Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\091112_OGL_CaecumContentPurifiedFrac50
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 55 **Hits:** 113
beginning to assemble proteins .... proteins assembled 0.017773 sec
proteins filtered by unique peptides 0.001589 sec
proteins filtered by score
calculated protein coverage maps 0.013994 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.000732 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 3 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	39	9	142.23	17	7.42e+010	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding d
1	1.1	38	8	131.23	27	7.42e+010	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (Co
2	2.1	12	7	114.39	20	3.51e+010	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp
2	2.1	12	7	114.39	35	3.51e+010	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [
3	3.1	4	3	43.24	5	9.10e+007	77517.5	PA_BS12:2189568391	PA_BS12:2189568391 or1689 Endoglucanase [B. setacea BS12] 725 bp
3	3.1	4	3	43.24	8	9.10e+007	50621.3	PA_Bse_meta_comb:2073574943	PA_Bse_meta_comb:2073574943 BaSeMet_00185990 Endoglucanase [Bankia setacea microbiome (Co
Totals:	109	37							

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1	1.1	39	9	142.23	17	7.42e+010	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding domain./Cel

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	084-0401.4615.4729.2	2	19.89	12.47	97.9	1.24e+010	(R)EWQDALVDYMVEK(D)	1625.752
2	084-0401.4734.4830.2	2	19.89	12.41	97.7	6.29e+009	(R)EWQDALVDYMVEK(D)	1625.752
3	084-0401.3560.3669.2	2	18.87	18.87	97.7	9.14e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
4	084-0401.7327.7375.0	3	17.91	17.91	88.6	2.28e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
5	084-0401.3429.3551.2	2	17.73	17.73	96.3	1.65e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
6	084-0401.3182.3226.0	3	17.61	8.96	87.0	7.94e+008	(R)AGWDEHFGYLR(D)	1350.623
7	084-0401.7679.7692.0	3	17.61	10.61	91.3	1.11e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
8	084-0401.3079.3175.2	2	17.57	17.57	92.3	2.34e+009	(R)AGWDEHFGYLR(D)	1350.623
9	084-0401.2978.3063.0	3	17.50	9.13	84.8	1.97e+009	(R)AGWDEHFGYLR(D)	1350.623
10	084-0401.5288.5397.0	3	17.49	11.94	89.2	2.94e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
11	084-0401.2977.3064.2	2	17.38	17.38	93.1	1.98e+009	(R)AGWDEHFGYLR(D)	1350.623
12	084-0401.8135.8167.0	3	17.15	9.34	92.6	7.24e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
13	084-0401.3181.3187.2	2	17.01	17.01	90.9	9.48e+008	(R)AGWDEHFGYLR(D)	1350.623
14	084-0401.4764.4764.3	3	16.88	5.62	96.5	2.79e+008	(R)EWQDALVDYMVEK(D)	1625.752
15	084-0401.7212.7296.0	3	16.62	16.62	85.4	3.28e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
16	084-0401.3078.3176.0	3	16.47	7.76	83.3	2.14e+009	(R)AGWDEHFGYLR(D)	1350.623
17	084-0401.10132.10178.0	3	16.39	13.32	88.1	3.49e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
18	084-0401.4637.4717.3	3	16.29	5.93	93.3	6.61e+008	(R)EWQDALVDYMVEK(D)	1625.752
19	084-0401.8497.8502.0	3	15.94	9.13	88.2	8.14e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050

20	084-0401.2906.2960.2	2	15.56	15.56	91.2	2.47e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
21	084-0401.2793.2916.3	3	15.40	8.36	85.2	1.68e+010	(R)AAEQEMWSHITPGVDR(E)	1826.850
22	084-0401.3360.3360.0	3	15.35	6.77	89.8	8.62e+006	(R)AGWDEHFGYLR(D)	1350.623
23	084-0401.10731.10784.0	3	15.29	15.29	81.2	8.53e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
24	084-0401.7796.7802.0	3	15.17	15.17	80.2	6.80e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
25	084-0401.10172.10172.0	3	15.12	10.03	83.3	2.11e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
26	084-0401.2920.2959.3	3	14.82	8.02	83.1	8.19e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
27	084-0401.1375.1474.0	2	14.78	7.13	91.2	2.97e+009	(R)LDANPPYADADR(E)	1317.608
28	084-0401.1477.1558.0	2	14.76	7.13	90.6	2.92e+009	(R)LDANPPYADADR(E)	1317.608
29	084-0401.9006.9006.0	3	14.74	11.37	83.8	3.96e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
30	084-0401.2788.2901.2	2	14.50	8.96	90.1	4.08e+009	(R)AAEQEMWSHITPGVDR(E)	1826.850
31	084-0401.3786.3791.2	2	14.42	7.70	88.4	3.86e+006	(R)EWQDALVDYMVEK(D)	1625.752
32	084-0401.6515.6546.0	3	14.33	14.33	79.3	1.64e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
33	084-0401.8093.8099.0	3	14.20	14.20	78.9	6.12e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
34	084-0401.9313.9372.0	3	13.78	6.96	85.0	4.73e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
35	084-0401.8959.8959.0	3	13.25	13.25	73.3	5.50e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
36	084-0401.10251.10251.0	3	12.15	12.15	72.3	2.43e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
37	084-0401.3367.3367.0	2	12.05	12.05	81.0	6.93e+006	(R)AGWDEHFGYLR(D)	1350.623
38	084-0401.1722.1726.2	2	11.00	6.40	85.2	2.03e+006	(K)NGSVFPVR(C)	875.474
39	084-0401.1174.1180.0	2	9.00	2.25	83.1	5.14e+005	(R)EGYEFTR(E)	901.406

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2	2.1	12	7	114.39	20	3.51e+010	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	MH^+ Matched (Da)
1	084-0401.2836.2938.0	3	19.68	19.68	95.6	1.84e+009	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
2	084-0401.2634.2711.2	2	19.39	10.88	97.2	8.84e+009	(R)IGAIEGPADGDGMGLR(E)	1528.743
3	084-0401.2532.2631.2	2	17.86	9.36	96.4	9.10e+009	(R)IGAIEGPADGDGMGLR(E)	1528.743
4	084-0401.6455.6521.0	3	17.48	14.32	86.7	6.07e+009	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
5	084-0401.7498.7498.2	2	16.78	11.59	75.3	2.36e+009	(R)WFPEAFQTLVENAYPAL(-)	1995.986
6	084-0401.6338.6444.0	3	16.39	8.12	85.3	6.76e+009	(R)YQDEYIAPIAEILSDPAYNNIR(I)	2568.262
7	084-0401.2051.2055.0	3	15.23	9.32	82.0	8.83e+006	(R)YADEGSGIMTGAMDNAPHAGR(W)	2120.913
8	084-0401.7529.7529.0	3	13.93	13.93	82.3	1.85e+007	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
9	084-0401.3372.3372.0	3	12.73	12.73	73.3	7.64e+006	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198
10	084-0401.7563.7595.0	3	11.90	6.15	70.4	4.58e+007	(R)EHLDETLAQGANLFMFVVYDLPNR(D)	2792.372
11	084-0401.10679.10679.0	3	10.28	5.84	73.4	7.25e+006	(K)SSDFYEFNSYLDELSFVQDWR(S)	2647.163
12	084-0401.3823.3823.0	3	9.29	9.29	72.2	6.54e+006	(R)NGWGGAARPSGASSSDDLETYVNESR(V)	2683.198

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	4	3	43.24	5	9.10e+007	77517.5	PA_BS12:2189568391	PA_BS12:2189568391 or1689 Endoglucanase [B. setacea BS12] 725 bp

MH^+

#	Filename	z	Score	Fwd-Rev Score	SPI (%)	Spectrum Intensity	Sequence	Matched (Da)
1	084-0401.3737.3741.2	2	16.06	12.42	88.8	2.39e+007	(R)DNESGWGEWGGFDER(K)	1740.689
2	084-0401.1746.1808.0	3	15.54	6.42	91.2	6.68e+006	(R)LDARPPYVDADR(D)	1387.697
3	084-0401.1780.1791.0	3	14.48	5.85	88.8	5.75e+006	(R)LDARPPYVDADR(D)	1387.697
4	084-0401.2974.2984.0	2	11.64	4.34	81.2	5.47e+007	(R)TIQQTMDEITAR(G)	1406.695