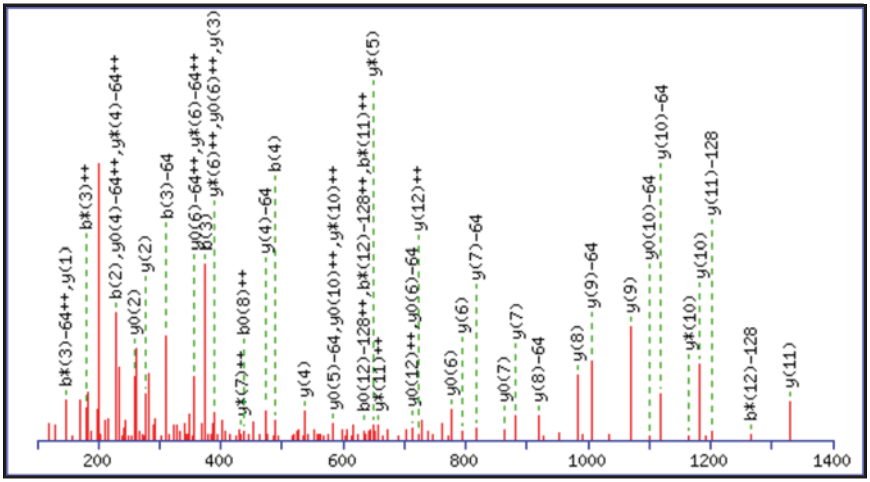
Peptide View

MS/MS Fragmentation of **NLMLSTSEEMIEK**
Found in **gi|6996658**, Apobec-1 complementation factor [Homo sapiens]

Match to Query 82: 1555.539048 from(778.776800,2+) intensity(1235.7059)

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1400 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1555.7109
Variable modifications:
M3 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
M10 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 49 **Expect:** 0.0052
Matches : 47/244 fragment ions using 69 most intense peaks (help)

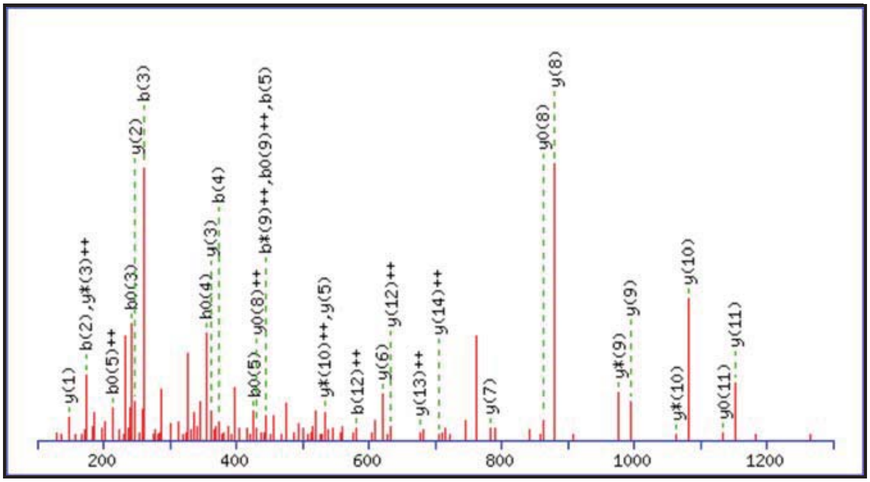
#	b	b^{++}	b*	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y*	y^{*++}	y^{0}	y^{0++}	#
1	115.0502	58.0287	98.0237	49.5155			N							13
2	**228.1343**	114.5708	211.1077	106.0575			L	1442.6753	721.8413	1425.6488	713.3280	1424.6647	712.8360	12
3	**375.1697**	188.0885	358.1431	179.5752			M	***1329.5912***	665.2993	1312.5647	656.7860	1311.5807	656.2940	11
4	**488.2537**	244.6305	471.2272	236.1172			L	***1182.5558***	591.7816	1165.5293	583.2683	1164.5453	582.7763	10
5	575.2858	288.1465	558.2592	279.6332	557.2752	279.1412	S	***1069.4718***	535.2395	1052.4452	526.7263	1051.4612	526.2342	9
6	676.3334	338.6704	659.3069	330.1571	658.3229	329.6651	T	***982.4398***	491.7235	965.4132	483.2102	964.4292	482.7182	8
7	763.3655	382.1864	746.3389	373.6731	745.3549	373.1811	S	***881.3921***	441.1997	864.3655	432.6864	863.3815	432.1944	7
8	892.4081	446.7077	875.3815	438.1944	874.3975	437.7024	E	***794.3600***	397.6837	777.3335	389.1704	776.3495	388.6784	6
9	1021.4507	511.2290	1004.4241	502.7157	1003.4401	502.2237	E	665.3175	333.1624	648.2909	324.6491	647.3069	324.1571	5
10	1168.4861	584.7467	1151.4595	576.2334	1150.4755	575.7414	M	***536.2749***	268.6411	519.2483	260.1278	518.2643	259.6358	4
11	1281.5701	641.2887	1264.5436	632.7754	1263.5596	632.2834	I	***389.2395***	195.1234	372.2129	186.6101	371.2289	186.1181	3
12	1410.6127	705.8100	1393.5862	697.2967	1392.6021	696.8047	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

Peptide View

MS/MS Fragmentation of **DGSLASNPYSGDLTK**
Found in **gi|11990132**, NICE-4 protein [Homo sapiens]

Match to Query 69: 1523.711248 from(762.862900,2+) intensity(263.4501)

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



`Monoisotopic mass of neutral peptide Mr(calc):` 1523.7104
`Ions Score:` 50 `Expect:` 0.0059
`Matches :` 31/154 fragment ions using 61 most intense peaks (help)

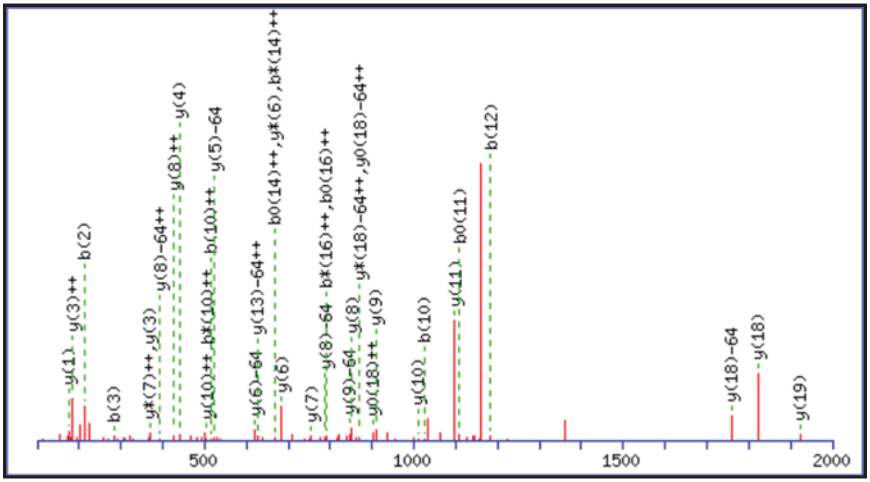
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	116.0342	58.5207			98.0237	49.5155	D							15
2	**173.0557**	87.0315			155.0451	78.0262	G	1409.6907	705.3490	1392.6642	696.8357	1391.6801	696.3437	14
3	**260.0877**	130.5475			242.0771	121.5422	S	1352.6692	676.8383	1335.6427	668.3250	1334.6587	667.8330	13
4	**373.1718**	187.0895			355.1612	178.0842	L	1265.6372	633.3222	1248.6107	624.8090	1247.6266	624.3170	12
5	**444.2089**	222.6081			426.1983	213.6028	A	***1152.5531***	576.7802	1135.5266	568.2669	1134.5426	567.7749	11
6	531.2409	266.1241			513.2304	257.1188	S	***1081.5160***	541.2617	1064.4895	532.7484	1063.5055	532.2564	10
7	645.2838	323.1456	628.2573	314.6323	627.2733	314.1403	N	***994.4840***	497.7456	977.4575	489.2324	976.4734	488.7404	9
8	742.3366	371.6719	725.3101	363.1587	724.3260	362.6667	P	***880.4411***	440.7242	863.4145	432.2109	862.4305	431.7189	8
9	905.3999	453.2036	888.3734	444.6903	887.3894	444.1983	Y	***783.3883***	392.1978	766.3618	383.6845	765.3777	383.1925	7
10	992.4320	496.7196	975.4054	488.2063	974.4214	487.7143	S	***620.3250***	310.6661	603.2984	302.1529	602.3144	301.6608	6
11	1049.4534	525.2304	1032.4269	516.7171	1031.4429	516.2251	G	***533.2930***	267.1501	516.2664	258.6368	515.2824	258.1448	5
12	1164.4804	582.7438	1147.4538	574.2305	1146.4698	573.7385	D	476.2715	238.6394	459.2449	230.1261	458.2609	229.6341	4
13	1277.5644	639.2859	1260.5379	630.7726	1259.5539	630.2806	L	***361.2445***	181.1259	344.2180	172.6126	343.2340	172.1206	3
14	1378.6121	689.8097	1361.5856	681.2964	1360.6015	680.8044	T	***248.1605***	124.5839	231.1339	116.0706	230.1499	115.5786	2
15							K	***147.1128***	74.0600	130.0863	65.5468			1

Peptide View

MS/MS Fragmentation of **IVAERPGTNSTGPAPMAPPR**
Found in **gi|1699027**, nuclear corepressor KAP-1 [Homo sapiens]

Match to Query 120: 2034.029472 from(679.017100,3+) intensity(353.5331)

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 2000 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 2034.0316
Variable modifications:
M16 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 42 **Expect:** 0.034
Matches : 37/300 fragment ions using 74 most intense peaks (help)

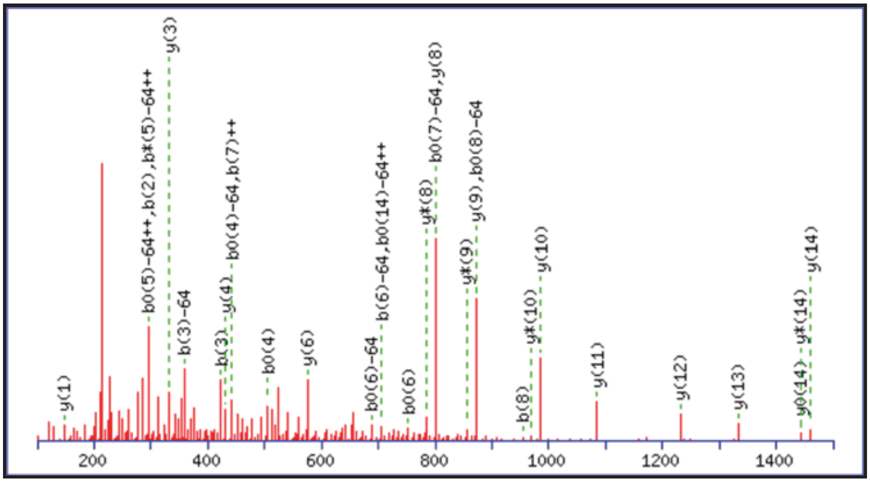
#	b	b^{++}	b*	b*$^{++}$	b^0	b^{0++}	Seq.	y	y^{++}	y*	y*$^{++}$	y^0	y^{0++}	#
1	114.0913	57.5493					I							20
2	**213.1598**	107.0835					V	***1921.9549***	961.4811	1904.9283	952.9678	1903.9443	952.4758	19
3	**284.1969**	142.6021					A	***1822.8865***	911.9469	1805.8599	903.4336	1804.8759	902.9416	18
4	413.2395	207.1234			395.2289	198.1181	E	1751.8493	876.4283	1734.8228	867.9150	1733.8388	867.4230	17
5	569.3406	285.1739	552.3140	276.6606	551.3300	276.1686	R	1622.8068	811.9070	1605.7802	803.3937	1604.7962	802.9017	16
6	666.3933	333.7003	649.3668	325.1870	648.3828	324.6950	P	1466.7056	733.8565	1449.6791	725.3432	1448.6951	724.8512	15
7	723.4148	362.2110	706.3883	353.6978	705.4042	353.2058	G	1369.6529	685.3301	1352.6263	676.8168	1351.6423	676.3248	14
8	824.4625	412.7349	807.4359	404.2216	806.4519	403.7296	T	1312.6314	656.8193	1295.6049	648.3061	1294.6208	647.8141	13
9	938.5054	469.7563	921.4789	461.2431	920.4948	460.7511	N	1211.5837	606.2955	1194.5572	597.7822	1193.5732	597.2902	12
10	**1025.5374**	513.2724	1008.5109	504.7591	1007.5269	504.2671	S	***1097.5408***	549.2740	1080.5143	540.7608	1079.5302	540.2688	11
11	1126.5851	563.7962	1109.5586	555.2829	1108.5745	554.7909	T	***1010.5088***	505.7580	993.4822	497.2448	992.4982	496.7527	10
12	**1183.6066**	592.3069	1166.5800	583.7937	1165.5960	583.3016	G	***909.4611***	455.2342	892.4346	446.7209			9
13	1280.6593	640.8333	1263.6328	632.3200	1262.6488	631.8280	P	***852.4396***	426.7235	835.4131	418.2102			8
14	1351.6965	676.3519	1334.6699	667.8386	1333.6859	667.3466	A	***755.3869***	378.1971	738.3603	369.6838			7
15	1448.7492	724.8782	1431.7227	716.3650	1430.7387	715.8730	P	***684.3498***	342.6785	667.3232	334.1652			6
16	1595.7846	798.3959	1578.7581	789.8827	1577.7741	789.3907	M	587.2970	294.1521	570.2704	285.6389			5
17	1666.8217	833.9145	1649.7952	825.4012	1648.8112	824.9092	A	***440.2616***	220.6344	423.2350	212.1212			4
18	1763.8745	882.4409	1746.8479	873.9276	1745.8639	873.4356	P	***369.2245***	185.1159	352.1979	176.6026			3
19	1860.9273	930.9673	1843.9007	922.4540	1842.9167	921.9620	P	272.1717	136.5895	255.1452	128.0762			2
20							R	***175.1190***	88.0631	158.0924	79.5498			1

Peptide View

MS/MS Fragmentation of **FMQTFVLAPEGSVANK**
Found in **gi|5031703**, ras GTPase-activating protein-binding protein 1 [Homo sapiens]

Match to Query 111: 1753.682248 from(877.848400,2+) intensity(2393.7693)

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1500 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): 1753.8709
Variable modifications:
M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983
Ions Score: 73 **Expect:** 2.7e-05
Matches : 31/246 fragment ions using 40 most intense peaks (help)

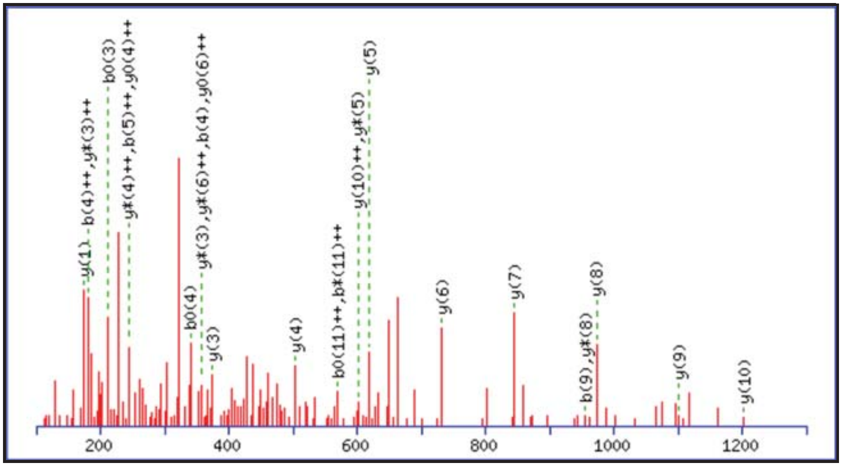
#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	148.0757	74.5415					F							16
2	**295.1111**	148.0592					M	1607.8098	804.4085	1590.7832	795.8952	1589.7992	795.4032	15
3	**423.1697**	212.0885	406.1431	203.5752			Q	***1460.7744***	730.8908	1443.7478	722.3775	1442.7638	721.8855	14
4	524.2173	262.6123	507.1908	254.0990	506.2068	253.6070	T	***1332.7158***	666.8615	1315.6892	658.3483	1314.7052	657.8563	13
5	671.2858	336.1465	654.2592	327.6332	653.2752	327.1412	F	***1231.6681***	616.3377	1214.6416	607.8244	1213.6575	607.3324	12
6	770.3542	385.6807	753.3276	377.1675	752.3436	376.6754	V	***1084.5997***	542.8035	1067.5732	534.2902	1066.5891	533.7982	11
7	883.4382	442.2228	866.4117	433.7095	865.4277	433.2175	L	***985.5313***	493.2693	968.5047	484.7560	967.5207	484.2640	10
8	**954.4754**	477.7413	937.4488	469.2280	936.4648	468.7360	A	***872.4472***	436.7272	855.4207	428.2140	854.4367	427.7220	9
9	1051.5281	526.2677	1034.5016	517.7544	1033.5176	517.2624	P	***801.4101***	401.2087	784.3836	392.6954	783.3995	392.2034	8
10	1180.5707	590.7890	1163.5442	582.2757	1162.5601	581.7837	E	704.3573	352.6823	687.3308	344.1690	686.3468	343.6770	7
11	1237.5922	619.2997	1220.5656	610.7865	1219.5816	610.2944	G	***575.3148***	288.1610	558.2882	279.6477	557.3042	279.1557	6
12	1324.6242	662.8157	1307.5977	654.3025	1306.6136	653.8105	S	518.2933	259.6503	501.2667	251.1370	500.2827	250.6450	5
13	1423.6926	712.3499	1406.6661	703.8367	1405.6821	703.3447	V	***431.2613***	216.1343	414.2347	207.6210			4
14	1494.7297	747.8685	1477.7032	739.3552	1476.7192	738.8632	A	***332.1928***	166.6001	315.1663	158.0868			3
15	1608.7727	804.8900	1591.7461	796.3767	1590.7621	795.8847	N	261.1557	131.0815	244.1292	122.5682			2
16							K	***147.1128***	74.0600	130.0863	65.5468			1

Peptide View

MS/MS Fragmentation of **GATQQILDEAER**
Found in **gi|5453603**, T-complex protein 1 subunit beta isoform 1 [Homo sapiens]

Match to Query 61: 1329.522648 from(665.768600,2+) intensity(352.0675)

Click mouse within plot area to zoom in by factor of two about that point
Or, Plot from 100 to 1300 Da Full range
Label all possible matches ○ Label matches used for scoring ●



Monoisotopic mass of neutral peptide Mr(calc): `1329.6524`
Ions Score: `41` **Expect:** `0.05`
Matches : `26/120 fragment ions using 43 most intense peaks` (help)

#	b	b^{++}	b^{*}	b^{*++}	b^{0}	b^{0++}	Seq.	y	y^{++}	y^{*}	y^{*++}	y^{0}	y^{0++}	#
1	58.0287	29.5180					G							12
2	129.0659	65.0366					A	1273.6383	637.3228	1256.6117	628.8095	1255.6277	628.3175	11
3	230.1135	115.5604			212.1030	106.5551	T	***1202.6012***	601.8042	1185.5746	593.2909	1184.5906	592.7989	10
4	358.1721	179.5897	341.1456	171.0764	340.1615	170.5844	Q	***1101.5535***	551.2804	1084.5269	542.7671	1083.5429	542.2751	9
5	486.2307	243.6190	469.2041	235.1057	468.2201	234.6137	Q	***973.4949***	487.2511	956.4684	478.7378	955.4843	478.2458	8
6	599.3148	300.1610	582.2882	291.6477	581.3042	291.1557	I	***845.4363***	423.2218	828.4098	414.7085	827.4258	414.2165	7
7	712.3988	356.7030	695.3723	348.1898	694.3883	347.6978	L	***732.3523***	366.6798	715.3257	358.1665	714.3417	357.6745	6
8	827.4258	414.2165	810.3992	405.7032	809.4152	405.2112	D	***619.2682***	310.1377	602.2416	301.6245	601.2576	301.1325	5
9	956.4684	478.7378	939.4418	470.2245	938.4578	469.7325	E	***504.2413***	252.6243	487.2147	244.1110	486.2307	243.6190	4
10	1027.5055	514.2564	1010.4789	505.7431	1009.4949	505.2511	A	***375.1987***	188.1030	358.1721	179.5897	357.1881	179.0977	3
11	1156.5481	578.7777	1139.5215	570.2644	1138.5375	569.7724	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