

Mascot Search Results

Peptide View

MS/MS Fragmentation of **NASTFEDVTQVSSAYQK**

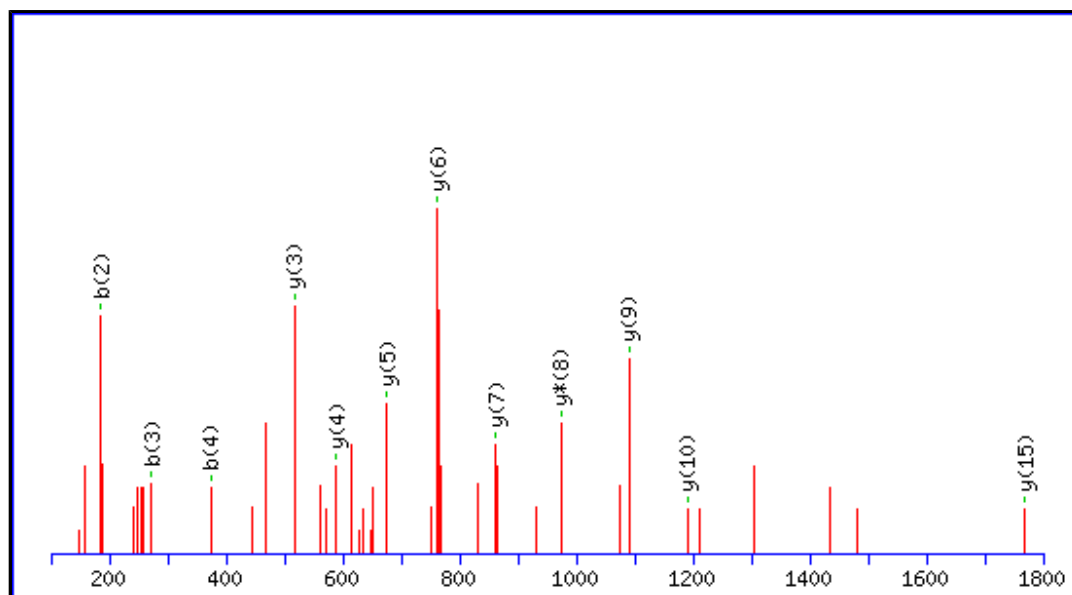
Found in **gi|20357552**, NP_005222.2| cortactin isoform a [Homo sapiens]

Match to Query 165: 1953.955448 from(977.985000,2+)

From data file hm160404_AK_SILAC3_Src_0006A.pkl

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): 1953.84

Fixed modifications: Oxidation (M)

Variable modifications:

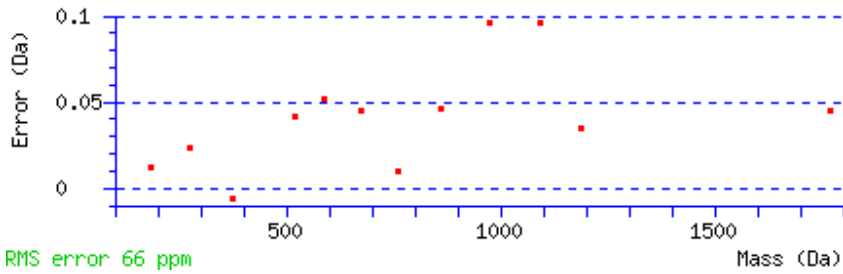
Y15 : Phospho (Y)

Ions Score: 42 **Expect:** 0.017

Matches (Bold Red): 12/192 fragment ions using 27 most intense peaks

#	a	a ⁺⁺	a*	a ^{*++}	b	b ⁺⁺	b*	b ^{*++}	Seq.	y	y ⁺⁺	y*	y ^{*++}	#
1	87.06	44.03	70.03	35.52	115.05	58.03	98.02	49.52	N					17
2	158.09	79.55	141.07	71.04	186.09	93.55	169.06	85.03	A	1840.80	920.90	1823.77	912.39	16
3	245.12	123.07	228.10	114.55	273.12	137.06	256.09	128.55	S	1769.76	885.39	1752.74	876.87	15
4	346.17	173.59	329.15	165.08	374.17	187.59	357.14	179.07	T	1682.73	841.87	1665.70	833.36	14
5	493.24	247.12	476.21	238.61	521.24	261.12	504.21	252.61	F	1581.68	791.35	1564.66	782.83	13
6	622.28	311.65	605.26	303.13	650.28	325.64	633.25	317.13	E	1434.61	717.81	1417.59	709.30	12
7	737.31	369.16	720.28	360.65	765.30	383.16	748.28	374.64	D	1305.57	653.29	1288.55	644.78	11
8	836.38	418.69	819.35	410.18	864.37	432.69	847.35	424.18	V	1190.55	595.78	1173.52	587.26	10
9	937.43	469.22	920.40	460.70	965.42	483.21	948.39	474.70	T	1091.48	546.24	1074.45	537.73	9
10	1065.48	533.25	1048.46	524.73	1093.48	547.24	1076.45	538.73	Q	990.43	495.72	973.40	487.20	8
11	1164.55	592.78	1147.52	574.27	1193.55	596.78	1176.52	589.26	N	862.27	431.60	845.24	422.18	7

11	1104.55	582.78	1147.55	574.27	1192.55	596.78	1175.52	588.20	V	802.57	451.09	845.54	425.18	7
12	1251.59	626.30	1234.56	617.78	1279.58	640.29	1262.55	631.78	S	763.30	382.15	746.28	373.64	6
13	1338.62	669.81	1321.59	661.30	1366.61	683.81	1349.59	675.30	S	676.27	338.64	659.24	330.13	5
14	1409.65	705.33	1392.63	696.82	1437.65	719.33	1420.62	710.81	A	589.24	295.12	572.21	286.61	4
15	1652.68	826.85	1635.66	818.33	1680.68	840.84	1663.65	832.33	Y	518.20	259.60	501.17	251.09	3
16	1780.74	890.87	1763.72	882.36	1808.74	904.87	1791.71	896.36	Q	275.17	138.09	258.14	129.58	2
17									K	147.11	74.06	130.09	65.55	1



NCBI **BLAST** search of NASTFEDVTQVSSAYQK

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **GPSYGLSAEVK**

Found in **gi|4502923**, NP_001830.1| calponin 3 [Homo sapiens]

Match to Query 362: 1186.545139 from(594.279845,2+)

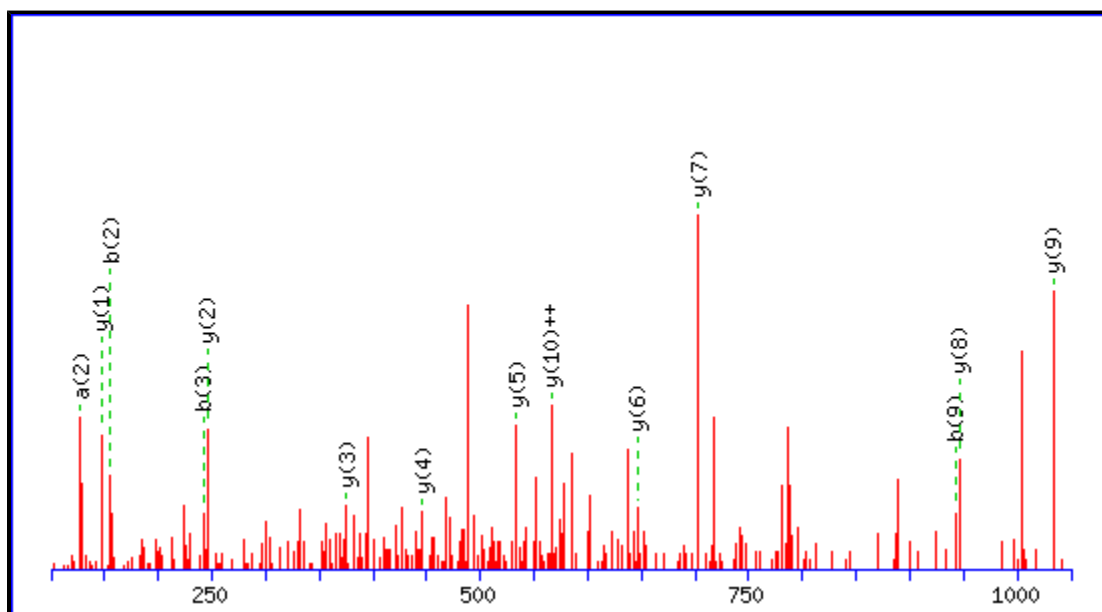
File: band_16_38kDa.wiff, Sample: band_16_38kDa3 (sample number 1), Elution: 17.26 min, Period: 1,

Cycle(s): 605 (Experiment 4)

From data file mas5.tmp

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): 1186.53

Fixed modifications: Oxidation (M)

Variable modifications:

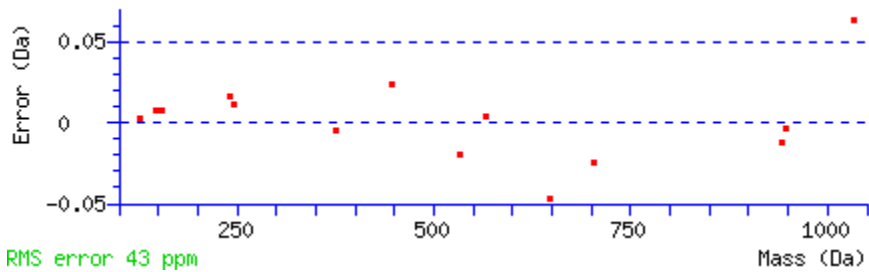
Y4 : Phospho (Y)

Ions Score: 46 **Expect:** 0.0078

Matches (Bold Red): 14/80 fragment ions using 41 most intense peaks

#	a	a ⁺⁺	b	b ⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	30.03	15.52	58.03	29.52	G					11
2	127.09	64.05	155.08	78.04	P	1130.51	565.76	1113.49	557.25	10
3	214.12	107.56	242.11	121.56	S	1033.46	517.23	1016.43	508.72	9
4	457.15	229.08	485.14	243.08	Y	946.43	473.72	929.40	465.20	8
5	514.17	257.59	542.16	271.59	G	703.40	352.20	686.37	343.69	7
6	627.25	314.13	655.25	328.13	L	646.38	323.69	629.35	315.18	6
7	714.29	357.65	742.28	371.64	S	533.29	267.15	516.27	258.64	5
8	785.32	393.17	813.32	407.16	A	446.26	223.63	429.23	215.12	4

9	914.37	457.69	942.36	471.68	E	375.22	188.12	358.20	179.60	3
10	1013.43	507.22	1041.43	521.22	V	246.18	123.59	229.15	115.08	2
11					K	147.11	74.06	130.09	65.55	1



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

MASCOT SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **QDHPSSMGVYGQESGGFSGPGENR**

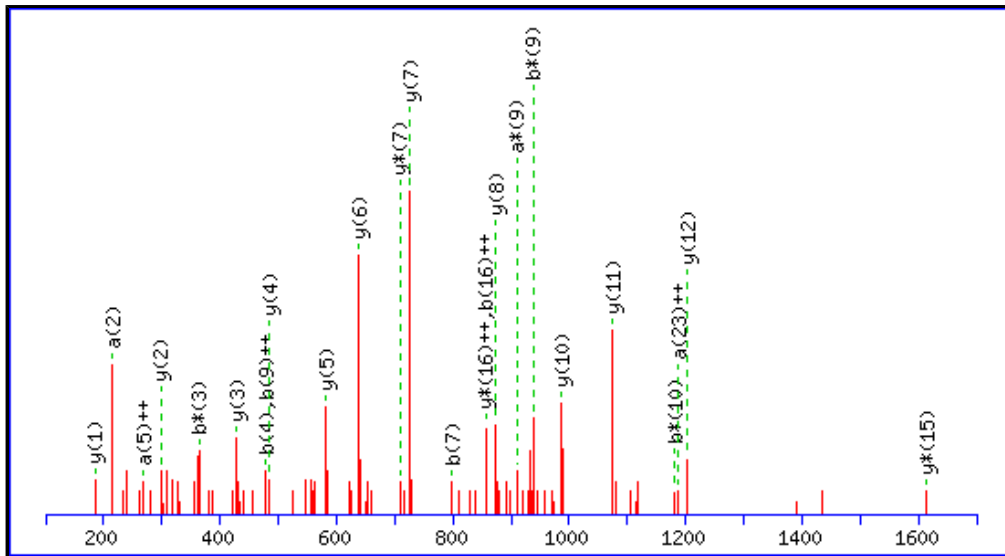
Found in **gi|4885225**, NP_005234.1| Ewing sarcoma breakpoint region 1 isoform EWS [Homo sapiens]

Match to Query 227: 2585.154972 from(862.725600,3+)

From data file hm160404_AK_SILAC3_Src_0005A.pkl

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): 2585.02

Fixed modifications: Oxidation (M)

Variable modifications:

Y10 : Phospho (Y)

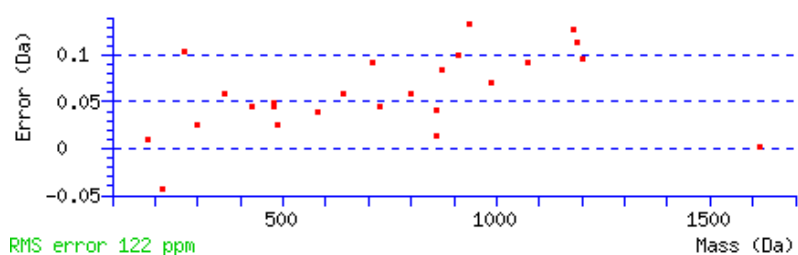
R24 : Arginine-13C615N4 (R-full)

Ions Score: 51 **Expect:** 0.001

Matches (Bold Red): 25/276 fragment ions using 47 most intense peaks

#	a	a ⁺⁺	a [*]	a ^{*++}	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	101.07	51.04	84.04	42.53	129.07	65.04	112.04	56.52	Q					24
2	216.10	108.55	199.07	100.04	244.09	122.55	227.07	114.04	D	2457.96	1229.49	2440.94	1220.97	23
3	353.16	177.08	336.13	168.57	381.15	191.08	364.13	182.57	H	2342.94	1171.97	2325.91	1163.46	22
4	450.21	225.61	433.18	217.10	478.20	239.61	461.18	231.09	P	2205.88	1103.44	2188.85	1094.93	21
5	537.24	269.12	520.22	260.61	565.24	283.12	548.21	274.61	S	2108.83	1054.92	2091.80	1046.40	20
6	624.27	312.64	607.25	304.13	652.27	326.64	635.24	318.12	S	2021.79	1011.40	2004.77	1002.89	19
7	771.31	386.16	754.28	377.64	799.30	400.16	782.28	391.64	M	1934.76	967.88	1917.73	959.37	18
8	828.33	414.67	811.30	406.16	856.33	428.67	839.30	420.15	G	1787.73	894.37	1770.70	885.85	17
9	927.40	464.20	910.37	455.69	955.39	478.20	938.37	469.69	V	1730.70	865.86	1713.68	857.34	16
10	1170.43	585.72	1153.40	577.20	1198.42	599.72	1181.40	591.20	Y	1631.64	816.32	1614.61	807.81	15
11	1227.45	614.23	1210.42	605.72	1255.44	628.23	1238.42	619.71	G	1388.61	694.81	1371.58	686.29	14
12	1355.51	678.26	1338.48	669.74	1383.50	692.26	1366.48	683.74	Q	1331.58	666.30	1314.56	657.78	13
13	1484.55	742.28	1467.50	734.27	1512.55	756.28	1495.50	748.26	D	1302.52	602.27	1286.50	592.75	12

13	1484.55	742.78	1407.52	754.27	1512.55	750.78	1495.52	748.20	E	1205.55	602.27	1180.50	595.75	12
14	1571.58	786.30	1554.56	777.78	1599.58	800.29	1582.55	791.78	S	1074.48	537.75	1057.46	529.23	11
15	1628.60	814.81	1611.58	806.29	1656.60	828.80	1639.57	820.29	G	987.45	494.23	970.43	485.72	10
16	1685.63	843.32	1668.60	834.80	1713.62	857.31	1696.59	848.80	G	930.43	465.72	913.40	457.21	9
17	1832.69	916.85	1815.67	908.34	1860.69	930.85	1843.66	922.34	F	873.41	437.21	856.38	428.69	8
18	1919.73	960.37	1902.70	951.85	1947.72	974.36	1930.69	965.85	S	726.34	363.67	709.31	355.16	7
19	1976.75	988.88	1959.72	980.36	2004.74	1002.88	1987.72	994.36	G	639.31	320.16	622.28	311.64	6
20	2073.80	1037.40	2056.77	1028.89	2101.80	1051.40	2084.77	1042.89	P	582.29	291.65	565.26	283.13	5
21	2130.82	1065.91	2113.80	1057.40	2158.82	1079.91	2141.79	1071.40	G	485.23	243.12	468.21	234.61	4
22	2259.86	1130.44	2242.84	1121.92	2287.86	1144.43	2270.83	1135.92	E	428.21	214.61	411.19	206.10	3
23	2373.91	1187.46	2356.88	1178.94	2401.90	1201.45	2384.88	1192.94	N	299.17	150.09	282.14	141.58	2
24									R	185.13	93.07	168.10	84.55	1



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

MATRIX SCIENCE Mascot Search Results

Peptide View

MS/MS Fragmentation of **IGGDAGTSLNSNDYGYGGQK**

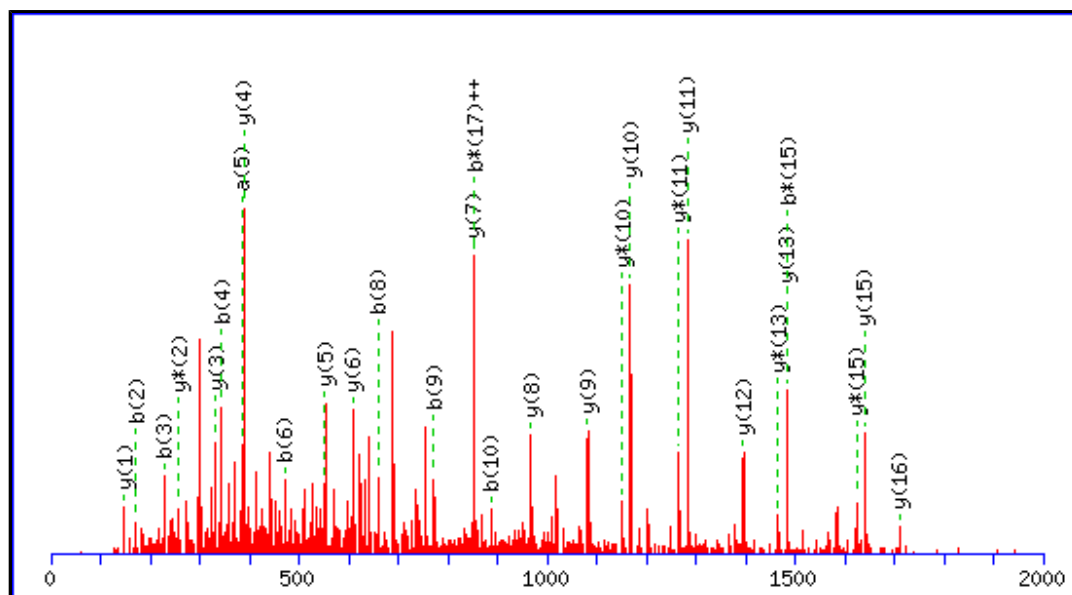
Found in **gi|17402900**, NP_003893.2] far upstream element-binding protein [Homo sapiens]

Match to Query 169: 2052.955248 from(1027.484900,2+)

From data file hm160404_AK_SILAC3_Src_0007A.pkl

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): 2052.84

Fixed modifications: Oxidation (M)

Variable modifications:

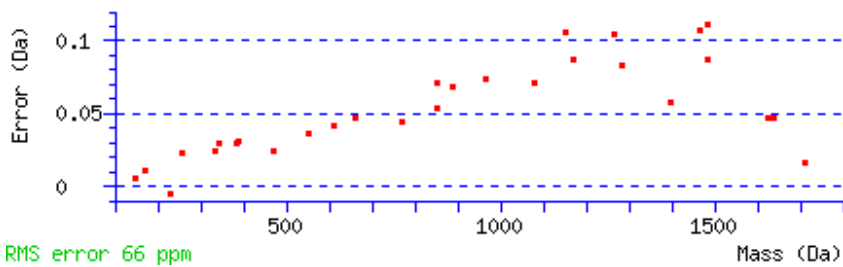
Y14 : Phospho (Y)

Ions Score: 65 **Expect:** 6.2e-05

Matches (Bold Red): 29/192 fragment ions using 91 most intense peaks

#	a	a ⁺⁺	a*	a* ⁺⁺	b	b ⁺⁺	b*	b* ⁺⁺	Seq.	y	y ⁺⁺	y*	y* ⁺⁺	#
1	86.10	43.55			114.09	57.55			I					20
2	143.12	72.06			171.11	86.06			G	1940.77	970.89	1923.74	962.37	19
3	200.14	100.57			228.13	114.57			G	1883.74	942.38	1866.72	933.86	18
4	315.17	158.09			343.16	172.08			D	1826.72	913.87	1809.70	905.35	17
5	386.20	193.61			414.20	207.60			A	1711.70	856.35	1694.67	847.84	16
6	443.22	222.12			471.22	236.11			G	1640.66	820.83	1623.63	812.32	15
7	544.27	272.64			572.27	286.64			T	1583.64	792.32	1566.61	783.81	14
8	631.30	316.16			659.30	330.15			S	1482.59	741.80	1465.56	733.29	13
9	744.39	372.70			772.38	386.70			L	1395.56	698.28	1378.53	689.77	12
10	858.43	429.72	841.41	421.21	886.43	443.72	869.40	435.20	N	1282.47	641.74	1265.45	633.23	11

11	945.46	473.24	928.44	464.72	973.46	487.23	956.43	478.72	S	1168.43	584.72	1151.40	576.21	10
12	1059.51	530.26	1042.48	521.74	1087.50	544.25	1070.47	535.74	N	1081.40	541.20	1064.37	532.69	9
13	1174.53	587.77	1157.51	579.26	1202.53	601.77	1185.50	593.25	D	967.36	484.18	950.33	475.67	8
14	1417.56	709.29	1400.54	700.77	1445.56	723.28	1428.53	714.77	Y	852.33	426.67	835.30	418.15	7
15	1474.58	737.80	1457.56	729.28	1502.58	751.79	1485.55	743.28	G	609.30	305.15	592.27	296.64	6
16	1637.65	819.33	1620.62	810.81	1665.64	833.33	1648.62	824.81	Y	552.28	276.64	535.25	268.13	5
17	1694.67	847.84	1677.64	839.33	1722.66	861.84	1705.64	853.32	G	389.21	195.11	372.19	186.60	4
18	1751.69	876.35	1734.66	867.84	1779.69	890.35	1762.66	881.83	G	332.19	166.60	315.17	158.09	3
19	1879.75	940.38	1862.72	931.87	1907.74	954.38	1890.72	945.86	Q	275.17	138.09	258.14	129.58	2
20									K	147.11	74.06	130.09	65.55	1



NCBI **BLAST** search of [IGGDAGTSLNSNDYGYGGQK](#)
 (Parameters: blastp, nr protein database, expect=20000, no filter, PAM30)
 Other BLAST [web gateways](#)

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

Mascot Search Results

Peptide View

MS/MS Fragmentation of **TDYNASVSPDSSGPER**

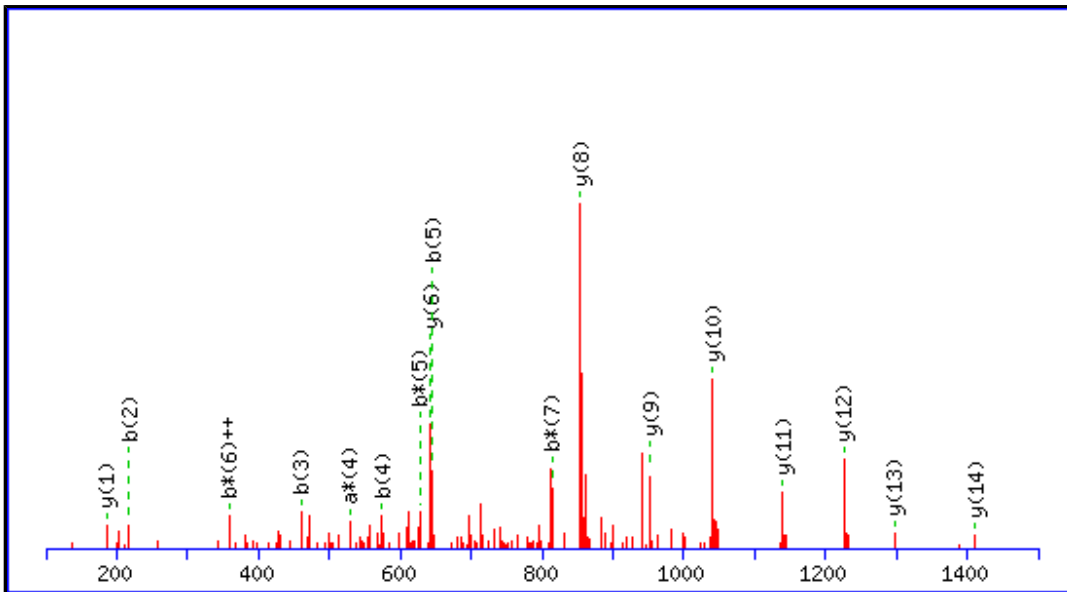
Found in **gi|14165435**, NP_112552.1| heterogeneous nuclear ribonucleoprotein K isoform b [Homo sapiens]

Match to Query 160: 1869.871448 from(935.943000,2+)

From data file hm160404_AK_SILAC3_Src_0009A.pkl

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): 1869.77

Fixed modifications: Oxidation (M)

Variable modifications:

Y3 : Phospho (Y)

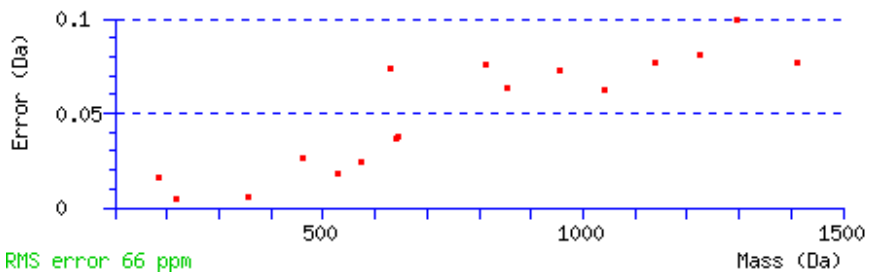
R17 : Arginine-13C615N4 (R-full)

Ions Score: 47 **Expect:** 0.005

Matches (Bold Red): 17/180 fragment ions using 37 most intense peaks

#	a	a ⁺⁺	a [*]	a ^{*++}	b	b ⁺⁺	b [*]	b ^{*++}	Seq.	y	y ⁺⁺	y [*]	y ^{*++}	#
1	74.06	37.53			102.05	51.53			T					17
2	189.09	95.05			217.08	109.04			D	1769.73	885.37	1752.70	876.85	16
3	432.12	216.56			460.11	230.56			Y	1654.70	827.85	1637.67	819.34	15
4	546.16	273.58	529.13	265.07	574.15	287.58	557.13	279.07	N	1411.67	706.34	1394.64	697.82	14
5	617.20	309.10	600.17	300.59	645.19	323.10	628.17	314.59	A	1297.63	649.32	1280.60	640.80	13
6	704.23	352.62	687.20	344.10	732.22	366.62	715.20	358.10	S	1226.59	613.80	1209.56	605.28	12
7	803.30	402.15	786.27	393.64	831.29	416.15	814.27	407.64	V	1139.56	570.28	1122.53	561.77	11
8	890.33	445.67	873.30	437.15	918.32	459.67	901.30	451.15	S	1040.49	520.75	1023.46	512.23	10
9	989.40	495.20	972.37	486.69	1017.39	509.20	1000.37	500.69	V	953.46	477.23	936.43	468.72	9
10	1086.45	543.73	1069.42	535.22	1114.45	557.73	1097.42	549.21	P	854.39	427.70	837.36	419.18	8

11	1201.48	601.24	1184.45	592.73	1229.47	615.24	1212.45	606.73	D	757.34	379.17	740.31	370.66	7
12	1288.51	644.76	1271.48	636.25	1316.50	658.76	1299.48	650.24	S	642.31	321.66	625.28	313.14	6
13	1375.54	688.27	1358.51	679.76	1403.54	702.27	1386.51	693.76	S	555.28	278.14	538.25	269.63	5
14	1432.56	716.79	1415.54	708.27	1460.56	730.78	1443.53	722.27	G	468.24	234.63	451.22	226.11	4
15	1529.62	765.31	1512.59	756.80	1557.61	779.31	1540.58	770.80	P	411.22	206.11	394.20	197.60	3
16	1658.66	829.83	1641.63	821.32	1686.65	843.83	1669.63	835.32	E	314.17	157.59	297.14	149.08	2
17									R	185.13	93.07	168.10	84.55	1



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