

**Supporting Information 2 (SI2):** Single peptide-based identifications

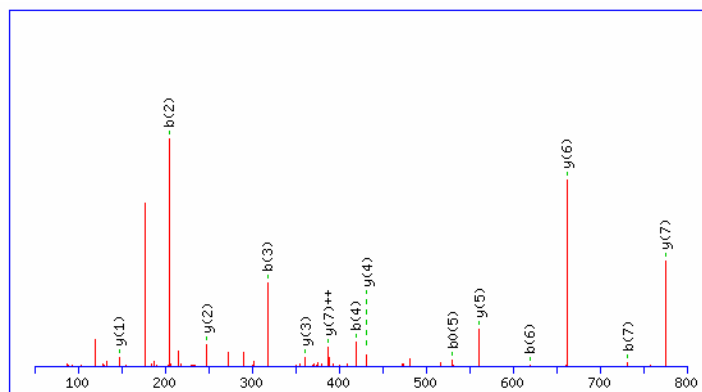
***C. neoformans* - protein 37:**

Q5KPX0 Expressed protein (Putative uncharacterized protein) Tax\_Id=5207 [*Cryptococcus neoformans*]

MW = 31335, pI = 5.43, Score = 57, Coverage = 3%, Unique peptides = 1

Start-End: 200-208. Observed mass: 490.2796 (2+). Mr (expt): 978.5446. Mr(calc): 978.5386 . Error (ppm): 6. Miss cleavage: 0. Sequence: R.GFITEALTK.N

MS/MS Spectrum:



Monoisotopic mass of neutral peptide Mr(calc): 978.5386

Ions Score: 57 Expect: 0.038

Matches (Bold Red): 14/72 fragment ions using 22 most intense peaks

#	b	b <sup>++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	58.0287	29.5180			G							9
2	205.0972	103.0522			F	922.5244	461.7658	905.4979	453.2526	904.5138	452.7606	8
3	318.1812	159.5942			I	775.4560	388.2316	758.4294	379.7184	757.4454	379.2264	7
4	419.2289	210.1181	401.2183	201.1128	T	662.3719	331.6896	645.3454	323.1763	644.3614	322.6843	6
5	548.2715	274.6394	530.2609	265.6341	E	561.3243	281.1658	544.2977	272.6525	543.3137	272.1605	5
6	619.3086	310.1579	601.2980	301.1527	A	432.2817	216.6445	415.2551	208.1312	414.2711	207.6392	4
7	732.3927	366.7000	714.3821	357.6947	L	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
8	833.4403	417.2238	815.4298	408.2185	T	248.1605	124.5839	231.1339	116.0706	230.1499	115.5786	2
9					K	147.1128	74.0600	130.0863	65.5468			1

### ***C. gattii* VGI - protein 2:**

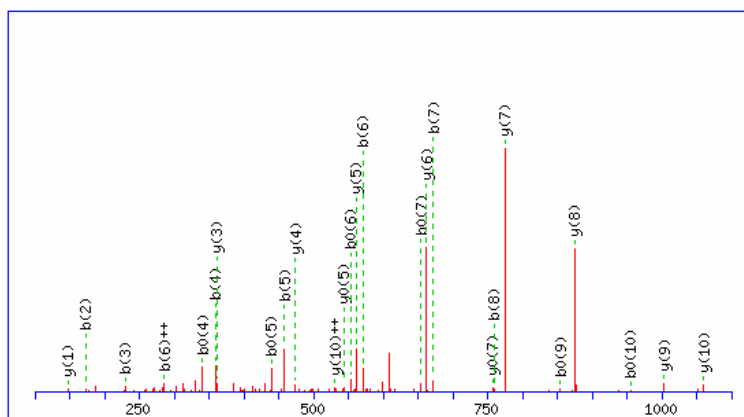
Q5KFM3Thioredoxin reductase Tax\_Id=5207 [*Cryptococcus neoformans*]

MW = 39839, pI = 5.14, Score = 73, Coverage = 3%, Unique peptides = 1

Start-End: 246 - 257. Observed mass: 616.8646 (2+). Mr (expt): 1231.7147. Mr(calc): 1231.6660. Error (ppm): 40. Miss

cleavage: 0. Sequence: K.GDGEVLTSLLTIK.N

MS/MS Spectrum:



Monoisotopic mass of neutral peptide Mr(calc): 1231.6660

Ions Score: 73. Expect: 0.00088

Matches (Bold Red): 26/104 fragment ions using 36 most intense peaks

#	b	b <sup>++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>***</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	58.0287	29.5180			G							12
2	<b>173.0557</b>	87.0315	155.0451	78.0262	D	1175.6518	588.3295	1158.6252	579.8163	1157.6412	579.3243	11
3	<b>230.0771</b>	115.5422	212.0666	106.5369	G	<b>1060.6249</b>	<b>530.8161</b>	1043.5983	522.3028	1042.6143	521.8108	10
4	<b>359.1197</b>	180.0635	<b>341.1092</b>	171.0582	E	<b>1003.6034</b>	502.3053	986.5768	493.7921	985.5928	493.3001	9
5	<b>458.1882</b>	229.5977	<b>440.1776</b>	220.5924	V	<b>874.5608</b>	437.7840	857.5342	429.2708	856.5502	428.7788	8
6	<b>571.2722</b>	<b>286.1397</b>	<b>553.2617</b>	277.1345	L	<b>775.4924</b>	388.2498	758.4658	379.7366	<b>757.4818</b>	379.2445	7
7	<b>672.3199</b>	336.6636	<b>654.3093</b>	327.6583	T	<b>662.4083</b>	331.7078	645.3818	323.1945	644.3978	322.7025	6
8	<b>759.3519</b>	380.1796	741.3414	371.1743	S	<b>561.3606</b>	281.1840	544.3341	272.6707	<b>543.3501</b>	272.1787	5
9	872.4360	436.7216	<b>854.4254</b>	427.7164	L	<b>474.3286</b>	237.6679	457.3021	229.1547	456.3180	228.6627	4

10	973.4837	487.2455	955.4731	478.2402	T	361.2445	181.1259	344.2180	172.6126	343.2340	172.1206	3
11	1086.5677	543.7875	1068.5572	534.7822	I	260.1969	130.6021	243.1703	122.0888			2
12					K	147.1128	74.0600	130.0863	65.5468			1

### ***C. gattii* VGI - protein 31:**

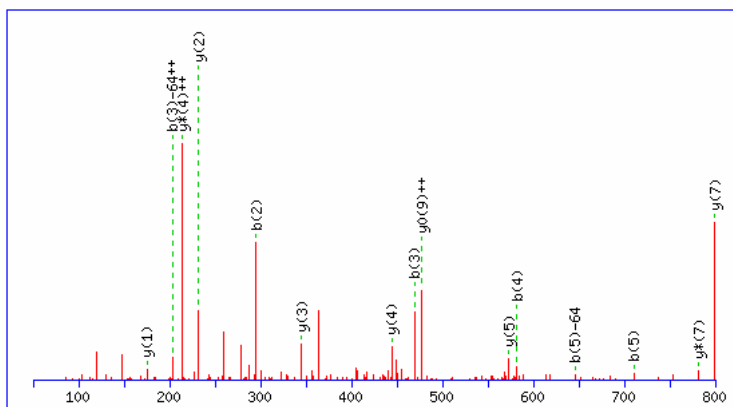
Q5KNQ6|Profilin Tax\_Id=5207 [Cryptococcus neoformans]

MW = 13658, pI = 6.56, Score = 86, Coverage = 11%, Unique peptides = 1

Start-End: 69-82. Observed mass: 840.9134 (2+). Mr (expt): 1679.8122 . Mr(calc): 1679.8011. Error (ppm): 7. Miss

cleavage: 0. Sequence: K.FMCIQATPEEVIGR.K Oxidation (M); Propionamide (C)

MS/MS Spectrum:



Monoisotopic mass of neutral peptide Mr(calc): 1679.8011

Variable modifications:

M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

C3 : Propionamide (C)

Ions Score: 86 Expect: 6.1e-005

Matches (Bold Red): 23/190 fragment ions using 32 most intense peaks

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	148.0757	74.5415					F							14
2	<b>295.1111</b>	148.0592					M	1533.7400	767.3736	1516.7134	758.8604	1515.7294	758.3683	13
3	<b>469.1574</b>	235.0823					C	<b>1386.7046</b>	693.8559	1369.6780	685.3426	1368.6940	684.8506	12
4	<b>582.2415</b>	291.6244					I	<b>1212.6583</b>	606.8328	1195.6317	598.3195	1194.6477	597.8275	11
5	<b>710.3000</b>	355.6537	693.2735	347.1404			Q	<b>1099.5742</b>	550.2907	1082.5477	541.7775	<b>1081.5636</b>	541.2855	10
6	781.3371	391.1722	764.3106	382.6589			A	<b>971.5156</b>	486.2615	954.4891	477.7482	953.5051	<b>477.2562</b>	9
7	<b>882.3848</b>	441.6960	865.3583	433.1828	864.3743	432.6908	T	<b>900.4785</b>	450.7429	883.4520	442.2296	<b>882.4680</b>	441.7376	8
8	979.4376	490.2224	962.4110	481.7092	961.4270	481.2171	P	<b>799.4308</b>	400.2191	<b>782.4043</b>	391.7058	781.4203	391.2138	7
9	1108.4802	554.7437	1091.4536	546.2305	1090.4696	545.7384	E	702.3781	351.6927	685.3515	343.1794	684.3675	342.6874	6
10	1237.5228	619.2650	1220.4962	610.7518	1219.5122	610.2597	E	<b>573.3355</b>	287.1714	556.3089	278.6581	555.3249	278.1661	5
11	1336.5912	668.7992	1319.5646	660.2860	1318.5806	659.7939	V	<b>444.2929</b>	222.6501	427.2663	<b>214.1368</b>			4
12	1449.6753	725.3413	1432.6487	716.8280	1431.6647	716.3360	I	<b>345.2245</b>	173.1159	328.1979	164.6026			3
13	1506.6967	753.8520	1489.6702	745.3387	1488.6861	744.8467	G	<b>232.1404</b>	116.5738	215.1139	108.0606			2
14							R	<b>175.1190</b>	88.0631	158.0924	79.5498			1

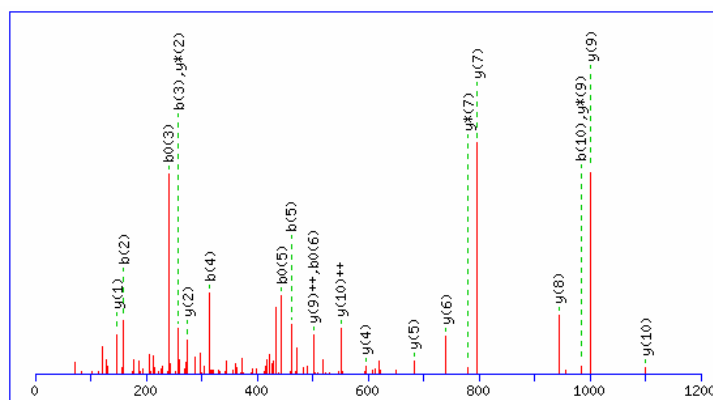
**C. gattii VGII - protein 1:**

A6DQH7 UDP-glucose 6-dehydrogenase Tax\_Id=313628 [*Lentisphaera araneosa* HTCC2155]

MW = 50148, pI = 4.97, Score = 90, Coverage = 2%, Unique peptides = 1

Start-End: 266-277. Observed mass: 629.8712 (2+). Mr (expt): 1257.7279. Mr(calc): 1257.6176. Error (ppm): 88. Miss cleavage: 1. Sequence: K.ASVGFGGSCFKK.D Propionamide (C)

MS/MS Spectrum:



Monoisotopic mass of neutral peptide Mr(calc): 1257.6176

Variable modifications:

C9 : Propionamide (C)

Ions Score: 90 Expect: 2.1e-005

Matches (Bold Red): 22/102 fragment ions using 23 most intense peaks

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	72.0444	36.5258					A							12
2	159.0764	80.0418			141.0659	71.0366	S	1187.5878	594.2975	1170.5612	585.7842	1169.5772	585.2922	11
3	258.1448	129.5761			240.1343	120.5708	V	1100.5557	550.7815	1083.5292	542.2682	1082.5452	541.7762	10
4	315.1663	158.0868			297.1557	149.0815	G	1001.4873	501.2473	984.4608	492.7340	983.4767	492.2420	9
5	462.2347	231.6210			444.2241	222.6157	F	944.4658	472.7366	927.4393	464.2233	926.4553	463.7313	8
6	519.2562	260.1317			501.2456	251.1264	G	797.3974	399.2024	780.3709	390.6891	779.3869	390.1971	7
7	576.2776	288.6425			558.2671	279.6372	G	740.3760	370.6916	723.3494	362.1783	722.3654	361.6863	6
8	663.3097	332.1585			645.2991	323.1532	S	683.3545	342.1809	666.3280	333.6676	665.3439	333.1756	5
9	837.3560	419.1816			819.3454	410.1763	C	596.3225	298.6649	579.2959	290.1516			4
10	984.4244	492.7158			966.4138	483.7105	F	422.2762	211.6417	405.2496	203.1285			3
11	1112.5193	556.7633	1095.4928	548.2500	1094.5088	547.7580	K	275.2078	138.1075	258.1812	129.5942			2
12							K	147.1128	74.0600	130.0863	65.5468			1

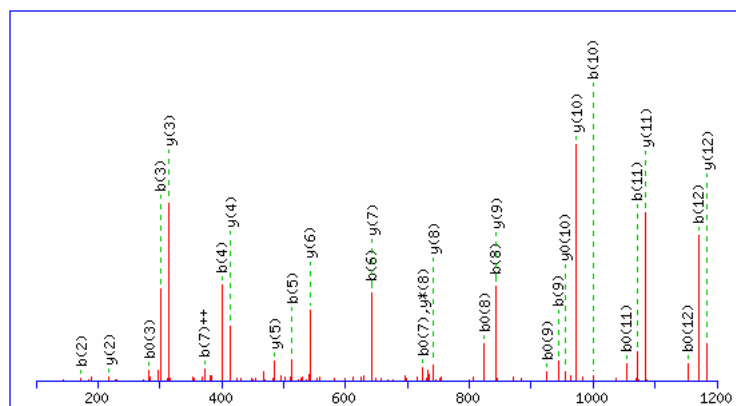
### ***C. gattii* VGII - protein 3:**

Q5KK55 Thioredoxin (Allergen cop c 2), putative (Putative uncharacterized protein) Tax\_Id=5207 [*Cryptococcus neoformans*]

MW = 11444, pI = 5.36, Score = 112, Coverage = 14%, Unique peptides = 1

Start-End: 80-94. Observed mass: 742.9188 (2+). Mr (expt): 1483.8231. Mr(calc): 1483.8246. Error (ppm): -1. Miss cleavage: 1. Sequence: K.DGKVIETVTGAVPAK.I

MS/MS Spectrum:



Monoisotopic mass of neutral peptide Mr(calc): 1483.8246

Ions Score: 112 Expect: 1.2e-007

Matches (Bold Red): 30/152 fragment ions using 33 most intense peaks

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	116.0342	58.5207			98.0237	49.5155	D							15
2	<b>173.0557</b>	87.0315			155.0451	78.0262	G	1369.8049	685.4061	1352.7784	676.8928	1351.7944	676.4008	14
3	<b>301.1506</b>	151.0790	284.1241	142.5657	<b>283.1401</b>	142.0737	K	1312.7835	656.8954	1295.7569	648.3821	1294.7729	647.8901	13
4	<b>400.2191</b>	200.6132	383.1925	192.0999	382.2085	191.6079	V	<b>1184.6885</b>	592.8479	1167.6620	584.3346	1166.6780	583.8426	12
5	<b>513.3031</b>	257.1552	496.2766	248.6419	495.2926	248.1499	I	<b>1085.6201</b>	543.3137	1068.5936	534.8004	1067.6095	534.3084	11
6	<b>642.3457</b>	321.6765	625.3192	313.1632	624.3352	312.6712	E	<b>972.5360</b>	486.7717	955.5095	478.2584	<b>954.5255</b>	477.7664	10
7	743.3934	<b>372.2003</b>	726.3668	363.6871	<b>725.3828</b>	363.1951	T	<b>843.4934</b>	422.2504	826.4669	413.7371	825.4829	413.2451	9
8	<b>842.4618</b>	421.7345	825.4353	413.2213	<b>824.4512</b>	412.7293	V	<b>742.4458</b>	371.7265	<b>725.4192</b>	363.2132	724.4352	362.7212	8
9	<b>943.5095</b>	472.2584	926.4829	463.7451	<b>925.4989</b>	463.2531	T	<b>643.3774</b>	322.1923	626.3508	313.6790	625.3668	313.1870	7
10	<b>1000.5310</b>	500.7691	983.5044	492.2558	982.5204	491.7638	G	<b>542.3297</b>	271.6685	525.3031	263.1552			6
11	<b>1071.5681</b>	536.2877	1054.5415	527.7744	<b>1053.5575</b>	527.2824	A	<b>485.3082</b>	243.1577	468.2817	234.6445			5



12	1170.6365	585.8219	1153.6099	577.3086	1152.6259	576.8166	V	414.2711	207.6392	397.2445	199.1259			4
13	1267.6892	634.3483	1250.6627	625.8350	1249.6787	625.3430	P	315.2027	158.1050	298.1761	149.5917			3
14	1338.7264	669.8668	1321.6998	661.3535	1320.7158	660.8615	A	218.1499	109.5786	201.1234	101.0653			2
15							K	147.1128	74.0600	130.0863	65.5468			1

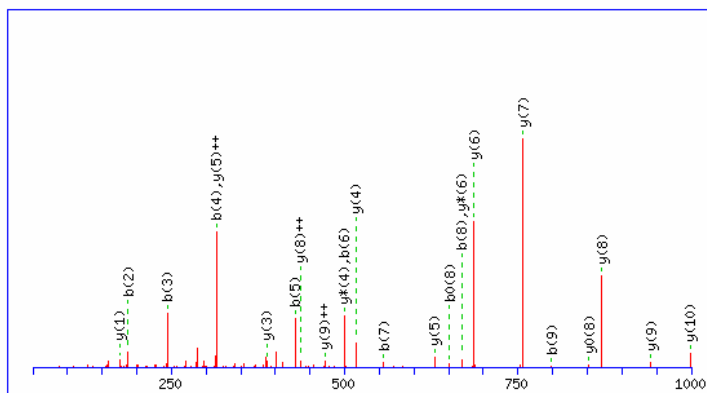
### ***C. gattii* VGII - protein 7:**

Q5KPD7 Heat shock protein sks2 (Heat shock cognate protein hsc1), putative Tax\_Id=5207 [*Cryptococcus neoformans*]

MW = 67085, pI = 5.37, Score = 74, Coverage = 1%, Unique peptides = 1

Start-End: 164-175. Observed mass: 592.8284 (2+). Mr (expt): 1183.6423. Mr(calc): 1183.6561. Error (ppm): -12. Miss cleavage: 0. Sequence: K.DAGAIAGLEVLR.I

MS/MS Spectrum:



Monoisotopic mass of neutral peptide Mr(calc): 1183.6561

Ions Score: 74 Expect: 0.0007

Matches (Bold Red): 24/104 fragment ions using 32 most intense peaks

#	b	b <sup>++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	116.0342	58.5207	98.0237	49.5155	D							12
2	<b>187.0713</b>	94.0393	169.0608	85.0340	A	1069.6364	535.3218	1052.6099	526.8086	1051.6259	526.3166	11
3	<b>244.0928</b>	122.5500	226.0822	113.5448	G	<b>998.5993</b>	499.8033	981.5728	491.2900	980.5887	490.7980	10
4	<b>315.1299</b>	158.0686	297.1193	149.0633	A	<b>941.5778</b>	<b>471.2926</b>	924.5513	462.7793	923.5673	462.2873	9
5	<b>428.2140</b>	214.6106	410.2034	205.6053	I	<b>870.5407</b>	<b>435.7740</b>	853.5142	427.2607	<b>852.5302</b>	426.7687	8
6	<b>499.2511</b>	250.1292	481.2405	241.1239	A	<b>757.4567</b>	379.2320	740.4301	370.7187	739.4461	370.2267	7
7	<b>556.2726</b>	278.6399	538.2620	269.6346	G	<b>686.4196</b>	343.7134	<b>669.3930</b>	335.2001	668.4090	334.7081	6
8	<b>669.3566</b>	335.1819	<b>651.3461</b>	326.1767	L	<b>629.3981</b>	<b>315.2027</b>	612.3715	306.6894	611.3875	306.1974	5
9	<b>798.3992</b>	399.7032	780.3886	390.6980	E	<b>516.3140</b>	258.6606	<b>499.2875</b>	250.1474	498.3035	249.6554	4
10	897.4676	449.2375	879.4571	440.2322	V	<b>387.2714</b>	194.1394	370.2449	185.6261			3
11	1010.5517	505.7795	992.5411	496.7742	L	288.2030	144.6051	271.1765	136.0919			2
12					R	<b>175.1190</b>	88.0631	158.0924	79.5498			1

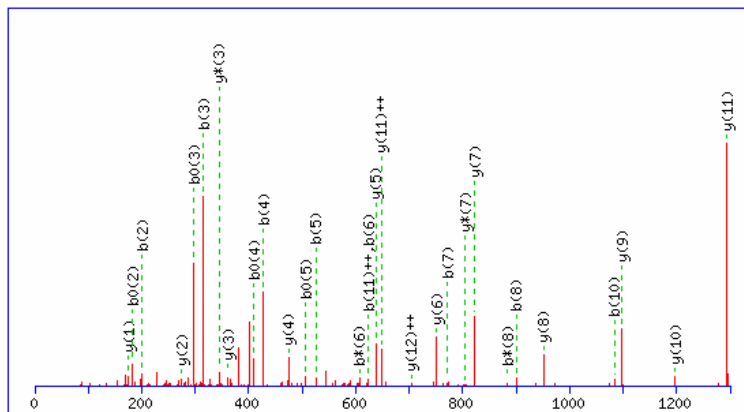
**C. gattii VGII - protein 12:**

Q96VZ5 Acetohydroxyacid reductoisomerase Tax\_Id=5207 [*Cryptococcus neoformans*]

MW = 44407, pI = 7.71, Score = 71, Coverage = 3%, Unique peptides = 1

Start-End: 335-349. Observed mass: 861.4116 (2+). Mr (expt): 1720.8087. Mr(calc): 1720.8784. Error (ppm): -41. Miss cleavage: 0. Sequence: K.EANLPVFEALYNSVR.D

MS/MS Spectrum:



Monoisotopic mass of neutral peptide Mr(calc): 1720.8784

Ions Score: 71 Expect: 0.0015

Matches (Bold Red): 30/160 fragment ions using 55 most intense peaks

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	130.0499	65.5286			112.0393	56.5233	E							15
2	<b>201.0870</b>	101.0471			<b>183.0764</b>	92.0418	A	1592.8431	796.9252	1575.8166	788.4119	1574.8326	787.9199	14
3	<b>315.1299</b>	158.0686	298.1034	149.5553	<b>297.1193</b>	149.0633	N	1521.8060	761.4066	1504.7795	752.8934	1503.7954	752.4014	13
4	<b>428.2140</b>	214.6106	411.1874	206.0974	<b>410.2034</b>	205.6053	L	1407.7631	<b>704.3852</b>	1390.7365	695.8719	1389.7525	695.3799	12
5	<b>525.2667</b>	263.1370	508.2402	254.6237	<b>507.2562</b>	254.1317	P	<b>1294.6790</b>	<b>647.8431</b>	1277.6525	639.3299	1276.6684	638.8379	11
6	<b>624.3352</b>	312.6712	<b>607.3086</b>	304.1579	606.3246	303.6659	V	<b>1197.6262</b>	599.3168	1180.5997	590.8035	1179.6157	590.3115	10
7	<b>771.4036</b>	386.2054	754.3770	377.6921	753.3930	377.2001	F	<b>1098.5578</b>	549.7826	1081.5313	541.2693	1080.5473	540.7773	9
8	<b>900.4462</b>	450.7267	<b>883.4196</b>	442.2134	882.4356	441.7214	E	<b>951.4894</b>	476.2483	934.4629	467.7351	933.4789	467.2431	8
9	971.4833	486.2453	954.4567	477.7320	953.4727	477.2400	A	<b>822.4468</b>	411.7271	<b>805.4203</b>	403.2138	804.4363	402.7218	7

10	1084.5673	542.7873	1067.5408	534.2740	1066.5568	533.7820	L	751.4097	376.2085	734.3832	367.6952	733.3991	367.2032	6
11	1247.6307	624.3190	1230.6041	615.8057	1229.6201	615.3137	Y	638.3257	319.6665	621.2991	311.1532	620.3151	310.6612	5
12	1361.6736	681.3404	1344.6470	672.8272	1343.6630	672.3352	N	475.2623	238.1348	458.2358	229.6215	457.2518	229.1295	4
13	1448.7056	724.8564	1431.6791	716.3432	1430.6951	715.8512	S	361.2194	181.1133	344.1928	172.6001	343.2088	172.1081	3
14	1547.7740	774.3907	1530.7475	765.8774	1529.7635	765.3854	V	274.1874	137.5973	257.1608	129.0840			2
15							R	175.1190	88.0631	158.0924	79.5498			1

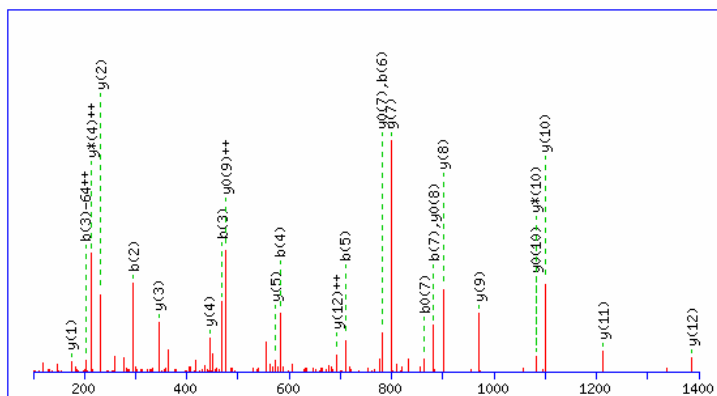
### ***C. gattii* VGII - protein 31:**

Q5KNQ6 Profilin Tax\_Id=5207 [Cryptococcus neoformans]

MW = 13658, pI = 6.56, Score = 87, Coverage = 11%, Unique peptides = 1

Start-End: 69-82. Observed mass: 840.9832 (2+). Mr (expt): 1679.9518. Mr(calc): 1679.8011. Error (ppm): 90. Miss cleavage: 0. Sequence: K.FMCIQATPEEVIGR.K Oxidation (M); Propionamide (C)

MS/MS Spectrum:



Monoisotopic mass of neutral peptide Mr(calc): 1679.8011

Variable modifications:

M2 : Oxidation (M), with neutral losses 0.0000(shown in table), 63.9983

C3 : Propionamide (C)

Ions Score: 87 Expect: 3.7e-005

Matches (Bold Red): 26/190 fragment ions using 35 most intense peaks

#	b	b <sup>++</sup>	b <sup>*</sup>	b <sup>+++</sup>	b <sup>0</sup>	b <sup>0++</sup>	Seq.	y	y <sup>++</sup>	y <sup>*</sup>	y <sup>+++</sup>	y <sup>0</sup>	y <sup>0++</sup>	#
1	148.0757	74.5415					F							14
2	<b>295.1111</b>	148.0592					M	1533.7400	767.3736	1516.7134	758.8604	1515.7294	758.3683	13
3	<b>469.1574</b>	235.0823					C	<b>1386.7046</b>	<b>693.8559</b>	1369.6780	685.3426	1368.6940	684.8506	12
4	<b>582.2415</b>	291.6244					I	<b>1212.6583</b>	606.8328	1195.6317	598.3195	1194.6477	597.8275	11
5	<b>710.3000</b>	355.6537	693.2735	347.1404			Q	<b>1099.5742</b>	550.2907	<b>1082.5477</b>	541.7775	<b>1081.5636</b>	541.2855	10
6	<b>781.3371</b>	391.1722	764.3106	382.6589			A	<b>971.5156</b>	486.2615	954.4891	477.7482	953.5051	<b>477.2562</b>	9
7	<b>882.3848</b>	441.6960	865.3583	433.1828	<b>864.3743</b>	432.6908	T	<b>900.4785</b>	450.7429	883.4520	442.2296	<b>882.4680</b>	441.7376	8
8	979.4376	490.2224	962.4110	481.7092	961.4270	481.2171	P	<b>799.4308</b>	400.2191	782.4043	391.7058	<b>781.4203</b>	391.2138	7
9	1108.4802	554.7437	1091.4536	546.2305	1090.4696	545.7384	E	702.3781	351.6927	685.3515	343.1794	684.3675	342.6874	6
10	1237.5228	619.2650	1220.4962	610.7518	1219.5122	610.2597	E	<b>573.3355</b>	287.1714	556.3089	278.6581	555.3249	278.1661	5
11	1336.5912	668.7992	1319.5646	660.2860	1318.5806	659.7939	V	<b>444.2929</b>	222.6501	427.2663	<b>214.1368</b>			4
12	1449.6753	725.3413	1432.6487	716.8280	1431.6647	716.3360	I	<b>345.2245</b>	173.1159	328.1979	164.6026			3
13	1506.6967	753.8520	1489.6702	745.3387	1488.6861	744.8467	G	<b>232.1404</b>	116.5738	215.1139	108.0606			2
14							R	<b>175.1190</b>	88.0631	158.0924	79.5498			1