Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\051111_OGL_BS21_1frac
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 147 **Hits:** 319
beginning to assemble proteins .... proteins assembled 0.047888 sec
proteins filtered by unique peptides 0.004622 sec
proteins filtered by score
calculated protein coverage maps 0.040805 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.004068 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 9 Proteins listed

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
1	1.1	73	10	184.07	28	8.11e+010	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding
1	1.1	73	10	184.07	48	8.11e+010	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (C
2	2.1	15	9	145.94	22	1.03e+009	80610.8	PA_BS12:2189571642	PA_BS12:2189571642 or0735 Carbohydrate binding domain. [B. setacea BS12] 763 bp
2	2.1	15	9	145.94	48	1.03e+009	37625.9	PA_Bse_meta_comb:2073592708	PA_Bse_meta_comb:2073592708 BaSeMet_00363640 hypothetical protein [Bankia setacea microbiome
2	2.1	2	2	37.21	3	3.60e+008	112354.2	PA_Bse_meta_comb:2073560170	PA_Bse_meta_comb:2073560170 BaSeMet_00038260 esterase, PHB depolymerase family [Bankia set
2	2.1	2	2	37.21	3	3.60e+008	112173.0	PA_Bse02:2503998147	PA_Bse02:2503998147 BS02DRAFT_00013240 esterase, PHB depolymerase family [B. setacea BS02
3	3.1	25	8	128.30	23	7.31e+010	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 b
3	3.1	25	8	128.30	40	7.31e+010	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
4	4.1	9	5	82.60	8	1.97e+009	104392.5	PA_BS12:2189569647	PA_BS12:2189569647 or2953 Beta-1,4-xylanase [B. setacea BS12] 986 bp
5	5.1	8	6	74.79	25	1.14e+009	43960.4	PA_Bse_meta_comb:2073561917	PA_Bse_meta_comb:2073561917 BaSeMet_00055730 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
5	5.1	3	3	37.72	5	3.13e+008	114184.0	PA_Bse_meta_comb:2073561915	PA_Bse_meta_comb:2073561915 BaSeMet_00055710 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
5	5.1	2	2	29.35	15	3.08e+008	23858.3	PA_Bse02:2504000230	PA_Bse02:2504000230 BS02DRAFT_00014530 Glycosyl hydrolases family 6. [B. setacea BS02 (Isolate
5	5.1	2	2	29.35	15	3.08e+008	23855.3	PA_Bse02:2503999190	PA_Bse02:2503999190 BS02DRAFT_00027250 Glycosyl hydrolases family 6. [B. setacea BS02 (Isolate
5	5.1	3	2	22.12	7	2.02e+008	38604.4	PA_Bse02:2503998988	PA_Bse02:2503998988 BS02DRAFT_00026880 Cellulose or protein binding domain./Cellulose binding
5	5.2	7	4	52.03	6	9.83e+008	112508.2	PA_Bse_meta_comb:2073561919	PA_Bse_meta_comb:2073561919 BaSeMet_00055750 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
5	5.2	6	3	37.88	4	7.66e+008	113016.6	PA_Bse02:2503999098	PA_Bse02:2503999098 BS02DRAFT_00001060 Cellulose or protein binding domain./Glycosyl hydrolase
6	6.1	2	2	32.91	7	2.19e+007	58225.4	PA_BS12:2189570192	PA_BS12:2189570192 or3423 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 560 b
6	6.1	2	2	32.91	8	2.19e+007	52443.2	PA_Bse_meta_comb:2073587378	PA_Bse_meta_comb:2073587378 BaSeMet_00310340 Cobalamin biosynthesis protein CobN and relate
7	7.1	4	2	30.51	6	3.87e+008	39939.7	PA_BS12:2189570962	PA_BS12:2189570962 or0231 Uncharacterized protein conserved in bacteria [B. setacea BS12] 383 bp
8	8.1	6	2	29.59	4	7.82e+007	70938.0	PA_Bse02:2504000681	PA_Bse02:2504000681 BS02DRAFT_00022770 Cellulose or protein binding domain./Glycosyl hydrolase
8	8.1	6	2	29.59	4	7.82e+007	70884.2	PA_Bse08:2503997525	PA_Bse08:2503997525 BS08DRAFT_00020200 Cellulose or protein binding domain./Glycosyl hydrolase
Totals:	290	95							

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
1	1.1	73	10	184.07	28	8.11e+010	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding domain./Cel

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	088-2301.5238.5238.0	3	21.25	15.28	95.7	1.94e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
2	088-2301.5381.5438.0	3	20.37	11.31	98.2	5.76e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
3	088-2301.4793.4867.0	3	19.63	11.61	95.6	2.43e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
4	088-2301.6670.6763.0	3	19.59	12.26	91.8	5.39e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050

5	088-2301.6022.6112.0	2	19.25	15.20	96.4	1.35e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
6	088-2301.6094.6140.0	3	19.20	11.56	94.3	2.18e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
7	088-2301.5611.5686.2	2	18.86	12.31	97.3	4.21e+008	(R)EWQDALVDYMVEK(D)	1625.752
8	088-2301.4381.4496.2	2	18.81	18.81	97.1	4.64e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
9	088-2301.7817.7845.3	3	18.58	14.08	91.7	2.35e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
10	088-2301.6985.7029.0	3	18.22	12.53	94.4	4.82e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
11	088-2301.9545.9671.3	3	17.86	17.86	88.9	3.29e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
12	088-2301.4009.4064.2	2	17.80	17.80	91.5	1.89e+008	(R)AGWDEHFGYLR(D)	1350.623
13	088-2301.11483.11571.2	2	17.74	12.67	95.9	3.15e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
14	088-2301.11609.11672.3	3	17.60	12.95	82.9	1.30e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
15	088-2301.11739.11829.2	2	17.59	13.97	93.8	2.70e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
16	088-2301.6441.6446.3	3	17.56	9.90	90.7	2.79e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
17	088-2301.6128.6141.0	2	17.35	17.35	83.0	1.02e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
18	088-2301.9681.9767.3	3	17.28	12.24	87.0	1.96e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
19	088-2301.5135.5232.0	3	17.11	11.99	77.0	2.06e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
20	088-2301.7109.7187.2	2	17.05	13.80	81.4	2.73e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
21	088-2301.7481.7552.0	3	17.01	17.01	87.0	4.46e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
22	088-2301.7423.7519.0	2	16.95	13.26	91.8	3.64e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
23	088-2301.6877.6885.0	2	16.94	11.87	91.0	3.76e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
24	088-2301.4690.4696.0	3	16.59	8.56	94.2	2.29e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
25	088-2301.6749.6864.2	2	16.52	11.26	92.3	6.07e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
26	088-2301.11308.11398.0	2	16.19	12.18	88.4	3.48e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
27	088-2301.3841.3876.2	2	16.14	16.14	92.6	4.79e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
28	088-2301.4515.4519.2	2	16.07	16.07	93.5	9.66e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
29	088-2301.11859.11859.2	2	16.05	11.84	84.6	1.61e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
30	088-2301.9598.9598.5	5	16.04	16.04	81.0	2.75e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
31	088-2301.3845.3860.2	2	15.82	15.82	91.9	4.83e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
32	088-2301.11248.11248.0	3	15.75	9.50	90.2	8.21e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
33	088-2301.6263.6317.3	3	15.72	9.09	85.9	5.09e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
34	088-2301.5752.5797.3	3	15.56	10.89	87.0	8.42e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
35	088-2301.6591.6640.2	2	15.52	12.17	81.0	3.94e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
36	088-2301.9997.10122.0	3	15.34	15.34	84.2	1.34e+009	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
37	088-2301.8657.8691.2	2	15.21	15.21	84.2	8.13e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
38	088-2301.7210.7284.0	2	15.16	11.82	82.4	2.63e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
39	088-2301.5992.6078.3	3	14.99	8.94	80.4	1.63e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
40	088-2301.7832.7904.0	3	14.75	14.75	82.3	5.35e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
41	088-2301.10452.10452.0	3	14.21	14.21	89.4	4.71e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
42	088-2301.3823.3875.3	3	14.16	4.73	81.3	2.50e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
43	088-2301.11453.11453.0	2	13.80	9.99	85.1	7.28e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
44	088-2301.7234.7325.2	2	13.73	8.78	88.0	4.12e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
45	088-2301.7982.7982.0	3	13.51	13.51	77.9	1.89e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
46	088-2301.11788.11840.0	3	13.40	9.41	71.6	4.52e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
47	088-2301.5778.5778.2	2	13.32	13.32	76.7	3.19e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
48	088-2301.10149.10149.0	3	13.10	13.10	84.8	6.97e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
49	088-2301.5754.5798.2	2	13.09	7.55	84.3	3.26e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
50	088-2301.12134.12153.0	3	12.70	6.44	84.0	8.02e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
51	088-2301.6442.6447.0	2	12.52	12.52	65.5	1.80e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
52	088-2301.7850.7850.0	3	12.49	12.49	78.3	3.81e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211

53	088-2301.11831.11831.0	2	12.27	12.27	79.3	5.57e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
54	088-2301.11254.11254.0	3	11.71	5.87	92.0	8.65e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
55	088-2301.11658.11658.0	2	11.60	11.60	72.5	6.13e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
56	088-2301.11853.11853.0	2	11.52	7.93	77.9	1.62e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
57	088-2301.6264.6270.2	2	11.44	7.59	61.3	2.20e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
58	088-2301.7345.7449.0	3	11.38	7.54	70.7	8.96e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
59	088-2301.11447.11447.0	2	11.25	6.93	64.9	7.35e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
60	088-2301.11577.11577.0	2	11.20	6.31	68.1	1.76e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
61	088-2301.11137.11137.0	3	11.18	11.18	72.1	5.57e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
62	088-2301.7539.7555.2	2	11.15	11.15	73.2	1.23e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
63	088-2301.7601.7601.0	2	10.15	10.15	70.6	1.93e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
64	088-2301.7597.7597.0	2	9.47	9.47	71.9	1.89e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
65	088-2301.9779.9779.0	2	9.36	9.36	72.4	2.50e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
66	088-2301.11774.11774.0	2	9.30	9.30	72.8	5.57e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
67	088-2301.7563.7563.0	2	8.68	4.87	67.4	1.43e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
68	088-2301.8263.8263.2	2	8.00	8.00	68.1	5.25e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
69	088-2301.12172.12172.2	2	7.67	7.67	67.4	4.13e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
70	088-2301.7715.7715.0	2	7.54	4.05	65.8	1.01e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
71	088-2301.7663.7663.0	2	6.74	6.74	61.8	1.05e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
72	088-2301.9084.9084.0	2	6.55	6.55	83.3	6.47e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
73	088-2301.9143.9143.0	2	6.53	6.53	63.0	5.65e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
2	2.1	15	9	145.94	22	1.03e+009	80610.8	PA_BS12:2189571642	PA_BS12:2189571642 or0735 Carbohydrate binding domain. [B. setacea BS12] 763 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	088-2301.5553.5563.2	2	20.64	20.64	95.3	3.27e+008	(K)FYDIYGSNHSAGSTVAWAWGVSR(M)	2531.174
2	088-2301.4771.4784.2	2	17.65	17.65	94.9	5.66e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
3	088-2301.4854.4860.2	2	17.28	9.84	88.8	7.87e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
4	088-2301.4710.4765.0	3	16.57	8.17	89.0	3.29e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
5	088-2301.3443.3497.0	3	15.63	5.92	75.6	5.19e+006	(K)GVAVVNFSNSEMGAHNGSGSR(G)	2076.952
6	088-2301.3581.3641.0	2	15.51	8.55	92.6	8.91e+006	(K)GAIVVGAFDER(I)	1133.595
7	088-2301.6389.6405.0	2	14.78	10.03	93.1	3.99e+007	(R)WIPWNTPILQ(-)	1267.684
8	088-2301.3659.3665.0	3	14.76	6.51	80.4	9.62e+006	(R)MIDVLQQTSGHNLDASR(I)	1884.924
9	088-2301.4764.4842.3	3	14.16	14.16	78.6	1.71e+008	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
10	088-2301.6053.6115.0	3	13.12	13.12	71.2	2.03e+008	(K)DAGANVQTASQIVGENPWMSANLDQFANNGTVTK(L)	3548.672
11	088-2301.4871.4947.0	3	13.04	13.04	71.9	3.14e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
12	088-2301.4849.4865.3	3	12.84	4.00	84.0	4.24e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
13	088-2301.4844.4844.0	2	9.00	9.00	76.9	1.54e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
14	088-2301.3734.3734.2	2	8.68	8.68	77.1	1.30e+006	(K)GAIVVGAFDER(I)	1133.595
15	088-2301.3816.3816.2	2	8.52	5.46	77.4	1.79e+006	(K)GAIVVGAFDER(I)	1133.595

Group	Subgroup	Spectra	Distinct Peptides	Distinct Summed MS/MS	% AA	Total Protein	Protein MW	Database	Protein Name

(#)	(#)	(#)	(#)	Search Score	Coverage	Spectral Intensity	(Da)	Accession #	
3	3.1	25	8	128.30	23	7.31e+010	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	088-2301.3308.3319.0	3	20.68	5.77	97.9	2.96e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
2	088-2301.3312.3312.0	3	20.66	11.40	98.2	2.45e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
3	088-2301.7856.7899.2	2	19.76	19.76	92.2	5.45e+009	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
4	088-2301.7855.7920.3	3	19.21	12.10	91.6	4.80e+009	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
5	088-2301.8225.8334.2	2	18.38	11.51	74.9	3.18e+010	(R)WFPEAFQTLVENAYPAL(-)	1995.986
6	088-2301.8103.8199.0	3	17.64	10.83	90.5	5.90e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
7	088-2301.8342.8455.2	2	17.33	10.94	75.0	2.76e+010	(R)WFPEAFQTLVENAYPAL(-)	1995.986
8	088-2301.4038.4094.3	3	16.51	10.61	95.6	3.89e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
9	088-2301.8143.8181.2	2	15.69	15.69	87.5	3.27e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
10	088-2301.8486.8486.0	3	15.20	11.33	79.3	1.14e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
11	088-2301.3725.3725.0	3	14.59	14.59	92.1	1.51e+007	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
12	088-2301.6287.6293.2	2	14.45	9.86	80.2	4.57e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
13	088-2301.4043.4106.2	2	14.44	14.44	87.7	3.78e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
14	088-2301.8565.8614.0	3	13.56	13.56	74.3	7.86e+007	(R)EHLDETLAQGANLFMFVVYDLPNR(D)	2792.372
15	088-2301.8509.8534.0	2	13.27	6.84	79.4	9.25e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
16	088-2301.6282.6311.3	3	12.06	3.86	76.5	2.52e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
17	088-2301.8482.8488.0	2	11.79	11.79	79.3	1.54e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
18	088-2301.3570.3570.0	2	10.37	5.93	91.0	6.72e+006	(R)IGAIEGPADGDGMGLR(E)	1528.743
19	088-2301.8567.8567.0	2	9.57	9.57	61.6	1.05e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
20	088-2301.11280.11280.0	3	9.47	9.47	81.8	3.95e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
21	088-2301.8813.8813.0	2	9.13	9.13	63.2	7.98e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
22	088-2301.3328.3328.2	2	8.56	8.56	76.6	2.92e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
23	088-2301.8867.8867.0	2	8.07	8.07	65.1	8.25e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
24	088-2301.3330.3330.2	2	7.46	7.46	61.2	2.85e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
25	088-2301.11561.11561.0	2	6.95	6.95	67.6	6.83e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
4	4.1	9	5	82.60	8	1.97e+009	104392.5	PA_BS12:2189569647	PA_BS12:2189569647 or2953 Beta-1,4-xylanase [B. setacea BS12] 986 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	088-2301.5316.5362.2	2	20.85	20.85	97.9	1.76e+008	(R)SDFGQYWDQITLENK(G)	1843.850
2	088-2301.6659.6686.2	2	18.06	10.40	92.2	6.81e+008	(R)IAALGLPIYISEYDIEK(T)	1908.037
3	088-2301.6696.6702.3	3	17.63	5.92	90.7	1.24e+008	(R)IAALGLPIYISEYDIEK(T)	1908.037
4	088-2301.6033.6114.3	3	16.54	8.66	86.3	5.02e+008	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
5	088-2301.4762.4802.0	3	15.83	15.83	85.1	4.40e+007	(K)WAQVEPQRDQYDWSGIDDAYNYAK(Q)	2918.302
6	088-2301.6045.6058.2	2	13.64	9.98	83.6	9.07e+007	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
7	088-2301.5343.5343.3	3	13.61	9.40	73.8	4.49e+007	(R)SDFGQYWDQITLENK(G)	1843.850
8	088-2301.6118.6118.0	3	12.57	8.47	70.6	3.06e+008	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
9	088-2301.4170.4170.0	2	11.32	6.93	73.6	2.65e+006	(K)AAEIEEWIR(D)	1116.569

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
5	5.1	8	6	74.79	25	1.14e+009	43960.4	PA_Bse_meta_comb:2073561917	PA_Bse_meta_comb:2073561917 BaSeMet_00055730 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [I

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	088-2301.5924.5973.2	2	16.05	16.05	90.4	5.18e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
2	088-2301.8984.9007.3	3	14.95	10.97	83.3	2.21e+008	(R)WFPEAFQTLLENAYPPL(-)	2036.017
3	088-2301.5173.5276.2	2	13.64	13.64	82.4	1.93e+008	(K)IAYESTFVWMDR(I)	1517.710
4	088-2301.8548.8553.2	2	13.30	13.30	70.4	2.56e+008	(R)SSDFYEWTQYLEELQFVQAWR(Q)	2725.258
5	088-2301.8976.8976.0	2	10.95	3.18	78.2	3.99e+008	(R)WFPEAFQTLLENAYPPL(-)	2036.017
6	088-2301.3913.3913.2	2	8.48	4.94	86.8	4.48e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
7	088-2301.3403.3403.0	3	8.37	8.37	74.2	5.40e+006	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
8	088-2301.3920.3920.0	2	8.03	4.33	88.1	4.31e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
5	5.2	7	4	52.03	6	9.83e+008	112508.2	PA_Bse_meta_comb:2073561919	PA_Bse_meta_comb:2073561919 BaSeMet_00055750 Cellobiohydrolase A (1,4-beta-cellobiosidase A)

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	088-2301.8124.8183.3	3	14.75	14.75	81.3	2.01e+008	(K)SSDFYEFNGYFDELSFVTDWR(N)	2624.126
2	088-2301.5258.5306.0	2	14.65	8.27	91.1	6.64e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
3	088-2301.7219.7222.2	2	14.15	14.15	84.5	2.16e+008	(R)VDNPFVGANWYIDPIWSAK(A)	2192.082
4	088-2301.8117.8117.0	2	12.23	12.23	64.3	2.12e+008	(K)SSDFYEFNGYFDELSFVTDWR(N)	2624.126
5	088-2301.8121.8180.2	2	11.71	11.71	71.8	2.78e+008	(K)SSDFYEFNGYFDELSFVTDWR(N)	2624.126
6	088-2301.3913.3913.2	2	8.48	4.94	86.8	4.48e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
7	088-2301.3920.3920.0	2	8.03	4.33	88.1	4.31e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
6	6.1	2	2	32.91	7	2.19e+007	58225.4	PA_BS12:2189570192	PA_BS12:2189570192 or3423 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 560 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	088-2301.4227.4227.0	3	18.47	12.33	76.1	5.35e+006	(K)AEGSSIVQTGSAVSNWNDSDLTAAGR(L)	2593.213
2	088-2301.5854.5859.0	2	14.44	9.53	90.2	1.66e+007	(K)SFAGNSFFWSNTEWGQER(F)	2149.937

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
7	7.1	4	2	30.51	6	3.87e+008	39939.7	PA_BS12:2189570962	

PA_BS12:2189570962 or0231 Uncharacterized protein conserved in bacteria [B. setacea BS12] 383 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	088-2301.6416.6464.3	3	18.80	15.34	96.2	2.40e+008	(K)ELVFWITKPGFSFDANR(T)	2027.039
2	088-2301.6434.6458.2	2	13.73	7.73	85.6	1.26e+008	(K)ELVFWITKPGFSFDANR(T)	2027.039
3	088-2301.2724.2756.2	2	11.71	5.67	87.9	1.15e+007	(R)HVIYGEWGR(D)	1116.559
4	088-2301.2736.2736.0	2	7.75	4.46	90.0	9.28e+006	(R)HVIYGEWGR(D)	1116.559

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
8	8.1	6	2	29.59	4	7.82e+007	70938.0	PA_Bse02:2504000681	PA_Bse02:2504000681 BS02DRAFT_00022770 Cellulose or protein binding domain./Glycosyl hydrolases family 11.

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	088-2301.5834.5879.0	3	17.65	17.65	89.7	3.48e+007	(R)VQQPSIEGTQTFYQYFSVR(S)	2278.114
2	088-2301.3479.3533.2	2	11.94	5.17	89.5	3.03e+006	(R)VITWDVDSR(D)	1090.553
3	088-2301.3307.3318.2	2	11.86	5.27	88.6	1.79e+007	(R)VITWDVDSR(D)	1090.553
4	088-2301.5855.5866.0	2	11.67	11.67	73.5	1.06e+007	(R)VQQPSIEGTQTFYQYFSVR(S)	2278.114
5	088-2301.5873.5873.0	2	10.29	10.29	71.4	1.08e+007	(R)VQQPSIEGTQTFYQYFSVR(S)	2278.114
6	088-2301.3648.3648.0	2	6.94	2.57	88.9	9.46e+005	(R)VITWDVDSR(D)	1090.553