Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\021511_OGL_Caec1_1st_set
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 114 **Hits:** 274
Data Directory: msdataSM\022011_OGL_Cae1_fractions
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 132 **Hits:** 308
beginning to assemble proteins .... proteins assembled 0.091784 sec
proteins filtered by unique peptides 0.007201 sec
proteins filtered by score
calculated protein coverage maps 0.046512 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.005512 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 20 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	35	7	114.95	17	4.39e+010	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding (
1	1.1	35	7	114.95	28	4.39e+010	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (Co
2	2.1	23	5	83.37	17	4.05e+009	54835.2	PA_BS12:2189568724	PA_BS12:2189568724 or2045 Beta-1,4-xylanase [B. setacea BS12] 511 bp
2	2.1	23	5	83.37	17	4.05e+009	54483.9	PA_Bse_meta_comb:2073587463	PA_Bse_meta_comb:2073587463 BaSeMet_00311190 Beta-1,4-xylanase [Bankia setacea microbiome (
2	2.2	6	2	34.77	3	8.08e+008	99497.3	PA_Bse08:2503994382	PA_Bse08:2503994382 BS08DRAFT_00000020 Cellulose or protein binding domain./Glycosyl hydrolase
3	3.1	25	5	78.52	9	1.51e+009	80610.8	PA_BS12:2189571642	PA_BS12:2189571642 or0735 Carbohydrate binding domain. [B. setacea BS12] 763 bp
3	3.1	25	5	78.52	20	1.51e+009	37625.9	PA_Bse_meta_comb:2073592708	PA_Bse_meta_comb:2073592708 BaSeMet_00363640 hypothetical protein [Bankia setacea microbiome
3	3.2	7	2	28.80	3	3.38e+008	112354.2	PA_Bse_meta_comb:2073560170	PA_Bse_meta_comb:2073560170 BaSeMet_00038260 esterase, PHB depolymerase family [Bankia set
3	3.2	7	2	28.80	3	3.38e+008	112173.0	PA_Bse02:2503998147	PA_Bse02:2503998147 BS02DRAFT_00013240 esterase, PHB depolymerase family [B. setacea BS02 (
4	4.1	33	4	71.02	10	2.32e+010	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp
4	4.1	33	4	71.02	18	2.32e+010	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
5	5.1	65	4	54.18	18	3.68e+010	34086.6	PA_BS12:2189568629	PA_BS12:2189568629 or1947 Cellulose or protein binding domain. [B. setacea BS12] 325 bp
5	5.1	65	4	54.18	19	3.68e+010	31845.8	PA_Bse_meta_comb:2073564373	PA_Bse_meta_comb:2073564373 BaSeMet_00080290 Cellulose or protein binding domain. [Bankia set
6	6.1	8	3	50.89	29	6.60e+008	11367.4	PA_Bse_meta_comb:2073565234	PA_Bse_meta_comb:2073565234 BaSeMet_00088900 Histones H3 and H4 [Bankia setacea microbiom
7	7.1	6	3	43.79	10	4.76e+008	46154.6	PA_Bse02:2503998146	PA_Bse02:2503998146 BS02DRAFT_00013230 Glycosyl hydrolase family 10. [B. setacea BS02 (Isolate
7	7.1	6	3	43.79	10	4.76e+008	46141.6	PA_Bse_meta_comb:2073560169	PA_Bse_meta_comb:2073560169 BaSeMet_00038250 Beta-1,4-xylanase [Bankia setacea microbiome (
8	8.1	18	3	39.05	13	1.37e+009	43960.4	PA_Bse_meta_comb:2073561917	PA_Bse_meta_comb:2073561917 BaSeMet_00055730 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
8	8.1	10	2	27.37	3	7.30e+008	114184.0	PA_Bse_meta_comb:2073561915	PA_Bse_meta_comb:2073561915 BaSeMet_00055710 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
8	8.2	10	3	35.67	4	6.75e+008	113016.6	PA_Bse02:2503999098	PA_Bse02:2503999098 BS02DRAFT_00001060 Cellulose or protein binding domain./Glycosyl hydrolase
8	8.2	10	3	35.67	4	6.75e+008	112508.2	PA_Bse_meta_comb:2073561919	PA_Bse_meta_comb:2073561919 BaSeMet_00055750 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
8	8.3	10	2	27.15	5	6.65e+008	77060.3	PA_BS12:2189570194	PA_BS12:2189570194 or3425 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 730 bp
8	8.3	10	2	27.15	7	6.65e+008	59632.4	PA_Bse_meta_comb:2073585294	PA_Bse_meta_comb:2073585294 BaSeMet_00289500 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
9	9.1	3	3	34.79	11	5.61e+007	56911.4	PA_Bse08:2503996762	PA_Bse08:2503996762 BS08DRAFT_00004980 esterase, PHB depolymerase family [B. setacea BS08 (
10	10.1	3	3	29.08	47	1.23e+008	8388.5	PA_Bse_meta_comb:2073588714	PA_Bse_meta_comb:2073588714 BaSeMet_00323700 hypothetical protein [Bankia setacea microbiome
11	11.1	9	2	28.84	1	1.35e+009	224278.3	PA_BS12:2189569050	PA_BS12:2189569050 or2363 Gluconolactonase [B. setacea BS12] 2124 bp
11	11.1	9	2	28.84	1	1.35e+009	223963.9	PA_Bse_meta_comb:2073579605	PA_Bse_meta_comb:2073579605 BaSeMet_00232610 Gluconolactonase [Bankia setacea microbiome (
12	12.1	2	2	26.99	5	2.96e+007	71955.5	PA_BS12:2189569712	PA_BS12:2189569712 or3019 Beta-1,4-xylanase [B. setacea BS12] 676 bp
12	12.1	2	2	26.99	5	2.96e+007	71160.6	PA_Bse_meta_comb:2073583496	PA_Bse_meta_comb:2073583496 BaSeMet_00271520 Beta-1,4-xylanase [Bankia setacea microbiome (
13	13.1	5	2	26.23	19	3.90e+008	12753.8	PA_Bse_meta_comb:2073593092	PA_Bse_meta_comb:2073593092 BaSeMet_00367480 Actin and related proteins [Bankia setacea micro
14	14.1	3	2	24.47	6	1.98e+008	39939.7	PA_BS12:2189570962	PA_BS12:2189570962 or0231 Uncharacterized protein conserved in bacteria [B. setacea BS12] 383 bp
15	15.1	3	2	24.34	4	8.54e+007	77470.6	PA_Bse08:2503996278	PA_Bse08:2503996278 BS08DRAFT_00001670 Cellulose or protein binding domain./Cellulose binding (
16	16.1	2	2	23.76	3	1.07e+008	70884.2	PA_Bse08:2503997525	PA_Bse08:2503997525 BS08DRAFT_00020200 Cellulose or protein binding domain./Glycosyl hydrolase

Totals: 511 102

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	35	7	114.95	17	4.39e+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	010-1701.5738.5809.3	3	19.34	7.24	96.2	2.43e+008	(R)EWQDALVDYMVEK(D)	1625.752
2	012-0801.5264.5264.3	3	18.84	6.07	96.4	4.42e+006	(R)EWQDALVDYMVEK(D)	1625.752
3	010-1702.5679.5787.2	2	18.37	7.93	97.3	6.16e+009	(R)EWQDALVDYMVEK(D)	1625.752
4	012-0801.5272.5296.2	2	18.30	11.90	96.3	3.57e+007	(R)EWQDALVDYMVEK(D)	1625.752
5	010-1702.5748.5832.3	3	18.28	6.11	94.9	2.51e+008	(R)EWQDALVDYMVEK(D)	1625.752
6	010-1701.5710.5825.2	2	18.27	9.76	95.4	6.35e+009	(R)EWQDALVDYMVEK(D)	1625.752
7	010-1702.5805.5871.2	2	18.22	10.33	94.6	4.43e+009	(R)EWQDALVDYMVEK(D)	1625.752
8	012-0801.3566.3614.3	3	17.53	10.59	88.9	4.47e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
9	011-0701.5155.5171.3	3	17.25	5.05	94.4	9.86e+006	(R)EWQDALVDYMVEK(D)	1625.752
10	010-1701.3489.3595.3	3	17.07	6.42	89.8	9.55e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
11	010-0601.4846.4936.0	3	17.01	8.53	81.8	2.52e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
12	012-0801.5680.5699.0	3	16.38	8.75	87.6	1.60e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
13	010-1702.2051.2081.0	2	16.37	9.19	95.0	1.16e+006	(R)LDANPPYADADR(E)	1317.608
14	010-0601.3498.3567.3	3	16.35	6.42	84.7	1.19e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
15	010-0601.3525.3546.2	2	16.05	12.94	92.3	1.59e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
16	010-1702.3467.3563.2	2	15.09	7.58	91.9	1.84e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
17	010-1701.3490.3597.2	2	15.03	9.35	92.1	2.26e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
18	010-0601.5142.5186.3	3	14.70	3.85	91.6	6.24e+007	(R)EWQDALVDYMVEK(D)	1625.752
19	011-0701.6360.6395.0	3	14.61	14.61	81.2	1.34e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
20	011-0701.3532.3532.2	2	14.41	11.11	88.8	6.21e+006	(R)AAEQEMWSHITPGVDR(E)	1826.850
21	010-0601.5129.5207.2	2	14.27	4.87	81.3	5.50e+008	(R)EWQDALVDYMVEK(D)	1625.752
22	010-1702.3456.3561.3	3	14.24	6.27	81.3	7.71e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
23	012-0801.3582.3588.2	2	14.06	8.54	90.4	7.80e+006	(R)AAEQEMWSHITPGVDR(E)	1826.850
24	012-1901.3758.3774.2	2	13.71	9.41	82.1	4.70e+007	(R)AGWDEHFGYLR(D)	1350.623
25	010-1701.2055.2079.0	2	13.26	5.45	89.7	1.07e+006	(R)LDANPPYADADR(E)	1317.608
26	010-1701.3636.3636.2	2	12.77	6.44	67.3	5.63e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
27	011-1801.3518.3530.2	2	12.12	7.24	69.5	2.16e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
28	010-1701.3705.3749.2	2	11.62	6.57	69.5	2.96e+008	(R)AGWDEHFGYLR(D)	1350.623
29	012-0801.6410.6482.0	3	11.45	11.45	72.1	6.29e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
30	012-1902.3794.3807.2	2	11.38	6.94	77.7	3.98e+007	(R)AGWDEHFGYLR(D)	1350.623
31	011-1801.3736.3747.2	2	10.61	7.26	71.1	5.28e+007	(R)AGWDEHFGYLR(D)	1350.623
32	012-1902.3598.3618.2	2	9.94	9.94	70.1	6.11e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
33	011-1802.3791.3796.2	2	9.71	4.17	70.1	1.79e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
34	010-1701.2068.2068.0	2	7.88	3.79	94.1	7.94e+005	(R)LDANPPYADADR(E)	1317.608
35	012-1901.3571.3574.2	2	7.62	7.62	63.1	5.21e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850

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

(#)	(#)	(#)	(#)	Search Score	Coverage	Spectral Intensity	(Da)	Accession #	
2	2.1	23	5	83.37	17	4.05e+009	54835.2	PA_BS12:2189568724	PA_BS12:2189568724 or2045 Beta-1,4-xylanase [B. setacea BS12] 511 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	009-0501.4190.4229.2	2	19.30	11.56	95.7	7.26e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
2	012-0801.4634.4634.0	3	17.54	10.64	92.7	2.73e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
3	011-0701.4268.4286.3	3	17.40	10.31	86.0	6.04e+006	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
4	012-0801.4516.4558.0	3	17.37	12.69	84.5	4.16e+007	(R)YPDTEMIDVVNESTPGHAPADFAR(D)	2632.199
5	011-1802.4996.5002.0	3	17.35	13.17	86.7	3.90e+008	(R)YPDTEMIDVVNESTPGHAPADFAR(D)	2632.199
6	012-0801.4336.4347.2	2	17.22	13.60	94.2	1.15e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
7	009-1601.4660.4713.0	2	16.77	8.94	93.8	3.00e+008	(R)DAFGNDWIIK(S)	1178.585
8	010-0601.4231.4251.2	2	16.66	9.55	91.8	1.35e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
9	011-0701.4258.4292.2	2	16.57	12.85	90.6	1.94e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
10	009-0501.4202.4220.3	3	16.37	9.85	85.4	1.66e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
11	009-1602.4913.4979.2	2	16.20	6.62	92.0	2.98e+008	(R)DAFGNDWIIK(S)	1178.585
12	009-1602.4741.4834.2	2	16.11	8.69	90.3	5.63e+008	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
13	011-1802.5031.5063.0	3	15.61	11.48	85.9	3.30e+008	(R)SDFTQYWDQITPENEGK(W)	2057.909
14	012-1901.4497.4549.2	2	15.26	10.82	83.9	6.31e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
15	009-1601.4500.4517.2	2	14.91	8.03	84.2	3.83e+008	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
16	012-1902.4559.4565.2	2	14.38	7.53	84.9	5.18e+007	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
17	012-1901.4695.4746.0	3	13.69	9.39	70.5	5.02e+008	(R)YPDTEMIDVVNESTPGHAPADFAR(D)	2632.199
18	012-1902.4739.4774.0	3	13.33	8.99	72.9	5.05e+008	(R)YPDTEMIDVVNESTPGHAPADFAR(D)	2632.199
19	010-1702.4585.4588.0	2	12.94	9.29	83.4	1.48e+008	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
20	011-1802.4729.4781.2	2	12.78	12.78	74.8	1.12e+008	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
21	012-0801.5871.5913.0	3	12.39	6.27	78.0	1.65e+007	(K)QHTLVWGSQFPSWINNLSNTEK(A)	2586.274
22	010-1701.4616.4616.0	2	11.87	7.44	68.3	1.53e+008	(R)DNYNWSGLDAAYNYAK(Q)	1864.814
23	012-0801.4511.4511.0	3	10.33	6.29	72.9	3.10e+007	(R)YPDTEMIDVVNESTPGHAPADFAR(D)	2632.199

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	2.2	6	2	34.77	3	8.08e+008	99497.3	PA_Bse08:2503994382	PA_Bse08:2503994382 BS08DRAFT_00000020 Cellulose or protein binding domain./Glycosyl hydrolase family 10./

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	012-0801.4634.4634.0	3	17.54	10.64	92.7	2.73e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909
2	009-0501.6057.6136.3	3	17.23	7.14	91.9	4.34e+007	(R)DQYNWGPLDAIYDYAR(A)	1959.888
3	010-0601.6244.6244.2	2	16.25	10.51	92.3	3.70e+007	(R)DQYNWGPLDAIYDYAR(A)	1959.888
4	009-0501.6054.6120.2	2	15.74	9.58	91.8	1.33e+008	(R)DQYNWGPLDAIYDYAR(A)	1959.888
5	011-1802.5031.5063.0	3	15.61	11.48	85.9	3.30e+008	(R)SDFTQYWDQITPENEGK(W)	2057.909
6	010-1702.6926.6976.2	2	10.16	6.25	61.1	2.37e+008	(R)DQYNWGPLDAIYDYAR(A)	1959.888

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name

3	3.1	25	5	78.52	9	1.51e+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	012-0801.4427.4452.0	3	17.85	10.03	87.1	5.64e+006	(K)LPVDNHELLGMVAPR(G)	1660.884
2	011-0701.4328.4344.0	3	16.77	7.35	85.3	1.69e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
3	008-0401.5888.5888.0	2	16.05	7.36	96.1	5.05e+007	(R)WIPWNTPILQ(-)	1267.684
4	008-0401.5883.5961.0	2	16.00	6.24	95.4	7.83e+007	(R)WIPWNTPILQ(-)	1267.684
5	011-0701.5915.5965.0	2	16.00	8.78	94.7	1.35e+007	(R)WIPWNTPILQ(-)	1267.684
6	009-0501.4430.4430.0	2	15.83	6.23	89.9	1.62e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
7	008-0401.4187.4247.3	3	15.19	6.04	81.6	7.46e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
8	008-0401.3332.3355.2	2	15.02	11.61	92.8	1.28e+007	(K)GAIVVGAFDER(I)	1133.595
9	011-1801.4685.4721.0	2	14.68	5.21	83.2	2.05e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
10	010-0601.4264.4325.0	3	13.82	5.23	78.4	2.12e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
11	010-0601.4443.4456.0	2	13.78	5.45	87.7	1.31e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
12	008-1502.3238.3243.2	2	13.77	10.04	79.4	4.48e+007	(R)MIDVLQQTSGHNLDASR(I)	1884.924
13	011-1802.4939.4971.0	2	13.54	5.06	77.3	2.17e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
14	009-0501.4262.4267.3	3	13.53	4.99	75.4	1.55e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
15	008-1501.3439.3461.0	2	13.23	7.68	86.4	3.62e+007	(K)GAIVVGAFDER(I)	1133.595
16	008-0401.4380.4385.0	2	13.13	5.24	80.3	3.44e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
17	010-0601.4447.4447.0	3	12.83	6.84	84.8	6.92e+006	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
18	009-1601.4719.4737.2	2	12.70	5.25	83.9	1.32e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
19	011-0701.4482.4482.0	2	12.54	2.88	87.4	1.67e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
20	008-1501.3484.3499.2	2	12.41	12.41	64.4	3.96e+007	(R)MIDVLQQTSGHNLDASR(I)	1884.924
21	012-0801.4579.4579.0	3	12.19	4.24	88.2	1.27e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
22	009-1602.4986.5015.0	2	12.08	4.45	78.3	1.30e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
23	010-1702.4834.4843.0	2	11.68	3.23	64.0	1.17e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
24	008-0401.3301.3301.2	2	9.70	9.70	76.1	6.01e+006	(K)GAIVVGAFDER(I)	1133.595
25	008-1501.4560.4649.2	2	9.06	2.02	63.5	1.96e+008	(K)LPVDNHELLGMVAPR(G)	1660.884

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
3	3.2	7	2	28.80	3	3.38e+008	112354.2	PA_Bse_meta_comb:2073560170	PA_Bse_meta_comb:2073560170 BaSeMet_00038260 esterase, PHB depolymerase family [Bankia set

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	012-0801.4427.4452.0	3	17.85	10.03	87.1	5.64e+006	(K)LPVDNHELLGMVAPR(G)	1660.884
2	011-0701.4328.4344.0	3	16.77	7.35	85.3	1.69e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
3	008-0401.4187.4247.3	3	15.19	6.04	81.6	7.46e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
4	010-0601.4264.4325.0	3	13.82	5.23	78.4	2.12e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
5	009-0501.4262.4267.3	3	13.53	4.99	75.4	1.55e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
6	008-0401.4618.4618.0	3	10.95	5.13	70.9	8.01e+006	(R)IQLWHGTNDETLNYNNFNEAIK(Q)	2634.259
7	008-1501.4560.4649.2	2	9.06	2.02	63.5	1.96e+008	(K)LPVDNHELLGMVAPR(G)	1660.884

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

(#)	(#)	(#)	(#)	Search Score	Coverage	Spectral Intensity	(Da)	Accession #	
4	4.1	33	4	71.02	10	2.32e+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	012-1901.3264.3350.2	2	19.61	11.38	96.3	3.72e+009	(R)IGAIEGPADGDGMGLR(E)	1528.743
2	011-0701.7602.7648.3	3	19.45	14.89	94.3	3.25e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
3	009-0501.7966.7976.3	3	19.41	12.74	93.8	1.44e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
4	006-1001.3103.3132.0	3	18.68	7.29	86.0	1.58e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
5	012-1902.3288.3371.2	2	18.58	11.09	95.4	3.93e+009	(R)IGAIEGPADGDGMGLR(E)	1528.743
6	010-0601.7973.8041.3	3	17.99	11.85	90.1	2.18e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
7	011-1802.3531.3577.2	2	17.81	9.81	95.1	2.50e+009	(R)IGAIEGPADGDGMGLR(E)	1528.743
8	010-1701.3304.3365.2	2	17.56	9.06	95.0	1.47e+009	(R)IGAIEGPADGDGMGLR(E)	1528.743
9	009-1601.3297.3315.2	2	17.55	9.45	95.1	3.98e+008	(R)IGAIEGPADGDGMGLR(E)	1528.743
10	010-1702.3277.3330.2	2	17.52	9.47	94.2	1.30e+009	(R)IGAIEGPADGDGMGLR(E)	1528.743
11	012-0801.3289.3354.2	2	17.04	10.43	94.6	1.19e+008	(R)IGAIEGPADGDGMGLR(E)	1528.743
12	012-1901.7874.7889.2	2	16.23	9.39	66.3	6.58e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
13	012-0801.7555.7614.2	2	16.18	7.52	71.8	3.14e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
14	011-0701.3315.3346.2	2	15.93	7.51	92.0	1.11e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
15	011-0701.7691.7703.2	2	15.78	9.51	65.2	2.54e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
16	011-1801.3240.3310.2	2	15.72	5.81	92.6	4.74e+009	(R)IGAIEGPADGDGMGLR(E)	1528.743
17	011-0701.7578.7619.2	2	15.49	8.03	86.1	4.81e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
18	010-1702.8725.8804.2	2	15.29	9.20	82.4	2.42e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
19	012-1902.7840.7918.2	2	13.81	7.07	65.2	7.77e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
20	006-1002.8166.8182.2	2	13.36	6.97	82.7	4.38e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
21	011-0701.6566.6587.0	3	13.28	2.25	72.9	6.35e+007	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
22	009-0501.7870.7945.2	2	13.13	6.02	61.4	7.35e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
23	012-0801.3295.3295.2	2	12.95	7.91	92.8	1.48e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
24	006-1001.7592.7627.2	2	12.72	8.30	79.3	1.30e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
25	006-1001.8130.8147.2	2	12.67	8.09	79.0	4.88e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
26	006-1001.7601.7601.2	2	12.13	5.27	76.1	1.15e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
27	009-0501.7980.7980.2	2	12.06	8.14	75.3	4.03e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
28	006-1001.7615.7615.2	2	11.75	7.89	71.2	1.02e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
29	010-0601.3334.3334.2	2	11.33	5.88	80.7	7.03e+006	(R)IGAIEGPADGDGMGLR(E)	1528.743
30	006-1002.8194.8194.2	2	10.76	6.87	70.9	3.63e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
31	006-1002.8171.8171.2	2	9.79	4.36	64.0	3.71e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
32	009-0501.7863.7863.2	2	9.33	9.33	64.4	1.14e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
33	006-1001.8113.8113.2	2	7.99	4.37	61.6	4.23e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986

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	65	4	54.18	18	3.68e+010	34086.6	PA_BS12:2189568629	PA_BS12:2189568629 or1947 Cellulose or protein binding domain. [B. setacea BS12] 325 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)

1	007-1402.2812.2894.2	2	16.65	8.03	87.5	4.13e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
2	012-1902.2896.2977.2	2	16.11	8.10	87.3	2.32e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
3	011-1802.3133.3216.2	2	16.10	8.59	86.9	2.04e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
4	012-1901.2865.2872.2	2	16.00	8.75	84.2	9.99e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
5	007-1402.10577.10637.0	3	15.82	15.82	81.6	8.51e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
6	008-1502.2825.2877.2	2	15.57	8.05	85.9	1.54e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
7	009-1601.5582.5582.0	3	15.54	11.08	83.5	3.19e+008	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
8	007-1401.2951.2956.2	2	15.20	7.48	88.8	6.43e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
9	012-1901.2969.3061.2	2	15.19	8.10	89.4	5.91e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
10	006-1002.3106.3111.2	2	15.12	8.09	87.4	3.55e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
11	006-1001.5566.5566.0	3	14.77	14.77	81.8	1.81e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
12	012-1901.3079.3079.2	2	14.65	9.01	88.1	4.86e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
13	009-1601.3096.3111.2	2	14.64	8.93	87.8	1.13e+009	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
14	012-0801.3012.3089.2	2	14.61	8.61	87.0	4.16e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
15	009-1602.3231.3318.2	2	14.60	9.67	86.4	8.67e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
16	007-1402.2937.3031.2	2	14.15	7.67	87.8	3.10e+009	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
17	007-1402.3035.3073.2	2	14.15	8.29	87.8	2.97e+009	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
18	009-1602.3350.3357.0	2	14.14	6.95	88.0	8.91e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
19	011-1802.3252.3322.2	2	14.13	7.80	87.3	1.31e+009	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
20	011-1801.2949.3062.2	2	14.10	7.59	86.5	1.34e+009	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
21	010-1702.3038.3038.2	2	14.08	7.81	85.4	8.21e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
22	010-1701.2917.2961.2	2	14.07	8.66	85.8	2.01e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
23	008-1501.3099.3177.2	2	14.04	8.15	84.3	2.28e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
24	009-0501.10246.10246.0	3	13.87	13.87	73.1	4.53e+006	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
25	010-1701.3039.3069.2	2	13.64	7.34	87.9	9.36e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
26	006-1001.3155.3249.2	2	13.63	7.08	87.4	2.24e+009	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
27	011-0701.3039.3061.2	2	13.62	7.00	86.8	3.89e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
28	010-1702.2920.3021.2	2	13.61	7.06	86.8	8.59e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
29	011-0701.5165.5225.0	3	13.59	13.59	73.3	6.41e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
30	006-1001.2984.3060.2	2	13.54	7.31	85.0	2.46e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
31	007-0301.5216.5284.0	3	13.53	13.53	73.4	5.07e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
32	006-1001.3270.3284.2	2	13.52	7.32	84.0	2.01e+009	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
33	006-1001.5192.5257.0	3	13.50	8.13	79.3	1.08e+008	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
34	011-1801.2852.2859.2	2	13.45	4.44	82.5	1.51e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
35	009-1601.2959.3053.2	2	13.38	8.47	80.8	1.07e+009	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
36	010-0601.5065.5112.0	3	13.35	13.35	75.3	9.48e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
37	006-1002.3298.3330.2	2	13.10	5.77	86.0	1.98e+009	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
38	012-1902.2983.3083.2	2	13.08	7.11	85.6	6.12e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
39	006-1002.3200.3290.2	2	13.07	6.03	85.6	2.22e+009	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
40	008-1502.2977.2987.2	2	13.06	7.54	84.7	1.40e+009	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
41	012-1902.3088.3088.2	2	13.05	7.55	83.5	4.94e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
42	012-0801.3079.3116.2	2	13.03	5.96	84.4	3.02e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
43	006-1001.3052.3090.2	2	12.87	4.38	80.1	6.32e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
44	006-1001.5103.5119.0	3	12.74	6.14	75.0	8.99e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
45	007-1401.3101.3204.2	2	12.55	5.59	84.3	3.73e+009	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
46	006-1002.10853.10853.0	3	12.53	12.53	74.0	8.76e+006	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
47	006-1001.3071.3077.2	2	12.50	5.63	82.5	1.34e+007	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
48	006-1001.6097.6124.0	3	12.18	12.18	71.5	2.62e+007	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072

49	007-0301.9063.9063.0	3	11.99	11.99	72.5	6.46e+006	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
50	009-1601.5564.5600.0	3	11.75	11.75	71.9	3.69e+008	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
51	012-1902.3263.3309.2	2	11.56	8.27	80.0	9.66e+007	(R)SQFGNNWFGGHR(N)	1406.635
52	012-1901.3244.3267.2	2	11.22	7.71	77.8	6.50e+007	(R)SQFGNNWFGGHR(N)	1406.635
53	011-0701.3112.3112.2	2	10.82	5.49	76.8	2.23e+006	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
54	007-0301.6545.6556.2	2	10.15	3.75	96.6	1.47e+008	(R)FWVEIPAI(-)	974.535
55	008-0401.6522.6531.2	2	10.10	4.15	94.7	2.06e+007	(R)FWVEIPAI(-)	974.535
56	012-0801.6561.6566.2	2	10.09	4.22	94.5	7.03e+006	(R)FWVEIPAI(-)	974.535
57	006-1001.6515.6524.2	2	10.08	3.77	94.0	3.26e+007	(R)FWVEIPAI(-)	974.535
58	011-0701.6500.6536.2	2	10.07	1.84	93.7	1.40e+007	(R)FWVEIPAI(-)	974.535
59	007-1401.7142.7165.2	2	9.68	4.63	97.2	1.46e+008	(R)FWVEIPAI(-)	974.535
60	006-1001.10999.10999.0	3	9.23	9.23	70.1	5.50e+006	(R)FLASAMMETEVMDTNYTYGDAK(S)	2488.072
61	006-1001.7035.7040.0	2	9.20	2.60	98.1	3.24e+007	(R)FWVEIPAI(-)	974.535
62	006-1002.7097.7120.2	2	9.20	2.63	98.1	2.89e+007	(R)FWVEIPAI(-)	974.535
63	006-1001.3415.3443.2	2	8.70	8.70	71.7	7.22e+007	(R)SQFGNNWFGGHR(N)	1406.635
64	010-1702.3080.3080.2	2	8.17	4.23	64.3	3.71e+008	(R)NGSTGLSNPNTQDIQNFK(A)	1934.921
65	012-1902.6888.6888.0	2	7.70	2.61	97.8	9.63e+006	(R)FWVEIPAI(-)	974.535

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	8	3	50.89	29	6.60e+008	11367.4	PA_Bse_meta_comb:2073565234	PA_Bse_meta_comb:2073565234 BaSeMet_00088900 Histones H3 and H4 [Bankia setacea microbiome

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	008-0401.4815.4881.0	2	17.82	9.40	95.2	6.36e+007	(K)TVTAMDVVYALK(R)	1310.703
2	008-1502.2886.2913.0	2	17.37	9.20	96.3	6.82e+007	(R)ISGLIYEETR(G)	1180.621
3	008-1501.3156.3161.2	2	16.80	10.86	94.5	6.59e+007	(R)ISGLIYEETR(G)	1180.621
4	008-0401.2992.3006.2	2	15.85	10.12	95.7	1.18e+007	(R)ISGLIYEETR(G)	1180.621
5	008-1502.3839.3854.2	2	15.70	6.01	97.9	2.28e+008	(K)VFLENVIR(D)	989.578
6	008-1501.4101.4105.2	2	15.22	6.02	98.9	2.12e+008	(K)VFLENVIR(D)	989.578
7	008-0401.3926.3931.0	2	14.73	5.43	98.9	7.34e+006	(K)VFLENVIR(D)	989.578
8	008-0401.4859.4859.0	3	12.00	6.71	83.3	2.68e+006	(K)TVTAMDVVYALK(R)	1310.703

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	6	3	43.79	10	4.76e+008	46154.6	PA_Bse02:2503998146	PA_Bse02:2503998146 BS02DRAFT_00013230 Glycosyl hydrolase family 10. [B. setacea BS02 (Isolate from shipw

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	009-0501.6057.6136.3	3	17.23	7.14	91.9	4.34e+007	(R)DQYNWGPLDAIYDYAR(A)	1959.888
2	010-0601.6244.6244.2	2	16.25	10.51	92.3	3.70e+007	(R)DQYNWGPLDAIYDYAR(A)	1959.888
3	009-0501.6054.6120.2	2	15.74	9.58	91.8	1.33e+008	(R)DQYNWGPLDAIYDYAR(A)	1959.888
4	010-0601.4412.4412.0	3	13.69	8.23	74.7	9.12e+006	(R)SDFSQYWDQITPENEGK(W)	2043.894
5	010-0601.5703.5738.0	3	12.87	12.87	74.3	1.69e+007	(K)RPAMDWLMNYLGR(-)	1622.794

6	010-1702.6926.6976.2	2	10.16	6.25	61.1	2.37e+008	(R)DQYNWGPLDAIYDYAR(A)	1959.888

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	18	3	39.05	13	1.37e+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	012-0801.5549.5581.2	2	15.45	11.92	89.4	1.38e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
2	011-0701.5445.5481.2	2	15.39	12.35	88.1	1.85e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
3	012-1902.5793.5884.0	2	14.90	8.43	87.7	7.86e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
4	012-0801.5465.5537.2	2	14.43	11.21	87.9	1.75e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
5	011-1802.6000.6090.0	2	13.50	7.25	80.4	8.95e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
6	010-1702.5984.6005.2	2	12.97	12.97	83.8	2.55e+008	(K)GFPSTLGMLIDTGR(N)	1464.752
7	012-1901.5827.5856.2	2	12.18	12.18	81.7	5.40e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
8	012-1901.3269.3304.0	3	11.92	3.52	73.1	1.49e+008	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
9	010-0601.5389.5423.2	2	11.70	11.70	70.2	4.26e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
10	012-1902.3656.3735.0	2	11.68	6.25	86.0	1.12e+008	(R)IGAIAGPADGDGLGLR(G)	1452.781
11	012-0801.3638.3680.2	2	11.54	7.73	73.7	1.34e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
12	011-1802.3845.3920.2	2	11.18	6.83	76.4	1.33e+008	(R)IGAIAGPADGDGLGLR(G)	1452.781
13	011-0701.5347.5347.0	2	11.04	7.88	73.5	1.17e+007	(K)GFPSTLGMLIDTGR(N)	1464.752
14	011-1801.3592.3619.0	2	9.74	4.38	82.0	1.34e+008	(R)IGAIAGPADGDGLGLR(G)	1452.781
15	011-0701.3636.3636.2	2	9.59	4.13	76.4	4.13e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
16	012-0801.3668.3668.2	2	7.99	7.99	67.8	3.63e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
17	010-1702.3629.3661.2	2	7.63	7.63	67.2	1.10e+008	(R)IGAIAGPADGDGLGLR(G)	1452.781
18	010-1701.3667.3697.2	2	6.65	6.65	61.5	1.32e+008	(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
8	8.2	10	3	35.67	4	6.75e+008	113016.6	PA_Bse02:2503999098	PA_Bse02:2503999098 BS02DRAFT_00001060 Cellulose or protein binding domain./Glycosyl hydrolases family 6.

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	012-0801.7376.7384.0	3	13.80	5.30	80.5	2.14e+007	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.304
2	012-1902.3656.3735.0	2	11.68	6.25	86.0	1.12e+008	(R)IGAIAGPADGDGLGLR(G)	1452.781
3	012-0801.3638.3680.2	2	11.54	7.73	73.7	1.34e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
4	011-1802.3845.3920.2	2	11.18	6.83	76.4	1.33e+008	(R)IGAIAGPADGDGLGLR(G)	1452.781
5	011-0701.4864.4864.0	2	10.19	6.62	75.1	1.04e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
6	011-1801.3592.3619.0	2	9.74	4.38	82.0	1.34e+008	(R)IGAIAGPADGDGLGLR(G)	1452.781
7	011-0701.3636.3636.2	2	9.59	4.13	76.4	4.13e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
8	012-0801.3668.3668.2	2	7.99	7.99	67.8	3.63e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
9	010-1702.3629.3661.2	2	7.63	7.63	67.2	1.10e+008	(R)IGAIAGPADGDGLGLR(G)	1452.781
10	010-1701.3667.3697.2	2	6.65	6.65	61.5	1.32e+008	(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
8	8.3	10	2	27.15	5	6.65e+008	77060.3	PA_BS12:2189570194	PA_BS12:2189570194 or3425 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 730 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	012-0801.5549.5581.2	2	15.45	11.92	89.4	1.38e+007	(K)GFPSTIGMLIDTGR(N)	1464.752
2	011-0701.5445.5481.2	2	15.39	12.35	88.1	1.85e+007	(K)GFPSTIGMLIDTGR(N)	1464.752
3	012-1902.5793.5884.0	2	14.90	8.43	87.7	7.86e+007	(K)GFPSTIGMLIDTGR(N)	1464.752
4	012-0801.5465.5537.2	2	14.43	11.21	87.9	1.75e+007	(K)GFPSTIGMLIDTGR(N)	1464.752
5	011-1802.6000.6090.0	2	13.50	7.25	80.4	8.95e+007	(K)GFPSTIGMLIDTGR(N)	1464.752
6	010-1702.5984.6005.2	2	12.97	12.97	83.8	2.55e+008	(K)GFPSTIGMLIDTGR(N)	1464.752
7	012-1901.5827.5856.2	2	12.18	12.18	81.7	5.40e+007	(K)GFPSTIGMLIDTGR(N)	1464.752
8	010-0601.5389.5423.2	2	11.70	11.70	70.2	4.26e+007	(K)GFPSTIGMLIDTGR(N)	1464.752
9	010-1702.3399.3403.0	3	11.70	6.79	71.9	8.39e+007	(R)NGWGGPNRPTGESSSSDLETYVNESR(I)	2796.246
10	011-0701.5347.5347.0	2	11.04	7.88	73.5	1.17e+007	(K)GFPSTIGMLIDTGR(N)	1464.752

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
9	9.1	3	3	34.79	11	5.61e+007	56911.4	PA_Bse08:2503996762	PA_Bse08:2503996762 BS08DRAFT_00004980 esterase, PHB depolymerase family [B. setacea BS08 (Isolate from

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	009-0501.6123.6160.0	2	15.05	10.76	79.5	4.63e+007	(R)DGGSDPVSIMSMIDYVK(Q)	1813.835
2	008-0401.4618.4618.0	3	10.95	5.13	70.9	8.01e+006	(R)LQLWHGTNDETLNYNNFNEAIK(Q)	2634.259
3	010-0601.3152.3152.0	3	8.79	5.33	88.1	1.88e+006	(K)QWTNVHGVSQTAAYTDSPESGITR(T)	2605.228

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
10	10.1	3	3	29.08	47	1.23e+008	8388.5	PA_Bse_meta_comb:2073588714	PA_Bse_meta_comb:2073588714 BaSeMet_00323700 hypothetical protein [Bankia setacea microbiome (

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	009-0501.6002.6076.0	2	11.17	7.73	69.6	1.01e+008	(K)DTGTFADFMEAFK(T)	1479.647
2	009-0501.4614.4614.2	2	9.99	2.22	85.7	1.90e+007	(K)FEEFIPLYK(E)	1185.620
3	009-0501.3215.3215.0	2	7.92	4.01	82.7	2.62e+006	(R)EGQGFISGAELR(H)	1263.633

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
11	11.1	9	2	28.84	1	1.35e+009	224278.3	PA_BS12:2189569050	PA_BS12:2189569050 or2363 Gluconolactonase [B. setacea BS12] 2124 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	012-1901.4165.4200.2	2	15.84	9.16	90.7	2.38e+008	(R)ALPENLDQVYLK(A)	1402.758
2	011-1802.4416.4464.0	2	14.84	7.30	90.4	1.90e+008	(R)ALPENLDQVYLK(A)	1402.758
3	011-1801.4161.4202.2	2	14.81	8.01	89.5	2.13e+008	(R)ALPENLDQVYLK(A)	1402.758
4	012-1902.4189.4202.0	2	13.82	6.22	89.6	1.74e+008	(R)ALPENLDQVYLK(A)	1402.758
5	008-1502.2354.2373.0	2	13.00	8.50	81.4	5.18e+006	(R)AFTGTQSVHFK(G)	1222.622
6	008-1501.2631.2637.0	2	12.01	7.58	76.0	4.40e+006	(R)AFTGTQSVHFK(G)	1222.622
7	010-1701.4268.4268.0	2	10.53	3.97	78.3	1.99e+008	(R)ALPENLDQVYLK(A)	1402.758
8	009-1601.4213.4254.0	2	9.85	2.67	70.4	1.69e+008	(R)ALPENLDQVYLK(A)	1402.758
9	009-1602.4462.4481.0	2	9.84	3.43	69.0	1.55e+008	(R)ALPENLDQVYLK(A)	1402.758

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
12	12.1	2	2	26.99	5	2.96e+007	71955.5	PA_BS12:2189569712	PA_BS12:2189569712 or3019 Beta-1,4-xylanase [B. setacea BS12] 676 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	008-0401.3735.3735.2	2	15.55	11.99	84.9	6.85e+006	(R)DNMSWGGVDTAYNYAR(S)	1819.771
2	008-0401.4858.4863.0	3	11.44	3.76	74.8	2.27e+007	(K)QHTFVWGSQEPSWIGNLSQSEQR(E)	2701.276

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
13	13.1	5	2	26.23	19	3.90e+008	12753.8	PA_Bse_meta_comb:2073593092	PA_Bse_meta_comb:2073593092 BaSeMet_00367480 Actin and related proteins [Bankia setacea microb

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	010-1702.5040.5059.0	3	13.75	3.81	78.5	2.58e+008	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
2	012-0801.4709.4735.0	3	13.14	4.04	74.0	7.57e+006	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
3	009-0501.4101.4139.0	3	12.48	5.74	71.3	3.20e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150
4	011-0701.4640.4667.0	3	12.23	2.85	77.7	1.21e+007	(K)DLYANTVLSGGSTMYPGIADR(M)	2201.055
5	010-1701.4428.4464.0	3	11.33	6.00	77.3	8.02e+007	(R)KDLYANTVLSGGSTMYPGIADR(M)	2329.150

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
14	14.1	3	2	24.47	6	1.98e+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	007-0301.5856.5903.0	3	17.57	14.44	94.3	1.87e+008	(K)ELVFWITKPGFSFDANR(T)	2027.039
2	007-0301.2612.2612.0	2	6.90	2.99	94.5	5.91e+006	(R)HVIYGEWGR(D)	1116.559
3	007-0301.2618.2618.0	2	6.79	2.88	90.2	4.79e+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
15	15.1	3	2	24.34	4	8.54e+007	77470.6	PA_Bse08:2503996278	PA_Bse08:2503996278 BS08DRAFT_00001670 Cellulose or protein binding domain./Cellulose binding domain./Cel

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	012-0801.4846.4891.0	3	14.88	6.42	77.0	3.65e+007	(R)FPIAPQTLDPNDAQGIGSVQNGGVLK(N)	2636.368
2	011-0701.4737.4761.0	3	14.40	6.15	78.0	4.63e+007	(R)FPIAPQTLDPNDAQGIGSVQNGGVLK(N)	2636.368
3	010-0601.2991.2991.2	2	9.46	6.15	87.8	2.60e+006	(K)ALGINVVR(F)	841.526

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
16	16.1	2	2	23.76	3	1.07e+008	70884.2	PA_Bse08:2503997525	PA_Bse08:2503997525 BS08DRAFT_00020200 Cellulose or protein binding domain./Glycosyl hydrolases family 11.

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	012-1902.3170.3175.2	2	11.98	7.75	76.3	1.33e+007	(R)YTSQWSNSTNNWVGGK(G)	1828.825
2	007-1401.3132.3145.2	2	11.78	5.30	76.3	9.32e+007	(R)VITWDVDSR(D)	1090.553