

Mascot Search Results

Peptide View

MS/MS Fragmentation of **SAGSRLTLSGR**

Found in **IP100111183**, Tax_Id=10090 Gene_Symbol=Npr1 Atrial natriuretic peptide receptor A

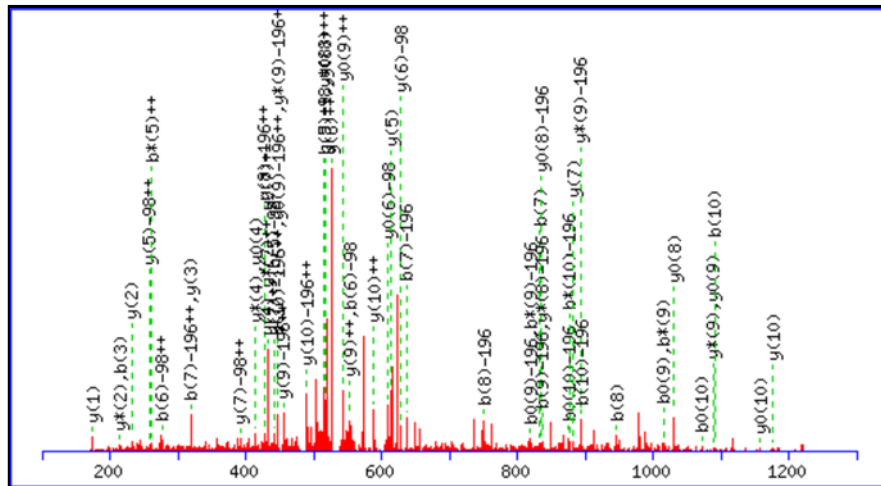
Match to Query 2130: 1263.535724 from(632.775138,2+)

Title: orbitrap001243.913.913.2.dta

Data file C:\Dokumente und Einstellungen\Juliane\Eigene Dateien\Orbitrap-Files\MA-IP, 2x 100 Schalen Juni09\msdata\orbitrap001243.RAW.mgf

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

Or, Plot from to Da



Monoisotopic mass of neutral peptide Mr(calc): 1263.5374

Fixed modifications: Carbamidomethyl (C)

Variable modifications:

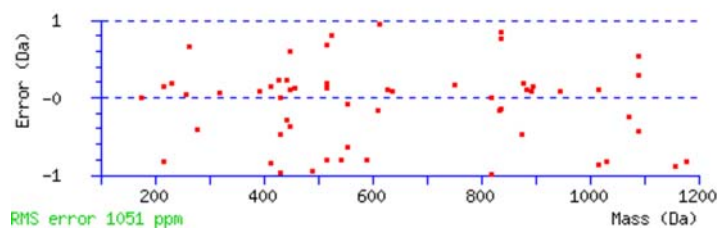
S4 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

T7 : Phospho (ST), with neutral losses 97.9769(shown in table), 0.0000

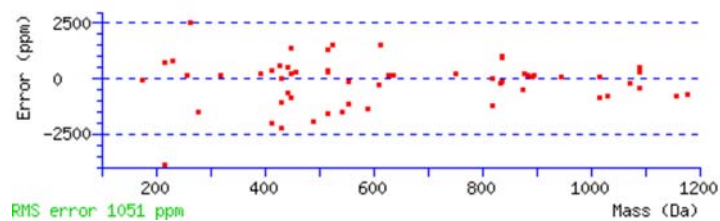
Ions Score: 28 Expect: 0.052

Matches (**Bold Red**): 58/184 fragment ions using 115 most intense peaks

#	b	b ⁺⁺	b [*]	b ⁺⁺	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ⁺⁺	y ⁰	y ⁰⁺⁺	#
1	88.0393	44.5233			70.0287	35.5180	S							11
2	159.0764	80.0418			141.0659	71.0366	A	981.5588	491.2830	964.5323	482.7698	963.5483	482.2778	10
3	216.0979	108.5526			198.0873	99.5473	G	910.5217	455.7645	893.4952	447.2512	892.5111	446.7592	9
4	285.1193	143.0633			267.1088	134.0580	S	853.5002	427.2538	836.4737	418.7405	835.4897	418.2485	8
5	441.2204	221.1139	424.1939	212.6006	423.2099	212.1086	R	784.4788	392.7430	767.4522	384.2298	766.4682	383.7378	7
6	554.3045	277.6559	537.2780	269.1426	536.2939	268.6506	L	628.3777	314.6925	611.3511	306.1792	610.3671	305.6872	6
7	637.3416	319.1744	620.3151	310.6612	619.3311	310.1692	T	515.2936	258.1504	498.2671	249.6372	497.2831	249.1452	5
8	750.4257	375.7165	733.3991	367.2032	732.4151	366.7112	L	432.2565	216.6319	415.2300	208.1186	414.2459	207.6266	4
9	837.4577	419.2325	820.4312	410.7192	819.4471	410.2272	S	319.1724	160.0899	302.1459	151.5766	301.1619	151.0846	3
10	894.4792	447.7432	877.4526	439.2300	876.4686	438.7379	G	232.1404	116.5738	215.1139	108.0606			2
11							R	175.1190	88.0631	158.0924	79.5498			1



RMS error 1051 ppm



NCBI BLAST search of [SAGSRLTLSGR](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
27.8	1263.5374	-0.0016	SAGSRLTLSGR
21.6	1263.5374	-0.0016	SAGSRLTLSGR
14.5	1262.5309	1.0048	VAILQDSTTR
14.4	1263.5374	-0.0016	SAGSRLTLSGR
13.2	1263.5414	-0.0057	REYDHMNGSR
11.4	1263.5319	0.0038	STFQMSLNTR
10.4	1262.5322	1.0035	RPPSFSRTR
9.3	1262.5309	1.0048	VAILQDSTTR
8.8	1263.5374	-0.0016	SAGSRLTLSGR
8.0	1263.5373	-0.0016	LSRAVSASSAR

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **GSNYGSLLTTEGQFQVFAK**

Found in **IPI00111183**, Tax_Id=10090 Gene_Symbol=Npr1 Atrial natriuretic peptide receptor A

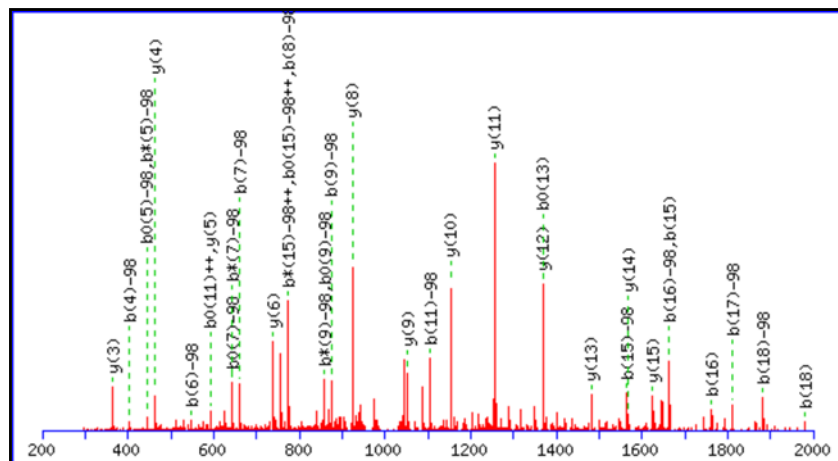
Match to Query 5266: 2126.985724 from(1064.500138,2+)

Title: orbitrap001243.4136.4136.2.dta

Data file C:\Dokumente und Einstellungen\Juliane\Eigene Dateien\Orbitrap-Files\MA-IP, 2x 100 Schalen Juni09\msdata\orbitrap001243.RAW.mgf

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

Or, to Da



Monoisotopic mass of neutral peptide Mr(calc): 2125.9722

Fixed modifications: Carbamidomethyl (C)

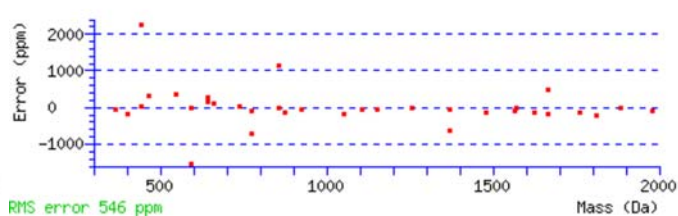
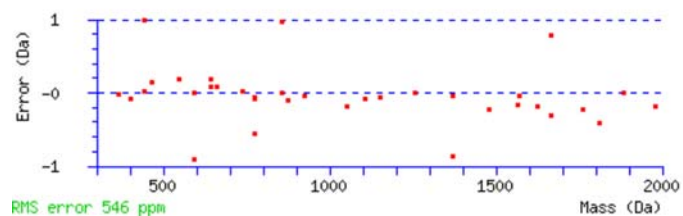
Variable modifications:

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

Ions Score: 105 Expect: 1.8e-009

Matches (Bold Red): 35/300 fragment ions using 38 most intense peaks

#	b	b ⁺⁺	b [*]	b ^{*++}	b ⁰	b ⁰⁺⁺	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	y ⁰	y ⁰⁺⁺	#
1	58.0287	29.5180					G							19
2	127.0502	64.0287			109.0396	55.0235	S	1971.9811	986.4942	1954.9545	977.9809	1953.9705	977.4889	18
3	241.0931	121.0502	224.0666	112.5369	223.0826	112.0449	N	1902.9596	951.9834	1885.9331	943.4702	1884.9490	942.9782	17
4	404.1565	202.5819	387.1299	194.0686	386.1459	193.5766	Y	1788.9167	894.9620	1771.8901	886.4487	1770.9061	885.9567	16
5	461.1779	231.0926	444.1514	222.5793	443.1674	222.0873	G	1625.8534	813.4303	1608.8268	804.9170	1607.8428	804.4250	15
6	548.2099	274.6086	531.1834	266.0953	530.1994	265.6033	S	1568.8319	784.9196	1551.8053	776.4063	1550.8213	775.9143	14
7	661.2940	331.1506	644.2675	322.6374	643.2834	322.1454	L	1481.7999	741.4036	1464.7733	732.8903	1463.7893	732.3983	13
8	774.3781	387.6927	757.3515	379.1794	756.3675	378.6874	L	1368.7158	684.8615	1351.6892	676.3483	1350.7052	675.8563	12
9	875.4258	438.2165	858.3992	429.7032	857.4152	429.2112	T	1255.6317	628.3195	1238.6052	619.8062	1237.6212	619.3142	11
10	976.4734	488.7404	959.4469	480.2271	958.4629	479.7351	T	1154.5841	577.7957	1137.5575	569.2824	1136.5735	568.7904	10
11	1105.5160	553.2616	1088.4895	544.7484	1087.5055	544.2564	E	1053.5364	527.2718	1036.5098	518.7586	1035.5258	518.2665	9
12	1162.5375	581.7724	1145.5109	573.2591	1144.5269	572.7671	G	924.4938	462.7505	907.4672	454.2373			8
13	1290.5961	645.8017	1273.5695	637.2884	1272.5855	636.7964	Q	867.4723	434.2398	850.4458	425.7265			7
14	1437.6645	719.3359	1420.6379	710.8226	1419.6539	710.3306	F	739.4137	370.2105	722.3872	361.6972			6
15	1565.7231	783.3652	1548.6965	774.8519	1547.7125	774.3599	Q	592.3453	296.6763	575.3188	288.1630			5
16	1664.7915	832.8994	1647.7649	824.3861	1646.7809	823.8941	V	464.2867	232.6470	447.2602	224.1337			4
17	1811.8599	906.4336	1794.8333	897.9203	1793.8493	897.4283	F	365.2183	183.1128	348.1918	174.5995			3
18	1882.8970	941.9521	1865.8705	933.4389	1864.8864	932.9469	A	218.1499	109.5786	201.1234	101.0653			2
19							K	147.1128	74.0600	130.0863	65.5468			1



NCBI **BLAST** search of [GSNYGSLLTTEGQFQVFAK](#)

(Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)

Other BLAST [web gateways](#)

All matches to this query

Score	Mr(calc):	Delta	Sequence
104.7	2125.9722	1.0136	GSNYGSLLTTEGQFQVFAK
81.5	2125.9722	1.0136	GSNYGSLLTTEGQFQVFAK
77.7	2125.9722	1.0136	GSNYGSLLTTEGQFQVFAK
43.3	2125.9722	1.0136	GSNYGSLLTTEGQFQVFAK
37.4	2125.9722	1.0136	GSNYGSLLTTEGQFQVFAK
10.7	2126.9809	0.0048	RLPPGSSVMGQNTGRALAR
5.2	2125.9780	1.0077	ATESLQEVSGPKEQSTEVK
3.9	2125.9881	0.9976	FNLTMHQRIHTGETPHK
3.9	2126.9809	0.0048	RLPPGSSVMGQNTGRALAR
3.7	2126.9959	-0.0102	YMNAIPSVVEGDNLTISPK

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