Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\051111_OGL_BS21_15fracs
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 726 **Hits:** 1510
beginning to assemble proteins .... proteins assembled 0.246512 sec
proteins filtered by unique peptides 0.026161 sec
proteins filtered by score
calculated protein coverage maps 0.096897 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.018022 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 27 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	253	17	286.52	34	4.24e+011	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding (
1	1.1	252	16	277.40	56	4.24e+011	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (Co
2	2.1	106	10	182.05	27	1.77e+011	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp
2	2.1	106	10	182.05	47	1.77e+011	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
3	3.1	56	9	161.19	14	5.27e+010	104392.5	PA_BS12:2189569647	PA_BS12:2189569647 or2953 Beta-1,4-xylanase [B. setacea BS12] 986 bp
3	3.2	3	2	28.37	4	2.86e+009	99497.3	PA_Bse08:2503994382	PA_Bse08:2503994382 BS08DRAFT_00000020 Cellulose or protein binding domain./Glycosyl hydrolase
4	4.1	58	9	153.51	22	5.49e+009	80610.8	PA_BS12:2189571642	PA_BS12:2189571642 or0735 Carbohydrate binding domain. [B. setacea BS12] 763 bp
4	4.1	58	9	153.51	48	5.49e+009	37625.9	PA_Bse_meta_comb:2073592708	PA_Bse_meta_comb:2073592708 BaSeMet_00363640 hypothetical protein [Bankia setacea microbiome
4	4.2	30	7	110.10	13	2.41e+009	112354.2	PA_Bse_meta_comb:2073560170	PA_Bse_meta_comb:2073560170 BaSeMet_00038260 esterase, PHB depolymerase family [Bankia seta
4	4.2	30	7	110.10	13	2.41e+009	112173.0	PA_Bse02:2503998147	PA_Bse02:2503998147 BS02DRAFT_00013240 esterase, PHB depolymerase family [B. setacea BS02 (
5	5.1	35	9	152.55	44	9.01e+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	10	4	70.28	39	2.50e+009	23858.3	PA_Bse02:2504000230	PA_Bse02:2504000230 BS02DRAFT_00014530 Glycosyl hydrolases family 6. [B. setacea BS02 (Isolate
5	5.1	19	4	66.43	7	2.33e+009	114184.0	PA_Bse_meta_comb:2073561915	PA_Bse_meta_comb:2073561915 BaSeMet_00055710 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
5	5.1	12	3	48.83	13	1.57e+009	38604.4	PA_Bse02:2503998988	PA_Bse02:2503998988 BS02DRAFT_00026880 Cellulose or protein binding domain./Cellulose binding (
5	5.1	8	2	32.36	15	1.92e+009	23855.3	PA_Bse02:2503999190	PA_Bse02:2503999190 BS02DRAFT_00027250 Glycosyl hydrolases family 6. [B. setacea BS02 (Isolate
5	5.2	32	9	141.60	14	3.07e+009	112508.2	PA_Bse_meta_comb:2073561919	PA_Bse_meta_comb:2073561919 BaSeMet_00055750 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
5	5.2	28	8	123.33	12	2.06e+009	113016.6	PA_Bse02:2503999098	PA_Bse02:2503999098 BS02DRAFT_00001060 Cellulose or protein binding domain./Glycosyl hydrolase
6	6.1	11	5	81.06	12	3.96e+008	74714.6	PA_Bse08:2503995453	PA_Bse08:2503995453 BS08DRAFT_00039170 Cellulose or protein binding domain./Cellulose binding (
6	6.2	2	2	23.42	3	2.46e+007	75758.3	PA_Bse_meta_comb:2073585828	PA_Bse_meta_comb:2073585828 BaSeMet_00294840 Endoglucanase [Bankia setacea microbiome (Co
6	6.2	2	2	23.42	3	2.46e+007	75690.3	PA_BSC2:2534572481	PA_BSC2:2534572481 Bsc2_00165 Endoglucanase [Alteromonadacea bacterium Bsc2]
7	7.1	15	5	63.54	14	5.05e+008	70938.0	PA_Bse02:2504000681	PA_Bse02:2504000681 BS02DRAFT_00022770 Cellulose or protein binding domain./Glycosyl hydrolase
7	7.1	12	2	22.55	4	1.89e+008	70884.2	PA_Bse08:2503997525	PA_Bse08:2503997525 BS08DRAFT_00020200 Cellulose or protein binding domain./Glycosyl hydrolase
8	8.1	6	4	56.78	16	3.24e+008	56911.4	PA_Bse08:2503996762	PA_Bse08:2503996762 BS08DRAFT_00004980 esterase, PHB depolymerase family [B. setacea BS08 (
9	9.1	11	3	53.35	11	1.09e+008	58225.4	PA_BS12:2189570192	PA_BS12:2189570192 or3423 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 560 bp
9	9.1	11	3	53.35	12	1.09e+008	52443.2	PA_Bse_meta_comb:2073587378	PA_Bse_meta_comb:2073587378 BaSeMet_00310340 Cobalamin biosynthesis protein CobN and relate
10	10.1	7	3	49.74	11	5.96e+008	46154.6	PA_Bse02:2503998146	PA_Bse02:2503998146 BS02DRAFT_00013230 Glycosyl hydrolase family 10. [B. setacea BS02 (Isolate
10	10.1	7	3	49.74	11	5.96e+008	46141.6	PA_Bse_meta_comb:2073560169	PA_Bse_meta_comb:2073560169 BaSeMet_00038250 Beta-1,4-xylanase [Bankia setacea microbiome (
11	11.1	6	3	43.13	4	2.45e+008	77470.6	PA_Bse08:2503996278	PA_Bse08:2503996278 BS08DRAFT_00001670 Cellulose or protein binding domain./Cellulose binding (
12	12.1	12	2	41.68	8	1.93e+009	62134.7	PA_Bse08:2503996242	PA_Bse08:2503996242 BS08DRAFT_00001300 Cellulose or protein binding domain./Cellulose binding (
13	13.1	14	2	41.23	41	2.90e+009	13375.7	PA_Bse_meta_comb:2073565643	PA_Bse_meta_comb:2073565643 BaSeMet_00092990 Histone H2A [Bankia setacea microbiome (Coml
14	14.1	5	3	40.38	6	1.47e+008	77517.5	PA_BS12:2189568391	PA_BS12:2189568391 or1689 Endoglucanase [B. setacea BS12] 725 bp
14	14.1	5	3	40.38	10	1.47e+008	50621.3	PA_Bse_meta_comb:2073574943	PA_Bse_meta_comb:2073574943 BaSeMet_00185990 Endoglucanase [Bankia setacea microbiome (Co
15	15.1	7	3	40.27	1	2.73e+008	224278.3	PA_BS12:2189569050	PA_BS12:2189569050 or2363 Gluconolactonase [B. setacea BS12] 2124 bp
15	15.1	7	3	40.27	1	2.73e+008	223963.9	PA_Bse_meta_comb:2073579605	PA_Bse_meta_comb:2073579605 BaSeMet_00232610 Gluconolactonase [Bankia setacea microbiome (
16	16.1	7	2	36.62	9	6.32e+008	43875.0	PA_Bse08:2503995778	PA_Bse08:2503995778 Cellulose or protein binding domain./Cellulase (glycosyl hydrolase family 5). [B. s

16	16.2	5	2	35.30	6	2.62e+008	60457.4	PA_BS12:2189569899	PA_BS12:2189569899 or3204 Cellulase (glycosyl hydrolase family 5)./Cellulose or protein binding doma
16	16.2	5	2	35.30	10	2.62e+008	39020.2	PA_Bse_meta_comb:2073558688	PA_Bse_meta_comb:2073558688 BaSeMet_00023440 Cellulase (glycosyl hydrolase family 5). [Bankia s
17	17.1	10	3	35.31	5	1.83e+009	73439.4	PA_Bse08:2503994248	PA_Bse08:2503994248 BS08DRAFT_00028400 Cellulose or protein binding domain./Chitin binding dom
18	18.1	15	2	34.08	6	4.04e+009	42518.1	PA_Bse02:2503998249	PA_Bse02:2503998249 BS02DRAFT_00014250 Cellulose or protein binding domain./Chitin binding dom
18	18.1	15	2	34.08	6	4.04e+009	42082.7	PA_Bse_meta_comb:2073581124	PA_Bse_meta_comb:2073581124 BaSeMet_00247800 Uncharacterized protein conserved in bacteria [E
18	18.2	13	2	30.50	6	1.90e+009	39939.7	PA_BS12:2189570962	PA_BS12:2189570962 or0231 Uncharacterized protein conserved in bacteria [B. setacea BS12] 383 bp
19	19.1	11	2	31.78	7	6.58e+007	55060.3	PA_BS12:2189568352	PA_BS12:2189568352 or0169 Cellulose or protein binding domain./Cellulose binding domain. [B. setace
20	20.1	10	2	28.96	8	1.01e+009	33117.2	PA_BS12:2189570963	PA_BS12:2189570963 or0232 Uncharacterized protein conserved in bacteria [B. setacea BS12] 320 bp
20	20.1	10	2	28.96	8	1.01e+009	31752.7	PA_Bse_meta_comb:2073593368	PA_Bse_meta_comb:2073593368 BaSeMet_00370240 Uncharacterized protein conserved in bacteria [E
21	21.1	20	1	21.88	4	3.97e+009	43475.8	PA_BS12:2189567935	PA_BS12:2189567935 or1258 Lysophospholipase L1 and related esterases [B. setacea BS12] 419 bp
21	21.1	20	1	21.88	4	3.97e+009	42177.2	PA_Bse_meta_comb:2073563649	PA_Bse_meta_comb:2073563649 BaSeMet_00073050 Predicted solute binding protein [Bankia setacea
Totals:	1377	209							

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	253	17	286.52	34	4.24e+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	083-1901.5201.5201.0	3	21.86	15.44	97.6	2.93e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
2	081-1701.6966.7001.0	3	21.45	13.22	99.3	1.30e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
3	084-2001.5335.5375.0	3	21.00	12.82	100.0	3.13e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
4	085-2101.5336.5374.0	3	20.96	11.61	99.4	2.56e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
5	082-1801.6705.6775.0	3	20.94	13.61	99.2	3.20e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
6	085-2101.5181.5181.0	3	20.71	13.78	95.4	4.79e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
7	083-1901.5572.5572.2	2	20.50	12.38	100.0	8.76e+008	(R)EWQDALVDYMVEK(D)	1625.752
8	082-1801.8017.8133.2	2	20.42	20.42	98.6	2.76e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
9	082-1801.8420.8543.3	3	20.13	20.13	95.6	5.12e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
10	082-1801.6590.6700.0	3	19.89	11.36	98.5	5.05e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
11	082-1801.6475.6580.0	3	19.87	19.87	98.2	4.09e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
12	085-2101.5049.5170.3	3	19.64	14.34	94.1	8.43e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
13	083-1901.5359.5426.0	3	19.42	11.40	98.9	3.26e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
14	085-2101.9601.9716.3	3	19.40	19.40	89.5	1.67e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
15	082-1801.8141.8259.2	2	19.36	19.36	97.6	5.03e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
16	084-2001.4275.4397.2	2	19.34	19.34	97.4	1.04e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
17	084-2001.10422.10489.0	3	19.32	19.32	93.4	4.30e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
18	082-1801.3883.3962.2	2	19.20	19.20	94.6	1.01e+009	(R)AGWDEHFGYLR(D)	1350.623
19	082-1801.4311.4428.2	2	19.04	19.04	93.0	5.12e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
20	082-1801.3972.3996.2	2	19.02	19.02	95.8	5.71e+008	(R)AGWDEHFGYLR(D)	1350.623
21	083-1901.6957.7055.3	3	19.00	19.00	94.0	5.31e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
22	082-1801.8263.8378.2	2	18.85	18.85	97.6	7.87e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
23	081-1701.6874.6958.0	3	18.83	9.93	97.7	1.38e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
24	081-1701.7355.7361.2	2	18.81	10.36	96.3	5.03e+007	(R)EWQDALVDYMVEK(D)	1625.752
25	082-1801.6351.6465.0	3	18.80	8.54	97.2	1.37e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
26	082-1801.7106.7200.2	2	18.76	11.35	95.5	2.36e+009	(R)EWQDALVDYMVEK(D)	1625.752
27	081-1701.7352.7356.2	2	18.69	14.75	95.7	1.34e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060

28	081-1701.10571.10571.0	3	18.67	11.92	96.2	5.46e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
29	082-1801.7912.8002.0	3	18.63	12.08	95.3	1.11e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
30	082-1801.7123.7222.2	2	18.44	15.30	94.0	2.08e+008	(R)AGWDEHFGYLR(D)	1350.623
31	082-1801.10415.10455.3	3	18.39	14.03	89.2	1.20e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
32	081-1701.7540.7638.2	2	18.27	18.27	96.2	2.43e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
33	082-1801.8414.8537.3	3	18.27	18.27	91.9	5.06e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
34	083-1901.4367.4432.2	2	18.27	18.27	96.3	7.98e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
35	082-1801.6440.6536.4	4	18.23	11.93	85.0	3.29e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
36	083-1901.4229.4356.2	2	18.22	18.22	95.5	1.63e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
37	084-2001.4401.4445.2	2	18.21	18.21	95.5	4.83e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
38	083-1901.5678.5754.2	2	18.12	18.12	95.4	3.48e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
39	082-1801.7999.8007.2	2	18.10	14.57	95.3	1.29e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
40	085-2101.5725.5815.2	2	18.09	15.01	95.0	8.24e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
41	082-1801.7981.8006.3	3	17.82	8.96	89.0	2.98e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
42	082-1801.7324.7442.2	2	17.81	11.39	96.4	4.88e+009	(R)EWQDALVDYMVEK(D)	1625.752
43	082-1801.7855.7973.3	3	17.81	9.15	88.8	6.21e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
44	085-2101.5724.5813.3	3	17.81	8.84	87.8	1.06e+010	(R)TIQQTMTEITAQGINVVR(L)	2003.060
45	082-1801.7206.7319.2	2	17.74	11.37	95.2	5.28e+009	(R)EWQDALVDYMVEK(D)	1625.752
46	081-1701.7824.7847.0	3	17.73	17.73	88.7	1.98e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
47	082-1801.7490.7609.3	3	17.72	10.14	87.2	5.48e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
48	085-2101.7053.7132.3	3	17.56	17.56	88.8	4.15e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
49	081-1701.7771.7844.2	2	17.53	17.53	96.2	3.46e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
50	082-1801.7507.7623.2	2	17.50	12.07	94.0	2.78e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
51	085-2101.5594.5719.2	2	17.50	12.31	94.1	1.65e+010	(R)TIQQTMTEITAQGINVVR(L)	2003.060
52	084-2001.5641.5733.2	2	17.47	13.79	93.5	6.74e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
53	083-1901.3766.3799.2	2	17.29	12.56	94.5	9.59e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
54	083-1901.8548.8565.0	3	17.29	17.29	89.8	2.24e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
55	082-1801.7615.7729.3	3	17.27	9.88	88.3	4.93e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
56	081-1701.7345.7397.3	3	17.25	9.99	89.1	3.79e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
57	082-1801.10153.10281.3	3	17.24	17.24	88.3	2.24e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
58	081-1701.7650.7762.2	2	17.19	17.19	95.1	4.92e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
59	082-1801.8384.8502.2	2	17.13	17.13	93.7	9.20e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
60	085-2101.4302.4416.2	2	17.12	17.12	94.1	5.41e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
61	082-1801.7629.7748.2	2	17.06	13.32	94.6	2.39e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
62	083-1901.7582.7655.0	3	17.02	17.02	87.3	3.43e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
63	082-1801.7874.7993.2	2	17.00	13.87	94.1	2.94e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
64	082-1801.7754.7868.2	2	16.96	13.34	93.6	2.74e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
65	082-1801.6370.6485.3	3	16.95	11.61	82.3	5.36e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
66	083-1901.7732.7797.0	3	16.89	16.89	86.5	3.63e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
67	082-1801.3679.3799.2	2	16.67	16.67	93.1	2.14e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
68	082-1801.7551.7559.0	2	16.65	16.65	94.0	1.12e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
69	082-1801.8669.8669.0	3	16.65	11.78	80.6	3.61e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
70	082-1801.7735.7849.3	3	16.63	9.96	85.8	5.77e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
71	084-2001.9682.9793.3	3	16.56	11.98	87.3	2.23e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
72	082-1801.8511.8592.2	2	16.48	16.48	95.4	6.24e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
73	083-1901.6030.6045.3	3	16.45	11.37	88.9	5.61e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
74	084-2001.6039.6044.2	2	16.41	12.93	79.3	4.75e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
75	081-1701.7296.7306.3	3	16.39	8.87	84.5	3.71e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850

76	085-2101.5589.5718.3	3	16.24	10.18	86.5	1.68e+010	(R)TIQQTMTEITAQGINVVR(L)	2003.060
77	084-2001.5636.5732.3	3	16.21	10.24	86.5	7.53e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
78	083-1901.6049.6053.2	2	16.13	16.13	75.2	6.27e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
79	084-2001.4631.4636.0	3	16.01	8.62	91.6	2.96e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
80	082-1801.6884.6944.2	2	15.97	15.97	91.3	7.28e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
81	082-1801.3789.3809.3	3	15.93	8.30	86.1	2.32e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
82	083-1901.6962.6962.0	3	15.93	11.55	82.4	2.52e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
83	083-1901.8540.8588.0	3	15.91	15.91	79.7	3.97e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
84	082-1801.7380.7497.2	2	15.90	12.43	93.0	2.17e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
85	083-1901.3756.3798.3	3	15.90	7.85	86.7	3.02e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
86	082-1801.9200.9221.0	3	15.87	15.87	80.2	1.18e+008	(R)AGWDEHFGYLRDQGYAMVIGEFGGNMDWPNGTR(A)	3746.655
87	081-1701.7096.7106.0	3	15.86	6.87	93.6	1.10e+007	(R)LDANPPYADADREGYEFTR(E)	2199.995
88	082-1801.11697.11749.0	3	15.62	10.32	82.5	1.64e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
89	084-2001.3764.3814.2	2	15.60	12.27	92.4	6.55e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
90	082-1801.8589.8680.0	3	15.56	9.10	79.8	4.25e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
91	085-2101.3778.3824.2	2	15.55	15.55	91.4	3.34e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
92	081-1701.6941.7034.0	3	15.53	9.36	81.5	8.02e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
93	083-1901.9351.9418.0	3	15.53	15.53	85.7	1.15e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
94	084-2001.11584.11584.0	3	15.52	15.52	84.1	1.22e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
95	083-1901.8055.8107.0	3	15.49	15.49	84.6	6.05e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
96	084-2001.6015.6092.3	3	15.45	8.41	88.4	7.24e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
97	082-1801.8548.8594.3	3	15.36	15.36	85.2	4.66e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
98	082-1801.11734.11734.0	3	15.32	15.32	79.2	8.34e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
99	085-2101.3771.3807.3	3	15.32	8.97	83.4	1.06e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
100	082-1801.4436.4469.2	2	15.17	15.17	90.3	1.59e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
101	082-1801.8161.8273.3	3	15.14	10.96	86.2	8.78e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
102	083-1901.5683.5776.3	3	15.03	6.93	83.7	4.68e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
103	083-1901.4803.4803.0	3	15.00	5.82	90.6	1.01e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
104	083-1901.7512.7551.0	3	15.00	11.14	84.7	2.64e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
105	083-1901.8986.9012.0	3	14.97	14.97	83.5	1.90e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
106	084-2001.3752.3813.3	3	14.91	7.28	86.1	2.70e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
107	082-1801.3806.3810.2	2	14.90	14.90	90.0	6.44e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
108	085-2101.11669.11669.0	3	14.82	14.82	76.6	7.35e+007	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
109	085-2101.7068.7134.2	2	14.81	8.74	68.8	1.39e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
110	082-1801.9172.9172.0	3	14.80	14.80	82.4	1.53e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
111	083-1901.7948.8017.3	3	14.76	14.76	78.2	4.17e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
112	084-2001.7566.7610.2	2	14.74	14.74	85.3	1.88e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
113	081-1701.9633.9754.3	3	14.66	14.66	70.8	9.94e+009	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
114	085-2101.6102.6203.0	2	14.65	9.65	80.9	7.37e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
115	085-2101.7638.7638.0	2	14.65	14.65	83.4	8.41e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
116	082-1801.11432.11474.0	2	14.63	14.63	84.8	4.61e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
117	082-1801.7240.7286.2	2	14.61	14.61	83.9	1.41e+008	(R)AGWDEHFGYLR(D)	1350.623
118	085-2101.11024.11029.0	3	14.59	8.06	80.4	5.05e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
119	085-2101.7916.7916.0	2	14.52	14.52	82.2	4.52e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
120	083-1901.11764.11820.0	3	14.42	8.01	77.3	1.41e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
121	083-1901.9269.9353.0	3	14.40	7.63	83.2	1.31e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
122	083-1901.7713.7806.2	2	14.38	14.38	78.0	1.61e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
123	082-1801.2266.2314.0	2	14.32	8.00	92.3	1.65e+007	(R)LDANPPYADADR(E)	1317.608

124	082-1801.9171.9176.0	3	14.32	14.32	79.6	1.73e+008	(R)AAEQEMWSHITPGVDREWQDALVDYMVEK(D)	3433.583
125	085-2101.9988.9988.0	3	14.22	14.22	79.5	4.13e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
126	082-1801.8969.9048.0	3	14.19	14.19	78.3	1.29e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
127	081-1701.6887.6932.2	2	14.14	9.15	89.9	3.96e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
128	083-1901.7843.7855.0	3	14.06	14.06	80.0	1.75e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
129	084-2001.6320.6420.0	3	14.03	14.03	78.8	4.05e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
130	083-1901.3948.3987.2	2	14.01	9.68	86.5	1.21e+008	(R)AGWDEHFGYLR(D)	1350.623
131	082-1801.7371.7484.3	3	13.91	7.33	81.3	3.69e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
132	082-1801.9163.9202.0	3	13.87	8.78	77.3	2.56e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
133	083-1901.11232.11250.0	3	13.86	13.86	77.0	1.70e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
134	083-1901.8007.8032.2	2	13.83	13.83	67.3	1.61e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
135	083-1901.10226.10351.3	3	13.76	6.57	72.2	1.97e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
136	081-1701.7474.7480.0	2	13.66	10.24	70.8	1.18e+008	(R)AGWDEHFGYLR(D)	1350.623
137	084-2001.11466.11501.0	3	13.66	6.08	82.0	1.01e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
138	084-2001.11860.11860.2	2	13.54	13.54	82.1	4.97e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
139	084-2001.11387.11393.0	3	13.52	10.17	77.4	1.51e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
140	085-2101.11210.11295.2	2	13.51	13.51	66.3	1.93e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
141	082-1801.9397.9443.0	3	13.44	13.44	77.4	5.27e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
142	083-1901.10215.10341.3	3	13.44	8.59	74.8	1.92e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
143	084-2001.12094.12118.0	3	13.18	7.26	82.4	1.03e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
144	085-2101.7384.7436.0	3	13.18	13.18	73.9	2.40e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
145	085-2101.12057.12057.0	3	13.13	13.13	76.8	3.08e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
146	085-2101.11271.11337.2	2	13.09	13.09	68.7	2.24e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
147	082-1801.11329.11384.0	3	13.06	6.75	70.1	6.18e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
148	082-1801.8356.8356.2	2	13.05	13.05	81.4	1.91e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
149	085-2101.11991.12045.0	3	13.05	7.57	79.5	1.07e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
150	084-2001.7409.7451.2	2	12.96	12.96	69.0	2.43e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
151	083-1901.11120.11120.0	2	12.90	12.90	90.0	3.48e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
152	083-1901.7258.7263.2	2	12.74	8.58	60.4	2.71e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
153	082-1801.6410.6468.2	2	12.63	7.05	88.9	2.82e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
154	083-1901.8129.8218.2	2	12.58	12.58	64.4	1.83e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
155	083-1901.7810.7810.2	2	12.53	12.53	72.4	8.27e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
156	083-1901.11052.11131.2	2	12.49	12.49	68.8	1.73e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
157	084-2001.8039.8039.0	3	12.42	12.42	70.2	1.68e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
158	083-1901.11180.11246.0	2	12.40	12.40	69.4	9.20e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
159	083-1901.9340.9340.0	3	12.37	12.37	84.8	9.75e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
160	083-1901.9010.9010.0	2	12.30	8.38	82.1	1.15e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
161	085-2101.6308.6387.0	3	12.28	8.92	73.7	5.58e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
162	084-2001.3956.3980.2	2	12.25	8.80	78.6	1.01e+008	(R)AGWDEHFGYLR(D)	1350.623
163	083-1901.6291.6394.3	3	12.12	5.23	78.0	7.00e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
164	080-1601.7298.7298.2	2	12.01	12.01	67.9	2.43e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
165	082-1801.10931.11000.0	3	11.83	11.83	74.3	9.32e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
166	083-1901.6985.7070.0	3	11.80	5.64	73.9	4.05e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
167	083-1901.5365.5365.0	3	11.76	8.08	79.0	2.67e+009	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
168	084-2001.11856.11856.0	2	11.76	11.76	77.9	5.18e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
169	085-2101.11615.11615.0	3	11.66	11.66	77.5	3.27e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
170	084-2001.11410.11432.2	2	11.56	7.67	66.4	1.64e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
171	082-1801.11096.11113.0	2	11.53	11.53	66.4	1.08e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050

172	083-1901.8114.8193.2	2	11.42	11.42	68.1	2.77e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
173	085-2101.7746.7758.0	2	11.41	11.41	68.7	5.72e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
174	085-2101.6526.6545.0	3	11.33	4.43	75.6	1.19e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
175	084-2001.10299.10333.0	3	11.22	11.22	72.8	1.02e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
176	085-2101.11509.11519.2	2	11.16	11.16	62.5	1.21e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
177	083-1901.9024.9024.0	2	11.12	11.12	73.4	1.09e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
178	085-2101.7057.7057.0	3	11.12	11.12	71.2	2.11e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
179	084-2001.11817.11817.0	3	11.05	11.05	73.6	1.19e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
180	085-2101.11673.11751.0	2	11.03	11.03	62.0	1.60e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
181	083-1901.7546.7618.2	2	11.02	11.02	71.5	1.65e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
182	082-1801.3895.3899.1	1	10.94	6.23	85.3	3.12e+008	(R)AGWDEHFGYLR(D)	1350.623
183	085-2101.10361.10361.0	3	10.91	10.91	72.7	1.26e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
184	084-2001.7920.7962.0	2	10.88	10.88	78.6	1.11e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
185	084-2001.11245.11245.0	2	10.87	10.87	66.4	5.39e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
186	082-1801.11225.11225.0	2	10.84	10.84	76.6	2.27e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
187	082-1801.7214.7330.0	2	10.81	10.81	63.5	2.04e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
188	085-2101.11164.11250.2	2	10.74	10.74	70.7	1.67e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
189	083-1901.11242.11242.0	2	10.64	10.64	76.1	1.90e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
190	082-1801.11116.11116.0	3	10.62	10.62	70.9	4.18e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
191	083-1901.2031.2037.0	2	10.55	4.37	83.9	1.40e+005	(R)EGYEFTR(E)	901.406
192	084-2001.7027.7046.0	2	10.53	10.53	64.0	3.22e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
193	085-2101.8128.8128.0	3	10.40	10.40	74.2	1.40e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
194	083-1901.11475.11522.2	2	10.32	10.32	72.2	4.83e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
195	082-1801.9294.9311.0	2	10.25	10.25	63.2	8.90e+007	(R)CGSWFGLEGQHEPK(D)	1574.706
196	085-2101.7613.7613.0	2	10.19	10.19	66.1	1.67e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
197	085-2101.7690.7690.0	2	10.09	10.09	70.7	6.55e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
198	084-2001.11709.11709.2	2	10.07	10.07	70.6	6.11e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
199	083-1901.7502.7605.0	2	10.00	10.00	62.3	3.79e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
200	085-2101.7111.7111.0	2	9.99	9.99	65.2	1.94e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
201	083-1901.8545.8569.2	2	9.86	9.86	61.0	2.36e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
202	084-2001.11633.11633.0	2	9.85	9.85	72.4	5.13e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
203	085-2101.11138.11138.0	2	9.84	5.94	71.0	6.75e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
204	083-1901.7379.7379.0	2	9.79	9.79	62.3	1.53e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
205	082-1801.8823.8893.0	2	9.70	9.70	60.6	1.19e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
206	084-2001.11824.11854.2	2	9.69	9.69	64.3	1.42e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
207	083-1901.7009.7092.2	2	9.68	9.68	64.6	3.29e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
208	084-2001.4864.4885.0	2	9.62	9.62	61.4	4.56e+007	(R)CGSWFGLEGQHEPK(D)	1574.706
209	083-1901.11390.11449.0	2	9.58	9.58	61.3	7.94e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
210	083-1901.7370.7370.0	2	9.54	6.42	77.5	1.46e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
211	082-1801.11275.11281.2	2	9.50	9.50	62.4	7.77e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
212	084-2001.6379.6476.2	2	9.50	9.50	62.7	3.75e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
213	085-2101.11323.11323.0	2	9.45	9.45	74.2	4.49e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
214	085-2101.11380.11477.0	2	9.42	6.14	64.7	3.08e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
215	084-2001.7541.7541.2	2	9.40	9.40	63.0	1.98e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
216	084-2001.11677.11677.0	2	9.29	9.29	70.6	1.69e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
217	084-2001.7537.7584.2	2	9.27	9.27	61.8	2.68e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
218	084-2001.8267.8267.2	2	9.27	9.27	66.3	1.52e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
219	082-1801.7113.7208.0	2	9.22	9.22	60.9	6.55e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050

220	084-2001.7791.7791.0	2	9.19	9.19	68.1	1.62e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
221	085-2101.3965.4022.0	2	9.14	9.14	64.0	1.21e+008	(R)AGWDEHFGYLR(D)	1350.623
222	082-1801.2634.2634.2	2	9.12	4.30	88.1	2.27e+005	(K)NGSVFPVR(C)	875.474
223	083-1901.4838.4874.0	2	9.12	9.12	60.9	5.59e+007	(R)CGSWFGLEGQHEPK(D)	1574.706
224	082-1801.11354.11354.0	2	9.10	9.10	77.2	1.67e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
225	084-2001.8755.8755.0	2	9.10	9.10	62.7	1.24e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
226	082-1801.9023.9073.0	2	9.09	9.09	62.5	2.10e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
227	085-2101.6329.6342.2	2	9.08	5.84	65.0	4.41e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
228	082-1801.7338.7428.0	2	8.90	8.90	60.2	1.84e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
229	084-2001.7685.7720.2	2	8.75	8.75	60.1	2.01e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
230	082-1801.11132.11132.2	2	8.70	8.70	61.6	2.62e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
231	083-1901.8900.8937.2	2	8.65	8.65	63.0	1.08e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
232	082-1801.8633.8697.0	2	8.49	5.26	61.8	1.88e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
233	082-1801.11297.11297.0	2	8.48	8.48	65.3	2.15e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
234	084-2001.11765.11765.0	2	8.17	8.17	69.9	3.57e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
235	084-2001.6531.6631.0	2	7.99	7.99	60.3	3.17e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
236	085-2101.11162.11162.0	2	7.96	7.96	65.7	7.14e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
237	084-2001.7068.7068.0	2	7.90	7.90	62.2	2.06e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
238	084-2001.11402.11402.0	2	7.72	7.72	63.3	4.75e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
239	084-2001.11644.11644.0	2	7.53	7.53	64.4	4.49e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
240	085-2101.7694.7694.0	2	7.28	7.28	66.8	6.37e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
241	082-1801.9281.9293.0	2	7.26	7.26	65.5	8.76e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
242	084-2001.8337.8337.0	2	7.10	7.10	61.7	6.50e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
243	082-1801.9232.9232.0	2	6.95	6.95	71.6	8.39e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
244	082-1801.9319.9319.0	2	6.94	6.94	63.2	7.03e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
245	085-2101.5522.5522.0	2	6.59	6.59	61.3	3.81e+008	(R)EWQDALVDYMVEK(D)	1625.752
246	084-2001.8315.8315.0	2	6.57	6.57	62.8	1.56e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
247	082-1801.11078.11078.0	2	6.54	6.54	65.7	3.88e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
248	082-1801.11127.11127.0	2	6.54	6.54	64.7	2.67e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
249	082-1801.11744.11744.2	2	6.42	6.42	60.3	1.17e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
250	083-1901.9439.9439.0	2	6.38	6.38	63.8	2.50e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
251	084-2001.7729.7729.0	2	6.27	6.27	60.4	9.05e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
252	083-1901.8976.8976.0	2	6.09	6.09	63.2	1.05e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
253	084-2001.7085.7085.0	2	6.07	6.07	65.4	2.08e+008	(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	106	10	182.05	27	1.77e+011	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	082-1801.3205.3252.0	3	22.25	10.50	100.0	6.56e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
2	085-2101.3228.3233.0	3	21.58	10.54	96.5	2.57e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
3	081-1701.8214.8218.2	2	21.48	16.14	99.3	7.62e+007	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
4	083-1901.8034.8105.3	3	20.49	15.12	94.8	5.27e+009	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
5	083-1901.8023.8106.2	2	20.26	20.26	96.2	4.33e+009	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163

6	081-1701.7040.7072.2	2	19.46	15.60	76.0	6.77e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
7	083-1901.8349.8462.0	2	19.40	11.56	76.8	2.21e+010	(R)WFPEAFQTLVENAYPAL(-)	1995.986
8	081-1701.8638.8715.0	2	19.39	11.58	96.4	1.60e+010	(R)WFPEAFQTLVENAYPAL(-)	1995.986
9	082-1801.9042.9139.0	2	19.39	11.59	76.8	8.14e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.986
10	081-1701.8707.8724.3	3	19.27	12.89	91.5	3.77e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
11	085-2101.8077.8141.2	2	19.15	19.15	94.3	3.82e+009	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
12	081-1701.5819.5913.2	2	19.11	11.15	96.5	1.79e+009	(R)IGAIEGPADGDGMGLR(E)	1528.743
13	081-1701.8690.8696.3	3	18.99	18.99	95.1	2.55e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.986
14	081-1701.5723.5807.2	2	18.89	10.46	97.3	1.50e+008	(R)IGAIEGPADGDGMGLR(E)	1528.743
15	081-1701.5610.5658.2	2	18.88	11.31	97.4	1.61e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
16	083-1901.9190.9204.0	3	18.82	12.54	86.8	1.49e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
17	081-1701.8705.8709.2	2	18.77	18.77	95.7	2.41e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
18	085-2101.8091.8140.3	3	18.71	10.74	85.7	3.84e+009	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
19	083-1901.3504.3550.2	2	18.60	10.01	95.9	2.05e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
20	082-1801.3454.3479.0	2	18.59	10.14	96.2	4.38e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
21	085-2101.7295.7339.2	2	18.42	13.92	83.6	8.45e+008	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
22	083-1901.8466.8534.2	2	18.37	10.44	75.1	1.60e+010	(R)WFPEAFQTLVENAYPAL(-)	1995.986
23	081-1701.8511.8630.0	2	18.36	11.93	75.1	1.89e+010	(R)WFPEAFQTLVENAYPAL(-)	1995.986
24	084-2001.8424.8505.2	2	18.36	12.66	77.0	1.34e+010	(R)WFPEAFQTLVENAYPAL(-)	1995.986
25	084-2001.8043.8060.2	2	18.33	18.33	92.1	3.37e+009	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
26	084-2001.3262.3270.2	2	18.27	18.27	95.9	5.50e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
27	082-1801.9158.9158.0	2	18.22	10.36	91.4	6.45e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.986
28	081-1701.7714.7820.3	3	18.09	11.88	95.3	1.46e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
29	081-1701.6051.6105.2	2	17.87	10.34	96.6	1.63e+009	(R)IGAIEGPADGDGMGLR(E)	1528.743
30	083-1901.9296.9375.0	3	17.67	12.24	83.4	2.78e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
31	082-1801.9151.9201.3	3	17.61	11.77	89.8	4.73e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
32	081-1701.5917.6046.2	2	17.59	10.10	95.8	3.23e+009	(R)IGAIEGPADGDGMGLR(E)	1528.743
33	085-2101.8460.8530.2	2	17.31	10.07	76.0	7.73e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.986
34	084-2001.8672.8723.0	3	17.17	9.90	93.0	4.24e+008	(R)EHLDETLAQGANLFMFVVYDLPNR(D)	2792.372
35	079-1501.7976.8002.2	2	17.16	9.36	72.2	1.11e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
36	084-2001.3507.3511.2	2	17.08	9.20	95.3	1.23e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
37	083-1901.9227.9244.0	2	16.72	10.02	91.7	3.06e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
38	082-1801.9165.9175.2	2	16.71	16.71	87.6	2.21e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
39	084-2001.3984.4008.3	3	16.61	11.91	92.9	3.30e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
40	084-2001.8538.8552.2	2	16.58	9.88	70.2	9.12e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.986
41	083-1901.9185.9207.2	2	16.28	16.28	88.6	1.29e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
42	082-1801.4008.4059.0	3	15.82	11.98	86.8	1.02e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
43	084-2001.3990.4067.2	2	15.58	12.37	90.3	7.35e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
44	079-1501.8011.8071.3	3	15.55	15.55	86.9	2.63e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
45	081-1701.5750.5821.2	2	15.38	15.38	87.1	6.75e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
46	080-1601.8312.8390.2	2	15.10	8.16	67.5	5.95e+008	(R)WFPEAFQTLVENAYPAL(-)	1995.986
47	082-1801.5545.5617.0	3	14.96	9.44	84.5	5.93e+006	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
48	083-1901.4000.4068.2	2	14.91	14.91	87.1	7.00e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
49	085-2101.6331.6451.2	2	14.70	9.04	87.5	5.55e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
50	085-2101.3507.3534.2	2	14.65	7.67	91.9	1.13e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743
51	081-1701.3374.3447.0	2	14.47	5.01	98.5	1.16e+006	(R)IADGGFQR(Y)	863.438
52	081-1701.6065.6106.2	2	14.43	14.43	87.1	1.29e+008	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
53	081-1701.7718.7821.2	2	14.19	8.64	86.9	1.49e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022

54	084-2001.6258.6365.2	2	14.16	9.03	86.3	4.33e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
55	083-1901.3988.4026.3	3	14.12	7.12	78.7	4.98e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
56	085-2101.3247.3255.2	2	14.07	10.12	85.7	4.12e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
57	085-2101.3996.4077.2	2	13.98	13.98	87.7	7.93e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
58	081-1701.5850.5889.2	2	13.91	10.78	86.5	6.14e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
59	081-1701.3458.3501.0	2	13.74	5.20	99.5	1.64e+006	(R)IADGGFQR(Y)	863.438
60	083-1901.6269.6350.2	2	13.64	8.48	85.5	3.79e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
61	080-1601.8319.8319.2	2	13.49	13.49	83.5	4.59e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
62	084-2001.4090.4090.2	2	13.37	9.33	85.9	4.07e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
63	082-1801.8395.8456.2	2	13.13	7.70	85.2	5.80e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
64	081-1701.6047.6107.3	3	13.11	8.90	84.2	1.64e+008	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
65	085-2101.8340.8389.0	3	13.05	7.16	79.6	1.40e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
66	081-1701.7086.7086.0	3	12.98	12.98	76.0	4.19e+007	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
67	082-1801.4009.4078.2	2	12.87	9.65	84.8	8.09e+006	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
68	080-1601.8316.8316.0	2	12.82	12.82	76.9	4.72e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
69	085-2101.8346.8372.2	2	12.78	12.78	81.3	1.18e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
70	084-2001.8731.8731.0	2	12.39	12.39	76.4	9.70e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
71	082-1801.3244.3244.2	2	12.27	12.27	95.4	5.61e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
72	082-1801.9188.9188.2	2	11.85	11.85	74.1	2.51e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
73	082-1801.8396.8490.3	3	11.84	11.84	79.7	4.75e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
74	081-1701.10572.10572.0	2	11.58	4.67	75.8	7.29e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
75	083-1901.9240.9240.0	2	11.51	2.52	74.9	2.47e+007	(R)WFPEAFQTLVENAYPAL(-)	1995.986
76	084-2001.7324.7330.2	2	11.50	7.70	73.5	2.10e+008	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
77	085-2101.8073.8073.2	2	11.33	11.33	63.5	2.51e+009	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
78	083-1901.6436.6442.2	2	11.08	6.55	70.9	9.09e+008	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
79	083-1901.7314.7320.2	2	11.00	6.50	66.0	1.26e+008	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
80	083-1901.9192.9192.0	2	10.72	10.72	77.9	9.96e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
81	083-1901.9361.9361.2	2	10.60	10.60	68.9	6.03e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
82	083-1901.7681.7740.2	2	10.28	10.28	64.5	9.55e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
83	083-1901.11280.11280.0	3	9.99	6.65	86.3	8.69e+006	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
84	081-1701.5499.5510.2	2	9.98	6.19	88.1	3.60e+006	(R)IGAIEGPADGDGMGLR(E)	1528.743
85	081-1701.6205.6205.0	2	9.90	5.62	75.4	1.59e+007	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
86	080-1601.6782.6790.2	2	9.71	9.71	62.9	5.65e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
87	084-2001.6450.6486.2	2	9.59	5.47	69.8	1.04e+009	(R)SSMINNGFPNSLGMLIDTGR(N)	2124.022
88	085-2101.3222.3222.0	3	9.45	5.86	84.7	2.22e+007	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
89	083-1901.8277.8295.2	2	9.43	9.43	70.1	3.15e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
90	084-2001.8569.8569.0	3	9.32	9.32	71.0	1.09e+008	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
91	081-1701.3652.3700.0	2	9.25	3.75	100.0	2.93e+005	(R)IADGGFQR(Y)	863.438
92	083-1901.9390.9390.0	2	8.99	8.99	67.9	2.93e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
93	083-1901.9451.9451.0	2	8.73	8.73	64.2	2.47e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
94	085-2101.3263.3263.2	2	8.50	8.50	100.0	4.12e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
95	085-2101.3243.3243.2	2	8.17	8.17	81.2	2.66e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
96	083-1901.3298.3298.2	2	8.09	8.09	80.1	6.10e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
97	082-1801.3255.3255.2	2	8.00	8.00	100.0	5.27e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
98	082-1801.3221.3221.2	2	7.74	4.25	93.7	5.55e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
99	083-1901.3266.3266.2	2	7.45	7.45	83.5	5.67e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
100	082-1801.5305.5305.0	2	7.11	2.97	79.8	5.12e+006	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
101	083-1901.3262.3262.2	2	7.00	7.00	100.0	5.67e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913

102	081-1701.3627.3627.0	2	6.75	1.14	100.0	4.05e+005	(R)IADGGFQR(Y)	863.438
103	082-1801.5202.5202.0	2	6.74	3.69	80.4	1.91e+006	(R)IGAIEGPADGDGMGLR(E)	1528.743
104	082-1801.5554.5554.2	2	6.47	6.47	61.8	2.52e+006	(K)ANGESNGSSISGYNTAVWMDR(I)	2215.968
105	082-1801.1482.1482.0	2	6.25	2.65	100.0	1.20e+005	(R)IADGGFQR(Y)	863.438
106	083-1901.3565.3565.0	2	6.06	2.03	69.9	1.31e+007	(R)IGAIEGPADGDGMGLR(E)	1528.743

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	56	9	161.19	14	5.27e+010	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	084-2001.4380.4386.2	2	21.94	14.89	98.6	1.36e+008	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
2	085-2101.5243.5249.2	2	21.50	21.50	100.0	2.06e+008	(R)SDFGQYWDQITLENK(G)	1843.850
3	081-1701.7146.7152.2	2	21.00	21.00	100.0	1.87e+008	(R)SDFGQYWDQITLENK(G)	1843.850
4	081-1701.5748.5818.2	2	20.91	11.99	98.2	2.83e+008	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
5	082-1801.5444.5448.0	2	20.89	13.16	97.8	1.25e+007	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
6	081-1701.5848.5871.2	2	20.39	12.00	97.8	8.82e+007	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
7	082-1801.8671.8677.0	3	20.37	13.83	91.8	4.94e+008	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
8	081-1701.5629.5701.2	2	19.84	13.08	96.7	1.29e+008	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
9	081-1701.8045.8056.0	3	19.64	11.99	94.9	1.51e+008	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
10	080-1601.6274.6280.2	2	19.56	10.66	96.0	2.25e+007	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
11	083-1901.7486.7504.3	3	19.43	19.43	90.1	5.70e+009	(R)YPDTEIIDVVNEATPGHAPANFAQDAFGNDWIIK(S)	3728.787
12	085-2101.4366.4400.2	2	19.28	10.28	95.2	2.54e+008	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
13	083-1901.5989.6022.3	3	19.27	12.95	89.1	3.56e+009	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
14	083-1901.5257.5281.2	2	19.21	19.21	96.0	1.90e+008	(R)SDFGQYWDQITLENK(G)	1843.850
15	082-1801.8640.8667.2	2	19.09	11.43	93.3	1.47e+009	(R)IAALGLPIYISEYDIEK(T)	1908.037
16	084-2001.6680.6724.2	2	19.09	11.47	93.4	8.22e+009	(R)IAALGLPIYISEYDIEK(T)	1908.037
17	081-1701.7988.8047.2	2	19.08	11.46	93.1	4.43e+009	(R)IAALGLPIYISEYDIEK(T)	1908.037
18	081-1701.5767.5851.3	3	18.70	12.53	94.2	3.61e+007	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
19	081-1701.5672.5752.3	3	18.67	14.12	93.7	2.72e+007	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
20	082-1801.5434.5481.3	3	18.59	12.08	92.0	3.81e+006	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
21	082-1801.6979.7007.2	2	18.42	18.42	92.2	2.26e+008	(R)SDFGQYWDQITLENK(G)	1843.850
22	082-1801.6892.6897.2	2	18.21	18.21	87.8	1.78e+008	(R)SDFGQYWDQITLENK(G)	1843.850
23	083-1901.6683.6747.2	2	18.08	9.33	92.7	3.53e+009	(R)IAALGLPIYISEYDIEK(T)	1908.037
24	081-1701.7324.7330.0	3	17.45	11.97	87.4	1.15e+008	(K)WAQVEPQRDQYDWSGIDDAYNYAK(Q)	2918.302
25	085-2101.6023.6057.3	3	17.42	10.21	84.6	3.93e+009	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
26	083-1901.6699.6709.3	3	17.38	7.63	90.4	4.32e+008	(R)IAALGLPIYISEYDIEK(T)	1908.037
27	084-2001.5951.6024.3	3	16.68	8.36	81.8	6.53e+009	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
28	081-1701.7990.8048.3	3	16.41	7.20	89.7	1.06e+009	(R)IAALGLPIYISEYDIEK(T)	1908.037
29	083-1901.4116.4116.0	2	16.29	8.86	90.5	8.41e+006	(K)AAEIEEWIR(D)	1116.569
30	082-1801.6901.6955.3	3	16.10	16.10	83.3	5.77e+007	(R)SDFGQYWDQITLENK(G)	1843.850
31	085-2101.4150.4173.0	2	15.98	7.14	93.0	8.41e+006	(K)AAEIEEWIR(D)	1116.569
32	083-1901.7418.7505.4	4	15.80	11.21	79.7	4.09e+009	(R)YPDTEIIDVVNEATPGHAPANFAQDAFGNDWIIK(S)	3728.787
33	083-1901.4105.4124.0	2	15.42	7.90	91.9	8.85e+006	(K)AAEIEEWIR(D)	1116.569
34	083-1901.5270.5270.3	3	15.16	15.16	79.1	2.92e+007	(R)SDFGQYWDQITLENK(G)	1843.850
35	084-2001.5267.5267.3	3	14.89	14.89	86.1	2.53e+007	(R)SDFGQYWDQITLENK(G)	1843.850

36	085-2101.5256.5256.3	3	14.55	14.55	75.0	4.19e+007	(R)SDFGQYWDQITLENK(G)	1843.850
37	084-2001.6694.6726.3	3	14.51	5.41	74.8	1.03e+009	(R)IAALGLPIYISEYDIEK(T)	1908.037
38	085-2101.6091.6091.4	4	14.51	14.51	78.7	6.74e+007	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
39	084-2001.4125.4131.0	2	14.22	6.78	87.9	6.57e+006	(K)AAEIEEWIR(D)	1116.569
40	082-1801.8690.8704.2	2	13.92	13.92	87.5	6.62e+007	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
41	084-2001.5957.6026.2	2	13.76	10.47	85.6	1.06e+009	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
42	081-1701.3841.3847.2	2	13.60	5.94	92.4	2.64e+006	(K)WAQVEPQR(D)	1013.517
43	085-2101.5227.5227.0	2	13.45	8.95	82.6	1.76e+008	(R)SDFGQYWDQITLENK(G)	1843.850
44	081-1701.7153.7182.3	3	13.33	13.33	75.5	5.45e+007	(R)SDFGQYWDQITLENK(G)	1843.850
45	085-2101.6037.6058.2	2	13.27	8.87	84.2	6.76e+008	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
46	084-2001.5237.5260.0	2	12.76	12.76	79.3	2.08e+008	(R)SDFGQYWDQITLENK(G)	1843.850
47	082-1801.4069.4075.0	2	12.51	5.68	83.2	7.73e+006	(K)AAEIEEWIR(D)	1116.569
48	083-1901.5998.6024.2	2	11.63	11.63	72.2	6.63e+008	(K)QHTFVWGSQYPNWIDSLSASEK(A)	2580.216
49	081-1701.8840.8865.2	2	11.52	7.68	86.1	1.57e+008	(R)DGTGLIQSNGQHRPAMDWLMNYIGR(-)	2830.352
50	081-1701.8781.8805.0	3	10.79	7.03	74.3	2.49e+009	(R)DGTGLIQSNGQHRPAMDWLMNYIGR(-)	2830.352
51	082-1801.5392.5392.0	2	10.07	5.82	88.2	5.33e+006	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
52	082-1801.1919.1919.2	2	9.95	2.95	93.6	1.36e+006	(K)WAQVEPQR(D)	1013.517
53	082-1801.6880.6880.2	2	8.38	8.38	62.0	1.04e+008	(R)SDFGQYWDQITLENK(G)	1843.850
54	082-1801.5542.5542.3	3	8.37	8.37	86.5	1.32e+006	(R)DQYDWSGIDDAYNYAK(Q)	1923.804
55	082-1801.7017.7017.2	2	7.95	7.95	64.6	8.61e+007	(R)SDFGQYWDQITLENK(G)	1843.850
56	082-1801.5386.5386.0	2	7.56	2.08	71.7	4.67e+006	(R)DQYDWSGIDDAYNYAK(Q)	1923.804

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
3	3.2	3	2	28.37	4	2.86e+009	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	081-1701.7806.7838.2	2	16.85	12.79	95.2	2.08e+008	(R)DQYNWGPLDAIYDYAR(A)	1959.888
2	081-1701.8840.8865.2	2	11.52	7.68	86.1	1.57e+008	(R)DGTGLIQSNGQHRPAMDWLMNYLGR(-)	2830.352
3	081-1701.8781.8805.0	3	10.79	7.03	74.3	2.49e+009	(R)DGTGLIQSNGQHRPAMDWLMNYLGR(-)	2830.352

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	58	9	153.51	22	5.49e+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	081-1701.7923.7962.2	2	21.21	21.21	96.7	1.35e+008	(K)FYDIYGSNHSAGSTVAWAWGVSR(M)	2531.174
2	083-1901.5433.5496.2	2	21.19	21.19	95.9	2.84e+008	(K)FYDIYGSNHSAGSTVAWAWGVSR(M)	2531.174
3	085-2101.4708.4714.2	2	20.92	20.92	98.8	1.14e+008	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
4	082-1801.8631.8651.2	2	20.70	20.70	96.1	1.44e+008	(K)FYDIYGSNHSAGSTVAWAWGVSR(M)	2531.174
5	085-2101.5414.5455.2	2	20.63	20.63	95.5	1.44e+008	(K)FYDIYGSNHSAGSTVAWAWGVSR(M)	2531.174
6	084-2001.5403.5436.2	2	19.48	19.48	93.4	2.68e+008	(K)FYDIYGSNHSAGSTVAWAWGVSR(M)	2531.174

7	082-1801.6162.6246.2	2	19.21	19.21	95.2	1.03e+008	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
8	083-1901.4702.4708.2	2	18.74	18.74	95.9	1.85e+008	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
9	082-1801.4663.4680.0	3	18.60	11.22	90.9	1.31e+006	(K)LPVDNHELLGMVAPR(G)	1660.884
10	084-2001.4685.4688.0	3	18.59	11.78	91.0	6.58e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
11	081-1701.6962.6962.2	2	17.64	17.64	94.3	8.82e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
12	084-2001.4806.4809.2	2	17.61	9.38	82.7	1.15e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
13	081-1701.7828.7846.3	3	17.59	10.10	90.1	1.95e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
14	082-1801.8596.8602.0	3	17.57	10.92	89.4	7.19e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
15	085-2101.4662.4666.0	3	17.55	11.02	89.2	9.10e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
16	083-1901.3599.3616.0	3	17.52	9.20	91.8	9.65e+006	(R)MIDVLQQTSGHNLDASR(I)	1884.924
17	085-2101.3608.3614.0	3	17.47	10.10	91.3	6.95e+006	(R)MIDVLQQTSGHNLDASR(I)	1884.924
18	084-2001.4714.4720.2	2	16.98	16.98	91.9	1.18e+008	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
19	081-1701.7033.7037.0	2	16.80	9.35	89.5	1.30e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
20	081-1701.6861.6884.2	2	16.58	16.58	93.0	6.12e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
21	082-1801.6383.6383.2	2	16.57	8.81	90.6	1.41e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
22	081-1701.6847.6859.0	3	16.48	16.48	83.0	6.91e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
23	084-2001.3595.3619.0	3	16.48	7.35	90.4	8.83e+006	(R)MIDVLQQTSGHNLDASR(I)	1884.924
24	083-1901.4669.4684.0	3	16.43	8.23	86.3	7.03e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
25	082-1801.4676.4676.0	3	16.17	8.57	83.4	1.26e+006	(K)LPVDNHELLGMVAPR(G)	1660.884
26	083-1901.3527.3568.2	2	16.07	9.37	94.5	2.16e+007	(K)GAIVVGAFDER(I)	1133.595
27	081-1701.7340.7344.0	3	15.89	15.89	81.0	1.21e+007	(K)DKGVAVVNFSNSEMGAHNGSGSR(G)	2320.074
28	083-1901.4790.4841.2	2	15.64	7.81	82.6	1.26e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
29	082-1801.5389.5394.0	3	15.62	6.96	91.3	1.79e+007	(K)FYDIYGSNHSAGSTVAWAWGVSR(M)	2531.174
30	082-1801.5632.5677.2	2	15.58	9.09	94.6	2.93e+006	(K)GAIVVGAFDER(I)	1133.595
31	084-2001.3523.3565.2	2	15.56	8.62	94.0	1.56e+007	(K)GAIVVGAFDER(I)	1133.595
32	082-1801.3468.3524.0	2	15.21	8.30	91.0	3.90e+007	(K)GAIVVGAFDER(I)	1133.595
33	081-1701.7836.7839.2	2	15.19	15.19	85.3	1.30e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
34	085-2101.4786.4792.0	2	15.18	8.05	83.7	1.55e+008	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
35	083-1901.4800.4805.3	3	14.93	5.50	87.1	3.41e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
36	081-1701.7230.7284.0	2	14.88	6.08	93.9	5.85e+008	(R)WIPWNTPILQ(-)	1267.684
37	085-2101.6506.6524.0	2	14.75	8.55	92.1	1.07e+008	(R)WIPWNTPILQ(-)	1267.684
38	081-1701.6291.6337.2	2	14.53	8.09	93.2	1.93e+007	(K)GAIVVGAFDER(I)	1133.595
39	085-2101.3526.3602.2	2	14.53	8.04	92.9	1.36e+007	(K)GAIVVGAFDER(I)	1133.595
40	082-1801.8603.8603.0	2	14.51	14.51	82.5	7.52e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
41	082-1801.5743.5743.2	2	14.43	10.71	97.3	1.79e+006	(K)GAIVVGAFDER(I)	1133.595
42	081-1701.6372.6444.0	2	14.33	8.43	87.0	4.20e+007	(K)GAIVVGAFDER(I)	1133.595
43	081-1701.7270.7275.0	2	14.33	9.17	84.1	1.11e+008	(R)MIDVLQQTSGHNLDASR(I)	1884.924
44	082-1801.7169.7216.0	2	14.28	10.05	92.2	1.00e+008	(R)WIPWNTPILQ(-)	1267.684
45	083-1901.6468.6474.0	2	14.26	10.25	92.5	7.44e+007	(R)WIPWNTPILQ(-)	1267.684
46	084-2001.6460.6464.0	2	14.21	10.39	91.7	8.63e+007	(R)WIPWNTPILQ(-)	1267.684
47	083-1901.4696.4701.3	3	13.84	13.84	79.9	4.09e+008	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
48	081-1701.7026.7060.3	3	13.68	4.97	86.3	6.71e+007	(R)ISLTIPQESGSGGVAAWR(V)	1828.956
49	085-2101.4692.4763.3	3	13.64	13.64	74.0	2.56e+008	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
50	082-1801.3482.3486.2	2	13.04	7.86	85.4	1.92e+007	(K)GAIVVGAFDER(I)	1133.595
51	083-1901.4825.4845.0	2	12.40	12.40	82.6	2.72e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
52	083-1901.4691.4691.2	2	11.62	11.62	73.8	2.04e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
53	084-2001.10344.10344.0	3	10.81	7.49	72.3	3.98e+007	(R)GLLVIENTGQEWLGNESTYTASVAAHEVWK(A)	3302.633
54	082-1801.3574.3574.2	2	9.78	6.55	83.1	3.59e+006	(R)MIDVLQQTSGHNLDASR(I)	1884.924

55	083-1901.3721.3721.0	2	9.02	4.26	83.7	2.90e+006	(K)GAIVVGAFDER(I)	1133.595
56	082-1801.5836.5836.0	2	8.50	5.30	100.0	4.77e+005	(K)GAIVVGAFDER(I)	1133.595
57	085-2101.4776.4776.0	2	7.43	7.43	67.6	3.77e+007	(K)FLLGNSSANTTIESTDGSFSVDR(N)	2418.142
58	081-1701.7326.7326.0	2	7.17	7.17	79.3	2.15e+008	(R)WIPWNTPILQ(-)	1267.684

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	4.2	30	7	110.10	13	2.41e+009	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	081-1701.7923.7962.2	2	21.21	21.21	96.7	1.35e+008	(K)FYDIYGSNHSAGSTVAWAWGVSR(I)	2531.174
2	083-1901.5433.5496.2	2	21.19	21.19	95.9	2.84e+008	(K)FYDIYGSNHSAGSTVAWAWGVSR(I)	2531.174
3	082-1801.8631.8651.2	2	20.70	20.70	96.1	1.44e+008	(K)FYDIYGSNHSAGSTVAWAWGVSR(I)	2531.174
4	085-2101.5414.5455.2	2	20.63	20.63	95.5	1.44e+008	(K)FYDIYGSNHSAGSTVAWAWGVSR(I)	2531.174
5	084-2001.5403.5436.2	2	19.48	19.48	93.4	2.68e+008	(K)FYDIYGSNHSAGSTVAWAWGVSR(I)	2531.174
6	082-1801.4663.4680.0	3	18.60	11.22	90.9	1.31e+006	(K)LPVDNHELLGMVAPR(G)	1660.884
7	084-2001.4685.4688.0	3	18.59	11.78	91.0	6.58e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
8	085-2101.5079.5096.0	3	17.71	17.71	84.2	1.51e+008	(R)YGSSGANAQVEAISLQGVPHNLPVEEEEAIR(F)	3264.614
9	081-1701.7828.7846.3	3	17.59	10.10	90.1	1.95e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
10	082-1801.8596.8602.0	3	17.57	10.92	89.4	7.19e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
11	085-2101.4662.4666.0	3	17.55	11.02	89.2	9.10e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
12	085-2101.4920.4932.2	2	16.84	16.84	89.2	1.78e+007	(R)IQLWHGTNDETLNYNNFNEAIK(Q)	2634.259
13	083-1901.4669.4684.0	3	16.43	8.23	86.3	7.03e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
14	082-1801.4676.4676.0	3	16.17	8.57	83.4	1.26e+006	(K)LPVDNHELLGMVAPR(G)	1660.884
15	082-1801.5389.5394.0	3	15.62	6.96	91.3	1.79e+007	(K)FYDIYGSNHSAGSTVAWAWGVSR(I)	2531.174
16	085-2101.4912.4912.0	3	15.37	6.86	80.9	1.48e+008	(R)IQLWHGTNDETLNYNNFNEAIK(Q)	2634.259
17	081-1701.7836.7839.2	2	15.19	15.19	85.3	1.30e+008	(K)LPVDNHELLGMVAPR(G)	1660.884
18	082-1801.8603.8603.0	2	14.51	14.51	82.5	7.52e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
19	083-1901.5097.5097.0	3	14.07	9.68	78.2	2.32e+008	(R)YGSSGANAQVEAISLQGVPHNLPVEEEEAIR(F)	3264.614
20	081-1701.7134.7165.0	3	13.29	6.17	83.3	5.19e+007	(K)QWTNVHGLSQTPTFTDQPSANATR(T)	2657.271
21	079-1501.6831.6837.0	3	13.18	6.85	72.9	3.05e+007	(R)YGSSGANAQVEAISLQGVPHNLPVEEEEAIR(F)	3264.614
22	084-2001.3733.3733.0	3	13.13	8.37	80.6	6.55e+006	(K)QWTNVHGLSQTPTFTDQPSANATR(T)	2657.271
23	081-1701.6414.6414.0	2	12.54	12.54	80.2	1.50e+007	(K)FLLGNDSANTTIVNSSK(V)	1780.908
24	083-1901.3736.3736.0	3	11.92	4.82	77.0	5.69e+006	(K)QWTNVHGLSQTPTFTDQPSANATR(T)	2657.271
25	083-1901.4691.4691.2	2	11.62	11.62	73.8	2.04e+007	(K)LPVDNHELLGMVAPR(G)	1660.884
26	085-2101.3740.3740.0	3	11.15	11.15	72.3	5.85e+006	(K)QWTNVHGLSQTPTFTDQPSANATR(T)	2657.271
27	081-1701.6453.6453.0	2	10.00	10.00	72.8	7.96e+006	(K)FLLGNDSANTTIVNSSK(V)	1780.908
28	081-1701.5446.5446.2	2	9.91	5.51	96.8	7.51e+005	(K)GAIVVGAMDER(I)	1117.568
29	081-1701.6440.6440.0	2	9.83	9.83	68.1	1.29e+007	(K)FLLGNDSANTTIVNSSK(V)	1780.908
30	083-1901.3730.3730.0	3	8.36	5.08	84.2	5.58e+006	(K)QWTNVHGLSQTPTFTDQPSANATR(T)	2657.271

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	35	9	152.55	44	9.01e+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	085-2101.5729.5751.0	3	19.26	19.26	87.1	3.04e+008	(K)GANSIAGFASNSANYTPVTEPYLQDPNLQVGGNPIR(S)	3732.826
2	083-1901.8026.8029.2	2	19.10	19.10	86.6	5.49e+007	(R)GHLDEALAQGANLFQFVVYDLPNR(D)	2687.358
3	085-2101.6064.6105.2	2	18.66	18.66	93.3	2.73e+008	(R)YQNEYIAGITEIIGDSK(Y)	1913.950
4	082-1801.9541.9584.0	2	18.47	10.89	60.7	1.36e+009	(R)WFPEAFQTLLENAYPPL(-)	2036.017
5	085-2101.5825.5873.2	2	18.03	13.27	94.4	3.58e+008	(K)GFPSTLGMLIDTGR(N)	1464.752
6	081-1701.9080.9097.0	2	17.43	9.91	96.8	1.56e+009	(R)WFPEAFQTLLENAYPPL(-)	2036.017
7	082-1801.8565.8569.2	2	17.16	17.16	93.4	2.23e+008	(K)GFPSTLGMLIDTGR(N)	1464.752
8	082-1801.9675.9675.2	2	16.83	16.83	83.5	3.10e+007	(R)GHLDEALAQGANLFQFVVYDLPNR(D)	2687.358
9	083-1901.5868.5913.2	2	16.67	16.67	91.6	1.68e+008	(K)GFPSTLGMLIDTGR(N)	1464.752
10	081-1701.7829.7845.2	2	16.63	16.63	92.8	2.38e+008	(K)GFPSTLGMLIDTGR(N)	1464.752
11	083-1901.5149.5202.2	2	16.36	16.36	87.1	4.10e+008	(K)IAYESTFVWMDR(I)	1517.710
12	084-2001.5837.5917.2	2	15.90	15.90	89.9	2.08e+008	(K)GFPSTLGMLIDTGR(N)	1464.752
13	084-2001.5135.5196.2	2	15.83	15.83	86.0	3.31e+008	(K)IAYESTFVWMDR(I)	1517.710
14	085-2101.5137.5139.2	2	15.35	15.35	86.5	2.80e+008	(K)IAYESTFVWMDR(I)	1517.710
15	084-2001.8019.8032.0	3	15.19	7.25	88.9	2.23e+008	(R)GHLDEALAQGANLFQFVVYDLPNR(D)	2687.358
16	085-2101.9061.9097.3	3	15.07	11.14	85.0	5.85e+007	(R)WFPEAFQTLLENAYPPL(-)	2036.017
17	083-1901.3350.3350.0	3	14.97	10.93	80.8	6.76e+006	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
18	083-1901.9544.9567.2	2	14.33	14.33	86.8	8.56e+007	(R)SSDFYEWTQYLEELQFVQAWR(Q)	2725.258
19	082-1801.9554.9585.3	3	14.05	9.88	84.4	5.37e+008	(R)WFPEAFQTLLENAYPPL(-)	2036.017
20	083-1901.3521.3521.0	3	13.84	13.84	78.0	3.47e+007	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
21	085-2101.3469.3475.0	3	13.68	5.95	78.7	2.75e+007	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
22	082-1801.3823.3836.0	2	13.37	8.32	90.8	6.96e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
23	084-2001.8646.8651.2	2	12.89	12.89	77.1	4.19e+008	(R)SSDFYEWTQYLEELQFVQAWR(Q)	2725.258
24	081-1701.7375.7375.2	2	12.51	8.87	68.8	1.98e+007	(K)IAYESTFVWMDR(I)	1517.710
25	081-1701.6432.6438.2	2	12.45	12.45	82.3	5.07e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
26	085-2101.8670.8674.2	2	10.77	10.77	69.9	2.22e+008	(R)SSDFYEWTQYLEELQFVQAWR(Q)	2725.258
27	081-1701.6331.6408.2	2	10.70	10.70	72.2	5.43e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
28	084-2001.3334.3334.0	3	10.49	10.49	91.6	7.61e+006	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
29	082-1801.7099.7132.2	2	10.48	10.48	74.2	7.71e+007	(K)IAYESTFVWMDR(I)	1517.710
30	081-1701.9085.9085.0	2	10.37	4.21	76.1	1.33e+009	(R)WFPEAFQTLLENAYPPL(-)	2036.017
31	083-1901.3344.3344.0	3	9.86	6.81	81.1	6.53e+006	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
32	084-2001.3573.3573.0	3	9.82	9.82	73.8	4.10e+006	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
33	085-2101.3313.3313.0	3	8.74	5.43	73.7	8.01e+006	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
34	082-1801.3301.3301.0	3	8.36	8.36	77.9	3.88e+006	(R)NGWGGANRPSGASSSTDLNTYVDESR(I)	2698.209
35	080-1601.6639.6639.2	2	6.89	6.89	67.1	2.64e+007	(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	32	9	141.60	14	3.07e+009	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	082-1801.5960.5988.2	2	19.38	19.38	97.9	8.90e+006	(K)AAGEPGGSAIANYNTAVWMDR(I)	2150.993
2	085-2101.4455.4461.0	2	19.33	19.33	97.1	4.44e+007	(K)AAGEPGGSAIANYNTAVWMDR(I)	2150.993
3	084-2001.4479.4497.2	2	19.20	19.20	94.5	3.61e+007	(K)AAGEPGGSAIANYNTAVWMDR(I)	2150.993
4	085-2101.7340.7410.2	2	18.27	18.27	86.5	2.14e+008	(R)VDNPFVGANWYIDPIWSAK(A)	2192.082
5	083-1901.4469.4474.2	2	18.18	18.18	94.4	5.63e+007	(K)AAGEPGGSAIANYNTAVWMDR(I)	2150.993
6	085-2101.8219.8219.2	2	18.04	12.17	88.1	2.67e+008	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.304
7	084-2001.7311.7385.2	2	17.88	13.40	88.0	3.15e+008	(R)VDNPFVGANWYIDPIWSAK(A)	2192.082
8	083-1901.7299.7390.2	2	17.73	12.84	84.8	3.58e+008	(R)VDNPFVGANWYIDPIWSAK(A)	2192.082
9	083-1901.8142.8205.2	2	17.61	11.25	89.8	1.39e+008	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.304
10	081-1701.5334.5340.0	2	15.84	10.24	91.3	5.02e+006	(R)VVLSNGDQWTR(N)	1274.649
11	085-2101.8161.8207.3	3	15.73	9.69	72.5	2.52e+008	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.304
12	083-1901.5225.5246.0	2	15.71	9.81	92.4	1.19e+008	(R)GLPSNIGMLIDTGR(N)	1443.763
13	083-1901.8119.8212.0	3	15.71	6.85	80.1	4.26e+008	(R)YQNEYIAPIVEILSDPAYANIR(I)	2552.304
14	085-2101.5202.5236.0	2	15.69	10.47	92.6	1.43e+008	(R)GLPSNIGMLIDTGR(N)	1443.763
15	082-1801.5970.5970.0	2	15.57	15.57	92.5	6.35e+006	(K)AAGEPGGSAIANYNTAVWMDR(I)	2150.993
16	084-2001.5227.5232.2	2	15.23	15.23	92.6	9.49e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
17	083-1901.8292.8296.2	2	14.41	14.41	72.6	2.50e+007	(K)SSDFYEFNGYFDELSFVTDWR(N)	2624.126
18	084-2001.5570.5570.0	3	13.82	13.82	79.0	3.22e+007	(R)GQEDYVIINIANEPVGNNQPSSMWINDHR(S)	3310.555
19	082-1801.7052.7069.0	2	13.43	8.07	86.0	6.05e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
20	082-1801.3823.3836.0	2	13.37	8.32	90.8	6.96e+006	(R)IGAIAGPADGDGLGLR(G)	1452.781
21	081-1701.7301.7310.0	2	12.84	7.12	86.1	2.50e+007	(R)GLPSNIGMLIDTGR(N)	1443.763
22	082-1801.2829.2859.2	2	12.76	12.76	73.7	3.45e+006	(R)HSLIELGR(L)	924.527
23	081-1701.6432.6438.2	2	12.45	12.45	82.3	5.07e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
24	085-2101.8337.8360.0	2	11.95	11.95	65.0	6.20e+007	(K)SSDFYEFNGYFDELSFVTDWR(N)	2624.126
25	084-2001.8321.8321.0	2	11.81	11.81	71.4	7.80e+007	(K)SSDFYEFNGYFDELSFVTDWR(N)	2624.126
26	082-1801.5955.5955.0	2	11.03	11.03	89.2	4.68e+006	(K)AAGEPGGSAIANYNTAVWMDR(I)	2150.993
27	083-1901.4523.4523.0	2	10.91	10.91	81.5	2.75e+007	(K)AAGEPGGSAIANYNTAVWMDR(I)	2150.993
28	081-1701.6331.6408.2	2	10.70	10.70	72.2	5.43e+007	(R)IGAIAGPADGDGLGLR(G)	1452.781
29	082-1801.5947.5947.0	2	9.56	6.43	82.4	3.48e+006	(K)AAGEPGGSAIANYNTAVWMDR(I)	2150.993
30	081-1701.6510.6510.0	2	9.25	9.25	79.9	5.75e+006	(K)AAGEPGGSAIANYNTAVWMDR(I)	2150.993
31	085-2101.7430.7430.0	2	8.19	8.19	63.6	1.23e+008	(R)VDNPFVGANWYIDPIWSAK(A)	2192.082
32	080-1601.6639.6639.2	2	6.89	6.89	67.1	2.64e+007	(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	11	5	81.06	12	3.96e+008	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	081-1701.6294.6300.0	3	19.24	19.24	96.2	2.25e+007	(R)LPIAPQTLDPNDPQGTGNVLK(N)	2188.161
2	081-1701.7243.7248.0	3	18.23	12.84	92.5	2.35e+007	(K)MFMDPAQPECEGLEGDEAGENDCNIVINATQLR(A)	3609.561
3	081-1701.8848.8925.2	2	16.63	11.55	91.0	2.05e+008	(R)KWSLLELTW(-)	1175.647
4	082-1801.9264.9279.2	2	16.36	11.34	91.0	5.75e+007	(R)KWSLLELTW(-)	1175.647
5	085-2101.3905.3930.0	3	14.65	6.88	95.5	1.70e+007	(R)LVYSPHTYGPSVFVQK(M)	1821.954
6	081-1701.6283.6356.2	2	14.12	9.31	89.6	1.16e+007	(R)LPIAPQTLDPNDPQGTGNVLK(N)	2188.161
7	084-2001.3906.3911.0	3	13.14	6.63	94.6	1.22e+007	(R)LVYSPHTYGPSVFVQK(M)	1821.954

8	083-1901.3904.3906.0	3	12.60	5.65	93.3	1.60e+007	(R)LVYSPHTYGPSVFVQK(M)	1821.954
9	081-1701.7549.7554.0	2	12.31	4.91	70.3	2.14e+007	(R)AGWEEHFGYLR(D)	1364.639
10	082-1801.5851.5851.0	3	11.62	7.38	87.3	1.16e+006	(R)LPIAPQTLDPNDPQGTGNVLK(N)	2188.161
11	081-1701.6290.6290.2	2	8.69	5.16	74.9	7.70e+006	(R)LPIAPQTLDPNDPQGTGNVLK(N)	2188.161

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	6.2	2	2	23.42	3	2.46e+007	75758.3	PA_Bse_meta_comb:2073585828	PA_Bse_meta_comb:2073585828 BaSeMet_00294840 Endoglucanase [Bankia setacea microbiome (Cor

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	081-1701.7549.7554.0	2	12.31	4.91	70.3	2.14e+007	(R)AGWEEHFGYLR(D)	1364.639
2	083-1901.3907.3907.0	3	11.11	3.64	92.0	3.25e+006	(R)LVYSPHTYGPSVFVQR(M)	1849.960

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	15	5	63.54	14	5.05e+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	081-1701.7122.7128.0	3	16.93	16.93	82.5	4.70e+007	(R)YTSQWSNSTNNWVGGLGWNPGGR(K)	2538.155
2	081-1701.6101.6129.0	2	15.06	5.97	93.8	2.22e+007	(R)VITWDVDSR(D)	1090.553
3	082-1801.3225.3278.2	2	14.55	5.76	93.4	1.04e+007	(R)VITWDVDSR(D)	1090.553
4	083-1901.3256.3271.0	2	14.39	6.61	89.7	2.08e+007	(R)VITWDVDSR(D)	1090.553
5	084-2001.3247.3323.0	2	13.47	5.96	91.3	2.01e+007	(R)VITWDVDSR(D)	1090.553
6	081-1701.6278.6278.2	2	12.44	4.33	89.1	1.08e+007	(R)VITWDVDSR(D)	1090.553
7	083-1901.5510.5510.0	3	12.17	12.17	77.8	2.35e+008	(K)VVSYSGSYNVSNSQNSYLALYGWTK(N)	2787.327
8	082-1801.8685.8685.0	3	11.89	4.82	78.5	3.46e+007	(K)GFGNISGTITVGNHFDFWASK(G)	2255.088
9	080-1601.6568.6589.2	2	11.71	4.25	91.0	6.00e+007	(R)VITWDVDSR(D)	1090.553
10	085-2101.3241.3251.0	2	11.61	4.18	87.9	6.45e+006	(R)VITWDVDSR(D)	1090.553
11	083-1901.3442.3442.0	2	9.54	2.27	65.9	2.50e+006	(R)VITWDVDSR(D)	1090.553
12	084-2001.3375.3375.0	2	8.86	2.48	86.0	2.16e+006	(R)VITWDVDSR(D)	1090.553
13	084-2001.3345.3345.0	2	8.27	2.46	72.8	4.33e+006	(R)VITWDVDSR(D)	1090.553
14	084-2001.5808.5808.0	2	7.49	7.49	65.3	2.74e+007	(R)VQQPSIEGTQTFYQYFSVR(S)	2278.114
15	082-1801.5240.5240.0	2	7.25	1.40	100.0	1.36e+006	(R)VITWDVDSR(D)	1090.553

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	4	56.78	16	3.24e+008	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	085-2101.4920.4932.2	2	16.84	16.84	89.2	1.78e+007	(R)LQLWHGTNDETLNYNNFNEAIK(Q)	2634.259

2	081-1701.7850.7850.2	2	16.76	16.76	88.7	5.80e+007	(R)DGGSDPVSIMSMIDYVK(Q)	1813.835
3	081-1701.7087.7092.0	3	15.59	11.63	80.3	2.53e+007	(K)QWTNVHGVSQTAAYTDSPESGITR(T)	2605.228
4	085-2101.4912.4912.0	3	15.37	6.86	80.9	1.48e+008	(R)LQLWHGTNDETLNYNNFNEAIK(Q)	2634.259
5	084-2001.3363.3363.0	3	9.20	9.20	81.3	1.88e+006	(K)QWTNVHGVSQTAAYTDSPESGITR(T)	2605.228
6	081-1701.8954.8954.0	2	7.59	3.98	64.9	7.31e+007	(R)VFVTGVSSGAMMTNVMIGLYPDVFK(A)	2663.329

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	11	3	53.35	11	1.09e+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	083-1901.4141.4155.0	3	20.83	20.83	89.6	1.06e+007	(K)AEGSSIVQTGSAVSNWNDSDLTAAGR(L)	2593.213
2	084-2001.2636.2653.3	3	17.52	11.31	90.7	2.74e+006	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
3	085-2101.2656.2656.3	3	16.17	9.59	83.3	2.38e+006	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
4	081-1701.7475.7511.2	2	15.00	15.00	91.2	5.06e+007	(K)SFAGNSFFWSNTEWGQER(F)	2149.937
5	081-1701.7477.7498.3	3	13.07	8.47	83.4	2.86e+007	(K)SFAGNSFFWSNTEWGQER(F)	2149.937
6	085-2101.2668.2668.3	3	12.71	5.55	92.3	2.27e+006	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
7	084-2001.2659.2659.2	2	9.91	6.35	96.3	2.74e+006	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
8	084-2001.2641.2641.3	3	9.58	5.20	88.6	2.36e+006	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
9	083-1901.2646.2646.3	3	9.49	4.17	84.3	2.37e+006	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
10	085-2101.2657.2657.2	2	8.00	8.00	100.0	2.34e+006	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911
11	083-1901.2647.2647.2	2	7.29	3.91	90.9	2.09e+006	(R)AALGADGEGSYSEDPSGNLSR(I)	2052.911

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	7	3	49.74	11	5.96e+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	081-1701.6584.6611.3	3	18.10	13.18	90.5	6.53e+007	(R)SDFSQYWDQITPENEGK(W)	2043.894
2	081-1701.7806.7838.2	2	16.85	12.79	95.2	2.08e+008	(R)DQYNWGPLDAIYDYAR(A)	1959.888
3	081-1701.6498.6556.3	3	16.46	9.72	86.7	6.44e+007	(R)SDFSQYWDQITPENEGK(W)	2043.894
4	082-1801.7066.7085.0	2	14.79	7.74	89.3	2.88e+007	(R)NYPPFFVGNITTNGSVR(S)	1882.945
5	081-1701.6501.6585.2	2	11.52	8.09	68.4	1.26e+008	(R)SDFSQYWDQITPENEGK(W)	2043.894
6	081-1701.7315.7320.3	3	10.75	4.31	75.4	5.93e+007	(R)NYPPFFVGNITTNGSVR(S)	1882.945
7	084-2001.5243.5243.2	2	8.29	3.37	61.2	4.55e+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
11	11.1	6	3	43.13	4	2.45e+008	77470.6	PA_Bse08:2503996278	PA_Bse08:2503996278 BS08DRAFT_00001670 Cellulose or protein binding domain./Cellulose binding domain./Cel

				Fwd-Rev	SPI	Spectrum		MH^+

#	Filename	z	Score	Score	(%)	Intensity	Sequence	Matched (Da)
1	085-2101.4467.4502.0	3	16.45	7.02	96.9	2.69e+007	(R)LIISPHTYGPSVFVQK(Q)	1785.990
2	082-1801.4471.4503.0	3	15.69	6.21	97.2	1.05e+008	(R)LIISPHTYGPSVFVQK(Q)	1785.990
3	084-2001.4495.4500.0	3	15.05	6.73	91.6	4.28e+007	(R)LIISPHTYGPSVFVQK(Q)	1785.990
4	082-1801.3096.3123.2	2	13.69	6.59	97.3	5.08e+005	(K)ALGINVVR(F)	841.526
5	083-1901.4477.4508.0	3	13.06	3.29	91.5	6.69e+007	(R)LIISPHTYGPSVFVQK(Q)	1785.990
6	082-1801.3037.3067.2	2	12.99	5.41	84.1	2.98e+006	(R)TIQQTMDEIK(A)	1206.604

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	12	2	41.68	8	1.93e+009	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	083-1901.6711.6733.3	3	21.85	12.03	96.9	2.59e+008	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.122
2	084-2001.3818.3822.0	3	19.83	13.64	95.0	9.24e+006	(R)LESSAALNPGASTTGDWSDSDLTQSGR(Y)	2723.240
3	083-1901.3822.3829.0	3	18.83	12.87	95.1	1.07e+007	(R)LESSAALNPGASTTGDWSDSDLTQSGR(Y)	2723.240
4	085-2101.6820.6836.3	3	18.75	12.79	94.5	2.43e+008	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.122
5	084-2001.6734.6738.0	3	18.21	10.07	93.2	2.83e+008	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.122
6	085-2101.3823.3831.0	3	17.16	11.35	90.9	1.19e+007	(R)LESSAALNPGASTTGDWSDSDLTQSGR(Y)	2723.240
7	083-1901.6717.6717.0	3	13.53	8.59	91.3	2.55e+008	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.122
8	084-2001.3854.3854.0	3	12.67	6.66	80.3	8.61e+006	(R)LESSAALNPGASTTGDWSDSDLTQSGR(Y)	2723.240
9	084-2001.6754.6754.0	3	12.09	4.53	89.7	2.81e+008	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.122
10	084-2001.6742.6753.0	2	11.42	2.99	78.7	3.37e+008	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.122
11	085-2101.6835.6850.0	2	10.24	4.54	73.6	2.23e+008	(R)GMSSLGLQWSDAAPWMNYDSIK(W)	2457.122
12	084-2001.3866.3866.0	3	9.48	5.54	89.8	6.13e+006	(R)LESSAALNPGASTTGDWSDSDLTQSGR(Y)	2723.240

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	14	2	41.23	41	2.90e+009	13375.7	PA_Bse_meta_comb:2073565643	PA_Bse_meta_comb:2073565643 BaSeMet_00092990 Histone H2A [Bankia setacea microbiome (Combi

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	082-1801.10908.10912.2	2	21.12	21.12	95.6	3.74e+007	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
2	079-1501.7880.7903.0	3	20.11	10.94	93.5	1.78e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
3	083-1901.8950.9008.3	3	19.00	10.58	92.1	1.57e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
4	084-2001.7769.7769.0	3	17.89	12.12	92.8	1.83e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
5	083-1901.9065.9065.3	3	17.36	9.04	85.7	3.01e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
6	084-2001.11249.11249.2	2	16.08	16.08	87.1	2.21e+007	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
7	085-2101.11124.11130.2	2	16.08	16.08	83.6	5.32e+007	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
8	081-1701.10325.10325.2	2	14.85	14.85	91.0	7.37e+008	(R)VGAGAPVYLAAVLEYLAAEVLELAGNAAR(D)	2871.562
9	083-1901.7641.7646.2	2	14.07	8.70	87.2	6.85e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
10	080-1601.8243.8243.3	3	13.43	8.30	77.9	3.37e+007	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
11	085-2101.7742.7790.2	2	11.82	5.35	82.1	3.64e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391

12	083-1901.8943.9029.2	2	10.70	5.00	78.4	2.29e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
13	082-1801.9001.9005.2	2	10.58	4.78	61.3	3.40e+008	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391
14	079-1501.7913.7913.2	2	8.11	2.61	64.8	9.02e+006	(K)LLSGVTIAQGGVLPNIQAVLLPK(K)	2301.391

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	5	3	40.38	6	1.47e+008	77517.5	PA_BS12:2189568391	PA_BS12:2189568391 or1689 Endoglucanase [B. setacea BS12] 725 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	081-1701.8220.8220.0	3	15.26	15.26	87.9	3.83e+007	(R)DQDRWDHISPGIDQEWQNAFVNYMSR(K)	3207.434
2	081-1701.9039.9039.0	2	14.10	7.86	88.7	2.32e+007	(R)KWSLLDML(-)	1005.544
3	081-1701.8203.8203.0	3	13.63	13.63	80.7	3.91e+007	(R)DQDRWDHISPGIDQEWQNAFVNYMSR(K)	3207.434
4	081-1701.8215.8215.0	3	12.40	12.40	78.6	3.95e+007	(R)DQDRWDHISPGIDQEWQNAFVNYMSR(K)	3207.434
5	081-1701.6445.6462.0	2	11.02	3.81	76.6	6.91e+006	(R)TIQQTMDEITAR(G)	1406.695

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	7	3	40.27	1	2.73e+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	081-1701.6673.6690.0	2	16.93	7.27	95.3	7.25e+007	(R)ALPENLDQVYLK(A)	1402.758
2	081-1701.6576.6659.0	2	16.40	6.79	93.8	1.10e+008	(R)ALPENLDQVYLK(A)	1402.758
3	080-1601.6716.6722.0	2	13.24	5.33	86.2	4.75e+007	(R)ALPENLDQVYLK(A)	1402.758
4	082-1801.2433.2439.0	3	12.12	4.84	93.3	1.53e+006	(K)SLGNEAGDNHEHIIGVK(G)	1789.883
5	081-1701.7158.7164.0	2	11.22	11.22	78.3	3.46e+007	(R)AFTGTQSVHFK(G)	1222.622
6	083-1901.2537.2543.0	2	11.12	11.12	69.8	2.78e+006	(R)AFTGTQSVHFK(G)	1222.622
7	085-2101.2545.2551.0	2	10.34	10.34	75.8	3.36e+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
16	16.1	7	2	36.62	9	6.32e+008	43875.0	PA_Bse08:2503995778	PA_Bse08:2503995778 Cellulose or protein binding domain./Cellulase (glycosyl hydrolase family 5). [B. setacea BS(

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	084-2001.4465.4472.0	3	20.78	16.91	97.7	1.02e+008	(R)GVNHAHAWYSGETGSIADIANTGANTIR(V)	2883.377
2	083-1901.4463.4473.0	3	19.54	19.54	95.2	1.19e+008	(R)GVNHAHAWYSGETGSIADIANTGANTIR(V)	2883.377
3	085-2101.4439.4443.0	3	19.53	15.49	94.7	1.99e+008	(R)GVNHAHAWYSGETGSIADIANTGANTIR(V)	2883.377
4	085-2101.4452.4452.2	2	18.00	13.30	87.0	2.84e+007	(R)GVNHAHAWYSGETGSIADIANTGANTIR(V)	2883.377
5	082-1801.8617.8626.0	3	16.42	16.42	86.9	9.58e+007	(R)GVNHAHAWYSGETGSIADIANTGANTIR(V)	2883.377
6	081-1701.7895.7903.0	3	16.08	16.08	85.6	8.38e+007	(R)GVNHAHAWYSGETGSIADIANTGANTIR(V)	2883.377
7	081-1701.5334.5340.0	2	15.84	10.24	91.3	5.02e+006	(R)VVLSNGDQWTR(N)	1274.649

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	16.2	5	2	35.30	6	2.62e+008	60457.4	PA_BS12:2189569899	PA_BS12:2189569899 or3204 Cellulase (glycosyl hydrolase family 5)./Cellulose or protein binding domain. [B. setace

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	084-2001.4460.4460.0	3	19.46	19.46	86.8	1.31e+008	(R)GVNHAHAWYTGETGSIADIANAGANTVR(V)	2853.367
2	083-1901.4475.4475.2	2	18.82	15.50	84.5	1.27e+007	(R)GVNHAHAWYTGETGSIADIANAGANTVR(V)	2853.367
3	085-2101.4440.4440.2	2	17.69	10.68	91.7	2.30e+007	(R)GVNHAHAWYTGETGSIADIANAGANTVR(V)	2853.367
4	081-1701.5334.5340.0	2	15.84	10.24	91.3	5.02e+006	(R)VVLSNGDQWTR(N)	1274.649
5	083-1901.4462.4465.0	3	15.32	15.32	73.9	9.04e+007	(R)GVNHAHAWYTGETGSIADIANAGANTVR(V)	2853.367

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
17	17.1	10	3	35.31	5	1.83e+009	73439.4	PA_Bse08:2503994248	PA_Bse08:2503994248 BS08DRAFT_00028400 Cellulose or protein binding domain./Chitin binding domain. [B. seta

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	080-1601.6577.6619.2	2	16.91	11.12	95.8	1.73e+009	(R)DLPAGVSTLYMK(A)	1294.672
2	081-1701.6313.6366.2	2	15.60	9.80	93.2	2.08e+007	(R)DLPAGVSTLYMK(A)	1294.672
3	084-2001.4173.4178.2	2	12.21	6.32	87.8	8.20e+006	(R)DLPAGVSTLYMK(A)	1294.672
4	083-1901.4161.4174.2	2	11.69	6.88	87.5	3.37e+007	(R)DLPAGVSTLYMK(A)	1294.672
5	085-2101.4197.4197.0	2	11.00	4.03	83.9	1.28e+007	(R)DLPAGVSTLYMK(A)	1294.672
6	082-1801.4197.4197.0	2	10.87	5.33	92.7	2.46e+006	(R)DLPAGVSTLYMK(A)	1294.672
7	080-1601.5807.5849.2	2	10.36	4.98	74.6	7.62e+006	(R)DLPAGVSTLYMK(A)	1294.672
8	083-1901.2866.2866.0	3	9.32	4.99	83.1	1.41e+006	(K)QLGNEPGDNHEHIFAVK(A)	1904.926
9	080-1601.7307.7307.2	2	9.08	9.08	64.7	1.13e+007	(R)HVIYAEWGR(N)	1130.575
10	082-1801.2837.2837.0	2	6.84	2.81	92.3	2.30e+006	(R)HVIYAEWGR(N)	1130.575

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
18	18.1	15	2	34.08	6	4.04e+009	42518.1	PA_Bse02:2503998249	PA_Bse02:2503998249 BS02DRAFT_00014250 Cellulose or protein binding domain./Chitin binding domain. [B. seta

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	084-2001.6378.6440.3	3	21.88	21.88	98.2	4.43e+008	(K)ELVFWITKPGFSFDENR(V)	2085.045
2	081-1701.8355.8444.3	3	20.84	20.84	97.8	1.03e+009	(K)ELVFWITKPGFSFDENR(V)	2085.045
3	085-2101.6459.6505.3	3	20.19	16.51	95.3	2.26e+008	(K)ELVFWITKPGFSFDENR(V)	2085.045
4	084-2001.6387.6408.2	2	17.94	11.43	97.5	2.36e+008	(K)ELVFWITKPGFSFDENR(V)	2085.045
5	083-1901.6384.6438.2	2	16.90	10.07	95.8	3.12e+008	(K)ELVFWITKPGFSFDENR(V)	2085.045
6	082-1801.8896.8905.2	2	15.33	8.82	93.3	9.13e+007	(K)ELVFWITKPGFSFDENR(V)	2085.045
7	081-1701.8364.8461.2	2	13.10	6.69	84.5	8.00e+008	(K)ELVFWITKPGFSFDENR(V)	2085.045
8	085-2101.6475.6494.2	2	12.78	7.01	90.9	1.38e+008	(K)ELVFWITKPGFSFDENR(V)	2085.045

9	084-2001.2665.2711.2	2	12.20	6.58	87.6	2.08e+007	(R)HVIYGEWGR(D)	1116.559
10	083-1901.2658.2715.0	2	11.70	6.28	87.4	3.81e+007	(R)HVIYGEWGR(D)	1116.559
11	082-1801.2656.2726.0	2	11.21	6.25	87.8	4.07e+007	(R)HVIYGEWGR(D)	1116.559
12	081-1701.7312.7318.0	2	10.53	3.19	81.6	8.48e+007	(R)HVIYGEWGR(D)	1116.559
13	083-1901.2848.2848.2	2	7.75	7.75	66.0	1.84e+006	(R)HVIYGEWGR(D)	1116.559
14	084-2001.2671.2671.0	2	6.76	3.59	89.3	1.58e+007	(R)HVIYGEWGR(D)	1116.559
15	081-1701.8354.8354.2	2	6.72	2.83	70.2	5.55e+008	(K)ELVFWITKPGFSFDENR(V)	2085.045

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
18	18.2	13	2	30.50	6	1.90e+009	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	085-2101.6496.6517.3	3	18.30	13.05	96.4	1.59e+008	(K)ELVFWITKPGFSFDANR(T)	2027.039
2	084-2001.6404.6438.3	3	17.79	13.90	96.4	2.94e+008	(K)ELVFWITKPGFSFDANR(T)	2027.039
3	083-1901.6408.6488.3	3	17.26	12.26	95.7	3.59e+008	(K)ELVFWITKPGFSFDANR(T)	2027.039
4	081-1701.8415.8433.2	2	15.56	10.74	91.9	2.92e+008	(K)ELVFWITKPGFSFDANR(T)	2027.039
5	084-2001.6426.6457.2	2	12.55	12.55	83.5	2.39e+008	(K)ELVFWITKPGFSFDANR(T)	2027.039
6	084-2001.2665.2711.2	2	12.20	6.58	87.6	2.08e+007	(R)HVIYGEWGR(D)	1116.559
7	083-1901.2658.2715.0	2	11.70	6.28	87.4	3.81e+007	(R)HVIYGEWGR(D)	1116.559
8	083-1901.6397.6444.2	2	11.70	11.70	79.4	2.66e+008	(K)ELVFWITKPGFSFDANR(T)	2027.039
9	082-1801.2656.2726.0	2	11.21	6.25	87.8	4.07e+007	(R)HVIYGEWGR(D)	1116.559
10	081-1701.7312.7318.0	2	10.53	3.19	81.6	8.48e+007	(R)HVIYGEWGR(D)	1116.559
11	085-2101.6537.6537.2	2	9.71	9.71	75.2	9.36e+007	(K)ELVFWITKPGFSFDANR(T)	2027.039
12	083-1901.2848.2848.2	2	7.75	7.75	66.0	1.84e+006	(R)HVIYGEWGR(D)	1116.559
13	084-2001.2671.2671.0	2	6.76	3.59	89.3	1.58e+007	(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
19	19.1	11	2	31.78	7	6.58e+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	084-2001.2951.2991.3	3	17.54	13.01	82.9	1.25e+007	(R)AHGGSNAVHFSGGANPAMIAR(A)	2021.973
2	082-1801.2955.2973.0	3	15.29	15.29	82.3	4.52e+006	(R)AHGGSNAVHFSGGANPAMIAR(A)	2021.973
3	083-1901.2956.3009.3	3	14.27	14.27	77.3	1.18e+007	(R)AHGGSNAVHFSGGANPAMIAR(A)	2021.973
4	084-2001.4130.4149.0	3	14.24	8.23	88.4	6.42e+006	(R)QLGMNPGDNHETLIALR(G)	1878.950
5	085-2101.2954.2995.3	3	14.23	10.60	79.8	1.07e+007	(R)AHGGSNAVHFSGGANPAMIAR(A)	2021.973
6	082-1801.4147.4156.0	3	12.59	7.12	81.1	6.20e+006	(R)QLGMNPGDNHETLIALR(G)	1878.950
7	083-1901.4135.4142.0	3	11.41	4.48	78.1	6.40e+006	(R)QLGMNPGDNHETLIALR(G)	1878.950
8	084-2001.2969.2969.2	2	9.34	9.34	94.3	1.57e+006	(R)AHGGSNAVHFSGGANPAMIAR(A)	2021.973
9	085-2101.2972.2972.2	2	8.46	8.46	86.5	2.28e+006	(R)AHGGSNAVHFSGGANPAMIAR(A)	2021.973
10	083-1901.2981.2981.2	2	6.68	6.68	89.0	1.93e+006	(R)AHGGSNAVHFSGGANPAMIAR(A)	2021.973

11	084-2001.2963.2963.2	2	6.45	6.45	82.6	1.49e+006	(R)AHGGSNAVHFSGGANPAMIAR(A)	2021.973

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
20	20.1	10	2	28.96	8	1.01e+009	33117.2	PA_BS12:2189570963	PA_BS12:2189570963 or0232 Uncharacterized protein conserved in bacteria [B. setacea BS12] 320 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	083-1901.6491.6527.0	3	18.79	12.77	95.6	1.35e+008	(K)ELVFWITKPSFNFDSGR(T)	2043.034
2	081-1701.8409.8484.3	3	18.12	13.46	93.0	2.52e+008	(K)ELVFWITKPSFNFDSGR(T)	2043.034
3	084-2001.6495.6499.0	3	17.72	11.61	94.4	9.14e+007	(K)ELVFWITKPSFNFDSGR(T)	2043.034
4	081-1701.7307.7314.2	2	10.17	6.66	86.0	2.92e+007	(R)HVIYSEWGR(D)	1146.570
5	081-1701.8403.8403.0	2	9.83	6.52	75.2	2.01e+008	(K)ELVFWITKPSFNFDSGR(T)	2043.034
6	083-1901.6510.6510.0	2	9.83	9.83	69.2	1.17e+008	(K)ELVFWITKPSFNFDSGR(T)	2043.034
7	081-1701.8397.8397.0	2	9.17	5.41	62.7	1.80e+008	(K)ELVFWITKPSFNFDSGR(T)	2043.034
8	082-1801.2608.2608.0	2	8.81	3.31	89.9	2.13e+006	(R)HVIYSEWGR(D)	1146.570
9	083-1901.2608.2612.0	2	7.82	4.29	91.2	1.69e+006	(R)HVIYSEWGR(D)	1146.570
10	082-1801.2613.2613.0	2	6.90	2.33	94.4	2.15e+006	(R)HVIYSEWGR(D)	1146.570

Group (#)	Subgroup (#)	Spectra (#)	Distinct Peptides (#)	Distinct Summed MS/MS Search Score	% AA Coverage	Total Protein Spectral Intensity	Protein MW (Da)	Database Accession #	Protein Name
21	21.1	20	1	21.88	4	3.97e+009	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	081-1701.10077.10083.0	2	21.88	18.26	98.6	8.28e+008	(R)STSLILQAFTDLVADMR(A)	1880.979
2	082-1801.10718.10722.3	3	20.73	20.73	96.8	1.25e+008	(R)STSLILQAFTDLVADMR(A)	1880.979
3	082-1801.10708.10727.0	2	20.09	20.09	95.3	3.08e+008	(R)STSLILQAFTDLVADMR(A)	1880.979
4	084-2001.11046.11046.0	2	19.96	19.96	95.0	6.90e+007	(R)STSLILQAFTDLVADMR(A)	1880.979
5	083-1901.10767.10772.0	2	19.63	15.93	95.5	1.75e+008	(R)STSLILQAFTDLVADMR(A)	1880.979
6	081-1701.10791.10862.0	2	18.85	18.85	92.6	5.31e+007	(R)STSLILQAFTDLVADMR(A)	1880.979
7	081-1701.10650.10725.0	2	16.09	16.09	81.5	7.95e+007	(R)STSLILQAFTDLVADMR(A)	1880.979
8	082-1801.11030.11068.0	3	15.33	10.81	82.1	3.30e+007	(R)STSLILQAFTDLVADMR(A)	1880.979
9	084-2001.9849.9906.2	2	14.82	14.82	81.7	5.73e+008	(R)STSLILQAFTDLVADMR(A)	1880.979
10	081-1701.10593.10673.2	2	14.65	14.65	79.7	1.20e+008	(R)STSLILQAFTDLVADMR(A)	1880.979
11	081-1701.10737.10743.0	3	13.44	13.44	76.3	2.38e+007	(R)STSLILQAFTDLVADMR(A)	1880.979
12	081-1701.10904.10909.2	2	13.35	13.35	68.7	4.06e+007	(R)STSLILQAFTDLVADMR(A)	1880.979
13	081-1701.10752.10752.0	2	12.94	12.94	77.0	3.85e+007	(R)STSLILQAFTDLVADMR(A)	1880.979
14	082-1801.11024.11024.0	3	11.85	11.85	74.1	2.95e+007	(R)STSLILQAFTDLVADMR(A)	1880.979
15	081-1701.10769.10769.0	2	11.72	11.72	66.3	3.79e+007	(R)STSLILQAFTDLVADMR(A)	1880.979
16	084-2001.10086.10086.0	3	10.96	6.48	89.5	9.18e+007	(R)STSLILQAFTDLVADMR(A)	1880.979
17	081-1701.10554.10554.2	2	10.87	10.87	68.0	2.45e+008	(R)STSLILQAFTDLVADMR(A)	1880.979
18	085-2101.9961.9961.0	2	10.79	10.79	60.2	5.27e+008	(R)STSLILQAFTDLVADMR(A)	1880.979
19	081-1701.10812.10812.0	2	9.67	9.67	71.9	2.39e+007	(R)STSLILQAFTDLVADMR(A)	1880.979

20	085-2101.9946.9946.0	2	8.95	8.95	62.2	5.52e+008	(R)STSLILQAFTDLVADMR(A)	1880.979