Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\061511_OGL_Cae2_GelFree
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 329 **Hits:** 667
beginning to assemble proteins .... proteins assembled 0.105844 sec
proteins filtered by unique peptides 0.011212 sec
proteins filtered by score
calculated protein coverage maps 0.076089 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.007908 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 19 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	186	15	267.84	33	1.08e+011	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding (
1	1.1	179	13	242.30	52	1.08e+011	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (Co
2	2.1	32	8	134.54	19	1.87e+009	80610.8	PA_BS12:2189571642	PA_BS12:2189571642 or0735 Carbohydrate binding domain. [B. setacea BS12] 763 bp
2	2.1	32	8	134.54	41	1.87e+009	37625.9	PA_Bse_meta_comb:2073592708	PA_Bse_meta_comb:2073592708 BaSeMet_00363640 hypothetical protein [Bankia setacea microbiome
2	2.2	9	2	35.53	4	8.82e+008	112354.2	PA_Bse_meta_comb:2073560170	PA_Bse_meta_comb:2073560170 BaSeMet_00038260 esterase, PHB depolymerase family [Bankia seta
2	2.2	9	2	35.53	4	8.82e+008	112173.0	PA_Bse02:2503998147	PA_Bse02:2503998147 BS02DRAFT_00013240 esterase, PHB depolymerase family [B. setacea BS02 (
3	3.1	24	8	113.65	17	1.74e+009	77470.6	PA_Bse08:2503996278	PA_Bse08:2503996278 BS08DRAFT_00001670 Cellulose or protein binding domain./Cellulose binding (
3	3.1	10	3	38.14	4	6.70e+008	78391.5	PA_Bse02:2503998382	PA_Bse02:2503998382 BS02DRAFT_00024320 Cellulose or protein binding domain./Cellulose binding (
3	3.1	10	3	38.14	7	6.70e+008	50267.5	PA_Bse_meta_comb:2073595739	PA_Bse_meta_comb:2073595739 BaSeMet_00393950 Endoglucanase [Bankia setacea microbiome (Co
3	3.1	5	2	23.51	14	2.93e+008	15283.0	PA_Bse_meta_comb:2073592399	PA_Bse_meta_comb:2073592399 BaSeMet_00360550 Cellulase (glycosyl hydrolase family 5). [Bankia s
4	4.1	24	5	89.04	7	4.06e+009	104392.5	PA_BS12:2189569647	PA_BS12:2189569647 or2953 Beta-1,4-xylanase [B. setacea BS12] 986 bp
5	5.1	13	4	58.46	8	1.84e+008	77941.2	PA_BS12:2189569979	PA_BS12:2189569979 or3290 Glycosyl hydrolase family 9./Cellulose or protein binding domain./N-termi
5	5.1	13	4	58.46	8	1.84e+008	77103.2	PA_Bse_meta_comb:2073565540	PA_Bse_meta_comb:2073565540 BaSeMet_00091960 cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) [
5	5.1	11	3	46.27	5	1.68e+008	90871.9	PA_Bse08:2503995091	PA_Bse08:2503995091 BS08DRAFT_00035590 Cellulose or protein binding domain./Cellulose binding (
6	6.1	8	4	57.24	11	2.36e+008	58225.4	PA_BS12:2189570192	PA_BS12:2189570192 or3423 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 560 b
6	6.1	8	4	57.24	13	2.36e+008	52443.2	PA_Bse_meta_comb:2073587378	PA_Bse_meta_comb:2073587378 BaSeMet_00310340 Cobalamin biosynthesis protein CobN and relate
6	6.1	3	2	24.98	4	6.89e+007	57718.9	PA_Bse08:2503996244	PA_Bse08:2503996244 BS08DRAFT_00001320 Cellulose or protein binding domain./Cellulose binding (
7	7.1	6	4	54.17	3	1.58e+008	224278.3	PA_BS12:2189569050	PA_BS12:2189569050 or2363 Gluconolactonase [B. setacea BS12] 2124 bp
7	7.1	6	4	54.17	3	1.58e+008	223963.9	PA_Bse_meta_comb:2073579605	PA_Bse_meta_comb:2073579605 BaSeMet_00232610 Gluconolactonase [Bankia setacea microbiome (
8	8.1	4	3	46.93	11	9.19e+007	46154.6	PA_Bse02:2503998146	PA_Bse02:2503998146 BS02DRAFT_00013230 Glycosyl hydrolase family 10. [B. setacea BS02 (Isolate
8	8.1	4	3	46.93	11	9.19e+007	46141.6	PA_Bse_meta_comb:2073560169	PA_Bse_meta_comb:2073560169 BaSeMet_00038250 Beta-1,4-xylanase [Bankia setacea microbiome (
8	8.2	2	2	29.57	3	5.83e+007	99497.3	PA_Bse08:2503994382	PA_Bse08:2503994382 BS08DRAFT_00000020 Cellulose or protein binding domain./Glycosyl hydrolase
9	9.1	8	3	39.66	6	1.80e+008	70884.2	PA_Bse08:2503997525	PA_Bse08:2503997525 BS08DRAFT_00020200 Cellulose or protein binding domain./Glycosyl hydrolase
9	9.1	4	2	25.84	7	1.03e+008	48213.7	PA_Bse08:2503997524	PA_Bse08:2503997524 BS08DRAFT_00020190 Cellulose or protein binding domain./Glycosyl hydrolase
9	9.2	6	3	36.16	7	1.12e+008	70938.0	PA_Bse02:2504000681	PA_Bse02:2504000681 BS02DRAFT_00022770 Cellulose or protein binding domain./Glycosyl hydrolase
10	10.1	4	2	35.07	4	9.21e+007	56911.4	PA_Bse08:2503996762	PA_Bse08:2503996762 BS08DRAFT_00004980 esterase, PHB depolymerase family [B. setacea BS08 (
11	11.1	2	2	31.02	5	5.08e+007	68058.0	PA_Bse02:2503998900	PA_Bse02:2503998900 BS02DRAFT_00018350 Cellulose binding domain./YceI-like domain. [B. setacea
11	11.1	2	2	31.02	9	5.08e+007	43274.1	PA_Bse_meta_comb:2073579119	PA_Bse_meta_comb:2073579119 BaSeMet_00227750 Cobalamin biosynthesis protein CobN and relate
12	12.1	5	2	29.50	8	2.18e+008	62134.7	PA_Bse08:2503996242	PA_Bse08:2503996242 BS08DRAFT_00001300 Cellulose or protein binding domain./Cellulose binding (
13	13.1	3	2	24.81	5	3.78e+007	74714.6	PA_Bse08:2503995453	PA_Bse08:2503995453 BS08DRAFT_00039170 Cellulose or protein binding domain./Cellulose binding (
14	14.1	2	2	22.97	6	6.48e+007	55060.3	PA_BS12:2189568352	PA_BS12:2189568352 or0169 Cellulose or protein binding domain./Cellulose binding domain. [B. setace
15	15.1	2	2	20.34	6	2.30e+007	39939.7	PA_BS12:2189570962	PA_BS12:2189570962 or0231 Uncharacterized protein conserved in bacteria [B. setacea BS12] 383 bp
16	16.1	3	1	20.20	4	1.56e+007	43475.8	PA_BS12:2189567935	PA_BS12:2189567935 or1258 Lysophospholipase L1 and related esterases [B. setacea BS12] 419 bp
16	16.1	3	1	20.20	4	1.56e+007	42177.2	PA_Bse_meta_comb:2073563649	PA_Bse_meta_comb:2073563649 BaSeMet_00073050 Predicted solute binding protein [Bankia setacea
Totals:	642	130							

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	186	15	267.84	33	1.08e+011	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	024-0401.6630.6715.3	3	21.83	16.94	96.6	1.05e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
2	027-1001.6635.6741.0	3	20.89	15.65	98.3	1.29e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
3	024-0401.6734.6760.0	3	20.70	14.35	94.5	8.91e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
4	024-0401.6749.6761.0	3	20.35	12.08	97.8	8.53e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
5	027-1001.6689.6762.4	4	20.33	10.91	96.4	3.26e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
6	026-0801.8543.8549.0	3	20.17	16.19	95.0	2.59e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
7	025-0601.7085.7089.2	2	19.93	11.68	98.8	2.21e+007	(R)EWQDALVDYMVEK(D)	1625.752
8	026-0801.6662.6782.0	3	19.84	9.46	97.7	2.07e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
9	027-1001.7130.7214.2	2	19.71	19.71	96.5	5.73e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
10	027-1001.6685.6787.3	3	19.64	15.91	93.2	5.08e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
11	027-1001.8474.8532.0	3	19.44	15.02	93.3	2.20e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
12	026-0801.7688.7803.0	2	19.36	19.36	97.6	4.24e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
13	024-0401.6650.6743.3	3	19.28	13.18	97.0	9.46e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
14	026-0801.6787.6906.0	3	19.27	15.54	96.9	6.82e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
15	026-0801.10247.10320.2	2	19.20	19.20	93.8	5.00e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
16	026-0801.6911.6935.0	3	19.19	13.41	95.2	5.07e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
17	027-1001.10233.10302.0	3	19.17	16.11	93.5	3.41e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
18	026-0801.7810.7848.3	3	18.99	18.99	94.6	1.78e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
19	024-0401.7125.7166.2	2	18.87	11.55	97.6	5.46e+007	(R)EWQDALVDYMVEK(D)	1625.752
20	026-0801.7334.7448.3	3	18.87	13.40	92.2	5.79e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
21	026-0801.9047.9052.0	3	18.75	14.70	92.4	7.70e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
22	026-0801.6820.6929.4	4	18.69	8.84	93.2	5.39e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
23	027-1001.9165.9165.0	3	18.68	11.81	93.5	1.54e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
24	026-0801.9419.9445.0	3	18.59	13.29	91.4	4.29e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
25	026-0801.6781.6903.3	3	18.51	14.89	91.3	7.40e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
26	026-0801.7187.7230.0	2	18.45	11.10	98.9	3.35e+008	(R)EWQDALVDYMVEK(D)	1625.752
27	027-1001.6888.6904.0	3	18.40	7.85	95.3	2.91e+007	(R)LDANPPYADADREGYEFTR(E)	2199.995
28	026-0801.7310.7423.3	3	18.37	12.48	92.4	5.76e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
29	027-1001.7213.7300.3	3	18.29	12.63	89.2	1.50e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
30	025-0601.7454.7478.2	2	18.25	18.25	95.0	5.19e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
31	024-0401.7017.7062.0	3	18.22	10.14	92.5	2.99e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
32	024-0401.7196.7196.0	3	18.14	12.73	94.2	1.42e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
33	025-0601.7057.7093.3	3	18.14	12.01	89.0	1.30e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
34	026-0801.10505.10557.0	3	18.14	11.92	92.9	4.22e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
35	026-0801.7330.7445.2	2	18.13	14.58	95.6	5.11e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
36	027-1001.6750.6847.0	3	18.10	9.64	93.9	2.89e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
37	027-1001.7217.7320.2	2	18.06	14.41	95.1	7.52e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
38	024-0401.7111.7177.2	2	17.93	17.93	94.1	2.02e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
39	027-1001.6801.6878.0	3	17.91	9.67	88.2	3.11e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
40	026-0801.9992.10072.3	3	17.64	17.64	88.4	7.23e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211

41	026-0801.7790.7846.3	3	17.61	10.99	94.7	4.43e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
42	026-0801.7231.7325.0	2	17.58	13.43	94.8	1.91e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
43	027-1001.10065.10070.2	2	17.55	17.55	91.2	2.04e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
44	027-1001.8854.8880.0	3	17.50	12.40	89.8	1.92e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
45	026-0801.7216.7296.3	3	17.35	12.17	90.9	9.15e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
46	026-0801.7558.7647.2	2	17.32	17.32	92.0	3.35e+009	(R)AGWDEHFGYLR(D)	1350.623
47	024-0401.7104.7189.3	3	17.24	10.69	90.4	3.58e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
48	025-0601.7082.7141.2	2	17.18	11.64	90.1	4.57e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
49	027-1001.9959.9987.2	2	17.15	17.15	92.2	2.15e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
50	026-0801.8411.8453.0	3	17.14	11.65	91.9	3.31e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
51	027-1001.8730.8799.0	3	17.14	11.21	92.5	2.59e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
52	027-1001.8550.8592.0	3	16.93	12.10	88.0	1.75e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
53	026-0801.7811.7847.2	2	16.85	16.85	93.8	3.15e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
54	025-0601.8673.8673.0	3	16.83	16.83	79.9	5.35e+007	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
55	026-0801.7491.7590.2	2	16.79	13.46	90.2	1.55e+009	(R)AGWDEHFGYLR(D)	1350.623
56	026-0801.7429.7473.3	3	16.67	8.27	88.9	4.62e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
57	027-1001.7106.7187.0	2	16.65	9.80	94.2	1.22e+008	(R)EWQDALVDYMVEK(D)	1625.752
58	024-0401.7237.7274.2	2	16.60	13.59	87.9	1.46e+008	(R)AGWDEHFGYLR(D)	1350.623
59	026-0801.7450.7474.2	2	16.51	12.71	94.0	2.97e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
60	027-1001.9675.9749.2	2	16.51	16.51	89.1	5.47e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
61	027-1001.9873.9901.2	2	16.51	16.51	89.7	1.98e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
62	027-1001.7126.7185.3	3	16.50	9.52	86.2	6.90e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
63	027-1001.7351.7418.2	2	16.50	13.41	90.2	7.29e+008	(R)AGWDEHFGYLR(D)	1350.623
64	027-1001.10265.10272.0	3	16.47	11.19	89.0	2.91e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
65	026-0801.9831.9915.0	3	16.44	16.44	87.2	1.33e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
66	026-0801.10256.10329.0	3	16.41	16.41	86.0	7.62e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
67	027-1001.8333.8363.0	3	16.36	16.36	87.9	1.51e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
68	027-1001.9407.9497.3	3	16.21	10.46	83.6	1.73e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
69	027-1001.8806.8817.5	5	16.15	16.15	79.6	1.48e+007	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
70	027-1001.7162.7192.0	2	16.09	8.76	93.1	1.22e+008	(R)EWQDALVDYMVEK(D)	1625.752
71	026-0801.8259.8303.0	3	16.02	16.02	86.8	3.98e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
72	024-0401.7472.7472.2	2	15.96	15.96	79.5	1.67e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
73	026-0801.10085.10162.3	3	15.91	10.99	86.4	6.37e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
74	026-0801.10253.10307.3	3	15.89	15.89	87.9	6.29e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
75	027-1001.9796.9871.0	3	15.86	9.91	85.9	5.78e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
76	027-1001.8107.8178.0	3	15.81	15.81	85.2	2.14e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
77	027-1001.7471.7478.2	2	15.77	15.77	91.1	2.94e+008	(R)AGWDEHFGYLR(D)	1350.623
78	026-0801.9606.9709.3	3	15.75	12.03	83.1	2.32e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
79	027-1001.9510.9582.0	3	15.74	12.41	84.9	1.17e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
80	026-0801.7573.7653.0	3	15.71	7.23	83.0	7.98e+007	(R)AGWDEHFGYLR(D)	1350.623
81	027-1001.7887.7941.0	3	15.71	10.85	81.8	1.60e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
82	025-0601.7198.7285.2	2	15.69	15.69	87.2	8.17e+007	(R)AGWDEHFGYLR(D)	1350.623
83	027-1001.9761.9810.0	2	15.68	15.68	78.1	3.97e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
84	026-0801.7245.7344.3	3	15.58	8.43	84.7	2.79e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
85	026-0801.9903.9910.2	2	15.54	15.54	76.2	6.80e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
86	026-0801.10084.10084.0	3	15.47	12.06	86.7	4.15e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
87	027-1001.9413.9503.0	3	15.47	12.26	86.6	2.14e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
88	026-0801.9195.9237.0	3	15.46	9.98	88.0	4.64e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050

89	027-1001.9865.9865.0	3	15.35	15.35	75.6	3.16e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
90	026-0801.7083.7128.3	3	15.30	6.85	82.7	2.79e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
91	027-1001.8369.8441.0	3	15.30	10.13	84.9	1.91e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
92	027-1001.8640.8685.0	3	15.29	8.71	84.6	1.81e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
93	024-0401.6158.6158.2	2	15.27	8.23	91.5	2.80e+007	(R)LDANPPYADADR(E)	1317.608
94	025-0601.7293.7343.2	2	15.23	15.23	88.1	8.52e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
95	026-0801.7687.7802.3	3	15.14	15.14	75.8	1.90e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
96	027-1001.9694.9755.3	3	15.13	15.13	83.1	6.90e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
97	026-0801.10104.10173.2	2	15.08	15.08	76.2	5.39e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
98	026-0801.7771.7832.0	2	15.06	15.06	77.0	4.64e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
99	026-0801.8573.8579.0	3	14.93	9.86	87.8	2.39e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
100	024-0401.7348.7364.0	2	14.91	14.91	91.1	7.89e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
101	027-1001.9506.9512.2	2	14.82	14.82	85.8	4.28e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
102	027-1001.9982.10057.3	3	14.80	5.86	85.5	8.63e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
103	027-1001.6195.6210.0	2	14.77	8.48	91.5	4.29e+007	(R)LDANPPYADADR(E)	1317.608
104	027-1001.10091.10111.3	3	14.76	10.62	84.0	4.57e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
105	027-1001.7495.7537.3	3	14.71	14.71	83.5	3.19e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
106	026-0801.8747.8747.0	3	14.55	14.55	80.6	2.02e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
107	026-0801.9555.9655.0	3	14.49	14.49	85.6	2.37e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
108	027-1001.10003.10021.2	2	14.47	14.47	80.5	8.54e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
109	027-1001.7523.7554.0	2	14.47	11.03	73.8	1.65e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
110	025-0601.6703.6707.0	3	14.41	7.40	78.2	2.81e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
111	027-1001.7395.7462.0	3	14.37	6.41	80.5	2.19e+007	(R)AGWDEHFGYLR(D)	1350.623
112	027-1001.7023.7029.2	2	14.26	14.26	82.6	3.15e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
113	027-1001.8989.8989.0	3	14.22	14.22	82.2	6.35e+006	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
114	026-0801.7085.7106.2	2	14.21	14.21	87.0	7.97e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
115	026-0801.8157.8230.0	3	14.19	9.64	81.0	5.43e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
116	026-0801.6170.6187.0	2	14.18	7.64	87.9	1.05e+008	(R)LDANPPYADADR(E)	1317.608
117	026-0801.7656.7663.2	2	14.18	11.04	89.0	2.36e+009	(R)AGWDEHFGYLR(D)	1350.623
118	026-0801.9465.9465.0	3	14.06	14.06	87.6	4.36e+006	(R)TIQQTMTEITAQGINVVR(L)	2003.060
119	026-0801.9703.9734.2	2	14.06	14.06	75.8	7.52e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
120	026-0801.10058.10100.0	2	14.04	14.04	72.9	1.33e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
121	027-1001.10033.10113.0	3	13.89	13.89	80.0	7.11e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
122	027-1001.7082.7119.3	3	13.85	5.09	77.3	1.08e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
123	026-0801.9443.9443.0	3	13.83	13.83	77.8	3.16e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
124	027-1001.9449.9528.2	2	13.81	13.81	70.5	2.08e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
125	027-1001.8889.8889.0	3	13.72	13.72	78.2	1.50e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
126	027-1001.8028.8028.0	3	13.69	13.69	75.1	1.52e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
127	026-0801.8376.8441.0	3	13.65	13.65	81.6	3.92e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
128	025-0601.6206.6215.0	2	13.50	6.56	81.5	2.99e+007	(R)LDANPPYADADR(E)	1317.608
129	024-0401.7034.7081.0	3	13.49	8.36	80.5	3.71e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
130	026-0801.9230.9230.0	3	13.47	13.47	81.9	1.83e+007	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
131	025-0601.6936.6953.0	3	13.43	6.44	85.9	2.48e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
132	027-1001.7910.7980.0	3	13.28	13.28	79.4	8.86e+007	(R)AAEQEMWSHITPGVDREWQDALVDYMVEK(D)	3433.583
133	027-1001.8287.8359.0	3	13.28	7.61	83.9	1.81e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
134	026-0801.8939.9019.0	3	13.27	5.51	82.8	5.56e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
135	026-0801.8192.8206.5	5	13.26	13.26	78.5	1.21e+007	(R)AAEQEMWSHITPGVDREWQDALVDYMVEK(D)	3433.583
136	027-1001.6722.6810.2	2	13.14	7.96	89.6	3.89e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410

137	027-1001.9121.9172.0	3	13.14	7.36	79.9	3.34e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
138	025-0601.6976.7000.0	3	13.12	13.12	72.8	3.55e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
139	024-0401.7871.7891.0	3	13.07	13.07	78.4	1.50e+007	(R)AAEQEMWSHITPGVDREWQDALVDYMVEK(D)	3433.583
140	026-0801.9708.9714.2	2	13.06	13.06	67.0	1.78e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
141	027-1001.9529.9583.3	3	13.04	6.67	79.0	1.09e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
142	026-0801.4866.4943.0	2	13.01	6.59	78.8	1.59e+006	(R)VDSQGNITK(N)	961.495
143	025-0601.6631.6658.0	3	12.98	7.71	82.1	1.40e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
144	027-1001.9230.9230.0	3	12.97	12.97	72.9	2.64e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
145	026-0801.9152.9152.0	3	12.73	12.73	73.8	2.28e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
146	026-0801.8670.8670.0	3	12.61	8.22	80.2	3.16e+006	(R)TIQQTMTEITAQGINVVR(L)	2003.060
147	027-1001.6999.7064.3	3	12.60	5.80	77.9	1.21e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
148	027-1001.8879.8879.0	3	12.58	12.58	81.7	1.70e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
149	027-1001.10308.10308.0	3	12.57	9.41	75.3	1.24e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
150	027-1001.8697.8703.0	3	12.54	12.54	72.4	1.47e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
151	027-1001.9205.9205.0	3	12.54	12.54	71.8	1.85e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
152	026-0801.6359.6375.2	2	12.53	6.85	87.1	3.97e+007	(K)NGSVFPVR(C)	875.474
153	026-0801.8748.8765.0	3	12.39	7.28	77.6	2.57e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
154	026-0801.6791.6909.2	2	12.32	5.99	61.8	6.37e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
155	027-1001.9440.9486.0	2	12.24	7.81	80.1	1.49e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
156	025-0601.7004.7016.2	2	12.04	7.28	77.7	2.08e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
157	024-0401.7060.7077.2	2	12.03	12.03	78.0	1.73e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
158	026-0801.8528.8528.0	3	11.95	3.96	79.7	3.69e+006	(R)TIQQTMTEITAQGINVVR(L)	2003.060
159	024-0401.7046.7046.2	2	11.87	7.87	78.1	2.66e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
160	026-0801.8214.8214.0	3	11.85	8.68	79.9	4.09e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
161	026-0801.4954.4991.0	2	11.80	6.68	80.7	1.39e+006	(R)VDSQGNITK(N)	961.495
162	027-1001.9218.9218.0	3	11.76	11.76	77.6	2.20e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
163	024-0401.6623.6708.2	2	11.60	6.19	75.6	1.60e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
164	027-1001.9540.9540.2	2	11.57	11.57	71.1	1.11e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
165	027-1001.6398.6423.2	2	11.49	5.72	86.2	1.64e+007	(K)NGSVFPVR(C)	875.474
166	026-0801.7174.7174.2	2	11.38	11.38	73.9	8.45e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
167	026-0801.10534.10534.0	3	11.34	7.48	70.4	1.19e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
168	027-1001.9827.9884.2	2	11.29	11.29	68.6	1.19e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
169	025-0601.6394.6404.2	2	11.24	6.70	85.9	5.81e+006	(K)NGSVFPVR(C)	875.474
170	026-0801.10564.10564.0	3	11.22	7.39	76.3	7.31e+006	(R)TIQQTMTEITAQGINVVR(L)	2003.060
171	024-0401.6417.6417.2	2	11.09	6.62	83.0	1.35e+007	(K)NGSVFPVR(C)	875.474
172	026-0801.7088.7137.0	2	11.01	6.34	64.1	6.19e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
173	027-1001.7610.7610.0	3	10.80	3.00	74.6	1.72e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
174	024-0401.6687.6718.4	4	10.64	3.96	72.8	2.09e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
175	026-0801.5043.5105.0	2	10.61	5.03	77.7	1.67e+006	(R)VDSQGNITK(N)	961.495
176	026-0801.8007.8007.0	3	10.55	10.55	75.8	2.87e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
177	026-0801.10265.10273.2	2	10.29	10.29	64.8	8.46e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
178	026-0801.10541.10541.0	3	10.14	10.14	72.0	2.60e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
179	027-1001.9060.9060.0	3	9.70	5.47	84.6	2.95e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
180	026-0801.7715.7715.0	2	9.37	5.14	86.7	8.16e+008	(R)AGWDEHFGYLR(D)	1350.623
181	027-1001.10311.10311.0	3	9.24	4.13	92.9	2.69e+006	(R)TIQQTMTEITAQGINVVR(L)	2003.060
182	026-0801.7606.7606.0	2	9.07	9.07	66.2	5.44e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
183	025-0601.6640.6640.0	3	8.81	2.15	73.3	8.36e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
184	026-0801.9005.9005.0	3	8.79	8.79	84.9	7.33e+006	(R)TIQQTMTEITAQGINVVR(L)	2003.060

185	027-1001.9323.9323.0	2	6.71	6.71	60.8	4.88e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
186	024-0401.9780.9780.0	2	6.24	6.24	60.6	1.51e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050

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	32	8	134.54	19	1.87e+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	025-0601.7315.7359.2	2	22.32	22.32	97.5	8.07e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
2	025-0601.7335.7335.2	2	20.08	20.08	94.9	7.61e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
3	026-0801.6924.6995.2	2	18.38	8.74	92.7	2.31e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
4	027-1001.6916.6952.0	3	18.33	6.03	95.5	1.45e+007	(K)GVAVVNFSNSEMGAHNGSGSR(G)	2076.952
5	024-0401.7401.7401.0	3	18.18	11.52	92.0	1.12e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
6	025-0601.6721.6779.2	2	17.82	9.72	90.5	8.94e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
7	025-0601.6654.6691.2	2	17.15	13.25	93.5	1.87e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
8	027-1001.6995.7010.0	3	16.93	8.43	88.7	1.71e+007	(R)MIDVLQQTSGHNLDASR(I)	1884.924
9	026-0801.7853.7864.2	2	16.70	16.70	82.3	1.37e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
10	025-0601.7297.7373.3	3	16.58	9.20	89.4	1.87e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
11	026-0801.7815.7881.3	3	16.49	9.07	87.4	2.02e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
12	025-0601.6529.6593.2	2	15.55	9.18	94.0	4.02e+007	(K)GAIVVGAFDER(I)	1133.595
13	025-0601.6881.6929.3	3	15.34	7.44	85.9	9.86e+007	(R)MIDVLQQTSGHNLDASR(I)	1884.924
14	026-0801.7071.7119.2	2	14.88	14.88	84.7	2.78e+007	(R)MIDVLQQTSGHNLDASR(I)	1884.924
15	024-0401.6770.6781.0	2	14.76	4.43	86.0	3.23e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
16	025-0601.6891.6921.2	2	14.53	11.20	79.4	2.70e+007	(R)MIDVLQQTSGHNLDASR(I)	1884.924
17	026-0801.6523.6540.2	2	13.80	13.80	86.7	5.82e+007	(K)GAIVVGAFDER(I)	1133.595
18	027-1001.7054.7074.0	2	13.76	8.96	91.5	1.48e+007	(R)WIPWNTPILQ(-)	1267.684
19	025-0601.7058.7065.0	2	13.71	9.48	91.0	5.16e+007	(R)WIPWNTPILQ(-)	1267.684
20	024-0401.6566.6566.2	2	13.60	8.17	87.7	1.59e+007	(K)GAIVVGAFDER(I)	1133.595
21	026-0801.7124.7162.0	2	13.42	9.57	88.0	5.24e+007	(R)WIPWNTPILQ(-)	1267.684
22	024-0401.6793.6807.3	3	13.27	6.51	81.6	1.84e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
23	024-0401.7014.7050.3	3	12.94	6.65	77.2	3.55e+007	(R)MIDVLQQTSGHNLDASR(I)	1884.924
24	026-0801.8243.8243.0	3	12.12	12.12	72.9	1.25e+007	(R)GLLVIENTGQEWLGNESTYTASVAAHEVWK(A)	3302.633
25	026-0801.6949.6949.3	3	11.17	3.98	78.6	8.92e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
26	026-0801.7858.7858.0	2	10.93	10.93	74.2	1.46e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
27	026-0801.8768.8768.0	3	10.86	10.86	74.0	7.69e+006	(R)GLLVIENTGQEWLGNESTYTASVAAHEVWK(A)	3302.633
28	026-0801.10192.10192.0	3	10.06	10.06	73.3	2.05e+007	(R)GLLVIENTGQEWLGNESTYTASVAAHEVWK(A)	3302.633
29	026-0801.9184.9184.0	3	9.57	5.20	93.8	1.08e+007	(R)GLLVIENTGQEWLGNESTYTASVAAHEVWK(A)	3302.633
30	026-0801.10011.10011.0	3	9.27	9.27	77.3	2.36e+007	(R)GLLVIENTGQEWLGNESTYTASVAAHEVWK(A)	3302.633
31	024-0401.7403.7403.0	2	9.02	9.02	66.2	1.34e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
32	026-0801.9455.9455.0	3	8.74	3.92	73.0	1.15e+007	(R)GLLVIENTGQEWLGNESTYTASVAAHEVWK(A)	3302.633

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

2	2.2	9	2	35.53	4	8.82e+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	025-0601.7315.7359.2	2	22.32	22.32	97.5	8.07e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
2	025-0601.7335.7335.2	2	20.08	20.08	94.9	7.61e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
3	024-0401.7401.7401.0	3	18.18	11.52	92.0	1.12e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
4	026-0801.7853.7864.2	2	16.70	16.70	82.3	1.37e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
5	025-0601.7297.7373.3	3	16.58	9.20	89.4	1.87e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
6	026-0801.7815.7881.3	3	16.49	9.07	87.4	2.02e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
7	024-0401.7151.7151.0	3	13.21	7.73	73.1	2.88e+007	(R)YGSSGANAQVEAISLQGVPHNLPVEEEEAIR(F)	3264.614
8	026-0801.7858.7858.0	2	10.93	10.93	74.2	1.46e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
9	024-0401.7403.7403.0	2	9.02	9.02	66.2	1.34e+007	(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	3.1	24	8	113.65	17	1.74e+009	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	027-1001.7787.7787.2	2	18.23	12.86	89.0	8.82e+006	(R)WDHIVPGVDEDWQNAFVDYMK(K)	2564.156
2	026-0801.8023.8043.0	3	16.53	16.53	82.3	3.80e+007	(R)WDHIVPGVDEDWQNAFVDYMK(K)	2564.156
3	026-0801.6980.6980.0	3	16.45	8.46	84.7	4.97e+008	(R)FPIAPQTLDPNDAQGIGSVQNGGVLK(N)	2636.368
4	027-1001.7465.7541.3	3	14.63	3.80	94.1	1.26e+008	(R)LIISPHTYGPSVFVQK(Q)	1785.990
5	027-1001.6845.6879.2	2	14.43	9.55	88.6	8.14e+007	(R)FPIAPQTLDPNDAQGIGSVQNGGVLK(N)	2636.368
6	027-1001.6535.6571.2	2	14.16	7.20	96.2	3.38e+007	(K)ALGINVVR(F)	841.526
7	026-0801.6535.6554.2	2	14.14	7.47	95.4	3.07e+007	(K)ALGINVVR(F)	841.526
8	026-0801.7843.7862.0	3	14.07	4.84	91.5	1.18e+008	(R)LIISPHTYGPSVFVQK(Q)	1785.990
9	024-0401.6542.6542.2	2	13.40	6.13	95.5	7.61e+006	(K)ALGINVVR(F)	841.526
10	024-0401.7963.7963.0	3	13.35	13.35	78.7	6.60e+006	(R)DQGYAMIIGEFGGMMDWPEGAAAHDLER(W)	3067.339
11	026-0801.6264.6303.0	2	13.32	6.62	84.3	1.01e+008	(R)TIQQTMDEIK(A)	1206.604
12	027-1001.6287.6343.0	2	13.24	6.65	83.2	9.59e+007	(R)TIQQTMDEIK(A)	1206.604
13	027-1001.7528.7543.0	2	13.18	13.18	77.6	5.46e+007	(R)LIISPHTYGPSVFVQK(Q)	1785.990
14	027-1001.6379.6379.0	2	12.86	5.75	84.4	5.14e+007	(R)TIQQTMDEIK(A)	1206.604
15	024-0401.7361.7389.0	3	12.85	3.12	82.1	2.85e+007	(R)LIISPHTYGPSVFVQK(Q)	1785.990
16	025-0601.6282.6337.0	2	12.71	5.03	83.1	2.03e+007	(R)TIQQTMDEIK(A)	1206.604
17	025-0601.6767.6767.0	3	12.61	12.61	77.6	2.48e+007	(R)FPIAPQTLDPNDAQGIGSVQNGGVLK(N)	2636.368
18	027-1001.6431.6513.0	2	12.40	4.08	91.4	4.63e+007	(R)QAMEDFIK(L)	981.471
19	026-0801.6415.6460.0	2	12.09	4.60	85.2	3.00e+007	(R)QAMEDFIK(L)	981.471
20	027-1001.6704.6731.0	2	11.11	3.69	83.4	1.92e+008	(R)LDAKPPYADAER(E)	1345.675
21	024-0401.6244.6327.0	2	10.66	4.15	75.6	6.74e+007	(R)TIQQTMDEIK(A)	1206.604
22	025-0601.6673.6673.0	2	9.24	4.18	88.2	1.86e+007	(R)LDAKPPYADAER(E)	1345.675
23	027-1001.7497.7497.0	2	8.98	8.98	66.3	4.93e+007	(R)LIISPHTYGPSVFVQK(Q)	1785.990
24	025-0601.6438.6458.0	2	8.19	3.13	67.5	6.43e+006	(R)QAMEDFIK(L)	981.471

				Distinct	Distinct			Total	

Group (#)	Subgroup (#)	Spectra (#)	Peptides (#)	Summed MS/MS Search Score	% AA Coverage	Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
4	4.1	24	5	89.04	7	4.06e+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	024-0401.6183.6270.2	2	21.95	14.09	98.9	1.63e+009	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
2	025-0601.6262.6324.2	2	21.50	13.13	100.0	6.47e+007	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
3	024-0401.6280.6335.2	2	21.46	12.92	99.1	1.57e+009	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
4	026-0801.6250.6300.2	2	21.45	13.65	99.0	4.19e+007	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
5	027-1001.6278.6294.2	2	20.87	11.97	97.2	3.26e+007	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
6	025-0601.6259.6299.3	3	19.19	14.50	93.3	1.55e+007	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
7	025-0601.6827.6899.0	2	18.40	18.40	85.9	4.39e+007	(R)SDFGQYWDQITLENK(G)	1843.850
8	025-0601.6857.6889.3	3	17.91	17.91	87.6	1.73e+007	(R)SDFGQYWDQITLENK(G)	1843.850
9	024-0401.6210.6307.3	3	17.90	12.40	88.3	2.32e+008	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
10	025-0601.7607.7647.3	3	17.09	7.09	90.4	1.12e+007	(R)IAALGLPIYISEYDIEK(T)	1908.037
11	027-1001.6285.6336.3	3	17.08	11.20	90.9	1.20e+007	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
12	024-0401.7595.7654.3	3	16.48	7.42	89.8	5.15e+007	(R)IAALGLPIYISEYDIEK(T)	1908.037
13	024-0401.7618.7645.0	3	16.04	6.76	87.9	3.67e+007	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
14	027-1001.7690.7713.3	3	15.98	6.58	89.1	1.10e+007	(R)IAALGLPIYISEYDIEK(T)	1908.037
15	026-0801.7939.7987.2	2	15.73	4.72	80.1	3.22e+007	(R)IAALGLPIYISEYDIEK(T)	1908.037
16	026-0801.7202.7206.0	3	15.56	6.83	83.0	1.82e+007	(K)WAQVEPQRDQYDWSGIDDAYNYAK(Q)	2918.302
17	027-1001.7688.7730.2	2	14.90	7.35	86.4	2.86e+007	(R)IAALGLPIYISEYDIEK(T)	1908.037
18	024-0401.7154.7154.0	3	14.00	14.00	76.3	8.10e+007	(K)WAQVEPQRDQYDWSGIDDAYNYAK(Q)	2918.302
19	025-0601.7079.7079.0	3	12.90	5.24	76.9	1.75e+007	(K)WAQVEPQRDQYDWSGIDDAYNYAK(Q)	2918.302
20	025-0601.7598.7598.0	2	12.59	5.25	76.2	1.21e+007	(R)IAALGLPIYISEYDIEK(T)	1908.037
21	024-0401.7118.7118.0	2	12.50	6.92	84.1	1.62e+007	(K)WAQVEPQRDQYDWSGIDDAYNYAK(Q)	2918.302
22	025-0601.7594.7594.2	2	12.31	5.81	82.0	1.95e+007	(R)IAALGLPIYISEYDIEK(T)	1908.037
23	025-0601.7083.7083.0	3	11.25	4.16	71.3	1.75e+007	(K)WAQVEPQRDQYDWSGIDDAYNYAK(Q)	2918.302
24	027-1001.6928.6976.0	2	11.00	11.00	71.3	4.32e+007	(R)SDFGQYWDQITLENK(G)	1843.850

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	13	4	58.46	8	1.84e+008	77941.2	PA_BS12:2189569979	PA_BS12:2189569979 or3290 Glycosyl hydrolase family 9./Cellulose or protein binding domain./N-terminal ig-like do

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	027-1001.7634.7671.0	3	19.01	19.01	89.3	3.30e+007	(K)MHDVGWTGLPLAPHEDSNER(A)	2261.041
2	025-0601.7561.7561.0	3	16.81	16.81	86.5	9.36e+006	(K)MHDVGWTGLPLAPHEDSNER(A)	2261.041
3	025-0601.7556.7556.0	3	15.55	15.55	91.3	1.00e+007	(K)MHDVGWTGLPLAPHEDSNER(A)	2261.041
4	027-1001.6993.7047.3	3	15.47	8.46	88.3	2.36e+007	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.153
5	025-0601.7539.7539.0	3	14.97	14.97	78.5	9.27e+006	(K)MHDVGWTGLPLAPHEDSNER(A)	2261.041
6	024-0401.7021.7029.0	2	14.77	5.05	88.0	1.67e+007	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.153
7	027-1001.7068.7068.2	2	12.74	6.78	86.2	9.54e+006	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.153
8	027-1001.7686.7686.0	3	12.20	7.96	77.9	2.43e+007	(K)MHDVGWTGLPLAPHEDSNER(A)	2261.041
9	027-1001.6295.6312.0	2	12.19	6.71	89.3	1.17e+007	(K)ASSNTAQTWELR(Q)	1363.661

10	027-1001.6944.6944.0	2	11.79	3.37	91.5	6.39e+006	(R)YFYHNR(S)	899.416
11	026-0801.7149.7149.0	3	10.30	3.17	81.7	9.87e+006	(K)FADGTLNIPESGNGVADILDEAR(W)	2374.153
12	025-0601.6290.6290.0	2	9.38	4.95	75.1	4.43e+006	(K)ASSNTAQTWELR(Q)	1363.661
13	024-0401.7562.7562.0	3	8.96	8.96	75.6	1.54e+007	(K)MHDVGWTGLPLAPHEDSNER(A)	2261.041

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	4	57.24	11	2.36e+008	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	024-0401.6203.6209.0	3	19.90	19.90	88.5	6.17e+007	(K)AEGSSIVQTGSAVSNWNDSDLTAAGR(L)	2593.213
2	024-0401.6316.6384.2	2	16.72	9.65	94.7	5.50e+007	(K)NDWNATIVR(A)	1088.549
3	025-0601.6348.6356.2	2	14.49	6.53	88.8	7.09e+006	(K)NDWNATIVR(A)	1088.549
4	024-0401.6238.6238.0	3	13.15	13.15	72.2	6.09e+007	(K)AEGSSIVQTGSAVSNWNDSDLTAAGR(L)	2593.213
5	024-0401.7276.7288.0	2	12.36	7.79	68.0	1.90e+007	(K)SFAGNSFFWSNTEWGQER(F)	2149.937
6	024-0401.6217.6217.2	2	11.98	8.28	86.6	9.89e+006	(K)AEGSSIVQTGSAVSNWNDSDLTAAGR(L)	2593.213
7	024-0401.7258.7265.0	3	11.75	5.34	80.2	1.57e+007	(K)SFAGNSFFWSNTEWGQER(F)	2149.937
8	024-0401.6951.6951.0	3	8.26	4.69	70.3	6.89e+006	(R)QNNISHLNWAVSDK(A)	1625.804

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	4	54.17	3	1.58e+008	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	024-0401.6401.6401.0	3	15.41	15.41	85.0	3.91e+007	(R)ASDGTLYFTDPDYQQGTTDGQSITGVYR(V)	3056.376
2	024-0401.7232.7303.0	3	15.12	5.42	93.4	4.02e+007	(K)SLGNEAGDNHEHIIGVK(G)	1789.883
3	025-0601.6624.6624.0	2	14.77	8.00	88.0	1.01e+007	(R)ALPENLDQVYLK(A)	1402.758
4	024-0401.6874.6931.0	2	8.87	8.87	68.5	3.59e+007	(R)AFTGTQSVHFK(G)	1222.622
5	024-0401.6943.6943.0	2	7.55	7.55	64.0	2.31e+007	(R)AFTGTQSVHFK(G)	1222.622
6	025-0601.6854.6854.2	2	7.24	7.24	60.7	9.49e+006	(R)AFTGTQSVHFK(G)	1222.622

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	4	3	46.93	11	9.19e+007	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	024-0401.7409.7434.3	3	17.18	8.87	88.6	2.03e+007	(R)DQYNWGPLDAIYDYAR(A)	1959.888
2	024-0401.6548.6608.3	3	15.90	9.14	84.4	2.52e+007	(R)SDFSQYWDQITPENEGK(W)	2043.894
3	024-0401.6547.6609.2	2	14.11	10.35	91.6	2.19e+007	(R)SDFSQYWDQITPENEGK(W)	2043.894
4	024-0401.7083.7088.0	2	13.85	6.00	91.7	2.45e+007	(R)NYPPFFVGNITTNGSVR(S)	1882.945

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	2	2	29.57	3	5.83e+007	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	024-0401.7409.7434.3	3	17.18	8.87	88.6	2.03e+007	(R)DQYNWGPLDAIYDYAR(A)	1959.888
2	024-0401.6645.6645.2	2	12.39	7.36	87.7	3.80e+007	(R)SDFTQYWDQITPENEGK(W)	2057.909

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	8	3	39.66	6	1.80e+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	026-0801.6482.6488.0	2	13.82	5.78	94.4	3.02e+007	(R)VITWDVDSR(D)	1090.553
2	024-0401.6182.6240.2	2	13.77	9.07	78.2	5.95e+007	(R)YTSQWSNSTNNWVGGK(G)	1828.825
3	027-1001.6507.6539.0	2	13.74	6.61	91.4	9.87e+006	(R)VITWDVDSR(D)	1090.553
4	025-0601.6476.6498.0	2	13.24	5.08	91.6	7.39e+006	(R)VITWDVDSR(D)	1090.553
5	024-0401.6456.6506.0	2	12.43	5.71	89.6	2.95e+007	(R)VITWDVDSR(D)	1090.553
6	024-0401.7084.7106.0	3	12.07	12.07	76.5	2.54e+007	(R)VQQPSIEGTQTFYQYFSVR(S)	2278.114
7	026-0801.6235.6235.0	2	10.13	5.52	90.4	1.01e+007	(R)YTSQWSNSTNNWVGGK(G)	1828.825
8	026-0801.6247.6247.0	2	7.76	4.18	90.4	8.45e+006	(R)YTSQWSNSTNNWVGGK(G)	1828.825

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	9.2	6	3	36.16	7	1.12e+008	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	026-0801.6482.6488.0	2	13.82	5.78	94.4	3.02e+007	(R)VITWDVDSR(D)	1090.553
2	027-1001.6507.6539.0	2	13.74	6.61	91.4	9.87e+006	(R)VITWDVDSR(D)	1090.553
3	025-0601.6476.6498.0	2	13.24	5.08	91.6	7.39e+006	(R)VITWDVDSR(D)	1090.553
4	024-0401.6456.6506.0	2	12.43	5.71	89.6	2.95e+007	(R)VITWDVDSR(D)	1090.553
5	024-0401.7084.7106.0	3	12.07	12.07	76.5	2.54e+007	(R)VQQPSIEGTQTFYQYFSVR(S)	2278.114
6	024-0401.6903.6903.0	2	10.27	3.53	72.6	9.95e+006	(R)YTSQWSNSTNNWVGGLGWNPGGR(K)	2538.155

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	4	2	35.07	4	9.21e+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	024-0401.7450.7457.2	2	20.33	15.96	97.1	2.38e+007	(R)DGGSDPVSIMSMIDYVK(Q)	1813.835
2	024-0401.6697.6697.0	2	14.74	7.17	89.4	2.76e+007	(K)TPEAWGDLVR(N)	1143.580
3	024-0401.7424.7424.0	2	9.92	9.92	68.3	1.87e+007	(R)DGGSDPVSIMSMIDYVK(Q)	1813.835
4	024-0401.7433.7433.0	2	9.47	9.47	68.1	2.20e+007	(R)DGGSDPVSIMSMIDYVK(Q)	1813.835

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	2	2	31.02	5	5.08e+007	68058.0	PA_Bse02:2503998900	PA_Bse02:2503998900 BS02DRAFT_00018350 Cellulose binding domain./Ycel-like domain. [B. setacea BS02 (Isol

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	024-0401.7625.7672.0	3	18.91	10.18	89.6	1.62e+007	(K)GGASPAQIIQALPAGVETLYMK(A)	2215.180
2	024-0401.6194.6206.0	2	12.11	2.38	81.8	3.46e+007	(K)GVLGTNEVPSDDISPR(Q)	1655.824

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	5	2	29.50	8	2.18e+008	62134.7	PA_Bse08:2503996242	PA_Bse08:2503996242 BS08DRAFT_00001300 Cellulose or protein binding domain./Cellulose binding domain./Cel

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	025-0601.7492.7514.3	3	18.82	9.72	95.8	4.04e+007	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.122
2	024-0401.7466.7468.0	3	17.68	10.36	93.1	6.11e+007	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.122
3	024-0401.7482.7535.2	2	14.59	8.09	83.3	8.31e+007	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.122
4	025-0601.6216.6216.2	2	10.68	6.87	70.1	1.12e+007	(R)LESSAALNPGASTTGDWSDSDLTQSGR(Y)	2723.240
5	025-0601.7501.7501.0	2	10.56	3.92	82.0	2.22e+007	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.122

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	3	2	24.81	5	3.78e+007	74714.6	PA_Bse08:2503995453	PA_Bse08:2503995453 BS08DRAFT_00039170 Cellulose or protein binding domain./Cellulose binding domain./Cel

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH+ Matched (Da)
1	027-1001.6524.6530.0	3	16.06	16.06	92.8	7.43e+006	(R)LPIAPQTLDPNDPQGTGNVLK(N)	2188.161
2	026-0801.6497.6528.0	3	15.62	15.62	82.3	2.12e+007	(R)LPIAPQTLDPNDPQGTGNVLK(N)	2188.161
3	026-0801.7275.7275.0	3	8.75	3.94	100.0	9.15e+006	(R)LVYSPHTYGPSVFVQK(M)	1821.954

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	2	2	22.97	6	6.48e+007	55060.3	PA_BS12:2189568352	PA_BS12:2189568352 or0169 Cellulose or protein binding domain./Cellulose binding domain. [B. setacea BS12] 541

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	024-0401.7375.7381.0	3	12.21	12.21	75.8	2.45e+007	(R)AHGGSNAVHFSGGANPAMIAR(A)	2021.973
2	024-0401.6321.6373.0	2	10.76	2.28	87.7	4.03e+007	(R)AIPSGTDTLYVR(A)	1292.685

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	2	2	20.34	6	2.30e+007	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	024-0401.7065.7090.2	2	10.68	4.51	86.3	2.05e+007	(R)HVIYGEWGR(D)	1116.559
2	027-1001.7890.7890.0	3	9.66	4.92	86.4	2.47e+006	(K)ELVFWITKPGFSFDANR(T)	2027.039

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	3	1	20.20	4	1.56e+007	43475.8	PA_BS12:2189567935	PA_BS12:2189567935 or1258 Lysophospholipase L1 and related esterases [B. setacea BS12] 419 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	024-0401.9065.9082.0	2	20.20	20.20	96.8	6.62e+006	(R)STSLILQAFTDLVADMR(A)	1880.979
2	024-0401.9054.9054.0	3	17.97	12.87	91.9	3.45e+006	(R)STSLILQAFTDLVADMR(A)	1880.979
3	024-0401.9088.9088.0	2	13.56	13.56	84.4	5.51e+006	(R)STSLILQAFTDLVADMR(A)	1880.979