Spectrum Mill - Protein Peptide/Summary

Results Shown Filtered by Validation Category: valid
Data Directory: msdataSM\051111_OGL_BS21_5fracs
hit table read - SpecFeatures read
valid hits read from tagSummary file - **Files:** 671 **Hits:** 1391
beginning to assemble proteins .... proteins assembled 0.226612 sec
proteins filtered by unique peptides 0.023152 sec
proteins filtered by score
calculated protein coverage maps 0.081404 sec
beginning to roll up proteins into groups ... . proteins rolled up into groups 0.013288 sec
protein groups ready for display
proteinGroupingMethod: oneSharedPeptideSubgrouped 22 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	298	14	248.28	31	3.00e+011	77520.7	PA_Bse02:2503999400	PA_Bse02:2503999400 BS02DRAFT_00002970 Cellulose or protein binding domain./Cellulose binding (
1	1.1	298	14	248.28	52	3.00e+011	48452.4	PA_Bse_meta_comb:2073585167	PA_Bse_meta_comb:2073585167 BaSeMet_00288230 Endoglucanase [Bankia setacea microbiome (Co
2	2.1	53	10	176.20	26	2.63e+009	80610.8	PA_BS12:2189571642	PA_BS12:2189571642 or0735 Carbohydrate binding domain. [B. setacea BS12] 763 bp
2	2.1	53	10	176.20	57	2.63e+009	37625.9	PA_Bse_meta_comb:2073592708	PA_Bse_meta_comb:2073592708 BaSeMet_00363640 hypothetical protein [Bankia setacea microbiome
2	2.2	20	6	105.10	13	2.67e+009	112354.2	PA_Bse_meta_comb:2073560170	PA_Bse_meta_comb:2073560170 BaSeMet_00038260 esterase, PHB depolymerase family [Bankia seta
2	2.2	20	6	105.10	13	2.67e+009	112173.0	PA_Bse02:2503998147	PA_Bse02:2503998147 BS02DRAFT_00013240 esterase, PHB depolymerase family [B. setacea BS02 (
3	3.1	112	9	168.34	26	2.23e+011	73729.2	PA_BS12:2189570195	PA_BS12:2189570195 or3426 Cellobiohydrolase A (1,4-beta-cellobiosidase A) [B. setacea BS12] 709 bp
3	3.1	112	9	168.34	45	2.23e+011	44290.5	PA_Bse_meta_comb:2073567998	PA_Bse_meta_comb:2073567998 BaSeMet_00116540 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
4	4.1	25	9	130.19	16	2.37e+009	112508.2	PA_Bse_meta_comb:2073561919	PA_Bse_meta_comb:2073561919 BaSeMet_00055750 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
4	4.1	21	8	114.65	14	1.73e+009	113016.6	PA_Bse02:2503999098	PA_Bse02:2503999098 BS02DRAFT_00001060 Cellulose or protein binding domain./Glycosyl hydrolase
4	4.2	24	8	118.10	40	3.94e+009	43960.4	PA_Bse_meta_comb:2073561917	PA_Bse_meta_comb:2073561917 BaSeMet_00055730 Cellobiohydrolase A (1,4-beta-cellobiosidase A)
4	4.2	7	3	41.30	13	7.96e+008	38604.4	PA_Bse02:2503998988	PA_Bse02:2503998988 BS02DRAFT_00026880 Cellulose or protein binding domain./Cellulose binding (
4	4.3	5	2	27.10	9	1.20e+008	43875.0	PA_Bse08:2503995778	PA_Bse08:2503995778 Cellulose or protein binding domain./Cellulase (glycosyl hydrolase family 5). [B. s
5	5.1	32	6	115.23	8	6.94e+009	104392.5	PA_BS12:2189569647	PA_BS12:2189569647 or2953 Beta-1,4-xylanase [B. setacea BS12] 986 bp
6	6.1	6	4	73.43	17	1.33e+009	56911.4	PA_Bse08:2503996762	PA_Bse08:2503996762 BS08DRAFT_00004980 esterase, PHB depolymerase family [B. setacea BS08 (
7	7.1	9	5	69.54	11	4.83e+008	77470.6	PA_Bse08:2503996278	PA_Bse08:2503996278 BS08DRAFT_00001670 Cellulose or protein binding domain./Cellulose binding (
8	8.1	7	4	51.64	9	2.93e+008	74714.6	PA_Bse08:2503995453	PA_Bse08:2503995453 BS08DRAFT_00039170 Cellulose or protein binding domain./Cellulose binding (
9	9.1	15	3	39.05	10	2.10e+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	15	3	39.05	11	2.10e+008	52443.2	PA_Bse_meta_comb:2073587378	PA_Bse_meta_comb:2073587378 BaSeMet_00310340 Cobalamin biosynthesis protein CobN and relate
10	10.1	12	2	33.87	41	1.57e+009	13375.7	PA_Bse_meta_comb:2073565643	PA_Bse_meta_comb:2073565643 BaSeMet_00092990 Histone H2A [Bankia setacea microbiome (Coml
11	11.1	7	3	33.14	5	1.62e+008	73439.4	PA_Bse08:2503994248	PA_Bse08:2503994248 BS08DRAFT_00028400 Cellulose or protein binding domain./Chitin binding dom
12	12.1	12	2	33.12	6	1.73e+009	42518.1	PA_Bse02:2503998249	PA_Bse02:2503998249 BS02DRAFT_00014250 Cellulose or protein binding domain./Chitin binding dom
12	12.1	12	2	33.12	6	1.73e+009	42082.7	PA_Bse_meta_comb:2073581124	PA_Bse_meta_comb:2073581124 BaSeMet_00247800 Uncharacterized protein conserved in bacteria [B
12	12.2	13	2	31.12	6	1.36e+009	39939.7	PA_BS12:2189570962	PA_BS12:2189570962 or0231 Uncharacterized protein conserved in bacteria [B. setacea BS12] 383 bp
13	13.1	12	2	31.89	4	2.70e+008	70938.0	PA_Bse02:2504000681	PA_Bse02:2504000681 BS02DRAFT_00022770 Cellulose or protein binding domain./Glycosyl hydrolase
13	13.1	12	2	31.89	4	2.70e+008	70884.2	PA_Bse08:2503997525	PA_Bse08:2503997525 BS08DRAFT_00020200 Cellulose or protein binding domain./Glycosyl hydrolase
14	14.1	6	2	28.54	7	3.73e+007	55060.3	PA_BS12:2189568352	PA_BS12:2189568352 or0169 Cellulose or protein binding domain./Cellulose binding domain. [B. setace
15	15.1	2	2	27.49	7	1.10e+008	46154.6	PA_Bse02:2503998146	PA_Bse02:2503998146 BS02DRAFT_00013230 Glycosyl hydrolase family 10. [B. setacea BS02 (Isolate
15	15.1	2	2	27.49	7	1.10e+008	46141.6	PA_Bse_meta_comb:2073560169	PA_Bse_meta_comb:2073560169 BaSeMet_00038250 Beta-1,4-xylanase [Bankia setacea microbiome (
16	16.1	4	2	25.13	1	9.92e+007	224278.3	PA_BS12:2189569050	PA_BS12:2189569050 or2363 Gluconolactonase [B. setacea BS12] 2124 bp
16	16.1	4	2	25.13	1	9.92e+007	223963.9	PA_Bse_meta_comb:2073579605	PA_Bse_meta_comb:2073579605 BaSeMet_00232610 Gluconolactonase [Bankia setacea microbiome (
17	17.1	3	2	22.19	3	6.15e+007	77941.2	PA_BS12:2189569979	PA_BS12:2189569979 or3290 Glycosyl hydrolase family 9./Cellulose or protein binding domain./N-termi
17	17.1	3	2	22.19	3	6.15e+007	77103.2	PA_Bse_meta_comb:2073565540	PA_Bse_meta_comb:2073565540 BaSeMet_00091960 cellulose 1,4-beta-cellobiosidase (EC 3.2.1.91) [
18	18.1	15	1	20.74	4	5.60e+009	43475.8	PA_BS12:2189567935	PA_BS12:2189567935 or1258 Lysophospholipase L1 and related esterases [B. setacea BS12] 419 bp
18	18.1	15	1	20.74	4	5.60e+009	42177.2	PA_Bse_meta_comb:2073563649	PA_Bse_meta_comb:2073563649 BaSeMet_00073050 Predicted solute binding protein [Bankia setacea

Totals: 1266 164

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	298	14	248.28	31	3.00e+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	086-2101.7486.7543.0	3	21.27	21.27	96.1	8.87e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
2	087-2201.5116.5224.0	3	20.69	13.45	94.8	1.32e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
3	086-2101.5140.5254.3	3	20.68	15.96	94.4	1.58e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
4	085-2001.5179.5233.0	3	20.67	17.48	94.8	3.45e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
5	085-2001.8804.8919.0	3	20.61	20.61	95.8	5.43e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
6	087-2201.5391.5391.0	3	20.40	10.14	98.5	3.21e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
7	087-2201.6029.6084.0	3	20.33	12.79	96.7	8.18e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
8	085-2001.5360.5405.0	3	19.88	10.58	98.2	9.73e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
9	085-2001.5084.5190.4	4	19.59	10.85	91.3	2.81e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
10	086-2101.9248.9302.0	3	19.56	19.56	94.3	8.61e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
11	085-2001.6019.6117.2	2	19.39	15.04	90.6	2.60e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
12	085-2001.8021.8097.3	3	19.28	10.99	95.2	3.76e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
13	086-2101.5407.5462.0	3	19.26	11.08	96.5	6.75e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
14	085-2001.8533.8606.3	3	19.18	15.24	93.8	4.79e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
15	085-2001.8052.8159.2	2	19.05	14.10	93.0	6.43e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
16	087-2201.5244.5251.0	3	19.05	19.05	92.8	8.34e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
17	085-2001.6007.6105.3	3	18.97	12.27	90.0	3.13e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
18	085-2001.6851.6972.3	3	18.72	12.42	94.2	1.62e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
19	083-1801.4979.5013.0	3	18.62	12.92	84.9	7.69e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
20	086-2101.11446.11482.0	2	18.61	13.95	93.4	2.42e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
21	084-1901.5279.5286.0	3	18.47	18.47	91.6	7.96e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
22	085-2001.11437.11476.0	2	18.42	13.54	91.0	3.87e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
23	086-2101.5668.5690.2	2	18.35	10.18	96.9	6.15e+008	(R)EWQDALVDYMVEK(D)	1625.752
24	085-2001.7254.7272.3	3	18.28	18.28	91.0	3.72e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
25	085-2001.11888.11968.2	2	18.23	13.09	95.4	3.37e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
26	085-2001.4190.4318.2	2	18.23	18.23	95.6	1.57e+009	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
27	083-1801.5916.6014.0	3	18.15	11.75	92.6	1.32e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
28	085-2001.8173.8245.0	3	18.13	14.89	92.2	2.82e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
29	086-2101.8159.8193.3	3	18.13	13.42	92.0	1.56e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
30	085-2001.7686.7692.0	3	18.12	10.13	92.6	2.15e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
31	087-2201.6271.6328.3	3	18.12	11.05	91.9	1.74e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
32	085-2001.5680.5685.0	3	18.11	10.77	95.2	2.31e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
33	085-2001.6128.6186.0	2	18.11	13.80	93.8	2.50e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
34	085-2001.7851.7927.0	3	18.06	13.85	90.9	3.34e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
35	085-2001.10838.10967.3	3	18.02	14.23	89.0	1.95e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
36	087-2201.4372.4461.2	2	18.01	18.01	92.5	1.56e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
37	087-2201.9370.9498.3	3	17.84	14.68	88.8	2.64e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
38	087-2201.10018.10137.0	3	17.79	17.79	79.4	1.17e+009	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843

39	086-2101.7056.7155.2	2	17.76	13.92	89.3	4.58e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
40	085-2001.8532.8636.0	2	17.67	11.49	94.4	7.24e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
41	085-2001.4327.4439.2	2	17.66	17.66	94.7	9.40e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
42	086-2101.3813.3879.3	3	17.66	10.13	93.6	2.38e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
43	087-2201.5612.5636.2	2	17.64	10.82	93.5	3.34e+008	(R)EWQDALVDYMVEK(D)	1625.752
44	085-2001.7162.7258.3	3	17.63	10.50	92.2	1.28e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
45	085-2001.8677.8768.0	3	17.63	17.63	88.8	4.65e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
46	085-2001.4791.4797.0	3	17.62	10.04	95.1	1.09e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
47	087-2201.12052.12086.0	3	17.61	14.10	92.0	2.74e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
48	085-2001.9998.10060.0	3	17.60	11.85	91.6	3.44e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
49	083-1801.6032.6092.0	3	17.59	12.04	91.8	5.95e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
50	085-2001.10253.10339.0	3	17.58	12.32	91.5	1.19e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
51	086-2101.10237.10315.0	3	17.58	12.47	91.6	1.24e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
52	086-2101.4394.4467.2	2	17.55	17.55	92.8	2.37e+008	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
53	085-2001.7420.7475.3	3	17.53	11.76	90.4	6.07e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
54	087-2201.11690.11774.2	2	17.49	12.41	92.5	3.88e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
55	085-2001.11335.11427.2	2	17.44	10.73	90.7	3.55e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
56	083-1801.6824.6829.0	3	17.33	17.33	89.5	5.54e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
57	085-2001.7397.7413.0	2	17.32	13.20	89.8	6.49e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
58	087-2201.5753.5837.3	3	17.20	10.61	89.0	4.95e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
59	085-2001.5067.5169.3	3	17.18	10.34	72.7	3.75e+009	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
60	086-2101.11574.11665.2	2	17.15	17.15	92.3	1.18e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
61	085-2001.6734.6834.3	3	17.09	11.08	91.1	1.57e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
62	085-2001.4312.4431.3	3	17.07	9.42	92.5	1.06e+010	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
63	083-1801.6434.6456.0	3	17.01	12.12	88.9	2.84e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
64	085-2001.6338.6338.2	2	17.01	12.13	74.2	5.70e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
65	086-2101.12036.12063.0	3	17.01	12.42	90.2	6.53e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
66	083-1801.6685.6725.0	3	16.91	9.81	86.2	2.65e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
67	085-2001.6026.6127.0	3	16.88	10.02	89.2	3.66e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
68	085-2001.7637.7642.2	2	16.85	16.85	89.6	3.24e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
69	087-2201.11366.11366.0	3	16.82	16.82	85.0	2.13e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
70	085-2001.8034.8038.0	3	16.73	16.73	89.7	5.17e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
71	085-2001.9709.9839.3	3	16.65	12.52	85.9	3.41e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
72	083-1801.8746.8835.0	3	16.61	12.52	85.5	3.96e+009	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
73	086-2101.9927.9977.0	3	16.59	9.58	91.4	1.52e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
74	085-2001.5232.5311.0	3	16.56	8.52	93.1	7.09e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
75	083-1801.6123.6188.0	3	16.55	11.31	91.1	4.39e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
76	085-2001.11800.11819.0	3	16.54	12.13	89.2	8.74e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
77	086-2101.6039.6124.3	3	16.54	9.41	91.4	1.61e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
78	086-2101.6958.7019.3	3	16.53	16.53	87.4	5.22e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
79	085-2001.7920.8020.0	3	16.50	16.50	87.2	8.65e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
80	083-1801.6612.6625.3	3	16.48	16.48	87.3	1.03e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
81	085-2001.7037.7152.3	3	16.46	9.49	89.3	1.49e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
82	085-2001.5596.5608.2	2	16.45	9.11	90.3	8.22e+008	(R)EWQDALVDYMVEK(D)	1625.752
83	085-2001.3405.3454.0	3	16.43	7.47	96.7	9.70e+006	(R)LDANPPYADADREGYEFTR(E)	2199.995
84	085-2001.6110.6185.3	3	16.43	9.58	89.2	4.49e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
85	087-2201.11368.11453.3	3	16.40	10.23	85.9	6.67e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
86	087-2201.11588.11594.0	3	16.37	16.37	81.4	3.15e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843

87	086-2101.11592.11679.2	2	16.35	12.11	89.8	2.93e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
88	085-2001.11407.11503.3	3	16.31	10.59	84.6	1.76e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
89	086-2101.11206.11277.2	2	16.31	11.50	89.3	2.91e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
90	085-2001.3676.3736.2	2	16.26	16.26	94.1	2.17e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
91	084-1901.6120.6126.2	2	16.16	12.59	87.5	1.75e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
92	086-2101.11301.11391.2	2	16.08	10.88	93.7	3.81e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
93	085-2001.5878.5914.0	3	16.05	7.90	92.3	2.18e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
94	087-2201.4683.4696.0	3	16.05	6.42	92.3	7.92e+006	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
95	086-2101.6072.6144.2	2	16.03	11.77	85.8	1.43e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
96	086-2101.8114.8171.0	3	16.00	10.62	84.0	4.89e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
97	083-1801.5748.5791.2	2	15.99	11.81	84.6	1.10e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
98	085-2001.9987.9996.0	2	15.98	11.30	90.9	2.42e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
99	085-2001.3984.4031.2	2	15.95	15.95	89.8	3.04e+007	(R)AGWDEHFGYLR(D)	1350.623
100	086-2101.9114.9114.0	3	15.91	10.04	88.2	4.75e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
101	087-2201.3803.3843.2	2	15.90	15.90	91.9	1.99e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
102	085-2001.7039.7039.0	2	15.89	11.81	84.2	7.46e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
103	085-2001.10167.10217.0	2	15.87	12.49	91.0	1.75e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
104	086-2101.3827.3880.2	2	15.86	15.86	92.6	4.56e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
105	085-2001.5731.5787.2	2	15.84	9.07	91.4	8.89e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
106	083-1801.6737.6737.0	3	15.77	15.77	75.4	9.84e+006	(R)AGWDEHFGYLRDQGYAMVIGEFGGNMDWPNGTR(A)	3746.655
107	083-1801.7221.7221.0	3	15.75	11.17	85.4	1.60e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
108	085-2001.7023.7136.3	3	15.75	15.75	84.4	1.15e+010	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
109	087-2201.5201.5220.2	2	15.75	15.75	92.5	8.64e+007	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
110	083-1801.5351.5375.2	2	15.73	9.11	85.2	5.98e+007	(R)EWQDALVDYMVEK(D)	1625.752
111	085-2001.3842.3873.2	2	15.73	15.73	90.9	6.66e+008	(R)AGWDEHFGYLR(D)	1350.623
112	084-1901.7030.7058.0	3	15.69	10.02	76.3	1.79e+008	(R)AGWDEHFGYLRDQGYAMVIGEFGGNMDWPNGTR(A)	3746.655
113	086-2101.11685.11685.0	2	15.69	15.69	87.5	1.68e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
114	086-2101.4010.4050.2	2	15.68	15.68	90.5	1.26e+008	(R)AGWDEHFGYLR(D)	1350.623
115	083-1801.7024.7040.0	3	15.65	12.52	84.4	1.67e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
116	085-2001.11847.11852.0	2	15.51	10.53	88.9	1.02e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
117	085-2001.5720.5786.3	3	15.47	10.51	83.9	1.94e+009	(R)TIQQTMTEITAQGINVVR(L)	2003.060
118	085-2001.9991.9991.0	2	15.47	11.12	91.0	2.61e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
119	085-2001.10266.10313.0	3	15.42	15.42	85.8	1.49e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
120	086-2101.8658.8665.0	3	15.37	9.66	87.6	1.12e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
121	087-2201.10322.10416.0	3	15.36	10.61	79.3	1.04e+009	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
122	085-2001.3664.3735.3	3	15.34	9.48	84.8	7.37e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
123	086-2101.8049.8162.0	3	15.32	15.32	84.6	5.11e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
124	086-2101.6137.6233.3	3	15.31	9.06	85.7	2.50e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
125	085-2001.11629.11675.2	2	15.29	15.29	85.9	1.25e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
126	085-2001.9420.9420.5	5	15.29	15.29	76.4	4.42e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
127	084-1901.3913.3940.0	3	15.27	8.40	83.1	1.34e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
128	086-2101.7615.7615.2	2	15.25	11.07	85.0	1.43e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
129	083-1801.6585.6658.3	3	15.23	15.23	84.7	1.12e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
130	085-2001.10113.10179.0	2	15.19	15.19	82.9	2.25e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
131	087-2201.11340.11433.2	2	15.18	10.90	87.5	2.66e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
132	087-2201.10706.10797.0	3	15.08	11.43	80.9	8.49e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
133	085-2001.5900.5905.0	3	14.91	7.49	81.6	4.39e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
134	085-2001.7839.7861.2	2	14.90	9.56	83.6	3.21e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050

135	083-1801.5506.5524.2	2	14.85	14.85	78.7	4.55e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
136	085-2001.9315.9442.3	3	14.84	8.24	70.1	4.15e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
137	083-1801.5491.5532.3	3	14.80	9.61	84.0	9.82e+007	(R)TIQQTMTEITAQGINVVR(L)	2003.060
138	085-2001.8183.8183.0	2	14.80	9.86	89.2	2.13e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
139	086-2101.7077.7146.0	3	14.78	8.45	85.8	4.11e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
140	085-2001.6235.6323.0	2	14.77	14.77	71.7	1.61e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
141	086-2101.11616.11695.0	3	14.76	10.42	83.3	9.63e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
142	087-2201.6457.6540.2	2	14.74	8.41	80.9	1.55e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
143	083-1801.7026.7026.0	3	14.70	14.70	75.0	3.58e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
144	086-2101.11279.11352.2	2	14.64	14.64	83.0	1.30e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
145	085-2001.8099.8192.2	2	14.57	14.57	82.4	3.05e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
146	086-2101.11643.11649.0	3	14.57	14.57	73.6	3.40e+008	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
147	086-2101.7591.7664.2	2	14.57	10.98	87.8	2.50e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
148	083-1801.5709.5790.3	3	14.56	7.46	82.5	2.09e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
149	084-1901.5495.5500.0	3	14.56	6.51	85.3	8.19e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
150	086-2101.5791.5849.3	3	14.53	9.37	84.0	9.70e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
151	085-2001.6234.6321.3	3	14.52	8.41	80.7	2.58e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
152	085-2001.7396.7498.3	3	14.51	14.51	81.1	3.18e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
153	086-2101.9829.9935.0	3	14.50	10.27	74.3	1.48e+010	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
154	085-2001.11740.11787.0	2	14.41	14.41	87.6	1.44e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
155	085-2001.2177.2196.2	2	14.35	8.02	93.8	8.37e+006	(R)LDANPPYADADR(E)	1317.608
156	087-2201.8174.8174.3	3	14.34	14.34	79.6	9.71e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
157	085-2001.12225.12242.0	3	14.33	10.07	86.1	7.60e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
158	085-2001.10045.10063.2	2	14.31	14.31	85.7	9.88e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
159	085-2001.6877.6965.0	2	14.19	9.79	71.0	1.47e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
160	085-2001.8883.8982.0	3	14.10	8.22	80.6	3.50e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
161	084-1901.7193.7240.3	3	14.07	14.07	82.4	5.65e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
162	087-2201.6588.6588.0	2	14.04	10.64	79.6	1.46e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
163	087-2201.6910.6955.2	2	14.04	7.55	72.6	9.25e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
164	087-2201.3814.3814.2	2	13.99	13.99	89.3	1.97e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
165	087-2201.5775.5832.2	2	13.96	10.10	88.0	2.22e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
166	086-2101.6572.6609.2	2	13.86	10.24	75.2	2.60e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
167	084-1901.5810.5816.2	2	13.83	13.83	77.7	3.06e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060
168	086-2101.11680.11680.0	2	13.81	13.81	83.7	5.87e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
169	086-2101.7347.7363.2	2	13.81	10.10	83.6	1.74e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
170	085-2001.8567.8667.2	2	13.78	13.78	73.7	3.94e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
171	086-2101.6489.6578.3	3	13.69	7.84	83.2	2.65e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
172	085-2001.6892.7014.3	3	13.68	13.68	76.3	1.22e+010	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
173	086-2101.6395.6429.0	2	13.66	13.66	70.0	2.59e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
174	087-2201.7011.7016.0	2	13.65	9.07	88.4	1.13e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
175	087-2201.3791.3842.3	3	13.64	8.68	80.8	1.31e+008	(R)AAEQEMWSHITPGVDR(E)	1826.850
176	084-1901.6811.6811.0	3	13.63	13.63	77.6	1.90e+008	(R)AAEQEMWSHITPGVDREWQDALVDYMVEK(D)	3433.583
177	083-1801.7195.7214.0	3	13.45	13.45	79.3	1.92e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
178	083-1801.8215.8215.0	3	13.45	13.45	85.7	1.19e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
179	085-2001.10035.10102.0	3	13.44	13.44	80.6	3.68e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
180	083-1801.6446.6446.0	3	13.42	13.42	79.5	2.27e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
181	083-1801.7889.7889.0	3	13.42	8.29	78.9	1.20e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
182	086-2101.5798.5850.2	2	13.39	13.39	83.4	3.94e+008	(R)TIQQTMTEITAQGINVVR(L)	2003.060

183	086-2101.8229.8255.0	2	13.38	9.92	85.2	1.52e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
184	086-2101.9277.9277.0	2	13.37	9.78	82.3	7.40e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
185	083-1801.5168.5168.0	3	13.26	7.09	80.6	1.44e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
186	086-2101.7671.7755.0	3	13.14	8.87	81.0	1.29e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
187	086-2101.7927.7939.0	3	13.02	13.02	76.1	1.65e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
188	085-2001.7493.7499.2	2	12.82	7.20	60.2	7.77e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
189	083-1801.6077.6120.2	2	12.80	12.80	76.5	1.97e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
190	087-2201.6009.6009.2	2	12.78	8.92	85.8	3.51e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
191	085-2001.6652.6706.0	2	12.77	12.77	66.8	7.93e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
192	085-2001.11681.11688.0	2	12.73	9.40	82.8	2.04e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
193	086-2101.8803.8803.0	2	12.73	12.73	88.4	9.97e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
194	086-2101.6960.6960.0	3	12.72	12.72	75.6	3.07e+009	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
195	085-2001.11402.11406.0	2	12.66	12.66	82.1	1.11e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
196	086-2101.5230.5232.2	2	12.61	5.46	88.7	1.02e+008	(R)LPIAPQTLDPNDPQGIGDIQNGGVLK(N)	2670.410
197	085-2001.6622.6728.3	3	12.56	7.01	76.6	1.38e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
198	085-2001.6502.6508.3	3	12.51	6.53	80.0	6.31e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
199	086-2101.9301.9301.2	2	12.50	7.43	82.1	7.17e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
200	087-2201.6329.6346.0	2	12.46	8.68	78.2	1.02e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
201	085-2001.6503.6509.0	2	12.29	9.07	61.4	4.09e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
202	086-2101.7659.7659.2	2	12.20	12.20	80.5	1.45e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
203	086-2101.10248.10248.0	3	12.19	12.19	70.9	1.20e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
204	087-2201.10164.10289.0	3	12.13	12.13	73.1	1.24e+009	(R)EIAGLPAQLGVDNIIGIDIFNEPWDYTWQEWK(T)	3730.843
205	084-1901.7206.7273.2	2	12.10	12.10	66.2	2.09e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
206	084-1901.5509.5509.0	3	12.01	12.01	70.5	8.01e+007	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
207	085-2001.5999.5999.0	3	12.01	12.01	75.5	1.62e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
208	085-2001.10202.10202.0	2	11.88	8.33	77.7	1.45e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
209	087-2201.11439.11439.0	2	11.81	11.81	75.8	1.32e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
210	087-2201.7369.7369.0	3	11.79	11.79	71.7	2.98e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
211	085-2001.11990.11990.0	2	11.75	11.75	76.9	3.28e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
212	086-2101.8838.8838.0	2	11.60	11.60	77.1	8.08e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
213	083-1801.6186.6186.0	2	11.55	7.49	79.2	1.20e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
214	087-2201.5374.5374.0	3	11.53	11.53	72.3	2.97e+008	(R)QFMDPSQSECTDLEGDAAGNADCNVVINPTVLR(A)	3509.562
215	085-2001.7175.7239.2	2	11.52	11.52	61.8	1.03e+009	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
216	087-2201.3985.4045.2	2	11.42	11.42	77.3	2.78e+007	(R)AGWDEHFGYLR(D)	1350.623
217	085-2001.9135.9135.0	2	11.41	11.41	78.1	2.08e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
218	086-2101.11364.11364.2	2	11.35	11.35	71.6	7.02e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
219	083-1801.6160.6160.2	2	11.34	8.04	78.3	1.26e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
220	085-2001.3851.3857.1	1	11.34	5.62	87.2	2.56e+008	(R)AGWDEHFGYLR(D)	1350.623
221	085-2001.9086.9105.2	2	11.31	6.83	81.4	2.29e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
222	085-2001.9146.9146.0	2	11.25	11.25	75.8	1.42e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
223	085-2001.8215.8220.2	2	11.17	11.17	63.3	1.61e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
224	087-2201.12088.12088.0	3	11.12	11.12	71.0	1.39e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
225	085-2001.8619.8619.0	2	11.09	11.09	72.6	1.98e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
226	085-2001.8527.8638.0	3	11.08	11.08	73.5	9.31e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
227	087-2201.11532.11532.0	2	11.07	11.07	79.0	1.66e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
228	086-2101.11262.11262.0	2	11.01	11.01	70.5	8.43e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
229	086-2101.3829.3829.2	2	11.01	11.01	92.8	4.20e+007	(R)AAEQEMWSHITPGVDR(E)	1826.850
230	086-2101.11338.11338.0	2	10.94	10.94	78.1	8.41e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211

231	086-2101.9077.9077.0	2	10.88	7.06	71.7	8.02e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
232	087-2201.12093.12093.0	3	10.87	10.87	73.8	1.26e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
233	086-2101.11307.11307.2	2	10.82	10.82	75.4	8.35e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
234	087-2201.11357.11357.0	2	10.70	10.70	68.4	4.99e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
235	086-2101.8654.8654.0	2	10.68	10.68	73.4	7.57e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
236	087-2201.11537.11537.0	2	10.67	10.67	74.4	1.49e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
237	086-2101.8320.8384.2	2	10.60	10.60	73.1	1.77e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
238	085-2001.8802.8802.0	2	10.58	10.58	76.6	3.39e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
239	087-2201.7250.7250.2	2	10.56	10.56	72.1	9.23e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
240	087-2201.11332.11332.0	2	10.47	10.47	68.9	1.40e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
241	086-2101.8640.8659.2	2	10.41	7.32	81.9	1.75e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
242	083-1801.10247.10247.0	2	10.39	10.39	74.0	3.80e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
243	086-2101.7600.7600.2	2	10.05	10.05	74.7	1.51e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
244	085-2001.4016.4016.0	3	9.89	4.64	75.8	3.09e+006	(R)AAEQEMWSHITPGVDR(E)	1826.850
245	085-2001.8797.8797.0	2	9.87	9.87	65.8	3.69e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
246	085-2001.4596.4646.2	2	9.85	9.85	76.2	3.01e+007	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
247	087-2201.11381.11381.0	2	9.80	9.80	73.9	5.67e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
248	086-2101.9063.9063.0	2	9.78	6.39	73.4	8.26e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
249	084-1901.11195.11195.0	2	9.76	9.76	70.5	4.30e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
250	083-1801.7393.7393.0	3	9.59	9.59	71.4	2.55e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
251	086-2101.7800.7839.2	2	9.46	9.46	63.4	1.41e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
252	083-1801.9995.9995.0	2	9.40	9.40	67.4	3.32e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
253	086-2101.4900.4900.0	3	9.35	4.02	86.0	5.44e+006	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
254	085-2001.10146.10165.2	2	9.29	9.29	68.8	6.35e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
255	086-2101.8858.8858.0	2	9.29	9.29	71.5	7.28e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
256	083-1801.5727.5727.0	2	9.26	9.26	71.7	3.64e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
257	085-2001.11872.11872.0	3	9.26	9.26	72.2	7.43e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
258	086-2101.11424.11424.0	2	9.25	9.25	63.5	7.07e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
259	085-2001.9129.9129.0	2	9.15	9.15	72.3	1.89e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
260	084-1901.11057.11057.0	2	9.13	5.79	65.2	4.37e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
261	086-2101.9048.9048.0	2	9.13	9.13	69.5	8.45e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
262	086-2101.11188.11188.0	2	9.02	9.02	69.5	8.63e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
263	084-1901.3927.3927.2	2	8.91	8.91	70.6	5.18e+006	(R)AAEQEMWSHITPGVDR(E)	1826.850
264	085-2001.8813.8813.0	2	8.89	3.21	89.1	3.45e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
265	084-1901.10853.10853.0	2	8.83	5.81	74.5	5.69e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
266	087-2201.11636.11636.2	2	8.82	8.82	68.8	1.52e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
267	085-2001.8596.8608.2	2	8.77	8.77	69.3	2.06e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
268	085-2001.9109.9109.0	2	8.77	8.77	70.0	1.29e+008	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
269	084-1901.11227.11227.0	2	8.66	8.66	66.7	2.83e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
270	086-2101.11197.11197.0	2	8.56	5.45	69.4	9.24e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
271	086-2101.9282.9282.0	2	8.56	8.56	68.3	7.04e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
272	087-2201.7552.7552.0	2	8.51	8.51	67.1	7.59e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
273	083-1801.10306.10306.0	2	8.49	8.49	84.1	4.73e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
274	086-2101.9951.9951.0	2	8.42	8.42	61.4	1.28e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
275	086-2101.7905.7905.0	2	8.41	8.41	60.8	1.38e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
276	084-1901.11222.11222.0	2	8.40	8.40	69.4	2.71e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
277	087-2201.11556.11556.0	2	8.32	8.32	61.1	5.69e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
278	084-1901.3933.3933.2	2	8.23	8.23	65.0	5.30e+006	(R)AAEQEMWSHITPGVDR(E)	1826.850

279	085-2001.12261.12261.2	2	8.17	8.17	61.7	5.37e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
280	085-2001.11252.11252.0	2	7.96	7.96	67.1	8.94e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
281	087-2201.6007.6007.0	2	7.76	3.38	69.8	3.04e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
282	086-2101.8453.8453.0	2	7.66	7.66	66.8	8.91e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
283	086-2101.11764.11764.0	2	7.45	7.45	67.0	5.51e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
284	086-2101.8757.8757.0	2	7.36	7.36	65.8	1.12e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
285	084-1901.11173.11173.0	2	7.30	7.30	62.0	3.14e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
286	085-2001.10412.10412.2	2	7.17	7.17	62.7	1.84e+007	(K)DADNNADGAPLELYVGNMWWADTGR(T)	2751.211
287	083-1801.6232.6232.2	2	7.09	7.09	60.5	1.09e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
288	086-2101.11199.11199.0	2	6.91	6.91	64.5	9.24e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
289	087-2201.11769.11769.0	2	6.91	6.91	64.8	2.06e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
290	085-2001.4822.4822.2	2	6.85	6.85	68.4	5.92e+006	(R)LVLSPHTYGPSVFVQR(Q)	1799.981
291	086-2101.7819.7819.0	2	6.74	6.74	65.8	1.61e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
292	086-2101.8786.8786.0	2	6.61	3.08	83.0	1.22e+008	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
293	086-2101.9086.9086.0	2	6.56	6.56	64.6	8.33e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
294	083-1801.9904.9904.0	2	6.49	6.49	65.0	2.88e+007	(R)DQGYAMVIGEFGGNMDWPNGTR(A)	2415.050
295	085-2001.11257.11257.0	2	6.42	6.42	60.7			