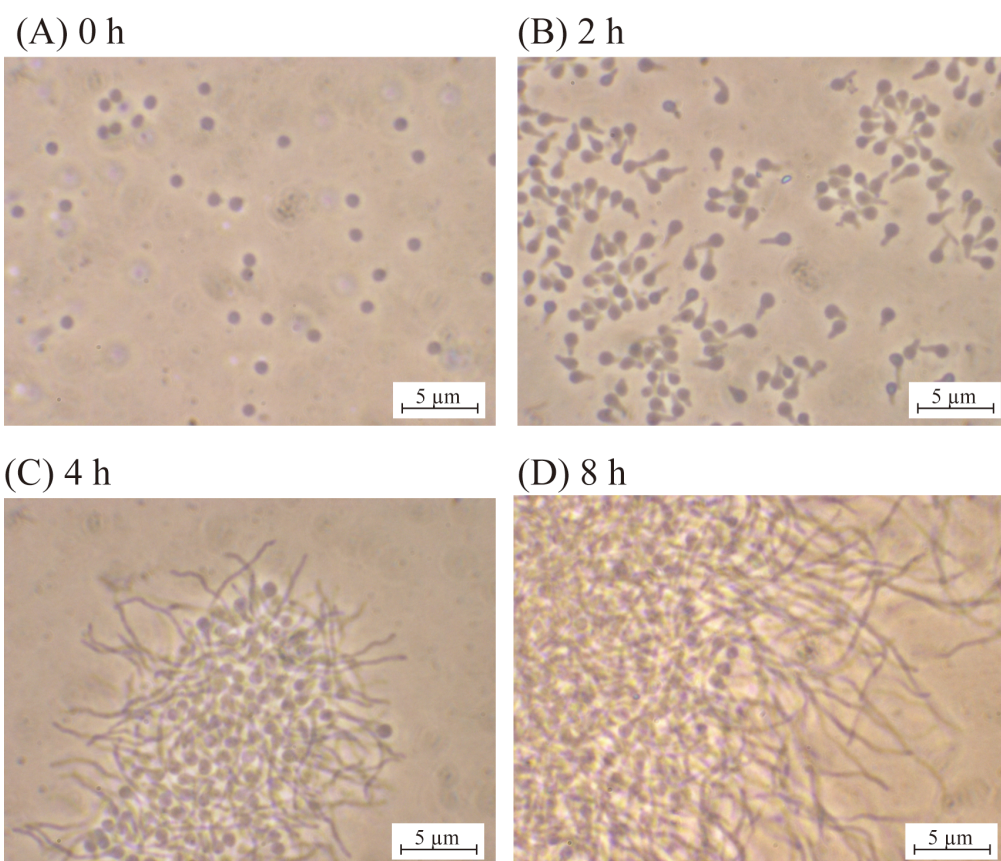
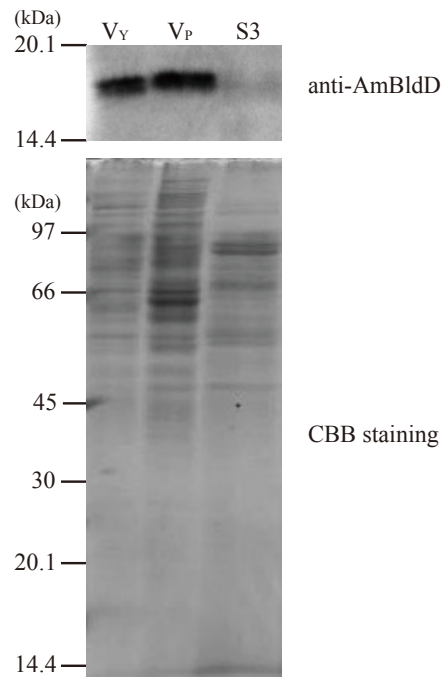


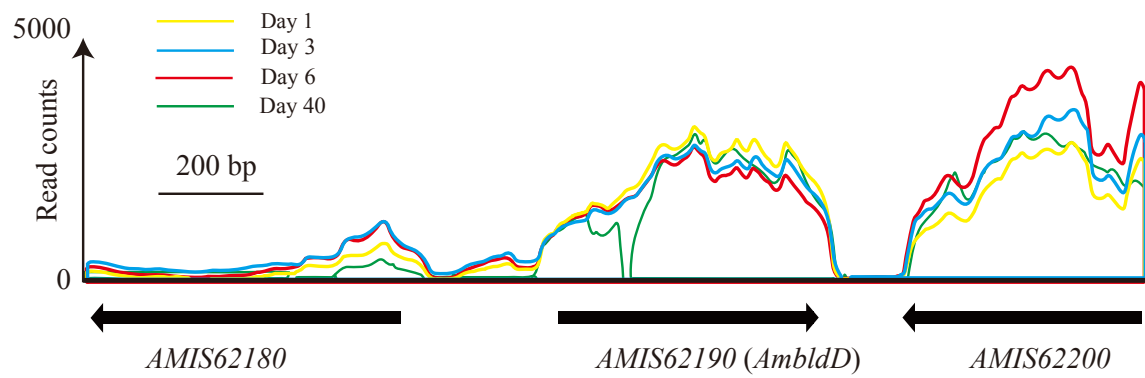
**Figure S1.** (A) Construction of the  $\Delta AmblD$  mutant. (B) Southern blotting using BamHI-digested genomic DNAs of the wild-type (wt) and  $\Delta AmblD$  strains. The probe position is shown in (A). (C) Nucleotide sequence of the *AmblD* locus in the  $\Delta AmblD$  strain. The hexameric -35 and -10 promoter sequences, transcription start point (tsp), start and termination codons, and AmBldD box are indicated. An inverted repeat sequence (palindrome sequence) that may serve as a transcription terminator is also indicated. Primers used for the qRT-PCR analysis in Table 2 and Fig. S7 are also indicated; RT.bldDup.f and RT.bldDup.r were used for the amplification of “AmblD upstream” and RT.bldDdown.f and RT.bldDdown.r were used for that of “AmblD downstream” .



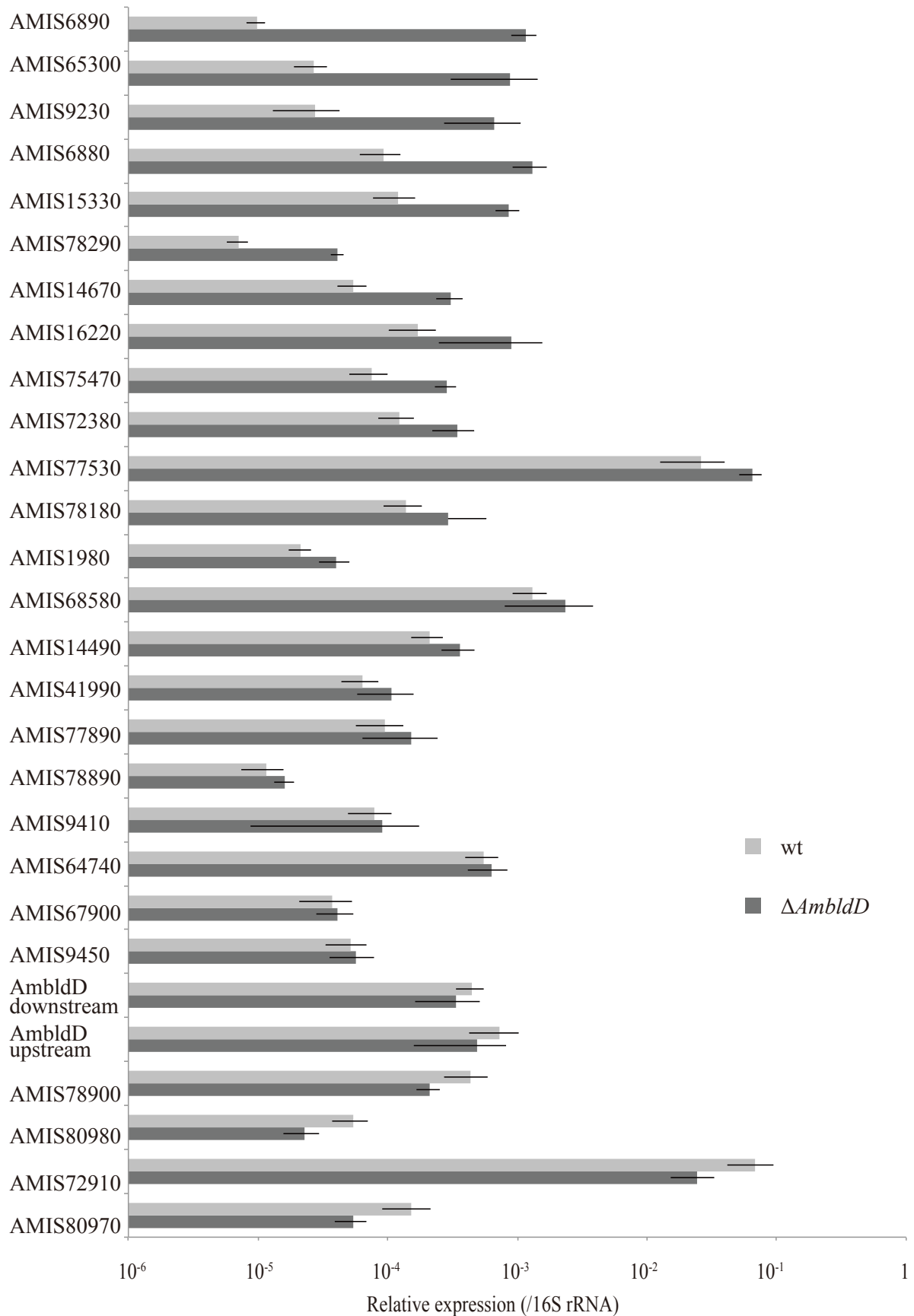
**Figure S2.** Light microscope observations of germinating cells. Zoospores were collected and shaken in PYM liquid at 30°C for (A) 0, (B) 2, (C) 4 and (D) 8 h.



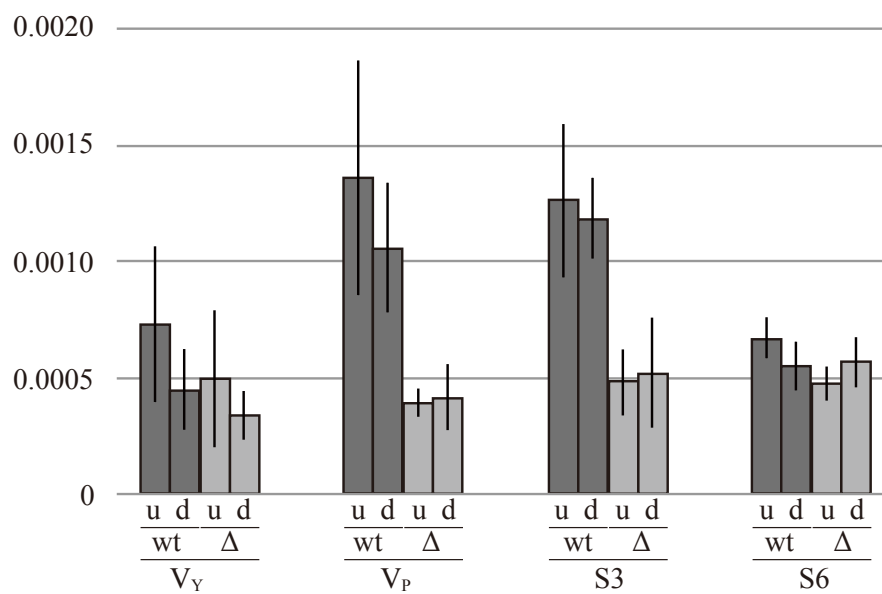
**Figure S3.** Protein levels of AmBldD. Protein concentrations were determined by the Bradford assay and equal amounts of proteins were used for SDS-PAGE. AmBldD was detected using the anti-AmBldD polyclonal antibody (upper panel). A CBB-stained gel is shown in the lower panel. Protein samples were prepared from vegetative mycelia grown on YBNM agar (V<sub>Y</sub>) and in PYM liquid (V<sub>P</sub>) at 30°C for 48 h, mixtures of substrate mycelium and immature sporangia grown on HAT agar at 30°C for 3 days (S3).



**Figure S4.** Transcription profiles of *AMIS62180*, *AMIS62190 (AmblD)* and *AMIS62200*. Yellow, blue, red and green lines indicate the distributions of the mapped read counts in the 1-, 3-, 6- and 40-day cultures, respectively. Arrows indicate the open reading frames.



**Figure S5.** Analysis of gene transcript levels to identify genes regulated by AmBlD. A qRT-PCR analysis of 27 genes was performed using the total RNAs extracted from the wt and  $\Delta AmblD$  strains grown in YBNM agar medium at 30°C for 2 days. The *AmblD* transcript was analyzed by two primer sets; one is for the 5' region of *AmblD* (AmblD upstream) and the other is for the 3' region (AmblD downstream). See Fig. S1(C) for the amplification regions. The data are means of three biological replicates  $\pm$  standard deviations.



**Figure S6.** Transcript levels of *AmbldD*. Transcripts of *AmbldD* in the wild-type (wt) and  $\Delta$  *AmbldD* ( $\Delta$ ) were measured by qRT-PCR amplifying “*AmbldD* upstream” (u) and “*AmbldD* downstream” (d). See Fig. S1(C) for the amplification regions. RNA samples were prepared from vegetative mycelia grown on YBNM agar (V<sub>Y</sub>) and in PYM liquid (V<sub>P</sub>) at 30°C for 48 h, mixtures of substrate mycelium and (immature) sporangia grown on HAT agar at 30°C for 3 and 6 days (S3 and S6).

**Table S1.** Primers used in this study.

Primer name	Sequence (5' to 3')	Used for
pColdI-BldD.f	TCGAATTCGACGGGTCGTTAAAGGATGTC	Protein expression
pColdI-BldD.r	TCTCTAGACCCGCGCTTCCTCAACGGTC	Protein expression
sRT.16SrRNA.f	AGAGTTTGATCCTGGCTCAG	Semi-qRT-PCR
sRT.16SrRNA.r	GGTACCTTGTACGACTT	Semi-qRT-PCR
sRT.bldD.f	GCGTCGAAGAGAAGTCCAAC	Semi-qRT-PCR
sRT.bldD.r	CGAGATGTCGTAGACGATGG	Semi-qRT-PCR
RT.16SrRNA.f	CAGTCGTGTCGTGAGATGT	qRT-PCR
RT.16SrRNA.r	AAGGGGCATGATGACTTGAC	qRT-PCR
RT.bldDup.f	GTAGCGATCCGCGAGGAAAG	qRT-PCR
RT.bldDup.r	CAGCGACTTGCGTACTCAG	qRT-PCR
RT.bldDdown.f	CGCCATCGTCTACGACATCT	qRT-PCR
RT.bldDdown.r	CTGGTGGCGCTCTGTGTC	qRT-PCR
RT.1980.f	ACACTGGAGATCGTCTGCTGA	qRT-PCR
RT.1980.r	ACCTCGGACTCGCGGAATC	qRT-PCR
RT.6880.f	ATGTCGAACGTTCCGAGACT	qRT-PCR
RT.6880.r	CGCACATCGTCTTTGCCTTG	qRT-PCR
RT.6890.f	GTCCTCGTGTGCGTCCGAAC	qRT-PCR
RT.6890.r	CCGTTCCGCCAGTCCGATCATG	qRT-PCR
RT.65300.f	AGTACCATTCGTCCAACGAC	qRT-PCR
RT.65300.r	TGCGTGGAACAACACATGGAC	qRT-PCR
RT.72910.f	ACTGGCGTCACGATGCGATC	qRT-PCR
RT.72910.r	GAGAGGCACGACTCGGTCAC	qRT-PCR
RT.78290.f	GTTTACCGATGGGGATGATC	qRT-PCR
RT.78290.r	GTCGGCGAGGCACTCGTAGC	qRT-PCR
RT.9230.f	CAGATCGCTGACGAGTTGTG	qRT-PCR
RT.9230.r	CACACGTTCCATGGTCTGAG	qRT-PCR
RT.9410.f	GTTTCGACTCGATGGAGCAGT	qRT-PCR
RT.9410.r	TGTGCGAGTGGTAGATGACC	qRT-PCR
RT.9450.f	CGTGTACGTACGTGGTGGTC	qRT-PCR
RT.9450.r	GCCCGTAGAAGGTGTAGACG	qRT-PCR
RT.14490.f	GATCATCGTTTGCCGGATT	qRT-PCR
RT.14490.r	ATCTGACCCTTGCGGTAGTG	qRT-PCR
RT.14670.f	GGTGATCGGTGTGGACATTC	qRT-PCR
RT.14670.r	GAAGTCCTGCTCCATCCAGA	qRT-PCR
RT.15330.f	CGAGTACGATCAGTCGCTCA	qRT-PCR
RT.15330.r	GCTCGAGCAGGTTGTTGG	qRT-PCR
RT.16220.f	GCAGAAGGTTCCGTTACGAC	qRT-PCR
RT.16220.r	TTACCGACGTACTIONCGATCACC	qRT-PCR
RT.41990.f	ACCGAGTCCCTGTCTTCT	qRT-PCR
RT.41990.r	TGTCCTCGAAGATGATGACC	qRT-PCR
RT.64740.f	CGAGTGCACACCTTCATC	qRT-PCR
RT.64740.r	GCACTCGAGGTTCTCGTTGT	qRT-PCR
RT.67900.f	GAGTGCCCCGGAAAATCT	qRT-PCR
RT.67900.r	CCATCACACGCACCCTCT	qRT-PCR
RT.68580.f	GTCTAGCAGCCGATGAACG	qRT-PCR
RT.68580.r	GGCCGCAGAACAAGAT	qRT-PCR
RT.72380.f	GTCAACGATGTGCTGACGAG	qRT-PCR
RT.72380.r	ATCCCGATGCTGTGATAAG	qRT-PCR
RT.75470.f	TCGTCCTGGTCGACTTCTG	qRT-PCR
RT.75470.r	GTGATCTCGGGGTGCTTCT	qRT-PCR

RT.77530.f	GGCAATCGAGACTAGGGTCA	qRT-PCR
RT.77530.r	ACCTCTTCGGCGTTCTCAG	qRT-PCR
RT.77890.f	AACAGCTCACTCGACGTGGT	qRT-PCR
RT.77890.r	AGTGGCGATCATCGGTAAAC	qRT-PCR
RT.78180.f	GGAGATGGACACGATCGAAG	qRT-PCR
RT.78180.r	TCTTCCCGGACAGAACGATA	qRT-PCR
RT.78890.f	CTCCGCTTTAGGATGCATGT	qRT-PCR
RT.78890.r	AGCAGAATGCGGAGAACG	qRT-PCR
RT.80970.f	CTACAGAGGCGAGCAGTCCCT	qRT-PCR
RT.80970.r	GGTATGTAGCCGCGTTTCTC	qRT-PCR
RT.80980.f	GCTGTACCCGACACTGAAGC	qRT-PCR
RT.80980.r	CTTCGGCCGTGATCTTGTAG	qRT-PCR
ΔbldD.up.f	TCGAATTCGCTCCGGCAGTTTGCTCATC	Gene deletion
ΔbldD.up.r	TCGCTAGCCAGCGACTTGGCGTACTCAG	Gene deletion
ΔbldD.down.f	TCGCTAGCGCGCTCGCCATCGTCTACGAC	Gene deletion
ΔbldD.down.r	TCAAGCTTCTGGTCGAGATGTGCCAGAC	Gene deletion
bldD.southern.f	GGTTGAGCACCAGGCCGTTCC	Southern blotting
bldD.southern.r	CTGGTCGAGATGTGGCCAGAC	Southern blotting
bldD-5'RACE-RT	CGCTGCTGCTGGATG	5'-RACE
bldD-5'RACE-A1	CGCTGCTGCTGGATG	5'-RACE
bldD-5'RACE-S1	GGCCGACTTCTACCGAGTGC	5'-RACE
bldD-5'RACE-A2	TCGAATTCGACTTCTCTTCGACGCCCTG	5'-RACE
bldD-5'RACE-S2	TCAAGCTTGAGAAGCTCTACGACACCAC	5'-RACE
whiD.5race.RT	CGCACATCGTCTTTG	5'-RACE
whiD.1st.S1	ATCGCCGACCTTTGGGACTG	5'-RACE
whiD.1st.A1	CGAACGTTTCGACATCAACAC	5'-RACE
whiD.2nd.S2	CAACGACTGGGCAATTGCCG	5'-RACE
whiD.2nd.A2	CGCGGAGTGTTTCGTCTGAG	5'-RACE
ssgB.5race.RT	GAAAGACCAGCTCAC	5'-RACE
ssgB.1st.S1	CGTACGCGGTCCATGTGTTG	5'-RACE
ssgB.1st.A1	CTGGGTTCGTACCCGAGACTG	5'-RACE
ssgB.2nd.S2	CCACGCAGAATCAGCCGGTG	5'-RACE
ssgB.2nd.A2	GCCGTTCGCGTCAGGCGCTAC	5'-RACE
wblA.5race.RT	GCACTCGTAGCGAAC	5'-RACE
wblA.1st.S1	TGACGCGCTGTTCGTGCAGG	5'-RACE
wblA.1st.A1	ACTCTGACACGCCGCCATGC	5'-RACE
wblA.2nd.S2	AACGTGGCGAAGAGGATCTG	5'-RACE
wblA.2nd.A2	AGTCGCTGATCATCCCCATC	5'-RACE
EMSA.bldD.f	GACCATGGTGACGTGCCTGAC	EMSA
EMSA.bldD.r	CAGCGACTTGGCGTACTCAG	EMSA
EMSA.A.f	CAGACGATCTCCAGTGTCCACAAC	EMSA
EMSA.A.r	CTTCACGCCCGGTAGCGGCGAATG	EMSA
EMSA.B.f	ACACGCACCATGTTCGATGTCTTC	EMSA
EMSA.B.r	CCGTTCCGCCAGTCGGATCATG	EMSA
EMSA.C.f	GAACCGAGTACCTGGGCAGAAC	EMSA
EMSA.C.r	GTTGGACGAATGGTACTCATG	EMSA
sense.f	GGATACAGCCGGTAACTTTG	DNase I footprinting
sense.r	CATACGGACACTCCCGGTAC	DNase I footprinting
anti-sense.f	GACGGGTCGTTAAAGGATGTC	DNase I footprinting
anti-sense.r	AGCCCACGACGACAGCCTTC	DNase I footprinting



**Table S2.** Zoospore-specific protein.

Spot	ORF no <sup>a</sup>	Gene product <sup>b</sup>
1	AMIS54020	putative ATPase associated with various cellular activities
2	AMIS37330	putative xylulose-5-phosphate/fructose-6-phosphate phosphoketolase
3	AMIS37880	putative catalase
4	AMIS64930	putative multi-sensor signal transduction histidine kinase
5	AMIS68770	putative methyl-accepting chemotaxis protein
6	AMIS65800	hypothetical protein
7, 28	AMIS49400	putative ABC transporter ATP-binding protein
8	AMIS73730	putative modulator of DNA gyrase
9	AMIS58720	putative UDP-N-acetylglucosamine 2-epimerase
10	AMIS56730	putative aminotransferase
11	AMIS30	putative 6-phosphogluconate dehydrogenase
12, 13	AMIS68250	hypothetical protein
14	AMIS61390	hypothetical protein
15	AMIS75470	putative thioredoxin
16, 24	AMIS80500	putative OsmC-like protein
17	AMIS72590	putative ATP-dependent Clp protease proteolytic subunit
18	AMIS10090	hypothetical protein
19	AMIS66160	hypothetical protein
20	AMIS54570	putative maltokinase
21	AMIS76190	putative flagellin domain protein
22	AMIS80580	hypothetical protein
23	AMIS76490	putative response regulator receiver domain protein CheY
25	AMIS76580	putative two-component system response regulator
26	AMIS68430	putative methylenetetrahydrofolate dehydrogenase/methenyltetrahydrofolate cyclohydrolase
27	AMIS4650	putative serine hydroxymethyltransferase
29	AMIS1780	hypothetical protein
30	AMIS37910	hypothetical protein

**a.** A total of 27 proteins were identified by peptide mass fingerprinting from the 30 spots indicated in Fig. 1A. AMIS49400, AMIS68250 and AMIS80500 were identified from two spots each.

**b.** Possible functions and classifications of the identified proteins are shown.

All these 'zoospore-specific' protein genes, except *AMIS75470*, are not the direct targets of AmBldD.

**Table S3.** AmBldD-binding sites detected by ChIP-seq analysis with a strict threshold (p-value < 0.0005).

No.	Region	MEME p-value	Upstream	BldD box	downstream
1	1009746..1010015	1.05E-05	CAACGCCGAC	GGGTCACTGGACGTAACGA	GAGAATTCGT
2	1047431..1047732	3.07E-06	GGGGCCTTTT	TCGTTACTGCCTGTGATCA	GGGGGCCGTG
3	1056800..1057128	1.05E-05	AAGATCTGCA	ACATTACATTCGGTAATCT	AGCTGTATCG
4	1080600..1080864	2.01E-04	AATCGCCCAC	ATGTAACCCAAGGTTACAT	TTATGACAAC
5	1103397..1103769	4.11E-06	AGCCAATCAG	CGTTCACACAACGTGACCG	TTTTTCGCGT
6	1163827..1164099	8.38E-05	TCCCAAGGCG	AGCCTACTGTGCGTAAGCT	GCCGCGGTTC
7	1219329..1219588	2.18E-05	ATCACGAGAC	CCATTACGCACCGTTGCTG	TGCATGCAGA
8	1230947..1231216	4.11E-06	CTGGCAAGGG	TGGTCACCTAGAGTCACCC	CCGTGCTGAT
9	1254784..1255042	1.35E-05	TACGTCCGAA	AAATTACGCCGGGTCACCG	ATAATTTAC
10	1264060..1264323	2.73E-05	GTAACCCAGA	CCGTGACCGAACGTGAAGA	GTGGGCGTTC
11	1264585..1264847	2.44E-05	GCCCGGAGGG	CGGTGACCGAGCGTGGTGG	CTACCGAGTG
12	1295021..1295279	1.21E-04	CACGGCGTTG	CTGTCACGTTGCGTGTGGT	GTCGGAACGT
13	143434..143700	8.14E-06	CACTTTCTCG	CGGTGACGGTGAGTCAGCA	AGTGAGGCAT
14	1488864..1489140	7.62E-05	CCGGCTGTTA	CAGCCACCGACCGTCACAG	CCCGAGGTCC
15	1511424..1511681	5.44E-06	TGGATTCAA	TGACTACTCAGCGTTACGG	CAGGGCGAGC
16	1533642..1533944	9.27E-06	TGATGGTGAA	AAAACACGTTGCGTGATCA	TGACTAGGAT
17	1552477..1552749	2.97E-04	TGTAAACCTC	CCATCGCCTTCTGTGATTG	TCGCCCTCGC
18	1573538..1573817	4.59E-04	TCATGATCTA	AGACTACGCGCAGTGCCCG	TCCGAACGCA
19	1626957..1627220	6.93E-07	ACATGTGTGC	CAATTACTGTGAGTGACAT	TTTCGGCCCT
20	1649128..1649396	7.62E-05	TTGTCGGGGC	TCCTCACCTTCCGTATCCT	TGCCACCCTC
21	1654530..1654837	2.55E-04	ACGACATCTC	CGGTAACGGTGCGTACACG	CACATGACCA
22	1751762..1752032	6.92E-05	TGATCACTTC	CGACTACTGTCCGTCACTC	TTTGGAATTGA
23	1808521..1808804	4.19E-05	CGTCAATCAT	CAGCGACGGCGAGTGACCG	CCTCCGGCTC
24	1821745..1822005	1.01E-04	TGACGACGTC	ATCATAAGCTGTGTAACCG	GCGAAGAGCT
25	1823811..1824068	2.44E-05	CCTGGAGTCC	CGCACACTCACCGTGATCG	GCTTGCCGGA
26	1861159..1861414	4.65E-05	CGCGGTGCA	ATCTGACTCTCCGTACAG	TCCGCTCTTC
27	1950647..1950915	1.64E-06	GAACGCAGGT	TGATCACTCTCCGTGAAGT	CCTTGGTCAC
28	1984962..1985249	1.44E-04	CCGTGGGCAA	CGAGCACGGAGAGTGGTCG	TTCGGGCGTA
29	2080681..2080944	2.55E-04	GCGATGTCGA	CGCTGACCAAACGTCACAA	ATAGTCGAAG
30	2211577..2211849	6.92E-05	TCACCCCGCA	TATCTACGCAGTGTTACTG	GCGGATGGTG
31	222486..222754	4.73E-06	CGAGAGACGC	CGGTTACGCGCAGTCACCT	CGAGCACCTG
32	223057..223315	9.90E-07	GAGCGGCCGG	TGGTCACGCTGAGTGTCCG	CTTGCTCGAT
33	226586..226880	6.92E-05	GTCGGTGAAC	GCGTCACCCGCCGTGAACA	CGAAGATCAG
34	2328090..2328352	4.65E-05	GCGCTTGAAT	CCGACACTCGCTGTGACGA	ATCGCTCACC
35	2343362..2343627	1.32E-04	GACGTTCCGC	CAGGCACGGAGAGTAGTCG	TTAGGCACTG
36	2419036..2419310	5.76E-07	GGCCTTCACC	ACGTCACCCTCAGTGACTT	CAAATTCAAA
37	245598..245861	9.90E-07	ACCCGCCCCC	AGGTCACCCTCCGTAATGT	CTCTAGATCA
38	250302..250609	5.69E-05	CCCGGCCATT	CGATCACGGGGCGTTAACG	GTCATCAAGC
39	2548123..2548393	1.57E-04	AGGAGTGCCA	GAACTACGCGGAGTCACTG	CGTCGGAATC
40	2584878..2585176	5.31E-08	CTCGTAGGGG	TAGTCACTCTCGGTGACCG	CCTGCTGGAA
41	2594..2851	2.44E-05	TCGATGTGGA	CAGACACTGTGCGTCACAA	ACTTGTCCAC
42	2795138..2795408	7.62E-05	CATCCAGCGC	ATGTCACGCCACGTGGCGG	GGTCACGCAG

43	3020327..3020590	2.18E-05	ACCGGACTCA	CGGTAACAGCGCGTGACGG	AGAAGGGCGG
44	3029050..3029322	1.20E-05	TCCGCCCCGA	TGCTCACACAGAGTGGTCG	TGGTGCGAGG
45	3082315..3082574	2.44E-05	TTGCTGTGAC	AACTAACTTAGAGTGATAA	CTTACTCGCG
46	3112623..3112892	7.62E-05	CGATCATCGA	TGGTTACGGGCTGTGGCAG	GTCGGGGTGC
47	330581..330840	8.38E-05	AGAGCCTCGT	TGGTGACGCGCTGTGAAAA	CGGTCAGACG
48	3367509..3367784	6.87E-08	CGAAGAGAAA	CCGTCACTGAGAGTGACGG	CTGTCCAGAG
49	354391..354667	3.04E-05	GTCAGCCGTT	TGATTACATTTCGGTCACCC	TTATGGCGAT
50	3559661..3559937	4.78E-07	CCGCAGGTTT	TGGTGACTCACGGTGACTG	CGCGCGGTGC
51	356374..356630	2.18E-05	TACATCATGG	TGGTCACCGGGCGTGTGCA	GAAGGGTCTG
52	3597235..3597545	3.77E-05	TGGCAGTTCC	ACGCCACTCACCGTATCGA	CGGCCGTAC
53	3772454..3772710	1.39E-06	GGTGACGGTT	AGGTTACGCTGGGTGAATA	GCTAGGGGGC
54	3786423..3786700	3.94E-07	AGGACGGTTG	CCGTTACGCTCGGTGACCT	GCGACTTGCG
55	3798364..3798628	3.04E-05	CCACCCCAT	CCGTCACGTAGAGTCGCAG	ACCGTCCGGG
56	3830196..3830461	1.87E-03	GTGGGGTAAC	CGCTCACTGCGCGGGGGG	GTCACCGTCG
57	3841135..3841418	4.28E-04	ACCGGCGGCG	TGGACACCGACGGTGAGAC	CGACGGCGAC
58	3989836..3990099	9.27E-06	ATGTGACCAG	AGGTGACGTAGTGTACGA	GGTGCATGTC
59	4054167..4054424	1.35E-05	TGTCAGCCGT	TCACTACTGTGCGTAGCTA	TCGACGGAAC
60	4140468..4140739	3.55E-06	TCGAGCGCGA	TGCTCACGCCAGTGACGA	CAGCGCGGTG
61	4141065..4141324	3.55E-06	ATGCAACGGC	TCGTCACCGATGGTGACCG	CGGTGGTGCC
62	41573..41887	2.01E-04	CCATCGAAGA	ATGTTGCGGAACGTCACCA	TCGCCGATCG
63	424760..425029	1.35E-05	TGTTACCAGG	CAGCGACTTTCCGTAATCA	AATCACCTCG
64	4265782..4266047	1.21E-04	CGCCAGGTGA	TCGACACGAGCCGTAACGG	CGGCGCGAGC
65	4266294..4266554	1.10E-04	ACCGGCTCCA	CCGTCACCGTCCGCAACGT	CTCCTGGAAC
66	4296677..4296939	1.20E-05	GTTTCGACACA	TCGTTACGCCTGGTGATCG	TGGTCGTGTT
67	4359905..4360166	4.73E-06	GATTCGAGCT	CGGTCACACAACGTAGTCA	GCTCGGCCAA
68	4369604..4369922	9.27E-06	CGTGACGATC	TCGTTACAGAGAGTCGCGA	TGCCGGTGGT
69	4379197..4379546	2.26E-06	GAGCCCCGCC	CGCTCACCGTGAGTGACCT	CTCCCCTCGC
70	4410559..4410844	1.72E-05	ACCGGAACAC	ACGTAACGCATGGTGACGG	GCTTGGCAGG
71	4676647..4676910	6.24E-06	GCGCCCCATG	AGGTCACTGCCAGTGACAG	GAGGTGGTTC
72	4825530..4825845	4.59E-04	CAGCCGAGAA	TACATACGCTCAGTGTGCG	ATTGACTACA
73	4906934..4907191	4.78E-07	GTCGGAGCCG	AGGTCACGCAGCGTGGCCA	TCCGCCGCTC
74	4959030..4959286	7.62E-05	CATCCCCGTC	AAACCACCCTAAGTAGTGA	ATTAGTTACG
75	5025249..5025506	4.78E-07	CGCCCCTCCC	TGCTCACCCCTGCGTGACGA	CGCCCCGGAG
76	5083238..5083493	1.94E-05	GCCACATCGA	CCCCCACCAGCGTGATCA	GGCTCTCAGC
77	5085477..5085740	2.44E-05	TTTCCATTAA	CCATTACACCTAGTAACCT	TCGACAGACT
78	5114683..5115065	4.11E-06	CCC GCGC	TGTTACCTTGAGTAATGT	GGTGACGAAT
79	5117418..5117685	3.55E-06	CCGGTAACCC	AGGTCACGCAGCGTCGCTA	AATCGCAGGT
80	5141027..5141303	1.39E-06	GACGGCGTTC	CGATCACGCTACGTACCT	GGCAACGCAC
81	5144261..5144522	6.24E-06	GCCCATCTCG	TCGTGACGGCGCGTGACGG	TCCCGCCGAG
82	5214684..5214944	2.97E-04	GGCTCCGTAA	CACTCACTGTGAGCGACGC	CTCCCACGGT
83	5229521..5229790	1.72E-05	GGCGTGGCGG	GGATCACCCAGCGTCATGT	TGATCTCGGT
84	5300865..5301132	8.14E-06	CGCACCATTC	CCCTTACGCAGCGTGCTA	AAATGGCCAC
85	5385915..5386182	4.73E-06	AGCCTAGCGA	CCGTCACGGAAGTATCCA	ACCAACCGAT
86	5403424..5403790	5.15E-05	ACCGAGTCGG	CAACCACTCTGCGTAGGCA	AACGTGAGGA
87	5419768..5420148	8.30E-07	TACTGCCAAA	CAATCACTTTGTGTGACTG	GCGGCTCATT

88	5635826..5636087	4.78E-07	GGGGGCCTTC	TCGTCACTCTGCGTGTCCA	CATAGGATTA
89	5732393..5732648	3.77E-05	GTGGGCTCCG	CCGTCACCGGTGGTAACCG	TTGTGCCGGG
90	577183..577565	3.94E-07	GAGAACTGTC	CGGTCACTGTGCGTGATCG	GAGCGTCCGA
91	5954432..5954693	1.74E-07	AAATCGTCAA	CAATCACACAGAGTGACCG	GGTGCGGATC
92	6194511..6194783	1.20E-05	CAGCGCCACC	GCCTTACCCAGCGTGACCG	TCACCGCGTC
93	6198514..6198774	1.93E-06	ACGGTGCTGA	CAGTCACTGAGCGTAGCTG	AGACGGAAAT
94	6233515..6233773	1.10E-04	TCACCGCCCT	TGATCACTCTGCGTTGATC	GACATATCAC
95	6687333..6687592	9.90E-07	AAACTCCGTA	CCGTCACGCAGCGTAGCGA	TCCGCGAGGA
96	670006..670313	4.73E-06	GAACACGACA	TCGTCAACCGTGCCTGAGAA	GTCGAAGGAA
97	6834433..6834691	4.73E-06	ATCACTCAAG	CAGTGACGCTAAGTAATAG	TTTTCTGCTC
98	688524..688843	1.35E-05	ACTATGGCAG	GCGTCACTGTGGGTACTG	GAGGGCGACG
99	6892302..6892566	1.94E-05	TAACCGTCCG	GCGTCACCCTCCGTAAGCG	TGGTGATCCC
100	6979498..6979789	6.43E-04	TTTCTCACCT	CGGTGACTTACTGTGCGGT	AACCGAAGCG
101	7081702..7081962	9.20E-05	CCACGCCCCG	GCCTCACCGAGAGTGGCCG	CCGCGTCGAA
102	719203..719467	1.10E-04	TCTGTAAACG	CATCAACGCAGCGTCACCG	TGTGTGTATC
103	7323797..7324058	8.83E-08	ATGCGTCGAG	AAGTCACTCTGCGTGACGT	CGCGGAGCTG
104	7358708..7358980	1.53E-05	CACCGGTCCG	AGATCACCCCTCCGTATTGA	TCTACGACGA
105	7365300..7365596	3.24E-07	GCGGTCCGGC	AGGTCACGCTGGGTACCA	CGACGTCGTC
106	7367211..7367488	1.94E-05	GGTGTGACGA	CCGTGACTCGCTGTGATCG	TTCTAACCCG
107	740983..741245	2.36E-04	CCCTGAGCTG	CGGTTACTCACCGCTATCC	CACTGTCTGTG
108	7429846..7430122	8.28E-04	ACCACCCGTA	CATCAACGGGTGGTGATCA	GACCGTTGTG
109	7484144..7484488	1.05E-05	CCGGAAACGA	CCGTCACCCCATGTGATCA	GGATGCCGGA
110	749647..749977	3.45E-04	AGATGAGCAA	CCGCTACGAGCTGTCACGA	TGGGCCGCTG
111	751801..752062	6.24E-06	GCGGAACGGC	CCATCACTGAGAGTCAGCG	CCTCGCGCTG
112	7526992..7527364	2.73E-05	CGCATTTACA	TAGTCACAGAGAGCAACCG	CAACCGGCC
113	7652398..7652677	1.32E-04	GCCTTCGCCA	TCGTGACTCCTTGTGACGC	GCTGCGTCTC
114	7674971..7675236	1.85E-04	GGTCATGGCA	CCAGCACTCCACGTGATCG	CCGGGCCTGG
115	7791515..7791776	7.62E-05	ACGAGGTGAA	CAGTGACCACACGTGACCG	GCAGCCCCTG
116	7844864..7845123	9.27E-06	ATCTCTGTGT	AAATAACTGACAGTAAGCA	AGAGTGCAAC
117	7852533..7852823	1.10E-04	GCTGGTCTGC	AAGTTACGCCACGTAGGCG	CGGAACGCCA
118	7866639..7866923	1.53E-05	AGCGGGTTGA	CCGCTACTGAACGTACCGA	ACACCGTGTG
119	7869344..7869599	4.78E-07	TTGCTGAGCG	TAGTCACGTACGGTGACCT	GGGGAAATCA
120	7872507..7872783	8.14E-06	CCCACCACGA	CCACGACGCAGCGTGACGA	CCGCCTGCCG
121	7886041..7886302	5.15E-05	CCCCCGGGTC	ACGTCACCCGCCGTAGCGG	GAAAGCTCTG
122	7906935..7907204	8.14E-06	CGCGGACCAC	CGGTAACCCAGAGTGAAC	AATCCGTTTA
123	7911162..7911418	6.28E-05	CACTTGACAT	TGGCCACTCGGGGTAGTGA	CACAGGCACC
124	7935382..7935650	6.24E-06	CCGGCCTGTT	CGGTAACCGAAAGTAATGG	CCGGATCTGC
125	8016907..8017210	9.90E-07	ACCGCCGCTA	CGATCACCCCTGGGTGATGG	CGAGGTTTTG
126	8076494..8076763	2.65E-07	AACCCGATTT	CAGTCACGCTGTGTAACCG	GTGGGTAAAG
127	8080825..8081114	1.12E-07	CGTAATGCTG	TGATTACTCAGCGTCATTA	CCGGCAGCTT
128	8167186..8167456	3.20E-04	AAGCCGATTG	TCATCACCGCAGGTACAC	CCGAGAGGGT
129	8168913..8169278	5.69E-05	CGACACCATC	CGCCTACTTTCAGTTACGA	TAGGTTGCC
130	8186072..8186327	6.28E-05	GTCGTCAAGG	CGGTACGGCGCGTAGCTC	CGATGAGGAG
131	8197191..8197509	1.53E-05	GATGAAAAAT	GAGTCACCCTCCGTAAGGA	GCTCGACACC
132	8232310..8232594	1.18E-03	CGTACGGAGA	CGAGCACTGGTCGTGTTCA	GTTTTACTCA

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133	8302647..8302992	2.26E-06	CACCCCGCGC	CCGTTACCCGGGGTGACCA	CAGTCCCCGC
134	8333790..8334050	1.53E-05	GATGATCTGC	TGCTCACGCTCGGTGAGGG	CCGGTCTTTC
135	8362838..8363113	3.04E-05	CGCTCGTCGT	CAATTACAGAGAGTGGCC	CAGGATGCGG
136	8378052..8378318	2.16E-07	GAAGCTGCCT	TAGTAACTCAAAGTGATCA	GCACGTCACG
137	8386105..8386366	3.24E-07	CCACGTCGCC	AAGTGACGCAGCGTGACGA	ATCATCACGC
138	8387412..8387672	6.28E-05	GCTGACCCTC	GGGTGACTCTGTGTAGTGG	GGTGGCCGAT
139	8406748..8407032	8.38E-05	CGTCATACTC	CGGCTGCGGAGCGTAACCA	GGCTCGGGCG
140	8411862..8412157	8.14E-06	TTCACGCGCT	CCTTCACCTTGGGTAAACGA	AACGGGCGCT
141	8447425..8447705	1.01E-04	GACCGCTGAA	TTGTCACTAGCGGTACCGG	CATTTCTGGT
142	8452173..8452447	8.14E-06	GACGCTTCCT	AAGTGACTATAAGTGACCT	CTTGGGCATC
143	8458114..8458496	2.65E-07	ATGTCCGTTT	CGGTCACCTTGGGTGACCA	AAAGGGGCGG
144	8462486..8462752	5.69E-05	CGTAGTTGGG	TGATTACGCAACGTTGTCC	CTCAAATACG
145	8496037..8496293	5.44E-06	ATGCCCGTCA	AGGCCACGCAGCGTAACAG	ATCGGCCAAG
146	8505092..8505357	1.35E-05	TGTACACGCA	TGACTACGCTGCGTGAATT	GTTAGCCCAG
147	8512657..8512941	9.27E-06	CGCGGCCCTT	GAGTCACGCTCCGTAGCTA	CTTAATGTCC
148	8520462..8520749	2.55E-04	GGTGCGGGCA	TCGTCACATATAGCGATTT	GTCCGTTTAC
149	8523931..8524195	1.39E-06	TCACCCAAAG	ATGTCACCCTGAGTGACAA	CCATCCGGTG
150	8528804..8529066	7.62E-05	AGGCGACACT	TCGTTACAAGGCGTAGCCG	GCTGCCACGA
151	8642381..8642649	6.28E-05	CAAGAGCGCA	ACGCTACGTAAAGTAATTC	TCGCCGAGGG
152	8656812..8657068	1.53E-05	TACCGCGAAC	TGATTACCGTCGGTCAGCA	CCTGGCCGAC
153	8666142..8666430	8.38E-05	GATCCAAAGG	TCGTGGCGGTGCGTAATCT	TTTTCCGGAT
154	8686973..8687341	4.59E-04	CGTAGGCACA	CGAGCACGTACGGTAGTTG	GAAAAGAGAG
155	8725272..8725534	2.21E-08	GACGTGCTTT	TGATCACTCACGGTGACCA	CCAAATGGAG
156	873292..873554	3.39E-05	TGAATCCGTT	TGCCTACGCTGAGTAATTC	CGGCGTGGTA
157	918289..918544	1.39E-06	AAGGAAGCGC	TCTTCACTCTCGGTGACCG	TCCCAGGGCG
158	939736..940004	4.28E-04	CAACTGCGGA	AACTACTCCCAGTATTTG	ACTCCCATGC
159	949656..949915	1.01E-04	CTTGCGGATT	TCGTTACACCGGTAGACT	CCAGTCCCCT
160	98496..98761	2.36E-04	AGGCCGCCGT	TCACCACCTGTAGTCACTA	AGTTATTACC
161	985912..986185	6.24E-06	TAGTGAGGTG	TTGTCACGCTGCGTGTTTCG	GGCTGAGAAG
162	986411..986710	1.94E-05	AGCCGTCATT	TGATCACGCTCGGTGAAGC	GATGTTTGCC
163	993227..993507	1.72E-05	CCAACACTTG	TAGTAACTGTCTGTCATGG	AGTTCTCGGC

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**Table S4.** BldD box-containing AmBldD-binding sites that were detected by a ChIP-seq analysis with a loosened threshold (p-value < 0.05).

No.	Region	MEMEp-value	Upstream	BldD box	Downstream
1	8725272..8725534	1.11E-08	GACGTGCTTT	TGATCACTCACGGTGACCA	CCAAATGGAG
2	3367509..3367784	2.53E-08	CGAAGAGAAA	CCGTCACTGAGAGTGACGG	CTGTCCAGAG
3	2584878..2585176	8.85E-08	CTCGTAGGGG	TAGTCACTCTCGGTGACCG	CCTGCTGGAA
4	577183..577565	1.16E-07	GAGAACTGTC	CGGTCACTGTTCGGTGATCG	GAGCGTCCGA
5	7323797..7324058	1.50E-07	ATGCGTCGAG	AAGTCACTCTGCGTGACGT	CGCGGAGCTG
6	8016907..8017210	1.94E-07	ACCGCCGCTA	CGATCACCCCTGGGTGATGG	CGAGGTTTTG
7	7804026..7804286	1.94E-07	CGGAGCACCG	GGGTCACTCAGCGTGACGG	CCAGGGTGGA
8	5025249..5025506	2.48E-07	CGCCCCTCCC	TGCTCACCCCTGCGTGACGA	CGCCC GGAG
9	3786423..3786700	2.48E-07	AGGACGGTTG	CCGTTACGCTCGGTGACCT	GCGACTTGCG
10	8458114..8458496	3.16E-07	ATGTCCGTTT	CGGTCACTTGGGTGACCA	AAAGGGGCGG
11	5954432..5954693	3.16E-07	AAATCGTCAA	CAATCACACAGAGTGACCG	GGTGCGGATC
12	8080825..8081114	3.99E-07	CGTAATGCTG	TGATTACTCAGCGTCATTA	CCGGCAGCTT
13	7365300..7365596	3.99E-07	GCGGTCCGGC	AGGTACGCTGGGTACCA	CGACGTCGTC
14	5635826..5636087	3.99E-07	GGGGCCTTC	TCGTCACTCTGCGTGCCA	CATAGGATTA
15	8386105..8386366	5.01E-07	CCACGTCGCC	AAGTGACGCAGCGTGACGA	ATCATCACGC
16	2909863..2910124	5.01E-07	GCGTCACCCG	TGATCACGGTCTGTGACTG	GCGGATGGTG
17	8076494..8076763	6.24E-07	AACCCGATTT	CAGTCACGCTGTGTAACGG	GTGGGTAAAG
18	6538086..6538438	6.24E-07	CGCCGACTGA	TAGTCAACGTCGGTGATGG	AGGAGCCAG
19	2419036..2419310	6.24E-07	GGCCTTCACC	ACGTCAACCTCAGTGACTT	CAAAATCAA
20	245598..245861	6.24E-07	ACCCGCCCCC	AGGTCAACCTCCGTAATGT	CTCTAGATCA
21	5753852..5754149	7.70E-07	CGAATACAAG	TGATCACTGTGCGTAAACG	CGGACGATAT
22	4906934..4907191	7.70E-07	GTCGGAGCCG	AGGTACGCAGCGTGCCCA	TCCGCCGCTC
23	1950647..1950915	7.70E-07	GAACGCAGGT	TGATCACTCTCCGTGAAGT	CCTTGGTAC
24	223057..223315	7.70E-07	GAGCGGCCGG	TGGTACGCTGAGTGTCGG	CTTGCTCGAT
25	7905201..7905495	9.45E-07	GTCGACCTGG	TCGTACGCTGGGTGGCGA	CGGCACGGTG
26	7869344..7869599	9.45E-07	TTGCTGAGCG	TAGTCACGTACGGTGACCT	GGGAAATCA
27	5493115..5493377	9.45E-07	CGCCGCCCGA	CCGTCAACGACCGTGAGCA	CCTGGTGCC
28	3559661..3559937	9.45E-07	CCGCAGGTTT	TGGTGA CTACGGTGACTG	CGCGCGGTGC
29	918289..918544	9.45E-07	AAGGAAGCGC	TCTTCACTCTCGGTGACCG	TCCCGAGGCG
30	911817..912103	9.45E-07	CACGATAGAG	GGATCACTGTGAGTGACGT	CATCGGAACG
31	8378052..8378318	1.15E-06	GAAGCTGCCT	TAGTAACTCAAAGTGATCA	GCACGTCACG
32	7012699..7012988	1.15E-06	CTCGTGAAC	CGGTCAACGAGCGTCACGT	ACAGATCCAG
33	6846686..6846957	1.15E-06	ACGGTCCGGG	CCATCACTGGGGTGACGA	GACCGTACCG
34	6687333..6687592	1.15E-06	AAACTCCGTA	CCGTACGCAGCGTAGCGA	TCCGCGAGGA
35	4284980..4285270	1.15E-06	GTGGTCCGCA	ACGCCACGCTGCGTGACGA	CGAGCTGATG
36	4141065..4141324	1.15E-06	ATGCAACGGC	TCGTCAACGATGGTGACCG	CGGTGGTGCC
37	4379197..4379546	1.40E-06	GAGCCCGCCC	CGCTCAACGTCAGTGACCT	CTCCCTCGC
38	5141027..5141303	1.69E-06	GACGGCGTTC	CGATCACGCTACGTACCT	GGCAACGCAC
39	1626957..1627220	1.69E-06	ACATGTGTGC	CAATTACTGTGAGTGACAT	TTTCGGCCCT
40	576356..576730	1.69E-06	GCCACTACGC	CCATCACGCACGGTGAGTA	GGGCATGTCT
41	8523931..8524195	2.04E-06	TCACCCAAAG	ATGTCAACCTGAGTGACAA	CCATCCGGTG

42	8302647..8302992	2.04E-06	CACCCCGCGC	CCGTTACCCGGGGTGACCA	CAGTCCCCGC
43	7758653..7758910	2.04E-06	GGGTGGGGGT	CCATCACGTAGCGTCATGG	TCACAGGTGG
44	6775588..6775882	2.04E-06	GGATCGTATT	GCATCACTGAGCGTCATCA	AAGAGCTTCG
45	4516206..4516489	2.44E-06	AGCGCCTCGG	TCATCACGGAGCGTAGCGG	GATGTGCTTG
46	4448179..4448464	2.44E-06	CCCGTCACAC	CGGTCACCGTGCGTGCCG	GGTAGCGGTG
47	4140468..4140739	2.44E-06	TCGAGCGCGA	TGCTCACGCCAGTGACGA	CAGCGCGGTG
48	3176481..3176763	2.44E-06	CGGAGCGGGA	TGGTGA CTCACAGTGAGGG	GGAGGGAGCG
49	2672017..2672390	2.44E-06	TAGGGCGATC	CCGTCACCGACGGTCACCG	ACAGATCAGA
50	670006..670313	2.44E-06	GAACACGACA	TCGTACCGTGCGTGAGAA	GTCGAAGGAA
51	3772454..3772710	2.91E-06	GGTGACGGTT	AGGTTACGCTGGGTGAATA	GCTAGGGGGC
52	446247..446522	2.91E-06	ACCCAGCGGA	TGGTCACCTACGGTCACGA	CGACGCGATC
53	8743341..8743630	3.46E-06	CCGGCGACCG	CCATCACACAGCGTGCCGA	CACAAC'TGCG
54	8324886..8325174	3.46E-06	GGCAGAGATG	CGGTTACTGAGCGTCATCC	TCGGTTCATC
55	5419768..5420148	3.46E-06	TACTGCCAAA	CAATCACTTTGTGTGACTG	GCGGCTCATT
56	5144261..5144522	3.46E-06	GCCCATCTCG	TCGTGACGGCGCGTGACGG	TCCC GCCGAG
57	4187437..4187700	3.46E-06	GCGGGGTAA	CGGTTACCAACTGTGACGA	ACCTCCTTCG
58	1047431..1047732	3.46E-06	GGGGCCTTTT	TCGTTACTGCCTGTGATCA	GGGGGCCGTG
59	8319506..8319774	4.10E-06	GCGGTCATCA	CCATCACGGTACGTAATGC	CGCGCCCGTG
60	7606839..7607214	4.10E-06	CGCCCGGCGC	ACGTCACCGCGGGTGATGA	CCTCGATCCG
61	6627585..6627866	4.10E-06	CGAAGTCTAA	CTATCACCGTGAGTGAGGA	TGGGAGGAGT
62	5993575..5993847	4.10E-06	GAGACCCGCT	GGGTCACGATGCGTGACAA	GCCGCCGGCG
63	2500909..2501247	4.10E-06		TA CCGTCACTTATCGTAATGT	CGGCAGCGCA
64	985912..986185	4.10E-06	TAGTGAGGTG	TTGTCACGCTGCGTGTTTCG	GGCTGAGAAG
65	751801..752062	4.10E-06	GGCGAACGGC	CCATCACTGAGAGTCAGCG	CCTCGCGCTG
66	7872507..7872783	4.83E-06	CCCACCACGA	CCACGACGCAGCGTGACGA	CCGCCTGCCG
67	6764873..6765128	4.83E-06		CAG TAGTCACCCTCGGTGGCGA	GGTAGTAGGC
68	986411..986710	5.68E-06	AGCCGTCAAT	TGATCACGCTCGGTGAAGC	GATGTTTGCC
69	8333790..8334050	6.67E-06	GATGATCTGC	TGCTCACGCTCGGTGAGGG	CCGGTCTTTC
70	7549682..7549956	6.67E-06	GGCCCCGGCG	CGACCACGCTGCGTCATCG	GGCTCGACCT
71	5385915..5386182	6.67E-06	AGCCTAGCGA	CCGTCACGGAAAGTATCCA	ACCAACCGAT
72	5229521..5229790	6.67E-06	GGCGTGCGCG	GGATCACCCAGCGTCATGT	TGATCTCGGT
73	4676647..4676910	6.67E-06	GCGCCCCATG	AGGTCACTGCCAGTGACAG	GAGGTGGTTC
74	4658870..4659133	6.67E-06	ATCAATCAGG	GCGTCACCATCGGTGACGA	CGCGATCGTC
75	2562586..2562803	6.67E-06	GACCCCTGCG	CGCTCACTCCCCGTGACCT	CACGTCGGCT
76	1230947..1231216	6.67E-06	CTGGCAAGGG	TGGTCACCTAGAGTCACCC	CCGTGCTGAT
77	1103397..1103769	6.67E-06	AGCCAATCAG	CGTTCACACAACGTGACCG	TTTTTCGCGT
78	7935382..7935650	7.80E-06	CCGGCCTGTT	CGGTAACCGAAAGTAATGG	CCGGATCTGC
79	7906935..7907204	7.80E-06	CGCGGACCAC	CGGTAACCCAGAGTGA ACT	AATCCGTTTA
80	7358708..7358980	7.80E-06	CACCGGTCGG	AGATCACCCCTCCGTATTGA	TCTACGACGA
81	6198514..6198774	7.80E-06	ACGGTGCTGA	CAGTCACTGAGCGTAGCTG	AGACGGAAAT
82	6194511..6194783	7.80E-06	CAGCGCCACC	GCCTTACCCAGCGTGACCG	TCACCGCGTC
83	5178014..5178394	7.80E-06	GCCAACCGTG	CCGTCACGCTGCGCGACGT	CGCCGGGCTC
84	5114683..5115065	7.80E-06		CCC GCGC TGTTACCTTGAGTAATGT	GGTGACGAAT
85	4410559..4410844	7.80E-06	ACCGGAACAC	ACGTAACGCATGGTGACGG	GCTTGGCAGG
86	4296677..4296939	7.80E-06	GTTTCGACACA	TCGTTACGCCTGGTGATCG	TGGTCGTGTT

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87	222486..222754	7.80E-06	CGAGAGACGC	CGGTTACGCGCAGTCACCT	CGAGCACCTG
88	8411862..8412157	9.10E-06	TTCACGCGCT	CCTTCACCTTGGGTAACGA	AACGGGCGCT
89	5117418..5117685	9.10E-06	CCGGTAACCC	AGGTCACGCAGCGTCGCTA	AATCGCAGGT
90	4466596..4466870	9.10E-06	CCGGCGGTTCG	CTGTTACGGGCCGTGATGG	CCGGGGCGGG
91	2545819..2546103	9.10E-06	CCTGTCGTGT	CCCTTACGGTCGGTCACCA	GCTCGACACT
92	1511424..1511681	9.10E-06	TGGATTCAAA	TGACTACTCAGCGTTACGG	CAGGGCGAGC
93	143434..143700	9.10E-06	CACTTTCTCG	CGGTGACGGTGAGTCAGCA	AGTGAGGCAT
94	8496037..8496293	1.06E-05	ATGCCCGTCA	AGGCCACGCAGCGTAACAG	ATCGGCCAAG
95	7903343..7903704	1.06E-05	GCCGGGCTTG	CCCTTACCCAGAGTGAGCG	GCTAGAGTCT
96	7484144..7484488	1.06E-05	CCGGAACGA	CCGTCACCCCATGTGATCA	GGATGCCGGA
97	6892302..6892566	1.06E-05	TAACCGTCCG	GCGTCACCCTCCGTAAGCG	TGGTGATCCC
98	5145804..5146059	1.06E-05	CAGCCGCTCA	CCATGACCATCGGTGACCG	ACAACAGCCG
99	5083238..5083493	1.06E-05	GCCACATCGA	CCCCACCCAGCGTGATCA	GGCTCTCAGC
100	1694759..1695044	1.06E-05	ATTCCGCGGG	TGGTTACCGAGCGTTAAGG	TGAGCGGCTG
101	1533642..1533944	1.06E-05	TGATGGTGAA	AAAACACGTTGCGTGATCA	TGACTAGGAT
102	1094153..1094431	1.06E-05	AGCAACCATT	ACGTCACCTTGGGTCACAA	TGACCTCGGA
103	1050581..1050963	1.06E-05	TCCGGCCCCA	CGGTGACGCATAGTCACCT	CCATGCTCGC
104	688524..688843	1.06E-05	ACTATGGCAG	GCGTCACTGTGGGTTACTG	GAGGGCGAGC
105	8656812..8657068	1.23E-05	TACCGCGAAC	TGATTACCGTCGGTCAGCA	CCTGGCCGAC
106	8448919..8449193	1.23E-05	GCCTGACCAC	TGGTGACGCTGCGTATCTG	CCGGCGCTCG
107	8441273..8441545	1.23E-05	CGTGCTCACC	TGATCACACGGCGTGAGGG	AGCACGGCTC
108	8197191..8197509	1.23E-05	GATGAAAAT	GAGTCACCCTCCGTAAGGA	GCTCGACACC
109	1823811..1824068	1.23E-05	CCTGGAGTCC	CGCACACTCACCGTGATCG	GCTTGCCGGA
110	1620466..1620734	1.23E-05	TCCGGCATA	CGGTCGCCGTGCGTGACGG	TCCGGCGGTA
111	1264060..1264323	1.23E-05	GGACACAAGA	GCCTCACCCCTCGGTGACCG	CTAGATCCCC
112	1189129..1189397	1.23E-05	CCAAATGGTC	ACATAACTTTCGTCATGA	CGGACGACGA
113	1171194..1171534	1.23E-05	AGTCACCGGG	CCATCGCGGTGCGTAACCG	CGTCGGCCGC
114	600084..600367	1.23E-05	CTTCGAGCAC	GAGTCACTGAACGTGACCC	TGGACGGTCC
115	356374..356630	1.23E-05	TACATCATGG	TGGTCACCGGGCGTGTCGA	GAAGGGTCTG
116	6737418..6737713	1.42E-05	TAGCAGGCAC	TCGTCACCGTCAGTGGGGA	CCGTGCGGCC
117	5803324..5803581	1.42E-05	GTCCCCGGG	TGCCTACCGAGCGTGACGA	GCGCCTGTTG
118	5300865..5301132	1.42E-05	CGCACCATTC	CCCTTACGCAGCGTGCTA	AAATGGCCAC
119	4359905..4360166	1.42E-05	GATTCGAGCT	CGGTCACACAACGTAGTCA	GCTCGGCCAA
120	1633890..1634168	1.42E-05	GATGTCACTG	GGGTCACTCACAGTAGTGG	GGCAGTACGC
121	1009746..1010015	1.42E-05	CAACGCCGAC	GGGTCACTGGACGTAACGA	GAGAATTCGT
122	7844864..7845123	1.64E-05	ATCTCTGTGT	AAATAACTGACAGTAAGCA	AGAGTGCAAC
123	7595196..7595458	1.64E-05	TCCGAGGCGA	AGGTCACGCTCAGTAGTAG	CCGCAGGGCC
124	7367211..7367488	1.64E-05	GGTGTGACGA	CCGTGACTCGCTGTGATCG	TTCTAACCCG
125	6834433..6834691	1.64E-05	ATCACTCAAG	CAGTGACGCTAAGTAATAG	TTTTCTGCTC
126	6102043..6102317	1.64E-05	CATCAGGTTCG	CGCTTACGGTCCGTGGTGA	ACTGTGAGTA
127	5853469..5853749	1.64E-05	TTGTTCACTG	ACGCCACTAAGCGTGACTG	ATCAGTAACG
128	5436060..5436427	1.64E-05	CGCCACGAGG	CCGACACGCCGCGTAACCG	CGGACCGGCC
129	3788149..3788413	1.64E-05	GAGCCGGCCA	GCGTCACAGGGCGTGACGG	CTCGTTGTGG
130	3020327..3020590	1.64E-05	ACCGGACTCA	CGGTAACAGCGCGTGACGG	AGAAGGGCGG
131	1264585..1264847	1.64E-05	GCCCGGAGGG	CGGTGACCGAGCGTGGTGG	CTACCGAGTG

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132	1037253..1037515	1.64E-05	CAAGTCCCGT	CGATCACCCCACGTGAGCA	AAAGGCTCGG
133	7457186..7457457	1.88E-05	TTCGTCGTAT	CGACGACGGAGAGTGACAA	GTCGGGCCAC
134	4748968..4749274	1.88E-05	TTGATCTGTG	TGGTGACCGAGGGTGTCCG	TGACGTGCGA
135	3029050..3029322	1.88E-05	TCCGCCCCGA	TGCTCACACAGAGTGGTCG	TGGTGCGAGG
136	2552506..2552845	1.88E-05	TGCGGTCATT	TCGTTACCTTCCGTTACCC	GAGGTTTCGT
137	1056800..1057128	1.88E-05	AAGATCTGCA	ACATTACATTCGGTAATCT	AGCTGTATCG
138	8720424..8720746	2.16E-05	AGTTGCCATT	CCAAAACGTGTCGGTGACGA	AGCGTCGTCC
139	8512657..8512941	2.16E-05	CGCGGCCCTT	GAGTCACGCTCCGTAGCTA	CTTAATGTCC
140	8452173..8452447	2.16E-05	GACGCTTCCT	AAGTGACTATAAGTGACCT	CTTGGGCATC
141	5732393..5732648	2.16E-05	GTGGGCTCCG	CCGTCACCGGTGGTAACCG	TTGTGCCGGG
142	5539798..5540064	2.16E-05	CGGCGCCAGC	AGGTCACCGCCGGTGAGCA	CCGTGAACAG
143	4369604..4369922	2.16E-05	CGTGACGATC	TCGTTACAGAGAGTCGCGA	TGCCGGTGGT
144	3989836..3990099	2.16E-05	ATGTGACCAG	AGGTGACGTAGTGTACGA	GGTGCATGTC
145	2380681..2380960	2.16E-05	CGTGAGAGCG	GCAATACTGAGAGTGACCT	TCCCTTTCAC
146	1219329..1219588	2.16E-05	TTCCGTGACC	TGCTCACGGGCGGTGACAA	GATCTATCAC
147	993227..993507	2.16E-05	CCAACACTTG	TAGTAACTGTCTGTATGG	AGTTCTCGGC
148	354391..354667	2.16E-05	ATGGCGATCT	TCGTTACGGTCGGTCTTGA	ACTATCGGTT
149	205525..205792	2.16E-05	GTGTCACCG	CCGTGACCGCGGTGATCT	CACCCAGAGC
150	8505092..8505357	2.47E-05	TGTACACGCA	TGACTACGCTGCGTGAATT	GTTAGCCAG
151	6761416..6761688	2.47E-05	TGGCACCTGA	TTGACACGCGGCGTGACCG	ACACACGGCG
152	2763391..2763698	2.47E-05	TTCATATGTA	TGGATACCGTAGGTGATCG	GATGCCGGTT
153	1254784..1255042	2.47E-05	TACGTCCGAA	AAATTACGCCGGGTACCG	ATAATTTTAC
154	1176103..1176391	2.47E-05	AGTGTCAGCT	TACTCACTCAGAGTTACTC	GTGCCATACG
155	7866639..7866923	2.82E-05	AGCGGGTTGA	CCGCTACTGAACGTCACGA	ACACCGTGTG
156	7744835..7745106	2.82E-05	TCCGTGTTGC	CGGCCACCCAGAGTGACAC	ACCTCACCCA
157	4271531..4271786	2.82E-05	GTTGTAGGCC	GCGTTACGAGCCGTGACCG	TCTCCCCGGA
158	2487754..2488064	2.82E-05	GTGGCCATGA	TCGTGACGGTGTGTGTTGG	TGCGGTAGTA
159	5351129..5351391	3.21E-05	CTTGTTTACG	CCTTCACGCATCGTGAAGT	TCACATTGGT
160	2790196..2790560	3.21E-05	TTCG	ACGTCACCCCCGGTGAGGG	ATTTCGATCCC
161	2328090..2328352	3.21E-05	GCGCTTGAAT	CCGACACTCGCTGTGACGA	ATCGCTCACC
162	250302..250609	3.21E-05	CCCGGCCATT	CGATCACGGGGCGTTAACG	GTCATCAAGC
163	226586..226880	3.21E-05	GTCGGTGAAC	GCGTCACCCGCCGTGAACA	CGAAGATCAG
164	2594..2851	3.21E-05	TCGATGTGGA	CAGACACTGTGCGTCACAA	ACTTGTCCAC
165	7526992..7527364	3.65E-05	CGCATTTACA	TAGTCACAGAGAGCAACCG	CAACGCGCCC
166	5940636..5940892	3.65E-05	GGCGGAGTGT	CGTTACAGTGGCGTCACCA	GCCGGCGGTC
167	5085477..5085740	3.65E-05	TTTCCATTAA	CCATTACACCTAGTAACCT	TCGACAGACT
168	4266294..4266554	3.65E-05	ACCGGCTCCA	CCGTCACCGTCCGCAACGT	CTCCTGGAAC
169	8657215..8657471	4.15E-05	CAACCGCGGC	CGGTCACCGCGGGTCAGCA	GCAGGCCCGA
170	8069961..8070241	4.15E-05	CCGGCTAGTG	TCGTCGCCGTGCGTCACTA	CGCCGCGTAT
171	7906062..7906445	4.15E-05	AACCGGAAGG	TGCTCACGATCCGTTACAG	AAACACGGTC
172	4014185..4014518	4.15E-05	TGAACTCAAT	ACATCACGAAAAGTATCGA	TGTCGTGACG
173	3597235..3597545	4.15E-05	TGGCAGTTCC	ACGCCACTCACCGTATCGA	CGGCCGTCAC
174	2363786..2364044	4.15E-05	CCACTCAAGG	CCATCACCCCTCCGTAAAAC	GCGCCCGGAA
175	424760..425029	4.15E-05	TGTTACCAGG	CAGCGACTTTCGGTAATCA	AATCACCTCG
176	139999..140270	4.15E-05	CATCCCGTTC	TCGGCACTCTGCGTGGTCA	GTGATCCGCG

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177	8666142..8666430	4.70E-05	GATCCAAAGG	TCGTGGCGGTGCGTAATCT	TTTTCCGGAT
178	8514945..8515293	4.70E-05	GGCGAAACCG	TGGTGACGGCTGGTGACTT	CAACGTCACG
179	6362675..6362935	4.70E-05	CACGGTGTTG	CCGTTGCTCAGCGTCACGT	TCCGCTTCCA
180	6019970..6020320	4.70E-05	CCAGGGTCCA	CGATGACGGTGCCTGTGCG	CTCATCCGGC
181	4054167..4054424	4.70E-05	TGTCAGCCGT	TCACTACTGTGCGTAGCTA	TGCACGGAAC
182	10826..11194	4.70E-05	CACTTGCCCTG	GAATCACCTTGAGTAAGGG	TTAACAGTGA
183	8362838..8363113	5.31E-05	CGCTCGTCGT	CAATTACAGAGAGTGGCCC	CAGGATGCGG
184	7886041..7886302	5.31E-05	CCCCGGGTC	ACGTCACCCGCCGTAGCGG	GAAAGCTCTG
185	5976115..5976409	5.31E-05	GGTAACGAGG	CGGTCACTGAGGGCTACGG	TCACGCCGGT
186	1861159..1861414	5.31E-05	CGCGGTCGCA	ATCTGACTCTCCGTACGA	TCCGCTCTTC
187	1441637..1441893	5.31E-05	ACCAGGGCG	ACGTCACAGGCCGTGGTCA	GCGTAGTCTC
188	368463..368812	5.31E-05	TCGAAGTAAA	TGGTGACAATCGGTAACAG	CGGACGTGCG
189	8135487..8135760	5.99E-05	GTAGTCACTT	AGGTTGCGCCGCGTGACCG	TGACCGGTGA
190	3798364..3798628	5.99E-05	CCACCCCAT	CCGTACGTAGAGTCGCAG	ACCGTCCGGG
191	3082315..3082574	5.99E-05	TTGCTGTGAC	AACTAACTTAGAGTGATAA	CTTACTCGCG
192	8525509..8525794	6.74E-05	CGTACCCGTT	CGATAACACAGCGTGCCGA	AAAGTCAGAC
193	7081702..7081962	6.74E-05	CCACGCCCG	GCCTCACCGAGAGTGGCCG	CCGCGTCGAA
194	6155744..6156048	6.74E-05	TGACGTCAGG	CCGTCACTCCTCGTATCGG	GGAACGGCCA
195	4410962..4411307	6.74E-05	CCCTGAAAGT	CGACTACGCACCGTAGCGT	AGTCACCCCG
196	4265782..4266047	6.74E-05	CGCCAGGTGA	TCGACACGAGCCGTAACGG	CGGCGCGAGC
197	2689490..2689766	6.74E-05	CACCCTGGAG	TGGTGACACTGCGTTGCCT	GCTTGTGGAC
198	1808521..1808804	6.74E-05	CGTCAATCAT	CAGCGACGGCGAGTGACCG	CCTCCGGCTC
199	1750664..1751040	6.74E-05	TCCGTGAGCA	TGATCACCGAGCGTCCCGT	CCGCCGACGG
200	289693..290013	6.74E-05	GTGACGATCT	CCTTCGCGCTGCGTAACGT	CGTGGACACC
201	8447425..8447705	7.58E-05	GACCGCTGAA	TTGTCACTAGCGGTCACGG	CATTTCTGGT
202	873292..873554	7.58E-05	TGAATCCGTT	TGCCTACGCTGAGTAATTC	CGGCGTGGTA
203	730583..730957	7.58E-05	GAGAGAAGGA	GGATCACTGTGCGTACCGT	CCTCGTGTGC
204	595894..596164	7.58E-05	ATCGGGTACG	TGGTCGCACACGGTGACCC	GGTCGAGCGT
205	8485715..8486036	8.50E-05	GGTCGCGGTG	GCCTCACCCCTCCGTGTTCC	GGTCGGTCGC
206	8462486..8462752	8.50E-05	CGTAGTTGGG	TGATTACGCAACGTTGTCC	CTCAAATACG
207	8406748..8407032	8.50E-05	CGTCATACTC	CGGCTGCGGAGCGTAACCA	GGCTCGGGCG
208	8378713..8378970	8.50E-05	GCTGATGAGC	CGGCTACCCGCTGTAATCA	TTCTGACCGA
209	8186072..8186327	8.50E-05	GTCGTCAAGG	CGGTCACGGCGCGTAGCTC	CGATGAGGAG
210	5267540..5267839	8.50E-05	TACCCGTCAA	AAGTGACGCACCGTTGCGG	GTCGATCCCC
211	1751762..1752032	8.50E-05	TGATCACTTC	CGACTACTGTCCGTCACTC	TTTGGATTGA
212	1649128..1649396	8.50E-05	TTGTCCGGGC	TCCTCACCTTCCGTATCCT	TGCCACCCTC
213	1488864..1489140	8.50E-05	CCGGCTGTTA	CAGCCACCGACCGTCACAG	CCCGAGGTCCG
214	1358859..1359165	8.50E-05	CAGCATCTTG	TGATCGCTGTCCGTATTCA	TCCACGGGGA
215	762712..763005	8.50E-05	GTGGGTGATA	TGGCGACCCTCTGTGAGCA	GGCGGAATGC
216	7791515..7791776	9.51E-05	ACGAGGTGAA	CAGTGACCACACGTGACCG	GCAGCCCCTG
217	7356973..7357307	9.51E-05	GTGGGCGATG	TCGTCACGGGCGGTGCCGG	TGACGGCCTG
218	3946708..3946983	9.51E-05	CCGGTGCCGG	TGATCACCCGCGGCGACGG	CTGCTATGTC
219	2795138..2795408	9.51E-05	GGGCAGCGGC	CGGTAACCGTCGGCGACCG	GCATGCCCAG
220	2364900..2365249	9.51E-05	AGTAGTTGAT	CCTTCACTGAGAGCAACTG	CCGCGCTAGC
221	2169162..2169427	9.51E-05	GGTATCGATG	TGATTACTCAGGGTGTGTC	GGATCGAGGA

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222	1984962..1985249	9.51E-05	CCGTGGGCAA	CGAGCACGGAGAGTGGTCG	TTCGGGCGTA
223	1026685..1026961	9.51E-05	CGTTCGGTAG	GAATAACTGAACGTTACCT	CTTAACTCCA
224	1021955..1022242	9.51E-05	GACGGCGTCG	GAATCACCCAGCGTGAGAC	ACCGCTGCTC
225	8387412..8387672	1.06E-04	GCTGACCCTC	GGGTGACTCTGTGTAGTGG	GGTGGCCGAT
226	7652398..7652677	1.06E-04	GCCTTCGCCA	TCGTGACTCCTTGTGACGC	GCTGCGTCTC
227	3212902..3213176	1.06E-04	CTCGCCGACG	ACGTACGCCGAGCAATGT	CCCGAGCGTG
228	1295021..1295279	1.06E-04	CACGGCGTTG	CTGTACGTTGCGTGTGGT	GTCGGAACGT
229	330581..330840	1.06E-04	AGAGCCTCGT	TGGTGACGCGCTGTGAAAA	CGGTCAAGACG
230	7911162..7911418	1.19E-04	CACTTGACAT	TGGCCACTCGGGGTAGTGA	CACAGGCACC
231	7846864..7847143	1.19E-04	TCTAGTCAGA	GTTCCACGCAGGGTGACGA	CGCACCCGAC
232	5116789..5117061	1.19E-04	CAGGGCGACG	ATGACACCGATGGTGACGG	TCCACCCGAG
233	4733507..4733779	1.19E-04	CAGCCCCTGG	CCAGCACGCAGCGTAGTCG	CACCCTTGAT
234	2648075..2648338	1.19E-04	GTCCCGGAGC	CGGTACGGGCGGTGCTGG	TTCGACCCAT
235	1453450..1453821	1.19E-04	CTCCAGCCCG	TGGAAACCGAACGTGACGC	CGGGCACCAT
236	1321420..1321757	1.19E-04	GTCGCTGTCC	TTGTCACTGCTCGTGTCCG	CATGAAAGGT
237	1080600..1080864	1.19E-04	AACGAAACCT	GCGTCACAATCAGTCACGC	CC
238	361392..361638	1.19E-04	TGGCCTCAAG	GCGTCGCTGAGTGTGATGT	CCGATCCGGC
239	310469..310784	1.19E-04	TGGCCTCGG	AGGTAGCTGTGCGTGACCC	CCTAGCGGAG
240	8168913..8169278	1.32E-04	GAAAGAGTTT	GCCTTACGGTCCGTATCTA	TGTGAAGGAC
241	7674971..7675236	1.32E-04	GGTCATGGCA	CCAGCACTCCACGTGATCG	CCGGGCCTGG
242	4272615..4272929	1.32E-04	TGAGCTGTGA	CGGATACCAAGTGTGAGCA	TGGTTGACGC
243	3112623..3112892	1.32E-04	CGATCATCGA	TGGTTACGGGCTGTGGCAG	GTCGGGGTGC
244	2879582..2879837	1.32E-04	GTGGTTTTTG	CAGTCACGGGGAGCAACTG	TACCATCCGA
245	2211577..2211849	1.32E-04	CTCGGCTCTT	CGGTGACTGTGTGTTGCTG	GGGTGGCCCC
246	1965600..1965892	1.32E-04	CATCCGTGCG	GGGTGACGCGCGGTACGT	GAAGCGGAAC
247	949656..949915	1.32E-04	TAAGTAAGAT	CCGTGACTGAGCGCTACCT	CGTCTGAACG
248	740983..741245	1.32E-04	CCCTGAGCTG	CGGTTACTCACCGCTATCC	CACTGTCGTG
249	8528804..8529066	1.47E-04	AGGCGACACT	TCGTTACAAGGCGTAGCCG	GCTGCCACGA
250	6610261..6610644	1.47E-04	CAAGTGATAG	ATATCACAATGGGTATCCA	GTGCCGCCCA
251	5560011..5560319	1.47E-04	AGCGGCGCCA	CGAGTACCCCGCGTGACTG	ACCCGCTCGC
252	2386332..2386598	1.47E-04	CACCGGGGGA	TTGACACCGAACGTAACAT	ATCAAATATC
253	2106157..2106477	1.47E-04	GAACCGTCCT	GGACCACGCAGGGTGAGCC	CCCGCTCGTG
254	1821745..1822005	1.47E-04	TTTGAACGCC	TTGTTACAACCTGGTGACGA	CGTCATCATA
255	763142..763403	1.47E-04	CACGGAATTG	GAATCACTCGGTGTAGCCA	AGCTATTTAC
256	8755310..8755587	1.63E-04	CACATTCTTG	GCATAACCGTAAGTGCCG	AACCCACTAC
257	6624245..6624509	1.63E-04	GGTGGTAGTC	ATGTCACTGACAGTAGGAA	ATCGTTAACG
258	5214684..5214944	1.63E-04	GGCTCCGTAA	CACTCACTGTGAGCGACGC	CTCCCACGGT
259	3966381..3966763	1.63E-04	AAACTAAGAT	CAATCACTCTCCGTGGGAC	AGAACCGAGT
260	1526402..1526762	1.63E-04	CTCAATCCGT	CAGTCACTCAACGTTGAGG	AGCCCGCAGG
261	1163827..1164099	1.63E-04	TCCAAGGCG	AGCCTACTGTGCGTAAGCT	GCCGCGGTTC
262	1126261..1126534	1.63E-04	AGGTTAATCC	CGATAACGGGCTGTCAATTT	GATCGCAGCT
263	8320551..8320818	1.81E-04	CAGTCCGTCA	CGGTACGGTGGGTGCGCC	GCCCCGTGGTG
264	5403424..5403790	1.81E-04	GCGCCCCGA	GGATTACCTTTCGTGTCCG	CCGCCACAGT
265	2343362..2343627	1.81E-04	GACGTTCCGC	CAGGCACGGAGAGTAGTCG	TTAGGCACTG
266	1552477..1552749	1.81E-04	TGTAAACCTC	CCATCGCCTTCTGTGATTG	TGCCCCTCGC

267	847230..847533	1.81E-04	AACGTAGCAT	CCTTCACTCACCGTTCCCG	ACCCGTAACG
268	719203..719467	1.81E-04	TCTGTAAACG	CATCAACGCAGCGTCACCG	TGTGTGTATC
269	87978..88232	1.81E-04	AGAGGTTTTTC	TCCTGACGCATCGTTAACG	GTATTTGTCC
270	7805256..7805598	2.00E-04	TCACGCGGGA	CGACAACGGGGTGTAAC TA	GTACGACGGG
271	7722472..7722823	2.00E-04	GTTACAGCCG	TGATCACGTCCCGTGCCAA	GCTGGATTAA
272	6241659..6241938	2.00E-04	CGCCGCTGAA	CACCTACTTAACGTAACGG	GCGGAGGCAC
273	4959030..4959286	2.00E-04	CATCCCCGTC	AAACCACCCTAAGTAGTGA	ATTAGTTACG
274	1824578..1824835	2.00E-04	AGGTTTCGCC	GCGTCACGGAGATTGACCG	AACGGACTAG
275	430249..430585	2.00E-04	CGCAGTGGGT	CCAACACGCTCTGTGCGTGA	CATCTGGGTG
276	360981..361267	2.00E-04	GACAGCGAGG	TAGTCGCCCATCGTCATGT	CGTCGAACGA
277	8642381..8642649	2.21E-04	CAAGAGCGCA	ACGCTACGTAAAGTAATTC	TCGCCGAGGG
278	7852533..7852823	2.21E-04	GGACTTGAC	CGAATACTCACCGTATGCG	ATGGAGCGCC
279	5067083..5067351	2.21E-04	CCTCGTCAGC	CCATCACGGGTCGCAATCG	GGTCTGTGCG
280	1654530..1654837	2.21E-04	ACGACATCTC	CGGTAACGGTGCGTACACG	CACATGACCA
281	1355945..1356216	2.21E-04	TTCCGCCATT	CATTCACTCCACGTAGTGA	TTCGCTACCA
282	8534120..8534389	2.44E-04	ACCTCAACGA	CAGCAACCACCGTCAACA	AGTCACCATC
283	8520462..8520749	2.44E-04	GGTGCGGGCA	TCGTACATATAGCGATTT	GTCCGTTTAC
284	3841135..3841418	2.44E-04	ACCGGCGGCG	TGGACACCGACGGTGAGAC	CGACGGCGAC
285	522107..522477	2.44E-04	CACGTTGAGT	CGAACACTGCTGGTCACCG	GCGGCGCCGG
286	187562..187916	2.44E-04	ACCTGCTGAA	AGAACACGCGGAGTCACTC	ACTGCGCGAT
287	93945..94327	2.44E-04	CGGCCGGCCT	TGGTCACTCCCCGTACGCT	CTGATGGGCC
288	41573..41887	2.44E-04	CCATCGAAGA	ATGTTGCGGAACGTCACCA	TCGCCGATCG
289	8167186..8167456	2.68E-04	AAGCCGATTG	TCATCACCGCAGGTACACAC	CCGAGAGGGT
290	7463467..7463722	2.68E-04	TTTTTCAAGC	TCACCACCAGGGGTGATGC	CACGATCACT
291	7041161..7041454	2.68E-04	TGAGATCAGC	GTATGGCGGAGCGTAACGA	CAGGGATCAC
292	6963157..6963539	2.68E-04	TTTGAGGCAT	GCCTTACCCTAATGTAATGG	ATCTTTCTGG
293	5438090..5438400	2.68E-04	GCTGGTTACC	TCTTGACTGTTGGTCAAGA	AGCGCTTCGG
294	5213501..5213788	2.68E-04	CTTGAGACC	TGCTCACCCAGGGTGCGGG	TGTCCTTCCA
295	3108370..3108729	2.68E-04	GATGGTGACT	TGTTGACGGTGGGTTGCTG	TCGTTGAGGT
296	1592069..1592446	2.68E-04	GGCGTCTCGC	AACCTACGTTGAGTAAGCA	GATTACACCC
297	977136..977432	2.68E-04	CCGGCGGGAG	TCACTACCGTGGGTGCTCG	CACAGGGTTG
298	8420679..8421010	2.95E-04	ACTGCCATCC	CGCCACCCTGAGTCTTGA	TGGTTCGGGT
299	6233515..6233773	2.95E-04	GCGGTGGTCA	TGGTCACCGCCCTTGATCA	CTCTGCGTTG
300	3346984..3347296	2.95E-04	ATAGCGCGAA	AGCACACCGAGGGTGCCCG	GTATGCGAAG
301	3272827..3273115	2.95E-04	TGAAGTCGTT	CGGTCACGATGAGTTCCAT	CAACGACGAG
302	2080681..2080944	2.95E-04	GCGATGTCGA	CGCTGACCAAACGTCACAA	ATAGTCGAAG
303	5955661..5956043	3.24E-04	CCTGTTAACC	GCGTTACGGTGAGTGCATG	AACGCACCGG
304	8087075..8087373	3.56E-04	CAGGCCATCG	TCGCCACGCTCGGCTACGT	CTTCTCGCCC
305	7137966..7138278	3.56E-04	GGCTTTTCGT	TGCTCACGTTCTGTAGATA	CGCCCCTTCA
306	7040470..7040805	3.56E-04	CGTAA	CGACCACGGAGCGTTTCTC	GGTTACCAAG
307	2654532..2654820	3.56E-04	AGCTGTCTGG	TTCGGACCGTCCGTGACCA	GCAACTACCC
308	2548123..2548393	3.56E-04	AGGAGTGCCA	GAACTACGCGGAGTCACTG	CGTCGGAATC
309	2546727..2547044	3.56E-04	CCGAGGATCA	GCCTCACTTTGAGCGATTG	CTCGGTGACG
310	749647..749977	3.56E-04	AGATGAGCAA	CCGCTACGAGCTGTACGA	TGGGCCGCTG
311	139556..139818	3.56E-04	GTCATGCAGC	CCACTACGCTGTGCAATCT	CGCATGTGGG

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312	8235173..8235552	3.90E-04	GGCGCTGTCT	CCGTCACGCATGGCATCGG	TAAGCCCTTG
313	3622897..3623225	3.90E-04	CGCCATCGGG	AGTCAACCATCCGTGACGT	AAAGATGAGC
314	931659..931925	3.90E-04	CTTGACATGG	TGGTTGCGGAGTGTGAATC	TAGAAGCACG
315	98496..98761	3.90E-04	AGGCCGCCGT	TCACCACCTGTAGTCACTA	AGTTATTACC
316	5232967..5233333	4.26E-04	TTCGTAATTG	TTTTAACTCCGGGTGTCGA	TTGATTGGCC
317	4824710..4824973	4.26E-04	CGGGTGGATT	CGGCCGCATACCGTGATCT	GCTGTCCTGG
318	7297693..7298067	4.65E-04	GGAGCGAAAA	CGCCAACGGCCCGTTACCA	GGATCCTGAT
319	7023985..7024274	4.65E-04	CACAGTCGAA	TAGCGACAGAGGGTGAAAG	GTTGAGGTCC
320	4825530..4825845	4.65E-04	CAGCCGAGAA	TACATACGCTCAGTGTCGC	ATTGACTACA
321	4088983..4089241	4.65E-04	CGCGTCAGTC	TGTCGACGCTTCGTGTTGA	GTTGTCACTT
322	849737..850015	4.65E-04	CAGTAGCTCC	GAGTGACCCGCGGTGGTGC	TGCTTCGCGG
323	44614..44993	4.65E-04	CCAAGCGCAA	CAGAAACGCACCGTGGGGG	GTTTCGGGGG
324	8585740..8586008	5.08E-04	ACTTTGACAG	AGAGAACGCTCCGTACAT	CATGAGTGAG
325	7507182..7507438	5.08E-04	TTCATCAAGG	TCAATACGTGGGGTAAATG	TCACCCAGGT
326	7211385..7211658	5.08E-04	CCCCGTCAAC	TCAACACGTGCCGTCAACT	CACAGTAGGC
327	1430658..1430981	5.08E-04	CGTCACGACA	TCGACACTATGAGTTGTGC	AAGTTGCACG
328	939736..940004	5.08E-04	GTTAGCGTCT	AGGTGACGAGGGGTGAATC	AGCAAAGTTC
329	7499624..7499886	5.53E-04	CCGCGCTTGG	AAAGCACAGGCAGTAACGT	GAAGCACCAT
330	1573538..1573817	5.53E-04	TCATGATCTA	AGACTACGCGCAGTGCCCG	TCCGAACGCA
331	8686973..8687341	6.02E-04	CGTAGGCACA	CGAGCACGTACGGTAGTTG	GAAAAGAGAG
332	6242786..6243052	6.02E-04	GCGGTAGCGG	GGGTACAGCTGGGCGCCCG	TACAGTGGTT
333	5730025..5730262	6.02E-04	CGCCGCGGGG	ACAGCACACTCTGTGGCCG	GAAGGGGCCG
334	1007267..1007618	6.02E-04	GGTGTGGGCA	CCGCCACCCCGGTGGCGC	GAAATACTTC
335	8531011..8531289	6.54E-04	ATCAGCC	GGATCACCAACTGCCATCA	CGGGCATCGC
336	549631..550012	7.10E-04	TACCGCCTGG	ACGTGGCGTTTCGGTGTCGA	GCCCGTTTAA
337	71932..72260	7.10E-04	GGGGGTGCCA	TCGTTGCGTACCGTTTCGT	TATCTCTTGC
338	6468886..6469183	7.69E-04	AGGACTCCGG	CCGTGACACCTTGTAGCGG	ATCAAACCGT
339	3416004..3416317	7.69E-04	CGCCACTGGT	TGATTACGTCGCGGAGGC	CGTGTCGCCT
340	8492249..8492625	8.33E-04	GCGGTGGCAC	CCGCTGCGGAAGGTCATCG	CGCGGTCTCG
341	1063647..1063902	8.33E-04	AGGGGCGGGC	GGCGGACGCAGAGTGAGCG	CAGGGCACCG
342	5233539..5233863	9.01E-04	AGAAGTGCCG	GTATTGCGATGGGTGACGC	TGGCCTTGAC
343	3960276..3960541	9.01E-04	AGGAAATCCT	CCGAAACTTTCAGTTTCTG	CGGTTTCAGCG
344	467387..467654	9.01E-04	TTGAGGGCAT	GGTTAACGGCTGGTGACGC	CTATTGCGCC
345	1846550..1846791	1.13E-03	GCACGTGAAG	GTGCCACTCGGCGGATCG	CCGATGATCT
346	4326961..4327218	1.41E-03	AGCCGTTTGA	ACGTCACTGTGGGCACGCG	TGGTCGACGG

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**Table S5.** List of the AmBldD target gene candidates.

a. The position of the central nucleotide of each AmBldD box is shown. The transcriptional start points predicted by previous RNA-Seq analyses were set as +1. The highlighted transcriptional start points of four genes (*AMIS6880*, *AMIS65300*, *AMIS62190* and *AMIS78290*) were determined by 5'-RACE. The RNA samples for the qRT-PCR experiment were used for the 5'-RACE experiment. The RNA-Seq analyses were performed using RNA samples prepared from the cells cultivated on HAT agar for 1, 3, 6 and 40 days (19).

b. Expression levels (RPKM) of each gene in the RNA-Seq analyses. Values above the threshold (RPKM > 200) are highlighted.

c. Amino acid sequence identity (left) and similarity (right) of each gene product with its orthologues (or homologues) in *Actinoplanes* sp. SE50/110 (ase), *Actinoplanes* sp. N902-109 (actn) and *Actinoplanes friuliensis* (afs) are shown. Values above the threshold (identity > 70%) are highlighted. "-" indicates that no homologue was found using the BLAST algorithm of the CLC Genomics Workbench (e-value < 0.0001).

Locus tag (AMIS number)	AmBldD box <sup>a</sup>	RPKM <sup>b</sup>				Identity / Similarity <sup>c</sup>			Definition	Classification
		Day 1	Day 3	Day 6	Day 40	ase	actn	afs		
660	40	128.1	16.4	11.8	3.1	38/58	44/59	44/62	putative subtilase-family protease	4.6 miscellaneous
780	30	138.9	194.8	180.2	136.0	87/92	85/92	88/94	putative branched-chain alpha keto acid dehydrogenase E1 alpha subunit	2.2 metabolism of amino acids and related molecules
830	-23	618.6	574.7	360.9	105.1	98/99	91/96	89/97	putative heat shock protein Hsp70 (DnaK)	4.1 adaptation of atypical condition
1980	25	48.0	2555.1	936.5	101.2	97/99	89/95	95/98	putative MerR-family transcriptional regulator	3.5.2 regulation
2230	-77	22.0	13.0	13.5	10.2	45/71	50/77	40/63	putative GntR-family transcriptional regulator	3.5.2 regulation
2990	23	155.0	43.0	28.8	12.3	98/99	91/97	93/98	putative IclR-family transcriptional regulator	3.5.2 regulation
3140	-26	56.3	52.8	45.0	30.5	88/95	86/93	88/94	putative haloacid dehalogenase-like hydrolase	4.6 miscellaneous
4020	-84	249.9	43.4	46.5	25.8	70/80	64/78	64/79	hypothetical protein	5 similar to unknown proteins
4030	-97	229.7	39.3	48.3	33.0	62/77	59/72	61/77	hypothetical protein	5 similar to unknown proteins
4090	-140	1.8	91.1	35.8	161.6	72/78	72/80	67/82	putative cysteine dioxygenase	2.2 metabolism of amino acids and related molecules
4100	-115	82.3	25.2	24.5	35.9	57/73	48/63	49/62	hypothetical protein	5 similar to unknown proteins
4820	-127	103.3	38.4	33.9	15.1	-	-	-	hypothetical protein	5 similar to unknown proteins
4830	40	125.3	93.9	78.5	42.7	81/91	26/44	31/47	putative NAD-dependent epimerase/dehydratase	4.6 miscellaneous
5080	-142	250.5	61.2	52.5	41.3	66/77	71/82	72/83	putative 5'-nucleotidase	2.3 metabolism of nucleotides and nucleic acids
5280	-153	15.3	107.4	65.8	26.3	69/76	-	57/69	hypothetical protein	6 no similarity
6500	-127	43.6	15.7	14.8	12.6	69/78	55/68	55/66	hypothetical protein	5 similar to unknown proteins
6510	-76	312.1	48.4	44.6	37.8	75/81	70/77	79/89	putative sensor-like histidine kinase	1.3 sensor
6800	-159	968.9	106.6	91.7	43.4	86/93	78/86	78/86	putative ABC transporter substrate-binding protein	1.2 transport / binding protein & lipoprotein
6880	-172 and -150	670.6	1351.1	631.9	225.5	98/99	93/96	95/97	putative WhiB-family transcriptional regulator	3.5.2 regulation
6890	10	83.8	443.4	206.4	74.3	94/95	87/90	86/89	putative LuxR-family transcriptional regulator	3.5.2 regulation
6970	-83	379.5	193.2	136.4	80.4	91/94	86/91	87/92	putative NUDIX hydrolase	4.6 miscellaneous
7140	-121	476.9	63.1	65.9	23.7	75/85	61/81	73/81	putative M23-family peptidase	4.6 miscellaneous
7150	-55	199.3	101.2	95.5	69.0	95/98	90/96	94/97	putative isobutyryl-CoA mutase chain B	2.4 metabolism of lipids
7950	-61	320.7	78.8	53.4	19.2	-	34/52	34/53	putative restriction endonuclease	4.1 adaptation of atypical condition
7960	-81	42.1	32.7	55.5	34.8	42/59	43/60	46/63	putative GntR-family transcriptional regulator	3.5.2 regulation
8500	-162	153.2	97.5	69.2	55.9	95/98	91/94	91/93	putative glycosyltransferase	4.6 miscellaneous
8700	-118	10.8	672.2	876.3	377.1	72/84	85/90	74/84	putative S-adenosyl-L-homocysteine hydrolase	2.2 metabolism of amino acids and related molecules
8770	-117	1281.8	1979.4	2169.1	2574.5	90/92	84/89	83/90	putative S30AE family protein	4.6 miscellaneous
8860	-40	489.6	184.7	147.6	73.4	98/99	97/99	97/99	putative cell division ATP-binding protein FtsE	1.7 cell division
9130	-23	36.8	25.5	16.4	8.4	57/66	63/73	63/74	hypothetical protein	6 no similarity
9140	-43	102.0	246.0	73.8	22.7	78/89	54/65	82/89	hypothetical protein	6 no similarity
9230	-20	2496.0	2233.9	2000.7	1082.4	95/98	85/94	86/94	hypothetical protein	6 no similarity
9260	31	53.6	44.6	22.4	10.4	78/86	69/78	73/83	putative diguanylate cyclase/phosphodiesterase with PAS sensor	1.3 sensor
9410	-38	1692.7	501.9	917.3	409.0	91/94	92/97	94/98	hypothetical protein of Mov34/MPN/PAD-1 family	5 similar to unknown proteins
9450	-134	151.1	241.1	221.7	50.0	94/97	89/95	88/95	hypothetical protein of metallo-beta-lactamase superfamily	5 similar to unknown proteins
9620	-7	96.7	101.8	93.6	81.8	81/91	-	-	putative S-adenosylmethionine decarboxylase	2.2 metabolism of amino acids and related molecules
9630	-163	86.3	31.0	23.0	23.1	71/78	62/81	-	hypothetical protein	5 similar to unknown proteins

9910	-138	1359.1	3194.7	3468.3	3236.2	87/94	69/81	68/81	hypothetical protein	5 similar to unknown proteins
10100	-100	176.9	85.9	62.1	29.7	69/77	42/60	67/78	putative integral membrane protein	4.6 miscellaneous
10230	-14	76.2	124.2	76.6	293.4	58/65	57/72	44/62	hypothetical protein	5 similar to unknown proteins
10520	-94	468.4	82.6	101.8	47.4	55/71	62/77	65/79	hypothetical protein of NlpC/P60 family	5 similar to unknown proteins
11040	-16	99.6	225.0	160.0	223.4	68/77	67/79	63/78	hypothetical protein	5 similar to unknown proteins
11190	-5	45.0	30.1	37.1	11.4	92/94	55/70	55/71	putative ArsR-family transcriptional regulator	3.5.2 regulation
11690	-76	55.2	87.2	37.5	9.6	67/79	59/75	65/78	hypothetical protein	5 similar to unknown proteins
12710	-70	78.4	162.1	58.9	19.1	43/53	47/60	51/66	hypothetical protein	5 similar to unknown proteins
12740	-113	72.4	91.2	53.6	21.3	-	-	-	hypothetical protein	6 no similarity
13400	-18	650.4	118.6	131.9	45.8	88/95	70/85	72/85	putative glyceraldehyde 3-phosphate dehydrogenase	2.1.2 main glycolytic pathways
13490	-63	83.5	103.1	121.6	106.0	83/89	77/85	79/86	putative NH <sub>3</sub> -dependent NAD <sup>+</sup> synthetase	2.5 metabolism of coenzymes
13500	-24	125.5	215.2	159.7	79.7	95/98	93/97	94/97	putative glutamine synthetase	2.2 metabolism of amino acids and related molecules
14070	-168	135.5	37.7	28.1	12.2	96/98	90/96	91/95	putative UDP-N-acetylglucosamine 1-carboxyvinyltransferase	3.5.2 regulation
14490	-50	667.1	260.3	271.4	161.9	99/99	93/97	93/96	putative transcriptional regulator containing cyclic nucleotide-binding domain	3.5.2 regulation
14500	-23	10.0	9.5	9.2	7.5	72/79	65/77	69/80	hypothetical protein	5 similar to unknown proteins
14670	-30	223.1	101.5	72.2	18.7	92/96	91/96	90/96	hypothetical protein	5 similar to unknown proteins
14860	-169	603.3	722.6	1318.7	229.0	74/84	70/80	70/80	putative succinate dehydrogenase cytochrome b-556 subunit	2.1.3 TCA cycle
15090	-115	342.6	116.8	104.7	97.8	93/95	90/93	92/95	putative ATPase associated with various cellular activities	4.6 miscellaneous
15100	-33	79.5	81.0	97.7	95.2	87/91	82/89	82/90	putative leucyl-tRNA synthetase	3.7.2 aminoacyl-tRNA transferases
15140	-62	260.6	15.5	22.1	10.1	68/84	65/76	69/83	hypothetical protein of NlpC/P60 family	5 similar to unknown proteins
15330	-30	207.4	241.1	223.1	131.9	95/97	87/92	91/94	putative TraR/DksA-family transcriptional regulator	3.5.2 regulation
15730	-89	252.1	605.0	527.8	210.1	95/97	88/94	88/93	putative pyruvate kinase	2.1.2 main glycolytic pathways
16220	-164	1271.8	1120.5	979.0	189.2	95/95	86/92	83/90	hypothetical protein	5 similar to unknown proteins
17080	42	28.6	58.8	43.7	217.2	44/61	59/74	54/70	putative RNA polymerase ECF-subfamily sigma factor	3.5.2 regulation
17210	-126	8.2	9.4	5.2	5.6	82/89	87/90	49/62	putative DNA polymerase IV	3.2 DNA modification & repair
17900	16	8.6	8.9	12.0	165.9	57/71	51/66	44/59	putative LuxR-family transcriptional regulator	3.5.2 regulation
18020	-140	0.8	1.5	2.4	97.8	67/74	-	29/40	putative diacylglycerol kinase	2.1 metabolism of carbohydrates and related molecules
18030	-28	1.9	3.8	28.1	566.7	51/68	50/68	50/68	putative polyphosphate kinase	2.6 metabolism of phosphate
20410	-28	55.2	32.5	32.0	24.2	40/54	51/64	-	hypothetical protein	6 no similarity
22420	-72	737.9	142.6	104.1	67.2	-	30/48	56/66	hypothetical protein	5 similar to unknown proteins
22570	-54	62.3	4.2	1.5	0.3	35/50	36/49	36/49	putative NUDIX hydrolase	2.4 metabolism of lipids
22780	-65	129.3	76.5	55.4	22.4	-	-	-	hypothetical protein	5 similar to unknown proteins
22980	-16	4.0	8.4	7.4	2.7	38/56	32/54	31/54	putative acyl-CoA dehydrogenase	2.4 metabolism of lipids
22990	-23	3.2	5.1	4.0	2.3	54/68	56/69	55/69	putative aldehyde dehydrogenase	4.6 miscellaneous
24370	-181	53.5	7.8	5.9	4.0	75/84	56/69	82/91	putative spore coat protein CotH	1.8 sporulation
24390	-27	17.7	60.3	204.3	45.0	71/80	66/79	58/73	hypothetical protein	6 no similarity
25310	25	19.1	16.4	13.0	5.0	29/44	31/43	34/50	putative TetR-family transcriptional regulator	3.5.2 regulation
25320	-83	19.9	3.1	1.1	0.6	32/52	36/56	28/48	hypothetical protein	5 similar to unknown proteins
25370	-5	31.2	219.2	84.3	4.8	94/96	66/76	-	hypothetical protein	5 similar to unknown proteins
25380	-140	14.1	6.4	3.6	1.8	52/63	69/78	-	putative sulfotransferase	2.7 metabolism of sulfur
25710	-11	21.5	27.4	9.8	6.2	-	-	33/54	putative response regulator receiver domain protein	3.5.2 regulation
26290	-8	102.6	24.5	15.5	6.2	30/42	35/45	33/46	putative trypsin-like serine protease	3.5.2 regulation
28700	-23	9.7	109.1	106.1	53.0	-	-	-	hypothetical protein	5 similar to unknown proteins
28800	-60	11.6	11.8	15.6	14.3	68/76	69/81	74/85	hypothetical protein of NlpC/P60 family	5 similar to unknown proteins
28810	-182	0.3	2.4	3.4	69.3	41/60	45/60	50/61	hypothetical protein	5 similar to unknown proteins
29340	-13	66.6	104.2	96.1	96.5	47/58	74/84	48/60	putative alcohol dehydrogenase	2.1.2 main glycolytic pathways

29540	-64	25.6	22.1	19.6	4.6	-	-	-	hypothetical protein	6 no similarity
29550	43	2.0	1.1	0.4	1.4	27/42	29/42	67/75	putative transposase	3.5.2 regulation
30270	-9	6.8	78.4	35.7	30.1	47/63	50/68	49/72	hypothetical protein	5 similar to unknown proteins
31170	-165	3.0	3.9	4.0	72.1	37/51	36/54	38/53	putative methyltransferase	4.6 miscellaneous
31180	-12	23.9	425.9	171.7	81.8	-	-	-	hypothetical protein	6 no similarity
31870	-40	35.1	899.3	317.7	11.0	-	34/48	34/49	hypothetical protein	6 no similarity
32070	-176	402.8	20.0	28.0	5.5	-	-	31/51	putative transcriptional regulator	3.5.2 regulation
32080	-143	94.2	7.3	13.6	2.8	-	-	-	hypothetical protein	6 no similarity
32410	-109	187.4	17.9	21.8	13.8	-	-	-	hypothetical protein	5 similar to unknown proteins
32420	-170	251.2	7.3	9.0	0.8	49/62	40/55	42/55	putative NRPS-related enzyme	4.3 antibiotic production
36070	-85	13.3	529.7	387.8	179.5	68/77	50/63	40/54	putative two-component system sensor kinase	3.5.2 regulation
36080	-21	117.4	971.6	749.1	327.8	84/89	47/63	48/65	putative response regulator receiver domain protein	3.5.2 regulation
36240	-169	123.9	109.6	87.2	35.2	-	-	-	hypothetical protein	6 no similarity
36250	-151	18.8	15.3	8.2	2.4	66/76	42/50	38/50	hypothetical protein	5 similar to unknown proteins
36260	-99	18.0	11.3	6.5	2.1	-	-	-	hypothetical protein	6 no similarity
37750	-148	628.7	9.3	6.4	3.1	79/88	71/82	67/81	putative ABC transporter substrate-binding protein	1.2 transport / binding protein & lipoprotein
37800	-83	7.6	159.4	99.8	16.2	35/49	32/45	-	hypothetical protein	5 similar to unknown proteins
37810	-3	11.0	12.5	6.0	1.7	-	-	40/51	hypothetical protein	5 similar to unknown proteins
38000	-23	10.5	7.1	2.8	1.2	77/87	-	35/54	putative TetR-family transcriptional regulator	3.5.2 regulation
38260	-8	65.3	57.3	49.3	26.5	63/77	62/72	-	hypothetical protein	5 similar to unknown proteins
39800	-65	110.5	64.3	43.2	72.2	62/78	70/82	73/82	putative glycosyltransferase	4.6 miscellaneous
41990	-113	127.2	213.7	189.7	122.8	82/87	80/89	79/90	hypothetical protein	5 similar to unknown proteins
42610	-184	39.1	109.4	54.5	22.0	68/80	70/83	46/60	putative cadmium resistance transporter	1.2 transport / binding protein & lipoprotein
44500	-112	15.4	110.3	134.5	5.6	68/77	65/77	33/55	hypothetical protein	5 similar to unknown proteins
45340	-40	100.2	15.3	12.5	3.3	-	-	-	hypothetical protein	5 similar to unknown proteins
46050	56	60.3	36.7	32.3	15.7	-	33/57	-	hypothetical protein	6 no similarity
47300	-56	42.6	700.3	183.6	33.1	64/74	50/62	51/61	hypothetical protein	5 similar to unknown proteins
47940	-188	49.9	7.1	15.4	7.3	48/64	-	-	hypothetical protein	5 similar to unknown proteins
48270	-24	7.1	2013.2	1271.2	1445.8	51/66	-	42/51	hypothetical protein	5 similar to unknown proteins
48400	-64	133.7	270.5	72.5	14.3	79/90	81/88	78/85	putative serine/threonine protein kinase	2.6 metabolism of phosphate
48760	-112	0.9	1.5	0.4	0.8	55/64	50/58	50/54	hypothetical protein	5 similar to unknown proteins
49410	-133	7.1	1177.1	1479.8	608.7	48/66	86/95	48/66	putative ABC transporter substrate-binding protein	1.2 transport / binding protein & lipoprotein
49500	-200	0.4	183.0	229.5	170.3	57/67	48/61	50/63	putative two-component system sensor kinase	3.5.2 regulation
49710	37	184.7	6.3	4.0	0.6	39/54	58/71	34/51	putative cysteine synthase	2.2 metabolism of amino acids and related molecules
49720	-136	91.1	5.5	2.9	1.3	32/44	29/42	30/43	hypothetical protein containing condensation domain of NRPS	5 similar to unknown proteins
50010	-93	590.9	131.4	141.1	76.6	75/83	58/73	64/77	hypothetical protein of NlpC/P60 family	5 similar to unknown proteins
50490	-73	37.9	1.9	1.1	0.3	28/40	29/41	29/42	putative oxidoreductase	4.6 miscellaneous
50500	-66	74.2	4.9	3.0	0.7	33/51	39/55	34/50	putative SARP-family transcriptional activator	3.5.2 regulation
50820	-136	667.4	219.1	225.1	259.6	73/87	-	-	hypothetical protein	6 no similarity
50970	-54	72.8	17.8	12.0	5.9	46/62	66/82	70/83	hypothetical protein containing YceI-like domain	5 similar to unknown proteins
50980	-94	44.4	38.5	19.1	7.7	60/79	-	-	hypothetical protein	5 similar to unknown proteins
51260	-9	2554.6	605.6	946.1	506.2	78/88	75/88	76/86	putative ABC transporter substrate-binding protein	1.2 transport / binding protein & lipoprotein
53060	26	2.7	2.2	0.7	0.2	-	-	-	putative LacI-family transcriptional regulator	3.5.2 regulation
53900	-137	30.5	21811.1	16345.1	3881.9	-	-	-	hypothetical protein	5 similar to unknown proteins
54130	-1	66.4	36.9	33.2	19.1	81/89	66/73	69/79	putative transcriptional regulator	3.5.2 regulation
54140	-169	82.1	141.0	54.7	7.9	73/84	69/79	70/79	putative ankyrin-like protein	4.6 miscellaneous



54550	-111	289.5	603.6	308.1	34.9	89/96	83/92	82/91	putative glycosyl hydrolase	2.1 metabolism of carbohydrates and related molecules
54930	-8	55.1	332.8	581.3	1367.7	69/81	53/71	53/71	hypothetical protein	6 no similarity
55770	-149	73.0	14.6	11.5	48.5	80/89	-	-	hypothetical protein	5 similar to unknown proteins
55780	-41	13.9	11.2	7.7	3.4	82/92	60/73	60/73	putative dehydrogenase	4.6 miscellaneous
55790	-5	6.0	4.9	5.0	11.0	71/79	37/52	31/55	putative TetR-family transcriptional regulator	3.5.2 regulation
57520	-108	42.2	31.5	20.7	8.3	-	-	-	hypothetical protein	5 similar to unknown proteins
57930	-80	50.7	10.0	18.4	8.5	52/63	63/77	60/72	hypothetical protein	5 similar to unknown proteins
58230	-7	282.3	229.5	146.3	73.3	59/71	59/73	49/63	hypothetical protein	5 similar to unknown proteins
58300	-13	35.7	40.1	28.7	14.2	89/95	37/55	88/96	putative LuxR-family transcriptional regulator	3.5.2 regulation
59370	-167	156.2	24.8	22.1	14.3	29/46	33/51	32/48	hypothetical protein	5 similar to unknown proteins
61610	-9	68.6	48.2	68.3	11.3	40/48	36/49	44/59	putative methyltransferase	4.6 miscellaneous
61620	-102	41.5	37.8	31.4	22.9	44/67	41/63	35/52	putative HxlR-family transcriptional regulator	3.5.2 regulation
61630	-28	34.5	22.4	17.1	13.8	85/91	79/88	76/85	putative glycosyl hydrolase	2.1 metabolism of carbohydrates and related molecules
61640	28	338.9	37.7	34.0	13.7	69/76	62/70	65/75	putative glutamylcysteine synthetase	2.2 metabolism of amino acids and related molecules
62190	-3	383.6	324.0	344.9	436.8	100/100	98/99	98/99	putative DNA-binding protein (AmblD)	3.5.2 regulation
62650	-71	58.0	40.8	45.6	43.7	88/92	87/92	88/93	putative serine/threonine protein kinase	2.6 metabolism of phosphate
62910	-164	82.8	165.2	82.4	22.0	90/95	85/92	88/94	putative translation elongation factor G	3.5.2 regulation
62970	-26	43.4	38.7	28.8	27.9	75/84	69/79	71/80	putative ADP-ribosylglycohydrolase	2.3 metabolism of nucleotides and nucleic acids
62980	-72	76.1	27.1	21.1	17.0	99/99	98/99	96/98	putative two-component system response regulator	3.5.2 regulation
63600	-92	94.4	35.1	32.4	15.2	88/94	75/85	80/88	hypothetical protein	5 similar to unknown proteins
64740	-76	2598.6	6395.9	5147.6	1122.2	83/91	73/85	71/84	hypothetical protein	5 similar to unknown proteins
64890	-180	63.2	119.2	66.2	20.9	67/79	65/76	65/77	hypothetical protein	5 similar to unknown proteins
65290	-82	61.4	142.3	167.2	90.4	64/78	66/82	72/88	putative membrane protein	4.6 miscellaneous
65300	-35	29.1	3670.2	3084.4	1223.7	99/100	99/100	100/100	putative SsgA-family protein	1.8 sporulation
66120	-11	41.1	58.7	181.9	52.4	66/79	56/70	53/71	hypothetical protein	5 similar to unknown proteins
67900	29	218.1	113.9	99.7	84.8	89/95	80/88	90/96	putative RNA polymerase ECF-subfamily sigma factor	3.5.2 regulation
68580	-63	5794.0	2461.9	3399.5	3162.6	93/96	91/94	87/91	hypothetical protein	5 similar to unknown proteins
68920	-88	313.8	58.7	115.5	110.9	94/97	79/85	84/92	putative ATP-binding protein	4.6 miscellaneous
69180	-56	109.8	117.5	103.6	18.4	87/93	78/89	77/88	putative luciferase-like monooxygenase	4.6 miscellaneous
69190	-15	89.7	49.3	20.0	10.6	85/92	75/84	75/87	hypothetical protein	5 similar to unknown proteins
69270	-88	70.9	63.4	48.6	62.2	88/93	86/93	85/93	hypothetical protein of radical SAM superfamily	5 similar to unknown proteins
69280	-40	6.5	5.0	2.7	1.3	-	-	43/60	hypothetical protein	5 similar to unknown proteins
71280	-68	775.6	4.1	1.8	1.7	49/66	82/89	88/92	putative cellobiose ABC transporter solute-binding protein	1.2 transport / binding protein & lipoprotein
71290	-90	151.6	50.2	36.5	20.4	91/96	80/89	83/92	putative LacI-family transcriptional regulator	3.5.2 regulation
71450	-55	41.6	198.5	97.6	42.9	85/88	76/88	80/91	hypothetical protein	5 similar to unknown proteins
71970	5	601.5	345.6	379.1	103.2	93/99	97/99	95/95	putative F-type proton-transporting ATPase C chain (AtpE)	1.4 membrane bioenergetics
72310	-27	36.8	23.0	16.2	5.7	-	-	57/71	putative capsular polysaccharide synthesis protein	1.1 cell wall / transformation & competence
72380	-17	479.9	417.0	273.0	196.7	97/99	93/95	94/96	hypothetical protein containing STAS domain	5 similar to unknown proteins
72710	-29	17.8	7.9	5.5	5.1	71/80	57/66	62/72	hypothetical protein	5 similar to unknown proteins
72910	-59	1109.9	1044.8	1349.8	463.4	98/98	96/98	96/96	putative WhiB-family transcriptional regulator	3.5.2 regulation
72950	-121	204.1	278.9	539.9	216.9	91/96	89/95	87/94	putative nitrite/sulphite reductase	2.7 metabolism of sulfur
73200	-132	61.9	22.4	26.4	23.9	85/91	60/78	66/76	hypothetical protein	5 similar to unknown proteins
73970	-167	145.1	67.2	56.0	58.6	86/92	78/87	80/89	hypothetical protein	5 similar to unknown proteins
74540	-41	126.5	125.0	92.8	73.4	93/95	88/93	89/94	putative dihydrolipoamide dehydrogenase	2.1.2 main glycolytic pathways
74550	-1	107.2	121.0	87.2	61.4	91/97	88/98	92/96	hypothetical protein	5 similar to unknown proteins
74660	-114	75.9	58.3	55.0	55.5	35/52	61/73	60/74	putative CDP-glycerol:polyglycerol phosphate glycerophosphotransferase	2.4 metabolism of lipids

74670	20	32.7	21.5	22.1	16.0	72/87	81/89	81/91	putative NUDIX hydrolase	4.6 miscellaneous
75120	-76	17.7	26.5	10.4	4.3	83/92	78/85	82/89	putative deoxyribonuclease	2.3 metabolism of nucleotides and nucleic acids
75130	-8	20.7	4.4	3.2	1.8	86/92	75/87	77/88	hypothetical protein	6 no similarity
75440	-74	827.1	971.1	685.0	132.5	-	92/94	92/94	hypothetical protein	5 similar to unknown proteins
75470	-17	957.5	2386.2	2421.0	2240.1	93/96	83/92	86/94	putative thioredoxin	3.5.2 regulation
76110	-35	13.5	1106.2	953.9	394.8	69/76	56/68	52/65	hypothetical protein	5 similar to unknown proteins
76150	-110	24.8	8512.2	8649.3	2880.4	88/95	79/90	74/86	putative flagellar assembly protein	1.1 cell wall / transformation & competence
76910	-112	42.5	150.9	92.6	46.8	74/82	78/85	79/86	putative phosphate ABC transporter substrate-binding protein (FliW)	1.2 transport / binding protein & lipoprotein
77370	41	14.9	6.8	6.7	5.8	60/73	45/58	37/52	putative AfsR-family transcriptional regulator	3.5.2 regulation
77530	-52	3812.9	3251.4	3757.6	2565.3	100/10	99/99	98/99	hypothetical protein	5 similar to unknown proteins
77540	-150	137.6	290.8	258.8	106.9	65/78	59/69	64/74	hypothetical protein	5 similar to unknown proteins
77620	-89	163.1	82.8	100.0	34.9	98/99	96/97	97/99	hypothetical protein	5 similar to unknown proteins
77890	-67	340.3	296.5	175.4	54.7	81/88	73/82	76/81	hypothetical protein	5 similar to unknown proteins
78120	-143	95.0	63.4	34.4	28.9	71/81	70/81	71/83	putative subtilase-family protease	4.6 miscellaneous
78170	-98	75.9	7.5	7.8	8.0	70/83	76/86	80/89	putative capsule synthesis protein	1.1 cell wall / transformation & competence
78180	-87	244.4	257.1	139.7	68.4	100/10	96/99	98/100	putative transcriptional regulator containing cyclic nucleotide-binding domain	3.5.2 regulation
78290	-41	42.3	1675.1	1362.2	2569.4	97/99	98/99	98/99	putative WhiB-family transcriptional regulator	3.5.2 regulation
78690	-136	170.0	40.5	31.2	17.3	61/73	56/71	52/65	hypothetical protein	5 similar to unknown proteins
78840	-43	117.9	24.1	38.7	111.9	65/77	61/74	63/75	putative diguanylate cyclase	1.3 sensor
78870	11	124.8	14.2	36.3	18.1	60/76	51/70	49/68	hypothetical protein	6 no similarity
78880	-43	165.3	51.8	61.4	27.6	97/97	81/85	84/89	hypothetical protein	5 similar to unknown proteins
78890	-44	236.8	83.7	85.1	48.4	88/93	87/93	86/92	putative DNA-binding protein	3.5.2 regulation
78900	26	1119.1	115.2	212.0	97.2	85/87	80/87	80/85	hypothetical protein	6 no similarity
79410	-57	19.4	15.5	12.6	16.6	41/54	31/49	35/51	putative TetR-family transcriptional regulator	3.5.2 regulation
79420	-22	3.2	2.6	2.3	2.1	38/49	37/52	56/75	putative short chain dehydrogenase	4.6 miscellaneous
79970	-102	96.0	62.0	61.1	23.7	87/93	79/87	79/88	putative polypeptide deformylase	2.2 metabolism of amino acids and related molecules
80800	-181	49.8	24.2	12.6	5.6	84/86	81/90	80/90	putative molybdopterin biosynthesis protein C	2.5 metabolism of coenzymes
80810	-95	55.6	36.5	25.0	9.6	75/83	56/69	58/72	putative diguanylate cyclase/phosphodiesterase	1.3 sensor
80840	-140	66.7	17.8	14.1	41.5	77/86	40/65	46/67	hypothetical protein	5 similar to unknown proteins
80970	-53	253.6	146.1	135.2	97.9	80/87	74/89	79/89	hypothetical protein	5 similar to unknown proteins
80980	-74	810.8	325.9	195.4	134.4	85/90	87/92	87/94	putative PadR-like family transcriptional regulator	3.5.2 regulation
81090	-70	24.2	23.7	21.5	9.7	75/83	72/83	64/72	putative RNA polymerase ECF-subfamily sigma factor	3.5.2 regulation