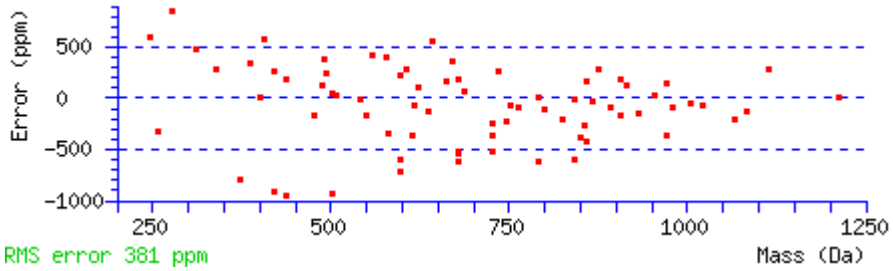


Monoisotopic mass of neutral peptide Mr(calc): 2103.7892 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 39 Expect: 0.018 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							17
2	143.0815	72.0444					A	2033.7594	1017.3834	2016.7329	1008.8701	2015.7489	1008.3781	16
3	271.1765	136.0919	254.1499	127.5786			K	1962.7223	981.8648	1945.6958	973.3515	1944.7118	972.8595	15
4	400.2191	200.6132	383.1925	192.0999	382.2085	191.6079	E	1834.6274	917.8173	1817.6008	909.3040	1816.6168	908.8120	14
5	567.2174	284.1123	550.1909	275.5991	549.2069	275.1071	S	1705.5848	853.2960	1688.5582	844.7827	1687.5742	844.2907	13
6	696.2600	348.6336	679.2335	340.1204	678.2494	339.6284	E	1538.5864	769.7968	1521.5599	761.2836	1520.5758	760.7916	12
7	825.3026	413.1549	808.2761	404.6417	807.2920	404.1497	E	1409.5438	705.2755	1392.5173	696.7623	1391.5333	696.2703	11
8	954.3452	477.6762	937.3186	469.1630	936.3346	468.6710	E	1280.5012	640.7543	1263.4747	632.2410	1262.4907	631.7490	10
9	1083.3878	542.1975	1066.3612	533.6843	1065.3772	533.1923	E	1151.4586	576.2330	1134.4321	567.7197	1133.4481	567.2277	9
10	1212.4304	606.7188	1195.4038	598.2056	1194.4198	597.7135	E	1022.4160	511.7117	1005.3895	503.1984	1004.4055	502.7064	8
11	1341.4730	671.2401	1324.4464	662.7269	1323.4624	662.2348	E	893.3734	447.1904	876.3469	438.6771	875.3629	438.1851	7
12	1470.5156	735.7614	1453.4890	727.2481	1452.5050	726.7561	E	764.3309	382.6691	747.3043	374.1558	746.3203	373.6638	6
13	1599.5582	800.2827	1582.5316	791.7694	1581.5476	791.2774	E	635.2883	318.1478	618.2617	309.6345	617.2777	309.1425	5
14	1700.6058	850.8066	1683.5793	842.2933	1682.5953	841.8013	T	506.2457	253.6265	489.2191	245.1132	488.2351	244.6212	4
15	1829.6484	915.3279	1812.6219	906.8146	1811.6379	906.3226	E	405.1980	203.1026	388.1714	194.5894	387.1874	194.0974	3
16	1958.6910	979.8492	1941.6645	971.3359	1940.6805	970.8439	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
17							K	147.1128	74.0600	130.0863	65.5468			1

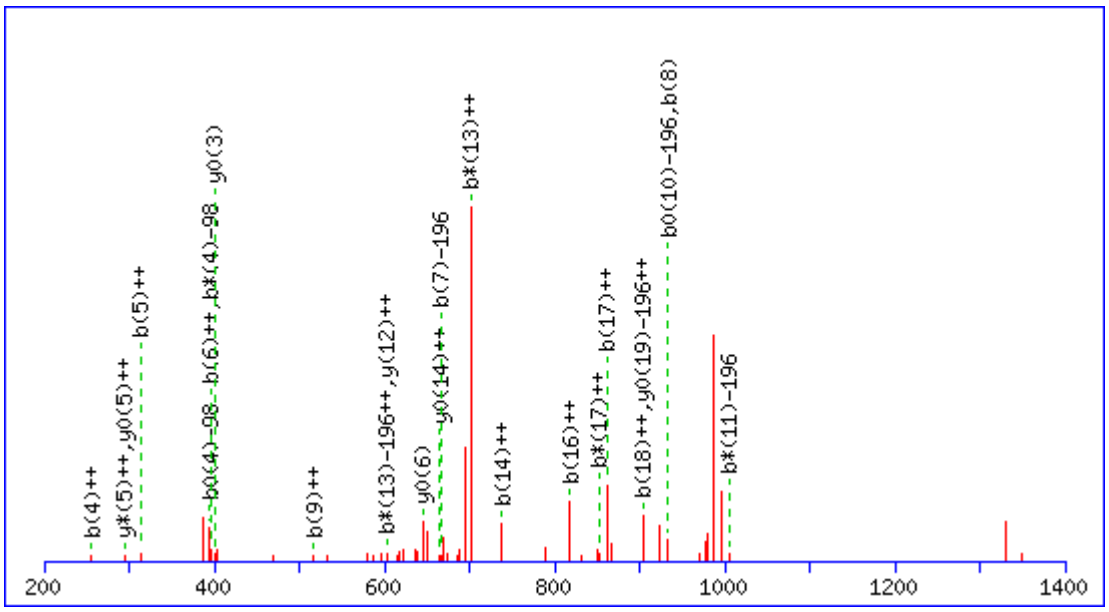


RMS error 381 ppm



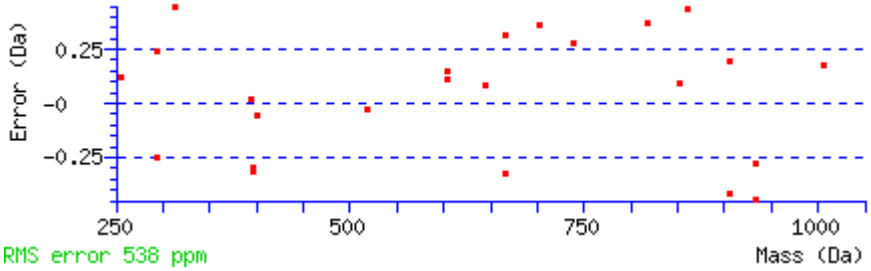
RMS error 381 ppm

IDENTIFICATION 95
MS/MS Fragmentation of NMPSLSAATLASLGGTSSRR
Found in IPI00117277



Monoisotopic mass of neutral peptide Mr(calc): 2136.9276
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
N1 : Deamidated (NQ)
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 25 Expect: 0.57 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207	99.0077	50.0075			N							20
2	247.0747	124.0410	230.0482	115.5277			M	2022.9079	1011.9576	2005.8814	1003.4443	2004.8974	1002.9523	19
3	344.1275	172.5674	327.1009	164.0541			P	1891.8674	946.4374	1874.8409	937.9241	1873.8569	937.4321	18
4	511.1258	256.0666	494.0993	247.5533	493.1153	247.0613	S	1794.8147	897.9110	1777.7881	889.3977	1776.8041	888.9057	17
5	624.2099	312.6086	607.1833	304.0953	606.1993	303.6033	L	1627.8163	814.4118	1610.7898	805.8985	1609.8058	805.4065	16
6	791.2082	396.1078	774.1817	387.5945	773.1977	387.1025	S	1514.7323	757.8698	1497.7057	749.3565	1496.7217	748.8645	15
7	862.2454	431.6263	845.2188	423.1130	844.2348	422.6210	A	1347.7339	674.3706	1330.7074	665.8573	1329.7233	665.3653	14
8	933.2825	467.1449	916.2559	458.6316	915.2719	458.1396	A	1276.6968	638.8520	1259.6702	630.3388	1258.6862	629.8468	13
9	1034.3302	517.6687	1017.3036	509.1554	1016.3196	508.6634	T	1205.6597	603.3335	1188.6331	594.8202	1187.6491	594.3282	12
10	1147.4142	574.2107	1130.3877	565.6975	1129.4037	565.2055	L	1104.6120	552.8096	1087.5854	544.2964	1086.6014	543.8044	11
11	1218.4513	609.7293	1201.4248	601.2160	1200.4408	600.7240	A	991.5279	496.2676	974.5014	487.7543	973.5174	487.2623	10
12	1305.4834	653.2453	1288.4568	644.7320	1287.4728	644.2400	S	920.4908	460.7490	903.4643	452.2358	902.4803	451.7438	9
13	1418.5674	709.7874	1401.5409	701.2741	1400.5569	700.7821	L	833.4588	417.2330	816.4322	408.7198	815.4482	408.2278	8
14	1475.5889	738.2981	1458.5623	729.7848	1457.5783	729.2928	G	720.3747	360.6910	703.3482	352.1777	702.3642	351.6857	7
15	1532.6104	766.8088	1515.5838	758.2955	1514.5998	757.8035	G	663.3533	332.1803	646.3267	323.6670	645.3427	323.1750	6
16	1633.6580	817.3327	1616.6315	808.8194	1615.6475	808.3274	T	606.3318	303.6695	589.3052	295.1563	588.3212	294.6643	5
17	1720.6901	860.8487	1703.6635	852.3354	1702.6795	851.8434	S	505.2841	253.1457	488.2576	244.6324	487.2736	244.1404	4
18	1807.7221	904.3647	1790.6955	895.8514	1789.7115	895.3594	S	418.2521	209.6297	401.2255	201.1164	400.2415	200.6244	3
19	1963.8232	982.4152	1946.7967	973.9020	1945.8126	973.4100	R	331.2201	166.1137	314.1935	157.6004			2
20							R	175.1190	88.0631	158.0924	79.5498			1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-0.25
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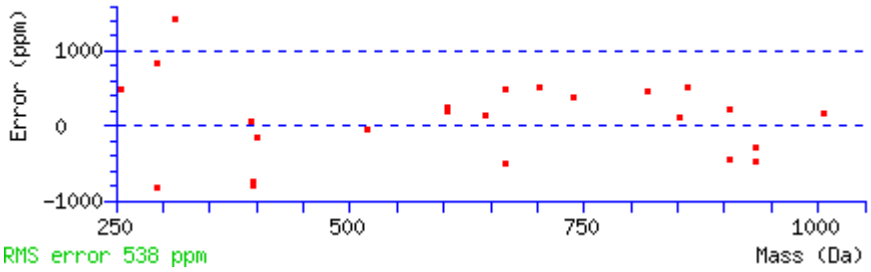
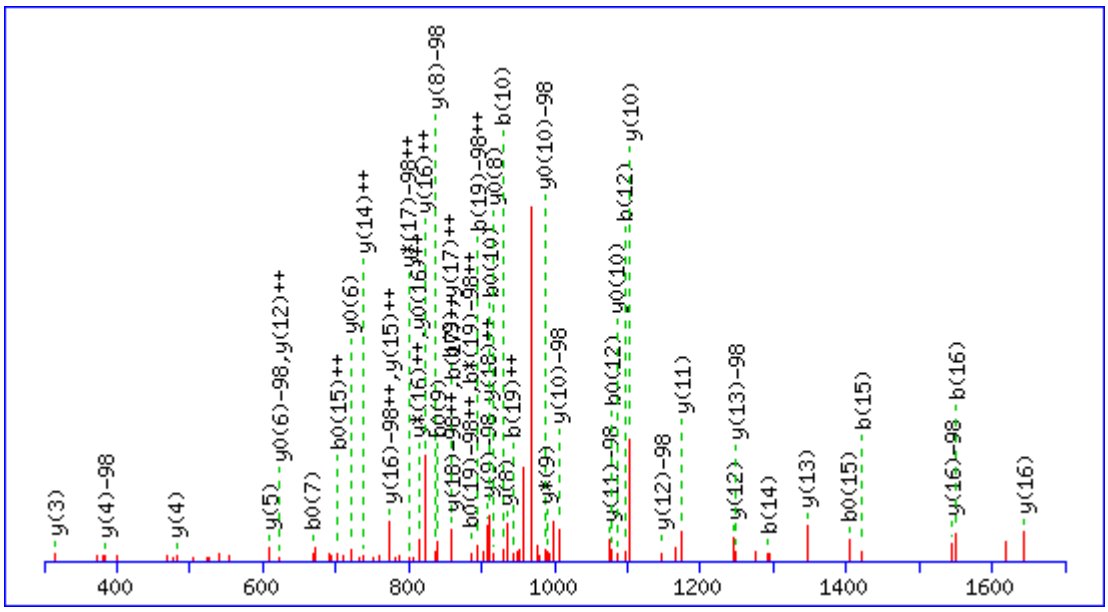
500
750
1000
RMS error 538 ppm
Mass (Da)

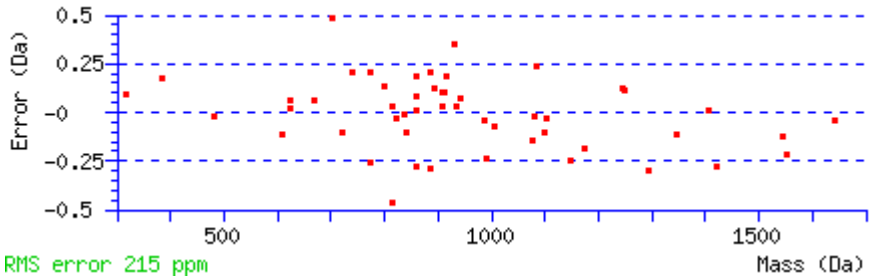

Error (ppm)
1000
0
-1000
250
500
750
1000
RMS error 538 ppm
Mass (Da)

IDENTIFICATION 96
MS/MS Fragmentation of SETAPAETAAPAPVEKSPAK
Found in IPI00230133

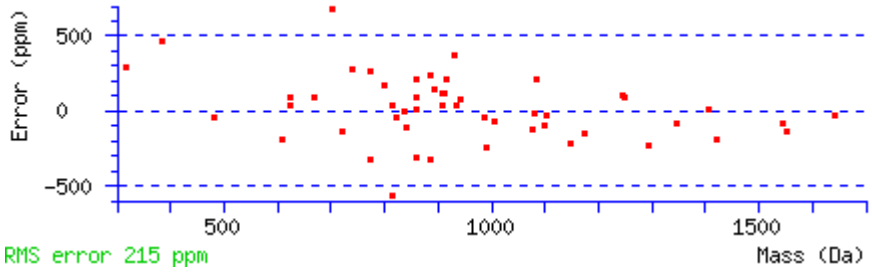


Monoisotopic mass of neutral peptide Mr(calc): 2030.9561
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S17 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 63 Expect: 7.7e-05 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							20
2	217.0819	109.0446			199.0713	100.0393	E	1944.9314	972.9693	1927.9049	964.4561	1926.9209	963.9641	19
3	318.1296	159.5684			300.1190	150.5631	T	1815.8888	908.4481	1798.8623	899.9348	1797.8783	899.4428	18
4	389.1667	195.0870			371.1561	186.0817	A	1714.8411	857.9242	1697.8146	849.4109	1696.8306	848.9189	17
5	486.2195	243.6134			468.2089	234.6081	P	1643.8040	822.4057	1626.7775	813.8924	1625.7935	813.4004	16
6	557.2566	279.1319			539.2460	270.1266	A	1546.7513	773.8793	1529.7247	765.3660	1528.7407	764.8740	15
7	686.2992	343.6532			668.2886	334.6479	E	1475.7142	738.3607	1458.6876	729.8474	1457.7036	729.3554	14
8	787.3468	394.1771			769.3363	385.1718	T	1346.6716	673.8394	1329.6450	665.3261	1328.6610	664.8341	13
9	858.3840	429.6956			840.3734	420.6903	A	1245.6239	623.3156	1228.5973	614.8023	1227.6133	614.3103	12
10	929.4211	465.2142			911.4105	456.2089	A	1174.5868	587.7970	1157.5602	579.2837	1156.5762	578.7917	11
11	1026.4738	513.7406			1008.4633	504.7353	P	1103.5497	552.2785	1086.5231	543.7652	1085.5391	543.2732	10
12	1097.5109	549.2591			1079.5004	540.2538	A	1006.4969	503.7521	989.4703	495.2388	988.4863	494.7468	9
13	1194.5637	597.7855			1176.5531	588.7802	P	935.4598	468.2335	918.4332	459.7203	917.4492	459.2282	8
14	1293.6321	647.3197			1275.6216	638.3144	V	838.4070	419.7071	821.3805	411.1939	820.3964	410.7019	7
15	1422.6747	711.8410			1404.6642	702.8357	E	739.3386	370.1729	722.3120	361.6597	721.3280	361.1677	6
16	1550.7697	775.8885	1533.7431	767.3752	1532.7591	766.8832	K	610.2960	305.6516	593.2695	297.1384	592.2854	296.6464	5
17	1717.7680	859.3877	1700.7415	850.8744	1699.7575	850.3824	S	482.2010	241.6042	465.1745	233.0909	464.1905	232.5989	4
18	1814.8208	907.9140	1797.7943	899.4008	1796.8102	898.9088	P	315.2027	158.1050	298.1761	149.5917			3
19	1885.8579	943.4326	1868.8314	934.9193	1867.8474	934.4273	A	218.1499	109.5786	201.1234	101.0653			2
20							K	147.1128	74.0600	130.0863	65.5468			1

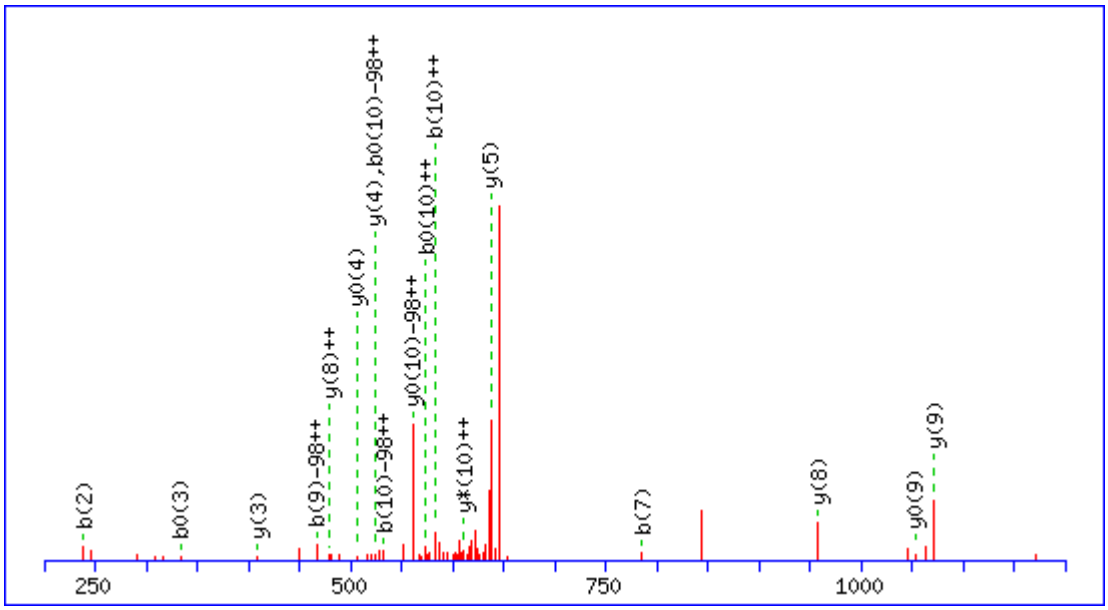


RMS error 215 ppm



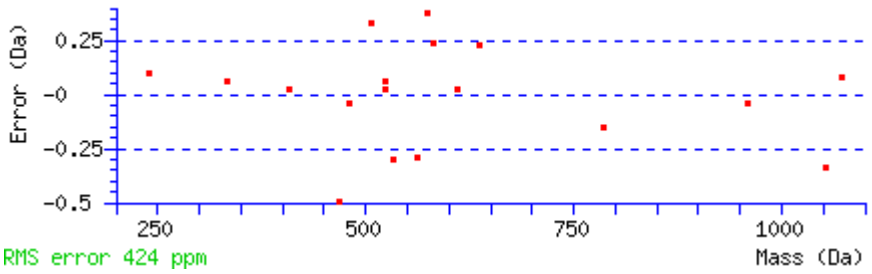
RMS error 215 ppm

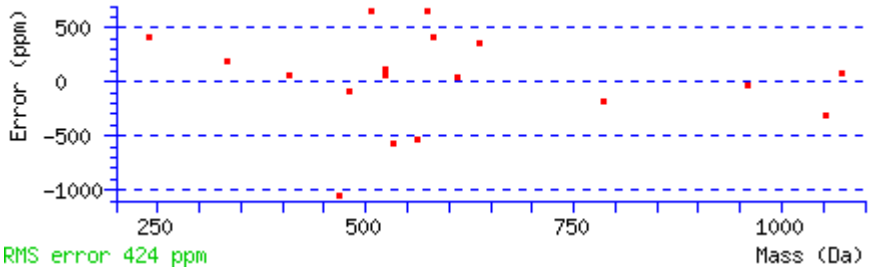
IDENTIFICATION 97
MS/MS Fragmentation of ASLAHLLDMMK
Found in
IPI00137400



Monoisotopic mass of neutral peptide Mr(calc): 1308.5971
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 26 Expect: 0.26 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258			A							11
2	239.0427	120.0250	221.0322	111.0197	S	1238.5673	619.7873	1221.5407	611.2740	1220.5567	610.7820	10
3	352.1268	176.5670	334.1162	167.5618	L	1071.5689	536.2881	1054.5424	527.7748	1053.5584	527.2828	9
4	423.1639	212.0856	405.1534	203.0803	A	958.4849	479.7461	941.4583	471.2328	940.4743	470.7408	8
5	560.2228	280.6151	542.2123	271.6098	H	887.4478	444.2275	870.4212	435.7142	869.4372	435.2222	7
6	673.3069	337.1571	655.2963	328.1518	L	750.3888	375.6981	733.3623	367.1848	732.3783	366.6928	6
7	786.3910	393.6991	768.3804	384.6938	L	637.3048	319.1560	620.2782	310.6428	619.2942	310.1507	5
8	901.4179	451.2126	883.4073	442.2073	D	524.2207	262.6140	507.1942	254.1007	506.2102	253.6087	4
9	1032.4584	516.7328	1014.4478	507.7276	M	409.1938	205.1005	392.1672	196.5873			3
10	1163.4989	582.2531	1145.4883	573.2478	M	278.1533	139.5803	261.1267	131.0670			2
11					K	147.1128	74.0600	130.0863	65.5468			1

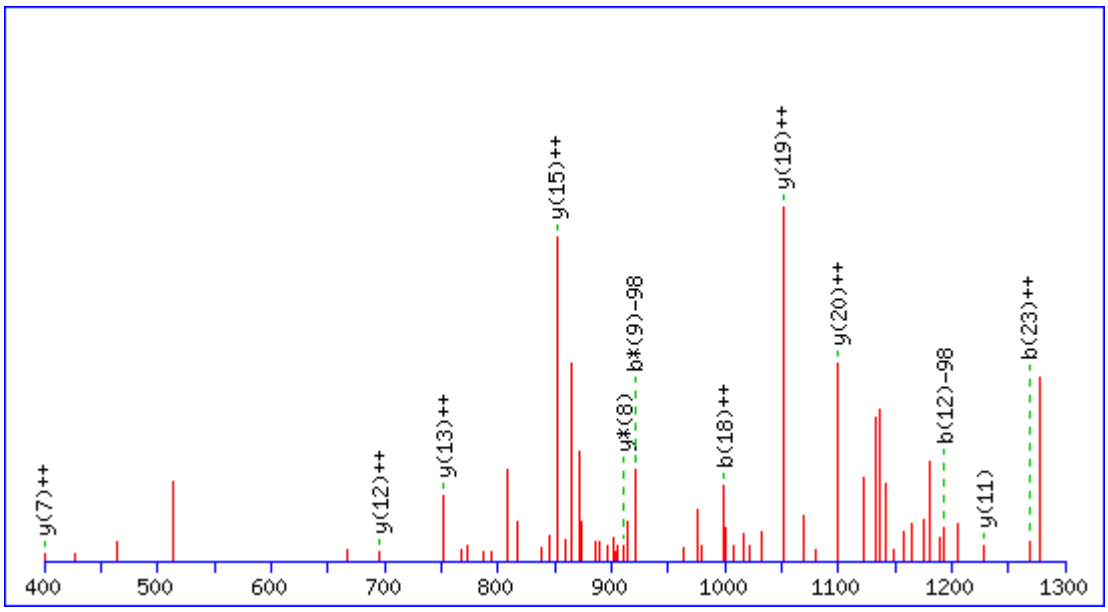




IDENTIFICATION 98

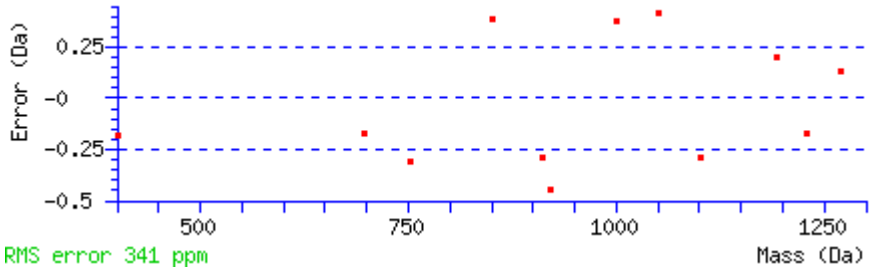
MS/MS Fragmentation of TGDELVNINGTPLYGSRQEALILIK

Found in IPI00752147

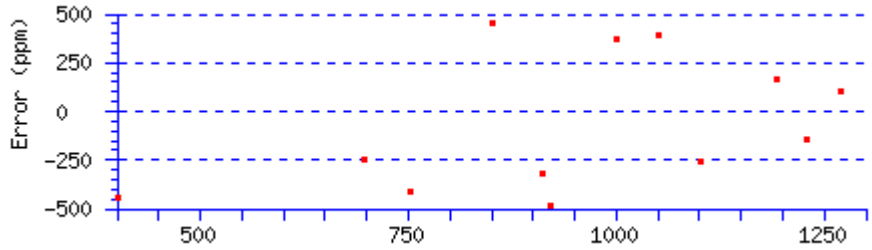


Monoisotopic mass of neutral peptide Mr(calc): 2794.4153
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Q18 : Deamidated (NQ)
Ions Score: 20 Expect: 0.9 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y_{0++}	#
1	182.0213	91.5143			164.0107	82.5090	T							25
2	239.0427	120.0250			221.0322	111.0197	G	2614.4087	1307.7080	2597.3821	1299.1947	2596.3981	1298.7027	24
3	354.0697	177.5385			336.0591	168.5332	D	2557.3872	1279.1972	2540.3606	1270.6840	2539.3766	1270.1920	23
4	483.1123	242.0598			465.1017	233.0545	E	2442.3603	1221.6838	2425.3337	1213.1705	2424.3497	1212.6785	22
5	596.1964	298.6018			578.1858	289.5965	L	2313.3177	1157.1625	2296.2911	1148.6492	2295.3071	1148.1572	21
6	695.2648	348.1360			677.2542	339.1307	V	2200.2336	1100.6204	2183.2070	1092.1072	2182.2230	1091.6152	20
7	809.3077	405.1575	792.2811	396.6442	791.2971	396.1522	N	2101.1652	1051.0862	2084.1386	1042.5730	2083.1546	1042.0809	19
8	922.3918	461.6995	905.3652	453.1862	904.3812	452.6942	I	1987.1223	994.0648	1970.0957	985.5515	1969.1117	985.0595	18
9	1036.4347	518.7210	1019.4081	510.2077	1018.4241	509.7157	N	1874.0382	937.5227	1857.0116	929.0095	1856.0276	928.5175	17
10	1093.4561	547.2317	1076.4296	538.7184	1075.4456	538.2264	G	1759.9953	880.5013	1742.9687	871.9880	1741.9847	871.4960	16
11	1194.5038	597.7556	1177.4773	589.2423	1176.4933	588.7503	T	1702.9738	851.9905	1685.9473	843.4773	1684.9632	842.9853	15
12	1291.5566	646.2819	1274.5300	637.7687	1273.5460	637.2767	P	1601.9261	801.4667	1584.8996	792.9534	1583.9156	792.4614	14
13	1404.6407	702.8240	1387.6141	694.3107	1386.6301	693.8187	L	1504.8734	752.9403	1487.8468	744.4270	1486.8628	743.9350	13
14	1567.7040	784.3556	1550.6774	775.8424	1549.6934	775.3503	Y	1391.7893	696.3983	1374.7627	687.8850	1373.7787	687.3930	12
15	1624.7254	812.8664	1607.6989	804.3531	1606.7149	803.8611	G	1228.7260	614.8666	1211.6994	606.3533	1210.7154	605.8613	11
16	1711.7575	856.3824	1694.7309	847.8691	1693.7469	847.3771	S	1171.7045	586.3559	1154.6780	577.8426	1153.6939	577.3506	10
17	1867.8586	934.4329	1850.8320	925.9197	1849.8480	925.4276	R	1084.6725	542.8399	1067.6459	534.3266	1066.6619	533.8346	9
18	1996.9012	998.9542	1979.8746	990.4410	1978.8906	989.9489	Q	928.5714	464.7893	911.5448	456.2760	910.5608	455.7840	8
19	2125.9438	1063.4755	2108.9172	1054.9622	2107.9332	1054.4702	E	799.5288	400.2680	782.5022	391.7547	781.5182	391.2627	7
20	2196.9809	1098.9941	2179.9543	1090.4808	2178.9703	1089.9888	A	670.4862	335.7467	653.4596	327.2335			6
21	2310.0649	1155.5361	2293.0384	1147.0228	2292.0544	1146.5308	L	599.4491	300.2282	582.4225	291.7149			5
22	2423.1490	1212.0781	2406.1225	1203.5649	2405.1384	1203.0729	I	486.3650	243.6861	469.3384	235.1729			4
23	2536.2331	1268.6202	2519.2065	1260.1069	2518.2225	1259.6149	L	373.2809	187.1441	356.2544	178.6308			3
24	2649.3171	1325.1622	2632.2906	1316.6489	2631.3066	1316.1569	I	260.1969	130.6021	243.1703	122.0888			2
25							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 341 ppm

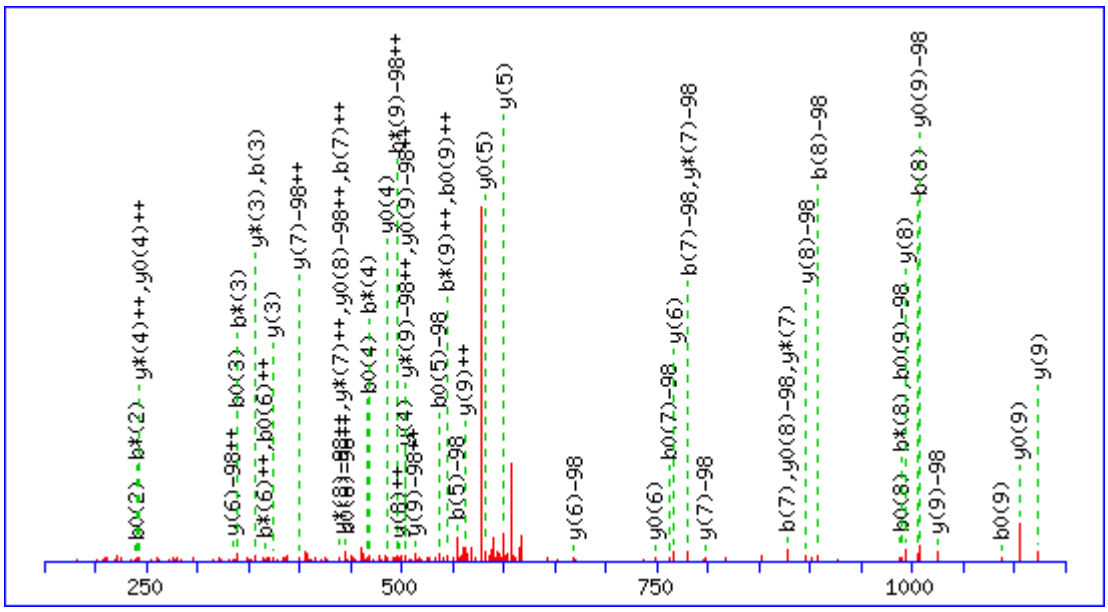


RMS error 341 ppm

IDENTIFICATION 99

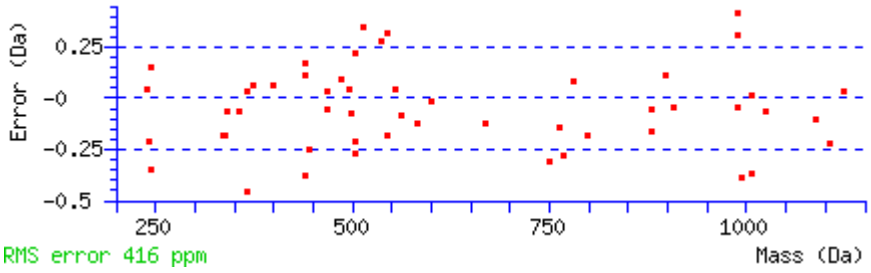
MS/MS Fragmentation of KEVQSPEQVK

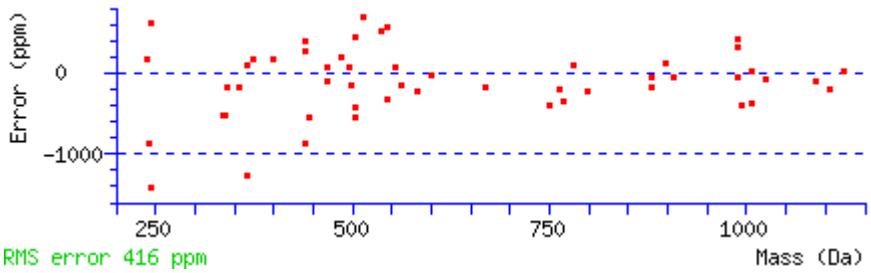
Found in IPI00169477



Monoisotopic mass of neutral peptide Mr(calc): 1250.5908 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 26 Expect: 0.26 (help)

#	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							10
2	258.1448	129.5761	241.1183	121.0628	240.1343	120.5708	E	1025.5262	513.2667	1008.4997	504.7535	1007.5156	504.2615	9
3	357.2132	179.1103	340.1867	170.5970	339.2027	170.1050	V	896.4836	448.7454	879.4571	440.2322	878.4730	439.7402	8
4	485.2718	243.1396	468.2453	234.6263	467.2613	234.1343	Q	797.4152	399.2112	780.3886	390.6980	779.4046	390.2060	7
5	554.2933	277.6503	537.2667	269.1370	536.2827	268.6450	S	669.3566	335.1819	652.3301	326.6687	651.3461	326.1767	6
6	651.3461	326.1767	634.3195	317.6634	633.3355	317.1714	P	600.3352	300.6712	583.3086	292.1579	582.3246	291.6659	5
7	780.3886	390.6980	763.3621	382.1847	762.3781	381.6927	E	503.2824	252.1448	486.2558	243.6316	485.2718	243.1396	4
8	908.4472	454.7272	891.4207	446.2140	890.4367	445.7220	Q	374.2398	187.6235	357.2132	179.1103			3
9	1007.5156	504.2615	990.4891	495.7482	989.5051	495.2562	V	246.1812	123.5942	229.1547	115.0810			2
10							K	147.1128	74.0600	130.0863	65.5468			1

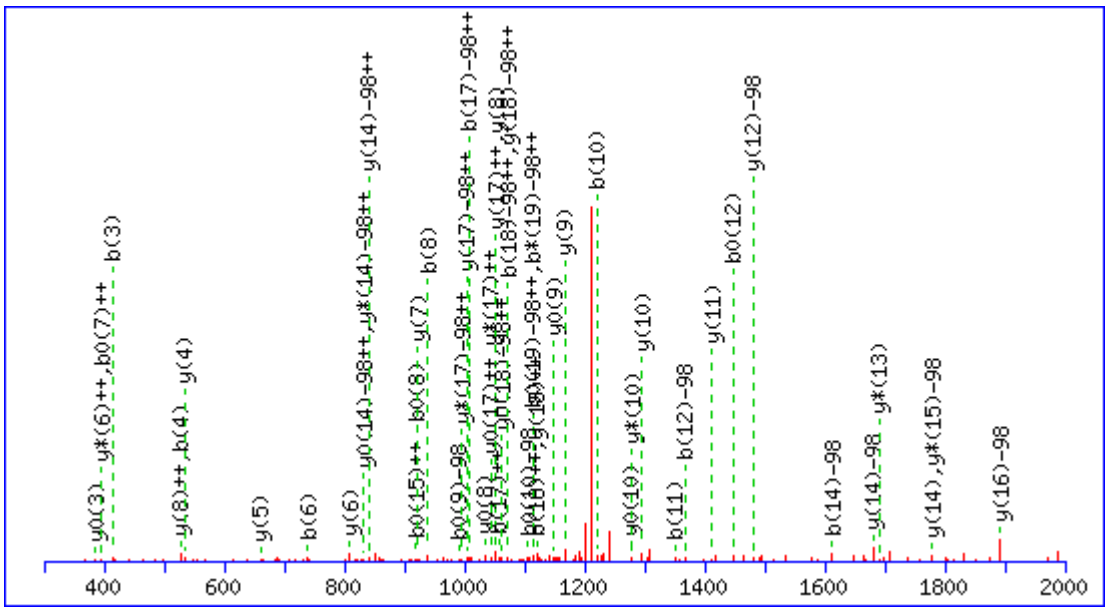




IDENTIFICATION 100

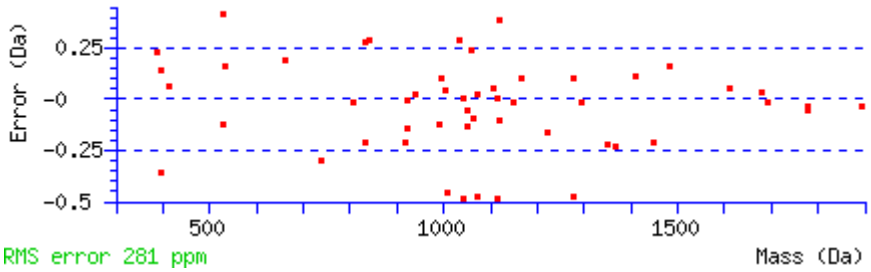
MS/MS Fragmentation of IYHLPDAESDEDEDFKEQTR

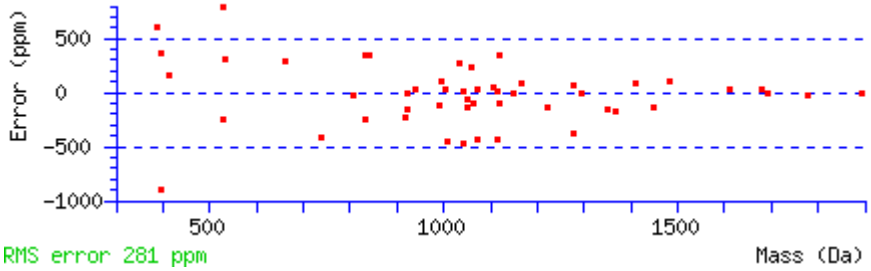
Found in IPI00114945



Monoisotopic mass of neutral peptide Mr(calc): 2516.0380 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 39 Expect: 0.026 (help)

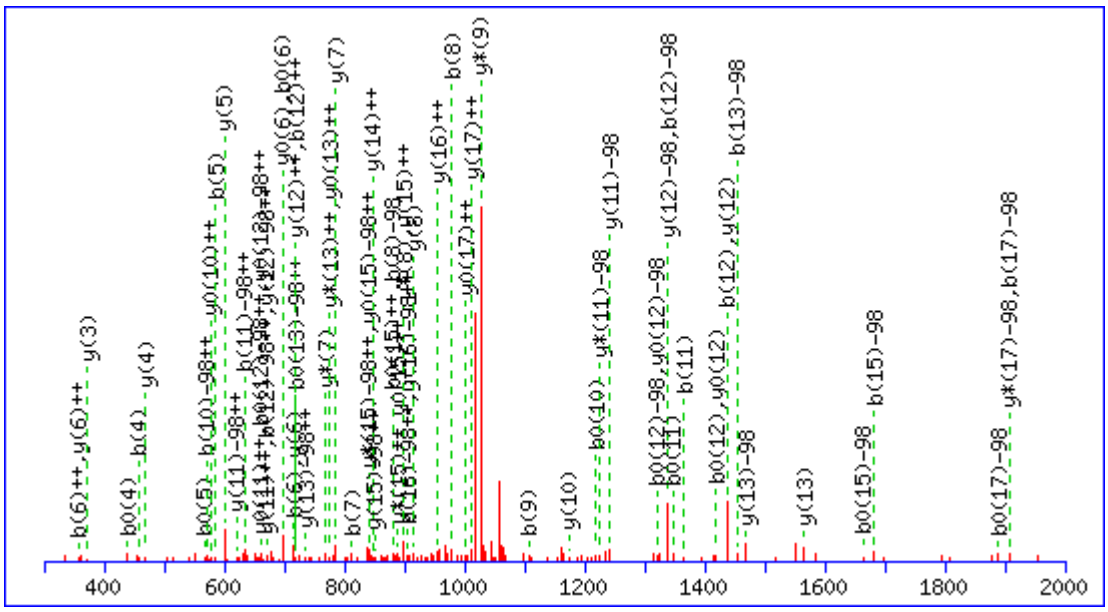
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							20
2	277.1547	139.0810					Y	2305.9844	1153.4958	2288.9578	1144.9826	2287.9738	1144.4905	19
3	414.2136	207.6104					H	2142.9210	1071.9642	2125.8945	1063.4509	2124.9105	1062.9589	18
4	527.2976	264.1525					L	2005.8621	1003.4347	1988.8356	994.9214	1987.8516	994.4294	17
5	624.3504	312.6788					P	1892.7781	946.8927	1875.7515	938.3794	1874.7675	937.8874	16
6	739.3774	370.1923			721.3668	361.1870	D	1795.7253	898.3663	1778.6988	889.8530	1777.7147	889.3610	15
7	810.4145	405.7109			792.4039	396.7056	A	1680.6984	840.8528	1663.6718	832.3395	1662.6878	831.8475	14
8	939.4571	470.2322			921.4465	461.2269	E	1609.6613	805.3343	1592.6347	796.8210	1591.6507	796.3290	13
9	1008.4785	504.7429			990.4680	495.7376	S	1480.6187	740.8130	1463.5921	732.2997	1462.6081	731.8077	12
10	1123.5055	562.2564			1105.4949	553.2511	D	1411.5972	706.3022	1394.5706	697.7890	1393.5866	697.2970	11
11	1252.5481	626.7777			1234.5375	617.7724	E	1296.5703	648.7888	1279.5437	640.2755	1278.5597	639.7835	10
12	1367.5750	684.2911			1349.5644	675.2859	D	1167.5277	584.2675	1150.5011	575.7542	1149.5171	575.2622	9
13	1496.6176	748.8124			1478.6070	739.8072	E	1052.5007	526.7540	1035.4742	518.2407	1034.4902	517.7487	8
14	1611.6445	806.3259			1593.6340	797.3206	D	923.4581	462.2327	906.4316	453.7194	905.4476	453.2274	7
15	1758.7130	879.8601			1740.7024	870.8548	F	808.4312	404.7192	791.4046	396.2060	790.4206	395.7139	6
16	1886.8079	943.9076	1869.7814	935.3943	1868.7973	934.9023	K	661.3628	331.1850	644.3362	322.6717	643.3522	322.1797	5
17	2015.8505	1008.4289	1998.8240	999.9156	1997.8399	999.4236	E	533.2678	267.1375	516.2413	258.6243	515.2572	258.1323	4
18	2143.9091	1072.4582	2126.8825	1063.9449	2125.8985	1063.4529	Q	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	3
19	2244.9568	1122.9820	2227.9302	1114.4687	2226.9462	1113.9767	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
20							R	175.1190	88.0631	158.0924	79.5498			1





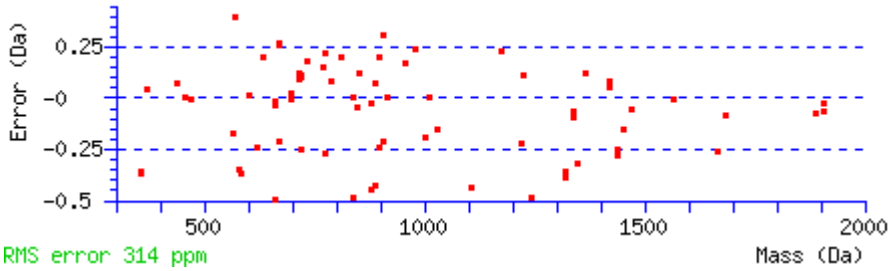
RMS error 281 ppm

IDENTIFICATION 101
MS/MS Fragmentation of EIITEEPSEEEADMPKPK
Found in IPI00120691



Monoisotopic mass of neutral peptide Mr(calc): 2150.9330 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S8 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 40 Expect: 0.019 (help)

#	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							18
2	243.1339	122.0706			225.1234	113.0653	I	1924.9208	962.9641	1907.8943	954.4508	1906.9103	953.9588	17
3	356.2180	178.6126			338.2074	169.6074	I	1811.8368	906.4220	1794.8102	897.9087	1793.8262	897.4167	16
4	457.2657	229.1365			439.2551	220.1312	T	1698.7527	849.8800	1681.7262	841.3667	1680.7421	840.8747	15
5	586.3083	293.6578			568.2977	284.6525	E	1597.7050	799.3562	1580.6785	790.8429	1579.6945	790.3509	14
6	715.3509	358.1791			697.3403	349.1738	E	1468.6624	734.8349	1451.6359	726.3216	1450.6519	725.8296	13
7	812.4036	406.7055			794.3931	397.7002	P	1339.6198	670.3136	1322.5933	661.8003	1321.6093	661.3083	12
8	881.4251	441.2162			863.4145	432.2109	S	1242.5671	621.7872	1225.5405	613.2739	1224.5565	612.7819	11
9	1010.4677	505.7375			992.4571	496.7322	E	1173.5456	587.2764	1156.5191	578.7632	1155.5351	578.2712	10
10	1139.5103	570.2588			1121.4997	561.2535	E	1044.5030	522.7551	1027.4765	514.2419	1026.4925	513.7499	9
11	1268.5529	634.7801			1250.5423	625.7748	E	915.4604	458.2339	898.4339	449.7206	897.4499	449.2286	8
12	1339.5900	670.2986			1321.5794	661.2933	A	786.4178	393.7126	769.3913	385.1993	768.4073	384.7073	7
13	1454.6169	727.8121			1436.6064	718.8068	D	715.3807	358.1940	698.3542	349.6807	697.3702	349.1887	6
14	1585.6574	793.3323			1567.6468	784.3271	M	600.3538	300.6805	583.3272	292.1673			5
15	1682.7102	841.8587			1664.6996	832.8534	P	469.3133	235.1603	452.2867	226.6470			4
16	1810.8051	905.9062	1793.7786	897.3929	1792.7946	896.9009	K	372.2605	186.6339	355.2340	178.1206			3
17	1907.8579	954.4326	1890.8314	945.9193	1889.8473	945.4273	P	244.1656	122.5864	227.1390	114.0731			2
18							K	147.1128	74.0600	130.0863	65.5468			1


Error (Da)
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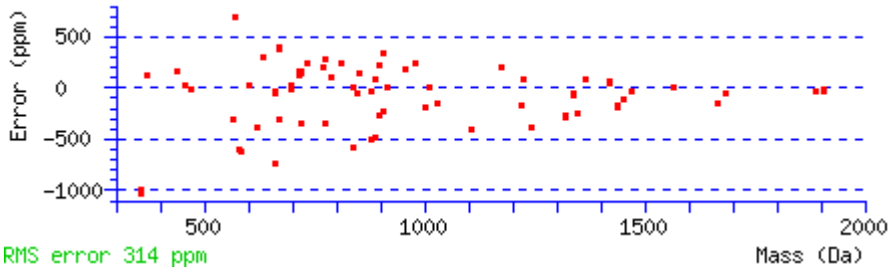
-0
-0.25
-0.5
500
1000
1500
2000
RMS error 314 ppm
Mass (Da)


Error (ppm)
500
0
-500
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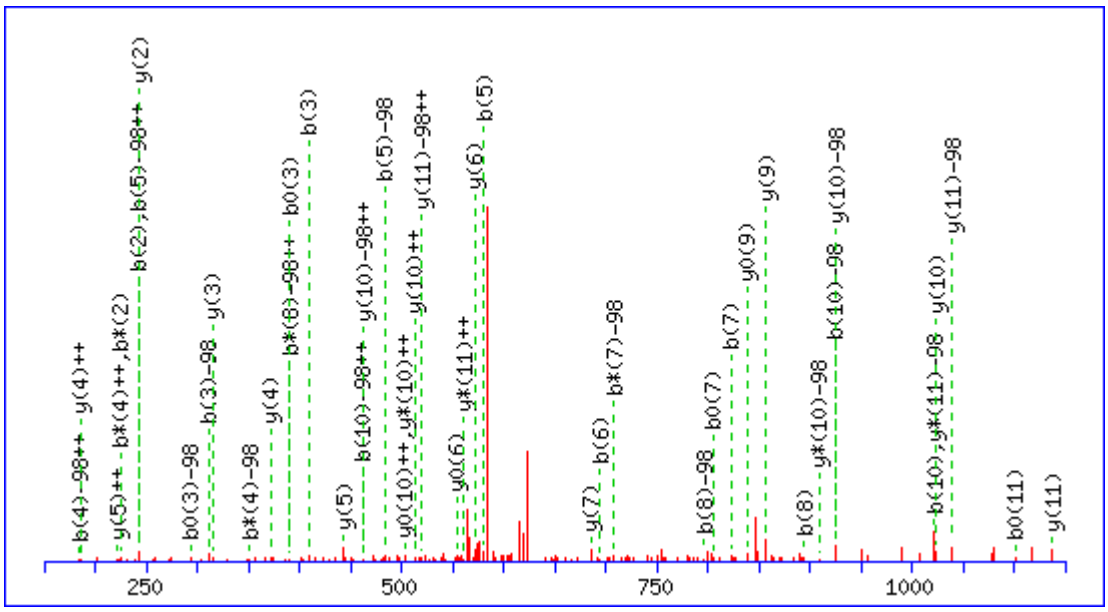
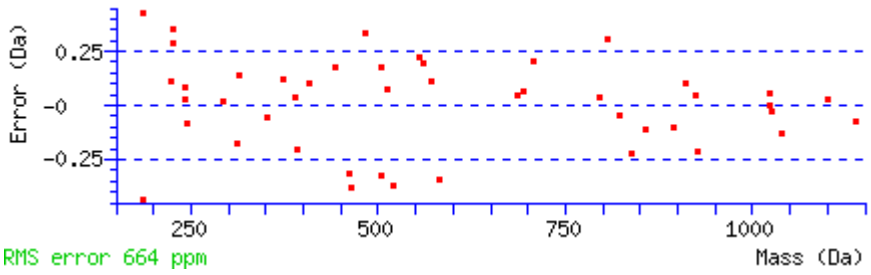
1000
1500
2000
RMS error 314 ppm
Mass (Da)

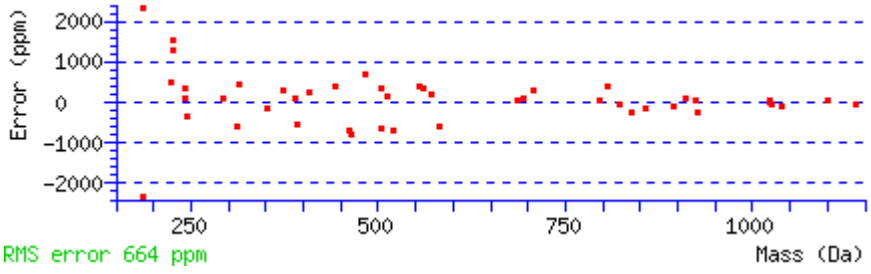
IDENTIFICATION 102
MS/MS Fragmentation of KLSGDLEAGAPK
Found in IPI00115660



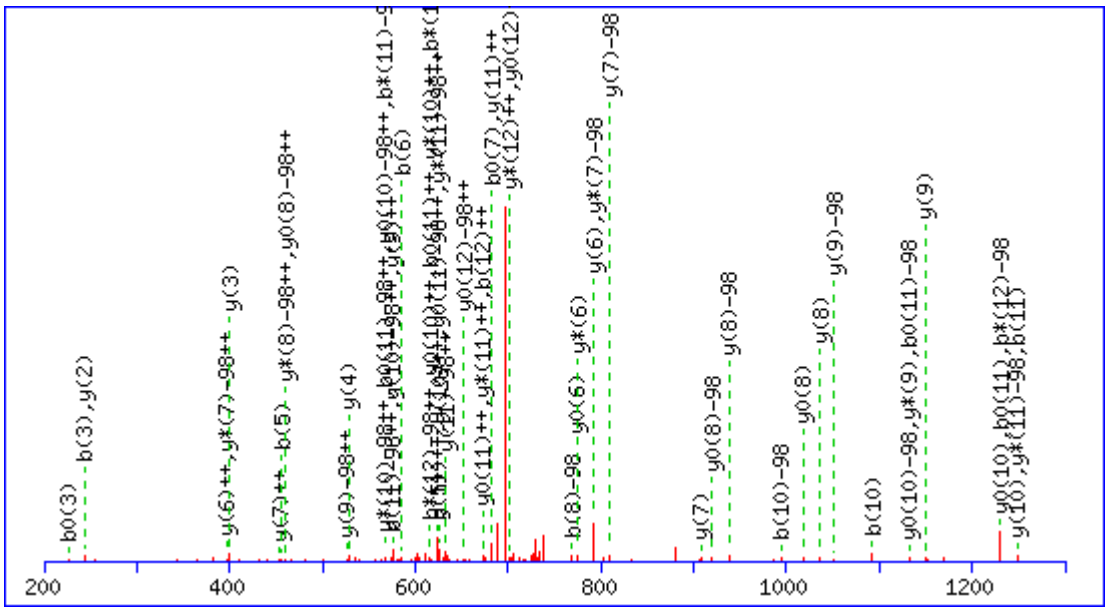
Monoisotopic mass of neutral peptide Mr(calc): 1264.6064
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 49 Expect: 0.0012 (help)

#	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							12
2	242.1863	121.5968	225.1598	113.0835			L	1039.5419	520.2746	1022.5153	511.7613	1021.5313	511.2693	11
3	311.2078	156.1075	294.1812	147.5942	293.1972	147.1022	S	926.4578	463.7325	909.4312	455.2193	908.4472	454.7272	10
4	368.2292	184.6183	351.2027	176.1050	350.2187	175.6130	G	857.4363	429.2218	840.4098	420.7085	839.4258	420.2165	9
5	483.2562	242.1317	466.2296	233.6184	465.2456	233.1264	D	800.4149	400.7111	783.3883	392.1978	782.4043	391.7058	8
6	596.3402	298.6738	579.3137	290.1605	578.3297	289.6685	L	685.3879	343.1976	668.3614	334.6843	667.3774	334.1923	7
7	725.3828	363.1951	708.3563	354.6818	707.3723	354.1898	E	572.3039	286.6556	555.2773	278.1423	554.2933	277.6503	6
8	796.4199	398.7136	779.3934	390.2003	778.4094	389.7083	A	443.2613	222.1343	426.2347	213.6210			5
9	853.4414	427.2243	836.4149	418.7111	835.4308	418.2191	G	372.2241	186.6157	355.1976	178.1024			4
10	924.4785	462.7429	907.4520	454.2296	906.4680	453.7376	A	315.2027	158.1050	298.1761	149.5917			3
11	1021.5313	511.2693	1004.5047	502.7560	1003.5207	502.2640	P	244.1656	122.5864	227.1390	114.0731			2
12							K	147.1128	74.0600	130.0863	65.5468			1



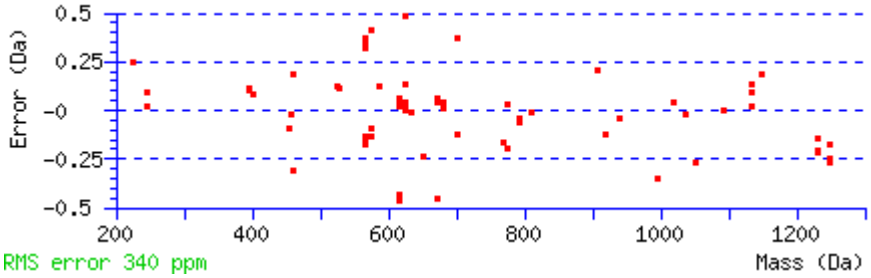


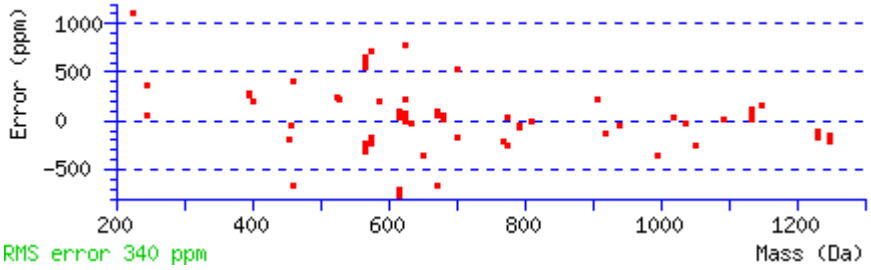
IDENTIFICATION 103
MS/MS Fragmentation of AGDVLEDSPKRPK
Found in IPI00313817



Monoisotopic mass of neutral peptide Mr(calc): 1490.7130
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S8 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 49 Expect: 0.0014 (help)

#	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	129.0659	65.0366					G	1420.6832	710.8452	1403.6566	702.3320	1402.6726	701.8399	12
3	244.0928	122.5500			226.0822	113.5448	D	1363.6617	682.3345	1346.6352	673.8212	1345.6512	673.3292	11
4	343.1612	172.0842			325.1506	163.0790	V	1248.6348	624.8210	1231.6082	616.3078	1230.6242	615.8157	10
5	456.2453	228.6263			438.2347	219.6210	L	1149.5664	575.2868	1132.5398	566.7735	1131.5558	566.2815	9
6	585.2879	293.1476			567.2773	284.1423	E	1036.4823	518.7448	1019.4558	510.2315	1018.4717	509.7395	8
7	700.3148	350.6610			682.3042	341.6558	D	907.4397	454.2235	890.4132	445.7102	889.4291	445.2182	7
8	867.3132	434.1602			849.3026	425.1549	S	792.4128	396.7100	775.3862	388.1967	774.4022	387.7047	6
9	964.3659	482.6866			946.3554	473.6813	P	625.4144	313.2108	608.3879	304.6976			5
10	1092.4609	546.7341	1075.4343	538.2208	1074.4503	537.7288	K	528.3616	264.6845	511.3351	256.1712			4
11	1248.5620	624.7846	1231.5355	616.2714	1230.5514	615.7794	R	400.2667	200.6370	383.2401	192.1237			3
12	1345.6148	673.3110	1328.5882	664.7977	1327.6042	664.3057	P	244.1656	122.5864	227.1390	114.0731			2
13							K	147.1128	74.0600	130.0863	65.5468			1

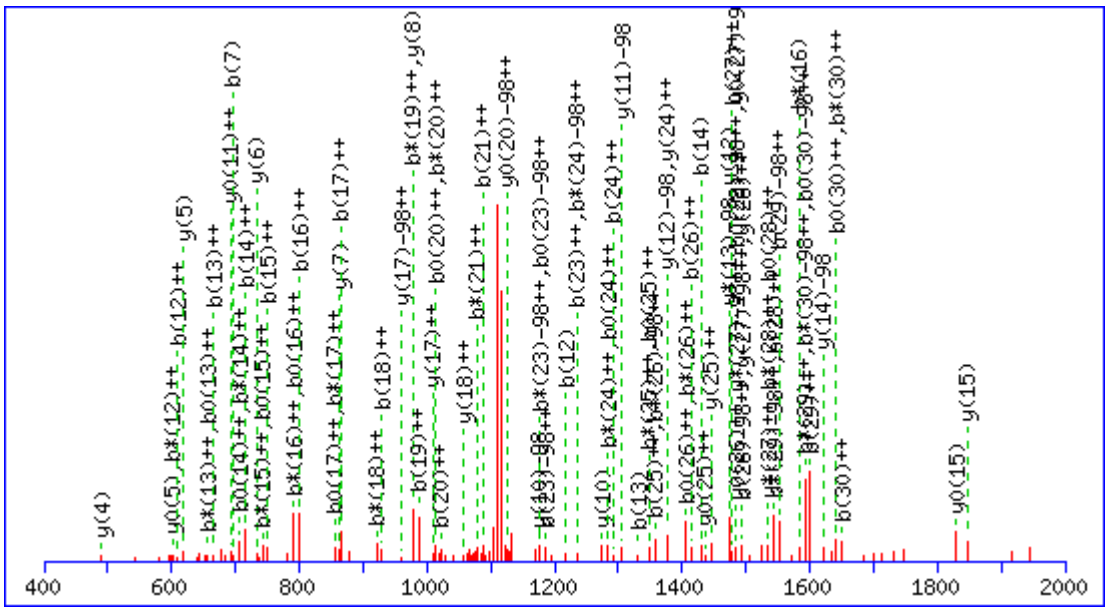

0.5
0.25
-0
-0.25
-0.5
Error (Da)
200
400
600
800
1000
1200
Mass (Da)
RMS error 340 ppm


1000
500
0
-500
Error (ppm)
200
400
600
800
1000
1200
Mass (Da)
RMS error 340 ppm

IDENTIFICATION 104

MS/MS Fragmentation of CGSGPVHISGQHLVAVEEDAESEDEDEEDVK

Found in IPI00127415



Monoisotopic mass of neutral peptide Mr(calc): 3445.4141

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

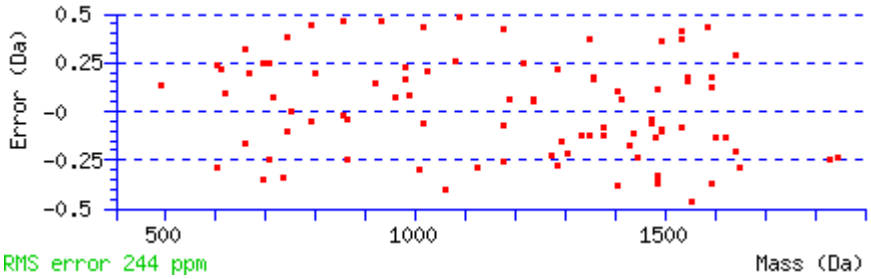
Variable modifications:

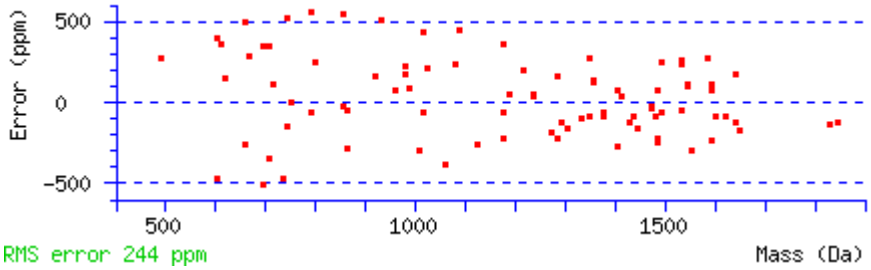
S22 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 89 Expect: 3.4e-07 (help)

#	b	b^{++}	b*	b*$^{++}$	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^{0}	y^{0++}	#
1	161.0379	81.0226					C							31
2	218.0594	109.5333					G	3286.3907	1643.6990	3269.3642	1635.1857	3268.3801	1634.6937	30
3	305.0914	153.0493			287.0809	144.0441	S	3229.3692	1615.1883	3212.3427	1606.6750	3211.3587	1606.1830	29
4	362.1129	181.5601			344.1023	172.5548	G	3142.3372	1571.6722	3125.3107	1563.1590	3124.3267	1562.6670	28
5	459.1656	230.0865			441.1551	221.0812	P	3085.3158	1543.1615	3068.2892	1534.6482	3067.3052	1534.1562	27
6	558.2341	279.6207			540.2235	270.6154	V	2988.2630	1494.6351	2971.2364	1486.1219	2970.2524	1485.6299	26
7	695.2930	348.1501			677.2824	339.1448	H	2889.1946	1445.1009	2872.1680	1436.5877	2871.1840	1436.0956	25
8	808.3770	404.6922			790.3665	395.6869	I	2752.1357	1376.5715	2735.1091	1368.0582	2734.1251	1367.5662	24
9	895.4091	448.2082			877.3985	439.2029	S	2639.0516	1320.0294	2622.0251	1311.5162	2621.0410	1311.0242	23
10	952.4305	476.7189			934.4200	467.7136	G	2552.0196	1276.5134	2534.9930	1268.0002	2534.0090	1267.5081	22
11	1080.4891	540.7482	1063.4626	532.2349	1062.4785	531.7429	Q	2494.9981	1248.0027	2477.9716	1239.4894	2476.9875	1238.9974	21
12	1217.5480	609.2776	1200.5215	600.7644	1199.5375	600.2724	H	2366.9395	1183.9734	2349.9130	1175.4601	2348.9290	1174.9681	20
13	1330.6321	665.8197	1313.6055	657.3064	1312.6215	656.8144	L	2229.8806	1115.4439	2212.8541	1106.9307	2211.8701	1106.4387	19
14	1429.7005	715.3539	1412.6739	706.8406	1411.6899	706.3486	V	2116.7966	1058.9019	2099.7700	1050.3886	2098.7860	1049.8966	18
15	1500.7376	750.8724	1483.7111	742.3592	1482.7270	741.8672	A	2017.7281	1009.3677	2000.7016	1000.8544	1999.7176	1000.3624	17
16	1599.8060	800.4066	1582.7795	791.8934	1581.7955	791.4014	V	1946.6910	973.8492	1929.6645	965.3359	1928.6805	964.8439	16
17	1728.8486	864.9279	1711.8221	856.4147	1710.8381	855.9227	E	1847.6226	924.3149	1830.5961	915.8017	1829.6120	915.3097	15
18	1857.8912	929.4492	1840.8647	920.9360	1839.8806	920.4440	E	1718.5800	859.7936	1701.5535	851.2804	1700.5695	850.7884	14
19	1972.9182	986.9627	1955.8916	978.4494	1954.9076	977.9574	D	1589.5374	795.2724	1572.5109	786.7591	1571.5269	786.2671	13
20	2043.9553	1022.4813	2026.9287	1013.9680	2025.9447	1013.4760	A	1474.5105	737.7589	1457.4839	729.2456	1456.4999	728.7536	12
21	2172.9979	1087.0026	2155.9713	1078.4893	2154.9873	1077.9973	E	1403.4734	702.2403	1386.4468	693.7270	1385.4628	693.2350	11
22	2339.9962	1170.5017	2322.9697	1161.9885	2321.9857	1161.4965	S	1274.4308	637.7190	1257.4042	629.2058	1256.4202	628.7137	10
23	2469.0388	1235.0230	2452.0123	1226.5098	2451.0282	1226.0178	E	1107.4324	554.2198	1090.4059	545.7066	1089.4219	545.2146	9
24	2584.0658	1292.5365	2567.0392	1284.0232	2566.0552	1283.5312	D	978.3898	489.6986	961.3633	481.1853	960.3793	480.6933	8
25	2713.1083	1357.0578	2696.0818	1348.5445	2695.0978	1348.0525	E	863.3629	432.1851	846.3363	423.6718	845.3523	423.1798	7
26	2828.1353	1414.5713	2811.1087	1406.0580	2810.1247	1405.5660	D	734.3203	367.6638	717.2937	359.1505	716.3097	358.6585	6
27	2957.1779	1479.0926	2940.1513	1470.5793	2939.1673	1470.0873	E	619.2933	310.1503	602.2668	301.6370	601.2828	301.1450	5

28	3086.2205	1543.6139	3069.1939	1535.1006	3068.2099	1534.6086	E	490.2508	245.6290	473.2242	237.1157	472.2402	236.6237	4
29	3201.2474	1601.1273	3184.2209	1592.6141	3183.2369	1592.1221	D	361.2082	181.1077	344.1816	172.5944	343.1976	172.1024	3
30	3300.3158	1650.6616	3283.2893	1642.1483	3282.3053	1641.6563	V	246.1812	123.5942	229.1547	115.0810			2
31							K	147.1128	74.0600	130.0863	65.5468			1

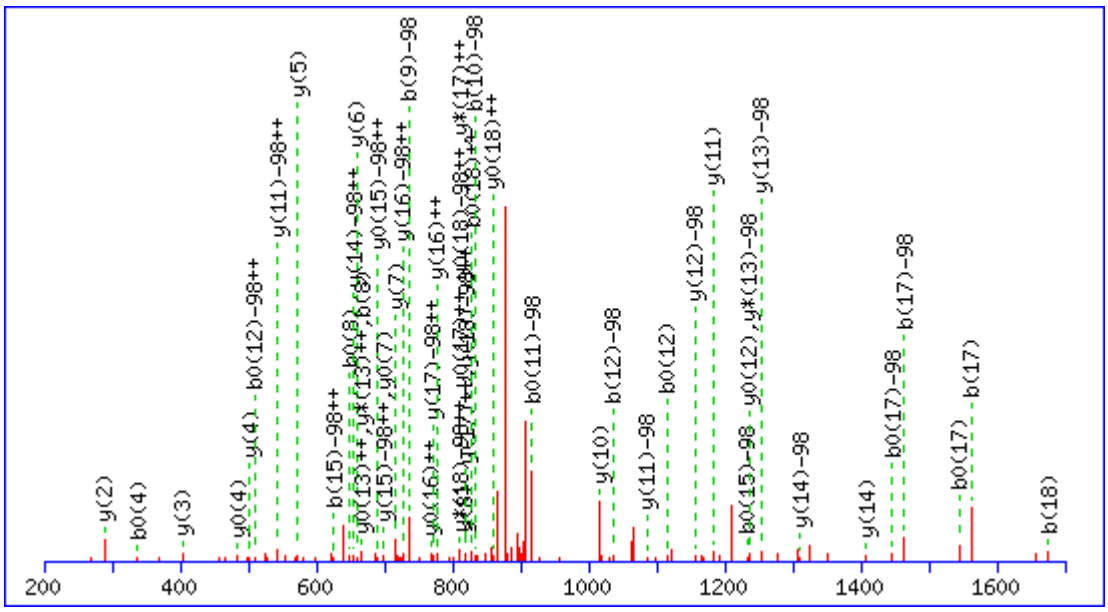




IDENTIFICATION 105

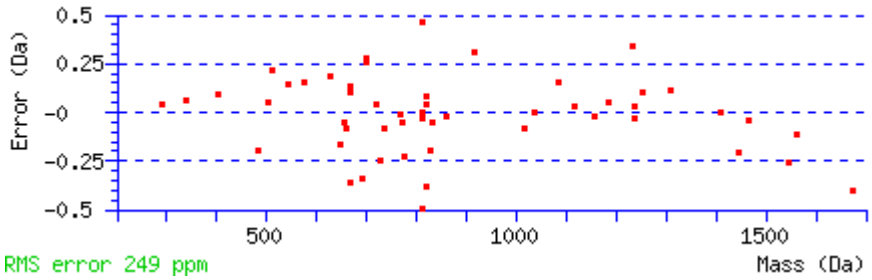
MS/MS Fragmentation of LPSGSGPASPTTGSAVDIR

Found in IPI00553798

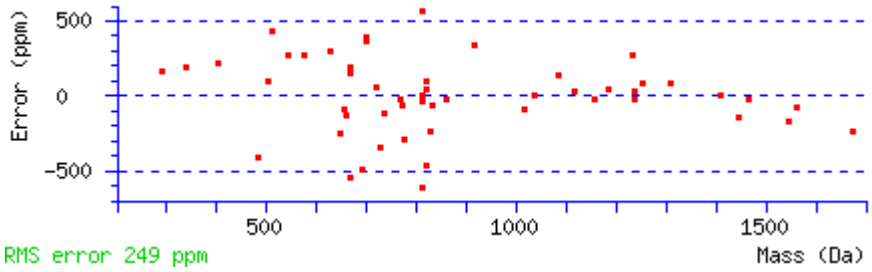


Monoisotopic mass of neutral peptide Mr(calc): 1848.8619 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 60 Expect: 0.00015 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							19
2	211.1441	106.0757			P	1638.8082	819.9077	1621.7816	811.3945	1620.7976	810.9025	18
3	298.1761	149.5917	280.1656	140.5864	S	1541.7554	771.3814	1524.7289	762.8681	1523.7449	762.3761	17
4	355.1976	178.1024	337.1870	169.0972	G	1454.7234	727.8653	1437.6968	719.3521	1436.7128	718.8601	16
5	442.2296	221.6184	424.2191	212.6132	S	1397.7019	699.3546	1380.6754	690.8413	1379.6914	690.3493	15
6	499.2511	250.1292	481.2405	241.1239	G	1310.6699	655.8386	1293.6434	647.3253	1292.6593	646.8333	14
7	596.3039	298.6556	578.2933	289.6503	P	1253.6484	627.3279	1236.6219	618.8146	1235.6379	618.3226	13
8	667.3410	334.1741	649.3304	325.1688	A	1156.5957	578.8015	1139.5691	570.2882	1138.5851	569.7962	12
9	736.3624	368.6849	718.3519	359.6796	S	1085.5586	543.2829	1068.5320	534.7696	1067.5480	534.2776	11
10	833.4152	417.2112	815.4046	408.2060	P	1016.5371	508.7722	999.5106	500.2589	998.5265	499.7669	10
11	934.4629	467.7351	916.4523	458.7298	T	919.4843	460.2458	902.4578	451.7325	901.4738	451.2405	9
12	1035.5106	518.2589	1017.5000	509.2536	T	818.4367	409.7220	801.4101	401.2087	800.4261	400.7167	8
13	1092.5320	546.7696	1074.5214	537.7644	G	717.3890	359.1981	700.3624	350.6849	699.3784	350.1928	7
14	1179.5640	590.2857	1161.5535	581.2804	S	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
15	1250.6012	625.8042	1232.5906	616.7989	A	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	5
16	1349.6696	675.3384	1331.6590	666.3331	V	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
17	1464.6965	732.8519	1446.6859	723.8466	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
18	1577.7806	789.3939	1559.7700	780.3886	I	288.2030	144.6051	271.1765	136.0919			2
19					R	175.1190	88.0631	158.0924	79.5498			1

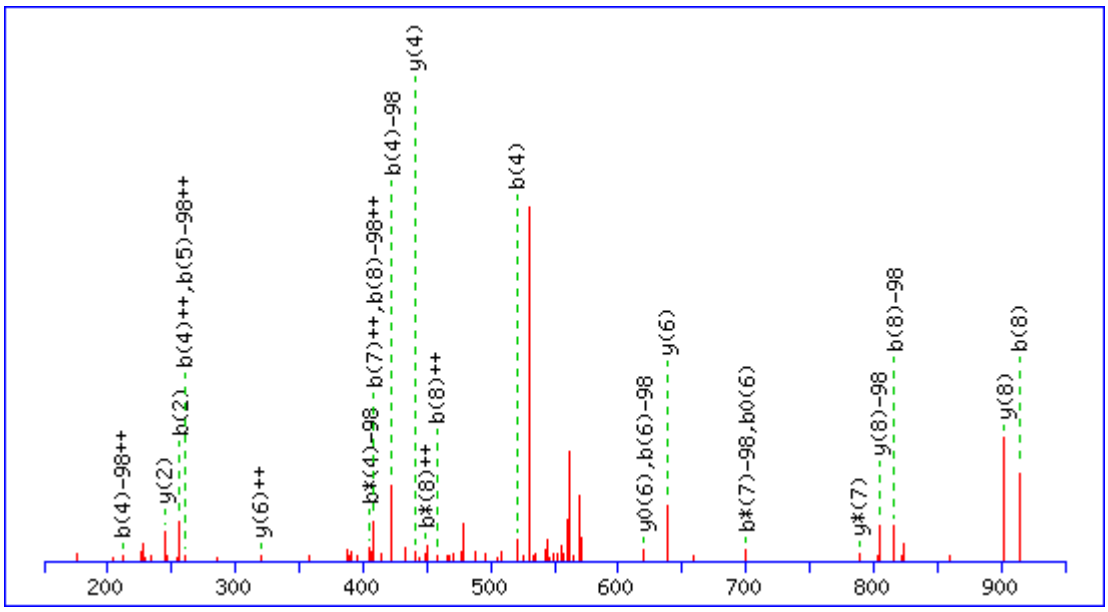


RMS error 249 ppm



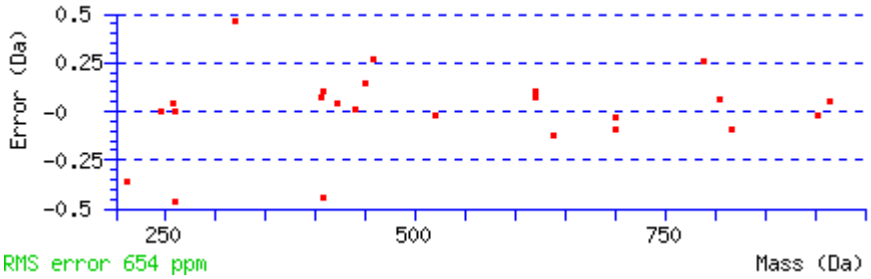
RMS error 249 ppm

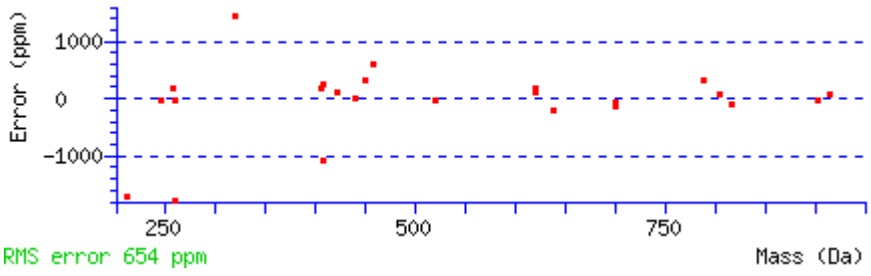
IDENTIFICATION 106
MS/MS Fragmentation of RVPSPTPVPK
Found in IPI00785240



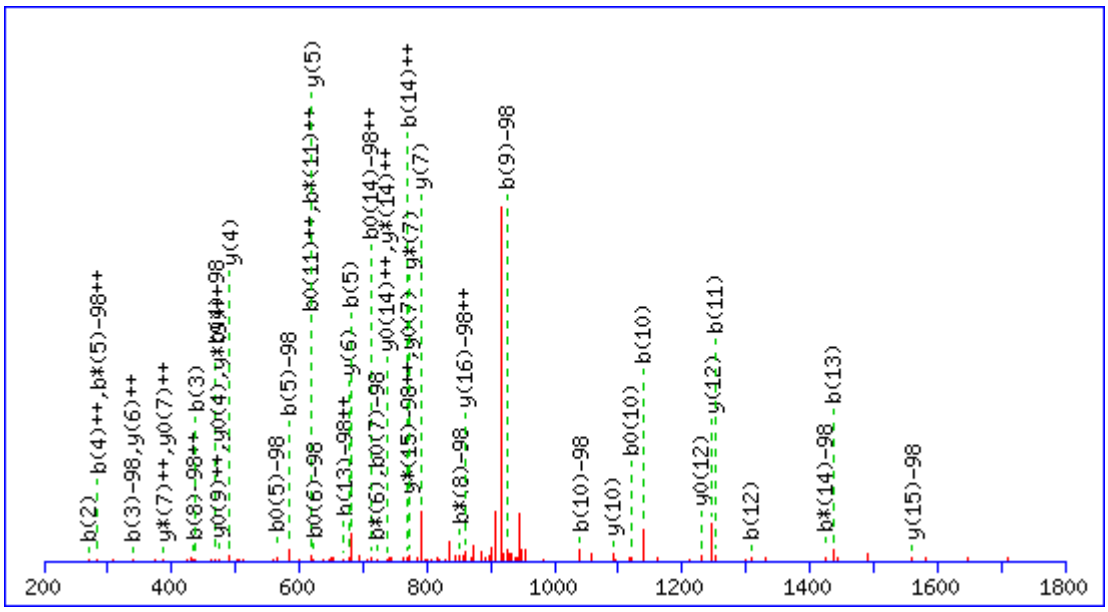
Monoisotopic mass of neutral peptide Mr(calc): 1156.6006
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.16 (help)

#	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							10
2	256.1768	128.5920	239.1503	120.0788			V	903.5298	452.2686	886.5033	443.7553	885.5193	443.2633	9
3	353.2296	177.1184	336.2030	168.6051			P	804.4614	402.7343	787.4349	394.2211	786.4509	393.7291	8
4	422.2510	211.6292	405.2245	203.1159	404.2405	202.6239	S	707.4087	354.2080	690.3821	345.6947	689.3981	345.2027	7
5	519.3038	260.1555	502.2772	251.6423	501.2932	251.1503	P	638.3872	319.6972	621.3606	311.1840	620.3766	310.6920	6
6	620.3515	310.6794	603.3249	302.1661	602.3409	301.6741	T	541.3344	271.1709	524.3079	262.6576	523.3239	262.1656	5
7	717.4042	359.2058	700.3777	350.6925	699.3937	350.2005	P	440.2867	220.6470	423.2602	212.1337			4
8	816.4726	408.7400	799.4461	400.2267	798.4621	399.7347	V	343.2340	172.1206	326.2074	163.6074			3
9	913.5254	457.2663	896.4989	448.7531	895.5148	448.2611	P	244.1656	122.5864	227.1390	114.0731			2
10							K	147.1128	74.0600	130.0863	65.5468			1



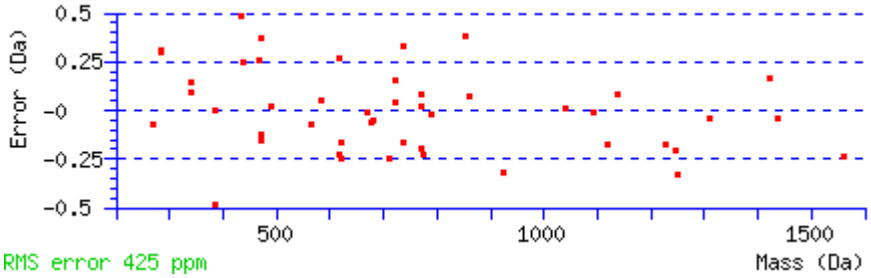


IDENTIFICATION 107
MS/MS Fragmentation of LRSEDGVEGDLGETQSR
Found in IPI00553798

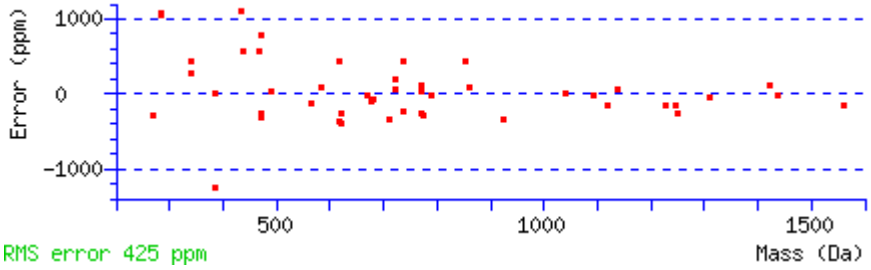


Monoisotopic mass of neutral peptide Mr(calc): 1926.8320 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 32 Expect: 0.11 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							17
2	270.1925	135.5999	253.1659	127.0866			R	1716.7783	858.8928	1699.7518	850.3795	1698.7678	849.8875	16
3	339.2139	170.1106	322.1874	161.5973	321.2033	161.1053	S	1560.6772	780.8423	1543.6507	772.3290	1542.6667	771.8370	15
4	468.2565	234.6319	451.2300	226.1186	450.2459	225.6266	E	1491.6558	746.3315	1474.6292	737.8182	1473.6452	737.3262	14
5	583.2835	292.1454	566.2569	283.6321	565.2729	283.1401	D	1362.6132	681.8102	1345.5866	673.2970	1344.6026	672.8049	13
6	640.3049	320.6561	623.2784	312.1428	622.2943	311.6508	G	1247.5862	624.2968	1230.5597	615.7835	1229.5757	615.2915	12
7	739.3733	370.1903	722.3468	361.6770	721.3628	361.1850	V	1190.5648	595.7860	1173.5382	587.2727	1172.5542	586.7807	11
8	868.4159	434.7116	851.3894	426.1983	850.4054	425.7063	E	1091.4964	546.2518	1074.4698	537.7385	1073.4858	537.2465	10
9	925.4374	463.2223	908.4108	454.7091	907.4268	454.2170	G	962.4538	481.7305	945.4272	473.2172	944.4432	472.7252	9
10	1040.4643	520.7358	1023.4378	512.2225	1022.4538	511.7305	D	905.4323	453.2198	888.4058	444.7065	887.4217	444.2145	8
11	1153.5484	577.2778	1136.5218	568.7646	1135.5378	568.2726	L	790.4054	395.7063	773.3788	387.1930	772.3948	386.7010	7
12	1210.5699	605.7886	1193.5433	597.2753	1192.5593	596.7833	G	677.3213	339.1643	660.2947	330.6510	659.3107	330.1590	6
13	1339.6124	670.3099	1322.5859	661.7966	1321.6019	661.3046	E	620.2998	310.6536	603.2733	302.1403	602.2893	301.6483	5
14	1440.6601	720.8337	1423.6336	712.3204	1422.6496	711.8284	T	491.2572	246.1323	474.2307	237.6190	473.2467	237.1270	4
15	1568.7187	784.8630	1551.6922	776.3497	1550.7081	775.8577	Q	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
16	1655.7507	828.3790	1638.7242	819.8657	1637.7402	819.3737	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

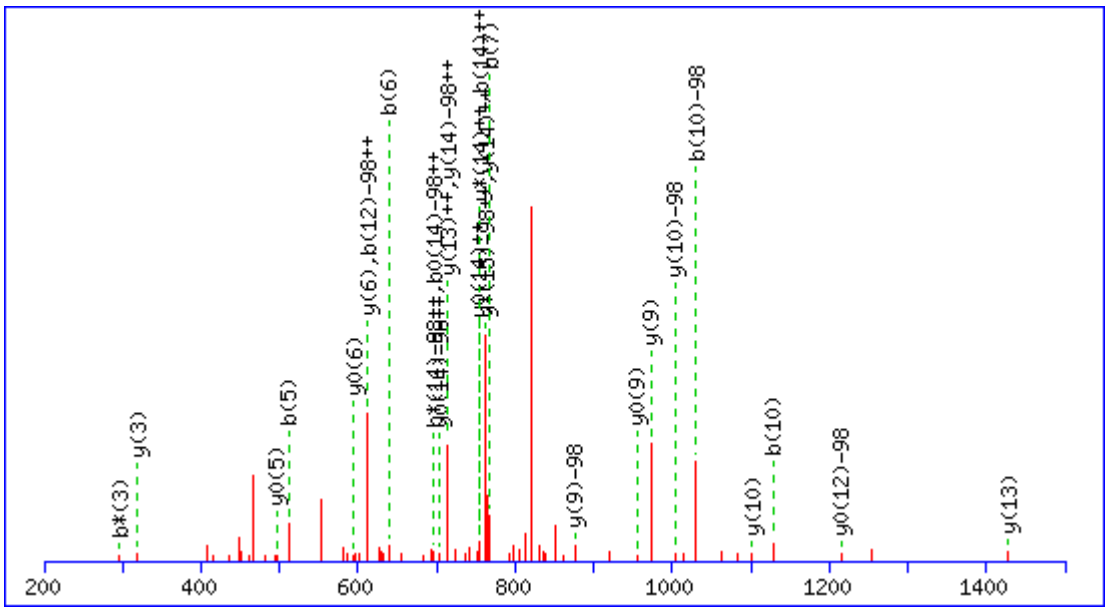


RMS error 425 ppm



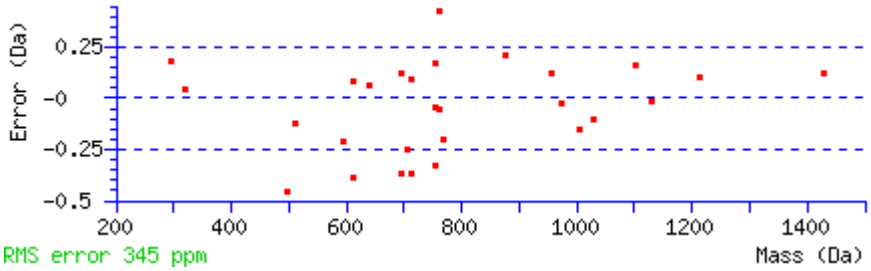
RMS error 425 ppm

IDENTIFICATION 108
MS/MS Fragmentation of TNPPTQKPPSPPVSGR
Found in IPI00454179



Monoisotopic mass of neutral peptide Mr(calc): 1738.8403
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 21 Expect: 0.91 (help)

#	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							16
2	216.0979	108.5526	199.0713	100.0393	198.0873	99.5473	N	1638.7999	819.9036	1621.7734	811.3903	1620.7894	810.8983	15
3	313.1506	157.0790	296.1241	148.5657	295.1401	148.0737	P	1524.7570	762.8821	1507.7305	754.3689	1506.7465	753.8769	14
4	410.2034	205.6053	393.1769	197.0921	392.1928	196.6001	P	1427.7043	714.3558	1410.6777	705.8425	1409.6937	705.3505	13
5	511.2511	256.1292	494.2245	247.6159	493.2405	247.1239	T	1330.6515	665.8294	1313.6249	657.3161	1312.6409	656.8241	12
6	639.3097	320.1585	622.2831	311.6452	621.2991	311.1532	Q	1229.6038	615.3055	1212.5773	606.7923	1211.5932	606.3003	11
7	767.4046	384.2060	750.3781	375.6927	749.3941	375.2007	K	1101.5452	551.2763	1084.5187	542.7630	1083.5347	542.2710	10
8	864.4574	432.7323	847.4308	424.2191	846.4468	423.7271	P	973.4503	487.2288	956.4237	478.7155	955.4397	478.2235	9
9	961.5102	481.2587	944.4836	472.7454	943.4996	472.2534	P	876.3975	438.7024	859.3710	430.1891	858.3869	429.6971	8
10	1128.5085	564.7579	1111.4820	556.2446	1110.4980	555.7526	S	779.3447	390.1760	762.3182	381.6627	761.3342	381.1707	7
11	1225.5613	613.2843	1208.5347	604.7710	1207.5507	604.2790	P	612.3464	306.6768	595.3198	298.1636	594.3358	297.6715	6
12	1322.6140	661.8107	1305.5875	653.2974	1304.6035	652.8054	P	515.2936	258.1504	498.2671	249.6372	497.2831	249.1452	5
13	1421.6825	711.3449	1404.6559	702.8316	1403.6719	702.3396	V	418.2409	209.6241	401.2143	201.1108	400.2303	200.6188	4
14	1508.7145	754.8609	1491.6879	746.3476	1490.7039	745.8556	S	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
15	1565.7360	783.3716	1548.7094	774.8583	1547.7254	774.3663	G	232.1404	116.5738	215.1139	108.0606			2
16							R	175.1190	88.0631	158.0924	79.5498			1


Error (Da)
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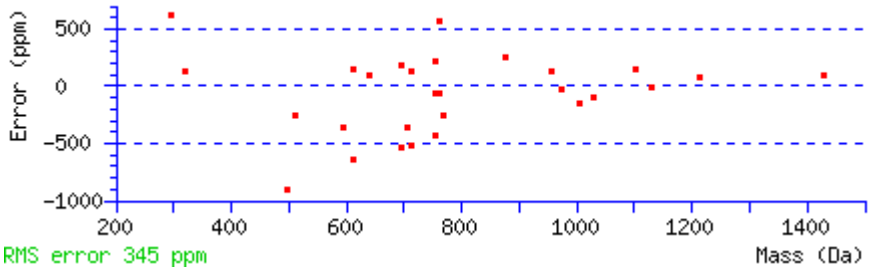
600
800
1000
1200
1400
Mass (Da)
RMS error 345 ppm


Error (ppm)
500
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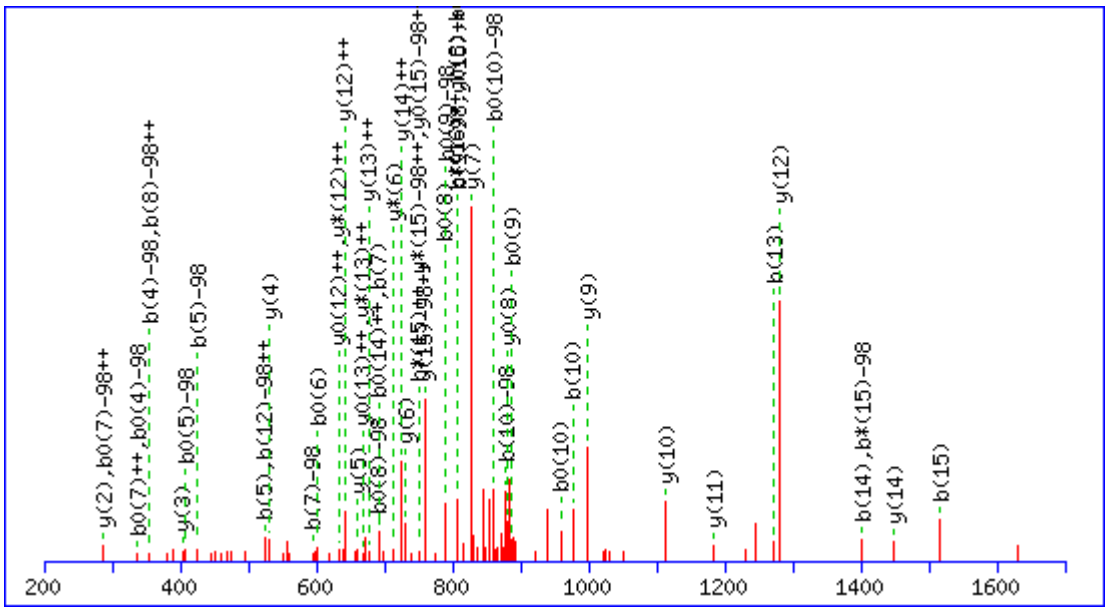
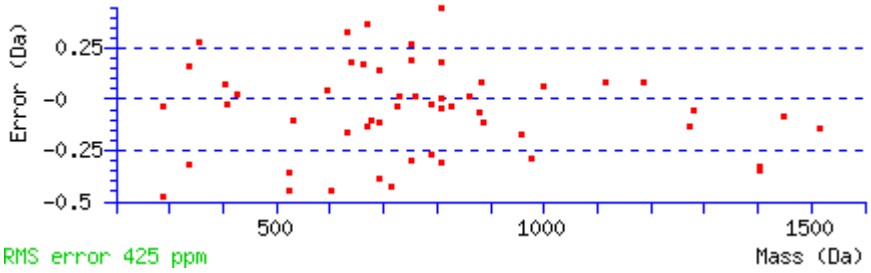
-500
-1000
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 345 ppm

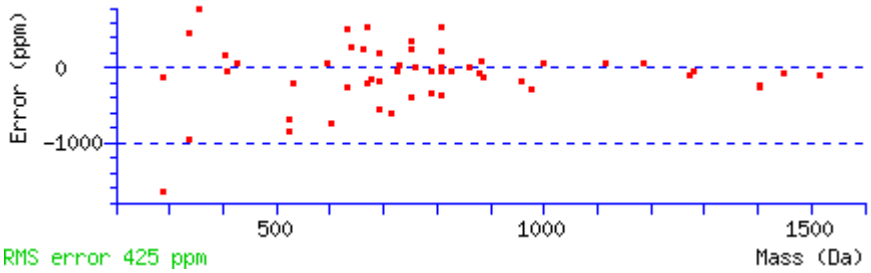
IDENTIFICATION 109
MS/MS Fragmentation of STSPAPADVAPAQEDLR
Found in IPI00130095



Monoisotopic mass of neutral peptide Mr(calc): 1803.8040 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 70 Expect: 1.7e-05 (help)

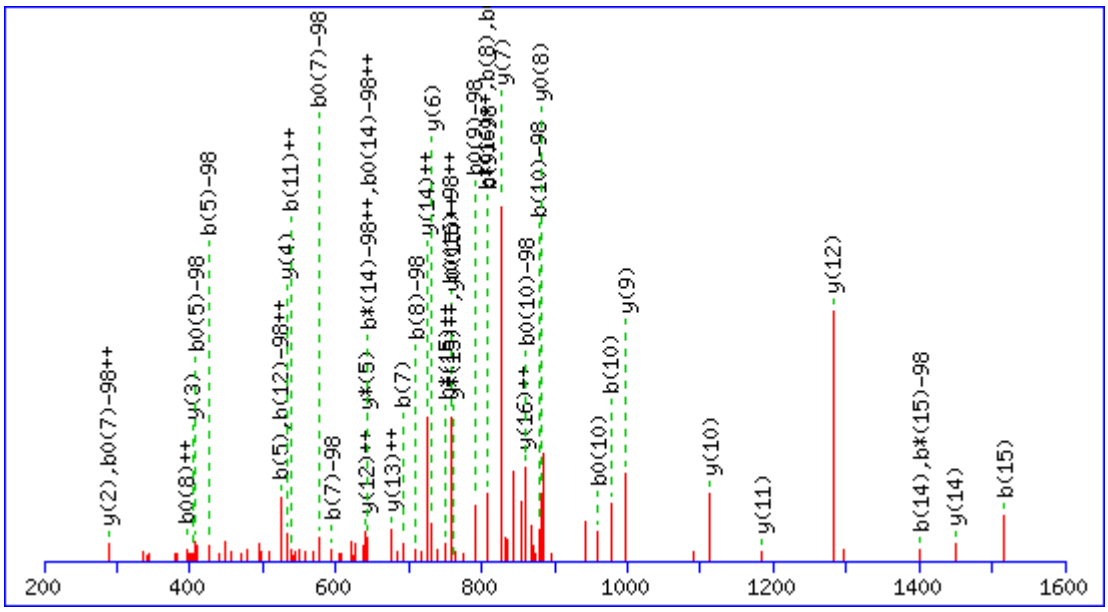
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							17
2	189.0870	95.0471			171.0764	86.0418	T	1619.8024	810.4048	1602.7758	801.8916	1601.7918	801.3995	16
3	258.1084	129.5579			240.0979	120.5526	S	1518.7547	759.8810	1501.7281	751.3677	1500.7441	750.8757	15
4	355.1612	178.0842			337.1506	169.0790	P	1449.7332	725.3703	1432.7067	716.8570	1431.7227	716.3650	14
5	426.1983	213.6028			408.1878	204.5975	A	1352.6805	676.8439	1335.6539	668.3306	1334.6699	667.8386	13
6	523.2511	262.1292			505.2405	253.1239	P	1281.6434	641.3253	1264.6168	632.8120	1263.6328	632.3200	12
7	594.2882	297.6477			576.2776	288.6425	A	1184.5906	592.7989	1167.5640	584.2857	1166.5800	583.7937	11
8	709.3151	355.1612			691.3046	346.1559	D	1113.5535	557.2804	1096.5269	548.7671	1095.5429	548.2751	10
9	808.3836	404.6954			790.3730	395.6901	V	998.5265	499.7669	981.5000	491.2536	980.5160	490.7616	9
10	879.4207	440.2140			861.4101	431.2087	A	899.4581	450.2327	882.4316	441.7194	881.4476	441.2274	8
11	976.4734	488.7404			958.4629	479.7351	P	828.4210	414.7141	811.3945	406.2009	810.4104	405.7089	7
12	1047.5106	524.2589			1029.5000	515.2536	A	731.3682	366.1878	714.3417	357.6745	713.3577	357.1825	6
13	1175.5691	588.2882	1158.5426	579.7749	1157.5586	579.2829	Q	660.3311	330.6692	643.3046	322.1559	642.3206	321.6639	5
14	1304.6117	652.8095	1287.5852	644.2962	1286.6012	643.8042	E	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
15	1419.6387	710.3230	1402.6121	701.8097	1401.6281	701.3177	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
16	1532.7227	766.8650	1515.6962	758.3517	1514.7122	757.8597	L	288.2030	144.6051	271.1765	136.0919			2
17							R	175.1190	88.0631	158.0924	79.5498			1





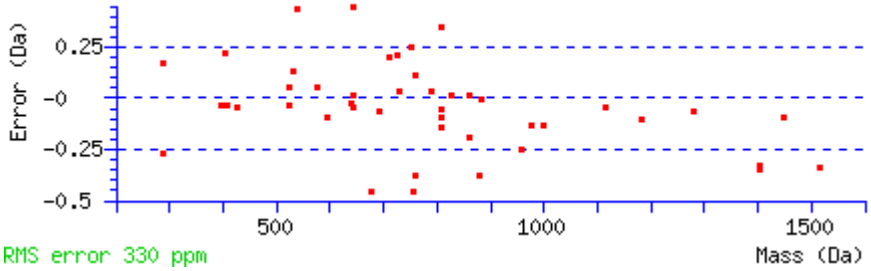
RMS error 425 ppm

IDENTIFICATION 110
MS/MS Fragmentation of STSPAPADVAPAQEDLR
Found in IPI00130095

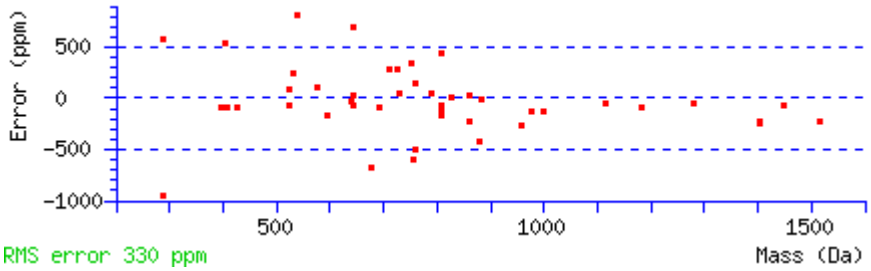


Monoisotopic mass of neutral peptide Mr(calc): 1803.8040
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 60 Expect: 0.00018 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							17
2	269.0533	135.0303			251.0427	126.0250	T	1717.7793	859.3933	1700.7527	850.8800	1699.7687	850.3880	16
3	356.0853	178.5463			338.0748	169.5410	S	1536.7653	768.8863	1519.7387	760.3730	1518.7547	759.8810	15
4	453.1381	227.0727			435.1275	218.0674	P	1449.7332	725.3703	1432.7067	716.8570	1431.7227	716.3650	14
5	524.1752	262.5912			506.1647	253.5860	A	1352.6805	676.8439	1335.6539	668.3306	1334.6699	667.8386	13
6	621.2280	311.1176			603.2174	302.1123	P	1281.6434	641.3253	1264.6168	632.8120	1263.6328	632.3200	12
7	692.2651	346.6362			674.2545	337.6309	A	1184.5906	592.7989	1167.5640	584.2857	1166.5800	583.7937	11
8	807.2920	404.1497			789.2815	395.1444	D	1113.5535	557.2804	1096.5269	548.7671	1095.5429	548.2751	10
9	906.3605	453.6839			888.3499	444.6786	V	998.5265	499.7669	981.5000	491.2536	980.5160	490.7616	9
10	977.3976	489.2024			959.3870	480.1971	A	899.4581	450.2327	882.4316	441.7194	881.4476	441.2274	8
11	1074.4503	537.7288			1056.4398	528.7235	P	828.4210	414.7141	811.3945	406.2009	810.4104	405.7089	7
12	1145.4874	573.2474			1127.4769	564.2421	A	731.3682	366.1878	714.3417	357.6745	713.3577	357.1825	6
13	1273.5460	637.2767	1256.5195	628.7634	1255.5355	628.2714	Q	660.3311	330.6692	643.3046	322.1559	642.3206	321.6639	5
14	1402.5886	701.7979	1385.5621	693.2847	1384.5781	692.7927	E	532.2726	266.6399	515.2460	258.1266	514.2620	257.6346	4
15	1517.6156	759.3114	1500.5890	750.7981	1499.6050	750.3061	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
16	1630.6996	815.8535	1613.6731	807.3402	1612.6891	806.8482	L	288.2030	144.6051	271.1765	136.0919			2
17							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 330 ppm

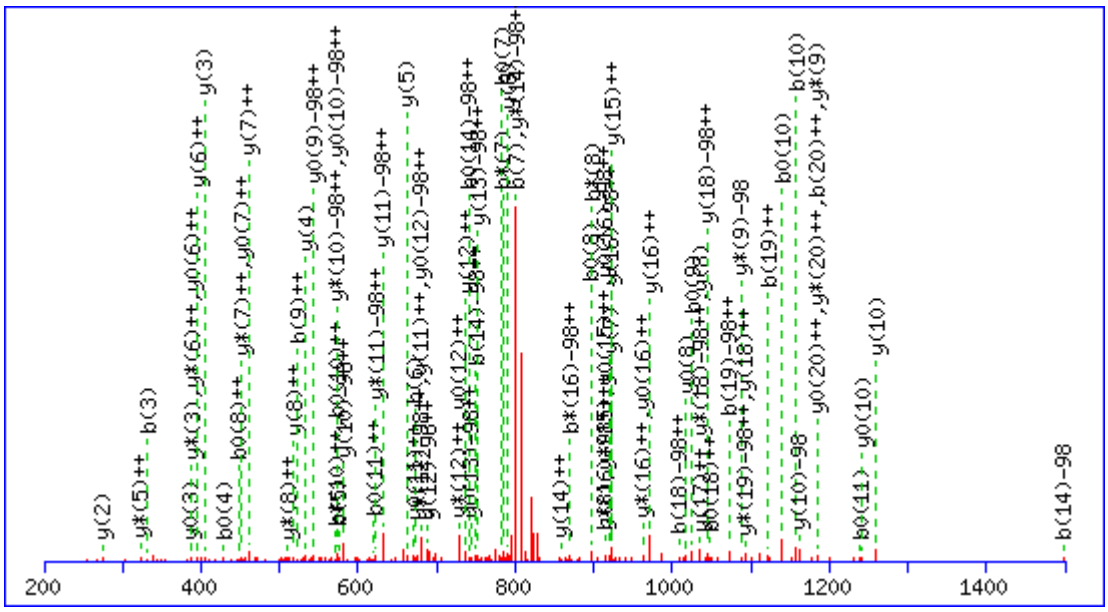


RMS error 330 ppm

IDENTIFICATION 111

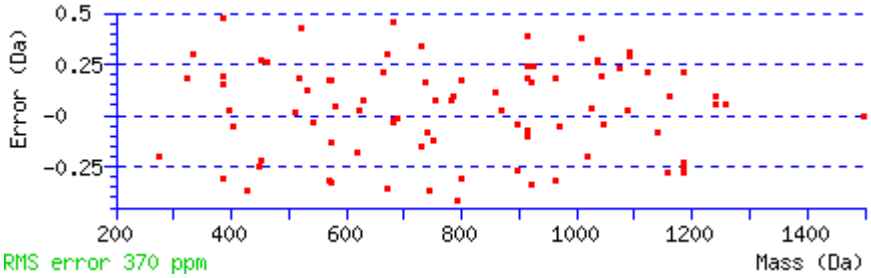
MS/MS Fragmentation of ESDDKPEIEDVGSDEEEEEKK

Found in IPI00330804



Monoisotopic mass of neutral peptide Mr(calc): 2515.0010 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S13 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 43 Expect: 0.0086 (help)

#	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							21
2	217.0819	109.0446			199.0713	100.0393	S	2288.9889	1144.9981	2271.9623	1136.4848	2270.9783	1135.9928	20
3	332.1088	166.5581			314.0983	157.5528	D	2201.9568	1101.4820	2184.9303	1092.9688	2183.9463	1092.4768	19
4	447.1358	224.0715			429.1252	215.0662	D	2086.9299	1043.9686	2069.9033	1035.4553	2068.9193	1034.9633	18
5	575.2307	288.1190	558.2042	279.6057	557.2202	279.1137	K	1971.9029	986.4551	1954.8764	977.9418	1953.8924	977.4498	17
6	672.2835	336.6454	655.2570	328.1321	654.2729	327.6401	P	1843.8080	922.4076	1826.7814	913.8944	1825.7974	913.4023	16
7	801.3261	401.1667	784.2996	392.6534	783.3155	392.1614	E	1746.7552	873.8812	1729.7287	865.3680	1728.7446	864.8760	15
8	914.4102	457.7087	897.3836	449.1954	896.3996	448.7034	I	1617.7126	809.3599	1600.6861	800.8467	1599.7021	800.3547	14
9	1043.4528	522.2300	1026.4262	513.7167	1025.4422	513.2247	E	1504.6286	752.8179	1487.6020	744.3046	1486.6180	743.8126	13
10	1158.4797	579.7435	1141.4532	571.2302	1140.4691	570.7382	D	1375.5860	688.2966	1358.5594	679.7833	1357.5754	679.2913	12
11	1257.5481	629.2777	1240.5216	620.7644	1239.5376	620.2724	V	1260.5590	630.7831	1243.5325	622.2699	1242.5485	621.7779	11
12	1314.5696	657.7884	1297.5430	649.2752	1296.5590	648.7831	G	1161.4906	581.2489	1144.4641	572.7357	1143.4800	572.2437	10
13	1383.5910	692.2992	1366.5645	683.7859	1365.5805	683.2939	S	1104.4691	552.7382	1087.4426	544.2249	1086.4586	543.7329	9
14	1498.6180	749.8126	1481.5914	741.2994	1480.6074	740.8073	D	1035.4477	518.2275	1018.4211	509.7142	1017.4371	509.2222	8
15	1627.6606	814.3339	1610.6340	805.8207	1609.6500	805.3286	E	920.4207	460.7140	903.3942	452.2007	902.4102	451.7087	7
16	1756.7032	878.8552	1739.6766	870.3420	1738.6926	869.8499	E	791.3781	396.1927	774.3516	387.6794	773.3676	387.1874	6
17	1885.7458	943.3765	1868.7192	934.8632	1867.7352	934.3712	E	662.3355	331.6714	645.3090	323.1581	644.3250	322.6661	5
18	2014.7884	1007.8978	1997.7618	999.3845	1996.7778	998.8925	E	533.2930	267.1501	516.2664	258.6368	515.2824	258.1448	4
19	2143.8310	1072.4191	2126.8044	1063.9058	2125.8204	1063.4138	E	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	3
20	2271.9259	1136.4666	2254.8994	1127.9533	2253.9154	1127.4613	K	275.2078	138.1075	258.1812	129.5942			2
21							K	147.1128	74.0600	130.0863	65.5468			1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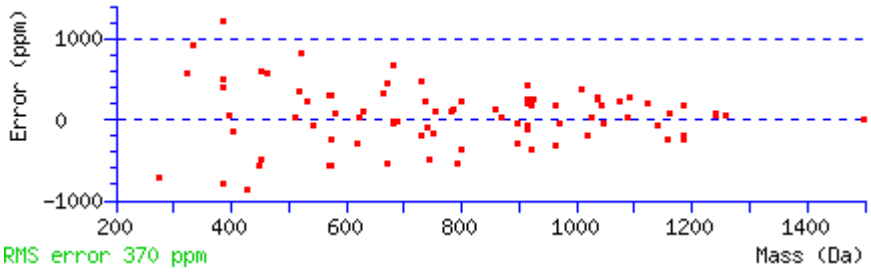
800
1000
1200
1400
Mass (Da)
RMS error 370 ppm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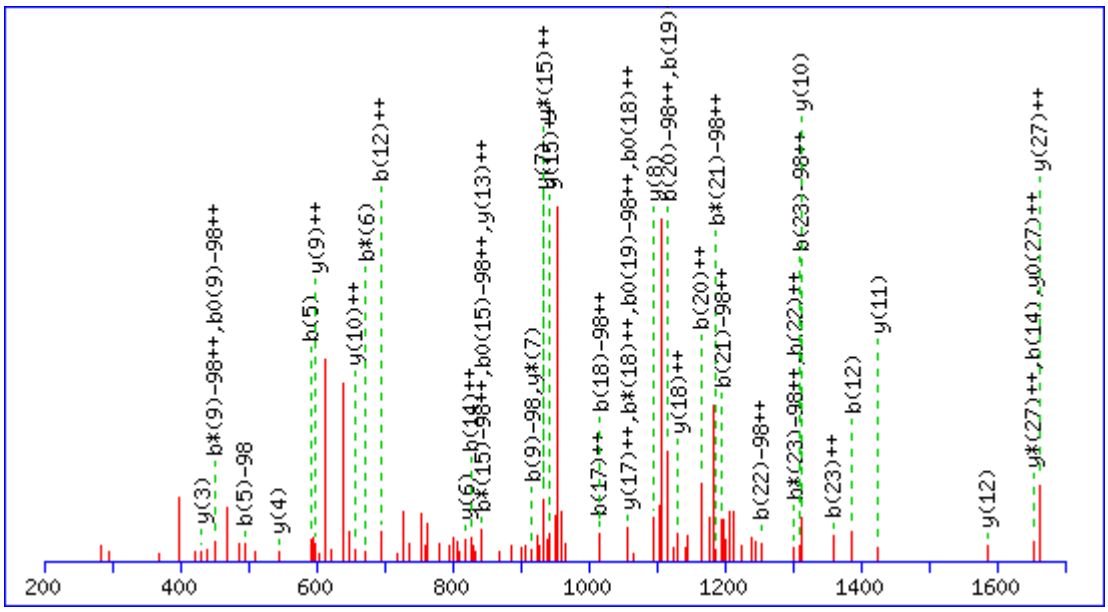
Error (ppm)
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 370 ppm

IDENTIFICATION 112

MS/MS Fragmentation of AKSPQPPVEEEDEHFDDTVVCLDTYNCDLHFK

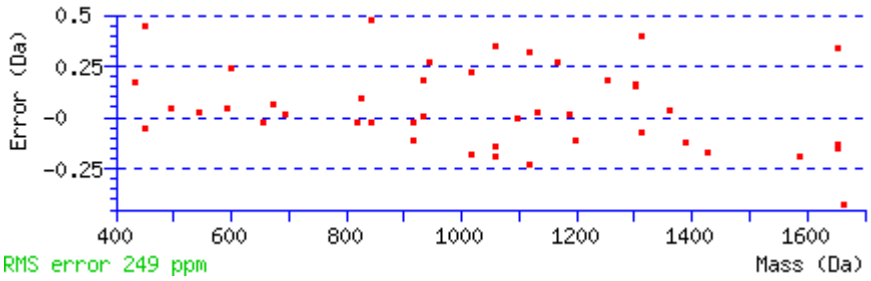
Found in IPI00458583

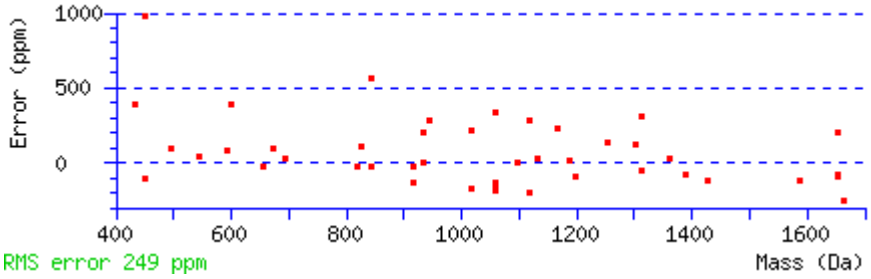


Monoisotopic mass of neutral peptide Mr(calc): 3913.6489 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 19 Expect: 4 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							32
2	200.1394	100.5733	183.1128	92.0600			K	3843.6190	1922.3131	3826.5925	1913.7999	3825.6085	1913.3079	31
3	367.1377	184.0725	350.1112	175.5592	349.1271	175.0672	S	3715.5241	1858.2657	3698.4975	1849.7524	3697.5135	1849.2604	30
4	464.1905	232.5989	447.1639	224.0856	446.1799	223.5936	P	3548.5257	1774.7665	3531.4991	1766.2532	3530.5151	1765.7612	29
5	592.2491	296.6282	575.2225	288.1149	574.2385	287.6229	Q	3451.4729	1726.2401	3434.4464	1717.7268	3433.4624	1717.2348	28
6	689.3018	345.1545	672.2753	336.6413	671.2913	336.1493	P	3323.4144	1662.2108	3306.3878	1653.6975	3305.4038	1653.2055	27
7	786.3546	393.6809	769.3280	385.1677	768.3440	384.6756	P	3226.3616	1613.6844	3209.3350	1605.1712	3208.3510	1604.6791	26
8	885.4230	443.2151	868.3964	434.7019	867.4124	434.2099	V	3129.3088	1565.1581	3112.2823	1556.6448	3111.2983	1556.1528	25
9	1014.4656	507.7364	997.4390	499.2232	996.4550	498.7312	E	3030.2404	1515.6238	3013.2139	1507.1106	3012.2298	1506.6186	24
10	1143.5082	572.2577	1126.4816	563.7445	1125.4976	563.2524	E	2901.1978	1451.1025	2884.1713	1442.5893	2883.1873	1442.0973	23
11	1272.5508	636.7790	1255.5242	628.2658	1254.5402	627.7737	E	2772.1552	1386.5813	2755.1287	1378.0680	2754.1447	1377.5760	22
12	1387.5777	694.2925	1370.5512	685.7792	1369.5672	685.2872	D	2643.1126	1322.0600	2626.0861	1313.5467	2625.1021	1313.0547	21
13	1516.6203	758.8138	1499.5938	750.3005	1498.6097	749.8085	E	2528.0857	1264.5465	2511.0591	1256.0332	2510.0751	1255.5412	20
14	1653.6792	827.3432	1636.6527	818.8300	1635.6687	818.3380	H	2399.0431	1200.0252	2382.0165	1191.5119	2381.0325	1191.0199	19
15	1800.7476	900.8775	1783.7211	892.3642	1782.7371	891.8722	F	2261.9842	1131.4957	2244.9576	1122.9825	2243.9736	1122.4904	18
16	1915.7746	958.3909	1898.7480	949.8777	1897.7640	949.3856	D	2114.9158	1057.9615	2097.8892	1049.4482	2096.9052	1048.9562	17
17	2030.8015	1015.9044	2013.7750	1007.3911	2012.7910	1006.8991	D	1999.8888	1000.4481	1982.8623	991.9348	1981.8783	991.4428	16
18	2131.8492	1066.4282	2114.8227	1057.9150	2113.8386	1057.4230	T	1884.8619	942.9346	1867.8353	934.4213	1866.8513	933.9293	15
19	2230.9176	1115.9624	2213.8911	1107.4492	2212.9071	1106.9572	V	1783.8142	892.4107	1766.7877	883.8975	1765.8036	883.4055	14
20	2329.9860	1165.4967	2312.9595	1156.9834	2311.9755	1156.4914	V	1684.7458	842.8765	1667.7192	834.3633	1666.7352	833.8713	13
21	2490.0167	1245.5120	2472.9901	1236.9987	2472.0061	1236.5067	C	1585.6774	793.3423	1568.6508	784.8291	1567.6668	784.3370	12
22	2603.1007	1302.0540	2586.0742	1293.5407	2585.0902	1293.0487	L	1425.6467	713.3270	1408.6202	704.8137	1407.6362	704.3217	11
23	2718.1277	1359.5675	2701.1011	1351.0542	2700.1171	1350.5622	D	1312.5627	656.7850	1295.5361	648.2717	1294.5521	647.7797	10
24	2819.1754	1410.0913	2802.1488	1401.5780	2801.1648	1401.0860	T	1197.5357	599.2715	1180.5092	590.7582	1179.5252	590.2662	9
25	2982.2387	1491.6230	2965.2121	1483.1097	2964.2281	1482.6177	Y	1096.4880	548.7477	1079.4615	540.2344	1078.4775	539.7424	8
26	3096.2816	1548.6444	3079.2551	1540.1312	3078.2711	1539.6392	N	933.4247	467.2160	916.3982	458.7027	915.4141	458.2107	7
27	3256.3123	1628.6598	3239.2857	1620.1465	3238.3017	1619.6545	C	819.3818	410.1945	802.3552	401.6813	801.3712	401.1892	6
28	3371.3392	1686.1732	3354.3127	1677.6600	3353.3286	1677.1680	D	659.3511	330.1792	642.3246	321.6659	641.3406	321.1739	5
29	3484.4233	1742.7153	3467.3967	1734.2020	3466.4127	1733.7100	L	544.3242	272.6657	527.2976	264.1525			4
30	3621.4822	1811.2447	3604.4556	1802.7315	3603.4716	1802.2394	H	431.2401	216.1237	414.2136	207.6104			3

31	3768.5506	1884.7789	3751.5241	1876.2657	3750.5400	1875.7737	F	294.1812	147.5942	277.1547	139.0810			2
32							K	147.1128	74.0600	130.0863	65.5468			1

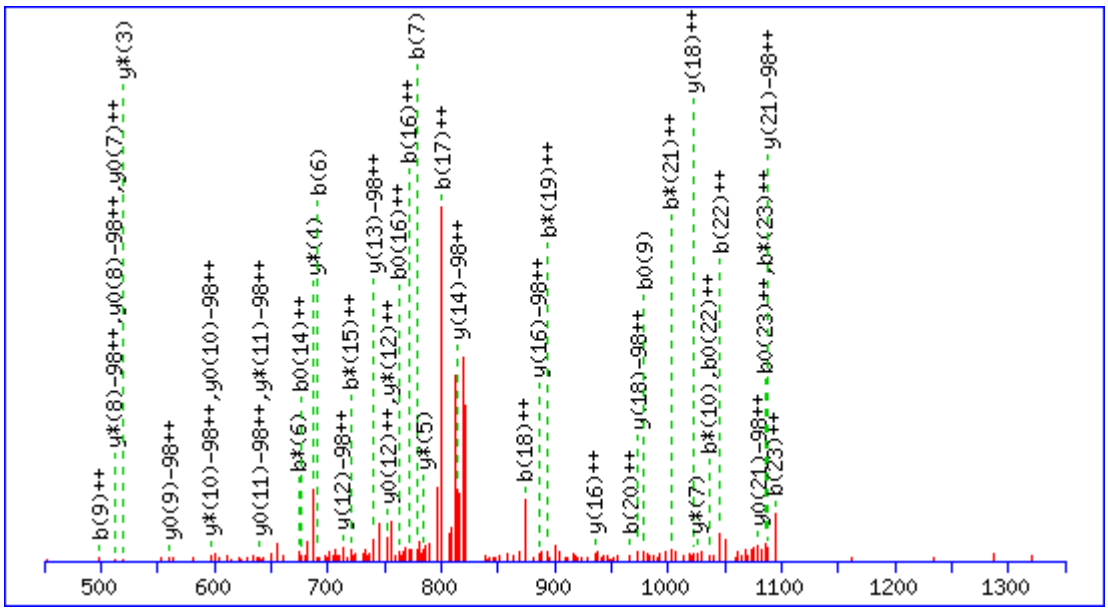




IDENTIFICATION 113

MS/MS Fragmentation of LPQQSHSAFGAASSSSGFGKSAPPQLPSFYK

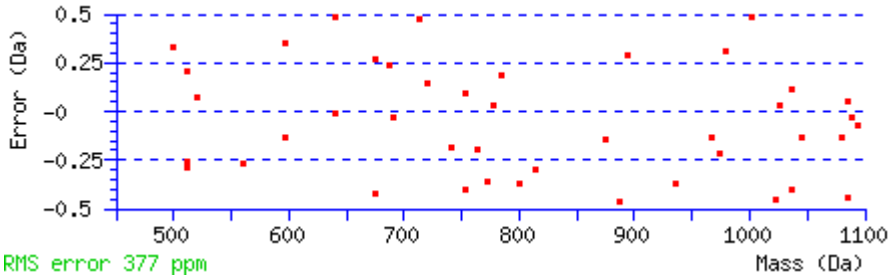
Found in IPI00329839

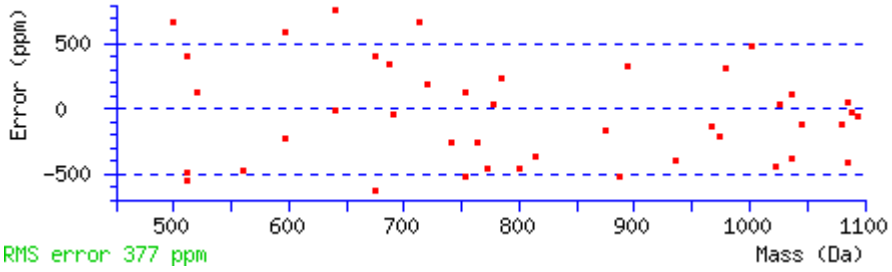


Monoisotopic mass of neutral peptide Mr(calc): 3325.4846
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S28 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Y30 : Phospho (Y)
Ions Score: 22 Expect: 1.9 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							31
2	211.1441	106.0757					P	3115.4309	1558.2191	3098.4044	1549.7058	3097.4204	1549.2138	30
3	339.2027	170.1050	322.1761	161.5917			Q	3018.3782	1509.6927	3001.3516	1501.1795	3000.3676	1500.6874	29
4	467.2613	234.1343	450.2347	225.6210			Q	2890.3196	1445.6634	2873.2931	1437.1502	2872.3090	1436.6582	28
5	554.2933	277.6503	537.2667	269.1370	536.2827	268.6450	S	2762.2610	1381.6341	2745.2345	1373.1209	2744.2505	1372.6289	27
6	691.3522	346.1797	674.3257	337.6665	673.3416	337.1745	H	2675.2290	1338.1181	2658.2024	1329.6049	2657.2184	1329.1129	26
7	778.3842	389.6958	761.3577	381.1825	760.3737	380.6905	S	2538.1701	1269.5887	2521.1435	1261.0754	2520.1595	1260.5834	25
8	849.4213	425.2143	832.3948	416.7010	831.4108	416.2090	A	2451.1381	1226.0727	2434.1115	1217.5594	2433.1275	1217.0674	24
9	996.4898	498.7485	979.4632	490.2352	978.4792	489.7432	F	2380.1009	1190.5541	2363.0744	1182.0408	2362.0904	1181.5488	23
10	1053.5112	527.2592	1036.4847	518.7460	1035.5007	518.2540	G	2233.0325	1117.0199	2216.0060	1108.5066	2215.0220	1108.0146	22
11	1124.5483	562.7778	1107.5218	554.2645	1106.5378	553.7725	A	2176.0111	1088.5092	2158.9845	1079.9959	2158.0005	1079.5039	21
12	1195.5854	598.2964	1178.5589	589.7831	1177.5749	589.2911	A	2104.9739	1052.9906	2087.9474	1044.4773	2086.9634	1043.9853	20
13	1282.6175	641.8124	1265.5909	633.2991	1264.6069	632.8071	S	2033.9368	1017.4721	2016.9103	1008.9588	2015.9263	1008.4668	19
14	1369.6495	685.3284	1352.6230	676.8151	1351.6389	676.3231	S	1946.9048	973.9560	1929.8783	965.4428	1928.8942	964.9508	18
15	1456.6815	728.8444	1439.6550	720.3311	1438.6710	719.8391	S	1859.8728	930.4400	1842.8462	921.9268	1841.8622	921.4347	17
16	1543.7136	772.3604	1526.6870	763.8471	1525.7030	763.3551	S	1772.8408	886.9240	1755.8142	878.4107	1754.8302	877.9187	16
17	1600.7350	800.8712	1583.7085	792.3579	1582.7245	791.8659	G	1685.8087	843.4080	1668.7822	834.8947	1667.7982	834.4027	15
18	1747.8034	874.4054	1730.7769	865.8921	1729.7929	865.4001	F	1628.7873	814.8973	1611.7607	806.3840	1610.7767	805.8920	14
19	1804.8249	902.9161	1787.7984	894.4028	1786.8143	893.9108	G	1481.7188	741.3631	1464.6923	732.8498	1463.7083	732.3578	13
20	1932.9199	966.9636	1915.8933	958.4503	1914.9093	957.9583	K	1424.6974	712.8523	1407.6708	704.3391	1406.6868	703.8470	12
21	2019.9519	1010.4796	2002.9253	1001.9663	2001.9413	1001.4743	S	1296.6024	648.8048	1279.5759	640.2916	1278.5919	639.7996	11
22	2090.9890	1045.9981	2073.9625	1037.4849	2072.9784	1036.9929	A	1209.5704	605.2888	1192.5438	596.7756	1191.5598	596.2836	10
23	2188.0418	1094.5245	2171.0152	1086.0112	2170.0312	1085.5192	P	1138.5333	569.7703	1121.5067	561.2570	1120.5227	560.7650	9
24	2285.0945	1143.0509	2268.0680	1134.5376	2267.0840	1134.0456	P	1041.4805	521.2439	1024.4540	512.7306	1023.4699	512.2386	8
25	2413.1531	1207.0802	2396.1266	1198.5669	2395.1425	1198.0749	Q	944.4277	472.7175	927.4012	464.2042	926.4172	463.7122	7
26	2526.2372	1263.6222	2509.2106	1255.1090	2508.2266	1254.6169	L	816.3692	408.6882	799.3426	400.1749	798.3586	399.6829	6
27	2623.2899	1312.1486	2606.2634	1303.6353	2605.2794	1303.1433	P	703.2851	352.1462	686.2586	343.6329	685.2745	343.1409	5

28	2692.3114	1346.6593	2675.2849	1338.1461	2674.3008	1337.6541	S	606.2323	303.6198	589.2058	295.1065	588.2218	294.6145	4
29	2839.3798	1420.1935	2822.3533	1411.6803	2821.3693	1411.1883	F	537.2109	269.1091	520.1843	260.5958			3
30	3082.4095	1541.7084	3065.3829	1533.1951	3064.3989	1532.7031	Y	390.1425	195.5749	373.1159	187.0616			2
31							K	147.1128	74.0600	130.0863	65.5468			1

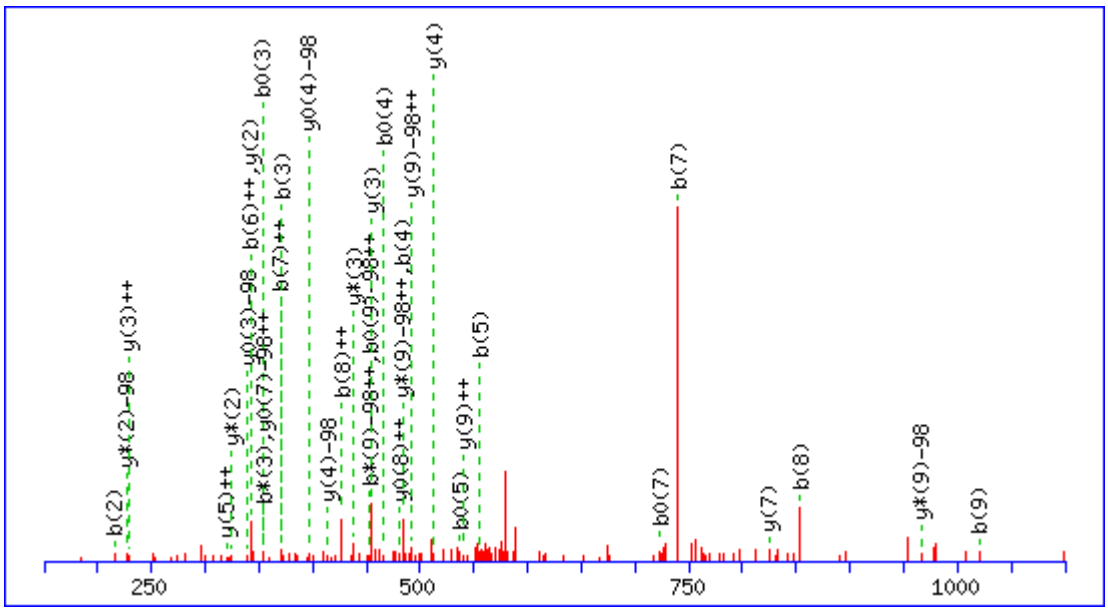




IDENTIFICATION 114

MS/MS Fragmentation of LTRLAQGLSR

Found in IPI00116996



Monoisotopic mass of neutral peptide Mr(calc): 1193.6281

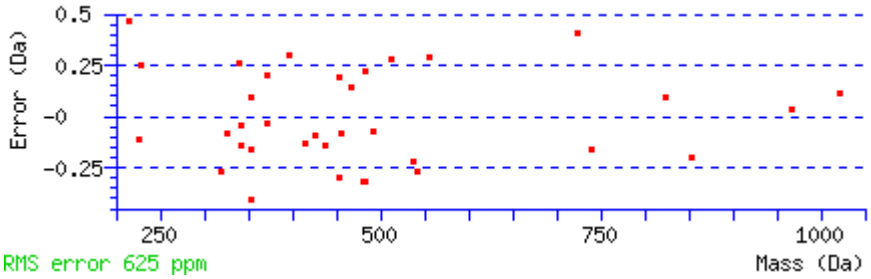
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

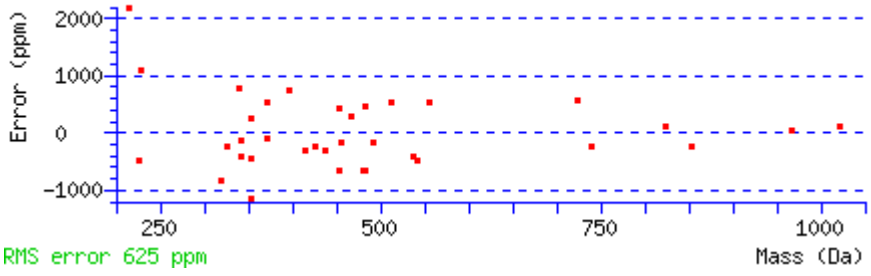
Variable modifications:

S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 26 Expect: 0.14 (help)

#	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	215.1390	108.0731			197.1285	99.0679	T	1081.5514	541.2793	1064.5248	532.7661	1063.5408	532.2740	9
3	371.2401	186.1237	354.2136	177.6104	353.2296	177.1184	R	980.5037	490.7555	963.4772	482.2422	962.4931	481.7502	8
4	484.3242	242.6657	467.2976	234.1525	466.3136	233.6605	L	824.4026	412.7049	807.3760	404.1917	806.3920	403.6997	7
5	555.3613	278.1843	538.3348	269.6710	537.3507	269.1790	A	711.3185	356.1629	694.2920	347.6496	693.3080	347.1576	6
6	683.4199	342.2136	666.3933	333.7003	665.4093	333.2083	Q	640.2814	320.6443	623.2549	312.1311	622.2709	311.6391	5
7	740.4414	370.7243	723.4148	362.2110	722.4308	361.7190	G	512.2228	256.6151	495.1963	248.1018	494.2123	247.6098	4
8	853.5254	427.2663	836.4989	418.7531	835.5148	418.2611	L	455.2014	228.1043	438.1748	219.5911	437.1908	219.0990	3
9	1020.5238	510.7655	1003.4972	502.2523	1002.5132	501.7602	S	342.1173	171.5623	325.0908	163.0490	324.1067	162.5570	2
10							R	175.1190	88.0631	158.0924	79.5498			1

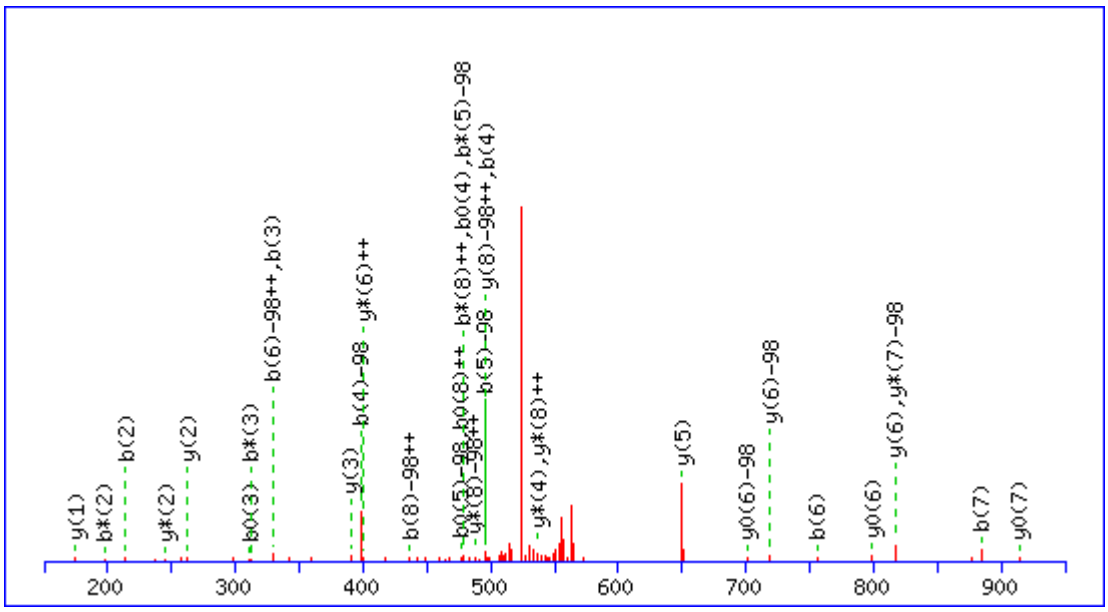




IDENTIFICATION 115

MS/MS Fragmentation of GRDSPYQSR

Found in IPI00132340



Monoisotopic mass of neutral peptide Mr(calc): 1144.4662

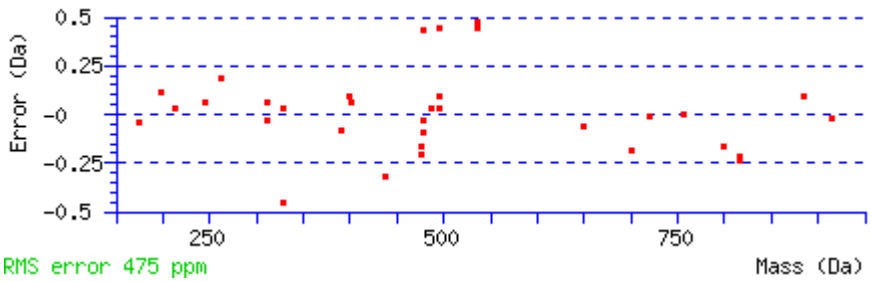
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

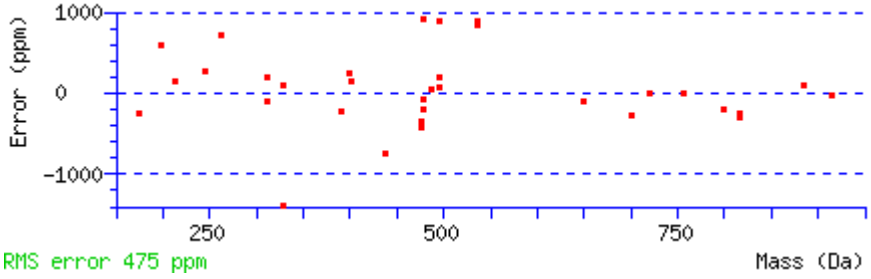
Variable modifications:

S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

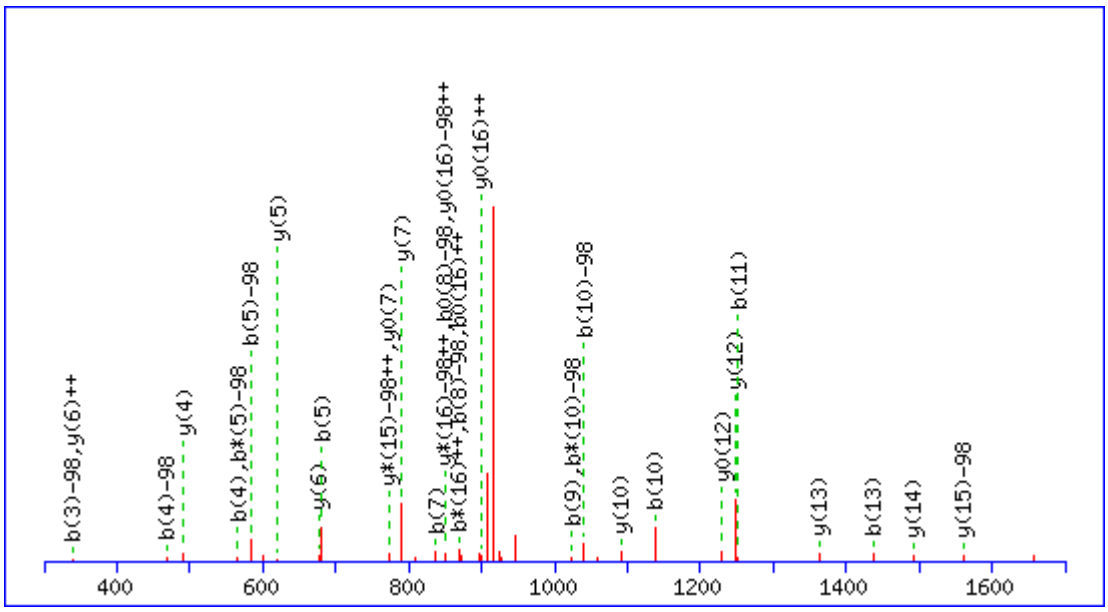
Ions Score: 35 Expect: 0.023 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b_{0++}	Seq.	y	y_{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							9
2	214.1299	107.5686	197.1033	99.0553			R	990.4752	495.7412	973.4486	487.2279	972.4646	486.7359	8
3	329.1568	165.0820	312.1302	156.5688	311.1462	156.0768	D	834.3741	417.6907	817.3475	409.1774	816.3635	408.6854	7
4	398.1783	199.5928	381.1517	191.0795	380.1677	190.5875	S	719.3471	360.1772	702.3206	351.6639	701.3365	351.1719	6
5	495.2310	248.1191	478.2045	239.6059	477.2205	239.1139	P	650.3257	325.6665	633.2991	317.1532	632.3151	316.6612	5
6	658.2944	329.6508	641.2678	321.1375	640.2838	320.6455	Y	553.2729	277.1401	536.2463	268.6268	535.2623	268.1348	4
7	786.3529	393.6801	769.3264	385.1668	768.3424	384.6748	Q	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
8	873.3850	437.1961	856.3584	428.6828	855.3744	428.1908	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
9							R	175.1190	88.0631	158.0924	79.5498			1



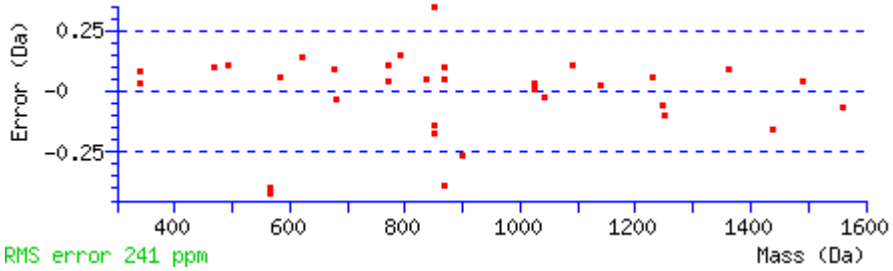


IDENTIFICATION 116
MS/MS Fragmentation of LRSEDGVEGDLGETQSR
Found in IPI00553798

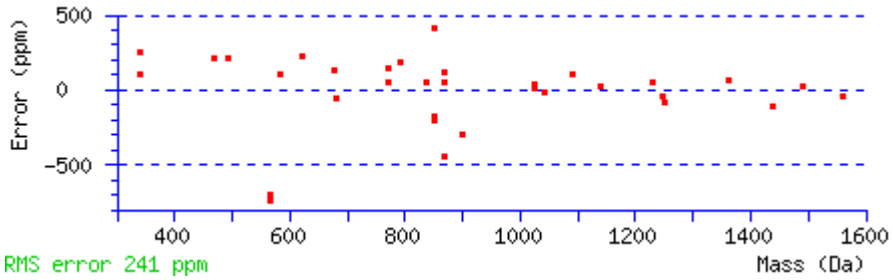


Monoisotopic mass of neutral peptide Mr(calc): 1926.8320
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 70 Expect: 1.9e-05 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							17
2	270.1925	135.5999	253.1659	127.0866			R	1716.7783	858.8928	1699.7518	850.3795	1698.7678	849.8875	16
3	339.2139	170.1106	322.1874	161.5973	321.2033	161.1053	S	1560.6772	780.8423	1543.6507	772.3290	1542.6667	771.8370	15
4	468.2565	234.6319	451.2300	226.1186	450.2459	225.6266	E	1491.6558	746.3315	1474.6292	737.8182	1473.6452	737.3262	14
5	583.2835	292.1454	566.2569	283.6321	565.2729	283.1401	D	1362.6132	681.8102	1345.5866	673.2970	1344.6026	672.8049	13
6	640.3049	320.6561	623.2784	312.1428	622.2943	311.6508	G	1247.5862	624.2968	1230.5597	615.7835	1229.5757	615.2915	12
7	739.3733	370.1903	722.3468	361.6770	721.3628	361.1850	V	1190.5648	595.7860	1173.5382	587.2727	1172.5542	586.7807	11
8	868.4159	434.7116	851.3894	426.1983	850.4054	425.7063	E	1091.4964	546.2518	1074.4698	537.7385	1073.4858	537.2465	10
9	925.4374	463.2223	908.4108	454.7091	907.4268	454.2170	G	962.4538	481.7305	945.4272	473.2172	944.4432	472.7252	9
10	1040.4643	520.7358	1023.4378	512.2225	1022.4538	511.7305	D	905.4323	453.2198	888.4058	444.7065	887.4217	444.2145	8
11	1153.5484	577.2778	1136.5218	568.7646	1135.5378	568.2726	L	790.4054	395.7063	773.3788	387.1930	772.3948	386.7010	7
12	1210.5699	605.7886	1193.5433	597.2753	1192.5593	596.7833	G	677.3213	339.1643	660.2947	330.6510	659.3107	330.1590	6
13	1339.6124	670.3099	1322.5859	661.7966	1321.6019	661.3046	E	620.2998	310.6536	603.2733	302.1403	602.2893	301.6483	5
14	1440.6601	720.8337	1423.6336	712.3204	1422.6496	711.8284	T	491.2572	246.1323	474.2307	237.6190	473.2467	237.1270	4
15	1568.7187	784.8630	1551.6922	776.3497	1550.7081	775.8577	Q	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
16	1655.7507	828.3790	1638.7242	819.8657	1637.7402	819.3737	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



RMS error 241 ppm

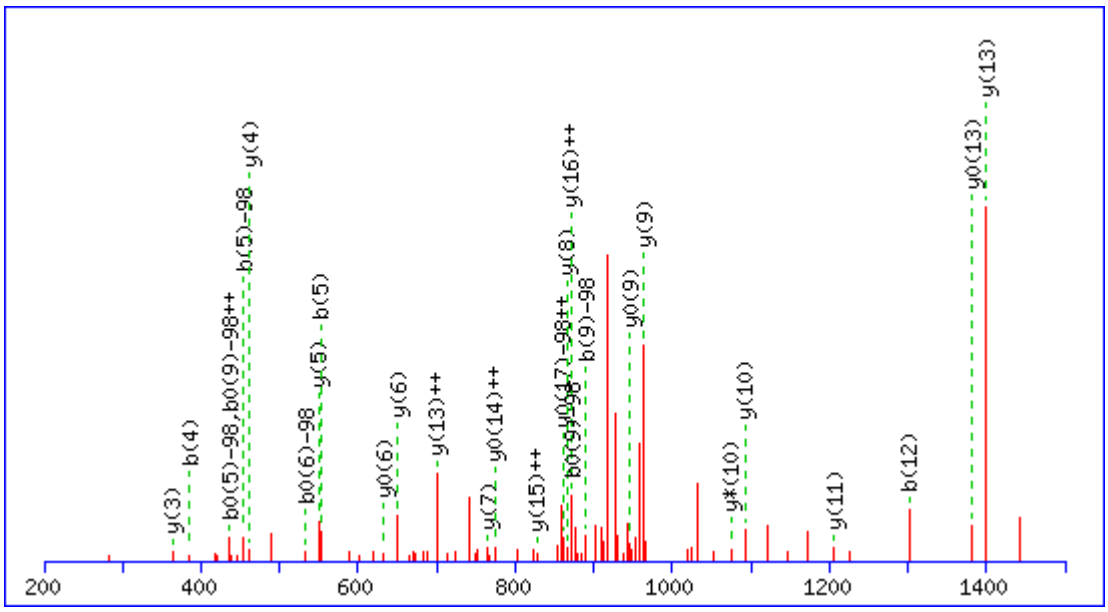


RMS error 241 ppm

IDENTIFICATION 117

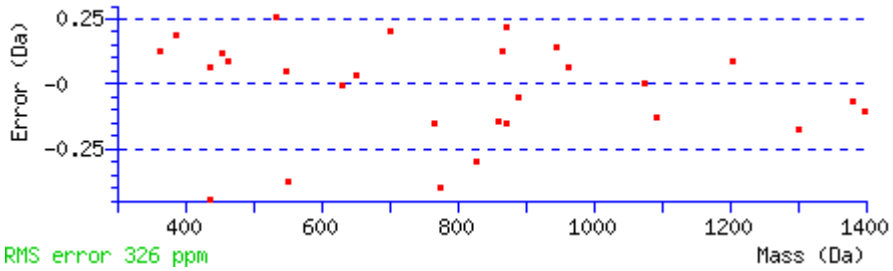
MS/MS Fragmentation of LPSSSPPLEPTDTSVTSR

Found in IPI00124959

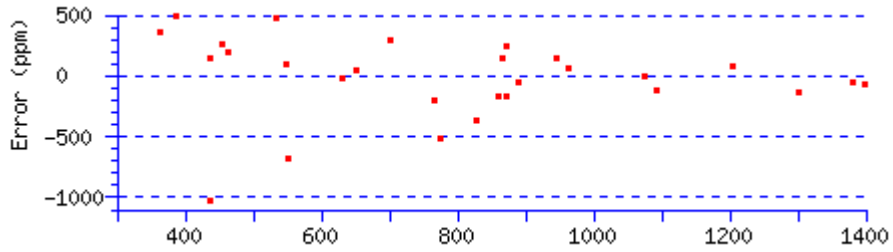


Monoisotopic mass of neutral peptide Mr(calc): 1949.8983 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 39 Expect: 0.024 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							18
2	211.1441	106.0757			P	1739.8446	870.4260	1722.8181	861.9127	1721.8341	861.4207	17
3	298.1761	149.5917	280.1656	140.5864	S	1642.7919	821.8996	1625.7653	813.3863	1624.7813	812.8943	16
4	385.2082	193.1077	367.1976	184.1024	S	1555.7598	778.3836	1538.7333	769.8703	1537.7493	769.3783	15
5	454.2296	227.6184	436.2191	218.6132	S	1468.7278	734.8675	1451.7013	726.3543	1450.7172	725.8623	14
6	551.2824	276.1448	533.2718	267.1395	P	1399.7064	700.3568	1382.6798	691.8435	1381.6958	691.3515	13
7	648.3352	324.6712	630.3246	315.6659	P	1302.6536	651.8304	1285.6270	643.3172	1284.6430	642.8251	12
8	761.4192	381.2132	743.4086	372.2080	L	1205.6008	603.3040	1188.5743	594.7908	1187.5903	594.2988	11
9	890.4618	445.7345	872.4512	436.7293	E	1092.5168	546.7620	1075.4902	538.2487	1074.5062	537.7567	10
10	987.5146	494.2609	969.5040	485.2556	P	963.4742	482.2407	946.4476	473.7274	945.4636	473.2354	9
11	1088.5623	544.7848	1070.5517	535.7795	T	866.4214	433.7143	849.3949	425.2011	848.4108	424.7091	8
12	1203.5892	602.2982	1185.5786	593.2930	D	765.3737	383.1905	748.3472	374.6772	747.3632	374.1852	7
13	1304.6369	652.8221	1286.6263	643.8168	T	650.3468	325.6770	633.3202	317.1638	632.3362	316.6717	6
14	1391.6689	696.3381	1373.6583	687.3328	S	549.2991	275.1532	532.2726	266.6399	531.2885	266.1479	5
15	1490.7373	745.8723	1472.7268	736.8670	V	462.2671	231.6372	445.2405	223.1239	444.2565	222.6319	4
16	1591.7850	796.3961	1573.7744	787.3909	T	363.1987	182.1030	346.1721	173.5897	345.1881	173.0977	3
17	1678.8170	839.9121	1660.8065	830.9069	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

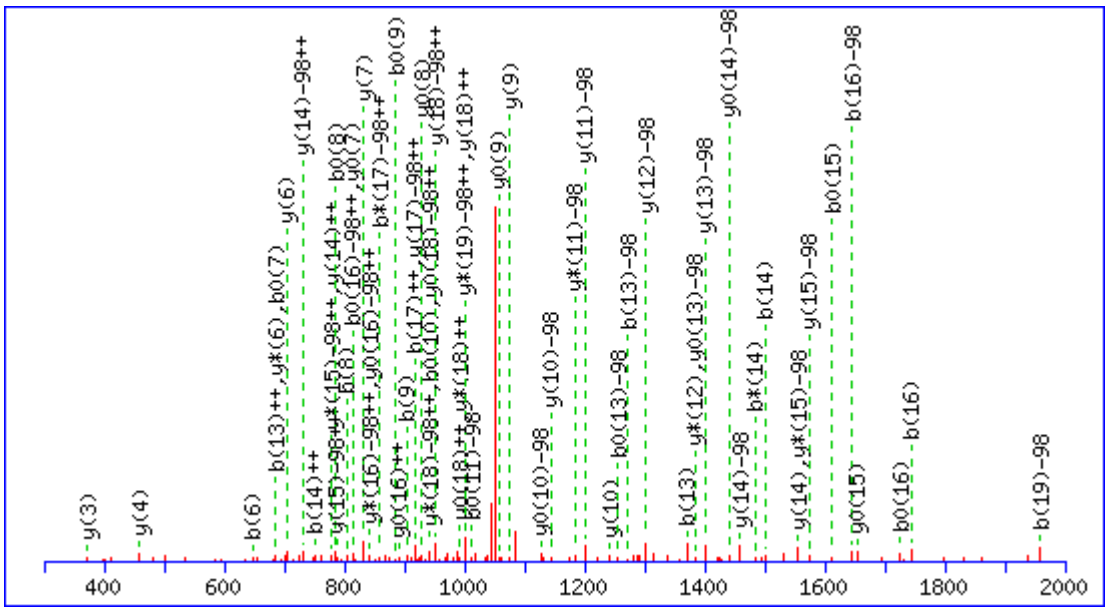


RMS error 326 ppm



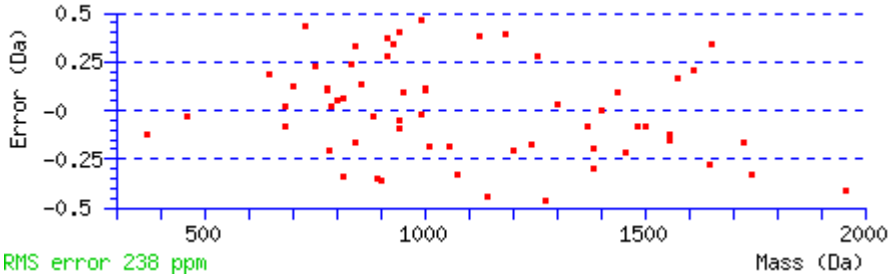
RMS error 326 ppm

IDENTIFICATION 118
MS/MS Fragmentation of SDAEEDGVTGSQDEEDSKPK
Found in IPI00119618

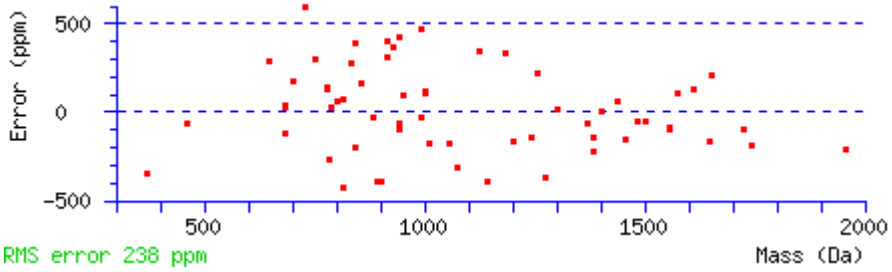


Monoisotopic mass of neutral peptide Mr(calc): 2201.8485
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 57 Expect: 0.00034 (help)

#	b	b^{++}	b*	b^{*++}	b_0	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^0	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							20
2	203.0662	102.0368			185.0557	93.0315	D	2017.8469	1009.4271	2000.8203	1000.9138	1999.8363	1000.4218	19
3	274.1034	137.5553			256.0928	128.5500	A	1902.8199	951.9136	1885.7934	943.4003	1884.8094	942.9083	18
4	403.1460	202.0766			385.1354	193.0713	E	1831.7828	916.3950	1814.7563	907.8818	1813.7723	907.3898	17
5	532.1885	266.5979			514.1780	257.5926	E	1702.7402	851.8738	1685.7137	843.3605	1684.7297	842.8685	16
6	647.2155	324.1114			629.2049	315.1061	D	1573.6976	787.3525	1556.6711	778.8392	1555.6871	778.3472	15
7	704.2370	352.6221			686.2264	343.6168	G	1458.6707	729.8390	1441.6441	721.3257	1440.6601	720.8337	14
8	803.3054	402.1563			785.2948	393.1510	V	1401.6492	701.3283	1384.6227	692.8150	1383.6387	692.3230	13
9	904.3530	452.6802			886.3425	443.6749	T	1302.5808	651.7940	1285.5543	643.2808	1284.5703	642.7888	12
10	961.3745	481.1909			943.3639	472.1856	G	1201.5331	601.2702	1184.5066	592.7569	1183.5226	592.2649	11
11	1030.3960	515.7016			1012.3854	506.6963	S	1144.5117	572.7595	1127.4851	564.2462	1126.5011	563.7542	10
12	1158.4546	579.7309	1141.4280	571.2176	1140.4440	570.7256	Q	1075.4902	538.2487	1058.4637	529.7355	1057.4796	529.2435	9
13	1273.4815	637.2444	1256.4549	628.7311	1255.4709	628.2391	D	947.4316	474.2195	930.4051	465.7062	929.4211	465.2142	8
14	1402.5241	701.7657	1385.4975	693.2524	1384.5135	692.7604	E	832.4047	416.7060	815.3781	408.1927	814.3941	407.7007	7
15	1531.5667	766.2870	1514.5401	757.7737	1513.5561	757.2817	E	703.3621	352.1847	686.3355	343.6714	685.3515	343.1794	6
16	1646.5936	823.8005	1629.5671	815.2872	1628.5831	814.7952	D	574.3195	287.6634	557.2930	279.1501	556.3089	278.6581	5
17	1733.6257	867.3165	1716.5991	858.8032	1715.6151	858.3112	S	459.2926	230.1499	442.2660	221.6366	441.2820	221.1446	4
18	1861.7206	931.3639	1844.6941	922.8507	1843.7101	922.3587	K	372.2605	186.6339	355.2340	178.1206			3
19	1958.7734	979.8903	1941.7468	971.3771	1940.7628	970.8850	P	244.1656	122.5864	227.1390	114.0731			2
20							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 238 ppm

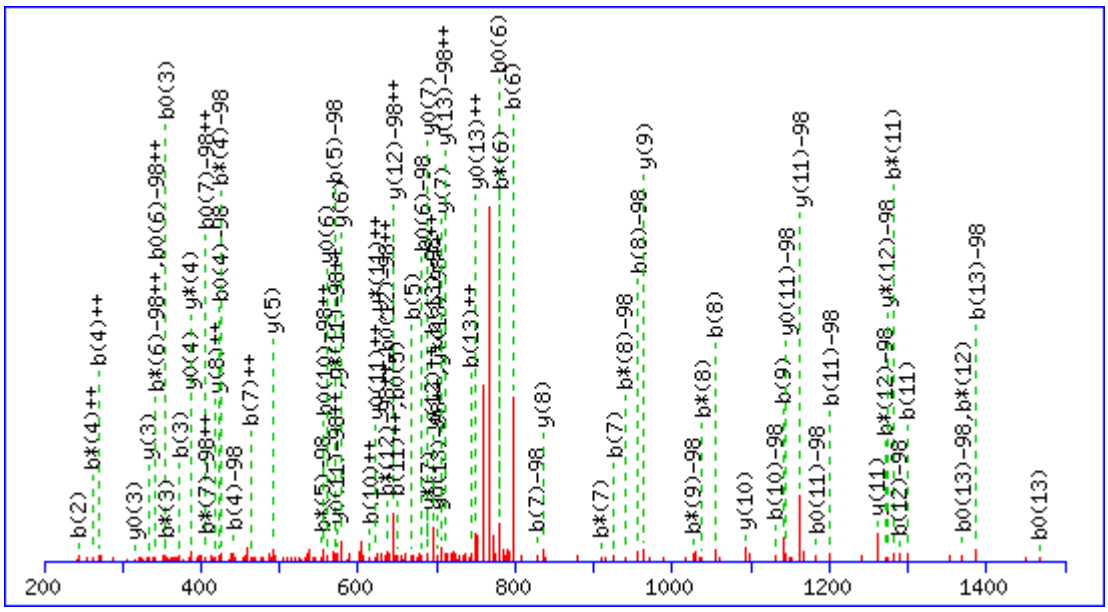


RMS error 238 ppm

IDENTIFICATION 119

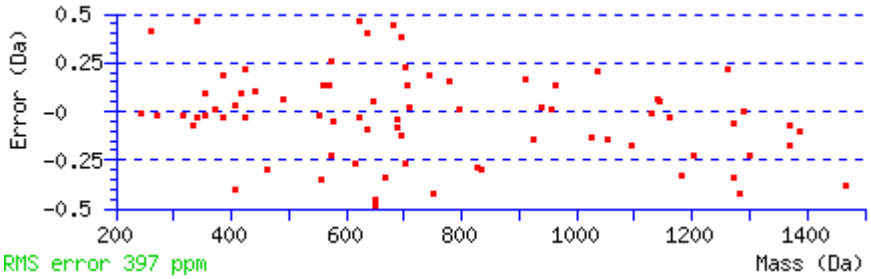
MS/MS Fragmentation of NEKSEEEQSSASVK

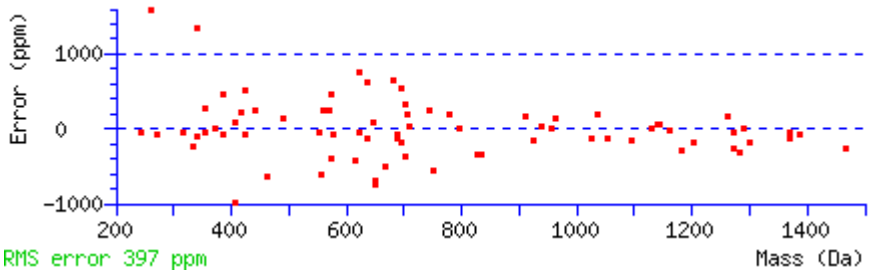
Found in IPI00130343



Monoisotopic mass of neutral peptide Mr(calc): 1630.6723 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 46 Expect: 0.0033 (help)

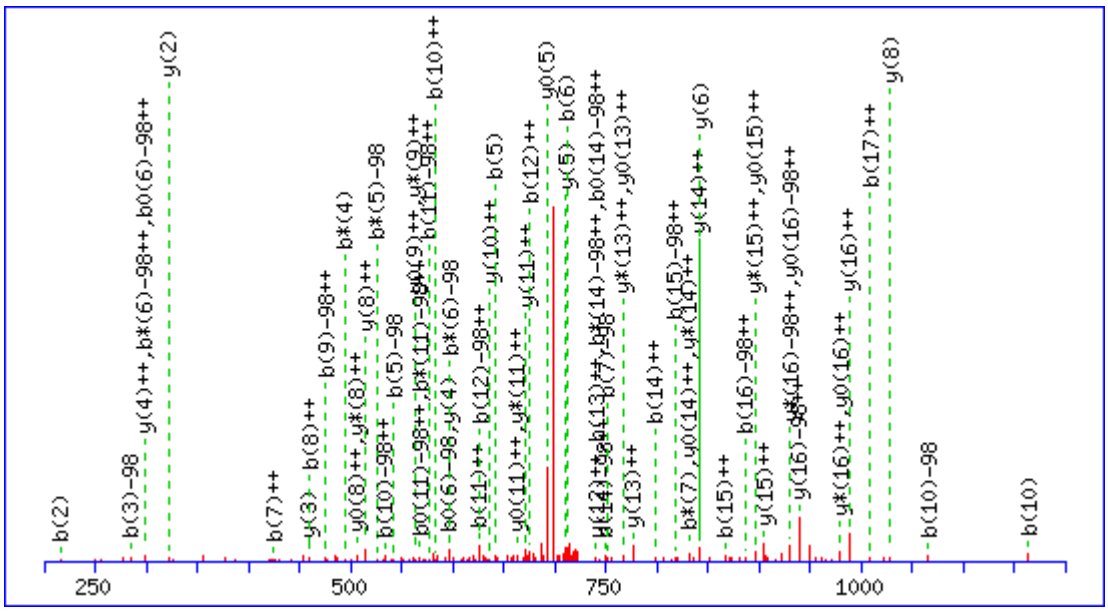
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							14
2	244.0928	122.5500	227.0662	114.0368	226.0822	113.5448	E	1419.6598	710.3335	1402.6332	701.8203	1401.6492	701.3283	13
3	372.1878	186.5975	355.1612	178.0842	354.1772	177.5922	K	1290.6172	645.8122	1273.5907	637.2990	1272.6066	636.8070	12
4	441.2092	221.1082	424.1827	212.5950	423.1987	212.1030	S	1162.5222	581.7648	1145.4957	573.2515	1144.5117	572.7595	11
5	570.2518	285.6295	553.2253	277.1163	552.2413	276.6243	E	1093.5008	547.2540	1076.4742	538.7408	1075.4902	538.2487	10
6	699.2944	350.1508	682.2679	341.6376	681.2838	341.1456	E	964.4582	482.7327	947.4316	474.2195	946.4476	473.7274	9
7	828.3370	414.6721	811.3105	406.1589	810.3264	405.6669	E	835.4156	418.2114	818.3890	409.6982	817.4050	409.2061	8
8	956.3956	478.7014	939.3690	470.1882	938.3850	469.6961	Q	706.3730	353.6901	689.3464	345.1769	688.3624	344.6849	7
9	1043.4276	522.2174	1026.4011	513.7042	1025.4170	513.2122	S	578.3144	289.6608	561.2879	281.1476	560.3039	280.6556	6
10	1130.4596	565.7335	1113.4331	557.2202	1112.4491	556.7282	S	491.2824	246.1448	474.2558	237.6316	473.2718	237.1395	5
11	1201.4967	601.2520	1184.4702	592.7387	1183.4862	592.2467	A	404.2504	202.6288	387.2238	194.1155	386.2398	193.6235	4
12	1288.5288	644.7680	1271.5022	636.2548	1270.5182	635.7627	S	333.2132	167.1103	316.1867	158.5970	315.2027	158.1050	3
13	1387.5972	694.3022	1370.5706	685.7890	1369.5866	685.2970	V	246.1812	123.5942	229.1547	115.0810			2
14							K	147.1128	74.0600	130.0863	65.5468			1





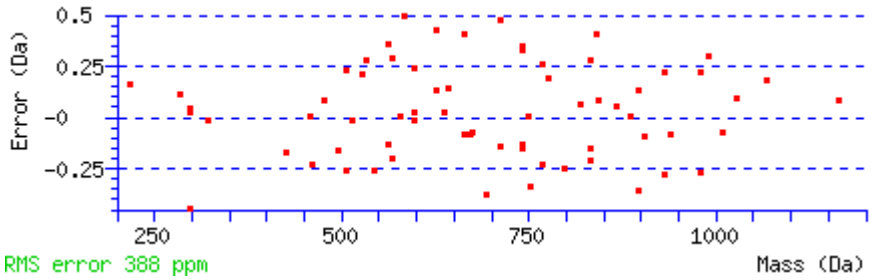
IDENTIFICATION 120

MS/MS Fragmentation of SKSEEAHAEDSVMDHHFR
Found in IPI00471475

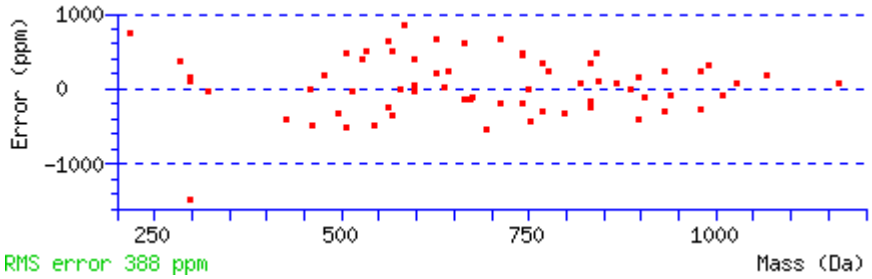


Monoisotopic mass of neutral peptide Mr(calc): 2190.8790 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 32 Expect: 0.12 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							18
2	216.1343	108.5708	199.1077	100.0575	198.1237	99.5655	K	2006.8773	1003.9423	1989.8508	995.4290	1988.8668	994.9370	17
3	285.1557	143.0815	268.1292	134.5682	267.1452	134.0762	S	1878.7824	939.8948	1861.7558	931.3816	1860.7718	930.8895	16
4	414.1983	207.6028	397.1718	199.0895	396.1878	198.5975	E	1809.7609	905.3841	1792.7344	896.8708	1791.7504	896.3788	15
5	543.2409	272.1241	526.2144	263.6108	525.2304	263.1188	E	1680.7183	840.8628	1663.6918	832.3495	1662.7078	831.8575	14
6	614.2780	307.6427	597.2515	299.1294	596.2675	298.6374	A	1551.6757	776.3415	1534.6492	767.8282	1533.6652	767.3362	13
7	751.3369	376.1721	734.3104	367.6588	733.3264	367.1668	H	1480.6386	740.8229	1463.6121	732.3097	1462.6281	731.8177	12
8	822.3741	411.6907	805.3475	403.1774	804.3635	402.6854	A	1343.5797	672.2935	1326.5532	663.7802	1325.5691	663.2882	11
9	951.4166	476.2120	934.3901	467.6987	933.4061	467.2067	E	1272.5426	636.7749	1255.5160	628.2617	1254.5320	627.7697	10
10	1066.4436	533.7254	1049.4170	525.2122	1048.4330	524.7202	D	1143.5000	572.2536	1126.4735	563.7404	1125.4894	563.2484	9
11	1153.4756	577.2414	1136.4491	568.7282	1135.4651	568.2362	S	1028.4731	514.7402	1011.4465	506.2269	1010.4625	505.7349	8
12	1252.5440	626.7757	1235.5175	618.2624	1234.5335	617.7704	V	941.4410	471.2242	924.4145	462.7109	923.4305	462.2189	7
13	1383.5845	692.2959	1366.5580	683.7826	1365.5740	683.2906	M	842.3726	421.6899	825.3461	413.1767	824.3621	412.6847	6
14	1498.6115	749.8094	1481.5849	741.2961	1480.6009	740.8041	D	711.3321	356.1697	694.3056	347.6564	693.3216	347.1644	5
15	1635.6704	818.3388	1618.6438	809.8256	1617.6598	809.3335	H	596.3052	298.6562	579.2786	290.1430			4
16	1772.7293	886.8683	1755.7027	878.3550	1754.7187	877.8630	H	459.2463	230.1268	442.2197	221.6135			3
17	1919.7977	960.4025	1902.7712	951.8892	1901.7871	951.3972	F	322.1874	161.5973	305.1608	153.0840			2
18							R	175.1190	88.0631	158.0924	79.5498			1

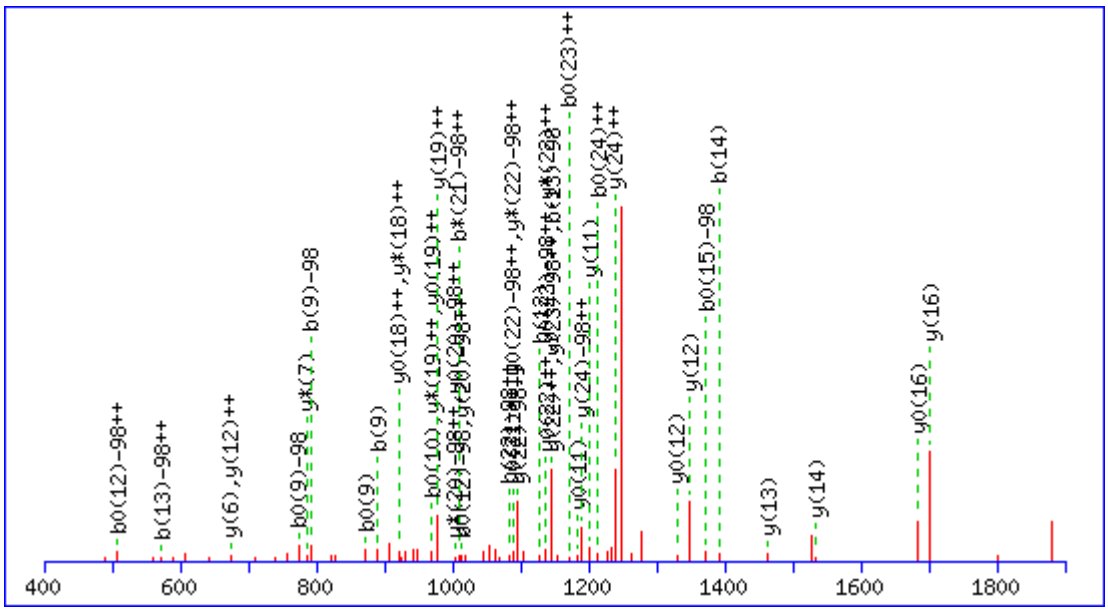


RMS error 388 ppm



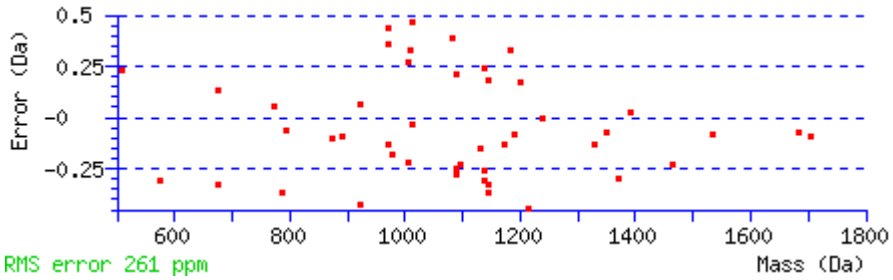
RMS error 388 ppm

IDENTIFICATION 121
MS/MS Fragmentation of DSVPASPGVPAADFPAETEQSKPSK
Found in IPI00122223

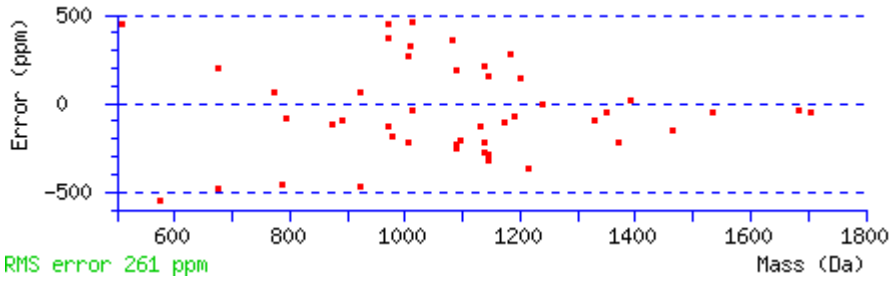


Monoisotopic mass of neutral peptide Mr(calc): 2591.1792
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S6 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.38 (help)

#	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	203.0662	102.0368			185.0557	93.0315	S	2379.1827	1190.0950	2362.1561	1181.5817	2361.1721	1181.0897	24
3	302.1347	151.5710			284.1241	142.5657	V	2292.1507	1146.5790	2275.1241	1138.0657	2274.1401	1137.5737	23
4	399.1874	200.0974			381.1769	191.0921	P	2193.0822	1097.0448	2176.0557	1088.5315	2175.0717	1088.0395	22
5	470.2245	235.6159			452.2140	226.6106	A	2096.0295	1048.5184	2079.0029	1040.0051	2078.0189	1039.5131	21
6	539.2460	270.1266			521.2354	261.1214	S	2024.9924	1012.9998	2007.9658	1004.4865	2006.9818	1003.9945	20
7	636.2988	318.6530			618.2882	309.6477	P	1955.9709	978.4891	1938.9444	969.9758	1937.9603	969.4838	19
8	693.3202	347.1638			675.3097	338.1585	G	1858.9181	929.9627	1841.8916	921.4494	1840.9076	920.9574	18
9	792.3886	396.6980			774.3781	387.6927	V	1801.8967	901.4520	1784.8701	892.9387	1783.8861	892.4467	17
10	889.4414	445.2243			871.4308	436.2191	P	1702.8283	851.9178	1685.8017	843.4045	1684.8177	842.9125	16
11	960.4785	480.7429			942.4680	471.7376	A	1605.7755	803.3914	1588.7489	794.8781	1587.7649	794.3861	15
12	1031.5156	516.2615			1013.5051	507.2562	A	1534.7384	767.8728	1517.7118	759.3596	1516.7278	758.8675	14
13	1146.5426	573.7749			1128.5320	564.7696	D	1463.7013	732.3543	1446.6747	723.8410	1445.6907	723.3490	13
14	1293.6110	647.3091			1275.6004	638.3039	F	1348.6743	674.8408	1331.6478	666.3275	1330.6638	665.8355	12
15	1390.6638	695.8355			1372.6532	686.8302	P	1201.6059	601.3066	1184.5794	592.7933	1183.5953	592.3013	11
16	1461.7009	731.3541			1443.6903	722.3488	A	1104.5531	552.7802	1087.5266	544.2669	1086.5426	543.7749	10
17	1590.7435	795.8754			1572.7329	786.8701	E	1033.5160	517.2617	1016.4895	508.7484	1015.5055	508.2564	9
18	1691.7911	846.3992			1673.7806	837.3939	T	904.4734	452.7404	887.4469	444.2271	886.4629	443.7351	8
19	1820.8337	910.9205			1802.8232	901.9152	E	803.4258	402.2165	786.3992	393.7032	785.4152	393.2112	7
20	1948.8923	974.9498	1931.8658	966.4365	1930.8817	965.9445	Q	674.3832	337.6952	657.3566	329.1819	656.3726	328.6899	6
21	2035.9243	1018.4658	2018.8978	1009.9525	2017.9138	1009.4605	S	546.3246	273.6659	529.2980	265.1527	528.3140	264.6606	5
22	2164.0193	1082.5133	2146.9928	1074.0000	2146.0087	1073.5080	K	459.2926	230.1499	442.2660	221.6366	441.2820	221.1446	4
23	2261.0721	1131.0397	2244.0455	1122.5264	2243.0615	1122.0344	P	331.1976	166.1024	314.1710	157.5892	313.1870	157.0972	3
24	2348.1041	1174.5557	2331.0775	1166.0424	2330.0935	1165.5504	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
25							K	147.1128	74.0600	130.0863	65.5468			1

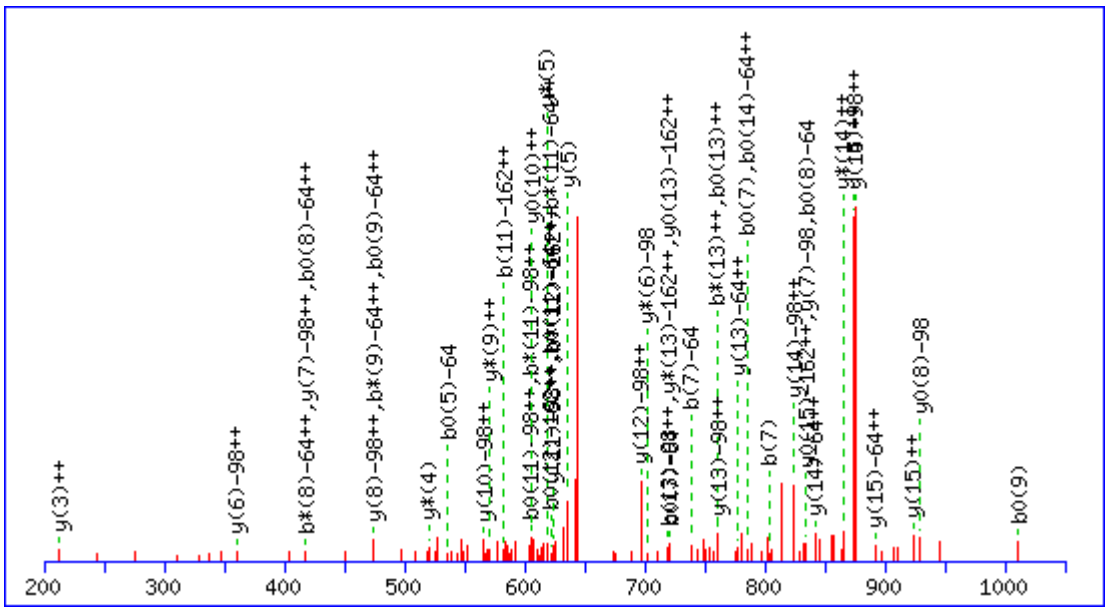


RMS error 261 ppm



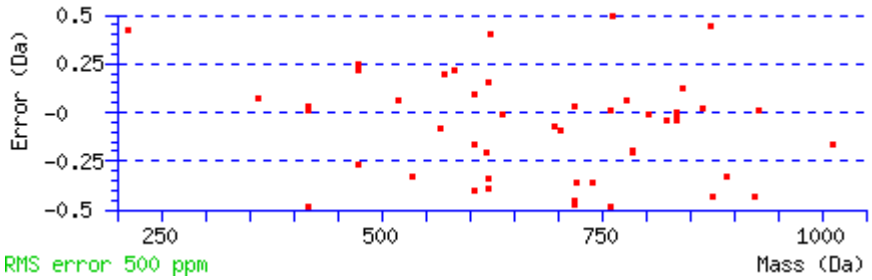
RMS error 261 ppm

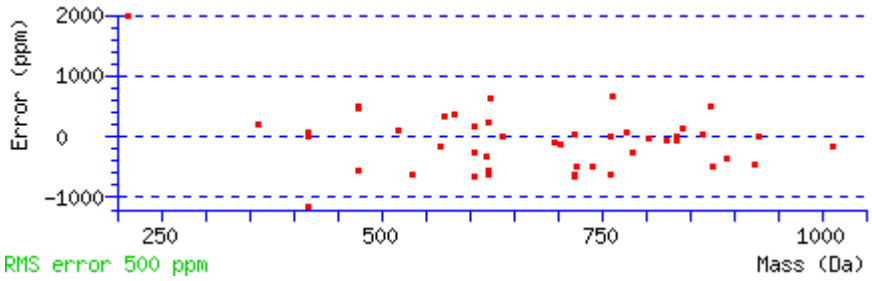
IDENTIFICATION 122
MS/MS Fragmentation of LTKQMNAIIDTVINYK
Found in IPI00460549



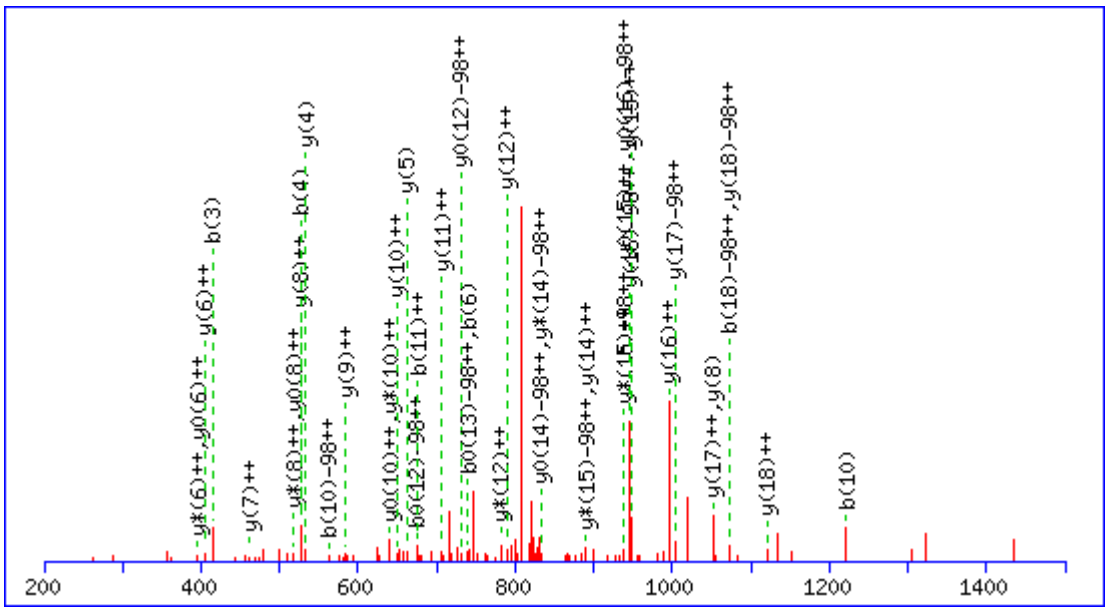
Monoisotopic mass of neutral peptide Mr(calc): 1959.9740 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: M5 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983 T11 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 27 Expect: 0.28 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							16
2	215.1390	108.0731			197.1285	99.0679	T	1749.9204	875.4638	1732.8938	866.9506	1731.9098	866.4585	15
3	343.2340	172.1206	326.2074	163.6074	325.2234	163.1153	K	1648.8727	824.9400	1631.8462	816.4267	1630.8621	815.9347	14
4	471.2926	236.1499	454.2660	227.6366	453.2820	227.1446	Q	1520.7777	760.8925	1503.7512	752.3792	1502.7672	751.8872	13
5	618.3280	309.6676	601.3014	301.1543	600.3174	300.6623	M	1392.7192	696.8632	1375.6926	688.3499	1374.7086	687.8579	12
6	732.3709	366.6891	715.3443	358.1758	714.3603	357.6838	N	1245.6838	623.3455	1228.6572	614.8322	1227.6732	614.3402	11
7	803.4080	402.2076	786.3815	393.6944	785.3974	393.2024	A	1131.6408	566.3241	1114.6143	557.8108	1113.6303	557.3188	10
8	916.4921	458.7497	899.4655	450.2364	898.4815	449.7444	I	1060.6037	530.8055	1043.5772	522.2922	1042.5932	521.8002	9
9	1029.5761	515.2917	1012.5496	506.7784	1011.5656	506.2864	I	947.5197	474.2635	930.4931	465.7502	929.5091	465.2582	8
10	1144.6031	572.8052	1127.5765	564.2919	1126.5925	563.7999	D	834.4356	417.7214	817.4090	409.2082	816.4250	408.7162	7
11	1227.6402	614.3237	1210.6136	605.8105	1209.6296	605.3184	T	719.4087	360.2080	702.3821	351.6947	701.3981	351.2027	6
12	1326.7086	663.8579	1309.6821	655.3447	1308.6980	654.8527	V	636.3715	318.6894	619.3450	310.1761			5
13	1439.7927	720.4000	1422.7661	711.8867	1421.7821	711.3947	I	537.3031	269.1552	520.2766	260.6419			4
14	1553.8356	777.4214	1536.8090	768.9082	1535.8250	768.4162	N	424.2191	212.6132	407.1925	204.0999			3
15	1716.8989	858.9531	1699.8724	850.4398	1698.8884	849.9478	Y	310.1761	155.5917	293.1496	147.0784			2
16							K	147.1128	74.0600	130.0863	65.5468			1


0.5
0.25
-0
-0.25
-0.5
Error (Da)
250
500
750
1000
Mass (Da)
RMS error 500 ppm

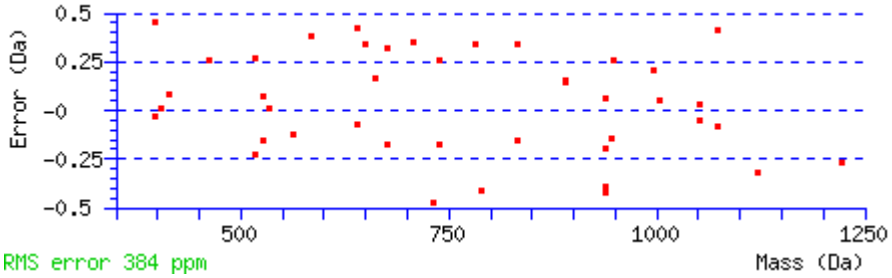

2000
1000
0
-1000
Error (ppm)
250
500
750
1000
Mass (Da)
RMS error 500 ppm

IDENTIFICATION 123
MS/MS Fragmentation of IYHLPDAESDEDEDFKEQTR
Found in IPI00114945

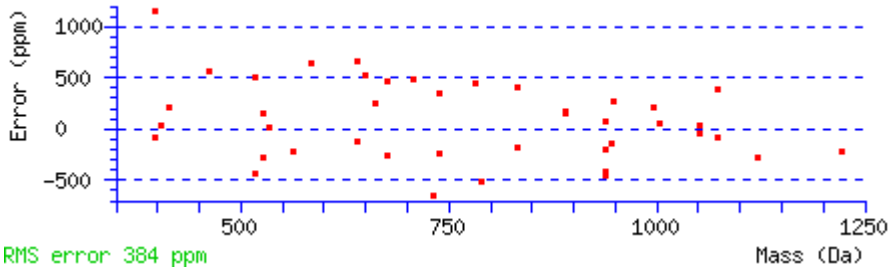


Monoisotopic mass of neutral peptide Mr(calc): 2516.0380
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 38 Expect: 0.038 (help)

#	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	277.1547	139.0810					Y	2403.9613	1202.4843	2386.9347	1193.9710	2385.9507	1193.4790	19
3	414.2136	207.6104					H	2240.8979	1120.9526	2223.8714	1112.4393	2222.8874	1111.9473	18
4	527.2976	264.1525					L	2103.8390	1052.4232	2086.8125	1043.9099	2085.8285	1043.4179	17
5	624.3504	312.6788					P	1990.7550	995.8811	1973.7284	987.3678	1972.7444	986.8758	16
6	739.3774	370.1923			721.3668	361.1870	D	1893.7022	947.3547	1876.6757	938.8415	1875.6916	938.3495	15
7	810.4145	405.7109			792.4039	396.7056	A	1778.6753	889.8413	1761.6487	881.3280	1760.6647	880.8360	14
8	939.4571	470.2322			921.4465	461.2269	E	1707.6381	854.3227	1690.6116	845.8094	1689.6276	845.3174	13
9	1106.4554	553.7313			1088.4449	544.7261	S	1578.5956	789.8014	1561.5690	781.2881	1560.5850	780.7961	12
10	1221.4824	611.2448			1203.4718	602.2395	D	1411.5972	706.3022	1394.5706	697.7890	1393.5866	697.2970	11
11	1350.5250	675.7661			1332.5144	666.7608	E	1296.5703	648.7888	1279.5437	640.2755	1278.5597	639.7835	10
12	1465.5519	733.2796			1447.5413	724.2743	D	1167.5277	584.2675	1150.5011	575.7542	1149.5171	575.2622	9
13	1594.5945	797.8009			1576.5839	788.7956	E	1052.5007	526.7540	1035.4742	518.2407	1034.4902	517.7487	8
14	1709.6214	855.3144			1691.6109	846.3091	D	923.4581	462.2327	906.4316	453.7194	905.4476	453.2274	7
15	1856.6898	928.8486			1838.6793	919.8433	F	808.4312	404.7192	791.4046	396.2060	790.4206	395.7139	6
16	1984.7848	992.8960	1967.7583	984.3828	1966.7742	983.8908	K	661.3628	331.1850	644.3362	322.6717	643.3522	322.1797	5
17	2113.8274	1057.4173	2096.8009	1048.9041	2095.8168	1048.4121	E	533.2678	267.1375	516.2413	258.6243	515.2572	258.1323	4
18	2241.8860	1121.4466	2224.8594	1112.9334	2223.8754	1112.4413	Q	404.2252	202.6162	387.1987	194.1030	386.2146	193.6110	3
19	2342.9337	1171.9705	2325.9071	1163.4572	2324.9231	1162.9652	T	276.1666	138.5870	259.1401	130.0737	258.1561	129.5817	2
20							R	175.1190	88.0631	158.0924	79.5498			1

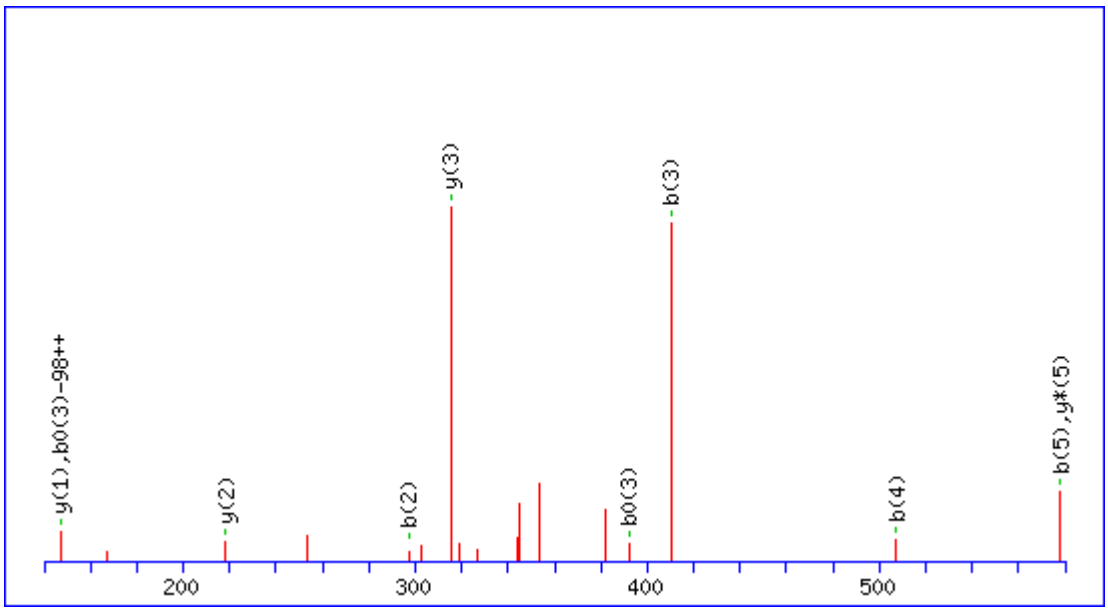


RMS error 384 ppm



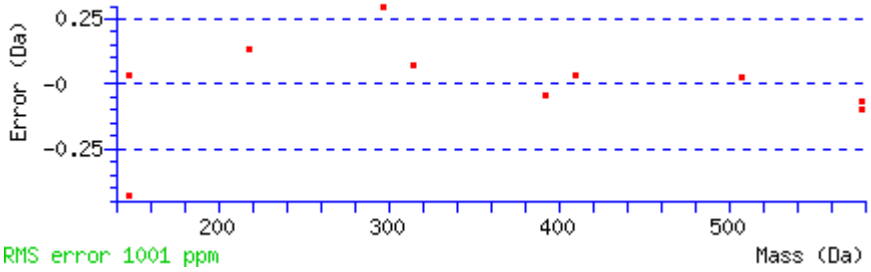
RMS error 384 ppm

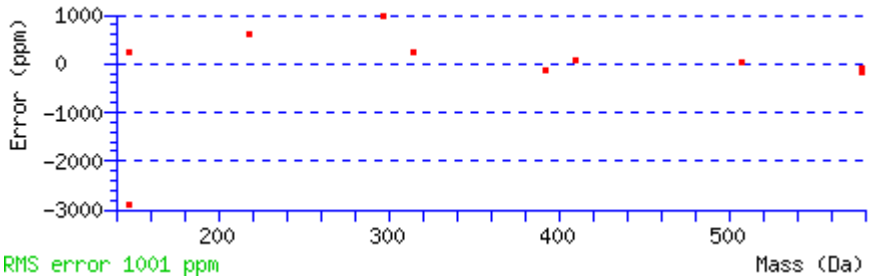
IDENTIFICATION 124
MS/MS Fragmentation of ESIPAK
Found in IPI00274795



Monoisotopic mass of neutral peptide Mr(calc): 723.3204
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S2 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.028 (help)

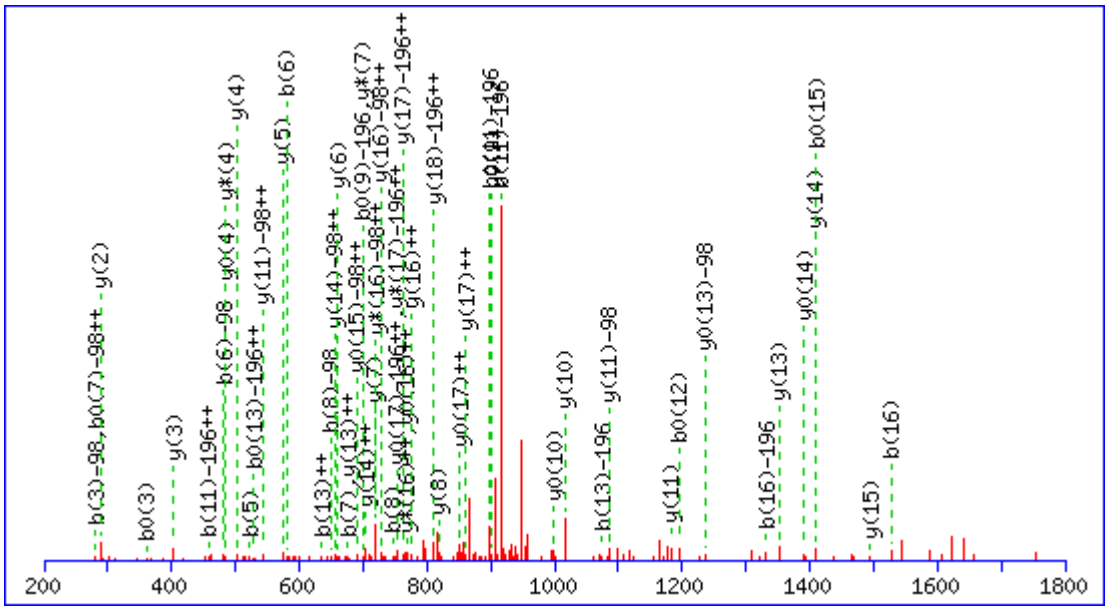
#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	130.0499	65.5286	112.0393	56.5233	E							6
2	297.0482	149.0278	279.0377	140.0225	S	595.2851	298.1462	578.2586	289.6329	577.2745	289.1409	5
3	410.1323	205.5698	392.1217	196.5645	I	428.2867	214.6470	411.2602	206.1337			4
4	507.1851	254.0962	489.1745	245.0909	P	315.2027	158.1050	298.1761	149.5917			3
5	578.2222	289.6147	560.2116	280.6094	A	218.1499	109.5786	201.1234	101.0653			2
6					K	147.1128	74.0600	130.0863	65.5468			1





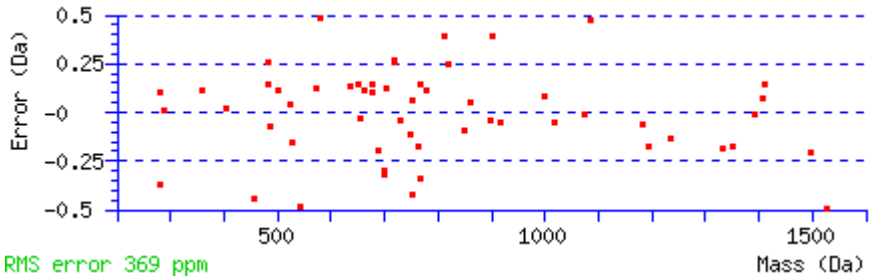
IDENTIFICATION 125
MS/MS Fragmentation of
LPSGSGPASPTTGSAVDIR

Found in IPI00553798

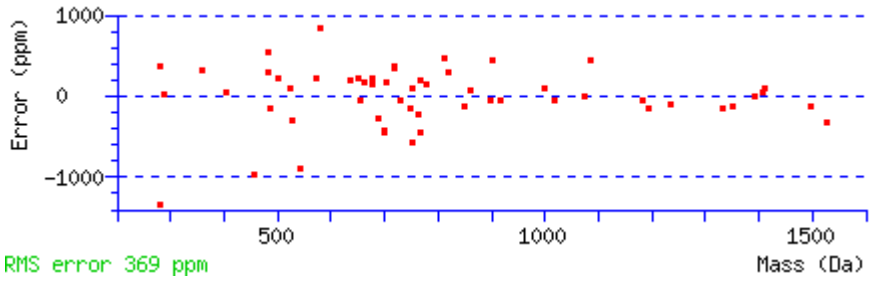


Monoisotopic mass of neutral peptide Mr(calc): 1928.8282 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 S9 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 33 Expect: 0.098 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							19
2	211.1441	106.0757			P	1816.7514	908.8793	1799.7249	900.3661	1798.7409	899.8741	18
3	378.1425	189.5749	360.1319	180.5696	S	1719.6987	860.3530	1702.6721	851.8397	1701.6881	851.3477	17
4	435.1639	218.0856	417.1534	209.0803	G	1552.7003	776.8538	1535.6737	768.3405	1534.6897	767.8485	16
5	522.1960	261.6016	504.1854	252.5963	S	1495.6788	748.3431	1478.6523	739.8298	1477.6683	739.3378	15
6	579.2174	290.1123	561.2069	281.1071	G	1408.6468	704.8270	1391.6203	696.3138	1390.6362	695.8218	14
7	676.2702	338.6387	658.2596	329.6334	P	1351.6253	676.3163	1334.5988	667.8030	1333.6148	667.3110	13
8	747.3073	374.1573	729.2967	365.1520	A	1254.5726	627.7899	1237.5460	619.2767	1236.5620	618.7846	12
9	914.3057	457.6565	896.2951	448.6512	S	1183.5355	592.2714	1166.5089	583.7581	1165.5249	583.2661	11
10	1011.3584	506.1828	993.3479	497.1776	P	1016.5371	508.7722	999.5106	500.2589	998.5265	499.7669	10
11	1112.4061	556.7067	1094.3955	547.7014	T	919.4843	460.2458	902.4578	451.7325	901.4738	451.2405	9
12	1213.4538	607.2305	1195.4432	598.2252	T	818.4367	409.7220	801.4101	401.2087	800.4261	400.7167	8
13	1270.4752	635.7413	1252.4647	626.7360	G	717.3890	359.1981	700.3624	350.6849	699.3784	350.1928	7
14	1357.5073	679.2573	1339.4967	670.2520	S	660.3675	330.6874	643.3410	322.1741	642.3570	321.6821	6
15	1428.5444	714.7758	1410.5338	705.7705	A	573.3355	287.1714	556.3089	278.6581	555.3249	278.1661	5
16	1527.6128	764.3100	1509.6022	755.3048	V	502.2984	251.6528	485.2718	243.1395	484.2878	242.6475	4
17	1642.6397	821.8235	1624.6292	812.8182	D	403.2300	202.1186	386.2034	193.6053	385.2194	193.1133	3
18	1755.7238	878.3655	1737.7132	869.3603	I	288.2030	144.6051	271.1765	136.0919			2
19					R	175.1190	88.0631	158.0924	79.5498			1

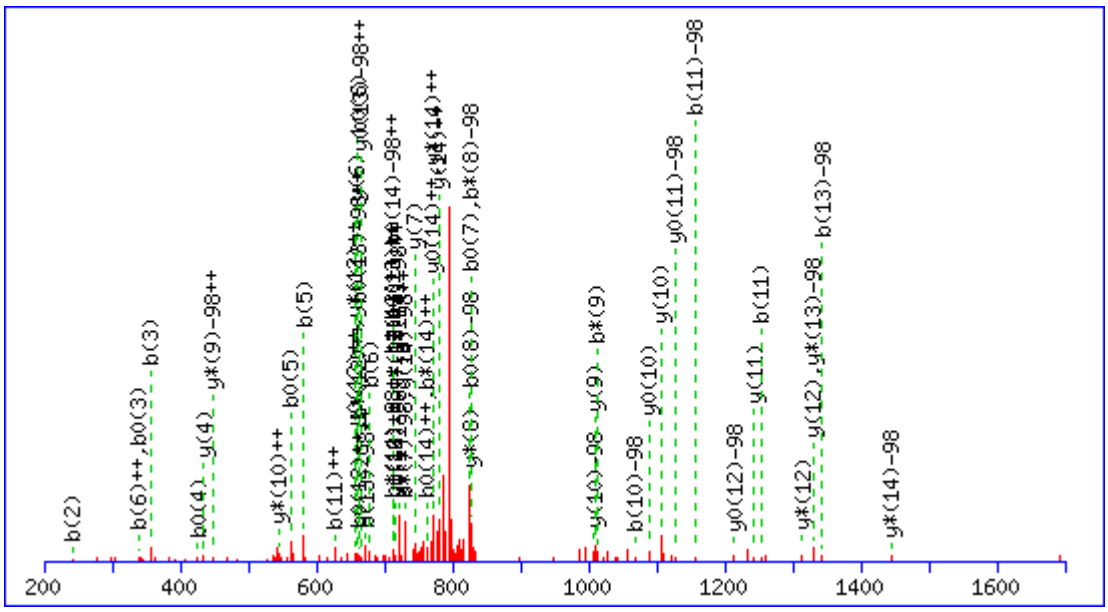


RMS error 369 ppm



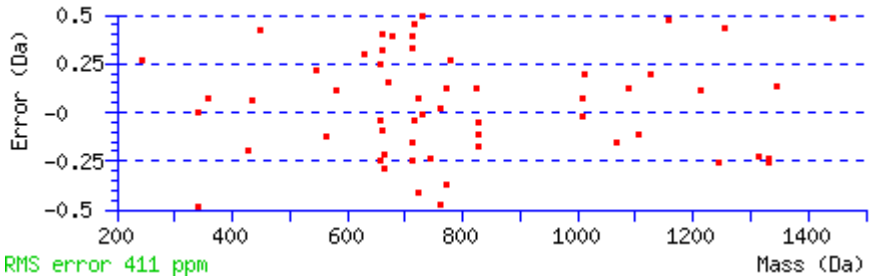
RMS error 369 ppm

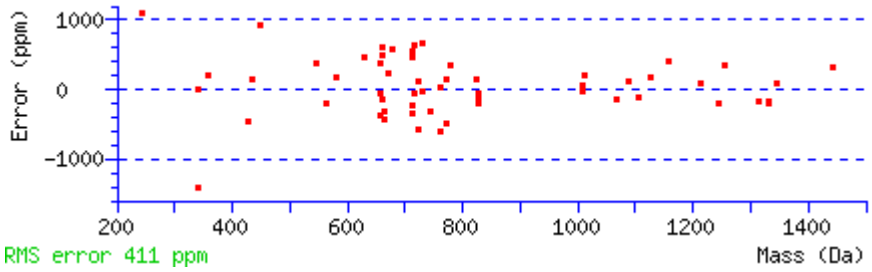
IDENTIFICATION 126
MS/MS Fragmentation of KIDSHPSPSHSSTVK
Found in IPI00664886



Monoisotopic mass of neutral peptide Mr(calc): 1685.7774
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 27 Expect: 0.33 (help)

#	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							15
2	242.1863	121.5968	225.1598	113.0835			I	1460.7128	730.8601	1443.6863	722.3468	1442.7023	721.8548	14
3	357.2132	179.1103	340.1867	170.5970	339.2027	170.1050	D	1347.6288	674.3180	1330.6022	665.8047	1329.6182	665.3127	13
4	444.2453	222.6263	427.2187	214.1130	426.2347	213.6210	S	1232.6018	616.8046	1215.5753	608.2913	1214.5913	607.7993	12
5	581.3042	291.1557	564.2776	282.6425	563.2936	282.1504	H	1145.5698	573.2885	1128.5432	564.7753	1127.5592	564.2833	11
6	678.3570	339.6821	661.3304	331.1688	660.3464	330.6768	P	1008.5109	504.7591	991.4843	496.2458	990.5003	495.7538	10
7	747.3784	374.1928	730.3519	365.6796	729.3678	365.1876	S	911.4581	456.2327	894.4316	447.7194	893.4476	447.2274	9
8	844.4312	422.7192	827.4046	414.2060	826.4206	413.7139	P	842.4367	421.7220	825.4101	413.2087	824.4261	412.7167	8
9	931.4632	466.2352	914.4367	457.7220	913.4526	457.2300	S	745.3839	373.1956	728.3573	364.6823	727.3733	364.1903	7
10	1068.5221	534.7647	1051.4956	526.2514	1050.5116	525.7594	H	658.3519	329.6796	641.3253	321.1663	640.3413	320.6743	6
11	1155.5541	578.2807	1138.5276	569.7674	1137.5436	569.2754	S	521.2930	261.1501	504.2664	252.6368	503.2824	252.1448	5
12	1242.5862	621.7967	1225.5596	613.2835	1224.5756	612.7914	S	434.2609	217.6341	417.2344	209.1208	416.2504	208.6288	4
13	1343.6339	672.3206	1326.6073	663.8073	1325.6233	663.3153	T	347.2289	174.1181	330.2023	165.6048	329.2183	165.1128	3
14	1442.7023	721.8548	1425.6757	713.3415	1424.6917	712.8495	V	246.1812	123.5942	229.1547	115.0810			2
15							K	147.1128	74.0600	130.0863	65.5468			1


0.5
0.25
-0
-0.25
-0.5
Error (Da)
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 411 ppm


1000
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Error (ppm)
200
400
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800
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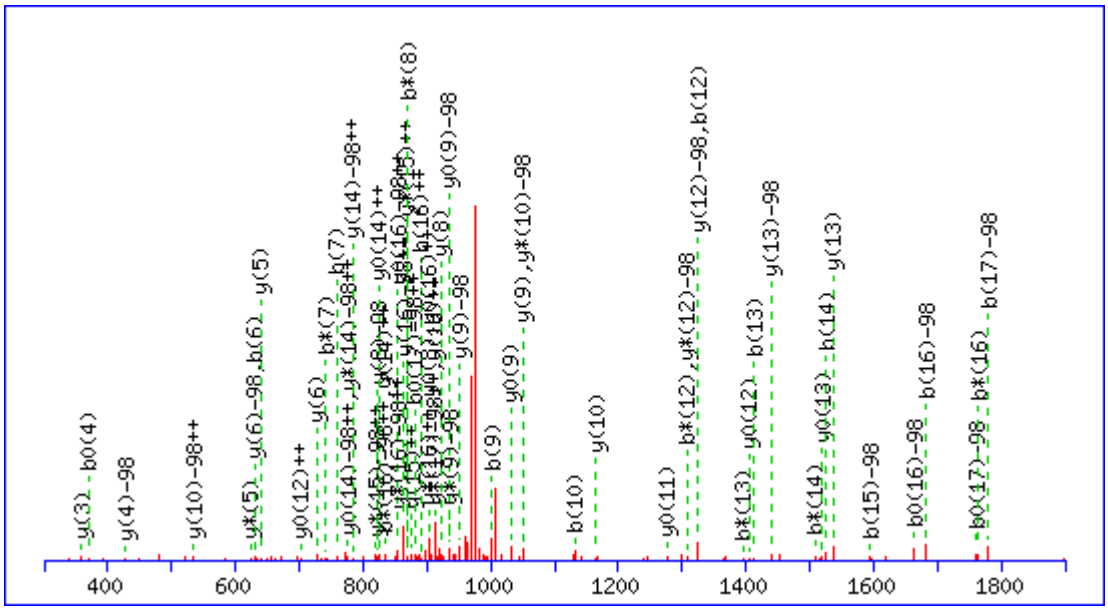
1200
1400
Mass (Da)
RMS error 411 ppm

IDENTIFICATION 127

MS/MS Fragmentation of IDASKNEEDEGHSNSSPR

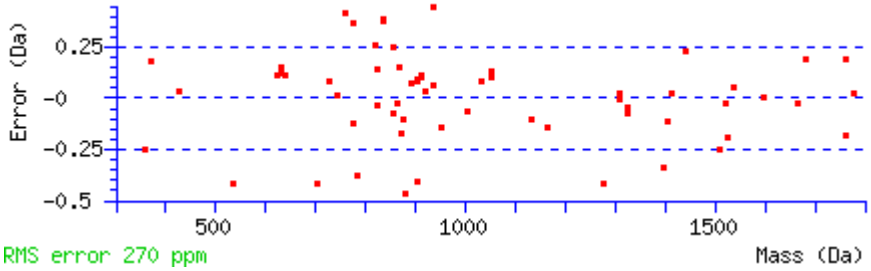
Found in

IPI00330958



Monoisotopic mass of neutral peptide Mr(calc): 2050.8229 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S15 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 40 Expect: 0.017 (help)

#	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	229.1183	115.0628			211.1077	106.0575	D	1840.7692	920.8883	1823.7427	912.3750	1822.7587	911.8830	17
3	300.1554	150.5813			282.1448	141.5761	A	1725.7423	863.3748	1708.7157	854.8615	1707.7317	854.3695	16
4	387.1874	194.0974			369.1769	185.0921	S	1654.7052	827.8562	1637.6786	819.3430	1636.6946	818.8509	15
5	515.2824	258.1448	498.2558	249.6316	497.2718	249.1395	K	1567.6732	784.3402	1550.6466	775.8269	1549.6626	775.3349	14
6	629.3253	315.1663	612.2988	306.6530	611.3148	306.1610	N	1439.5782	720.2927	1422.5516	711.7795	1421.5676	711.2874	13
7	758.3679	379.6876	741.3414	371.1743	740.3573	370.6823	E	1325.5353	663.2713	1308.5087	654.7580	1307.5247	654.2660	12
8	887.4105	444.2089	870.3840	435.6956	869.3999	435.2036	E	1196.4927	598.7500	1179.4661	590.2367	1178.4821	589.7447	11
9	1002.4374	501.7224	985.4109	493.2091	984.4269	492.7171	D	1067.4501	534.2287	1050.4235	525.7154	1049.4395	525.2234	10
10	1131.4800	566.2437	1114.4535	557.7304	1113.4695	557.2384	E	952.4231	476.7152	935.3966	468.2019	934.4126	467.7099	9
11	1188.5015	594.7544	1171.4750	586.2411	1170.4909	585.7491	G	823.3805	412.1939	806.3540	403.6806	805.3700	403.1886	8
12	1325.5604	663.2838	1308.5339	654.7706	1307.5498	654.2786	H	766.3591	383.6832	749.3325	375.1699	748.3485	374.6779	7
13	1412.5924	706.7999	1395.5659	698.2866	1394.5819	697.7946	S	629.3002	315.1537	612.2736	306.6404	611.2896	306.1484	6
14	1526.6354	763.8213	1509.6088	755.3080	1508.6248	754.8160	N	542.2681	271.6377	525.2416	263.1244	524.2576	262.6324	5
15	1595.6568	798.3321	1578.6303	789.8188	1577.6463	789.3268	S	428.2252	214.6162	411.1987	206.1030	410.2146	205.6110	4
16	1682.6889	841.8481	1665.6623	833.3348	1664.6783	832.8428	S	359.2037	180.1055	342.1772	171.5922	341.1932	171.1002	3
17	1779.7416	890.3744	1762.7151	881.8612	1761.7311	881.3692	P	272.1717	136.5895	255.1452	128.0762			2
18							R	175.1190	88.0631	158.0924	79.5498			1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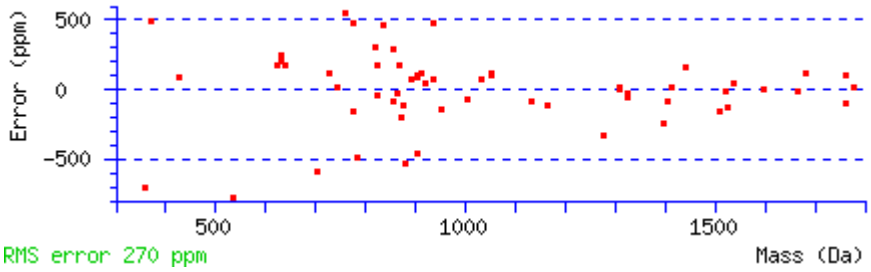
RMS error 270 ppm
Mass (Da)


Error (ppm)
500
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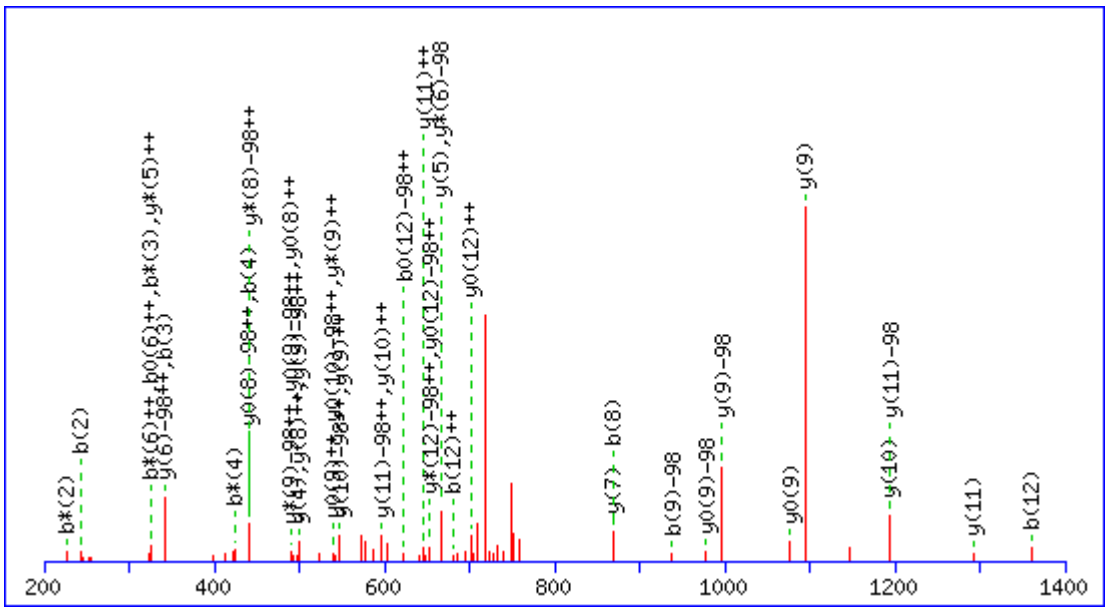
-500
500
1000
1500
RMS error 270 ppm
Mass (Da)

IDENTIFICATION 128
MS/MS Fragmentation of NQVVPESDSPVKR
Found in IPI00473314



Monoisotopic mass of neutral peptide Mr(calc):

1533.7188

Fixed modifications:

Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S9 :

Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score:

40

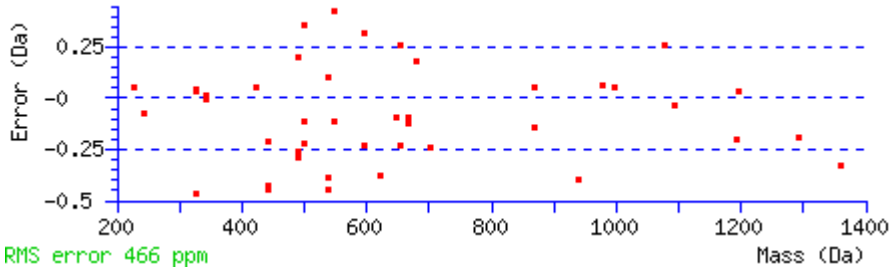
Expect:

0.014 (

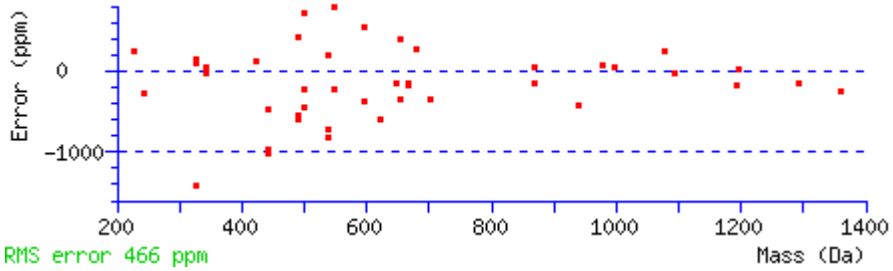
help

)

#	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	243.1088	122.0580	226.0822	113.5448			Q	1420.6832	710.8452	1403.6566	702.3320	1402.6726	701.8399	12
3	342.1772	171.5922	325.1506	163.0790			V	1292.6246	646.8159	1275.5981	638.3027	1274.6140	637.8107	11
4	441.2456	221.1264	424.2191	212.6132			V	1193.5562	597.2817	1176.5296	588.7685	1175.5456	588.2765	10
5	538.2984	269.6528	521.2718	261.1396			P	1094.4878	547.7475	1077.4612	539.2343	1076.4772	538.7422	9
6	667.3410	334.1741	650.3144	325.6608	649.3304	325.1688	E	997.4350	499.2211	980.4085	490.7079	979.4245	490.2159	8
7	754.3730	377.6901	737.3464	369.1769	736.3624	368.6849	S	868.3924	434.6998	851.3659	426.1866	850.3819	425.6946	7
8	869.3999	435.2036	852.3734	426.6903	851.3894	426.1983	D	781.3604	391.1838	764.3338	382.6706	763.3498	382.1786	6
9	1036.3983	518.7028	1019.3717	510.1895	1018.3877	509.6975	S	666.3335	333.6704	649.3069	325.1571	648.3229	324.6651	5
10	1133.4511	567.2292	1116.4245	558.7159	1115.4405	558.2239	P	499.3351	250.1712	482.3085	241.6579			4
11	1232.5195	616.7634	1215.4929	608.2501	1214.5089	607.7581	V	402.2823	201.6448	385.2558	193.1315			3
12	1360.6144	680.8109	1343.5879	672.2976	1342.6039	671.8056	K	303.2139	152.1106	286.1874	143.5973			2
13							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 466 ppm

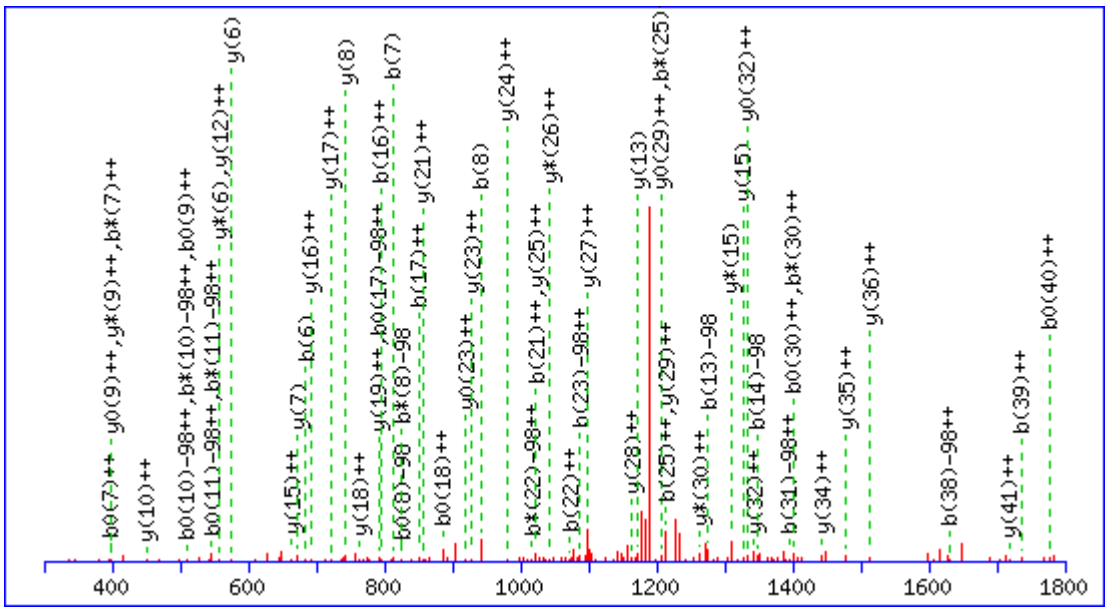


RMS error 466 ppm

IDENTIFICATION 129

MS/MS Fragmentation of SSEAETQQPPAAPAAALSAADTKPGSTGSGAGSGGPGGLTSAAPAGGDKK

Found in IPI00120886



Monoisotopic mass of neutral peptide Mr(calc): 4471.0776

Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

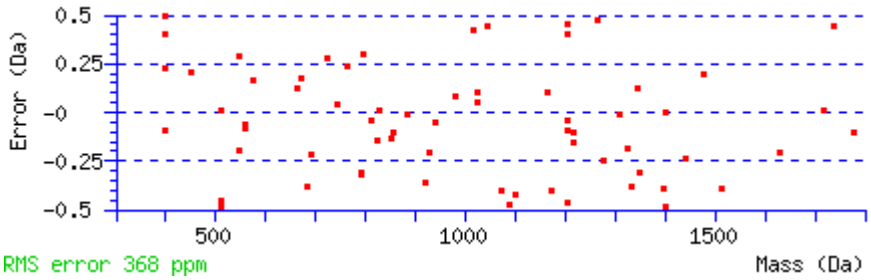
Variable modifications:

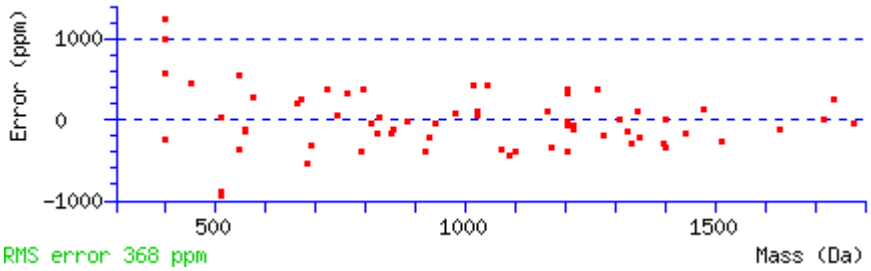
T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 26 Expect: 0.49 (help)

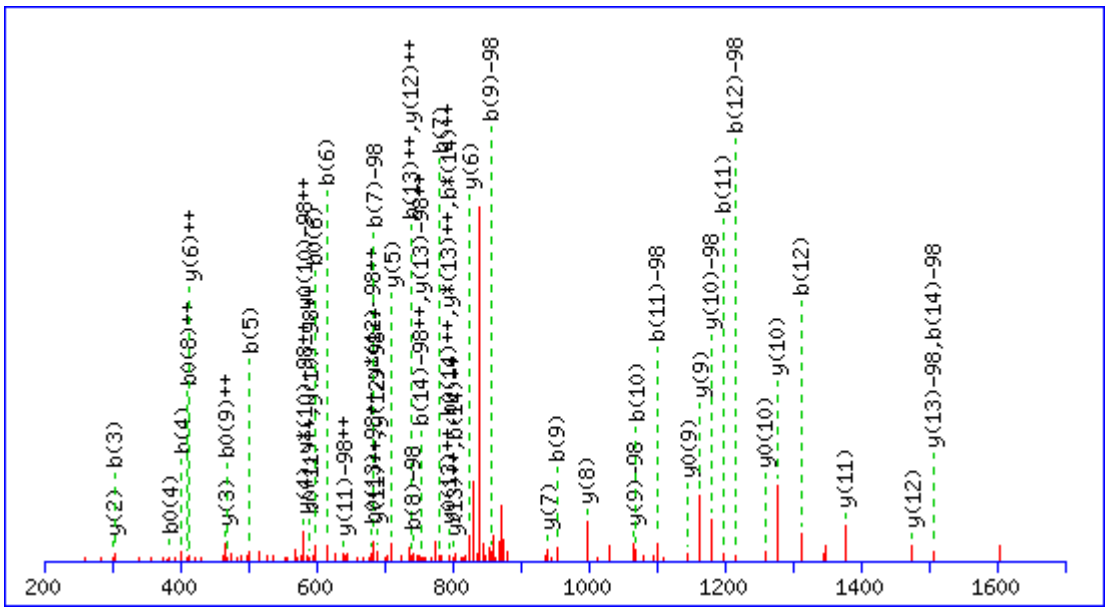
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							50
2	175.0713	88.0393			157.0608	79.0340	S	4385.0529	2193.0301	4368.0263	2184.5168	4367.0423	2184.0248	49
3	304.1139	152.5606			286.1034	143.5553	E	4298.0209	2149.5141	4280.9943	2141.0008	4280.0103	2140.5088	48
4	375.1510	188.0792			357.1405	179.0739	A	4168.9783	2084.9928	4151.9517	2076.4795	4150.9677	2075.9875	47
5	504.1936	252.6005			486.1831	243.5952	E	4097.9412	2049.4742	4080.9146	2040.9609	4079.9306	2040.4689	46
6	685.2076	343.1075			667.1971	334.1022	T	3968.8986	1984.9529	3951.8720	1976.4396	3950.8880	1975.9476	45
7	813.2662	407.1367	796.2397	398.6235	795.2557	398.1315	Q	3787.8846	1894.4459	3770.8580	1885.9326	3769.8740	1885.4406	44
8	941.3248	471.1660	924.2982	462.6528	923.3142	462.1608	Q	3659.8260	1830.4166	3642.7994	1821.9034	3641.8154	1821.4113	43
9	1038.3776	519.6924	1021.3510	511.1791	1020.3670	510.6871	P	3531.7674	1766.3873	3514.7408	1757.8741	3513.7568	1757.3821	42
10	1135.4303	568.2188	1118.4038	559.7055	1117.4198	559.2135	P	3434.7146	1717.8610	3417.6881	1709.3477	3416.7041	1708.8557	41
11	1206.4674	603.7374	1189.4409	595.2241	1188.4569	594.7321	A	3337.6619	1669.3346	3320.6353	1660.8213	3319.6513	1660.3293	40
12	1277.5046	639.2559	1260.4780	630.7426	1259.4940	630.2506	A	3266.6248	1633.8160	3249.5982	1625.3027	3248.6142	1624.8107	39
13	1374.5573	687.7823	1357.5308	679.2690	1356.5468	678.7770	P	3195.5876	1598.2975	3178.5611	1589.7842	3177.5771	1589.2922	38
14	1445.5944	723.3009	1428.5679	714.7876	1427.5839	714.2956	A	3098.5349	1549.7711	3081.5083	1541.2578	3080.5243	1540.7658	37
15	1516.6315	758.8194	1499.6050	750.3061	1498.6210	749.8141	A	3027.4978	1514.2525	3010.4712	1505.7392	3009.4872	1505.2472	36
16	1587.6687	794.3380	1570.6421	785.8247	1569.6581	785.3327	A	2956.4607	1478.7340	2939.4341	1470.2207	2938.4501	1469.7287	35
17	1700.7527	850.8800	1683.7262	842.3667	1682.7422	841.8747	L	2885.4235	1443.2154	2868.3970	1434.7021	2867.4130	1434.2101	34
18	1787.7848	894.3960	1770.7582	885.8827	1769.7742	885.3907	S	2772.3395	1386.6734	2755.3129	1378.1601	2754.3289	1377.6681	33
19	1858.8219	929.9146	1841.7953	921.4013	1840.8113	920.9093	A	2685.3074	1343.1574	2668.2809	1334.6441	2667.2969	1334.1521	32
20	1929.8590	965.4331	1912.8324	956.9199	1911.8484	956.4278	A	2614.2703	1307.6388	2597.2438	1299.1255	2596.2598	1298.6335	31
21	2044.8859	1022.9466	2027.8594	1014.4333	2026.8754	1013.9413	D	2543.2332	1272.1202	2526.2067	1263.6070	2525.2227	1263.1150	30
22	2145.9336	1073.4704	2128.9071	1064.9572	2127.9230	1064.4652	T	2428.2063	1214.6068	2411.1797	1206.0935	2410.1957	1205.6015	29
23	2274.0286	1137.5179	2257.0020	1129.0046	2256.0180	1128.5126	K	2327.1586	1164.0829	2310.1320	1155.5697	2309.1480	1155.0777	28
24	2371.0813	1186.0443	2354.0548	1177.5310	2353.0708	1177.0390	P	2199.0636	1100.0355	2182.0371	1091.5222	2181.0531	1091.0302	27
25	2428.1028	1214.5550	2411.0762	1206.0418	2410.0922	1205.5498	G	2102.0109	1051.5091	2084.9843	1042.9958	2084.0003	1042.5038	26
26	2515.1348	1258.0710	2498.1083	1249.5578	2497.1243	1249.0658	S	2044.9894	1022.9983	2027.9629	1014.4851	2026.9788	1013.9931	25
27	2616.1825	1308.5949	2599.1560	1300.0816	2598.1719	1299.5896	T	1957.9574	979.4823	1940.9308	970.9691	1939.9468	970.4770	24

28	2673.2040	1337.1056	2656.1774	1328.5923	2655.1934	1328.1003	G	1856.9097	928.9585	1839.8831	920.4452	1838.8991	919.9532	23
29	2760.2360	1380.6216	2743.2094	1372.1084	2742.2254	1371.6164	S	1799.8882	900.4478	1782.8617	891.9345	1781.8777	891.4425	22
30	2817.2575	1409.1324	2800.2309	1400.6191	2799.2469	1400.1271	G	1712.8562	856.9317	1695.8297	848.4185	1694.8456	847.9265	21
31	2888.2946	1444.6509	2871.2680	1436.1376	2870.2840	1435.6456	A	1655.8347	828.4210	1638.8082	819.9077	1637.8242	819.4157	20
32	2945.3160	1473.1617	2928.2895	1464.6484	2927.3055	1464.1564	G	1584.7976	792.9025	1567.7711	784.3892	1566.7871	783.8972	19
33	3032.3481	1516.6777	3015.3215	1508.1644	3014.3375	1507.6724	S	1527.7762	764.3917	1510.7496	755.8784	1509.7656	755.3864	18
34	3089.3695	1545.1884	3072.3430	1536.6751	3071.3590	1536.1831	G	1440.7441	720.8757	1423.7176	712.3624	1422.7336	711.8704	17
35	3146.3910	1573.6991	3129.3644	1565.1859	3128.3804	1564.6939	G	1383.7227	692.3650	1366.6961	683.8517	1365.7121	683.3597	16
36	3243.4438	1622.2255	3226.4172	1613.7122	3225.4332	1613.2202	P	1326.7012	663.8542	1309.6747	655.3410	1308.6906	654.8490	15
37	3300.4652	1650.7362	3283.4387	1642.2230	3282.4547	1641.7310	G	1229.6484	615.3279	1212.6219	606.8146	1211.6379	606.3226	14
38	3357.4867	1679.2470	3340.4601	1670.7337	3339.4761	1670.2417	G	1172.6270	586.8171	1155.6004	578.3039	1154.6164	577.8118	13
39	3470.5707	1735.7890	3453.5442	1727.2757	3452.5602	1726.7837	L	1115.6055	558.3064	1098.5790	549.7931	1097.5949	549.3011	12
40	3571.6184	1786.3129	3554.5919	1777.7996	3553.6079	1777.3076	T	1002.5215	501.7644	985.4949	493.2511	984.5109	492.7591	11
41	3658.6505	1829.8289	3641.6239	1821.3156	3640.6399	1820.8236	S	901.4738	451.2405	884.4472	442.7272	883.4632	442.2352	10
42	3729.6876	1865.3474	3712.6610	1856.8341	3711.6770	1856.3421	A	814.4417	407.7245	797.4152	399.2112	796.4312	398.7192	9
43	3800.7247	1900.8660	3783.6981	1892.3527	3782.7141	1891.8607	A	743.4046	372.2060	726.3781	363.6927	725.3941	363.2007	8
44	3897.7774	1949.3924	3880.7509	1940.8791	3879.7669	1940.3871	P	672.3675	336.6874	655.3410	328.1741	654.3570	327.6821	7
45	3968.8146	1984.9109	3951.7880	1976.3976	3950.8040	1975.9056	A	575.3148	288.1610	558.2882	279.6477	557.3042	279.1557	6
46	4025.8360	2013.4216	4008.8095	2004.9084	4007.8255	2004.4164	G	504.2776	252.6425	487.2511	244.1292	486.2671	243.6372	5
47	4082.8575	2041.9324	4065.8309	2033.4191	4064.8469	2032.9271	G	447.2562	224.1317	430.2296	215.6185	429.2456	215.1264	4
48	4197.8844	2099.4459	4180.8579	2090.9326	4179.8739	2090.4406	D	390.2347	195.6210	373.2082	187.1077	372.2241	186.6157	3
49	4325.9794	2163.4933	4308.9528	2154.9801	4307.9688	2154.4881	K	275.2078	138.1075	258.1812	129.5942			2
50							K	147.1128	74.0600	130.0863	65.5468			1



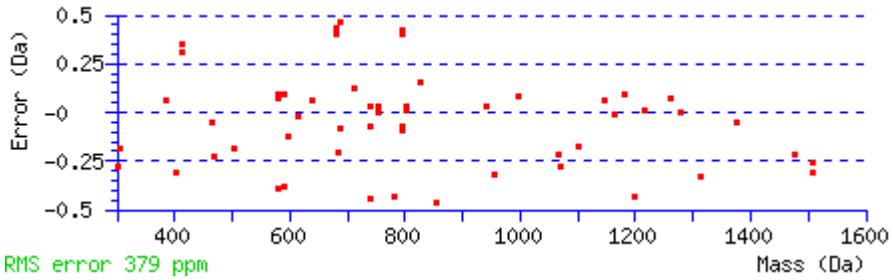


IDENTIFICATION 130
MS/MS Fragmentation of SSEVVLSGDDEDYQR
Found in IPI00553798

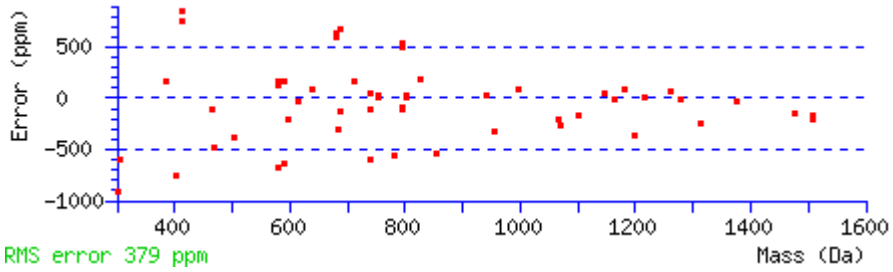


Monoisotopic mass of neutral peptide Mr(calc): 1777.7044 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 58 Expect: 0.00025 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*}_{++}	y^{0}	y_{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							15
2	175.0713	88.0393			157.0608	79.0340	S	1593.7027	797.3550	1576.6762	788.8417	1575.6922	788.3497	14
3	304.1139	152.5606			286.1034	143.5553	E	1506.6707	753.8390	1489.6441	745.3257	1488.6601	744.8337	13
4	403.1823	202.0948			385.1718	193.0895	V	1377.6281	689.3177	1360.6016	680.8044	1359.6175	680.3124	12
5	502.2508	251.6290			484.2402	242.6237	V	1278.5597	639.7835	1261.5331	631.2702	1260.5491	630.7782	11
6	615.3348	308.1710			597.3243	299.1658	L	1179.4913	590.2493	1162.4647	581.7360	1161.4807	581.2440	10
7	684.3563	342.6818			666.3457	333.6765	S	1066.4072	533.7072	1049.3807	525.1940	1048.3966	524.7020	9
8	741.3777	371.1925			723.3672	362.1872	G	997.3857	499.1965	980.3592	490.6832	979.3752	490.1912	8
9	856.4047	428.7060			838.3941	419.7007	D	940.3643	470.6858	923.3377	462.1725	922.3537	461.6805	7
10	971.4316	486.2195			953.4211	477.2142	D	825.3373	413.1723	808.3108	404.6590	807.3268	404.1670	6
11	1100.4742	550.7407			1082.4637	541.7355	E	710.3104	355.6588	693.2838	347.1456	692.2998	346.6536	5
12	1215.5012	608.2542			1197.4906	599.2489	D	581.2678	291.1375	564.2413	282.6243	563.2572	282.1323	4
13	1378.5645	689.7859			1360.5539	680.7806	Y	466.2409	233.6241	449.2143	225.1108			3
14	1506.6231	753.8152	1489.5965	745.3019	1488.6125	744.8099	Q	303.1775	152.0924	286.1510	143.5791			2
15							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 379 ppm



RMS error 379 ppm

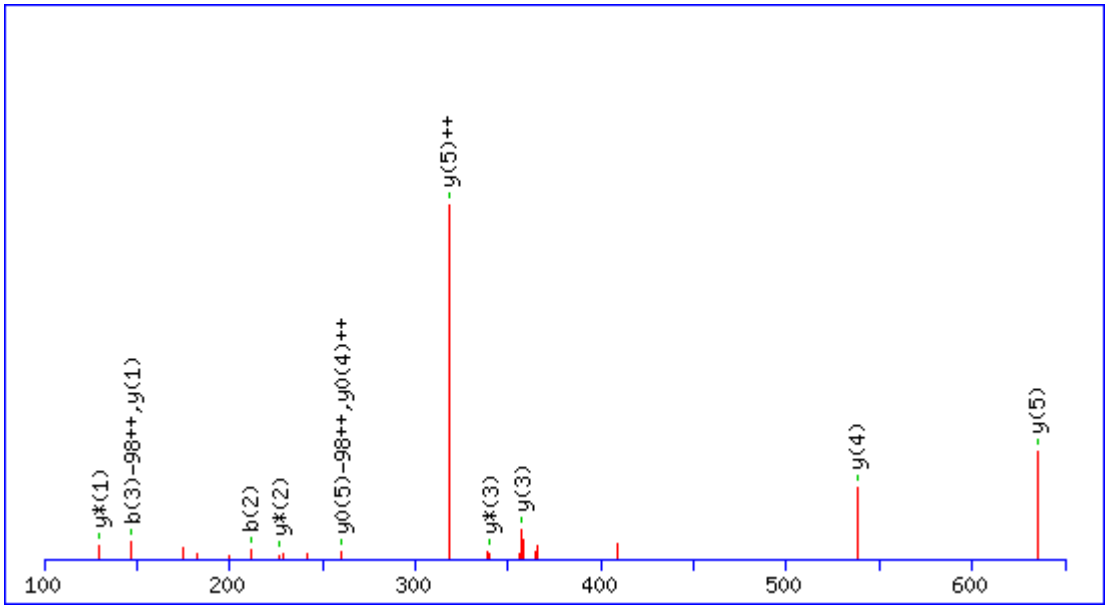
IDENTIFICATION 131

MS/MS Fragmentation of

LPTLPK

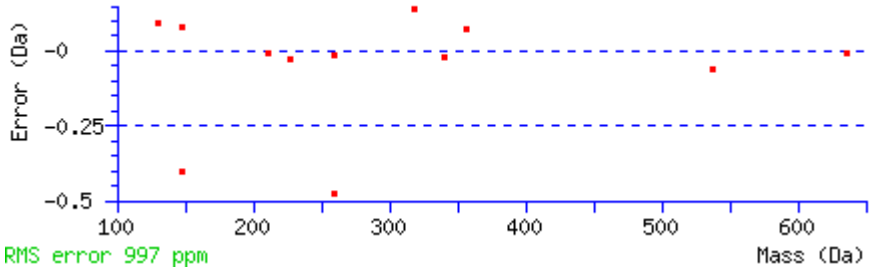
Found in

IPI00127493

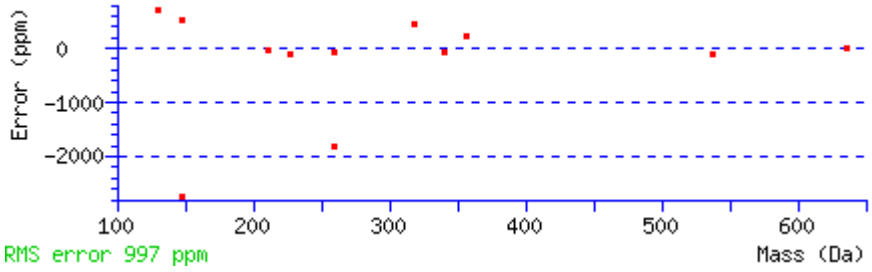


Monoisotopic mass of neutral peptide Mr(calc): 747.3932 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 43 Expect: 0.0032 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493			L							6
2	211.1441	106.0757			P	635.3164	318.1618	618.2899	309.6486	617.3058	309.1566	5
3	392.1581	196.5827	374.1475	187.5774	T	538.2636	269.6355	521.2371	261.1222	520.2531	260.6302	4
4	505.2422	253.1247	487.2316	244.1194	L	357.2496	179.1285	340.2231	170.6152			3
5	602.2949	301.6511	584.2844	292.6458	P	244.1656	122.5864	227.1390	114.0731			2
6					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 997 ppm

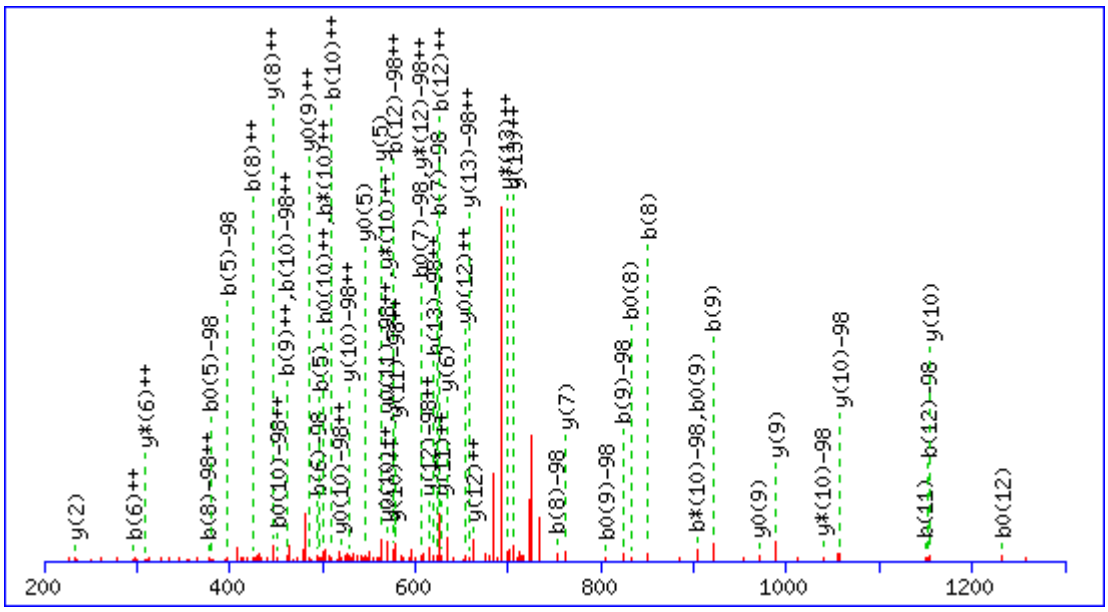


RMS error 997 ppm

IDENTIFICATION 132

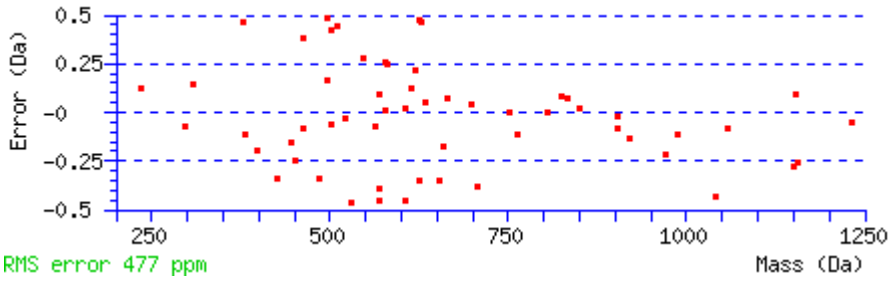
MS/MS Fragmentation of ASAVSPEKAPMTSK

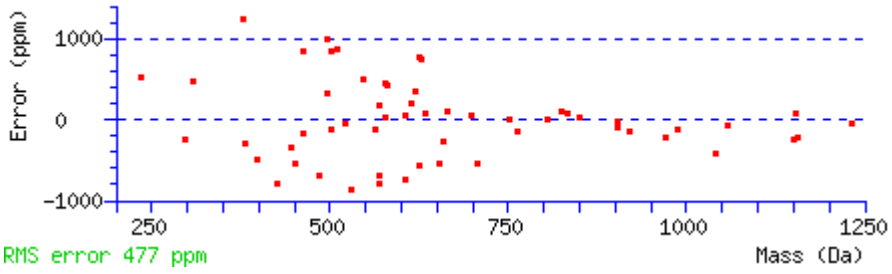
Found in IPI00115660



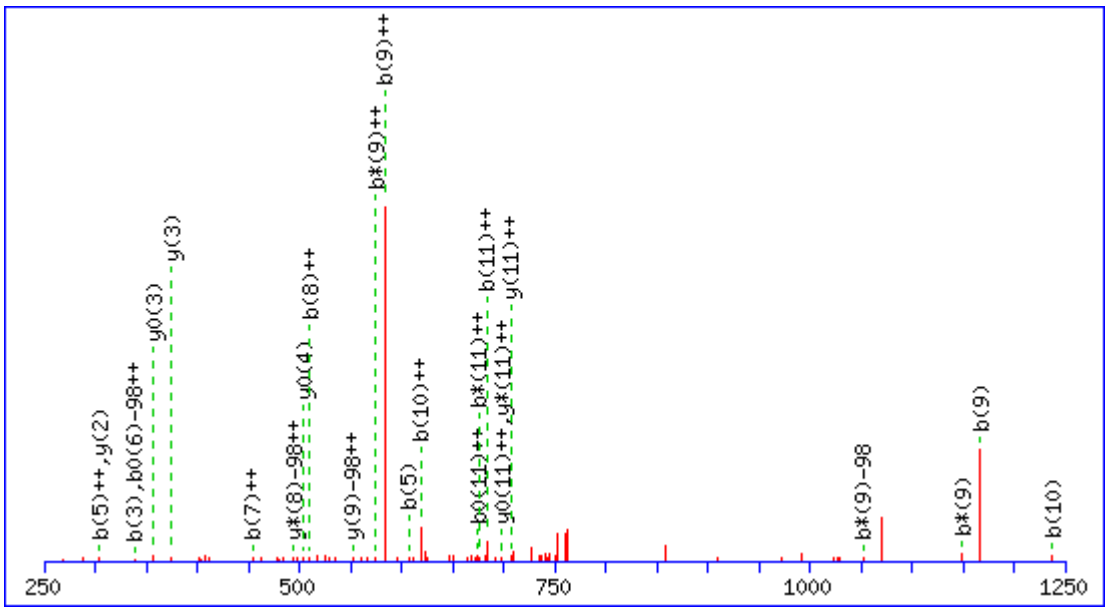
Monoisotopic mass of neutral peptide Mr(calc): 1482.6789 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S5 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 28 Expect: 0.24 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							14
2	159.0764	80.0418			141.0659	71.0366	S	1314.6722	657.8397	1297.6457	649.3265	1296.6616	648.8345	13
3	230.1135	115.5604			212.1030	106.5551	A	1227.6402	614.3237	1210.6136	605.8105	1209.6296	605.3184	12
4	329.1819	165.0946			311.1714	156.0893	V	1156.6031	578.8052	1139.5765	570.2919	1138.5925	569.7999	11
5	398.2034	199.6053			380.1928	190.6001	S	1057.5347	529.2710	1040.5081	520.7577	1039.5241	520.2657	10
6	495.2562	248.1317			477.2456	239.1264	P	988.5132	494.7602	971.4866	486.2470	970.5026	485.7550	9
7	624.2988	312.6530			606.2882	303.6477	E	891.4604	446.2339	874.4339	437.7206	873.4499	437.2286	8
8	752.3937	376.7005	735.3672	368.1872	734.3832	367.6952	K	762.4178	381.7126	745.3913	373.1993	744.4073	372.7073	7
9	823.4308	412.2191	806.4043	403.7058	805.4203	403.2138	A	634.3229	317.6651	617.2963	309.1518	616.3123	308.6598	6
10	920.4836	460.7454	903.4571	452.2322	902.4730	451.7402	P	563.2858	282.1465	546.2592	273.6332	545.2752	273.1412	5
11	1051.5241	526.2657	1034.4975	517.7524	1033.5135	517.2604	M	466.2330	233.6201	449.2064	225.1069	448.2224	224.6149	4
12	1152.5718	576.7895	1135.5452	568.2762	1134.5612	567.7842	T	335.1925	168.0999	318.1660	159.5866	317.1819	159.0946	3
13	1239.6038	620.3055	1222.5773	611.7923	1221.5932	611.3003	S	234.1448	117.5761	217.1183	109.0628	216.1343	108.5708	2
14							K	147.1128	74.0600	130.0863	65.5468			1



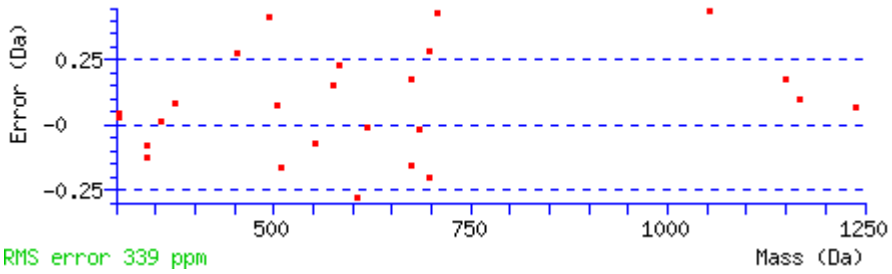


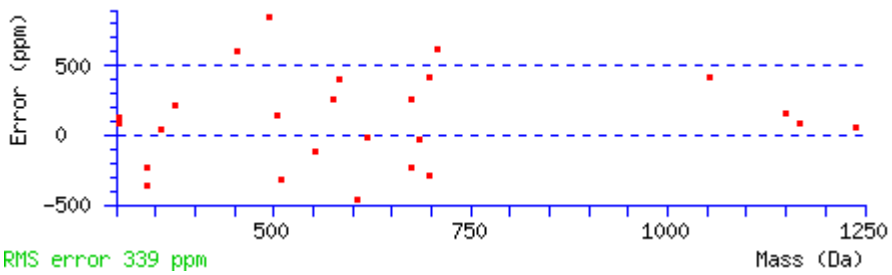
IDENTIFICATION 133
MS/MS Fragmentation of KPLTSWILFAER
Found in IPI00756871



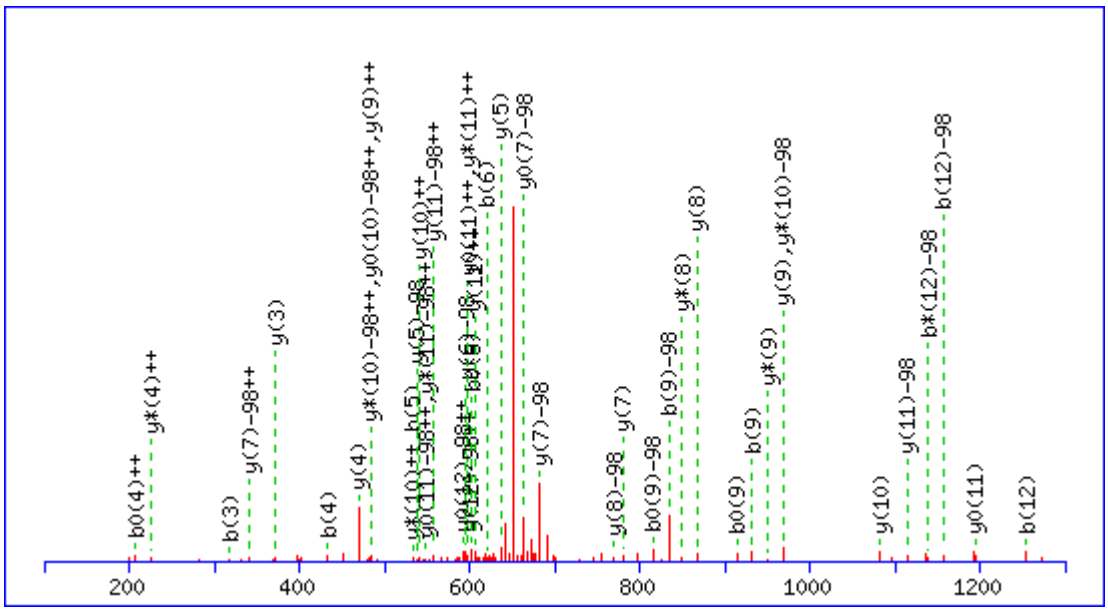
Monoisotopic mass of neutral peptide Mr(calc): 1539.7850 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S5 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 23 Expect: 0.37 (help)

#	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							12
2	226.1550	113.5811	209.1285	105.0679			P	1412.6974	706.8523	1395.6708	698.3391	1394.6868	697.8470	11
3	339.2391	170.1232	322.2125	161.6099			L	1315.6446	658.3259	1298.6181	649.8127	1297.6341	649.3207	10
4	440.2867	220.6470	423.2602	212.1337	422.2762	211.6417	T	1202.5606	601.7839	1185.5340	593.2706	1184.5500	592.7786	9
5	607.2851	304.1462	590.2586	295.6329	589.2745	295.1409	S	1101.5129	551.2601	1084.4863	542.7468	1083.5023	542.2548	8
6	793.3644	397.1858	776.3379	388.6726	775.3539	388.1806	W	934.5145	467.7609	917.4880	459.2476	916.5039	458.7556	7
7	906.4485	453.7279	889.4219	445.2146	888.4379	444.7226	I	748.4352	374.7212	731.4087	366.2080	730.4246	365.7160	6
8	1019.5325	510.2699	1002.5060	501.7566	1001.5220	501.2646	L	635.3511	318.1792	618.3246	309.6659	617.3406	309.1739	5
9	1166.6010	583.8041	1149.5744	575.2908	1148.5904	574.7988	F	522.2671	261.6372	505.2405	253.1239	504.2565	252.6319	4
10	1237.6381	619.3227	1220.6115	610.8094	1219.6275	610.3174	A	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
11	1366.6807	683.8440	1349.6541	675.3307	1348.6701	674.8387	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1



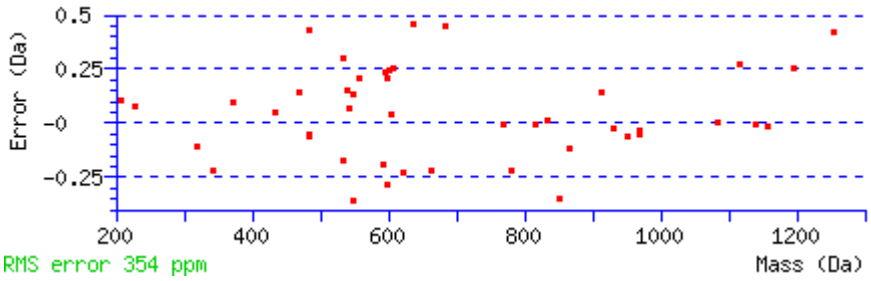


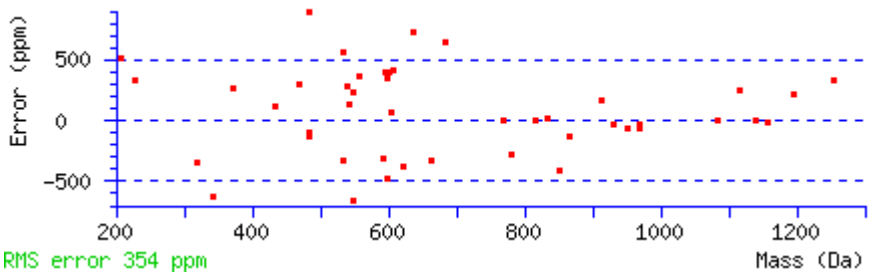
IDENTIFICATION 134
MS/MS Fragmentation of TSEDTSSGSPPKK
Found in IPI00399961



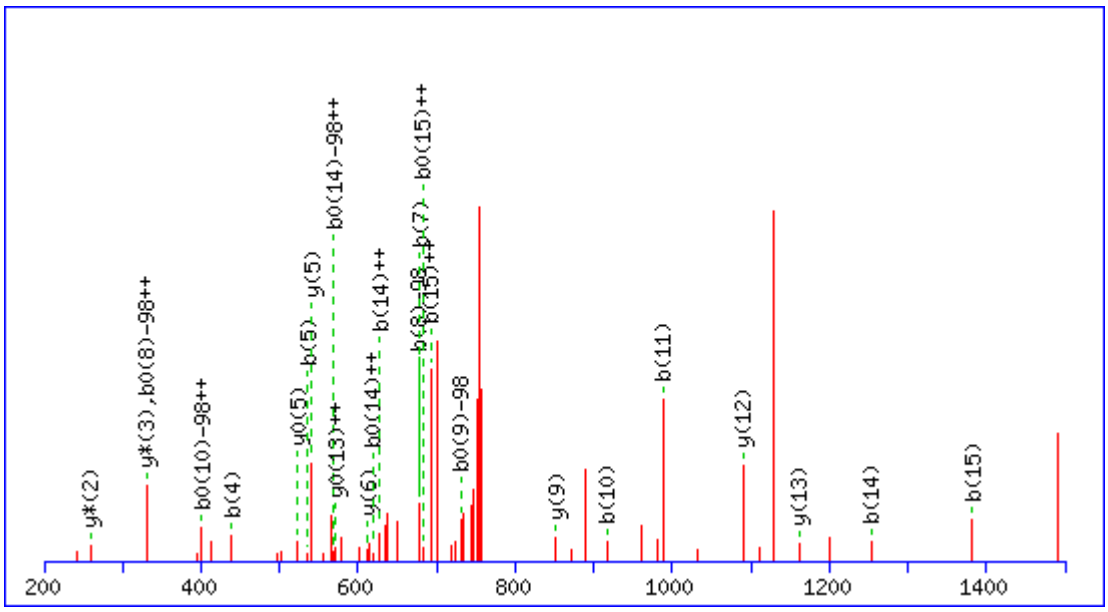
Monoisotopic mass of neutral peptide Mr(calc): 1399.5868 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 31 Expect: 0.078 (help)

#	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							13
2	189.0870	95.0471			171.0764	86.0418	S	1201.5695	601.2884	1184.5430	592.7751	1183.5590	592.2831	12
3	318.1296	159.5684			300.1190	150.5631	E	1114.5375	557.7724	1097.5109	549.2591	1096.5269	548.7671	11
4	433.1565	217.0819			415.1460	208.0766	D	985.4949	493.2511	968.4684	484.7378	967.4843	484.2458	10
5	534.2042	267.6057			516.1936	258.6005	T	870.4680	435.7376	853.4414	427.2243	852.4574	426.7323	9
6	621.2362	311.1218			603.2257	302.1165	S	769.4203	385.2138	752.3937	376.7005	751.4097	376.2085	8
7	708.2683	354.6378			690.2577	345.6325	S	682.3883	341.6978	665.3617	333.1845	664.3777	332.6925	7
8	765.2897	383.1485			747.2792	374.1432	G	595.3562	298.1817	578.3297	289.6685	577.3457	289.1765	6
9	834.3112	417.6592			816.3006	408.6539	S	538.3348	269.6710	521.3082	261.1577	520.3242	260.6657	5
10	931.3639	466.1856			913.3534	457.1803	P	469.3133	235.1603	452.2867	226.6470			4
11	1028.4167	514.7120			1010.4061	505.7067	P	372.2605	186.6339	355.2340	178.1206			3
12	1156.5117	578.7595	1139.4851	570.2462	1138.5011	569.7542	K	275.2078	138.1075	258.1812	129.5942			2
13							K	147.1128	74.0600	130.0863	65.5468			1



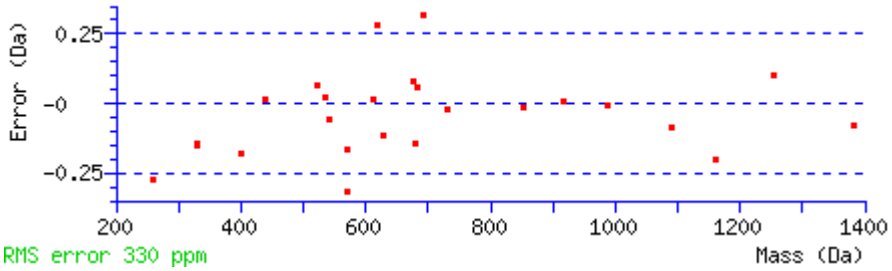


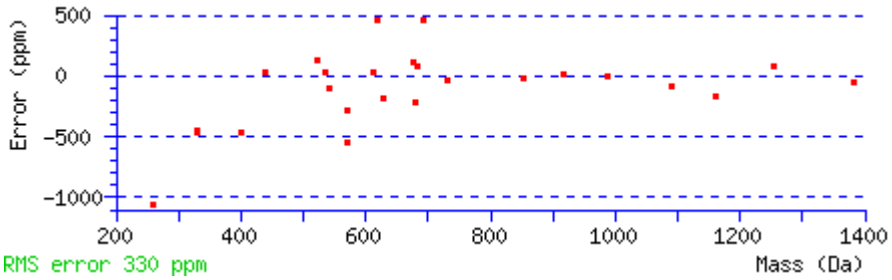
IDENTIFICATION 135
MS/MS Fragmentation of SEAAPAAPAAAPPAEK
Found in IPI00223713



Monoisotopic mass of neutral peptide Mr(calc): 1527.6970 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S1 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 27 Expect: 0.27 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	168.0056	84.5065	149.9951	75.5012	S							16
2	297.0482	149.0278	279.0377	140.0225	E	1361.7060	681.3566	1344.6794	672.8433	1343.6954	672.3513	15
3	368.0853	184.5463	350.0748	175.5410	A	1232.6634	616.8353	1215.6368	608.3220	1214.6528	607.8300	14
4	439.1225	220.0649	421.1119	211.0596	A	1161.6263	581.3168	1144.5997	572.8035	1143.6157	572.3115	13
5	536.1752	268.5912	518.1647	259.5860	P	1090.5891	545.7982	1073.5626	537.2849	1072.5786	536.7929	12
6	607.2123	304.1098	589.2018	295.1045	A	993.5364	497.2718	976.5098	488.7585	975.5258	488.2665	11
7	678.2494	339.6284	660.2389	330.6231	A	922.4993	461.7533	905.4727	453.2400	904.4887	452.7480	10
8	775.3022	388.1547	757.2916	379.1495	P	851.4621	426.2347	834.4356	417.7214	833.4516	417.2294	9
9	846.3393	423.6733	828.3288	414.6680	A	754.4094	377.7083	737.3828	369.1951	736.3988	368.7030	8
10	917.3764	459.1919	899.3659	450.1866	A	683.3723	342.1898	666.3457	333.6765	665.3617	333.1845	7
11	988.4136	494.7104	970.4030	485.7051	A	612.3352	306.6712	595.3086	298.1579	594.3246	297.6659	6
12	1085.4663	543.2368	1067.4558	534.2315	P	541.2980	271.1527	524.2715	262.6394	523.2875	262.1474	5
13	1182.5191	591.7632	1164.5085	582.7579	P	444.2453	222.6263	427.2187	214.1130	426.2347	213.6210	4
14	1253.5562	627.2817	1235.5456	618.2765	A	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
15	1382.5988	691.8030	1364.5882	682.7977	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
16					K	147.1128	74.0600	130.0863	65.5468			1





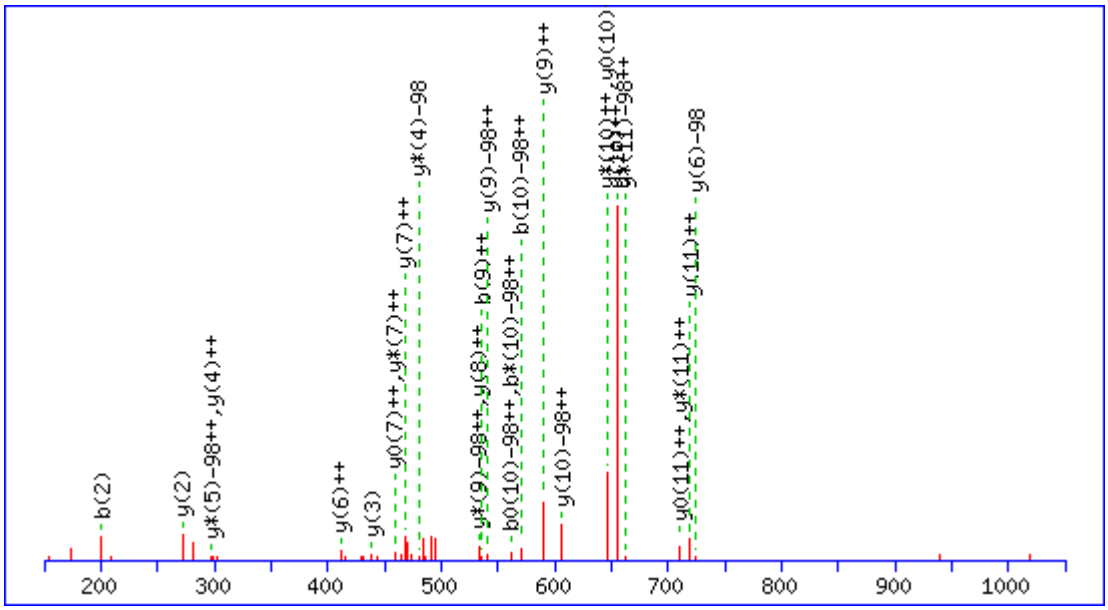
RMS error 330 ppm

IDENTIFICATION 136

MS/MS Fragmentation of

AEEDEILNRSPR

Found in IPI00119618



Monoisotopic mass of neutral peptide Mr(calc):

1507.6667

Fixed modifications:

Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S10 :

Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score:

29

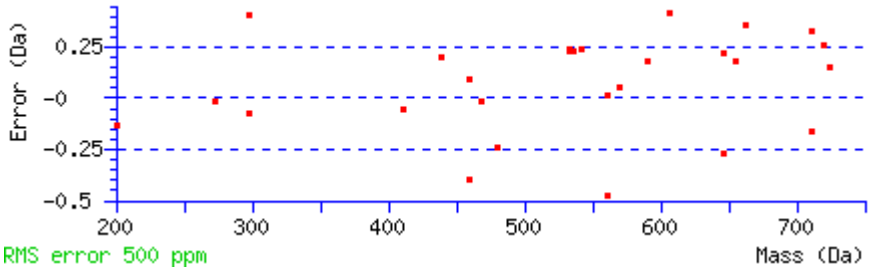
Expect:

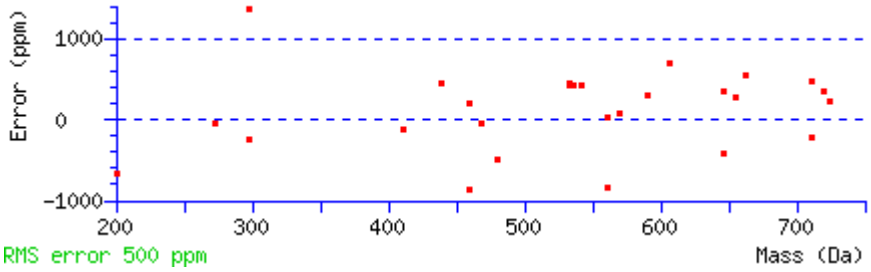
0.17 (

help

)

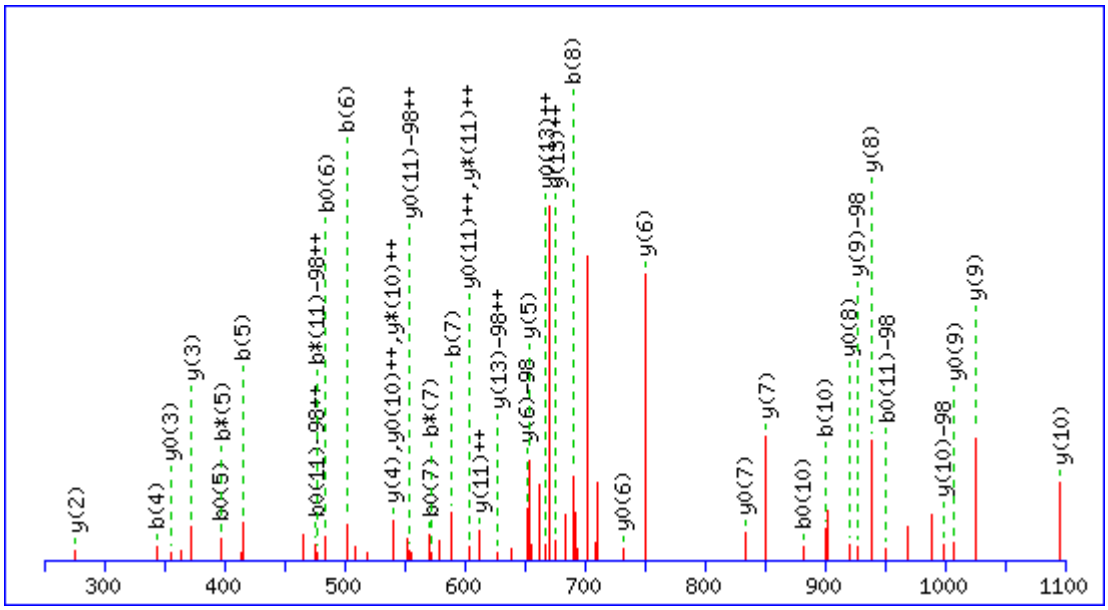
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	72.0444	36.5258					A							12
2	201.0870	101.0471			183.0764	92.0418	E	1437.6370	719.3221	1420.6104	710.8088	1419.6264	710.3168	11
3	330.1296	165.5684			312.1190	156.5631	E	1308.5944	654.8008	1291.5678	646.2875	1290.5838	645.7955	10
4	445.1565	223.0819			427.1460	214.0766	D	1179.5518	590.2795	1162.5252	581.7663	1161.5412	581.2742	9
5	574.1991	287.6032			556.1885	278.5979	E	1064.5248	532.7661	1047.4983	524.2528	1046.5143	523.7608	8
6	687.2832	344.1452			669.2726	335.1399	I	935.4822	468.2448	918.4557	459.7315	917.4717	459.2395	7
7	800.3672	400.6873			782.3567	391.6820	L	822.3982	411.7027	805.3716	403.1895	804.3876	402.6974	6
8	914.4102	457.7087	897.3836	449.1954	896.3996	448.7034	N	709.3141	355.1607	692.2876	346.6474	691.3035	346.1554	5
9	1070.5113	535.7593	1053.4847	527.2460	1052.5007	526.7540	R	595.2712	298.1392	578.2446	289.6260	577.2606	289.1339	4
10	1237.5096	619.2585	1220.4831	610.7452	1219.4991	610.2532	S	439.1701	220.0887	422.1435	211.5754	421.1595	211.0834	3
11	1334.5624	667.7848	1317.5359	659.2716	1316.5518	658.7796	P	272.1717	136.5895	255.1452	128.0762			2
12							R	175.1190	88.0631	158.0924	79.5498			1


Error (Da)
0.25
-0
-0.25
-0.5
200
300
400
500
600
700
RMS error 500 ppm
Mass (Da)


Error (ppm)
1000
0
-1000
200
300
400
500
600
700
RMS error 500 ppm
Mass (Da)

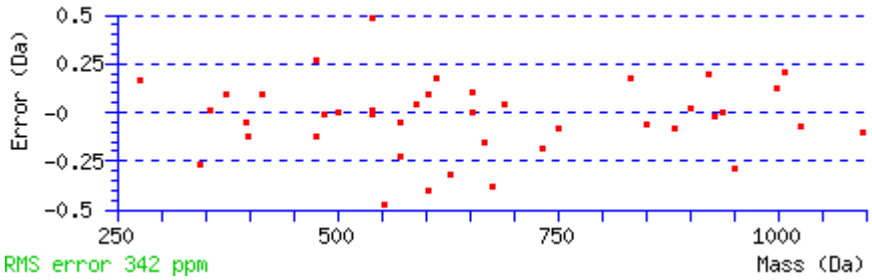
IDENTIFICATION 137
MS/MS Fragmentation of
SGAQASSTPLSPTR

Found in IPI00400300

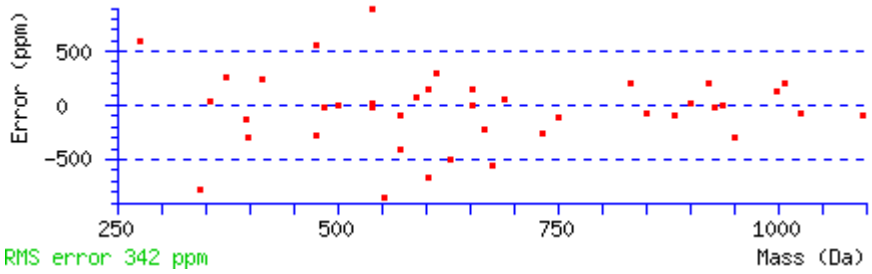


Monoisotopic mass of neutral peptide Mr(calc): 1438.6453
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S11 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 69 Expect: 1.7e-05 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							14
2	145.0608	73.0340			127.0502	64.0287	G	1352.6206	676.8139	1335.5940	668.3007	1334.6100	667.8086	13
3	216.0979	108.5526			198.0873	99.5473	A	1295.5991	648.3032	1278.5726	639.7899	1277.5886	639.2979	12
4	344.1565	172.5819	327.1299	164.0686	326.1459	163.5766	Q	1224.5620	612.7846	1207.5355	604.2714	1206.5514	603.7794	11
5	415.1936	208.1004	398.1670	199.5872	397.1830	199.0951	A	1096.5034	548.7554	1079.4769	540.2421	1078.4929	539.7501	10
6	502.2256	251.6164	485.1991	243.1032	484.2150	242.6112	S	1025.4663	513.2368	1008.4398	504.7235	1007.4558	504.2315	9
7	589.2576	295.1325	572.2311	286.6192	571.2471	286.1272	S	938.4343	469.7208	921.4077	461.2075	920.4237	460.7155	8
8	690.3053	345.6563	673.2788	337.1430	672.2947	336.6510	T	851.4023	426.2048	834.3757	417.6915	833.3917	417.1995	7
9	787.3581	394.1827	770.3315	385.6694	769.3475	385.1774	P	750.3546	375.6809	733.3280	367.1677	732.3440	366.6756	6
10	900.4421	450.7247	883.4156	442.2114	882.4316	441.7194	L	653.3018	327.1545	636.2753	318.6413	635.2913	318.1493	5
11	1067.4405	534.2239	1050.4139	525.7106	1049.4299	525.2186	S	540.2178	270.6125	523.1912	262.0992	522.2072	261.6072	4
12	1164.4933	582.7503	1147.4667	574.2370	1146.4827	573.7450	P	373.2194	187.1133	356.1928	178.6001	355.2088	178.1081	3
13	1265.5409	633.2741	1248.5144	624.7608	1247.5304	624.2688	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

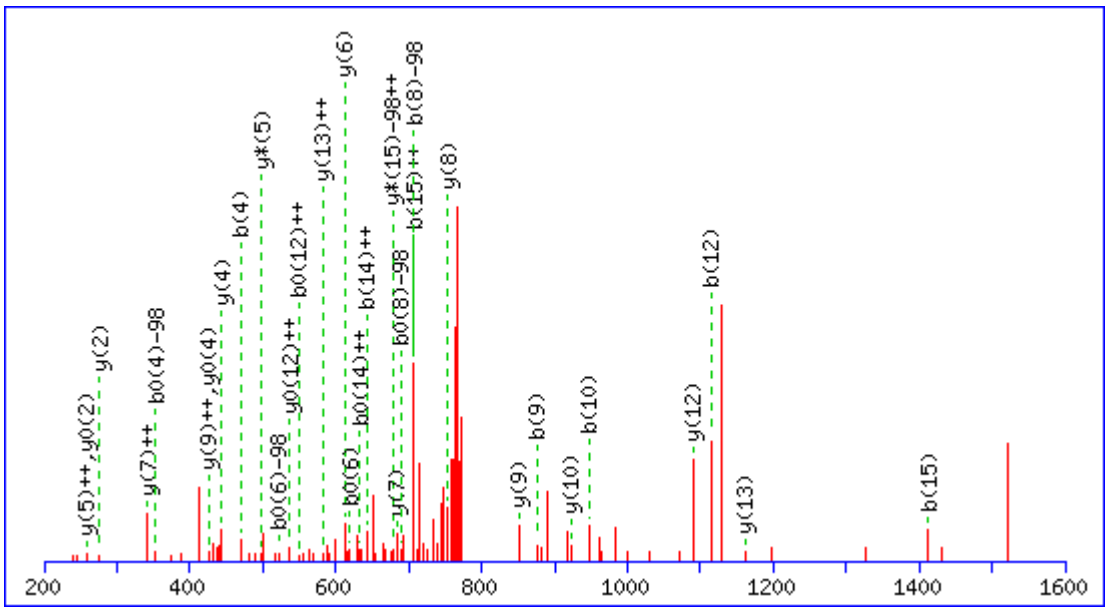


RMS error 342 ppm



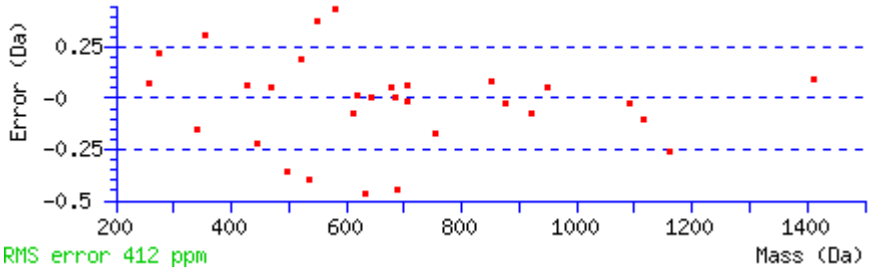
RMS error 342 ppm

IDENTIFICATION 138
MS/MS Fragmentation of SETAPAAPAAPAPAEK
Found in IPI00223714

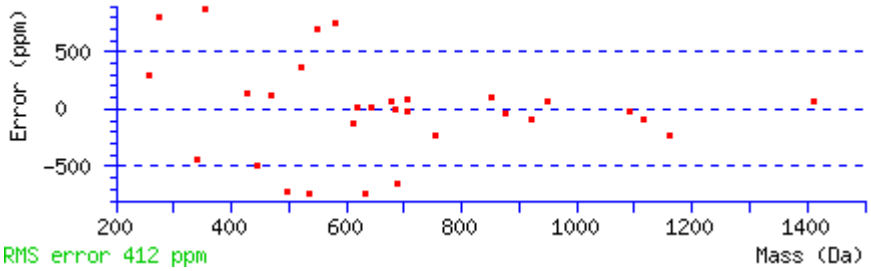


Monoisotopic mass of neutral peptide Mr(calc): 1557.7076
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.072 (help)

#	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							16
2	217.0819	109.0446	199.0713	100.0393	E	1471.6829	736.3451	1454.6563	727.8318	1453.6723	727.3398	15
3	398.0959	199.5516	380.0853	190.5463	T	1342.6403	671.8238	1325.6137	663.3105	1324.6297	662.8185	14
4	469.1330	235.0701	451.1225	226.0649	A	1161.6263	581.3168	1144.5997	572.8035	1143.6157	572.3115	13
5	566.1858	283.5965	548.1752	274.5912	P	1090.5891	545.7982	1073.5626	537.2849	1072.5786	536.7929	12
6	637.2229	319.1151	619.2123	310.1098	A	993.5364	497.2718	976.5098	488.7586	975.5258	488.2665	11
7	708.2600	354.6336	690.2494	345.6284	A	922.4993	461.7533	905.4727	453.2400	904.4887	452.7480	10
8	805.3128	403.1600	787.3022	394.1547	P	851.4621	426.2347	834.4356	417.7214	833.4516	417.2294	9
9	876.3499	438.6786	858.3393	429.6733	A	754.4094	377.7083	737.3828	369.1951	736.3988	368.7030	8
10	947.3870	474.1971	929.3764	465.1919	A	683.3723	342.1898	666.3457	333.6765	665.3617	333.1845	7
11	1044.4398	522.7235	1026.4292	513.7182	P	612.3352	306.6712	595.3086	298.1579	594.3246	297.6659	6
12	1115.4769	558.2421	1097.4663	549.2368	A	515.2824	258.1448	498.2558	249.6316	497.2718	249.1396	5
13	1212.5296	606.7685	1194.5191	597.7632	P	444.2453	222.6263	427.2187	214.1130	426.2347	213.6210	4
14	1283.5668	642.2870	1265.5562	633.2817	A	347.1925	174.0999	330.1660	165.5866	329.1819	165.0946	3
15	1412.6094	706.8083	1394.5988	697.8030	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
16					K	147.1128	74.0600	130.0863	65.5468			1



RMS error 412 ppm



RMS error 412 ppm

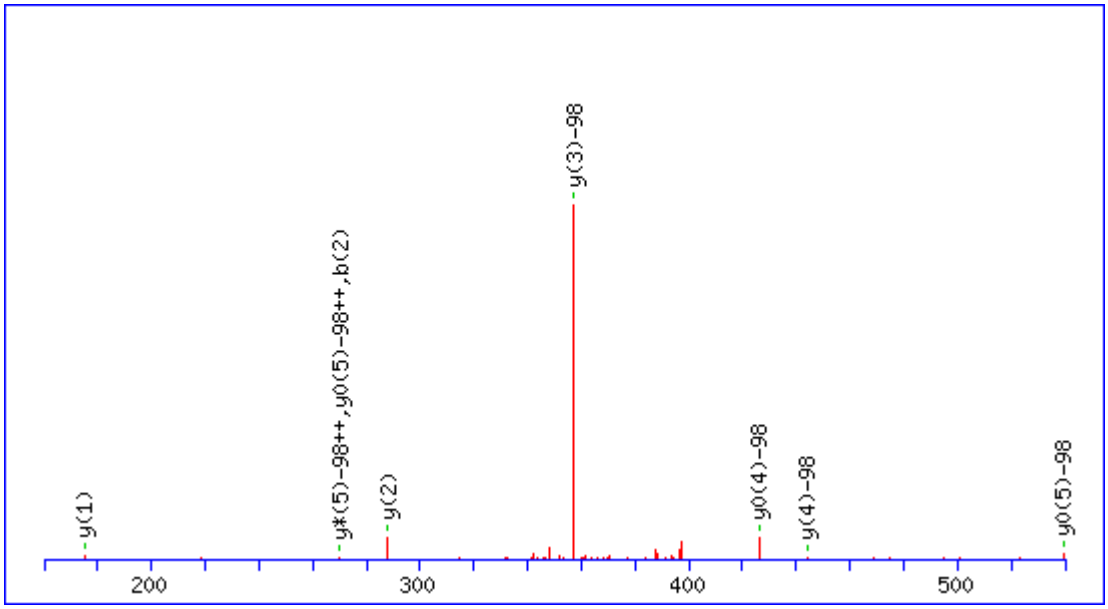
IDENTIFICATION 139

MS/MS Fragmentation of

RLSSLR

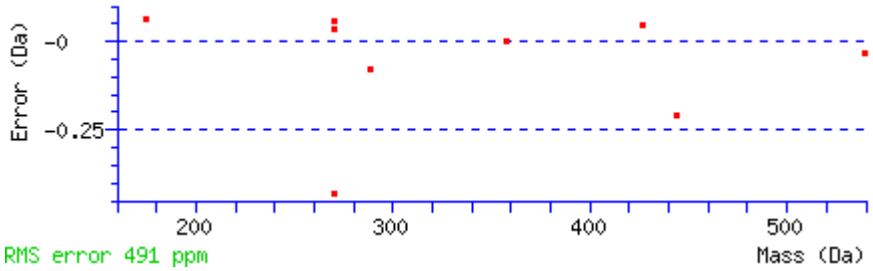
Found in

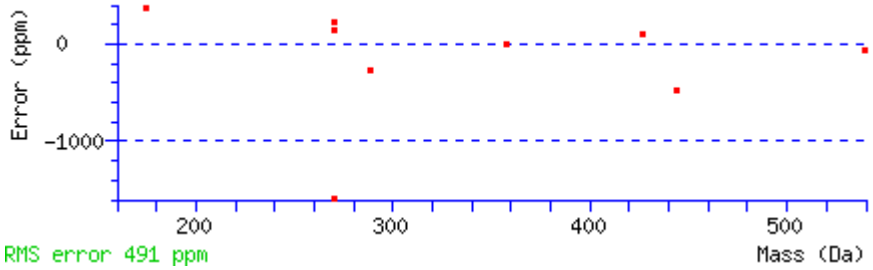
IPI00108454



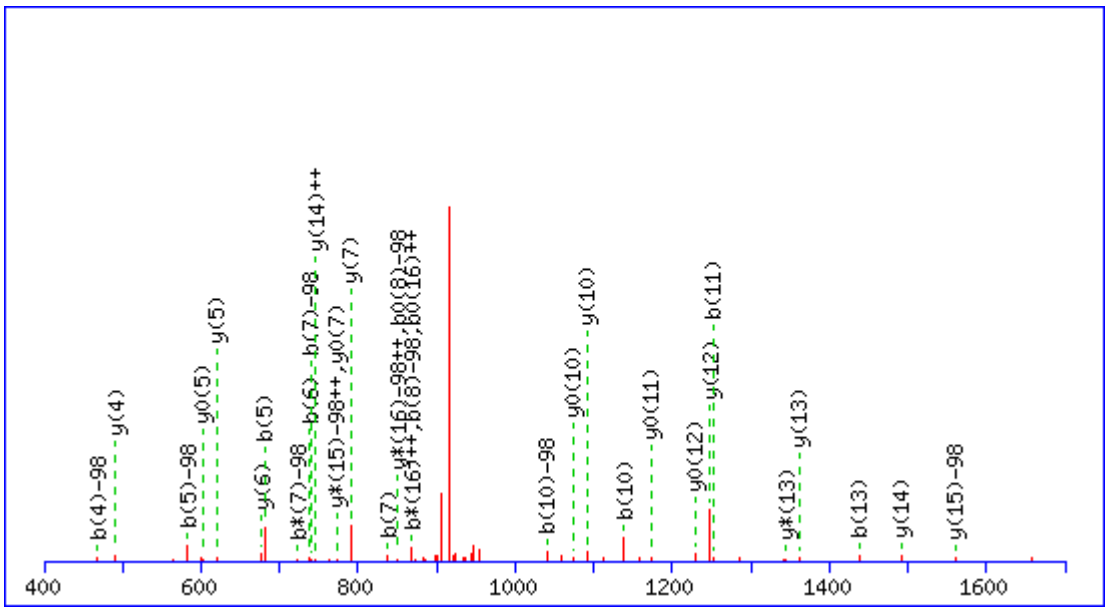
Monoisotopic mass of neutral peptide Mr(calc): 810.4113 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 38 Expect: 0.0065 (help)

#	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							6
2	270.1925	135.5999	253.1659	127.0866			L	557.3406	279.1739	540.3140	270.6606	539.3300	270.1686	5
3	357.2245	179.1159	340.1979	170.6026	339.2139	170.1106	S	444.2565	222.6319	427.2300	214.1186	426.2459	213.6266	4
4	426.2459	213.6266	409.2194	205.1133	408.2354	204.6213	S	357.2245	179.1159	340.1979	170.6026	339.2139	170.1106	3
5	539.3300	270.1686	522.3035	261.6554	521.3194	261.1634	L	288.2030	144.6051	271.1765	136.0919			2
6							R	175.1190	88.0631	158.0924	79.5498			1


Error (Da)
-0
-0.25
200
300
400
500
RMS error 491 ppm
Mass (Da)

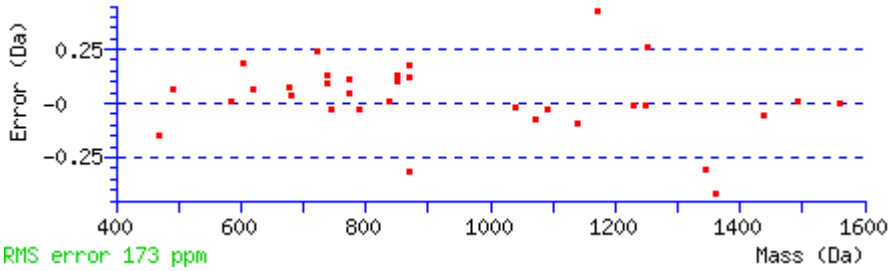

Error (ppm)
0
-1000
200
300
400
500
RMS error 491 ppm
Mass (Da)

IDENTIFICATION 140
MS/MS Fragmentation of LRSEDGVEGDLGETQSR
Found in IPI00553798

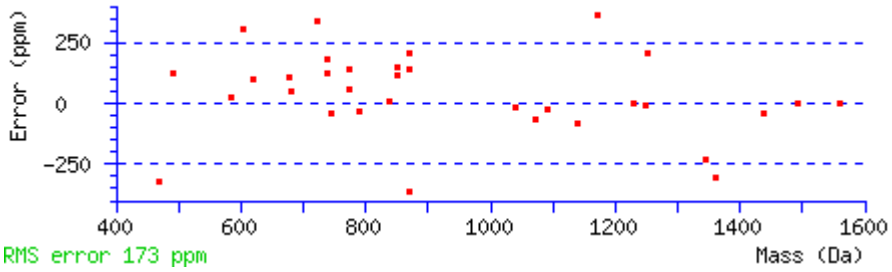


Monoisotopic mass of neutral peptide Mr(calc): 1926.8320 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S3 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 67 Expect: 3.8e-05 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					L							17
2	270.1925	135.5999	253.1659	127.0866			R	1716.7783	858.8928	1699.7518	850.3795	1698.7678	849.8875	16
3	339.2139	170.1106	322.1874	161.5973	321.2033	161.1053	S	1560.6772	780.8423	1543.6507	772.3290	1542.6667	771.8370	15
4	468.2565	234.6319	451.2300	226.1186	450.2459	225.6266	E	1491.6558	746.3315	1474.6292	737.8182	1473.6452	737.3262	14
5	583.2835	292.1454	566.2569	283.6321	565.2729	283.1401	D	1362.6132	681.8102	1345.5866	673.2970	1344.6026	672.8049	13
6	640.3049	320.6561	623.2784	312.1428	622.2943	311.6508	G	1247.5862	624.2968	1230.5597	615.7835	1229.5757	615.2915	12
7	739.3733	370.1903	722.3468	361.6770	721.3628	361.1850	V	1190.5648	595.7860	1173.5382	587.2727	1172.5542	586.7807	11
8	868.4159	434.7116	851.3894	426.1983	850.4054	425.7063	E	1091.4964	546.2518	1074.4698	537.7385	1073.4858	537.2465	10
9	925.4374	463.2223	908.4108	454.7091	907.4268	454.2170	G	962.4538	481.7305	945.4272	473.2172	944.4432	472.7252	9
10	1040.4643	520.7358	1023.4378	512.2225	1022.4538	511.7305	D	905.4323	453.2198	888.4058	444.7065	887.4217	444.2145	8
11	1153.5484	577.2778	1136.5218	568.7646	1135.5378	568.2726	L	790.4054	395.7063	773.3788	387.1930	772.3948	386.7010	7
12	1210.5699	605.7886	1193.5433	597.2753	1192.5593	596.7833	G	677.3213	339.1643	660.2947	330.6510	659.3107	330.1590	6
13	1339.6124	670.3099	1322.5859	661.7966	1321.6019	661.3046	E	620.2998	310.6536	603.2733	302.1403	602.2893	301.6483	5
14	1440.6601	720.8337	1423.6336	712.3204	1422.6496	711.8284	T	491.2572	246.1323	474.2307	237.6190	473.2467	237.1270	4
15	1568.7187	784.8630	1551.6922	776.3497	1550.7081	775.8577	Q	390.2096	195.6084	373.1830	187.0951	372.1990	186.6031	3
16	1655.7507	828.3790	1638.7242	819.8657	1637.7402	819.3737	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

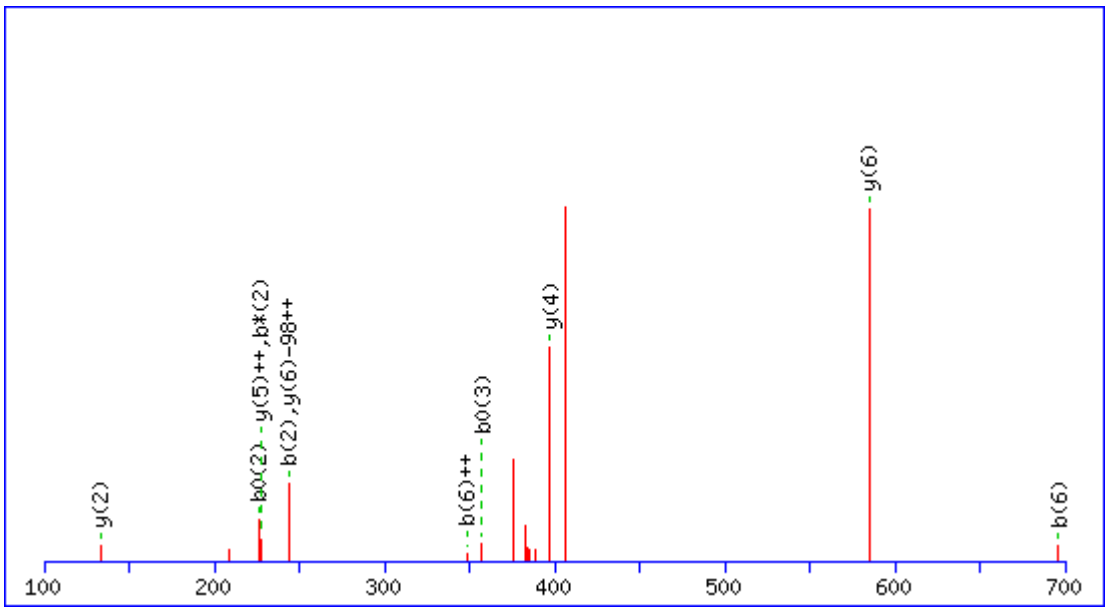


RMS error 173 ppm



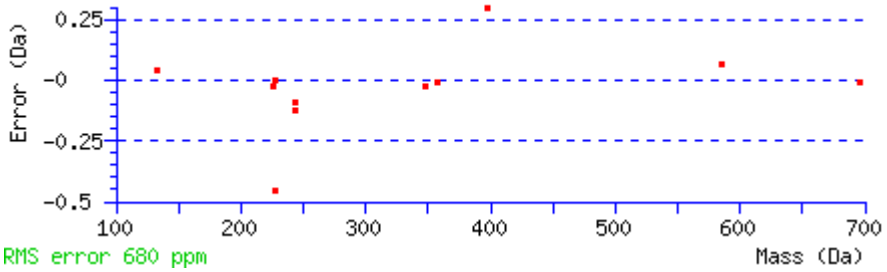
RMS error 173 ppm

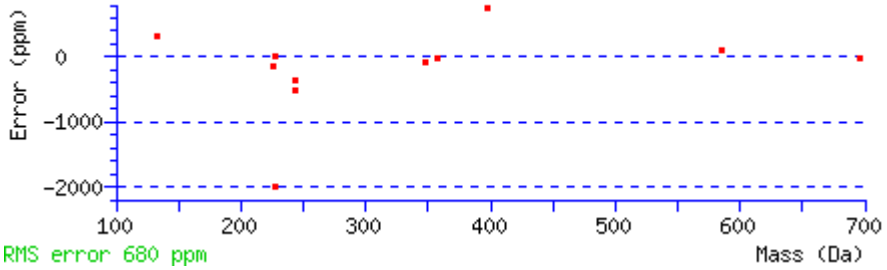
IDENTIFICATION 141
MS/MS Fragmentation of SRMGPSGG
Found in IPI00649088



Monoisotopic mass of neutral peptide Mr(calc): 827.2997 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 26 Expect: 0.083 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							8
2	244.1404	122.5738	227.1139	114.0606	226.1298	113.5686	R	741.2750	371.1411	724.2484	362.6278	723.2644	362.1358	7
3	375.1809	188.0941	358.1544	179.5808	357.1703	179.0888	M	585.1738	293.0906			567.1633	284.0853	6
4	432.2024	216.6048	415.1758	208.0915	414.1918	207.5995	G	454.1334	227.5703			436.1228	218.5650	5
5	529.2551	265.1312	512.2286	256.6179	511.2446	256.1259	P	397.1119	199.0596			379.1013	190.0543	4
6	696.2535	348.6304	679.2269	340.1171	678.2429	339.6251	S	300.0591	150.5332			282.0486	141.5279	3
7	753.2750	377.1411	736.2484	368.6278	735.2644	368.1358	G	133.0608	67.0340					2
8							G	76.0393	38.5233					1

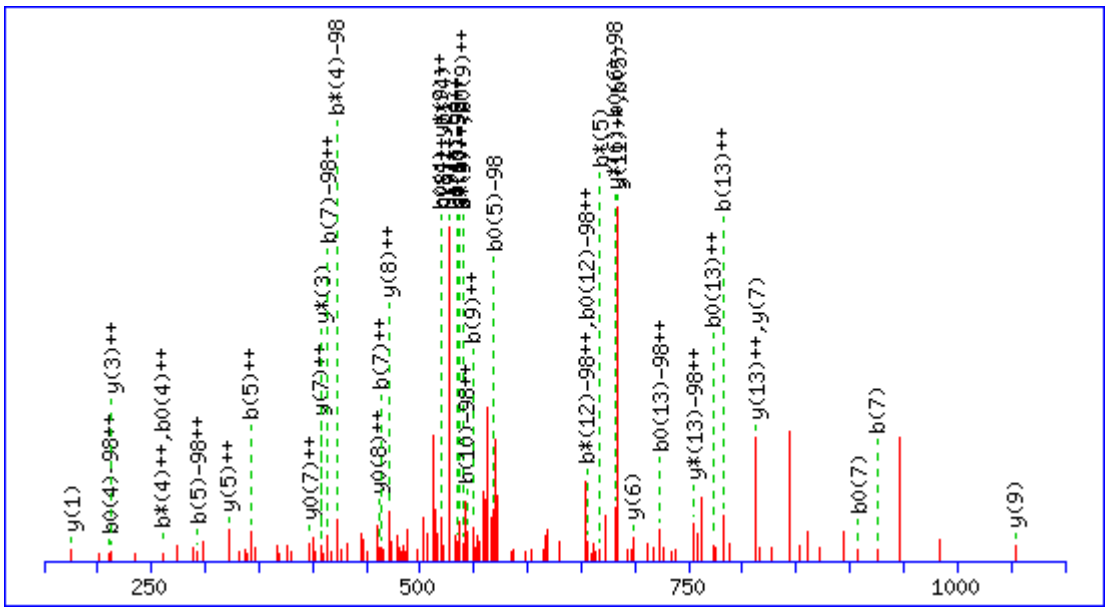




IDENTIFICATION 142

MS/MS Fragmentation of IQKSFIQNGSELHR

Found in IPI00855179



Monoisotopic mass of neutral peptide Mr(calc):

1735.8407

Fixed modifications:

Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S4 :

Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score:

23

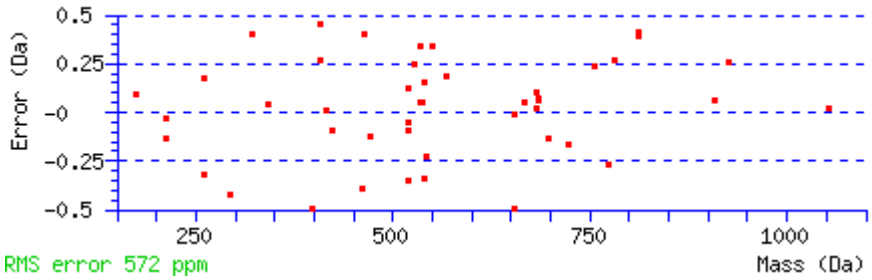
Expect:

0.59 (

help

)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							14
2	242.1499	121.5786	225.1234	113.0653			Q	1623.7639	812.3856	1606.7373	803.8723	1605.7533	803.3803	13
3	370.2449	185.6261	353.2183	177.1128			K	1495.7053	748.3563	1478.6788	739.8430	1477.6948	739.3510	12
4	537.2432	269.1253	520.2167	260.6120	519.2327	260.1200	S	1367.6104	684.3088	1350.5838	675.7955	1349.5998	675.3035	11
5	684.3117	342.6595	667.2851	334.1462	666.3011	333.6542	F	1200.6120	600.8096	1183.5854	592.2964	1182.6014	591.8044	10
6	797.3957	399.2015	780.3692	390.6882	779.3852	390.1962	I	1053.5436	527.2754	1036.5170	518.7622	1035.5330	518.2701	9
7	925.4543	463.2308	908.4277	454.7175	907.4437	454.2255	Q	940.4595	470.7334	923.4330	462.2201	922.4490	461.7281	8
8	1039.4972	520.2522	1022.4707	511.7390	1021.4867	511.2470	N	812.4009	406.7041	795.3744	398.1908	794.3904	397.6988	7
9	1096.5187	548.7630	1079.4921	540.2497	1078.5081	539.7577	G	698.3580	349.6826	681.3315	341.1694	680.3474	340.6774	6
10	1183.5507	592.2790	1166.5242	583.7657	1165.5402	583.2737	S	641.3365	321.1719	624.3100	312.6586	623.3260	312.1666	5
11	1312.5933	656.8003	1295.5668	648.2870	1294.5827	647.7950	E	554.3045	277.6559	537.2780	269.1426	536.2940	268.6506	4
12	1425.6774	713.3423	1408.6508	704.8290	1407.6668	704.3370	L	425.2619	213.1346	408.2354	204.6213			3
13	1562.7363	781.8718	1545.7097	773.3585	1544.7257	772.8665	H	312.1779	156.5926	295.1513	148.0793			2
14							R	175.1190	88.0631	158.0924	79.5498			1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0.25
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-0.5
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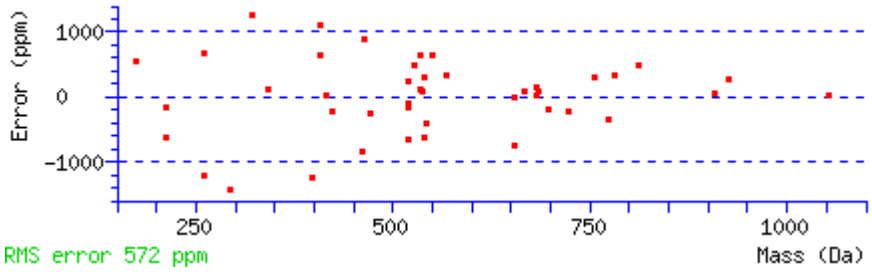
500
750
1000
Mass (Da)
RMS error 572 ppm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Error (ppm)
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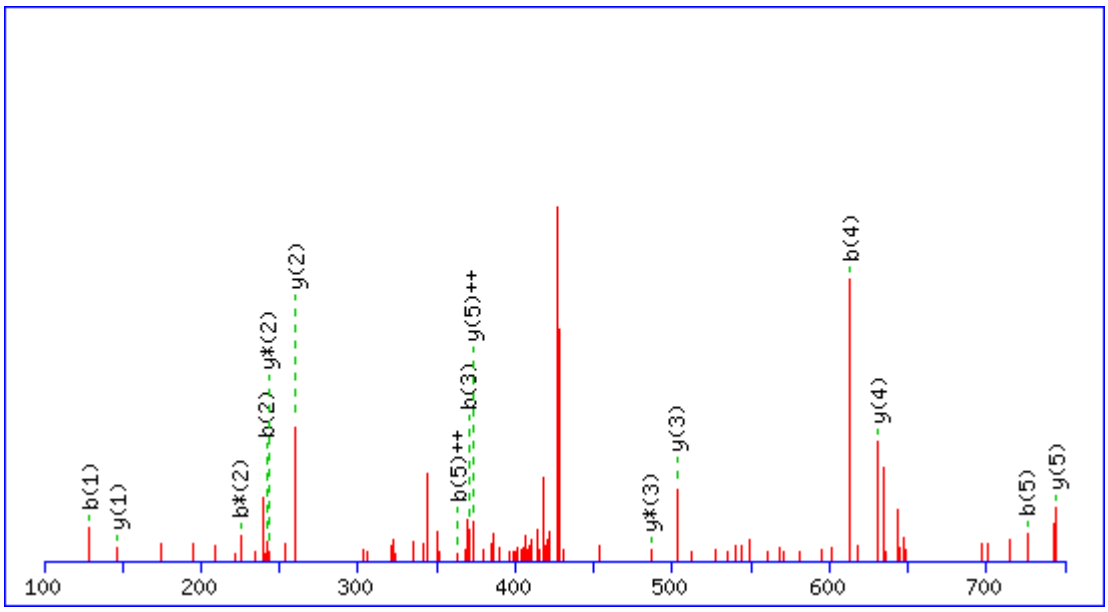
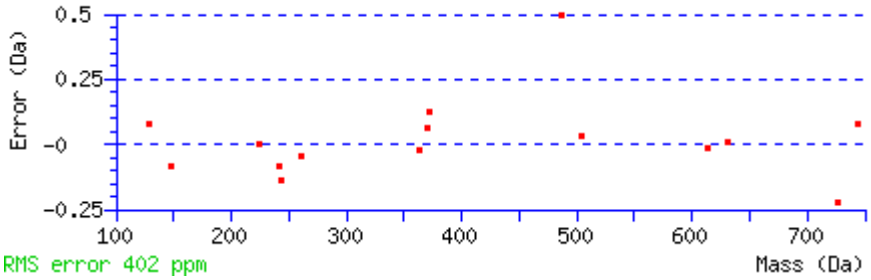
750
1000
Mass (Da)
RMS error 572 ppm

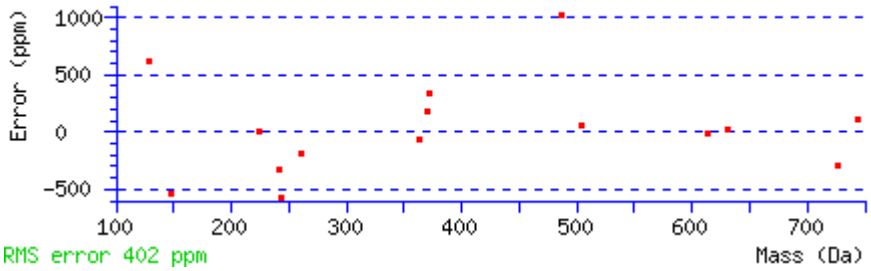
IDENTIFICATION 143
MS/MS Fragmentation of QLQYLK
Found in IPI00129298



Monoisotopic mass of neutral peptide Mr(calc): 871.4204 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: Y4 : Phospho (Y) Ions Score: 33 Expect: 0.027 (help)

#	b	b^{++}	b*	b^{*++}	Seq.	y	y^{++}	y*	y^{*++}	#
1	129.0659	65.0366	112.0393	56.5233	Q					6
2	242.1499	121.5786	225.1234	113.0653	L	744.3692	372.6882	727.3426	364.1749	5
3	370.2085	185.6079	353.1819	177.0946	Q	631.2851	316.1462	614.2586	307.6329	4
4	613.2382	307.1227	596.2116	298.6094	Y	503.2265	252.1169	486.2000	243.6036	3
5	726.3222	363.6647	709.2957	355.1515	L	260.1969	130.6021	243.1703	122.0888	2
6					K	147.1128	74.0600	130.0863	65.5468	1



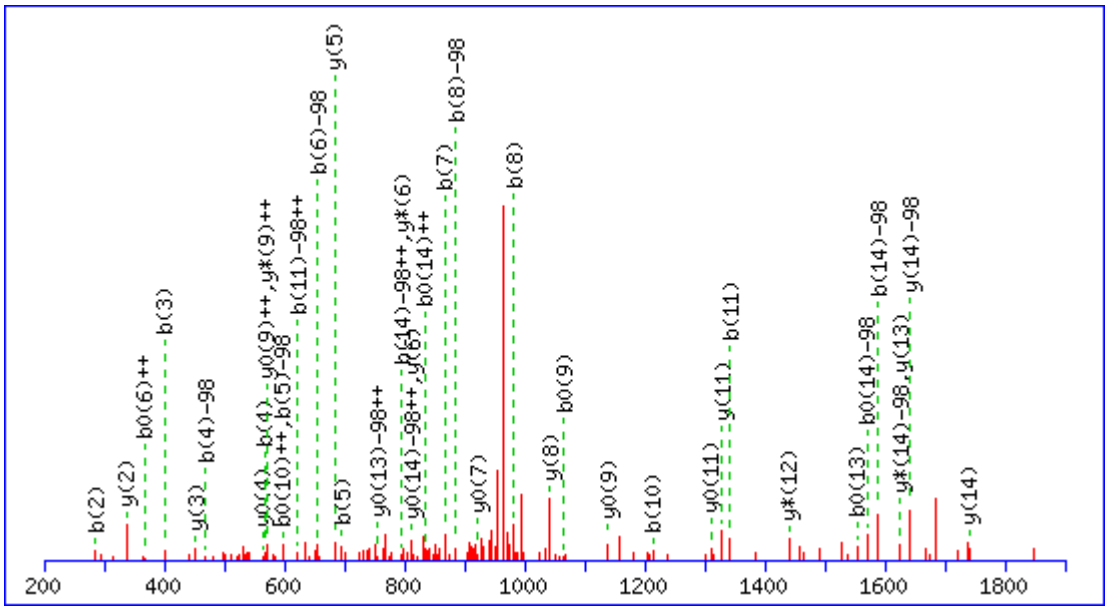


IDENTIFICATION 144

MS/MS Fragmentation of FHDSEGDDTEETEDYR

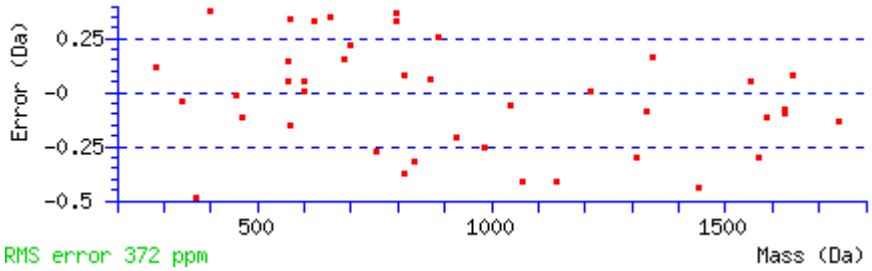
Found in

IPI00169477

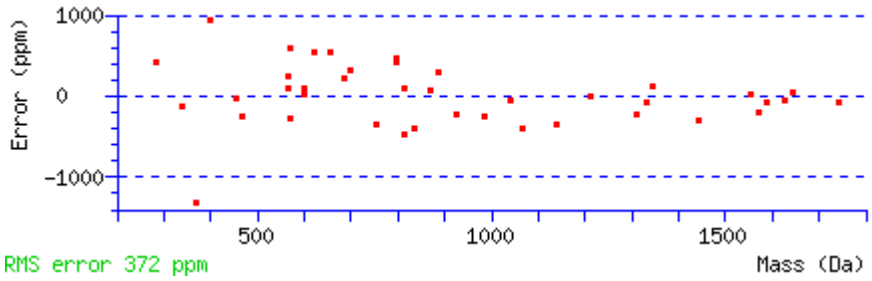


Monoisotopic mass of neutral peptide Mr(calc): 2023.6956
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 33 Expect: 0.035 (help)

#	b	b^{++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415			F							16
2	285.1346	143.0709			H	1877.6345	939.3209	1860.6080	930.8076	1859.6240	930.3156	15
3	400.1615	200.5844	382.1510	191.5791	D	1740.5756	870.7914	1723.5491	862.2782	1722.5650	861.7862	14
4	567.1599	284.0836	549.1493	275.0783	S	1625.5487	813.2780	1608.5221	804.7647	1607.5381	804.2727	13
5	696.2025	348.6049	678.1919	339.5996	E	1458.5503	729.7788	1441.5238	721.2655	1440.5397	720.7735	12
6	753.2240	377.1156	735.2134	368.1103	G	1329.5077	665.2575	1312.4812	656.7442	1311.4971	656.2522	11
7	868.2509	434.6291	850.2403	425.6238	D	1272.4862	636.7468	1255.4597	628.2335	1254.4757	627.7415	10
8	983.2778	492.1426	965.2673	483.1373	D	1157.4593	579.2333	1140.4328	570.7200	1139.4487	570.2280	9
9	1084.3255	542.6664	1066.3150	533.6611	T	1042.4324	521.7198	1025.4058	513.2065	1024.4218	512.7145	8
10	1213.3681	607.1877	1195.3576	598.1824	E	941.3847	471.1960	924.3581	462.6827	923.3741	462.1907	7
11	1342.4107	671.7090	1324.4001	662.7037	E	812.3421	406.6747	795.3155	398.1614	794.3315	397.6694	6
12	1443.4584	722.2328	1425.4478	713.2276	T	683.2995	342.1534	666.2729	333.6401	665.2889	333.1481	5
13	1572.5010	786.7541	1554.4904	777.7488	E	582.2518	291.6295	565.2253	283.1163	564.2413	282.6243	4
14	1687.5279	844.2676	1669.5174	835.2623	D	453.2092	227.1083	436.1827	218.5950	435.1987	218.1030	3
15	1850.5913	925.7993	1832.5807	916.7940	Y	338.1823	169.5948	321.1557	161.0815			2
16					R	175.1190	88.0631	158.0924	79.5498			1



RMS error 372 ppm

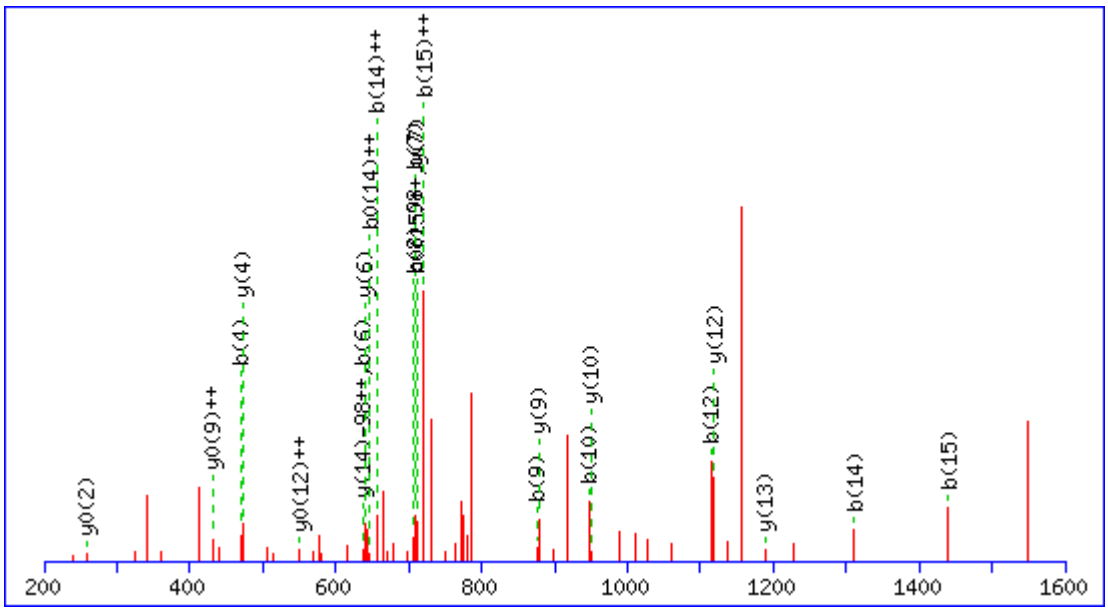


RMS error 372 ppm

IDENTIFICATION 145

MS/MS Fragmentation of SETAPAAPAAPAPVEK

Found in IPI00331597



Monoisotopic mass of neutral peptide Mr(calc): 1585.7389

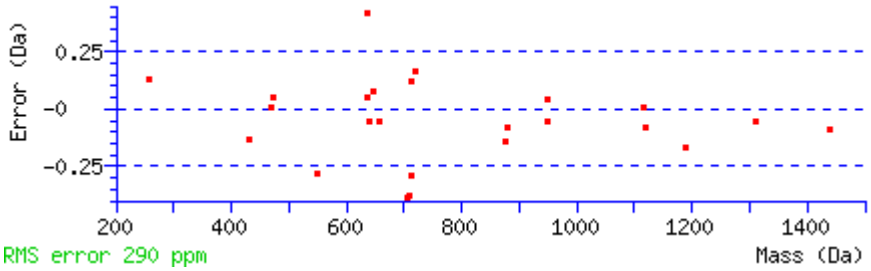
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

T3 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score: 33 Expect: 0.072 (help)

#	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							16
2	217.0819	109.0446	199.0713	100.0393	E	1499.7142	750.3607	1482.6876	741.8474	1481.7036	741.3554	15
3	398.0959	199.5516	380.0853	190.5463	T	1370.6716	685.8394	1353.6450	677.3261	1352.6610	676.8341	14
4	469.1330	235.0701	451.1225	226.0649	A	1189.6576	595.3324	1172.6310	586.8191	1171.6470	586.3271	13
5	566.1858	283.5965	548.1752	274.5912	P	1118.6204	559.8139	1101.5939	551.3006	1100.6099	550.8086	12
6	637.2229	319.1151	619.2123	310.1098	A	1021.5677	511.2875	1004.5411	502.7742	1003.5571	502.2822	11
7	708.2600	354.6336	690.2494	345.6284	A	950.5306	475.7689	933.5040	467.2556	932.5200	466.7636	10
8	805.3128	403.1600	787.3022	394.1547	P	879.4934	440.2504	862.4669	431.7371	861.4829	431.2451	9
9	876.3499	438.6786	858.3393	429.6733	A	782.4407	391.7240	765.4141	383.2107	764.4301	382.7187	8
10	947.3870	474.1971	929.3764	465.1919	A	711.4036	356.2054	694.3770	347.6921	693.3930	347.2001	7
11	1044.4398	522.7235	1026.4292	513.7182	P	640.3665	320.6869	623.3399	312.1736	622.3559	311.6816	6
12	1115.4769	558.2421	1097.4663	549.2368	A	543.3137	272.1605	526.2871	263.6472	525.3031	263.1552	5
13	1212.5296	606.7685	1194.5191	597.7632	P	472.2766	236.6419	455.2500	228.1287	454.2660	227.6366	4
14	1311.5981	656.3027	1293.5875	647.2974	V	375.2238	188.1155	358.1973	179.6023	357.2132	179.1103	3
15	1440.6407	720.8240	1422.6301	711.8187	E	276.1554	138.5813	259.1288	130.0681	258.1448	129.5761	2
16					K	147.1128	74.0600	130.0863	65.5468			1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400
600
800
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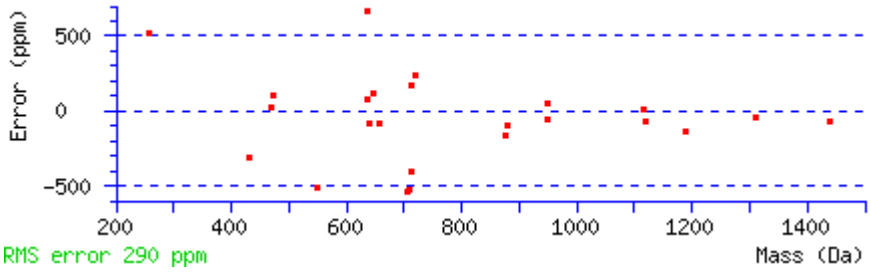
1200
1400
Mass (Da)
RMS error 290 ppm


Error (ppm)
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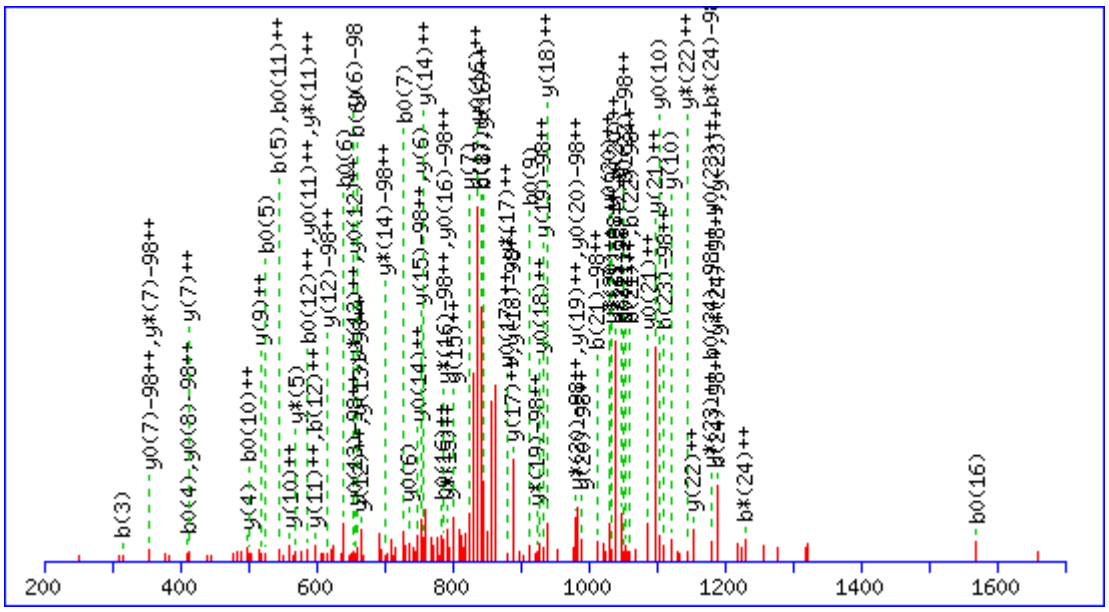
0
-500
200
400
600
800
1000
1200
1400
Mass (Da)
RMS error 290 ppm

IDENTIFICATION 146

MS/MS Fragmentation of EDALDDSVSSSSVHASPLASSPVRK

Found in IPI00337844



Monoisotopic mass of neutral peptide Mr(calc):

2620.2018

Fixed modifications:

Carbamidomethyl (C) (apply to specified residues or termini only)

Variable modifications:

S20 :

Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

Ions Score:

59

Expect:

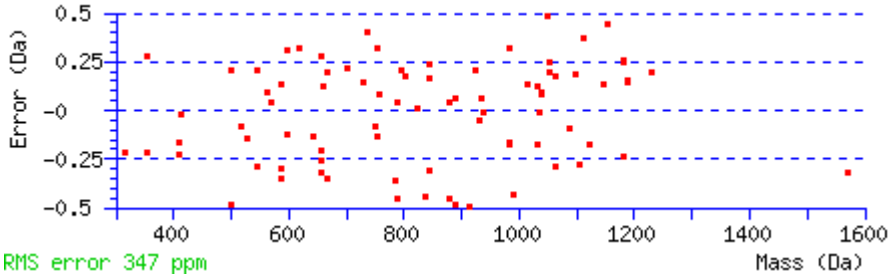
0.00024 (

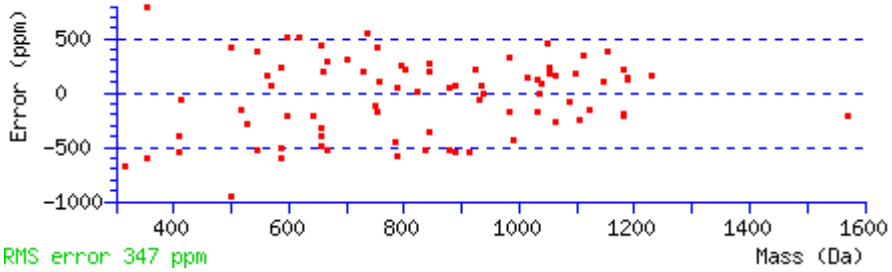
help

)

#	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							25
2	245.0768	123.0420			227.0662	114.0368	D	2492.1665	1246.5869	2475.1399	1238.0736	2474.1559	1237.5816	24
3	316.1139	158.5606			298.1034	149.5553	A	2377.1395	1189.0734	2360.1130	1180.5601	2359.1289	1180.0681	23
4	429.1980	215.1026			411.1874	206.0974	L	2306.1024	1153.5548	2289.0758	1145.0416	2288.0918	1144.5496	22
5	544.2249	272.6161			526.2144	263.6108	D	2193.0183	1097.0128	2175.9918	1088.4995	2175.0078	1088.0075	21
6	659.2519	330.1296			641.2413	321.1243	D	2077.9914	1039.4993	2060.9648	1030.9861	2059.9808	1030.4940	20
7	746.2839	373.6456			728.2733	364.6403	S	1962.9644	981.9859	1945.9379	973.4726	1944.9539	972.9806	19
8	845.3523	423.1798			827.3418	414.1745	V	1875.9324	938.4698	1858.9059	929.9566	1857.9219	929.4646	18
9	932.3843	466.6958			914.3738	457.6905	S	1776.8640	888.9356	1759.8375	880.4224	1758.8534	879.9304	17
10	1019.4164	510.2118			1001.4058	501.2065	S	1689.8320	845.4196	1672.8054	836.9064	1671.8214	836.4143	16
11	1106.4484	553.7278			1088.4378	544.7226	S	1602.7999	801.9036	1585.7734	793.3903	1584.7894	792.8983	15
12	1193.4804	597.2439			1175.4699	588.2386	S	1515.7679	758.3876	1498.7414	749.8743	1497.7574	749.3823	14
13	1292.5488	646.7781			1274.5383	637.7728	V	1428.7359	714.8716	1411.7093	706.3583	1410.7253	705.8663	13
14	1429.6078	715.3075			1411.5972	706.3022	H	1329.6675	665.3374	1312.6409	656.8241	1311.6569	656.3321	12

15	1500.6449	750.8261			1482.6343	741.8208	A	1192.6086	596.8079	1175.5820	588.2946	1174.5980	587.8026	11
16	1587.6769	794.3421			1569.6663	785.3368	S	1121.5714	561.2894	1104.5449	552.7761	1103.5609	552.2841	10
17	1684.7297	842.8685			1666.7191	833.8632	P	1034.5394	517.7733	1017.5129	509.2601	1016.5289	508.7681	9
18	1797.8137	899.4105			1779.8032	890.4052	L	937.4867	469.2470	920.4601	460.7337	919.4761	460.2417	8
19	1868.8508	934.9291			1850.8403	925.9238	A	824.4026	412.7049	807.3760	404.1917	806.3920	403.6997	7
20	2035.8492	1018.4282			2017.8386	1009.4230	S	753.3655	377.1864	736.3389	368.6731	735.3549	368.1811	6
21	2122.8812	1061.9443			2104.8707	1052.9390	S	586.3671	293.6872	569.3406	285.1739	568.3566	284.6819	5
22	2219.9340	1110.4706			2201.9234	1101.4654	P	499.3351	250.1712	482.3085	241.6579			4
23	2319.0024	1160.0048			2300.9918	1150.9996	V	402.2823	201.6448	385.2558	193.1315			3
24	2475.1035	1238.0554	2458.0770	1229.5421	2457.0930	1229.0501	R	303.2139	152.1106	286.1874	143.5973			2
25							K	147.1128	74.0600	130.0863	65.5468			1

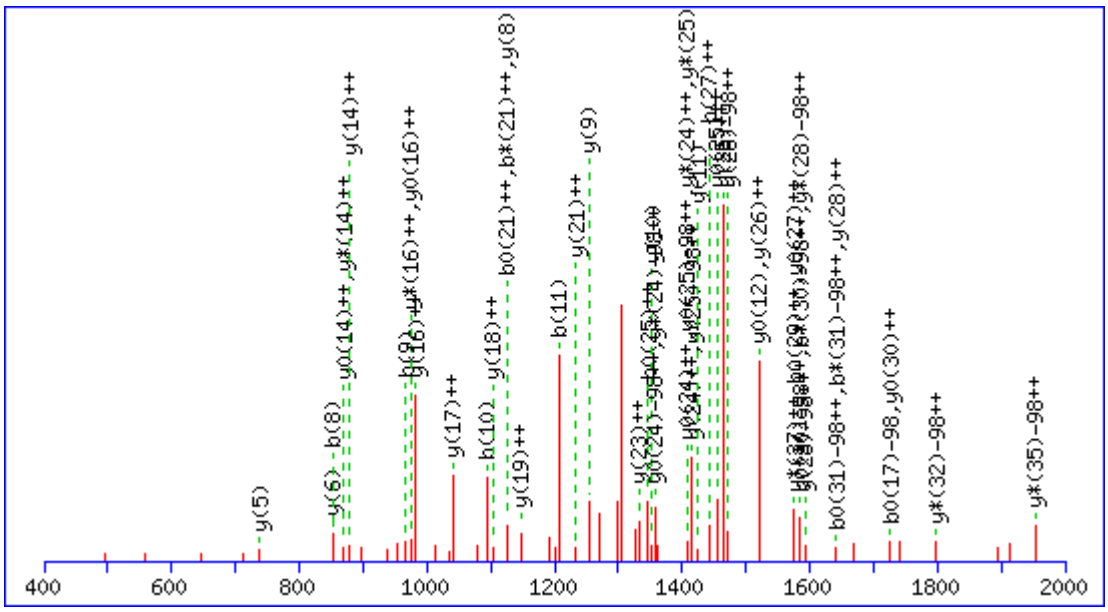




IDENTIFICATION 147

MS/MS Fragmentation of IIPTLEEGLQLPSPTATSQLPLESDAVECLNYQHYK

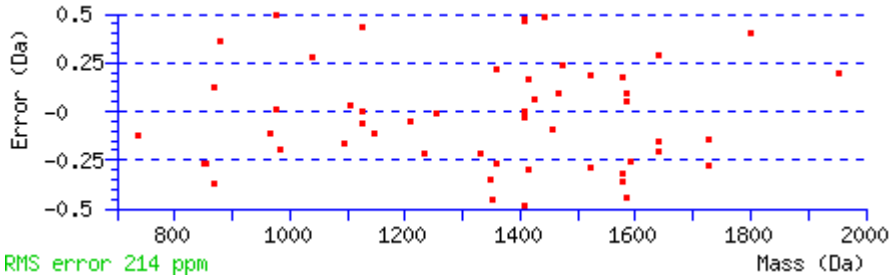
Found in IPI00223253

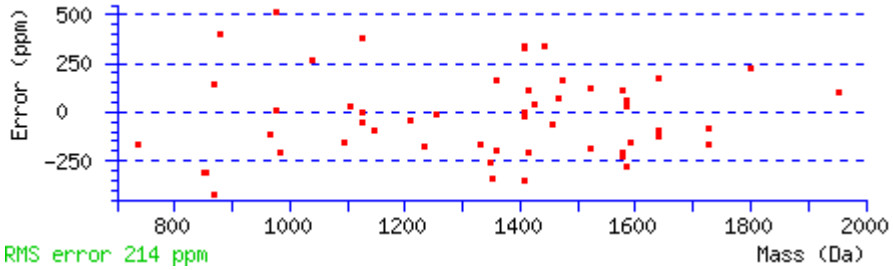


Monoisotopic mass of neutral peptide Mr(calc): 4133.9908 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S13 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 51 Expect: 0.0011 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	114.0913	57.5493					I							36
2	227.1754	114.0913					I	4021.9141	2011.4607	4004.8875	2002.9474	4003.9035	2002.4554	35
3	324.2282	162.6177					P	3908.8300	1954.9186	3891.8034	1946.4054	3890.8194	1945.9134	34
4	425.2758	213.1416			407.2653	204.1363	T	3811.7772	1906.3923	3794.7507	1897.8790	3793.7667	1897.3870	33
5	538.3599	269.6836			520.3493	260.6783	L	3710.7296	1855.8684	3693.7030	1847.3551	3692.7190	1846.8631	32
6	667.4025	334.2049			649.3919	325.1996	E	3597.6455	1799.3264	3580.6189	1790.8131	3579.6349	1790.3211	31
7	796.4451	398.7262			778.4345	389.7209	E	3468.6029	1734.8051	3451.5763	1726.2918	3450.5923	1725.7998	30
8	853.4666	427.2369			835.4560	418.2316	G	3339.5603	1670.2838	3322.5338	1661.7705	3321.5497	1661.2785	29
9	966.5506	483.7790			948.5401	474.7737	L	3282.5388	1641.7731	3265.5123	1633.2598	3264.5283	1632.7678	28
10	1094.6092	547.8082	1077.5827	539.2950	1076.5986	538.8030	Q	3169.4548	1585.2310	3152.4282	1576.7178	3151.4442	1576.2257	27
11	1207.6933	604.3503	1190.6667	595.8370	1189.6827	595.3450	L	3041.3962	1521.2017	3024.3696	1512.6885	3023.3856	1512.1965	26
12	1304.7460	652.8767	1287.7195	644.3634	1286.7355	643.8714	P	2928.3121	1464.6597	2911.2856	1456.1464	2910.3016	1455.6544	25
13	1471.7444	736.3758	1454.7178	727.8626	1453.7338	727.3706	S	2831.2594	1416.1333	2814.2328	1407.6200	2813.2488	1407.1280	24
14	1568.7972	784.9022	1551.7706	776.3889	1550.7866	775.8969	P	2664.2610	1332.6341	2647.2345	1324.1209	2646.2504	1323.6289	23
15	1669.8448	835.4261	1652.8183	826.9128	1651.8343	826.4208	T	2567.2082	1284.1078	2550.1817	1275.5945	2549.1977	1275.1025	22
16	1740.8819	870.9446	1723.8554	862.4313	1722.8714	861.9393	A	2466.1606	1233.5839	2449.1340	1225.0706	2448.1500	1224.5786	21
17	1841.9296	921.4685	1824.9031	912.9552	1823.9191	912.4632	T	2395.1235	1198.0654	2378.0969	1189.5521	2377.1129	1189.0601	20
18	1928.9617	964.9845	1911.9351	956.4712	1910.9511	955.9792	S	2294.0758	1147.5415	2277.0492	1139.0283	2276.0652	1138.5362	19
19	2057.0202	1029.0138	2039.9937	1020.5005	2039.0097	1020.0085	Q	2207.0437	1104.0255	2190.0172	1095.5122	2189.0332	1095.0202	18
20	2170.1043	1085.5558	2153.0777	1077.0425	2152.0937	1076.5505	L	2078.9852	1039.9962	2061.9586	1031.4829	2060.9746	1030.9909	17
21	2267.1571	1134.0822	2250.1305	1125.5689	2249.1465	1125.0769	P	1965.9011	983.4542	1948.8746	974.9409	1947.8905	974.4489	16
22	2380.2411	1190.6242	2363.2146	1182.1109	2362.2306	1181.6189	L	1868.8483	934.9278	1851.8218	926.4145	1850.8378	925.9225	15
23	2509.2837	1255.1455	2492.2572	1246.6322	2491.2732	1246.1402	E	1755.7643	878.3858	1738.7377	869.8725	1737.7537	869.3805	14
24	2596.3157	1298.6615	2579.2892	1290.1482	2578.3052	1289.6562	S	1626.7217	813.8645	1609.6951	805.3512	1608.7111	804.8592	13
25	2711.3427	1356.1750	2694.3161	1347.6617	2693.3321	1347.1697	D	1539.6897	770.3485	1522.6631	761.8352	1521.6791	761.3432	12
26	2782.3798	1391.6935	2765.3533	1383.1803	2764.3692	1382.6883	A	1424.6627	712.8350	1407.6362	704.3217	1406.6521	703.8297	11
27	2881.4482	1441.2277	2864.4217	1432.7145	2863.4377	1432.2225	V	1353.6256	677.3164	1336.5991	668.8032	1335.6150	668.3112	10
28	3010.4908	1505.7490	2993.4643	1497.2358	2992.4802	1496.7438	E	1254.5572	627.7822	1237.5306	619.2690	1236.5466	618.7769	9
29	3170.5215	1585.7644	3153.4949	1577.2511	3152.5109	1576.7591	C	1125.5146	563.2609	1108.4880	554.7477			8
30	3283.6055	1642.3064	3266.5790	1633.7931	3265.5950	1633.3011	L	965.4839	483.2456	948.4574	474.7323			7

31	3397.6484	1699.3279	3380.6219	1690.8146	3379.6379	1690.3226	N	852.3999	426.7036	835.3733	418.1903			6
32	3560.7118	1780.8595	3543.6852	1772.3463	3542.7012	1771.8542	Y	738.3570	369.6821	721.3304	361.1688			5
33	3688.7704	1844.8888	3671.7438	1836.3755	3670.7598	1835.8835	Q	575.2936	288.1504	558.2671	279.6372			4
34	3825.8293	1913.4183	3808.8027	1904.9050	3807.8187	1904.4130	H	447.2350	224.1212	430.2085	215.6079			3
35	3988.8926	1994.9499	3971.8660	1986.4367	3970.8820	1985.9447	Y	310.1761	155.5917	293.1496	147.0784			2
36							K	147.1128	74.0600	130.0863	65.5468			1

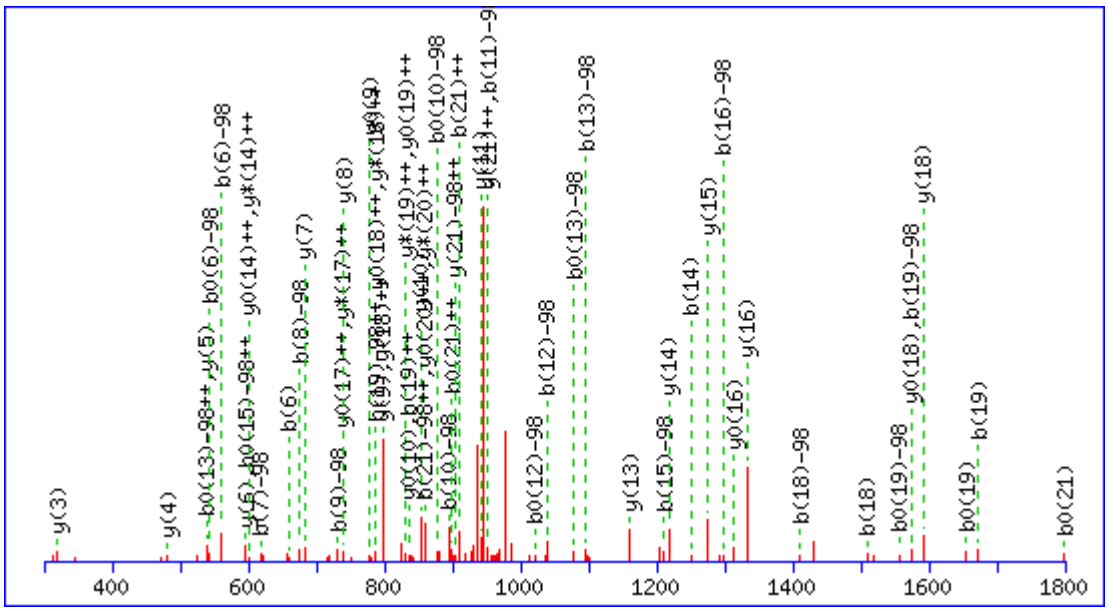




IDENTIFICATION 148

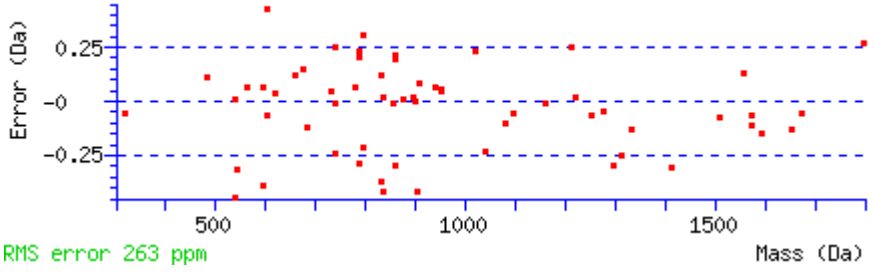
MS/MS Fragmentation of SSGSPYGGGYGSGGGSGGYGSR

Found in IPI00269661

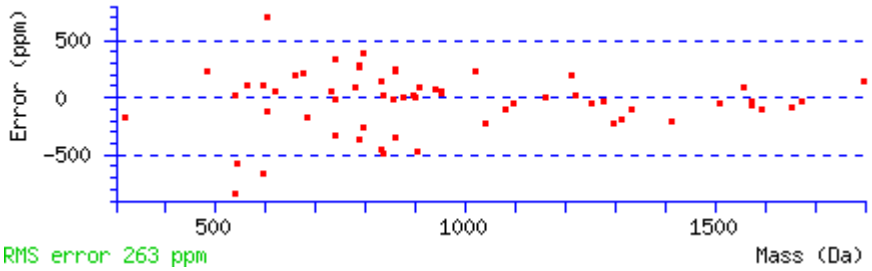


Monoisotopic mass of neutral peptide Mr(calc): 1989.7491 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: S2 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000 Ions Score: 111 Expect: 1e-09 (help)

#	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							22
2	157.0608	79.0340	139.0502	70.0287	S	1805.7474	903.3773	1788.7208	894.8641	1787.7368	894.3720	21
3	214.0822	107.5448	196.0717	98.5395	G	1736.7259	868.8666	1719.6994	860.3533	1718.7154	859.8613	20
4	301.1143	151.0608	283.1037	142.0555	S	1679.7045	840.3559	1662.6779	831.8426	1661.6939	831.3506	19
5	398.1670	199.5871	380.1565	190.5819	P	1592.6724	796.8399	1575.6459	788.3266	1574.6619	787.8346	18
6	561.2304	281.1188	543.2198	272.1135	Y	1495.6197	748.3135	1478.5931	739.8002	1477.6091	739.3082	17
7	618.2518	309.6295	600.2413	300.6243	G	1332.5563	666.7818	1315.5298	658.2685	1314.5458	657.7765	16
8	675.2733	338.1403	657.2627	329.1350	G	1275.5349	638.2711	1258.5083	629.7578	1257.5243	629.2658	15
9	732.2947	366.6510	714.2842	357.6457	G	1218.5134	609.7603	1201.4869	601.2471	1200.5028	600.7551	14
10	895.3581	448.1827	877.3475	439.1774	Y	1161.4919	581.2496	1144.4654	572.7363	1143.4814	572.2443	13
11	952.3795	476.6934	934.3690	467.6881	G	998.4286	499.7179	981.4021	491.2047	980.4180	490.7127	12
12	1039.4116	520.2094	1021.4010	511.2041	S	941.4071	471.2072	924.3806	462.6939	923.3966	462.2019	11
13	1096.4330	548.7202	1078.4225	539.7149	G	854.3751	427.6912	837.3486	419.1779	836.3646	418.6859	10
14	1153.4545	577.2309	1135.4439	568.2256	G	797.3537	399.1805	780.3271	390.6672	779.3431	390.1752	9
15	1210.4760	605.7416	1192.4654	596.7363	G	740.3322	370.6697	723.3056	362.1565	722.3216	361.6645	8
16	1297.5080	649.2576	1279.4974	640.2523	S	683.3107	342.1590	666.2842	333.6457	665.3002	333.1537	7
17	1354.5294	677.7684	1336.5189	668.7631	G	596.2787	298.6430	579.2522	290.1297	578.2681	289.6377	6
18	1411.5509	706.2791	1393.5403	697.2738	G	539.2572	270.1323	522.2307	261.6190	521.2467	261.1270	5
19	1574.6142	787.8108	1556.6037	778.8055	Y	482.2358	241.6215	465.2092	233.1082	464.2252	232.6162	4
20	1631.6357	816.3215	1613.6251	807.3162	G	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
21	1718.6677	859.8375	1700.6572	850.8322	S	262.1510	131.5791	245.1244	123.0659	244.1404	122.5738	2
22					R	175.1190	88.0631	158.0924	79.5498			1



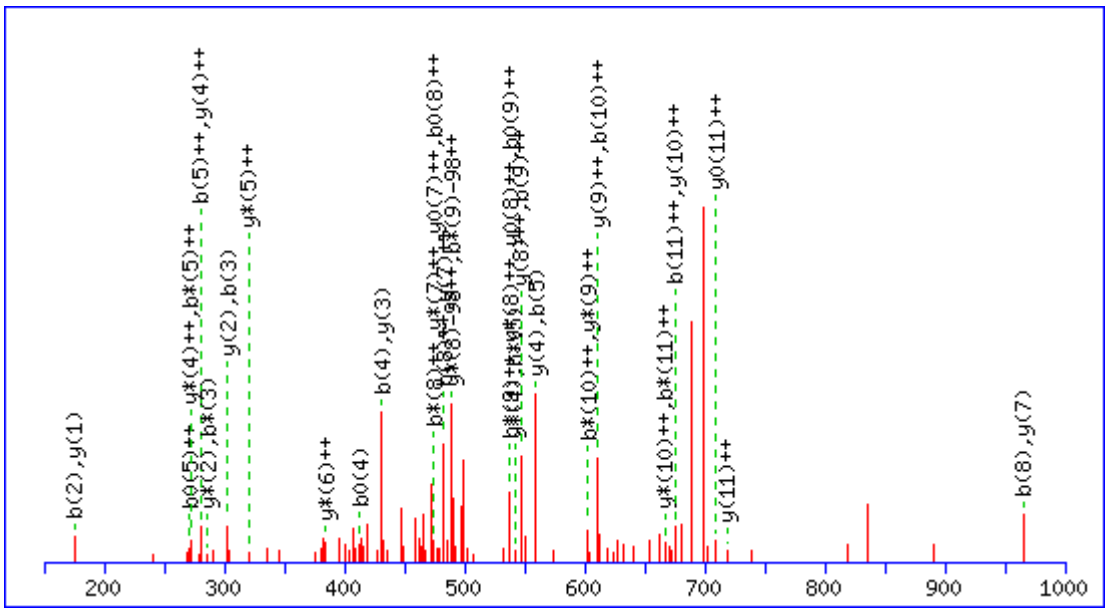
RMS error 263 ppm



RMS error 263 ppm

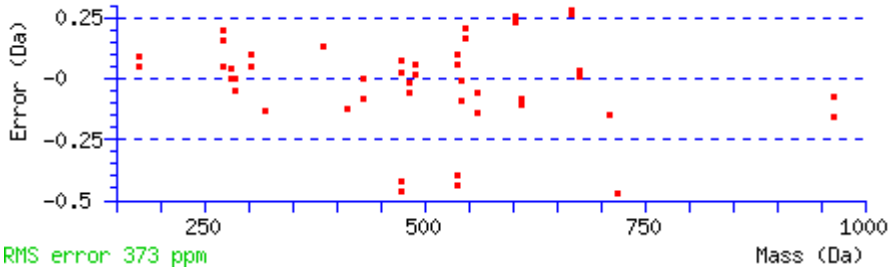
IDENTIFICATION 149

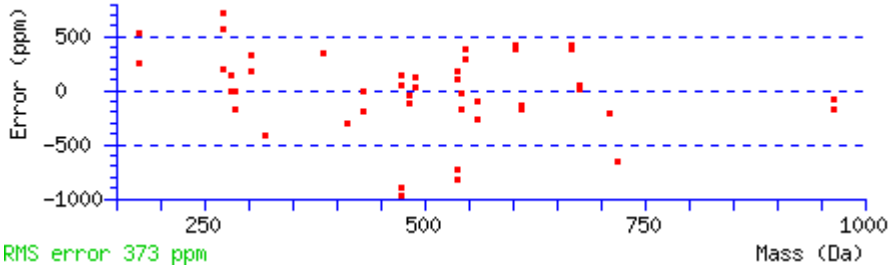
MS/MS Fragmentation of SSQQQTQPQKQR
Found in
IPI00135207



Monoisotopic mass of neutral peptide Mr(calc): 1522.6889 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: T6 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 37 Expect: 0.029 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	88.0393	44.5233			70.0287	35.5180	S							12
2	175.0713	88.0393			157.0608	79.0340	S	1436.6642	718.8357	1419.6376	710.3225	1418.6536	709.8304	11
3	303.1299	152.0686	286.1034	143.5553	285.1193	143.0633	Q	1349.6322	675.3197	1332.6056	666.8064	1331.6216	666.3144	10
4	431.1885	216.0979	414.1619	207.5846	413.1779	207.0926	Q	1221.5736	611.2904	1204.5470	602.7772	1203.5630	602.2851	9
5	559.2471	280.1272	542.2205	271.6139	541.2365	271.1219	Q	1093.5150	547.2611	1076.4885	538.7479	1075.5044	538.2559	8
6	740.2611	370.6342	723.2345	362.1209	722.2505	361.6289	T	965.4564	483.2318	948.4299	474.7186	947.4459	474.2266	7
7	868.3197	434.6635	851.2931	426.1502	850.3091	425.6582	Q	784.4424	392.7248	767.4159	384.2116			6
8	965.3724	483.1898	948.3459	474.6766	947.3619	474.1846	P	656.3838	328.6956	639.3573	320.1823			5
9	1093.4310	547.2191	1076.4044	538.7059	1075.4204	538.2139	Q	559.3311	280.1692	542.3045	271.6559			4
10	1221.5260	611.2666	1204.4994	602.7533	1203.5154	602.2613	K	431.2725	216.1399	414.2459	207.6266			3
11	1349.5845	675.2959	1332.5580	666.7826	1331.5740	666.2906	Q	303.1775	152.0924	286.1510	143.5791			2
12							R	175.1190	88.0631	158.0924	79.5498			1





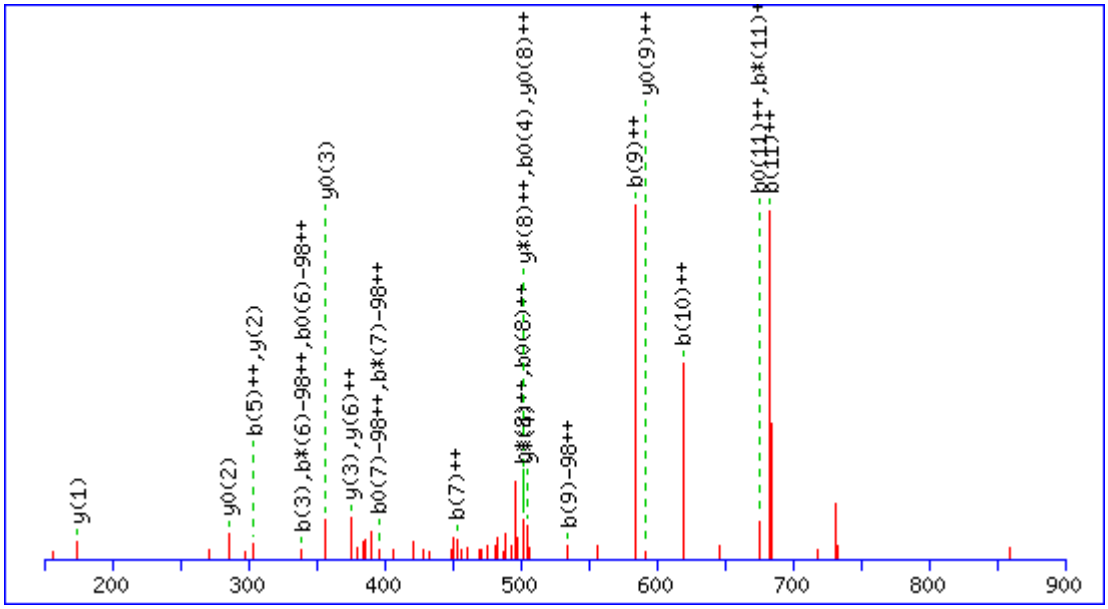
IDENTIFICATION 150

MS/MS Fragmentation of

KPLTSWILFAER

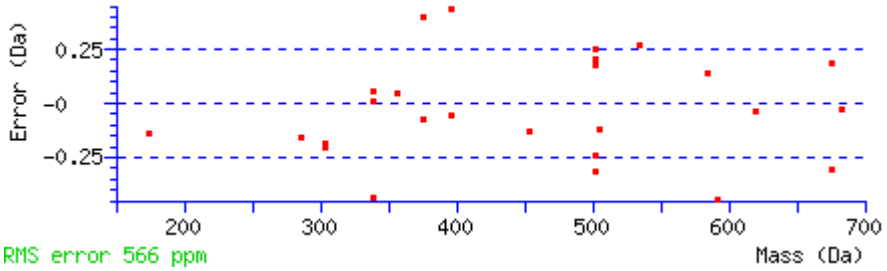
Found in

IPI00756871

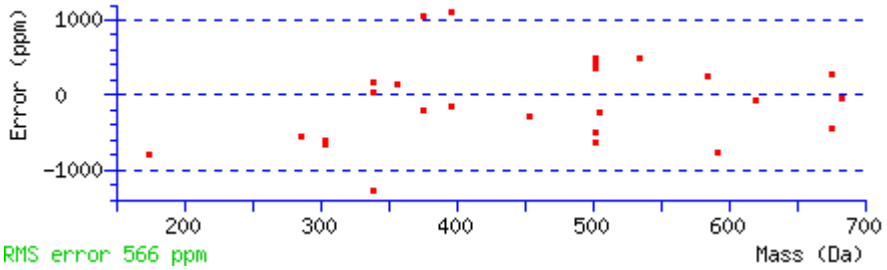


Monoisotopic mass of neutral peptide Mr(calc): 1539.7850 Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only) Variable modifications: T4 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769 Ions Score: 24 Expect: 0.33 (help)

#	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							12
2	226.1550	113.5811	209.1285	105.0679			P	1412.6974	706.8523	1395.6708	698.3391	1394.6868	697.8470	11
3	339.2391	170.1232	322.2125	161.6099			L	1315.6446	658.3259	1298.6181	649.8127	1297.6341	649.3207	10
4	520.2531	260.6302	503.2265	252.1169	502.2425	251.6249	T	1202.5606	601.7839	1185.5340	593.2706	1184.5500	592.7786	9
5	607.2851	304.1462	590.2586	295.6329	589.2745	295.1409	S	1021.5465	511.2769	1004.5200	502.7636	1003.5360	502.2716	8
6	793.3644	397.1858	776.3379	388.6726	775.3539	388.1806	W	934.5145	467.7609	917.4880	459.2476	916.5039	458.7556	7
7	906.4485	453.7279	889.4219	445.2146	888.4379	444.7226	I	748.4352	374.7212	731.4087	366.2080	730.4246	365.7160	6
8	1019.5325	510.2699	1002.5060	501.7566	1001.5220	501.2646	L	635.3511	318.1792	618.3246	309.6659	617.3406	309.1739	5
9	1166.6010	583.8041	1149.5744	575.2908	1148.5904	574.7988	F	522.2671	261.6372	505.2405	253.1239	504.2565	252.6319	4
10	1237.6381	619.3227	1220.6115	610.8094	1219.6275	610.3174	A	375.1987	188.1030	358.1721	179.5897	357.1881	179.0977	3
11	1366.6807	683.8440	1349.6541	675.3307	1348.6701	674.8387	E	304.1615	152.5844	287.1350	144.0711	286.1510	143.5791	2
12							R	175.1190	88.0631	158.0924	79.5498			1

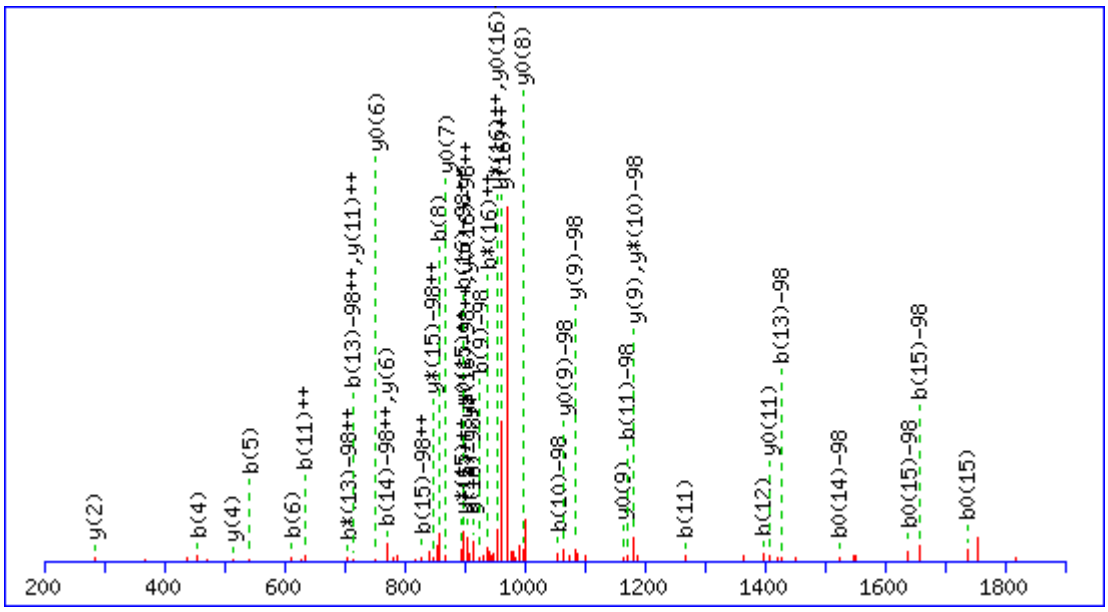


RMS error 566 ppm



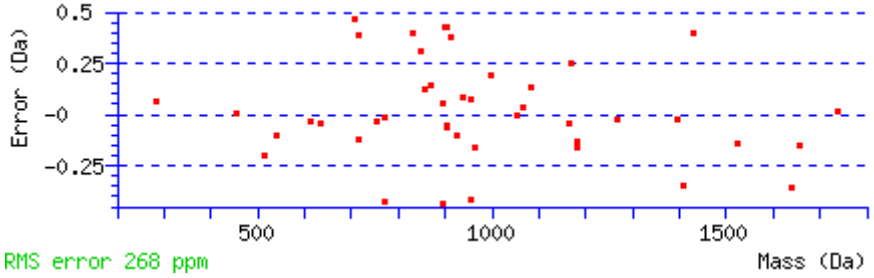
RMS error 566 ppm

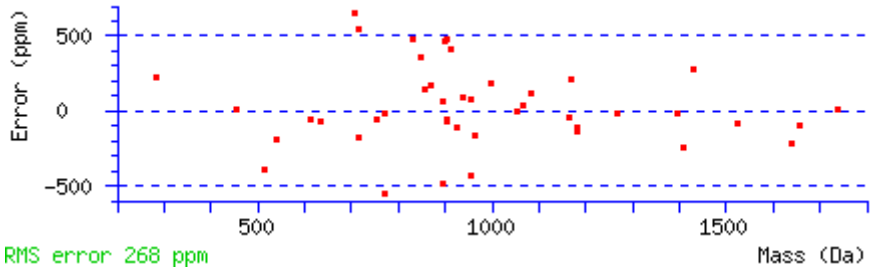
IDENTIFICATION 151
MS/MS Fragmentation of DDSHSAEDSEDEKDDHK
Found in IPI00341869



Monoisotopic mass of neutral peptide Mr(calc): 2037.7073
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S9 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000
Ions Score: 35 Expect: 0.026 (help)

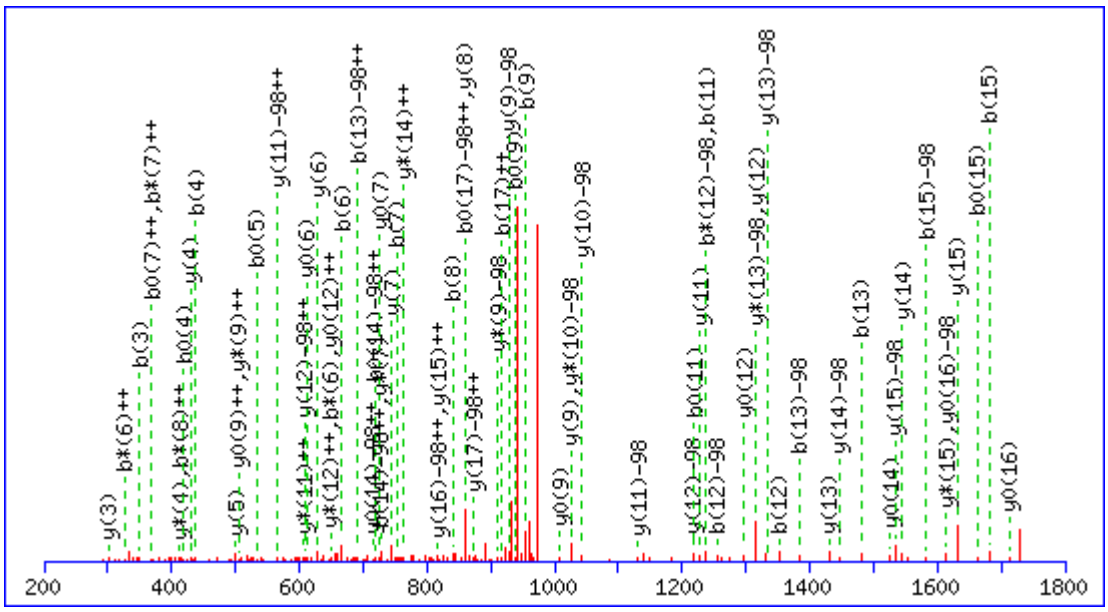
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							17
2	231.0612	116.0342			213.0506	107.0289	D	1825.7107	913.3590	1808.6842	904.8457	1807.7002	904.3537	16
3	318.0932	159.5502			300.0826	150.5450	S	1710.6838	855.8455	1693.6572	847.3323	1692.6732	846.8402	15
4	455.1521	228.0797			437.1415	219.0744	H	1623.6517	812.3295	1606.6252	803.8162	1605.6412	803.3242	14
5	542.1841	271.5957			524.1736	262.5904	S	1486.5928	743.8001	1469.5663	735.2868	1468.5823	734.7948	13
6	613.2212	307.1143			595.2107	298.1090	A	1399.5608	700.2840	1382.5343	691.7708	1381.5502	691.2788	12
7	742.2638	371.6356			724.2533	362.6303	E	1328.5237	664.7655	1311.4971	656.2522	1310.5131	655.7602	11
8	857.2908	429.1490			839.2802	420.1437	D	1199.4811	600.2442	1182.4546	591.7309	1181.4705	591.2389	10
9	926.3122	463.6598			908.3017	454.6545	S	1084.4542	542.7307	1067.4276	534.2174	1066.4436	533.7254	9
10	1055.3548	528.1811			1037.3443	519.1758	E	1015.4327	508.2200	998.4061	499.7067	997.4221	499.2147	8
11	1170.3818	585.6945			1152.3712	576.6892	D	886.3901	443.6987	869.3636	435.1854	868.3795	434.6934	7
12	1299.4244	650.2158			1281.4138	641.2105	E	771.3632	386.1852	754.3366	377.6719	753.3526	377.1799	6
13	1427.5193	714.2633	1410.4928	705.7500	1409.5088	705.2580	K	642.3206	321.6639	625.2940	313.1506	624.3100	312.6586	5
14	1542.5463	771.7768	1525.5197	763.2635	1524.5357	762.7715	D	514.2256	257.6164	497.1991	249.1032	496.2150	248.6112	4
15	1657.5732	829.2902	1640.5467	820.7770	1639.5627	820.2850	D	399.1987	200.1030	382.1721	191.5897	381.1881	191.0977	3
16	1794.6321	897.8197	1777.6056	889.3064	1776.6216	888.8144	H	284.1717	142.5895	267.1452	134.0762			2
17							K	147.1128	74.0600	130.0863	65.5468			1





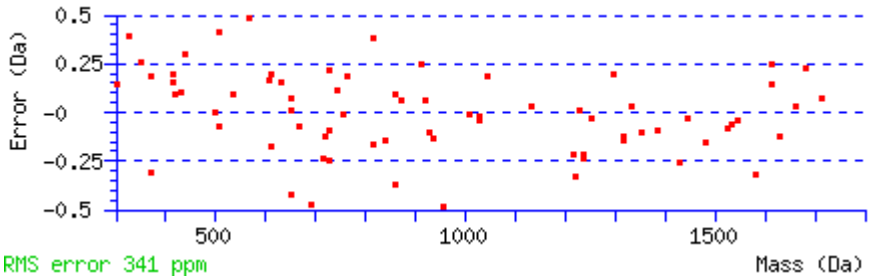
RMS error 268 ppm

IDENTIFICATION 152
MS/MS Fragmentation of HIVSNDSSDSDDEAQGPK
Found in IPI00111169

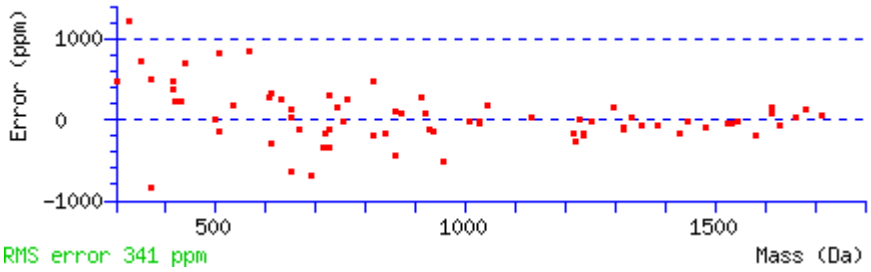


Monoisotopic mass of neutral peptide Mr(calc): 1979.7746
Fixed modifications: Carbamidomethyl (C) (apply to specified residues or termini only)
Variable modifications:
S10 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769
Ions Score: 65 Expect: 5.2e-05 (help)

#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	138.0662	69.5367					H							18
2	251.1503	126.0788					I	1843.7229	922.3651	1826.6964	913.8518	1825.7124	913.3598	17
3	350.2187	175.6130					V	1730.6389	865.8231	1713.6123	857.3098	1712.6283	856.8178	16
4	437.2507	219.1290			419.2401	210.1237	S	1631.5705	816.2889	1614.5439	807.7756	1613.5599	807.2836	15
5	551.2936	276.1504	534.2671	267.6372	533.2831	267.1452	N	1544.5384	772.7729	1527.5119	764.2596	1526.5279	763.7676	14
6	666.3206	333.6639	649.2940	325.1506	648.3100	324.6586	D	1430.4955	715.7514	1413.4690	707.2381	1412.4849	706.7461	13
7	753.3526	377.1799	736.3260	368.6667	735.3420	368.1747	S	1315.4686	658.2379	1298.4420	649.7246	1297.4580	649.2326	12
8	840.3846	420.6959	823.3581	412.1827	822.3741	411.6907	S	1228.4365	614.7219	1211.4100	606.2086	1210.4260	605.7166	11
9	955.4116	478.2094	938.3850	469.6961	937.4010	469.2041	D	1141.4045	571.2059	1124.3780	562.6926	1123.3939	562.2006	10
10	1122.4099	561.7086	1105.3834	553.1953	1104.3994	552.7033	S	1026.3776	513.6924	1009.3510	505.1791	1008.3670	504.6871	9
11	1237.4369	619.2221	1220.4103	610.7088	1219.4263	610.2168	D	859.3792	430.1932	842.3527	421.6800	841.3686	421.1880	8
12	1352.4638	676.7355	1335.4373	668.2223	1334.4532	667.7303	D	744.3523	372.6798	727.3257	364.1665	726.3417	363.6745	7
13	1481.5064	741.2568	1464.4799	732.7436	1463.4958	732.2516	E	629.3253	315.1663	612.2988	306.6530	611.3148	306.1610	6
14	1552.5435	776.7754	1535.5170	768.2621	1534.5330	767.7701	A	500.2827	250.6450	483.2562	242.1317			5
15	1680.6021	840.8047	1663.5755	832.2914	1662.5915	831.7994	Q	429.2456	215.1264	412.2191	206.6132			4
16	1737.6236	869.3154	1720.5970	860.8021	1719.6130	860.3101	G	301.1870	151.0972	284.1605	142.5839			3
17	1834.6763	917.8418	1817.6498	909.3285	1816.6658	908.8365	P	244.1656	122.5864	227.1390	114.0731			2
18							K	147.1128	74.0600	130.0863	65.5468			1



RMS error 341 ppm



RMS error 341 ppm