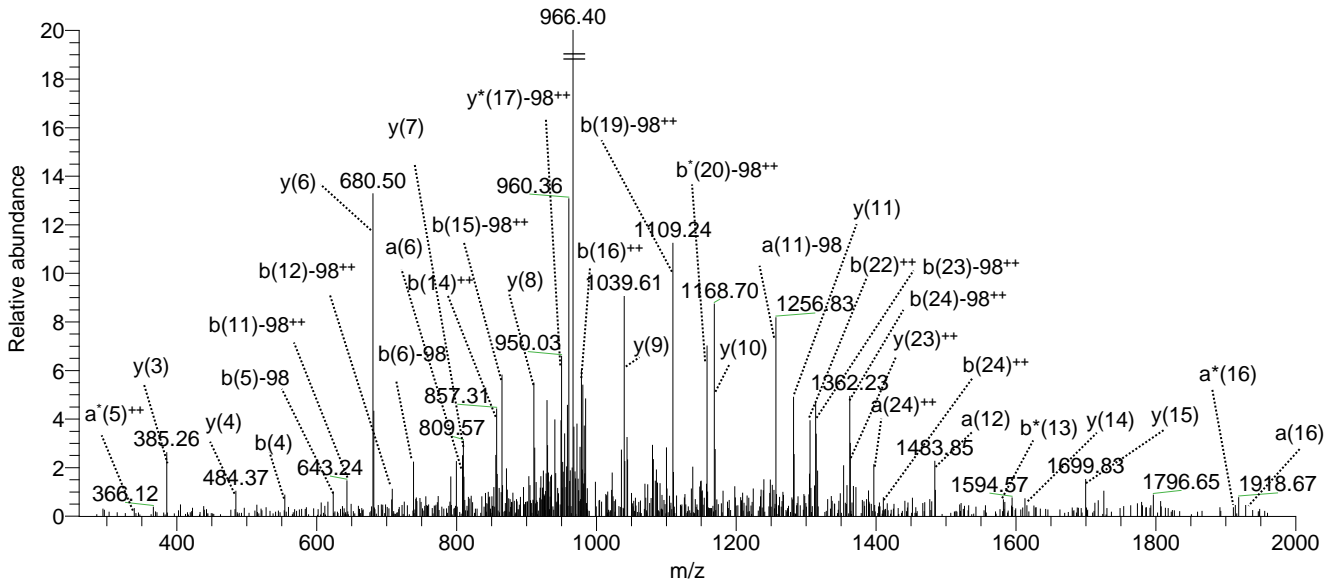
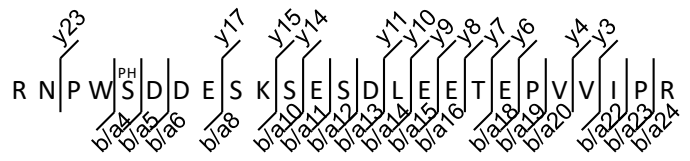


# Erk1\_S1336, S1340, S1344



Match to Query 12003: 2993.331402 from(998.784410,3+) intensity(19394.5762) rtinseconds(2576) rawfile(SN221363\_deTOP2B\_Erk1\_1ul.raw) scans(8614) index(6914)

**Monoisotopic mass of neutral peptide Mr(calc):** 2993.3291

**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

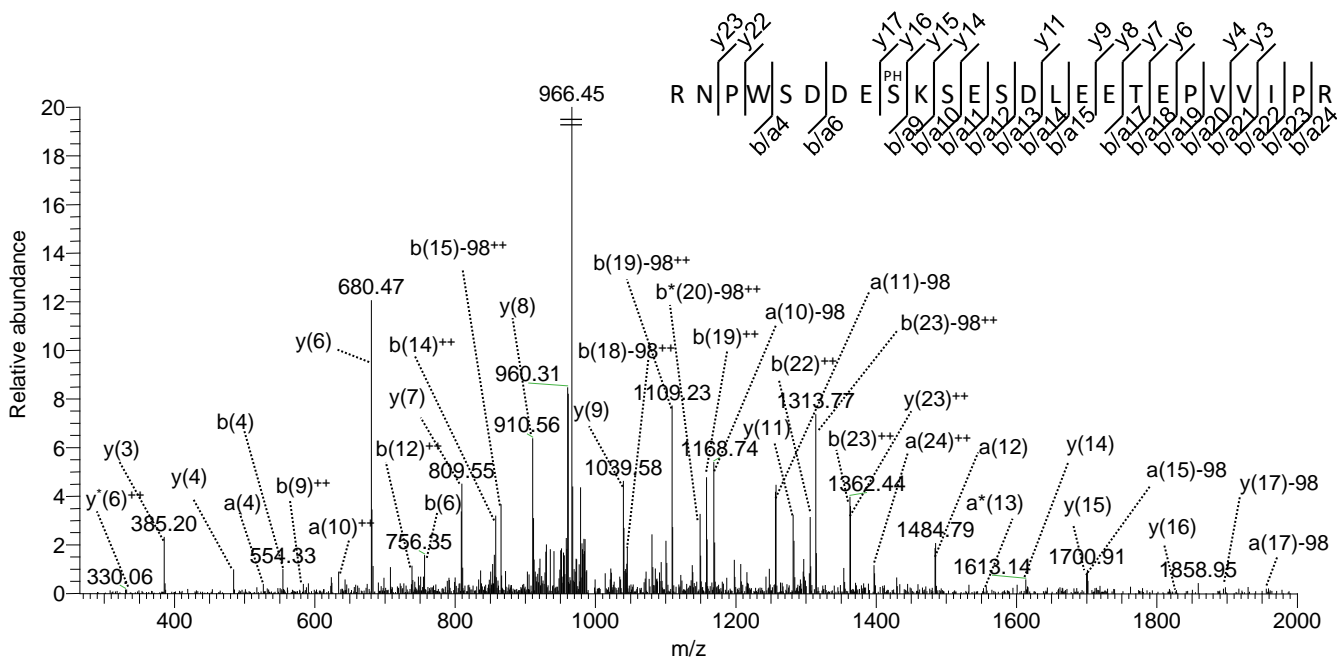
**Ions Score:** 52 **Expect:** 0.00025 **Matches :** 74/464 fragment ions using 85 most intense peaks

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	129.11	65.06	112.09	56.55	157.11	79.06	140.08	70.54	R					25
2	243.16	122.08	226.13	113.57	271.15	136.08	254.12	127.57	N	2740.26	1370.63	2723.23	1362.12	24
3	340.21	170.61	323.18	162.09	368.20	184.61	351.18	176.09	P	2626.22	1313.61	2609.19	1305.10	23
4	526.29	263.65	509.26	255.13	554.28	277.65	537.26	269.13	W	2529.16	1265.09	2512.14	1256.57	22
5	595.31	298.16	578.28	289.65	623.30	312.16	606.28	303.64	S	2343.08	1172.05	2326.06	1163.53	21
6	710.34	355.67	693.31	347.16	738.33	369.67	721.31	361.16	D	2274.06	1137.53	2257.04	1129.02	20
7	825.36	413.19	808.34	404.67	853.36	427.18	836.33	418.67	D	2159.04	1080.02	2142.01	1071.51	19
8	954.41	477.71	937.38	469.19	982.40	491.70	965.37	483.19	E	2044.01	1022.51	2026.98	1013.99	18
9	1041.44	521.22	1024.41	512.71	1069.43	535.22	1052.41	526.71	S	1914.97	957.99	1897.94	949.47	17
10	1169.53	585.27	1152.51	576.76	1197.53	599.27	1180.50	590.75	K	1827.93	914.47	1810.91	905.96	16
11	1256.57	628.79	1239.54	620.27	1284.56	642.78	1267.53	634.27	S	1699.84	850.42	1682.81	841.91	15
12	1385.61	693.31	1368.58	684.79	1413.60	707.31	1396.58	698.79	E	1612.81	806.91	1595.78	798.39	14
13	1472.64	736.82	1455.61	728.31	1500.64	750.82	1483.61	742.31	S	1483.76	742.39	1466.74	733.87	13
14	1587.67	794.34	1570.64	785.82	1615.66	808.33	1598.64	799.82	D	1396.73	698.87	1379.71	690.36	12
15	1700.75	850.88	1683.72	842.37	1728.75	864.88	1711.72	856.36	L	1281.70	641.36	1264.68	632.84	11
16	1829.79	915.40	1812.77	906.89	1857.79	929.40	1840.76	920.88	E	1168.62	584.81	1151.59	576.30	10
17	1958.84	979.92	1941.81	971.41	1986.83	993.92	1969.80	985.41	E	1039.58	520.29	1022.55	511.78	9
18	2059.88	1030.45	2042.86	1021.93	2087.88	1044.44	2070.85	1035.93	T	910.54	455.77	893.51	447.26	8
19	2188.93	1094.97	2171.90	1086.45	2216.92	1108.96	2199.89	1100.45	E	809.49	405.25	792.46	396.73	7
20	2285.98	1143.49	2268.95	1134.98	2313.97	1157.49	2296.95	1148.98	P	680.45	340.73	663.42	332.21	6
21	2385.05	1193.03	2368.02	1184.51	2413.04	1207.02	2396.02	1198.51	V	583.39	292.20	566.37	283.69	5
22	2484.12	1242.56	2467.09	1234.05	2512.11	1256.56	2495.08	1248.05	V	484.32	242.67	467.30	234.15	4
23	2597.20	1299.10	2580.17	1290.59	2625.20	1313.10	2608.17	1304.59	I	385.26	193.13	368.23	184.62	3
24	2694.25	1347.63	2677.23	1339.12	2722.25	1361.63	2705.22	1353.11	P	272.17	136.59	255.15	128.08	2
25									R	175.12	88.06	158.09	79.55	1

## All matches to this query

Score	Mr(calc)	Delta	Site Analysis
52.4	2993.329	0.0023	Phospho S5 82.30%
44.9	2993.329	0.0023	Phospho S9 14.60%
37.6	2993.329	0.0023	Phospho S11 2.71%
29.1	2993.329	0.0023	Phospho S13 0.38%
6.9	2993.329	0.0023	Phospho T18 0.00%

# Erk1\_S1336, S1340, S1344



Match to Query 12001: 2993.325072 from(998.782300,3+) intensity(15240.2246) rtinseconds(2551) rawfile(SN221363\_deTOP2B\_Erk1\_1ul.raw) scans(8507) index(6815)

**Monoisotopic mass of neutral peptide Mr(calc):** 2993.3291

**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

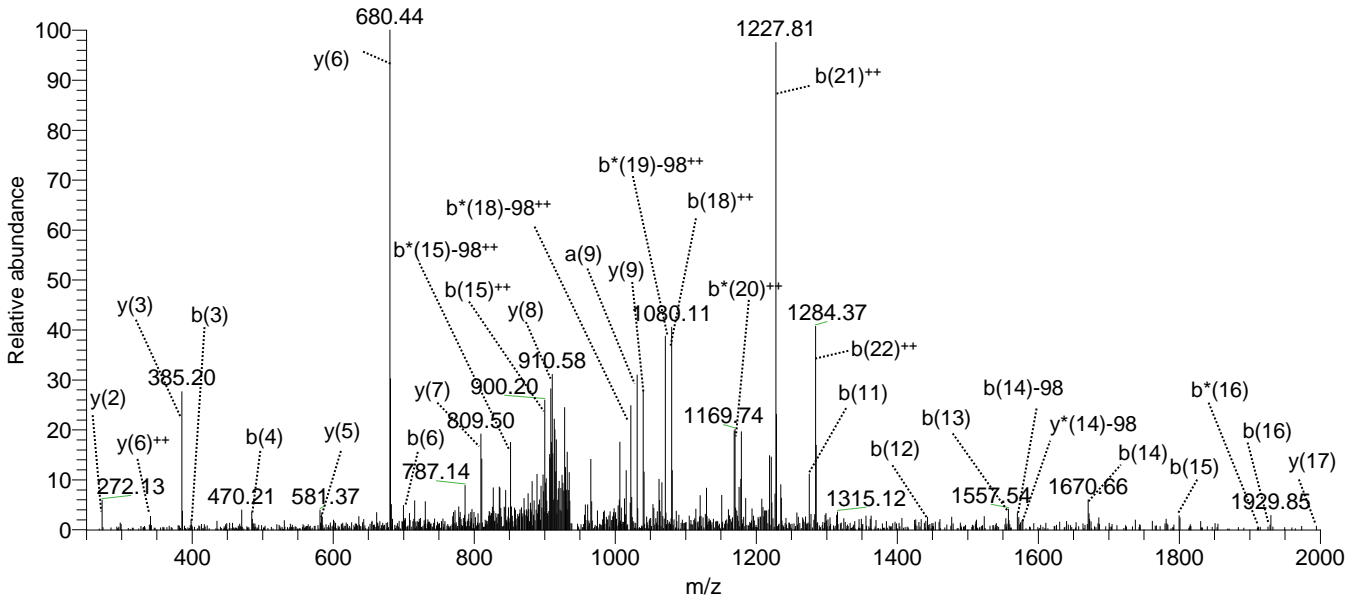
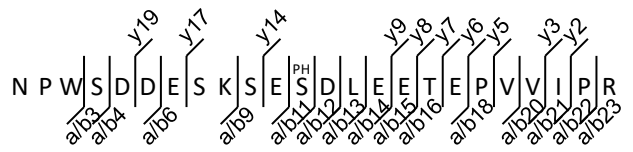
**Ions Score:** 67 **Expect:** 4.3e-06 **Matches :** 59/448 fragment ions using 68 most intense peaks

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	129.11	65.06	112.09	56.55	157.11	79.06	140.08	70.54	R					25
2	243.16	122.08	226.13	113.57	271.15	136.08	254.12	127.57	N	2740.26	1370.63	2723.23	1362.12	24
3	340.21	170.61	323.18	162.09	368.20	184.61	351.18	176.09	P	2626.22	1313.61	2609.19	1305.10	23
4	526.29	263.65	509.26	255.13	554.28	277.65	537.26	269.13	W	2529.16	1265.09	2512.14	1256.57	22
5	613.32	307.16	596.29	298.65	641.32	321.16	624.29	312.65	S	2343.08	1172.05	2326.06	1163.53	21
6	728.35	364.68	711.32	356.16	756.34	378.67	739.32	370.16	D	2256.05	1128.53	2239.02	1120.02	20
7	843.37	422.19	826.35	413.68	871.37	436.19	854.34	427.68	D	2141.02	1071.02	2124.00	1062.50	19
8	972.42	486.71	955.39	478.20	1000.41	500.71	983.39	492.20	E	2026.00	1013.50	2008.97	1004.99	18
9	1041.44	521.22	1024.41	512.71	1069.43	535.22	1052.41	526.71	S	1896.95	948.98	1879.93	940.47	17
10	1169.53	585.27	1152.51	576.76	1197.53	599.27	1180.50	590.75	K	1827.93	914.47	1810.91	905.96	16
11	1256.57	628.79	1239.54	620.27	1284.56	642.78	1267.53	634.27	S	1699.84	850.42	1682.81	841.91	15
12	1385.61	693.31	1368.58	684.79	1413.60	707.31	1396.58	698.79	E	1612.81	806.91	1595.78	798.39	14
13	1472.64	736.82	1455.61	728.31	1500.64	750.82	1483.61	742.31	S	1483.73	742.39	1466.74	733.87	13
14	1587.67	794.34	1570.64	785.82	1615.66	808.33	1598.64	799.82	D	1396.73	698.87	1379.71	690.36	12
15	1700.75	850.88	1683.72	842.37	1728.75	864.88	1711.72	856.36	L	1281.70	641.36	1264.68	632.84	11
16	1829.79	915.40	1812.77	906.89	1857.79	929.40	1840.76	920.88	E	1168.62	584.81	1151.59	576.30	10
17	1958.84	979.92	1941.81	971.41	1986.83	993.92	1969.80	985.41	E	1039.58	520.29	1022.55	511.78	9
18	2059.88	1030.45	2042.86	1021.93	2087.88	1044.44	2070.85	1035.93	T	910.54	455.77	893.51	447.26	8
19	2188.93	1094.97	2171.90	1086.45	2216.92	1108.96	2199.89	1100.45	E	809.49	405.25	792.46	396.73	7
20	2285.98	1143.49	2268.95	1134.98	2313.97	1157.49	2296.95	1148.98	P	680.45	340.73	663.42	332.21	6
21	2385.05	1193.03	2368.02	1184.51	2413.04	1207.02	2396.02	1198.51	V	583.39	292.20	566.37	283.69	5
22	2484.12	1242.56	2467.09	1234.05	2512.11	1256.56	2495.08	1248.05	V	484.32	242.67	467.30	234.15	4
23	2597.20	1299.10	2580.17	1290.59	2625.20	1313.10	2608.17	1304.59	I	385.26	193.13	368.23	184.62	3
24	2694.25	1347.63	2677.23	1339.12	2722.25	1361.63	2705.22	1353.11	P	272.17	136.59	255.15	128.08	2
25									R	175.12	88.06	158.09	79.55	1

## All matches to this query

Score	Mr(calc)	Delta	Site Analysis
66.6	2993.329	-0.004	Phospho S9 78.41%
59.9	2993.329	-0.004	Phospho S5 16.88%
54.3	2993.329	-0.004	Phospho S11 4.62%
37.3	2993.329	-0.004	Phospho S13 0.09%
11.6	2993.329	-0.004	Phospho T18 0.00%

# Erk1\_S1336, S1340, S1344



Match to Query 11588: 2837.230062 from(946.750630,3+) intensity(15514.4561) rtinseconds(2595) rawfile(SN221363\_deTOP2B\_Erk1\_1ul.raw) scans(8693) index(6987)

**Monoisotopic mass of neutral peptide Mr(calc):** 2837.2280

**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

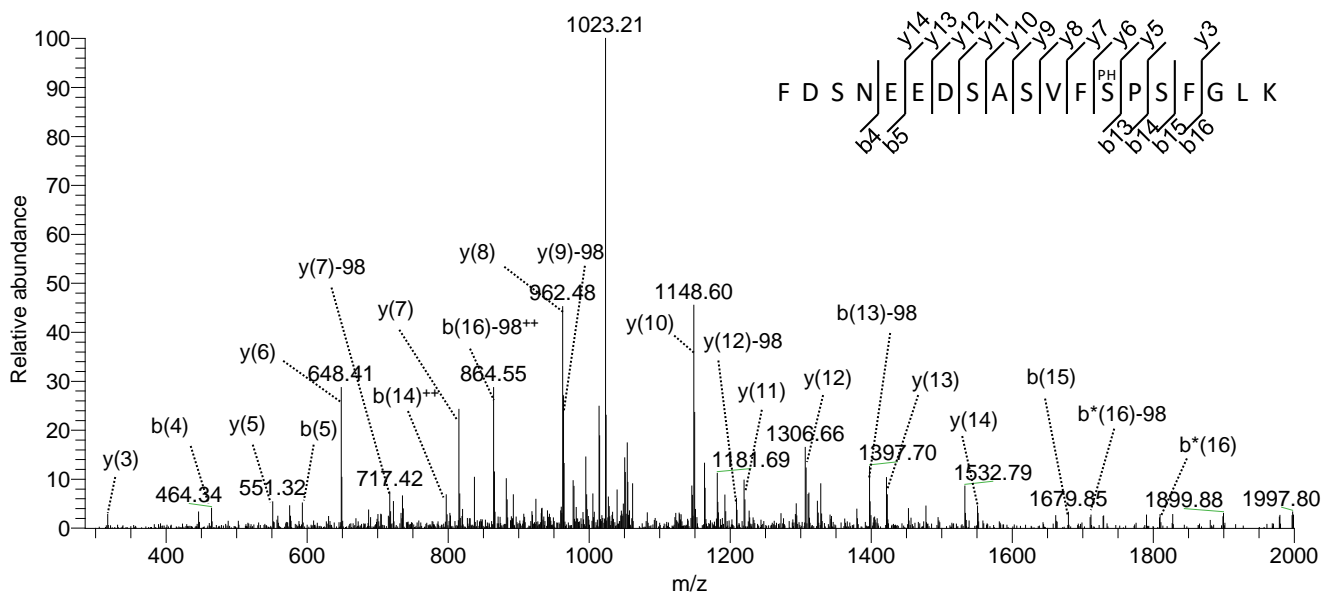
**Ions Score:** 60 **Expect:** 7e-05 **Matches :** 43/416 fragment ions using 53 most intense peaks

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	87.06	44.03	70.03	35.52	115.05	58.03	98.02	49.52	N					24
2	184.11	92.56	167.08	84.04	212.10	106.56	195.08	98.04	P	2724.19	1362.60	2707.17	1354.09	23
3	370.19	185.60	353.16	177.08	398.18	199.59	381.16	191.08	W	2627.14	1314.07	2610.11	1305.56	22
4	457.22	229.11	440.19	220.60	485.21	243.11	468.19	234.60	S	2441.06	1221.03	2424.03	1212.52	21
5	572.25	286.63	555.22	278.11	600.24	300.62	583.21	292.11	D	2354.03	1177.52	2337.00	1169.00	20
6	687.27	344.14	670.25	335.63	715.27	358.14	698.24	349.62	E	2239.00	1120.00	2221.97	1111.49	19
7	816.32	408.66	799.29	400.15	844.31	422.66	827.28	414.15	D	2123.97	1062.49	2106.95	1053.98	18
8	903.35	452.18	886.32	443.66	931.34	466.18	914.32	457.66	S	1994.93	997.97	1977.91	989.46	17
9	1031.44	516.23	1014.42	507.71	1059.44	530.22	1042.41	521.71	K	1907.90	954.45	1890.87	945.94	16
10	1118.47	559.74	1101.45	551.23	1146.47	573.74	1129.44	565.23	S	1779.80	890.41	1762.78	881.89	15
11	1247.52	624.26	1230.49	615.75	1275.51	638.26	1258.49	629.75	E	1692.77	846.89	1675.75	838.38	14
12	1414.52	707.76	1397.49	699.25	1442.51	721.76	1425.48	713.25	S	1563.73	782.37	1546.70	773.86	13
13	1529.54	765.28	1512.52	756.76	1557.54	779.27	1540.51	770.76	D	1396.73	698.87	1379.71	690.36	12
14	1642.63	821.82	1625.60	813.30	1670.62	835.81	1653.60	827.30	L	1281.70	641.36	1264.68	632.84	11
15	1771.67	886.34	1754.64	877.83	1799.66	900.34	1782.64	891.82	E	1168.62	584.81	1151.59	576.30	10
16	1900.71	950.86	1883.69	942.35	1928.71	964.86	1911.68	956.34	E	1039.58	520.29	1022.55	511.78	9
17	2001.76	1001.38	1984.73	992.87	2029.75	1015.38	2012.73	1006.87	T	910.54	455.77	893.51	447.26	8
18	2130.80	1065.90	2113.78	1057.39	2158.80	1079.90	2141.77	1071.39	E	809.49	405.25	792.46	396.73	7
19	2227.86	1114.43	2210.83	1105.92	2255.85	1128.43	2238.82	1119.92	P	680.45	340.73	663.42	332.21	6
20	2326.92	1163.97	2309.90	1155.45	2354.92	1177.96	2337.89	1169.45	V	583.39	292.20	566.37	283.69	5
21	2425.99	1213.50	2408.97	1204.99	2453.99	1227.50	2436.96	1218.98	V	484.32	242.67	467.30	234.15	4
22	2539.08	1270.04	2522.05	1261.53	2567.07	1284.04	2550.04	1275.53	I	385.26	193.13	368.23	184.62	3
23	2636.13	1318.57	2619.10	1310.05	2664.12	1332.57	2647.10	1324.05	P	272.17	136.59	255.15	128.08	2
24									R	175.12	88.06	158.09	79.55	1

## All matches to this query

Score	Mr(calc)	Delta	Site Analysis
60.3	2837.228	0.002	Phospho S12 67.34%
54.1	2837.228	0.002	Phospho S10 16.15%
54.1	2837.228	0.002	Phospho S8 16.15%
37	2837.228	0.002	Phospho S4 0.31%
27.7	2837.228	0.002	Phospho T17 0.04%

# Erk1m\_S1476



Match to Query 9544: 2141.881308 from(1071.947930,2+) intensity(22847.6758) rtinseconds(3249) rawfile(SN221365\_deTOP2B\_Erk1m1\_1ul.raw) scans(11219) index(9272)

**Monoisotopic mass of neutral peptide Mr(calc):** 2141.8831

**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

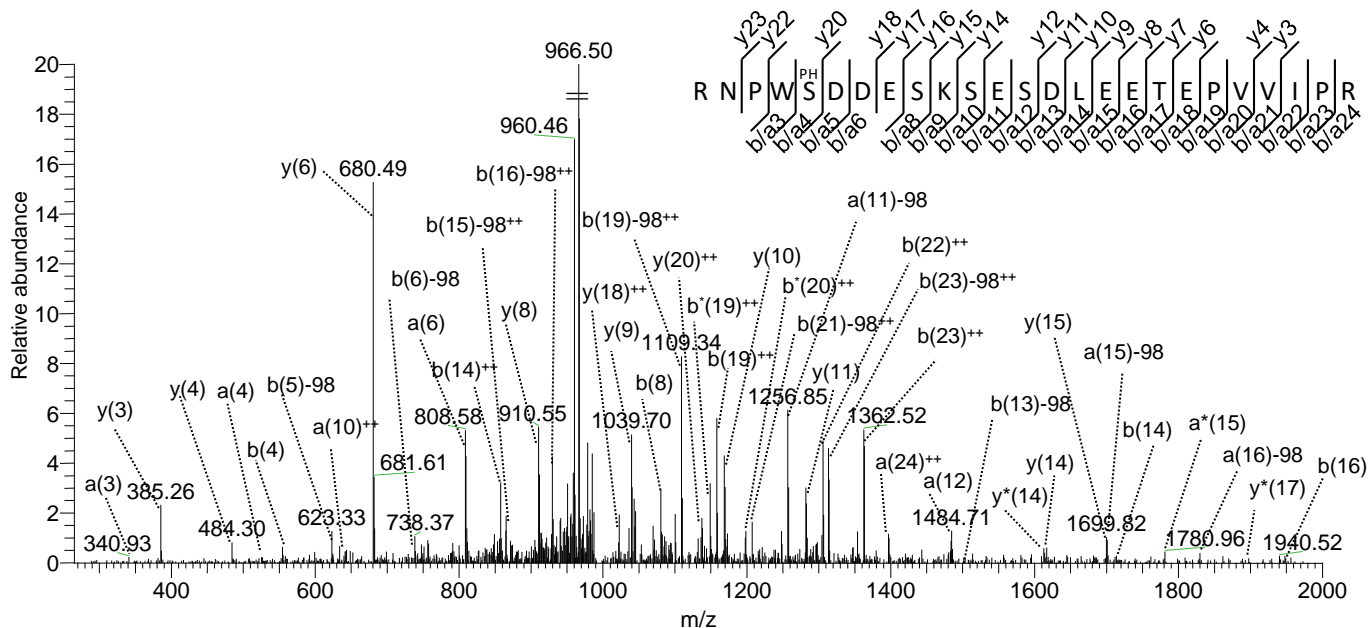
**Ions Score:** 82 **Expect:** 1.5e-07 **Matches :** 25/300 fragment ions using 34 most intense peaks

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	120.1	60.5			148.1	74.5			F					19
2	235.1	118.1			263.1	132.1			D	1995.8	998.4	1978.8	989.9	18
3	322.1	161.6			350.1	175.6			S	1880.8	940.9	1863.8	932.4	17
4	436.2	218.6	419.2	210.1	464.2	232.6	447.2	224.1	N	1793.8	897.4	1776.7	888.9	16
5	565.2	283.1	548.2	274.6	593.2	297.1	576.2	288.6	E	1679.7	840.4	1662.7	831.9	15
6	694.3	347.6	677.2	339.1	722.3	361.6	705.2	353.1	E	1550.7	775.8	1533.7	767.3	14
7	809.3	405.2	792.3	396.6	837.3	419.1	820.3	410.6	D	1421.6	711.3	1404.6	702.8	13
8	896.3	448.7	879.3	440.2	924.3	462.7	907.3	454.2	S	1306.6	653.8	1289.6	645.3	12
9	967.4	484.2	950.3	475.7	995.4	498.2	978.3	489.7	A	1219.6	610.3	1202.5	601.8	11
10	1054.4	527.7	1037.4	519.2	1082.4	541.7	1065.4	533.2	S	1148.5	574.8	1131.5	566.3	10
11	1153.5	577.2	1136.4	568.7	1181.5	591.2	1164.4	582.7	V	1061.5	531.3	1044.5	522.7	9
12	1300.5	650.8	1283.5	642.3	1328.5	664.8	1311.5	656.3	F	962.4	481.7	945.4	473.2	8
13	1467.5	734.3	1450.5	725.8	1495.5	748.3	1478.5	739.8	S	815.4	408.2	798.3	399.7	7
14	1564.6	782.8	1547.6	774.3	1592.6	796.8	1575.6	788.3	P	648.4	324.7	631.3	316.2	6
15	1651.6	826.3	1634.6	817.8	1679.6	840.3	1662.6	831.8	S	551.3	276.2	534.3	267.6	5
16	1798.7	899.8	1781.7	891.3	1826.7	913.8	1809.7	905.3	F	464.3	232.6	447.3	224.1	4
17	1855.7	928.4	1838.7	919.8	1883.7	942.4	1866.7	933.8	G	317.2	159.1	300.2	150.6	3
18	1968.8	984.9	1951.8	976.4	1996.8	998.9	1979.8	990.4	L	260.2	130.6	243.2	122.1	2
19									K	147.1	74.1	130.1	65.5	1

## All matches to this query

Score	Mr(calc)	Delta	Site Analysis
81.6	2141.8831	-0.0017	Phospho S13 99.26%
59	2141.8831	-0.0017	Phospho S10 0.55%
54.2	2141.8831	-0.0017	Phospho S15 0.18%
38.2	2141.8831	-0.0017	Phospho S8 0.00%
24.8	2141.8831	-0.0017	Phospho S3 0.00%

# Erk2\_S1336, S1340, S1344



Match to Query 11699: 2993.329722 from(998.783850,3+) intensity(20973.7480) rtinseconds(2565) rawfile(SN221364\_deTOP2B\_Erk2\_1ul.raw) scans(8366) index(6632)

**Monoisotopic mass of neutral peptide Mr(calc):** 2993.3291

**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

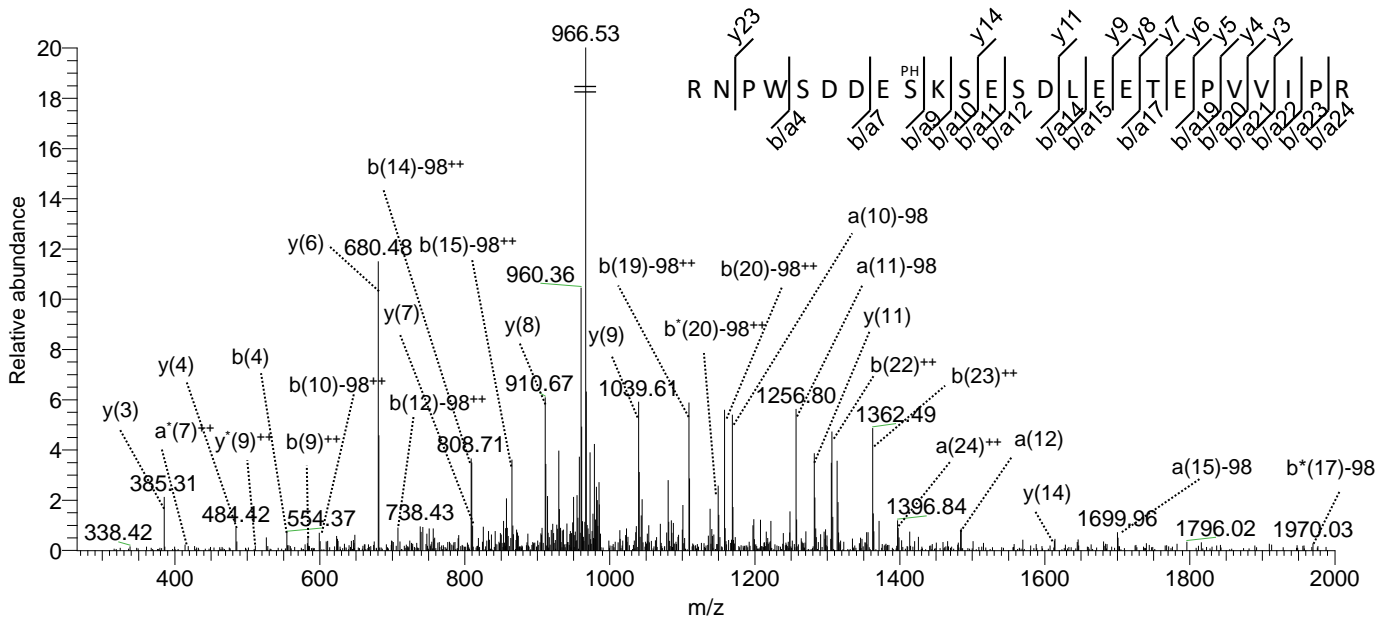
**Ions Score:** 63 **Expect:** 1e-05 **Matches :** 112/464 fragment ions using 153 most intense peaks

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	129.1	65.1	112.1	56.5	157.1	79.1	140.1	70.5	R					25
2	243.2	122.1	226.1	113.6	271.2	136.1	254.1	127.6	N	2838.2	1419.6	2821.2	1411.1	24
3	340.2	170.6	323.2	162.1	368.2	184.6	351.2	176.1	P	2724.2	1362.6	2707.2	1354.1	23
4	526.3	263.6	509.3	255.1	554.3	277.6	537.3	269.1	W	2627.1	1314.1	2610.1	1305.6	22
5	693.3	347.1	676.3	338.6	721.3	361.1	704.3	352.6	S	2441.1	1221.0	2424.0	1212.5	21
6	808.3	404.7	791.3	396.1	836.3	418.7	819.3	410.1	D	2274.1	1137.5	2257.0	1129.0	20
7	923.3	462.2	906.3	453.7	951.3	476.2	934.3	467.7	D	2159.0	1080.0	2142.0	1071.5	19
8	1052.4	526.7	1035.4	518.2	1080.4	540.7	1063.4	532.2	E	2044.0	1022.5	2027.0	1014.0	18
9	1139.4	570.2	1122.4	561.7	1167.4	584.2	1150.4	575.7	S	1915.0	958.0	1897.9	949.5	17
10	1267.5	634.3	1250.5	625.7	1295.5	648.3	1278.5	639.7	K	1827.9	914.5	1810.9	906.0	16
11	1354.5	677.8	1337.5	669.3	1382.5	691.8	1365.5	683.3	S	1699.8	850.4	1682.8	841.9	15
12	1483.6	742.3	1466.6	733.8	1511.6	756.3	1494.6	747.8	E	1612.8	806.9	1595.8	798.4	14
13	1570.6	785.8	1553.6	777.3	1598.6	799.8	1581.6	791.3	S	1483.8	742.4	1466.7	733.9	13
14	1685.6	843.3	1668.6	834.8	1713.6	857.3	1696.6	848.8	D	1396.7	698.9	1379.7	690.4	12
15	1798.7	899.9	1781.7	891.4	1826.7	913.9	1809.7	905.4	L	1281.7	641.4	1264.7	632.8	11
16	1927.8	964.4	1910.7	955.9	1955.8	978.4	1938.7	969.9	E	1168.6	584.8	1151.6	576.3	10
17	2056.8	1028.9	2039.8	1020.4	2084.8	1042.9	2067.8	1034.4	E	1039.6	520.3	1022.6	511.8	9
18	2157.9	1079.4	2140.8	1070.9	2185.9	1093.4	2168.8	1084.9	T	910.5	455.8	893.5	447.3	8
19	2286.9	1144.0	2269.9	1135.4	2314.9	1158.0	2297.9	1149.4	E	809.5	405.2	792.5	396.7	7
20	2384.0	1192.5	2366.9	1184.0	2412.0	1206.5	2394.9	1198.0	P	680.4	340.7	663.4	332.2	6
21	2483.0	1242.0	2466.0	1233.5	2511.0	1256.0	2494.0	1247.5	V	583.4	292.2	566.4	283.7	5
22	2582.1	1291.6	2565.1	1283.0	2610.1	1305.5	2593.1	1297.0	V	484.3	242.7	467.3	234.2	4
23	2695.2	1348.1	2678.2	1339.6	2723.2	1362.1	2706.1	1353.6	I	385.3	193.1	368.2	184.6	3
24	2792.2	1396.6	2775.2	1388.1	2820.2	1410.6	2803.2	1402.1	P	272.2	136.6	255.1	128.1	2
25									R	175.1	88.1	158.1	79.5	1

## All matches to this query

Score	Mr(calc)	Delta	Site Analysis
63.1	2993.329	0.0006	Phospho S5 75.56%
58	2993.329	0.0006	Phospho S9 23.78%
42.2	2993.329	0.0006	Phospho S11 0.62%
30	2993.329	0.0006	Phospho S13 0.04%

# Erk2\_S1336, S1340, S1344



Match to Query 11698: 2993.329182 from(998.783670,3+) intensity(20568.6523) rtinseconds(2558) rawfile(SN221364\_deTOP2B\_Erk2\_1ul.raw) scans(8339) index(6607)

**Monoisotopic mass of neutral peptide Mr(calc):** 2993.3291

**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

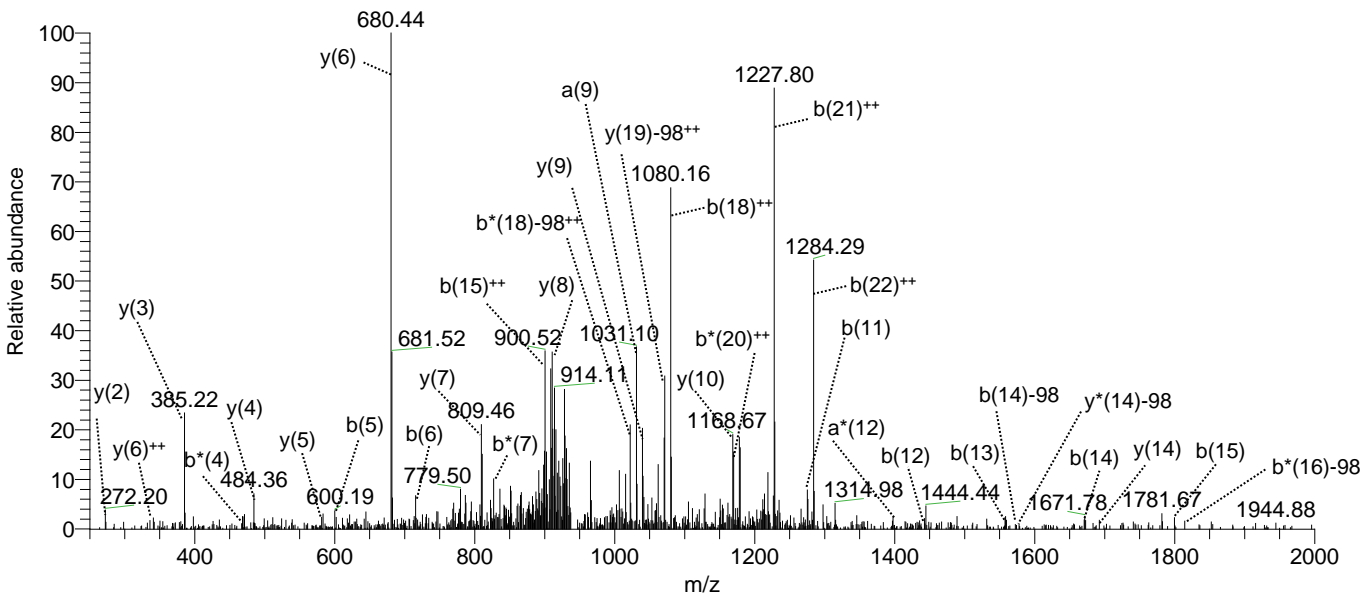
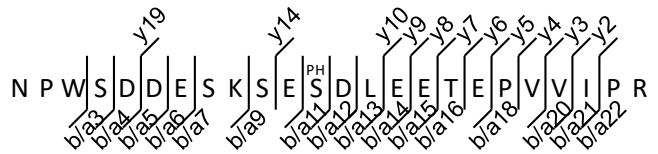
**Ions Score:** 63 **Expect:** 2.4e-05 **Matches :** 44/448 fragment ions using 51 most intense peaks

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	129.1	65.1	112.1	56.5	157.1	79.1	140.1	70.5	R					25
2	243.2	122.1	226.1	113.6	271.2	136.1	254.1	127.6	N	2740.3	1370.6	2723.2	1362.1	24
3	340.2	170.6	323.2	162.1	368.2	184.6	351.2	176.1	P	2626.2	1313.6	2609.2	1305.1	23
4	526.3	263.6	509.3	255.1	554.3	277.6	537.3	269.1	W	2529.2	1265.1	2512.1	1256.6	22
5	613.3	307.2	596.3	298.7	641.3	321.2	624.3	312.6	S	2343.1	1172.0	2326.1	1163.5	21
6	728.3	364.7	711.3	356.2	756.3	378.7	739.3	370.2	D	2256.1	1128.5	2239.0	1120.0	20
7	843.4	422.2	826.3	413.7	871.4	436.2	854.3	427.7	D	2141.0	1071.0	2124.0	1062.5	19
8	972.4	486.7	955.4	478.2	1000.4	500.7	983.4	492.2	E	2026.0	1013.5	2009.0	1005.0	18
9	1041.4	521.2	1024.4	512.7	1069.4	535.2	1052.4	526.7	S	1897.0	949.0	1879.9	940.5	17
10	1169.5	585.3	1152.5	576.8	1197.5	599.3	1180.5	590.8	K	1827.9	914.5	1810.9	906.0	16
11	1256.6	628.8	1239.5	620.3	1284.6	642.8	1267.5	634.3	S	1699.8	850.4	1682.8	841.9	15
12	1385.6	693.3	1368.6	684.8	1413.6	707.3	1396.6	698.8	E	1612.8	806.9	1595.8	798.4	14
13	1472.6	736.8	1455.6	728.3	1500.6	750.8	1483.6	742.3	S	1483.8	742.4	1466.7	733.9	13
14	1587.7	794.3	1570.6	785.8	1615.7	808.3	1598.6	799.8	D	1396.7	698.9	1379.7	690.4	12
15	1700.8	850.9	1683.7	842.4	1728.7	864.9	1711.7	856.4	L	1281.7	641.4	1264.7	632.8	11
16	1829.8	915.4	1812.8	906.9	1857.8	929.4	1840.8	920.9	E	1168.6	584.8	1151.6	576.3	10
17	1958.8	979.9	1941.8	971.4	1986.8	993.9	1969.8	985.4	E	1039.6	520.3	1022.6	511.8	9
18	2059.9	1030.4	2042.9	1021.9	2087.9	1044.4	2070.9	1035.9	T	910.5	455.8	893.5	447.3	8
19	2188.9	1095.0	2171.9	1086.5	2216.9	1109.0	2199.9	1100.5	E	809.5	405.2	792.5	396.7	7
20	2286.0	1143.5	2269.0	1135.0	2314.0	1157.5	2296.9	1149.0	P	680.4	340.7	663.4	332.2	6
21	2385.0	1193.0	2368.0	1184.5	2413.0	1207.0	2396.0	1198.5	V	583.4	292.2	566.4	283.7	5
22	2484.1	1242.6	2467.1	1234.0	2512.1	1256.6	2495.1	1248.0	V	484.3	242.7	467.3	234.2	4
23	2597.2	1299.1	2580.2	1290.6	2625.2	1313.1	2608.2	1304.6	I	385.3	193.1	368.2	184.6	3
24	2694.3	1347.6	2677.2	1339.1	2722.2	1361.6	2705.2	1353.1	P	272.2	136.6	255.1	128.1	2
25									R	175.1	88.1	158.1	79.5	1

## All matches to this query

Score	Mr(calc)	Delta	Site Analysis
63	2993.3291	0.0001	Phospho S9 58.20%
61.2	2993.3291	0.0001	Phospho S5 38.90%
49.9	2993.3291	0.0001	Phospho S11 2.86%
31	2993.3291	0.0001	Phospho S13 0.04%

# Erk2\_S1336, S1340, S1344



Match to Query 11292: 2837.226972 from(946.749600,3+) intensity(9996.0352) rtinseconds(2605) rawfile(SN221364\_deTOP2B\_Erk2\_1ul.raw) scans(8539) index(6791)

**Monoisotopic mass of neutral peptide Mr(calc):** 2837.2280

**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

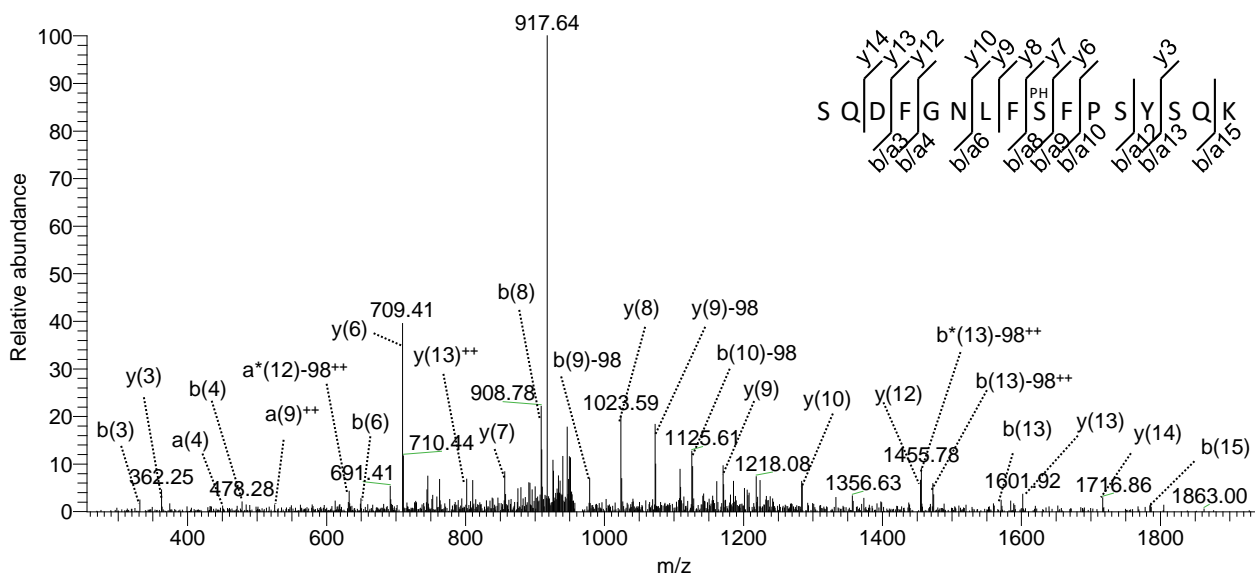
**Ions Score:** 59 **Expect:** 0.00013 **Matches :** 46/416 fragment ions using 54 most intense peaks

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	129.1	65.1	112.1	56.5	157.1	79.1	140.1	70.5	R					25
2	243.2	122.1	226.1	113.6	271.2	136.1	254.1	127.6	N	2838.2	1419.6	2821.2	1411.1	24
3	<b>340.2</b>	170.6	323.2	162.1	<b>368.2</b>	184.6	351.2	176.1	P	2724.2	<b>1362.6</b>	2707.2	<b>1354.1</b>	23
4	<b>526.3</b>	263.6	509.3	255.1	<b>554.3</b>	277.6	537.3	269.1	W	2627.1	<b>1314.1</b>	2610.1	<b>1305.6</b>	22
5	693.3	347.1	676.3	338.6	721.3	361.1	704.3	352.6	S	2441.1	1221.0	2424.0	1212.5	21
6	<b>808.3</b>	404.7	791.3	396.1	836.3	418.7	819.3	410.1	D	2274.1	<b>1137.5</b>	2257.0	1129.0	20
7	923.3	462.2	906.3	453.7	951.3	476.2	934.3	467.7	D	2159.0	<b>1080.0</b>	2142.0	1071.5	19
8	1052.4	<b>526.7</b>	<b>1035.4</b>	518.2	<b>1080.4</b>	540.7	1063.4	532.2	E	2044.0	<b>1022.5</b>	2027.0	1014.0	18
9	1139.4	570.2	1122.4	561.7	1167.4	<b>584.2</b>	1150.4	<b>575.7</b>	S	1915.0	<b>958.0</b>	<b>1897.9</b>	949.5	17
10	1267.5	<b>634.3</b>	1250.5	625.7	1295.5	<b>648.3</b>	1278.5	639.7	K	<b>1827.9</b>	914.5	1810.9	906.0	16
11	<b>1354.5</b>	677.8	1337.5	669.3	1382.5	691.8	1365.5	<b>683.3</b>	S	<b>1699.8</b>	850.4	1682.8	841.9	15
12	<b>1483.6</b>	742.3	1466.6	733.8	1511.6	<b>756.3</b>	1494.6	<b>747.8</b>	E	<b>1612.8</b>	806.9	<b>1595.8</b>	798.4	14
13	1570.6	785.8	1553.6	777.3	1598.6	799.8	1581.6	791.3	S	<b>1483.8</b>	742.4	1466.7	733.9	13
14	1685.6	843.3	1668.6	834.8	<b>1713.6</b>	<b>857.3</b>	1696.6	<b>848.8</b>	D	<b>1396.7</b>	<b>698.9</b>	1379.7	690.4	12
15	<b>1798.7</b>	899.9	<b>1781.7</b>	891.4	1826.7	913.9	<b>1809.7</b>	905.4	L	<b>1281.7</b>	<b>641.4</b>	1264.7	632.8	11
16	1927.8	964.4	1910.7	955.9	<b>1955.8</b>	<b>978.4</b>	1938.7	969.9	E	<b>1168.6</b>	<b>584.8</b>	1151.6	<b>576.3</b>	10
17	2056.8	1028.9	2039.8	1020.4	2084.8	<b>1042.9</b>	2067.8	1034.4	E	<b>1039.6</b>	520.3	<b>1022.6</b>	511.8	9
18	2157.9	1079.4	2140.8	1070.9	2185.9	1093.4	2168.8	1084.9	T	<b>910.5</b>	455.8	893.5	447.3	8
19	2286.9	1144.0	2269.9	1135.4	2314.9	<b>1158.0</b>	2297.9	<b>1149.4</b>	E	<b>809.5</b>	405.2	792.5	396.7	7
20	2384.0	1192.5	2366.9	1184.0	2412.0	1206.5	2394.9	<b>1198.0</b>	P	<b>680.4</b>	<b>340.7</b>	663.4	332.2	6
21	2483.0	1242.0	2466.0	1233.5	2511.0	1256.0	2494.0	<b>1247.5</b>	V	<b>583.4</b>	292.2	566.4	283.7	5
22	2582.1	1291.6	2565.1	<b>1283.0</b>	2610.1	<b>1305.5</b>	2593.1	1297.0	V	<b>484.3</b>	242.7	467.3	234.2	4
23	2695.2	1348.1	2678.2	1339.6	2723.2	<b>1362.1</b>	2706.1	<b>1353.6</b>	I	<b>385.3</b>	193.1	<b>368.2</b>	184.6	3
24	2792.2	<b>1396.6</b>	2775.2	1388.1	2820.2	1410.6	2803.2	1402.1	P	272.2	136.6	255.1	128.1	2
25									R	175.1	88.1	158.1	79.5	1

## All matches to this query

Score	Mr(calc)	Delta	Site Analysis
59.4	2837.228	-0.001	Phospho S12 94.58%
42.9	2837.228	-0.001	Phospho S10 2.08%
42.9	2837.228	-0.001	Phospho S8 2.08%
40.6	2837.228	-0.001	Phospho S4 1.25%
21.5	2837.228	-0.001	Phospho T17 0.02%

# Erk2m\_S1449



Match to Query 8559: 1930.811788 from(966.413170,2+) intensity(12163.2783) rtinseconds(3270) rawfile(SN221366\_deTOP2B\_Erk2m\_1ul.raw) scans(11317) index(9361)

**Monoisotopic mass of neutral peptide Mr(calc):** 1930.8139

**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:** 66 **Expect:** 2.6e-06 **Matches :** 29/264 fragment ions using 34 most intense peaks

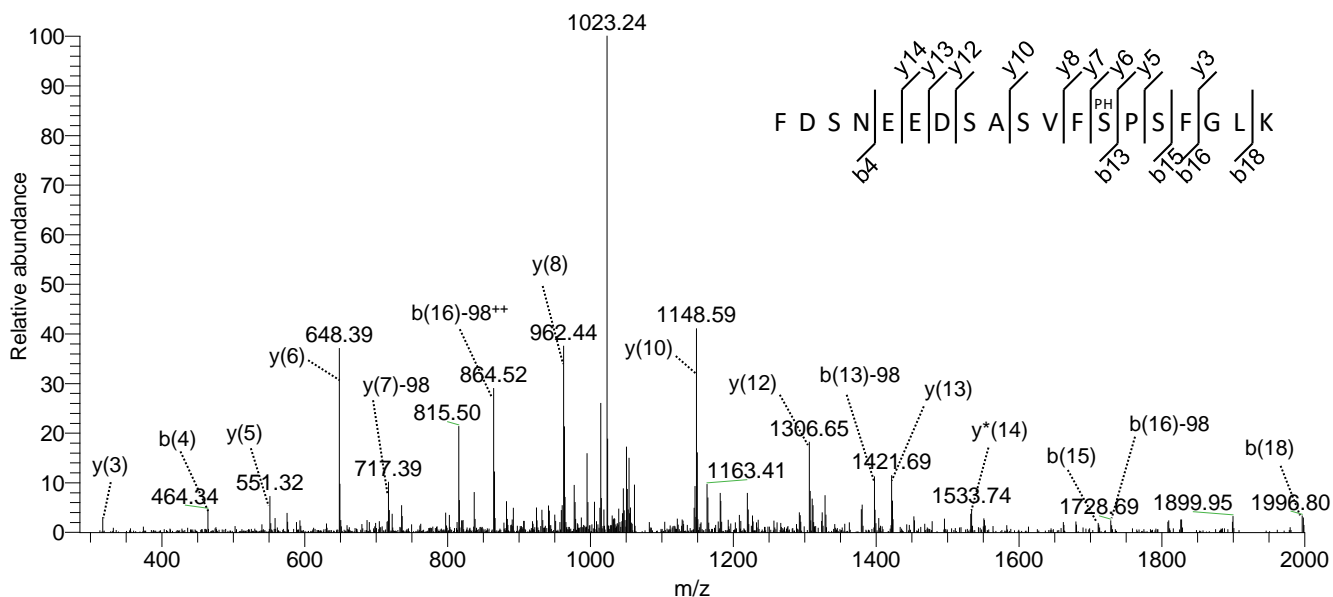
#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	60.0	30.5			88.0	44.5			S					16
2	188.1	94.6	171.1	86.0	216.1	108.6	199.1	100.0	Q	1844.8	922.9	1827.8	914.4	15
3	303.1	152.1	286.1	143.6	331.1	166.1	314.1	157.6	D	1716.7	858.9	1699.7	850.4	14
4	450.2	225.6	433.2	217.1	478.2	239.6	461.2	231.1	F	1601.7	801.4	1584.7	792.8	13
5	507.2	254.1	490.2	245.6	535.2	268.1	518.2	259.6	G	1454.6	727.8	1437.6	719.3	12
6	621.3	311.1	604.2	302.6	649.3	325.1	632.2	316.6	N	1397.6	699.3	1380.6	690.8	11
7	734.3	367.7	717.3	359.2	762.3	381.7	745.3	373.2	L	1283.6	642.3	1266.5	633.8	10
8	881.4	441.2	864.4	432.7	909.4	455.2	892.4	446.7	F	1170.5	585.7	1153.5	577.2	9
9	1048.4	524.7	1031.4	516.2	1076.4	538.7	1059.4	530.2	S	1023.4	512.2	1006.4	503.7	8
10	1195.5	598.2	1178.5	589.7	1223.5	612.2	1206.5	603.7	F	856.4	428.7	839.4	420.2	7
11	1292.5	646.8	1275.5	638.3	1320.5	660.8	1303.5	652.3	P	709.4	355.2	692.3	346.7	6
12	1379.6	690.3	1362.5	681.8	1407.6	704.3	1390.5	695.8	S	612.3	306.7	595.3	298.1	5
13	1542.6	771.8	1525.6	763.3	1570.6	785.8	1553.6	777.3	Y	525.3	263.1	508.2	254.6	4
14	1629.7	815.3	1612.6	806.8	1657.7	829.3	1640.6	820.8	S	362.2	181.6	345.2	173.1	3
15	1757.7	879.4	1740.7	870.9	1785.7	893.4	1768.7	884.8	Q	275.2	138.1	258.1	129.6	2
16									K	147.1	74.1	130.1	65.5	1

## All matches to this query

Score	Mr(calc)	Delta	Site Analysis
65.8	1930.8139	-0.0021	Phospho S9 99.81%
38.3	1930.8139	-0.0021	Phospho S12 0.18%
23	1930.8139	-0.0021	Phospho Y13 0.01%
21.6	1930.8139	-0.0021	Phospho S14 0.00%
13.2	1930.8139	-0.0021	Phospho S1 0.00%



# Erk2m\_S1476



Match to Query 9274: 2141.882588 from(1071.948570,2+) intensity(21991.7324) rtinseconds(3251) rawfile(SN221366\_deTOP2B\_Erk2m\_1ul.raw) scans(11238) index(9288)

**Monoisotopic mass of neutral peptide Mr(calc):** 2141.8831

**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

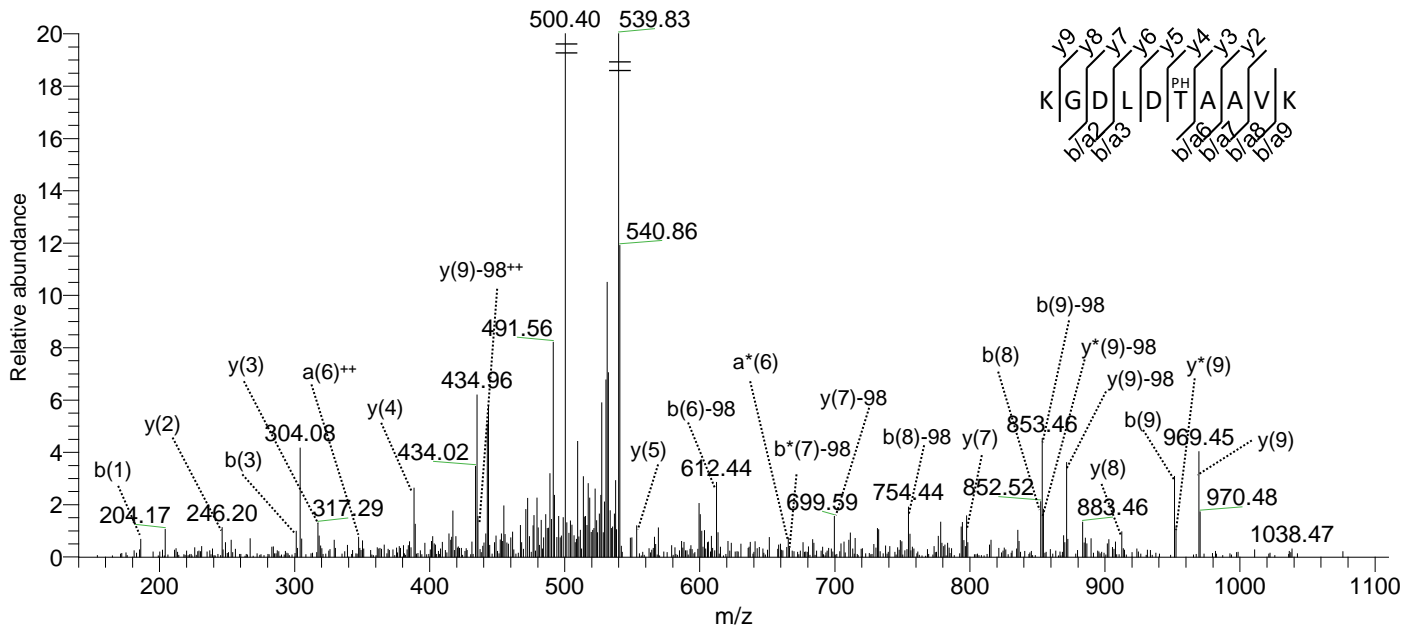
**Ions Score:** 80 **Expect:** 6.9e-08 **Matches :** 19/300 fragment ions using 17 most intense peaks z

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	120.1	60.5			148.1	74.5			F					19
2	235.1	118.1			263.1	132.1			D	1995.8	998.4	1978.8	989.9	18
3	322.1	161.6			350.1	175.6			S	1880.8	940.9	1863.8	932.4	17
4	436.2	218.6	419.2	210.1	464.2	232.6	447.2	224.1	N	1793.8	897.4	1776.7	888.9	16
5	565.2	283.1	548.2	274.6	593.2	297.1	576.2	288.6	E	1679.7	840.4	1662.7	831.9	15
6	694.3	347.6	677.2	339.1	722.3	361.6	705.2	353.1	E	1550.7	775.8	1533.7	767.3	14
7	809.3	405.2	792.3	396.6	837.3	419.1	820.3	410.6	D	1421.6	711.3	1404.6	702.8	13
8	896.3	448.7	879.3	440.2	924.3	462.7	907.3	454.2	S	1306.6	653.8	1289.6	645.3	12
9	967.4	484.2	950.3	475.7	995.4	498.2	978.3	489.7	A	1219.6	610.3	1202.5	601.8	11
10	1054.4	527.7	1037.4	519.2	1082.4	541.7	1065.4	533.2	S	1148.5	574.8	1131.5	566.3	10
11	1153.5	577.2	1136.4	568.7	1181.5	591.2	1164.4	582.7	V	1061.5	531.3	1044.5	522.7	9
12	1300.5	650.8	1283.5	642.3	1328.5	664.8	1311.5	656.3	F	962.4	481.7	945.4	473.2	8
13	1467.5	734.3	1450.5	725.8	1495.5	748.3	1478.5	739.8	S	815.4	408.2	798.3	399.7	7
14	1564.6	782.8	1547.6	774.3	1592.6	796.8	1575.6	788.3	P	648.4	324.7	631.3	316.2	6
15	1651.6	826.3	1634.6	817.8	1679.6	840.3	1662.6	831.8	S	551.3	276.2	534.3	267.6	5
16	1798.7	899.8	1781.7	891.3	1826.7	913.8	1809.7	905.3	F	464.3	232.6	447.3	224.1	4
17	1855.7	928.4	1838.7	919.8	1883.7	942.4	1866.7	933.8	G	317.2	159.1	300.2	150.6	3
18	1968.8	984.9	1951.8	976.4	1996.8	998.9	1979.8	990.4	L	260.2	130.6	243.2	122.1	2
19									K	147.1	74.1	130.1	65.5	1

## All matches to this query

Score	Mr(calc)	Delta	Site Analysis
80.2	2141.8831	-0.0005	Phospho S13 99.06%
59.6	2141.8831	-0.0005	Phospho S10 0.86%
46.4	2141.8831	-0.0005	Phospho S15 0.04%
45.3	2141.8831	-0.0005	Phospho S8 0.03%
19.4	2141.8831	-0.0005	Phospho S3 0.00%

# Erk2m\_T1267



Match to Query 2189: 1096.516888 from(549.265720,2+) intensity(10601.1406) rtinseconds(1259) rawfile(SN221366\_deTOP2B\_Erk2m\_1ul.raw) scans(2924) index(1760)

**Monoisotopic mass of neutral peptide Mr(calc):** 1096.5165

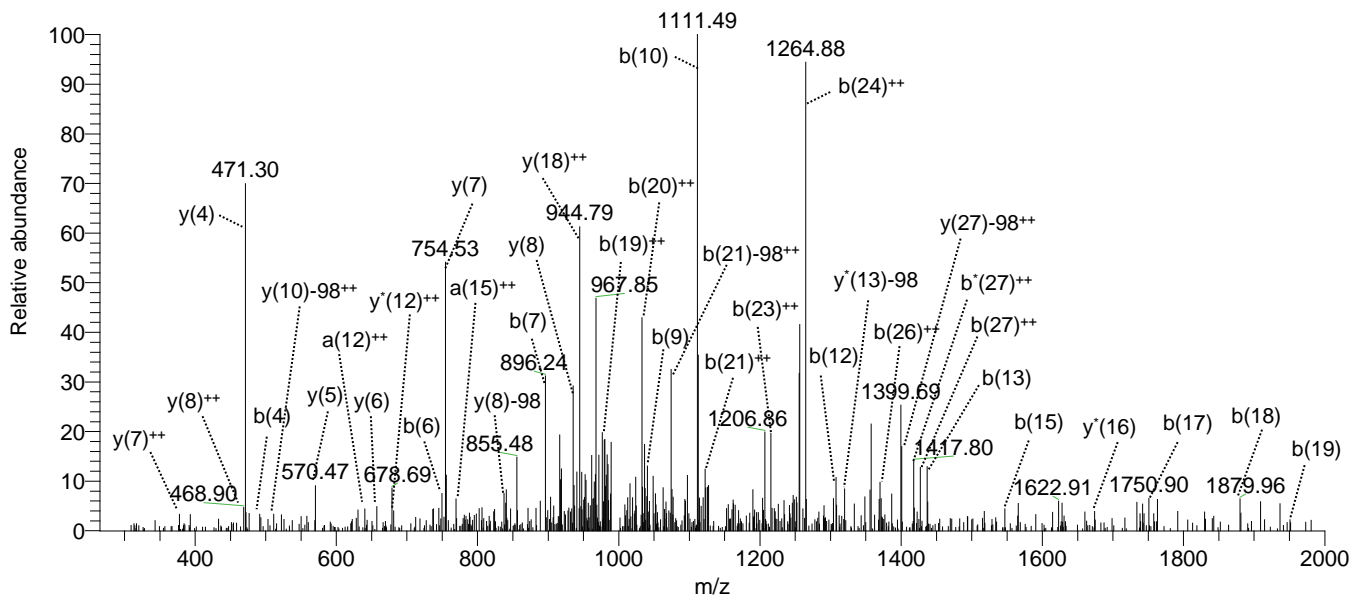
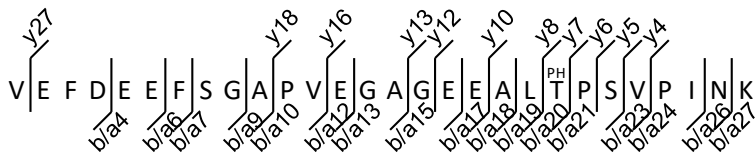
**Fixed modifications:** Carbamidomethyl (C) (apply to specified residues or termini only)

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

**Ions Score:** 40 **Expect:** 0.0052 **Matches :** 27/160 fragment ions using 64 most intense peaks

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	101.1	51.1	84.1	42.5	129.1	65.1	112.1	56.5	K					10
2	158.1	79.6	141.1	71.1	186.1	93.6	169.1	85.1	G	969.4	485.2	952.4	476.7	9
3	273.2	137.1	256.1	128.6	301.2	151.1	284.1	142.6	D	912.4	456.7	895.4	448.2	8
4	386.2	193.6	369.2	185.1	414.2	207.6	397.2	199.1	L	797.4	399.2	780.4	390.7	7
5	501.3	251.1	484.2	242.6	529.3	265.1	512.2	256.6	D	684.3	342.7	667.3	334.1	6
6	682.3	341.6	665.3	333.1	710.3	355.6	693.2	347.1	T	569.3	285.1	552.2	276.6	5
7	753.3	377.2	736.3	368.6	781.3	391.2	764.3	382.6	A	388.3	194.6	371.2	186.1	4
8	824.4	412.7	807.3	404.2	852.3	426.7	835.3	418.2	A	317.2	159.1	300.2	150.6	3
9	923.4	462.2	906.4	453.7	951.4	476.2	934.4	467.7	V	246.2	123.6	229.2	115.1	2
10									K	147.1	74.1	130.1	65.5	1

# Erk1m\_T1292



Match to Query 11653: 2997.348372 from(1000.123400,3+) intensity(71701.7266) rtinseconds(2936) rawfile(SN221365\_deTOP2B\_Erk1m\_1ul.raw) scans(9928) index(8092)

**Monoisotopic mass of neutral peptide Mr(calc):** 2997.3532

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

**Variable modifications:** T21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

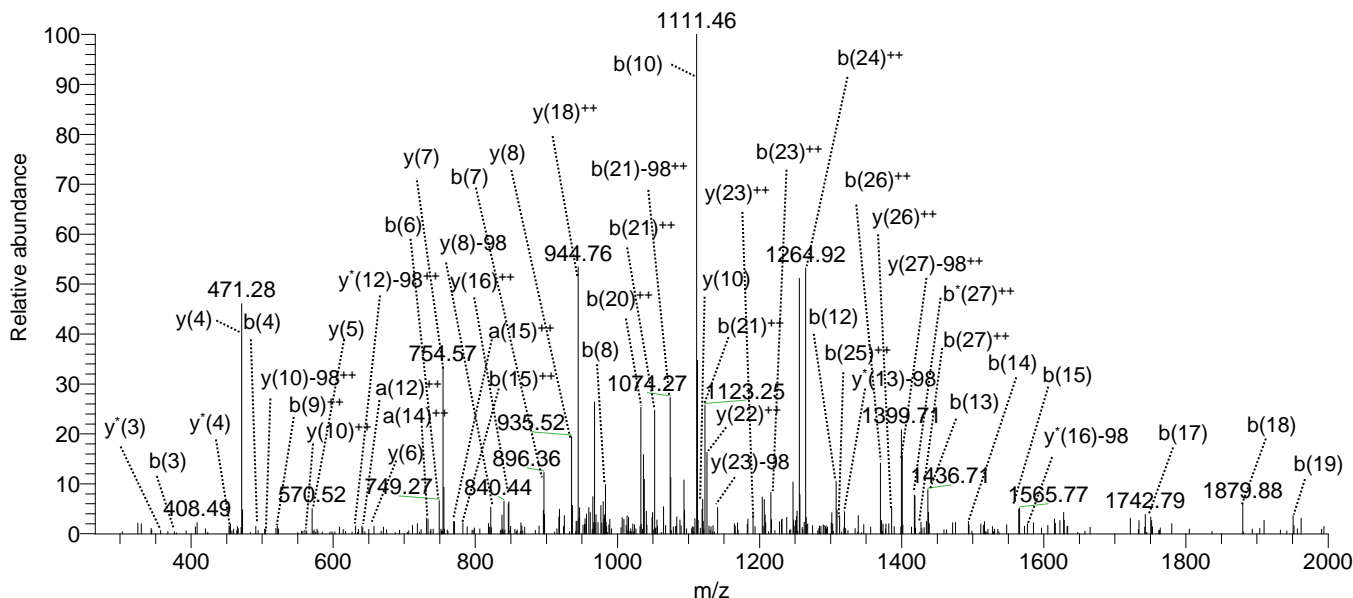
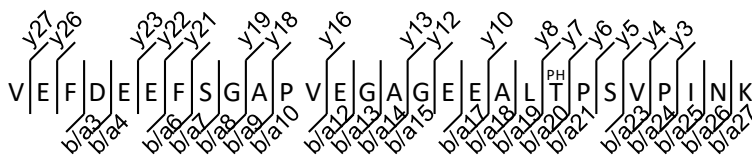
**Ions Score:** 40 **Expect:** 0.00073 **Matches :** 46/332 fragment ions using 85 most intense peaks

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1.0	72.1	36.5			100.1	50.5			V					28.0
2.0	201.1	101.1			229.1	115.1			E	2899.3	1450.1	2882.3	1441.6	27.0
3.0	348.2	174.6			376.2	188.6			F	2770.2	1385.6	2753.2	1377.1	26.0
4.0	463.2	232.1			491.2	246.1			D	2623.2	1312.1	2606.2	1303.6	25.0
5.0	592.3	296.6			620.3	310.6			E	2508.2	1254.6	2491.1	1246.1	24.0
6.0	721.3	361.2			749.3	375.2			E	2379.1	1190.1	2362.1	1181.5	23.0
7.0	868.4	434.7			896.4	448.7			F	2250.1	1125.5	2233.0	1117.0	22.0
8.0	955.4	478.2			983.4	492.2			S	2103.0	1052.0	2086.0	1043.5	21.0
9.0	1012.4	506.7			1040.4	520.7			G	2016.0	1008.5	1998.9	1000.0	20.0
10.0	1083.5	542.2			1111.5	556.2			A	1958.9	980.0	1941.9	971.5	19.0
11.0	1180.5	590.8			1208.5	604.8			P	1887.9	944.5	1870.9	935.9	18.0
12.0	1279.6	640.3			1307.6	654.3			V	1790.9	895.9	1773.8	887.4	17.0
13.0	1408.6	704.8			1436.6	718.8			E	1691.8	846.4	1674.8	837.9	16.0
14.0	1465.6	733.3			1493.6	747.3			G	1562.7	781.9	1545.7	773.4	15.0
15.0	1536.7	768.8			1564.7	782.8			A	1505.7	753.4	1488.7	744.9	14.0
16.0	1593.7	797.4			1621.7	811.4			G	1434.7	717.8	1417.7	709.3	13.0
17.0	1722.7	861.9			1750.7	875.9			E	1377.7	689.3	1360.6	680.8	12.0
18.0	1851.8	926.4			1879.8	940.4			E	1248.6	624.8	1231.6	616.3	11.0
19.0	1922.8	961.9			1950.8	975.9			A	1119.6	560.3	1102.6	551.8	10.0
20.0	2035.9	1018.5			2063.9	1032.5			L	1048.5	524.8	1031.5	516.3	9.0
21.0	2216.9	1109.0			2244.9	1123.0			T	935.5	468.2	918.4	459.7	8.0
22.0	2314.0	1157.5			2342.0	1171.5			P	754.4	377.7	737.4	369.2	7.0
23.0	2401.0	1201.0			2429.0	1215.0			S	657.4	329.2	640.4	320.7	6.0
24.0	2500.1	1250.5			2528.1	1264.5			V	570.4	285.7	553.3	277.2	5.0
25.0	2597.1	1299.1			2625.1	1313.1			P	471.3	236.1	454.3	227.6	4.0
26.0	2710.2	1355.6			2738.2	1369.6			I	374.2	187.6	357.2	179.1	3.0
27.0	2824.3	1412.6	2807.2	1404.1	2852.3	1426.6	2835.2	1418.1	N	261.2	131.1	244.1	122.6	2.0
28.0									K	147.1	74.1	130.1	65.5	1.0

## All matches to this query

Score	Mr(calc)	Delta	Site Analysis
39.9	2997.353	-0.0049	Phospho T21 90.98%
29.8	2997.353	-0.0049	Phospho S23 8.91%
10.8	2997.353	-0.0049	Phospho S8 0.11%

# Erk2m\_T1292



Match to Query 11387: 2997.351552 from(1000.124460,3+) intensity(543952.3750) rtinseconds(2940) rawfile(Z:\%SN22%SN221366\_deTOP2B\_Erk2m\_1ul.raw) scans(9948) index(8112)  
 Title: SpectrumID: "8131"; File: "SN221366\_deTOP2B\_Erk2m\_1ul.raw"

**Monoisotopic mass of neutral peptide Mr(calc):** 2997.3532

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

**Variable modifications:** T21 : Phospho (ST), with neutral losses 0.0000(shown in table), 97.9769

**Ions Score:** 55 **Expect:** 7.8e-05 **Matches :** 65/332 fragment ions using 133 most intense peaks

#	a	a <sup>++</sup>	a <sup>*</sup>	a <sup>+++</sup>	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	#
1	72.1	36.5			100.1	50.5			V					28
2	201.1	101.1			229.1	115.1			E	2899.3	1450.1	2882.3	1441.6	27
3	348.2	174.6			376.2	188.6			F	2770.2	1385.6	2753.2	1377.1	26
4	463.2	232.1			491.2	246.1			D	2623.2	1312.1	2606.2	1303.6	25
5	592.3	296.6			620.3	310.6			E	2508.2	1254.6	2491.1	1246.1	24
6	721.3	361.2			749.3	375.2			E	2379.1	1190.1	2362.1	1181.5	23
7	868.4	434.7			896.4	448.7			F	2250.1	1125.5	2233.0	1117.0	22
8	955.4	478.2			983.4	492.2			S	2103.0	1052.0	2086.0	1043.5	21
9	1012.4	506.7			1040.4	520.7			G	2016.0	1008.5	1998.9	1000.0	20
10	1083.5	542.2			1111.5	556.2			A	1958.9	980.0	1941.9	971.5	19
11	1180.5	590.8			1208.5	604.8			P	1887.9	944.5	1870.9	935.9	18
12	1279.6	640.3			1307.6	654.3			V	1790.9	895.9	1773.8	887.4	17
13	1408.6	704.8			1436.6	718.8			E	1691.8	846.4	1674.8	837.9	16
14	1465.6	733.3			1493.6	747.3			G	1562.7	781.9	1545.7	773.4	15
15	1536.7	768.8			1564.7	782.8			A	1505.7	753.4	1488.7	744.9	14
16	1593.7	797.4			1621.7	811.4			G	1434.7	717.8	1417.7	709.3	13
17	1722.7	861.9			1750.7	875.9			E	1377.7	689.3	1360.6	680.8	12
18	1851.8	926.4			1879.8	940.4			E	1248.6	624.8	1231.6	616.3	11
19	1922.8	961.9			1950.8	975.9			A	1119.6	560.3	1102.6	551.8	10
20	2035.9	1018.5			2063.9	1032.5			L	1048.5	524.8	1031.5	516.3	9
21	2216.9	1109.0			2244.9	1123.0			T	935.5	468.2	918.4	459.7	8
22	2314.0	1157.5			2342.0	1171.5			P	754.4	377.7	737.4	369.2	7
23	2401.0	1201.0			2429.0	1215.0			S	657.4	329.2	640.4	320.7	6
24	2500.1	1250.5			2528.1	1264.5			V	570.4	285.7	553.3	277.2	5
25	2597.1	1299.1			2625.1	1313.1			P	471.3	236.1	454.3	227.6	4
26	2710.2	1355.6			2738.2	1369.6			I	374.2	187.6	357.2	179.1	3
27	2824.3	1412.6	2807.2	1404.1	2852.3	1426.6	2835.2	1418.1	N	261.2	131.1	244.1	122.6	2
28									K	147.1	74.1	130.1	65.5	1

## All matches to this query

Score	Mr(calc)	Delta	Site Analysis
54.6	2997.353	-0.0017	Phospho T21 83.30%
47.6	2997.353	-0.0017	Phospho S23 16.70%