

Supporting files

Genome Structure of *Bacillus cereus* tsu1 and Genes Involved in Cellulose Degradation and Poly-3-hydroxybutyrate Synthesis

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Figure S1. The phylogenetic tree of *Bacillus cereus* tsu1

The *Bacillus cereus* tsu1 genome sequence data was generated using next generation sequencing analysis. It was assembled into 36 scaffolds. The annotated assembled contigs were also deposited in the Integrated Microbial Genomes & Microbiomes databases (Join Genome Institute, accession 2648501652). The phylogenetic COGs ranking was developed by comparing *B. cereus* tsu1 with the deposited genomes in the Bacteria domain.

Figure S2. Extracellular proteins of *B. cereus* tsu1 separated on SDS-PAGE gel

Extracellular proteins of *B. cereus* tsu1 growing in M9 minimal medium supplemented with 1% CMC broth were extracted and loaded on 10-20% SDS-PAGE gel, five bands at 25, 35, 40, 65, and 150 kDa were cut for subsequent MS analysis.

Figure S3. Amino acid composition of the aqueous extracts of rapeseed cake

Rapeseed cake samples (25 g per sample) were soaked in 1 L water overnight under constant stirring. The supernatant filtered through a 0.22 μm filtration system (EMD Millipore, Massachusetts) was submitted for amino acid analysis on an L-8800 Hitachi analyzer in the Molecular Structure Facility at University of California at Davis.

Figure S4. Schematic representation of the pathways for the generation of poly-(R)-3-hydroxybutyrate (PHB) based on the genomic structure of *Bacillus cereus* tsu1 and composition of rapeseed cake

The first PHB biosynthesis pathway using acetyl-CoA substrate involves an acetoacetyl-CoA thiolase (1), acetoacetyl-coA reductase (2) and a 3HB-CoA dehydrogenase (3). The second alternative metabolic route is from γ -amino-butyric acid (GABA). Genes identified in *Bacillus cereus* tsu1 involves the following processes: GABA and Glutamate uptake; endogenous formation of Glutamate from alpha-KG involving a glutamate dehydrogenase (4, GenBank ID: KGT44639.1), then into GABA through glutamate decarboxylase (5, GenBank ID: KGT45792.1); conversion of GABA into succinate-semialdehyde (SSA) through a GABA transaminase (6, GenBank ID: KGT45608.1) and conversion of Succinyl-CoA through SSA dehydrogenase (7, GenBank ID: KGT45610.1); SSA reduction by the γ -hydroxybutyric acid (GHB) dehydrogenase (8, GenBank ID: KGT41557.1); and activated to 4-hydroxybutyryl-CoA by a co-enzyme A transferase enzyme (9, GenBank ID: KGT44257.1); and polymerization of GHB and 3-HB by PHB synthase (3, GenBank ID: KGT44863.1). The third pathway is that phaJ gene, encoding R-specific enoyl-CoA hydratase (11, GenBank ID: KGT44860.1), work together with another acyl-CoA dehydrogenase (10, GenBank ID: KGT41138.1) to form (R)-3HB-CoA via crotonyl-CoA intermediate from fatty acid β -oxidation.

Table S2 Five genes from PHB biosynthesis pathway were cloned.			
PHB biosynthesis pathway genes			
Protein Name	Scaffold location	GenBank ID/locus_tag	Primers Designed for Cloning
Name=Acetyl-CoA acetyltransferase (PhaA)	BCtsu1_scaffold17_size11011_09_322327..323502	KGT41550.1/ IY08_20320	F:CACCATGCATAATGTTGTTATTACAGC R:TAGTGCTTCTATAAATAAGGCA
Name=Acetoacetyl-CoA reductase (PhaB)	BCtsu1_scaffold9_size945600_552131..552874	KGT44864.1/ IY08_06450	F:CACCATGGTTCAATTAATGAAAAAGTAGC R:CATATATAATCCGCCGTTAATGTTT
Name=poly(R)-hydroxyalkanoic acid synthase (PhaC)	BCtsu1_scaffold9_size945600_552958..554043	KGT44865.1/ IY08_06455	F:CACCATGACTACATTGCAACAGAATG R:ATTAGAACGCTCTTCAAGCCAA
Name=PhaP_Bmeg	BCtsu1_scaffold9_size945600_550280..550804	KGT44861.1/ IY08_06435	F:CACCATGGAAACTAAACCATACGAATTAGTC R:CTTGATGGAAGTAAATAGATTTTTTTGA
Name=PhaR protein (synthase subunit)	BCtsu1_scaffold9_size945600_551498..551980	KGT44863.1/ IY08_06445	F:CACCGTGATTGATCAAAAATTTCGATCC R:TTTTTTATTTTCTGGCTTATTCGC
Gene Sequences			
<p>phaA: ATGCATAATGTTGTTATTACAGCTGCAGTTCGTTCCGCAATTGGAACTTTTGGAGGAGCGCTAAAAATGTAACGCCAGTAGAATTAGCTGTTCCGTACTTCAGGAAGCTGTAAAACGAGGCGGGGTAGAACCCACATGAAGTTGATGAAGTAATTTTAGGTCATTGTATTCAAAGAACTGATGAAGCAAATACGGCGAGAACAGCTGCATTAGCGGCAGGATTTCTTGACACAGTTACGGGATATACAATCCAACGCCAATGTTCTTCAGGTATGCAAGCAATTATGTCAGCTGCAATGCAAATCCAATTAGGTGTAAGTGATGTTGTTGTTGTCAGGTGGAGTAGAAGCGATGAGTTCGAGCCCTTATGCATTGAACAGCACCGCTGGGGACAACGTCTACAGCACGGAGAAATTCGTGATACGGTGTGGGAAGTGTTAGAAGACCCGATTACCATATTATGATGGGTGAAACAGCGGAAAAATTTAGTTGAACAATATGAATTTACAAGAGAGGAACAAGATGAAGTTGCTCTTCGCAGTCATACATTGGCACTGAAGGCAATCGAGTCTGGATACTTTGACGATCAAATTGTTCCATTACAATAAAAGAGCGTAGAAAAAGAAAGTTATATTTTCGAAGGATGAACATCCACGTGCAGATATTACAGCTGAAAAATTAGCTGGATTGAAGCCGGCATTCCGTAAAGATGGATCAGTGACTGCGGGGAATGCATCTGGCCTTAATGACGGGAGTG CAGTTCTAGTATTAATGAGCGAAGAAAAAGCGAAAGAAAAAGGTTTACAACCGTTAGCTAGAATTGTTGGATATTCAGTAGCTGGAGTAGATCCAAAAATTATGGGTATTGGACCAGCACCAGCAATTCGTAAAGGTTTAGAAAAAGTAGATTGGTCATTGGAAGATGCAGATTTACTTGAATTAATGAAGCTTTCGCGGCTCAATATTTAGCTGTAGAGAAAGAGTTAGGCTTAGACCGTGAAAAAGTGAACGTAAACGGTAGTGGCGTAGGACTTGGGCATCCAATTGGTTGTACAGGGGCTCGTATTACAGTAAGTTAATTACGAATTA AAAAGACGTGGGTAGAAAAAGGAATTGCCTCTTTATGCGTCGGTGCGGTATCGGGGTTGCCTTATTTATAGAAGCACTATAA</p>			
<p>phaB: ATGGTTCAATTAATGAAAAAGTAGCAATCGTAACAGGTGGAGCAAAAGGAATTGGAAAAGCGATTACAGTAGCATTAGCACAAAGAGGGAGCAAAAGTAGTTATTA ACTATAATAGCAGTAAAGAACAGCTGAAAACTTAGTAAACGAATTAGGAAAAGACGGACATGACGTTTATGCAGTGCAAGCGGATGTTTCTAAAGTAGAAGATGCAAACCGACTTG TAGAAGAAGCTGTGAATCATTTTGGTAAAGTTGATATTCTTGTTAATAATGCTGGTATTACAAGAGATCGTACATTCAAAAAGTTAAATCGTGAAGATTGGGAGCGCGTAATTGACGTGAATTTAAGTAGCGTATTTAATACGACAAGCGCGGTTCTTCCATACATAACTGAAGCGGAAGAAGGAAGGATTATTAGCATTCTTCTATTATTGGTCAAGCAGGTGGATTGGCCAAACAACTACTCAGCAGCAAAAGCAGGTATGCTAGGATTTACAAAATCGTTAGCGTTAGA ACTTGCAAAAACAAATGTCACGTGTAACGCTATTGCCCAGGATTTATTGATACTGAAATGGTAGCAGAAGTACCAGAAGAAGTACGTCAAAAAATCGTTGCAAAAATCCCGAAAAACGTTTGGTCAAGCCGATGAAATTGCAAAAAGGTGTAGTATACCTATGCCGTGACGGTGC GTATATCACAGGTCAACAATTAAACATTAAACGGCGGATTATATATGTAA</p>			

phaC: **ATG**ACTACATTTCGCAACAGAATGGGAAAAGCAATTAGAGCTATACCCAGAAGAGTACCGAAAAAGCATACCGCCGAGTGAAAAGGGCGAGTGAAATTTTATTACGTGAACCAGAGCCGCAAGT
AGGGTTAACGCCGAAAGAGGTTATTTGGACGAAGAATAAGACGAAGCTTTATCGCTACATTCCAAAACAAGAAAAAACACAAAGAGTTCCAATTCTGTAAATATATGCTCTTATTAATAAACCATAT
ATTATGGATTTAACTCCTGGAAATAGTTTAGTGGAATATCTAGTGGATCGTGGTTTTGATGTGTATATGCTTGATTGGGGCACATTTGGTTTAGAAGATAGTCATTTGAAATTTGATGATTTTGTGT
TTGATTATATTGCAAAAGCAGTAAAAAAGTAATGCGAACTGCAAAATCGGACGAGATTTCTTTACTTGGTTATTGCATGGGTGGAACGCTAACTTCTATTTATGCAGCACTTCATCCGCACATGCC
AATTCGTAATTTAATTTTCATGACAAGTCCTTTTGATTCTCTGAAACAGGATTGTATGGCCCTTTATTAGATGAGAAATACTTCAATTTAGATAAAGCGGTTGATACATTTGGAAATATTCCGCCA
GAAATGATTGATTTTCGGAACAAAATGTTAAAGCCAATTACGAACTTTGTTGGTCCATATGTTGCTTTAGTAGATCGTTCAGAGAATGAGCGCTTCGTCGAAAGCTGGAGATTGGTTCAAAAGTGGG
TTGGTGATGGTATTCCGTTCCCAGGTGAATCATACAGACAGTGGATTCTGTGATTTTTATCAAAATAATAAGTTGGTTAAGGGTGAAGTTCGTTATTCGCGGACAAAAGGTAGACCTTGCAAATATTAA
GGCGAATGTCCTTAAATATTTCCGGGAAACGTGATCATATCGCTTTGCCATGTCAAGTAGAAGCATTACTAGACCATATTTCTAGCACAGATAAAACAATATGTATGTTTACCAACAGGGCATATGTCT
ATCGTTTACGGTGGAACAGCTGTAAAACAAACATATCCGACGATTGGAAATTGGCTTGAAGAGCGTTCTAAT**TAA**

phaR: **GTG**ATTGATCAAAAATTCGATCCACTACAAGCATGGAAAAATGCTTATGAACAAACCGAAACATTTTGGGGAAAAGCGCTCAATGAACAATTAACAGAGAATATTCTGCTTGGATGGG
CAGCGTTCTAGATTTGAATTTGTTTTATCAAAAAGCATTAAATGATACGACAAAAAACTATTTAGAACAAGTAAATGTGCCGACGAAAGAGGATATCGCAAGAGTAGCTACGCTAGTTATTAACCTTA
GAAAATAAAGTAGATAACATTGAGGAGTTCTAGAGGAAAAAGTAGATTCTTTAGGACAAGCTCCTACATTAAAGCGTGATGTAACGAAAGTAAACAAGATATTCGTACGCTTGAAACAAAAGTAG
ATCAAATTTTGAATTGCTAGAAAAGCAAAATGCAGTACTAGCTAACTACAAGTACCTGTAAAAGAAGAGGTAAAGCCTGCGAATAAGCCAGAAAATAAAAA**TGA**

phaP: **ATG**GAAACTAAACCATACGAATTAGTCGATGCATTTTGGAAAACTGGTCTCAATCACTTTCCCTTTTCTCTTCAGCTGGGAAACAATTAGAGCAGCTTACTTTAGAAACATTAAAAACAACA
ACAAGACGCTTTGCATAAATTAACATCAGGAGTAGATGAACTAGAAAAAGAACTACAACAACCTACTGCTCAGTTCAACAACCAATATACAGATTACGTGAAACAATTAAGTGGAACTCCTTAAAT
GATCAAATTAACGAGTGGCAGGACAAATGGAAGGAACCTTCTGCTCATATGCATCAACTTACTGTTTCTCCTACAAAAACATCTTTGTCAATTCTTACACAAACAAGCGGTCAATTTGAAGAAACAA
CAAAACAATTTATTGTGCAACAACAATTACAACGTGAAGAGGCTCAAAAAACAGTTAGAGGGTTTTTTTGAAGAGTTCAAGTCAAAACAGTTGGAAGTTCGCAAAAAAGTTCGAGGAAACCTCAAAAA
TCTATTTACTTCCATCAAG**TAA**

Table S3 The alignment of peptide sequences of recombinant proteins to predicted proteins in PHB biosynthesis pathway in *Bacillus cereus* tsu1^a

Protein name	Peptides identified 2D-MS ^b
PhaA	MHNVVITA AVR;SPIGTFGGALK;NVTPVELAVPVLQEAVK;R;GGVEPHEVDEVILGHCIQR;TDEANTAR;TAALAAGFPDVTVTGYTIQR;QCSSGMQAIMSAAMQIQLGVSDV VVAGGVEAMSSSPYALK;QHR;WGQR;LQHGEIR;DTVWEVLEDPIHHIMMGETAENLVEQYEITR;EEQDEVALR;SHTLALK;AIESGYFDDQIVPITIK;ERR;KEVIFSK;DEHPR;ADITAEK;LAGLK;PAFRK;DGSVTAGNASGLNDGSAVLVLMSEEK;AK;EK;GLQPLAR;IVGYSVAGVDPK;IMGIGPAPAIRK;GLEK;VDWSLEDADLLEINEAFAAQYLAVEK;ELGLDR;EK;VNVNGSGVGLGHPIGCTGAR;ITVSLIHELK;RR;GLEK;GIASLCVGGGIGVALFIEAL;
PhaB	MVQLNGK;VAIVTGGAK;GIGK;AITVALAQEGAK;VVINYNSSKEAAENLVNELGK;DGHVYAVQADVSK;VEDANR;LVEEAVNHFGK;VDILVNNAGITR;DR;TFKK;LNREDWER;VIDVNLSSVFNTTSAVL PYITEAEEGR;IISISSIIGQAGGFGQTNYSAAK;AGMLGFTK;SLALELAK;TNVTVNAICPGFIDTEMVAEVPEEVR;QK;IVAK;IPKK;RFGQADEIAK;GVVYLCR;DGAYITGQQLNINGGLYM;
PhaC	MTTFATEWEK;QLELYPEEYRK;AYRR;VKR;ASEILLR;EPEPQVGLTPK;EVIWTK;NK;TK;LYRYIPK;QEK;TQR;VPILLIYALINK;PYIMDLTPGNSLVEY;LVDR;GFDVYMLDWGTFGLEDSHLK;FDDDFVFDYIAK;AVKK;VMRTAK;SDEISLLGYCMGGTLTSIYAALHPHMPPIR;NLIFMTPFDFSETGLYGPLLDEK;YFNLDK;AVDTFGNIPPEMIDFGNK;MLK;PITNFVGPYVALVDR;SENER;FVESWR;LVQK;WVG DGIPFPGESYR;QWIR;DFYQNNK;LVK;GELVIR;GQK;VDLANIK;ANVLNISGKR;DHIALPCQVEALLDHISSTDK;QYVCLPTGHMSIVYGGTAVK;QTYPTIGNWLEER;SN;
PhaR	VIDQK;FDPLQAWK;NAYEQTETFWGK;ALNETIK;TEEYSAWMGSVLDLNLFYQK;ALNDTTK;NYLEQVNVPTK;EDIAR;VATLVINLENK;VDNIEEFLEEK;VDSL GQAPTLK;RDVTK;VK;QDIR;TLETK;VDQILELLEK;QNAVLAK;LQVPVK;EEVK;PANK;PENKK;
PhaP	METK;PYELVDAFWK;NWSQSLSLFSSAGK;QLEQLTLETTLK;QQQDALHK;LTSGVDELEK;ELQQLTAQFNNQYTDYVK;QLTGNSLNDQINWQDK;WK;ELSAHMHQLTVSPTK;TSLSILTQTSQGFEETTK;QFIVQQLQR;EEAQK;QLEGFLEEFK;SK;QLELAKK;FEENSK;NLFTSIK;

^aPeptide sequences and tryptic fragments of PHB biosynthesis proteins predicted from the respective

genes in the annotated genome of *B. cereus* tsu1

^bThe 2D gels is data result from LC-MS (Q-TOF). Regions marked in green are the trptic peptides identified in the recombinant proteins using the liquid chromatography mass spectrometry analysis.

Table S4 HPLC analysis of purity of poly-(R)-3-hydroxybutyrate (PHB) extracts from *Bacillus cereus* tsu1^a

Samples (replicates)	Mass of sample weighted out (mg)	Peak area (PHB)	Predicated mg of PHB in original extracts	% of PHB in samples (mg PHB/mg TSS*100) ^b
HL2	3.50	2034.10	3.37	96.30
HL4	3.07	1654.00	2.75	89.50
HL6	2.36	1238.80	2.06	87.50
Average				91.1± 4.3 %

^aEach PHB was extracted from 20 mg dried bacterial cells;

^bTSS: total suspended solids

Table S6 The peak positions at known vibrational modes for poly-(R)-3-hydroxybutyrate (PHB) produced by *Bacillus cereus* tsu1 on rapeseed cake substrates^a

Vibrational mode	Raman Peak position (cm ⁻¹)	FTIR peak position (cm ⁻¹)
C-O-C deformation + C-CH ₃ deformation	363.1	Not in IR range
CCO deformation	434.3	Not in IR range
C-CH ₃ deformation and CCO deformation	513.9	Not in IR range
C-CH ₃ deformation and CCO deformation	601.6	Not in IR range
C=O deformation (out-of-plane)	681.1	Not in IR range
C=O deformation (in-plane)	694.8	Not in IR range

C-COO stretching	840.1	826.03
?	897.7	895.34
?	908.7	No peak
?	938.8	937.8
?	947.0	No peak
	979.9	978.8
?	No peak	1043.9
C-O stretching	1059.5	1054.9
COC symmetric stretching	1103.3	1100.2
CH ₃ asymmetric rocking	1136.2	1130.8
?	No peak	1181.6
COC asymmetric stretching	1221.2	1227.5
C-O-C stretching and CH deformation	1262.3	1261.6
	No peak	1276.5
CH deformation	1298	No peak
CH deformation and CH ₃ symmetric deformation	1363.8	No peak
?	No peak	1379.23
CH ₃ symmetric deformation	1402.2	
?	1413.1	No peak
CH ₃ asymmetric deformation	1451.5	1452.9
C=O stretching	1731.2	1719.23

CH stretching	2880.2	No peak
?	2900.7	No peak
CH ₃ antisymmetric stretching	2935.4	2934.3
CH ₃ asymmetric stretching	2976.6	2976.7
CH ₃ asymmetric stretching	3002.9	No peak

^aA majority of the vibrational modes in PHB are asymmetric, therefore they can be observed both in the FTIR as well as in the Raman spectra. Same peaks were observed on PHB standard (Sigma).

Table S7 *Bacillus cereus* tsu1 genes for cellulose degradation and PHB biosynthesis.

Function	Protein Name	Scaffold location	GenBank ID/locus_tag
Cellulose degradation			
	Name=Endoglucanase C	BCtsu1_scaffold16_size198830_9489..10395	KGT42715.1/ IY08_17770
	Name=Endoglucanase (chitosanase)	BCtsu1_scaffold13_size480439_95775..97104	KGT43479.1/ IY08_13235
	Name=Oligo-1,6-glucosidase	BCtsu1_scaffold17_size1101109_314793..316469	KGT41541.1/ IY08_20275
	Name=Bifunctional xylanase/deacetylase	BCtsu1_scaffold10_size252322_32315..33019	KGT44235.1/ IY08_08835
PHB biosynthesis			
	Name=Acetyl-CoA acetyltransferase (PhaA)	BCtsu1_scaffold19_size558666_390769..391950	KGT41140.1/ IY08_26925
	Name=Acetyl-CoA acetyltransferase (PhaA)	BCtsu1_scaffold17_size1101109_322327..323502	KGT41550.1/ IY08_20320
	Name=3-hydroxybutyryl-CoA dehydratase (PhaJ)	BCtsu1_scaffold9_size945600_549735..550178	KGT44860.1/ IY08_06430
	Name=PhaP_Bmeg	BCtsu1_scaffold9_size945600_550280..550804	KGT44861.1/ IY08_06435
	Name=PadR (PhaQ)	BCtsu1_scaffold9_size945600_550847..551299	KGT44862.1/ IY08_06440
	Name=PhaR protein (PhaC synthase subunit)	BCtsu1_scaffold9_size945600_551498..551980	KGT44863.1/ IY08_06445
	Name=Acetoacetyl-CoA reductase (PhaB)	BCtsu1_scaffold9_size945600_552131..552874	KGT44864.1/ IY08_06450
	Name=poly(R)-hydroxyalkanoic acid synthase (PhaC)	BCtsu1_scaffold9_size945600_552958..554043	KGT44865.1/ IY08_06455
	Name= Glutamate dehydrogenase	BCtsu1_scaffold9_size945600_706717..708003	KGT44639.1/ IY08_07350
	Name=Glutamate decarboxylase	BCtsu1_scaffold5_size27344_7346..8815	KGT45792.1/ IY08_01265
	Name=GABA transaminase	BCtsu1_scaffold7_size212786_39367..40731	KGT45608.1/ IY08_01640
	Name=SSA dehydrogenase	BCtsu1_scaffold7_size212786_42207..43658	KGT45610.1/ IY08_01650
	Name= Gamma-hydroxybutyric acid (GHB) dehydrogenase	BCtsu1_scaffold17_size1101109_327528..328304	KGT41557.1/ IY08_20360
	Name=Co-enzyme A transferase enzyme	BCtsu1_scaffold10_size252162_53175..54689	KGT44257.1/ IY08_08955
	Name=Acyl-CoA dehydrogenase	BCtsu1_scaffold19_size558666_388664..389794	KGT41138.1/ IY08_26915

Figure S1



Figure S2

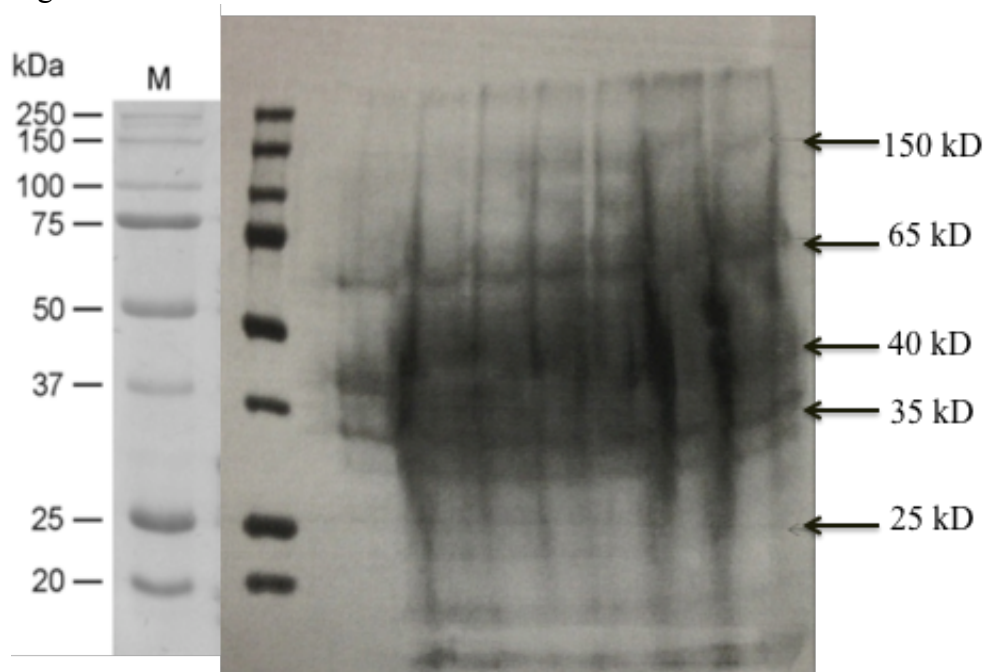
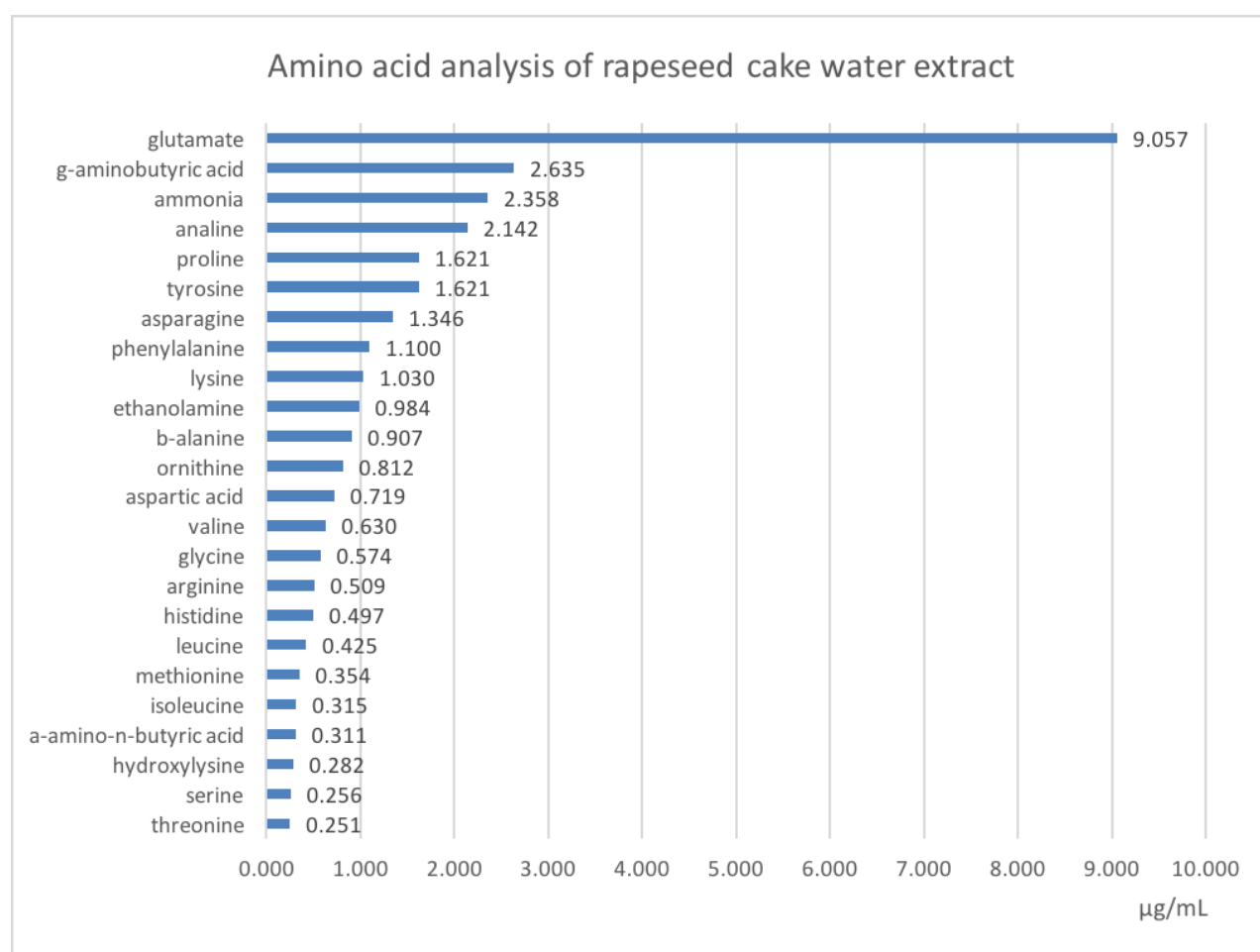


Figure S3



The diagram illustrates the metabolic pathways for the synthesis of P3HB, P4HB, and co-polymers. The pathways are as follows:

- Glycolysis** leads to **Pyruvate**.
- Pyruvate** is converted to **Acetyl-CoA**.
- Acetyl-CoA** enters the **TCA** cycle.
- Acetyl-CoA** is also converted to **Acetoacetyl-CoA** (step 1).
- Acetoacetyl-CoA** is converted to **R-3-HB-CoA** (step 2).
- R-3-HB-CoA** is converted to **P3HB, P4HB, co-polymers** (step 3).
- Acetoacetyl-CoA** is also converted to **Acyl-CoA**.
- Acyl-CoA** is converted to **Crotonyl-CoA** (step 10).
- Crotonyl-CoA** is converted to **R-3-HB-CoA** (step 11).
- Alpha-KG** is converted to **Glutamate** (step 4).
- Glutamate** is converted to **GABA** (step 5).
- GABA** is converted to **SSA** (step 6).
- SSA** is converted to **4-HB** (step 8).
- 4-HB** is converted to **4-HB-CoA** (step 9).
- 4-HB-CoA** is converted to **P3HB, P4HB, co-polymers** (step 3).
- Succinyl-CoA** is converted to **SSA** (step 7).

Table S1 Genome assembled scaffolds used for creating circular genome map of *Bacillus cereus* tsu1

The 36 scaffolds were annotated using the NCBI Prokaryotic Genome Annotation Pipeline GenBank: KN321896-KN321931).

This table shows the localizations of annotated genes on these scaffolds and on the reconstructed circular map

	On circular map		On NCBI scaffolds		Annotation on original scaffold		
	start	stop	start	stop			
scaffold1							
gene	122	1096	122	1096	gene=IY08_00005	protein=hypothetical protein	protein_id=KGT46009.1
gene	1340	2803	1340	2803	gene=IY08_00010	protein=inosine-5-monophosphate dehydrogenase	protein_id=KGT46010.1
gene	2908	4224	2908	4224	gene=IY08_00015	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT46011.1
gene	4385	5272	4385	5272	gene=IY08_00020	protein=pyridoxal biosynthesis protein	protein_id=KGT46012.1
gene	5291	5881	5291	5881	gene=IY08_00025	protein=glutamine amidotransferase	protein_id=KGT46013.1
gene	6209	7483	6209	7483	gene=IY08_00030	protein=seryl-tRNA synthetase	protein_id=KGT46014.1
gene	7638	7730	7638	7730	tRNA		
gene	7897	8289	7897	8289	gene=IY08_00040	protein=cytoplasmic protein	protein_id=KGT46015.1
gene	8325	8993	8325	8993	gene=IY08_00045	protein=deoxycytidine kinase	protein_id=KGT46016.1
gene	8996	9631	8996	9631	gene=IY08_00050	protein=deoxyguanosine kinase	protein_id=KGT46017.1
gene	9757	10296	9757	10296	gene=IY08_00055	protein=isochorismatase	protein_id=KGT46018.1
gene	10274	10413	10274	10413	pseudo		
gene	10406	10906	10406	10906	gene=IY08_00065	protein=adenosine deaminase	protein_id=KGT46019.1
gene	11383	13071	11383	13071	gene=IY08_00070	protein=DNA polymerase III subunit gamma	
gene	13094	13423	13094	13423	gene=IY08_00075	protein=nucleoid-associated protein	protein_id=KGT46021.1
gene	13438	14034	13438	14034	gene=IY08_00080	protein=recombinase RecR	protein_id=KGT46022.1
gene	14049	14270	14049	14270	gene=IY08_00085	protein=hypothetical protein	protein_id=KGT46023.1
gene	14432	14701	14432	14701	gene=IY08_00090	protein=sigma-K factor-processing regulatory protein BofA	protein_id=KGT46024.1
scaffold2							
gene	14941	14974	1	34	5s rRNA		
gene	15223	15402	283	462	gene=IY08_00100	protein=carnitine--CoA ligase	protein_id=KGT45959.1
gene	15474	16895	534	1955	gene=IY08_00105	protein=arginine decarboxylase	protein_id=KGT45960.1
gene	16897	17523	1957	2583	gene=IY08_00110	protein=thymidylate kinase	protein_id=KGT45961.1
gene	17559	18542	2619	3602	gene=IY08_00115	protein=DNA polymerase III subunit delta'	protein_id=KGT45962.1
gene	18548	19375	3608	4435	gene=IY08_00120	protein=stage 0 sporulation protein	protein_id=KGT45963.1

gene	19390	19740	4450	4800	gene=IY08_00125	protein=DNA replication initiation control protein YabA	protein_id=KGT45964.1
gene	19823	20563	4883	5623	gene=IY08_00130	protein=hypothetical protein	protein_id=KGT45965.1
gene	20550	20840	5610	5900	gene=IY08_00135	protein=hypothetical protein	protein_id=KGT45966.1
gene	20809	21684	5869	6744	gene=IY08_00140	protein=16S rRNA methyltransferase	protein_id=KGT45967.1
gene	21705	21989	6765	7049	gene=IY08_00145	protein=transition state regulator Abh	protein_id=KGT45968.1
gene	22475	24457	7535	9517	gene=IY08_00150	protein=methionine--tRNA ligase	protein_id=KGT45969.1
gene	24624	29450	9684	14510	gene=IY08_00155	protein=hydrolase TatD	protein_id=KGT45970.1
gene	25606	26163	10666	11223	gene=IY08_00160	protein=ribonuclease M5	protein_id=KGT45971.1
gene	26160	27038	11220	12098	gene=IY08_00165	protein=16S rRNA methyltransferase	protein_id=KGT45972.1
gene	27149	28012	12209	13072	gene=IY08_00170	protein=peptidase	protein_id=KGT45973.1
gene	28238	28498	13298	13558	gene=IY08_00175	protein=ABC transporter permease	protein_id=KGT45974.1
gene	28611	28769	13671	13829	gene=IY08_00180	protein=protein sspF	protein_id=KGT45975.1
gene	28957	29835	14017	14895	gene=ipk	protein=4-diphosphocytidyl-2C-methyl-D-erythritol kinase	protein_id=KGT45976.1
gene	29890	30738	14950	15798	gene=IY08_00190	protein=pur operon repressor	protein_id=KGT45977.1
gene	30858	31232	15918	16292	gene=IY08_00195	protein=endoribonuclease L-PSP	protein_id=KGT45978.1
gene	31385	31678	16445	16738	gene=IY08_00200	protein=septation protein spoVG	protein_id=KGT45979.1
gene	31991	33370	17051	18430	gene=IY08_00205	protein=glucosamine-1-phosphate N-acetyltransferase	protein_id=KGT45980.1
gene	33392	34345	18452	19405	gene=IY08_00210	protein=ribose-phosphate pyrophosphokinase	protein_id=KGT45981.1
gene	34355	34978	19415	20038	gene=IY08_00215	protein=peptidyl-tRNA hydrolase	protein_id=KGT45982.1
gene	35049	35273	20109	20333	gene=IY08_00220	protein=peptide ABC transporter permease	protein_id=KGT45983.1
gene	35379	38909	20439	23969	gene=IY08_00225	protein=transcription-repair coupling factor	protein_id=KGT45984.1
gene	39046	39582	24106	24642	gene=IY08_00230	protein=stage VI sporulation protein D	protein_id=KGT45985.1
gene	39813	41414	24873	26474	gene=IY08_00235	protein=sugar transporter	protein_id=KGT45986.1
gene	41427	42887	26487	27947	gene=IY08_00240	protein=hypothetical protein	protein_id=KGT45987.1
gene	42902	43177	27962	28237	gene=IY08_00245	protein=hypothetical protein	protein_id=KGT45988.1
gene	43236	43544	28296	28604	gene=IY08_00250	protein=spore coat protein	protein_id=KGT45989.1
gene	43541	44194	28601	29254	gene=IY08_00255	protein=spore cortex biosynthesis protein	protein_id=KGT45990.1
gene	44191	44550	29251	29610	gene=IY08_00260	protein=cell division protein DIVIC	protein_id=KGT45991.1
gene	44638	45123	29698	30183	gene=IY08_00265	protein=RNA-binding protein	protein_id=KGT45992.1
gene	45283	45356	30343	30416	tRNA		
gene	45370	45441	30430	30501	tRNA		

gene	45701	48172	30761	33232	gene=IY08_00280	protein=stage II sporulation protein E	protein_id=KGT45993.1
gene	48403	49833	33463	34893	gene=IY08_00285	protein=tRNA(Ile)-lysine synthetase	protein_id=KGT45994.1
gene	49830	50372	34890	35432	gene=IY08_00290	protein=hypoxanthine phosphoribosyltransferase	protein_id=KGT45995.1
gene	50458	52359	35518	37419	gene=IY08_00295	protein=cell division protein FtsH	protein_id=KGT45996.1
gene	52604	53392	37664	38452	gene=IY08_00300	protein=pantothenate kinase	protein_id=KGT45997.1
gene	53399	54274	38459	39334	gene=IY08_00305	protein=heat shock protein Hsp33	protein_id=KGT45998.1
gene	54388	55311	39448	40371	gene=IY08_00310	protein=cysteine synthase	protein_id=KGT45999.1
gene	55534	56931	40594	41991	gene=IY08_00315	protein=aminobenzoate synthetase	protein_id=KGT46000.1
gene	56937	57524	41997	42584	gene=IY08_00320	protein=anthranilate synthase component II	protein_id=KGT46001.1
gene	57518	58390	42578	43450	gene=IY08_00325	protein=4-amino-4-deoxychorismate lyase	protein_id=KGT46002.1
gene	58365	59225	43425	44285	gene=IY08_00330	protein=dihydropteroate synthase	protein_id=KGT46003.1
gene	59226	59588	44286	44648	gene=IY08_00335	protein=dihydroneopterin aldolase	protein_id=KGT46004.1
gene	59585	60100	44645	45160	gene=IY08_00340	protein=2-amino-4-hydroxy-6-hydroxymethyldihydropteridine pyrophosphokinase	protein_id=KGT46005.1
gene	60052	60255	45112	45315	gene=IY08_00345	protein=XRE family transcriptional regulator	protein_id=KGT46006.1
gene	60279	61277	45339	46337	gene=IY08_00350	protein=tRNA-dihydrouridine synthase	protein_id=KGT46007.1
gene	61437	62936	46497	47996	gene=IY08_00355	protein=lysyl-tRNA synthetase	protein_id=KGT46008.1
scaffold3							
gene	63662	64123	302	763	gene=IY08_00375	protein=CtsR family transcriptional regulator	protein_id=KGT45885.1
gene	64294	64842	934	1482	gene=IY08_00380	protein=hypothetical protein	protein_id=KGT45886.1
gene	64847	65911	1487	2551	gene=IY08_00385	protein=ATP:guanido phosphotransferase	protein_id=KGT45887.1
gene	65934	68369	2574	5009	gene=IY08_00390	protein=Clp protease ClpX	protein_id=KGT45888.1
gene	68465	69841	5105	6481	gene=IY08_00395	protein=DNA repair protein RadA	protein_id=KGT45889.1
gene	69845	70918	6485	7558	gene=IY08_00400	protein=DNA integrity scanning protein DisA	protein_id=KGT45890.1
gene	71079	72188	7719	8828	gene=IY08_00405	protein=hypothetical protein	protein_id=KGT45891.1
gene	72205	72885	8845	9525	gene=IY08_00410	protein=2-C-methyl-D-erythritol 4-phosphate cytidyltransferase	protein_id=KGT45892.1
gene	73002	73478	9642	10118	gene=IY08_00415	protein=2-C-methyl-D-erythritol 2,4-cyclodiphosphate	protein_id=KGT45893.1
gene	73568	75025	10208	11665	gene=IY08_00420	protein=glutamyl-tRNA synthetase	protein_id=KGT45894.1
gene	75470	76135	12110	12775	gene=IY08_00425	protein=serine acetyltransferase	protein_id=KGT45895.1
gene	76116	77513	12756	14153	gene=IY08_00430	protein=cysteinyl-tRNA synthetase	protein_id=KGT45896.1

gene	77516	77923	14156	14563	gene=IY08_00435	protein=ribonuclease III	protein_id=KGT45897.1
gene	77920	78663	14560	15303	gene=IY08_00440	protein=RNA methyltransferase	protein_id=KGT45898.1
gene	78667	79179	15307	15819	gene=IY08_00445	protein=hypothetical protein	protein_id=KGT45899.1
gene	79247	79906	15887	16546	gene=IY08_00450	protein=RNA polymerase factor sigma-70	protein_id=KGT45900.1
gene	80043	80189	16683	16829	gene=IY08_00455	protein=50S ribosomal protein L33	protein_id=KGT45901.1
gene	80222	80401	16862	17041	gene=IY08_00460	protein=preprotein translocase subunit SecE	protein_id=KGT45902.1
gene	80533	81066	17173	17706	gene=IY08_00465	protein=antitermination protein NusG	protein_id=KGT45903.1
gene	81234	81659	17874	18299	gene=IY08_00470	protein=50S ribosomal protein L11	protein_id=KGT45904.1
gene	81836	82528	18476	19168	gene=IY08_00475	protein=50S ribosomal protein L1	protein_id=KGT45905.1
gene	82762	83262	19402	19902	gene=IY08_00480	protein=50S ribosomal protein L10	protein_id=KGT45906.1
gene	83330	83689	19970	20329	gene=rplL	protein=50S ribosomal protein L7/L12	protein_id=KGT45907.1
gene	83766	84365	20406	21005	gene=IY08_00490	protein=16S rRNA methyltransferase	protein_id=KGT45908.1
gene	84657	88190	21297	24830	gene=IY08_00495	protein=DNA-directed RNA polymerase subunit beta	protein_id=KGT45909.1
gene	88228	91839	24868	28479	gene=IY08_00500	protein=DNA-directed RNA polymerase subunit beta'	protein_id=KGT45910.1
gene	91953	92201	28593	28841	gene=IY08_00505	protein=50S ribosomal protein L7	protein_id=KGT45911.1
gene	92316	92738	28956	29378	gene=IY08_00510	protein=30S ribosomal protein S12	protein_id=KGT45912.1
gene	92768	93238	29408	29878	gene=IY08_00515	protein=30S ribosomal protein S7	protein_id=KGT45913.1
gene	93447	95525	30087	32165	gene=fusA	protein=elongation factor G	protein_id=KGT45914.1
gene	95643	96830	32283	33470	gene=tuf	protein=elongation factor Tu	protein_id=KGT45915.1
gene	97231	97539	33871	34179	gene=IY08_00530	protein=30S ribosomal protein S10	protein_id=KGT45916.1
gene	97574	98206	34214	34846	gene=IY08_00535	protein=50S ribosomal protein L3	protein_id=KGT45917.1
gene	98232	98855	34872	35495	gene=IY08_00540	protein=50S ribosomal protein L4	protein_id=KGT45918.1
gene	98855	99145	35495	35785	gene=IY08_00545	protein=50S ribosomal protein L23	protein_id=KGT45919.1
gene	99174	100004	35814	36644	gene=rplB	protein=50S ribosomal protein L2	protein_id=KGT45920.1
gene	100065	100343	36705	36983	gene=IY08_00555	protein=30S ribosomal protein S19	protein_id=KGT45921.1
gene	100361	100702	37001	37342	gene=IY08_00560	protein=50S ribosomal protein L22	protein_id=KGT45922.1
gene	100706	101365	37346	38005	gene=IY08_00565	protein=30S ribosomal protein S3	protein_id=KGT45923.1
gene	101367	101801	38007	38441	gene=IY08_00570	protein=50S ribosomal protein L16	protein_id=KGT45924.1
gene	101791	101991	38431	38631	gene=IY08_00575	protein=50S ribosomal protein L29	protein_id=KGT45925.1
gene	102012	102275	38652	38915	gene=IY08_00580	protein=30S ribosomal protein S17	protein_id=KGT45926.1
gene	102319	102687	38959	39327	gene=IY08_00585	protein=50S ribosomal protein L14	protein_id=KGT45927.1

gene	102726	103037	39366	39677	gene=IY08_00590	protein=50S ribosomal protein L24	protein_id=KGT45928.1
gene	103064	103603	39704	40243	gene=IY08_00595	protein=50S ribosomal protein L5	protein_id=KGT45929.1
gene	103637	103822	40277	40462	gene=rpsN	protein=30S ribosomal protein S14	protein_id=KGT45930.1
gene	103852	104250	40492	40890	gene=IY08_00605	protein=30S ribosomal protein S8	protein_id=KGT45931.1
gene	104283	104822	40923	41462	gene=IY08_00610	protein=50S ribosomal protein L6	protein_id=KGT45932.1
gene	104854	105216	41494	41856	gene=IY08_00615	protein=50S ribosomal protein L18	protein_id=KGT45933.1
gene	105238	105738	41878	42378	gene=IY08_00620	protein=30S ribosomal protein S5	protein_id=KGT45934.1
gene	105752	105934	42392	42574	gene=IY08_00625	protein=50S ribosomal protein L30	protein_id=KGT45935.1
gene	105968	106408	42608	43048	gene=IY08_00630	protein=50S ribosomal protein L15	protein_id=KGT45936.1
gene	106408	107709	43048	44349	gene=IY08_00635	protein=preprotein translocase subunit SecY	protein_id=KGT45937.1
gene	107766	108416	44406	45056	gene=IY08_00640	protein=adenylate kinase	protein_id=KGT45938.1
gene	108416	109162	45056	45802	gene=IY08_00645	protein=methionine aminopeptidase	protein_id=KGT45939.1
gene	109231	109449	45871	46089	gene=infA	protein=translation initiation factor IF-1	protein_id=KGT45940.1
gene	109485	109598	46125	46238	gene=rpmJ	protein=50S ribosomal protein L36	protein_id=KGT45941.1
gene	109620	109985	46260	46625	gene=IY08_00660	protein=30S ribosomal protein S13	protein_id=KGT45942.1
gene	110010	110399	46650	47039	gene=IY08_00665	protein=30S ribosomal protein S11	protein_id=KGT45943.1
gene	110580	111524	47220	48164	gene=IY08_00670	protein=DNA-directed RNA polymerase subunit alpha	protein_id=KGT45944.1
gene	111560	111922	48200	48562	gene=IY08_00675	protein=50S ribosomal protein L17	protein_id=KGT45945.1
gene	112026	112868	48666	49508	gene=cbiO	protein=cobalt transporter ATP-binding subunit	protein_id=KGT45946.1
gene	112844	113725	49484	50365	gene=cbiO	protein=cobalt transporter ATP-binding subunit	protein_id=KGT45947.1
gene	113713	114507	50353	51147	gene=IY08_00690	protein=cobalt ABC transporter permease	protein_id=KGT45948.1
gene	114507	115265	51147	51905	gene=IY08_00695	protein=tRNA pseudouridine synthase A	protein_id=KGT45949.1
gene	115418	115855	52058	52495	gene=IY08_00700	protein=50S ribosomal protein L13	protein_id=KGT45950.1
gene	115877	116269	52517	52909	gene=IY08_00705	protein=30S ribosomal protein S9	protein_id=KGT45951.1
gene	116431	116859	53071	53499	gene=IY08_00710	protein=KINB signaling pathway activation protein	protein_id=KGT45952.1
gene	116926	117639	53566	54279	gene=IY08_00715	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT45953.1
gene	117785	118849	54425	55489	gene=IY08_00720	protein=chromosome partitioning protein ParA	protein_id=KGT45954.1
gene	119011	119628	55651	56268	gene=IY08_00725	protein=spore germination protein GerD	protein_id=KGT45955.1
gene	119768	120379	56408	57019	gene=IY08_00730	protein=KINB signaling pathway activation protein	protein_id=KGT45956.1
gene	120497	121261	57137	57901	gene=IY08_00735	protein=polysaccharide deacetylase	protein_id=KGT45957.1
gene	121432	121650	58072	58290	gene=IY08_00740	protein=hypothetical protein	protein_id=KGT45958.1

gene	121872	123347	58512	59987	16S rRNA		
scaffold4							
gene	123510	123582	8	79	tRNA		
gene	123428	123499	90	162	tRNA		
gene	123700	124845	280	1425	gene=IY08_00760	protein=glycerate kinase	protein_id=KGT45802.1
gene	125056	125949	1636	2529	gene=IY08_00765	protein=arginase	protein_id=KGT45803.1
gene	126198	127019	2778	3599	gene=IY08_00770	protein=membrane protein	protein_id=KGT45804.1
gene	127012	128499	3592	5079	gene=IY08_00775	protein=hypothetical protein	protein_id=KGT45805.1
gene	128492	129838	5072	6418	gene=IY08_00780	protein=phosphoglucosamine mutase	protein_id=KGT45806.1
gene	130127	130312	6707	6892	gene=IY08_00785	protein=hypothetical protein	protein_id=KGT45807.1
gene	130325	132127	6905	8707	gene=IY08_00790	protein=glucosamine--fructose-6-phosphate	protein_id=KGT45808.1
gene	132266	133381	8846	9961	gene=IY08_00795	protein=membrane protein	protein_id=KGT45809.1
gene	133982	135946	10562	12526	gene=IY08_00800	protein=peptidase S9	protein_id=KGT45810.1
gene	136054	136620	12634	13200	gene=IY08_00805	protein=hypothetical protein	protein_id=KGT45811.1
gene	136693	137199	13273	13779	gene=IY08_00810	protein=DoxX	protein_id=KGT45812.1
gene	137595	138371	14175	14951	gene=IY08_00815	protein=3-ketoacyl-ACP reductase	protein_id=KGT45813.1
gene	138410	139078	14990	15658	gene=IY08_00820	protein=metal ABC transporter permease	protein_id=KGT45814.1
gene	139053	140093	15633	16673	gene=IY08_00825	protein=methionine ABC transporter ATP-binding protein	protein_id=KGT45815.1
gene	140106	140918	16686	17498	gene=IY08_00830	protein=dioxygenase	protein_id=KGT45816.1
gene	141198	142106	17778	18686	gene=IY08_00835	protein=NADPH:quinone reductase	protein_id=KGT45817.1
gene	142264	143028	18844	19608	gene=IY08_00840	protein=lipoprotein	protein_id=KGT45818.1
gene	143095	144531	19675	21111	gene=IY08_00845	protein=FAD-binding protein	protein_id=KGT45819.1
gene	144528	145061	21108	21641	gene=IY08_00850	protein=MFS transporter	protein_id=KGT45820.1
gene	145140	146858	21720	23438	gene=IY08_00855	protein=hypothetical protein	protein_id=KGT45821.1
gene	147039	148235	23619	24815	gene=IY08_00860	protein=MFS transporter	protein_id=KGT45822.1
gene	148497	149000	25077	25580	gene=IY08_00865	protein=lipoprotein	protein_id=KGT45823.1
gene	149048	149515	25628	26095	gene=IY08_00870	protein=hypothetical protein	protein_id=KGT45824.1
gene	149688	150587	26268	27167	gene=IY08_00875	protein=transcriptional regulator	protein_id=KGT45825.1
gene	150606	150797	27186	27377	gene=IY08_00880	protein=hypothetical protein	protein_id=KGT45826.1
gene	150794	151144	27374	27724	gene=IY08_00885	protein=hypothetical protein	protein_id=KGT45827.1
gene	151185	152825	27765	29405	gene=IY08_00890	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT45828.1

gene	153230	154870	29810	31450	gene=IY08_00895	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT45829.1
gene	155260	156093	31840	32673	gene=IY08_00900	protein=glyoxal reductase	protein_id=KGT45830.1
gene	156095	156898	32675	33478	gene=IY08_00905	protein=pyrroline-5-carboxylate reductase	protein_id=KGT45831.1
gene	157184	158035	33764	34615	gene=IY08_00910	protein=glucose transporter GlcU	protein_id=KGT45832.1
gene	158336	159010	34916	35590	gene=IY08_00915	protein=molybdenum ABC transporter permease	protein_id=KGT45833.1
gene	159016	159822	35596	36402	gene=IY08_00920	protein=molybdenum ABC transporter substrate-binding	protein_id=KGT45834.1
gene	159983	160903	36563	37483	gene=IY08_00925	protein=hypothetical protein	protein_id=KGT45835.1
gene	160969	161070	37549	37650	gene=IY08_00930	protein=hypothetical protein	protein_id=KGT45836.1
gene	161083	161184	37663	37764	gene=IY08_00935	protein=hypothetical protein	protein_id=KGT45837.1
gene	161325	162191	37905	38771	gene=IY08_00940	protein=LysR family transcriptional regulator	protein_id=KGT45838.1
gene	162319	163287	38899	39867	gene=IY08_00945	protein=transporter	protein_id=KGT45839.1
gene	163309	163449	39889	40029	gene=IY08_00950	protein=hypothetical protein	protein_id=KGT45840.1
gene	163618	163719	40198	40299	gene=IY08_00960	protein=hypothetical protein	protein_id=KGT45841.1
gene	163943	164548	40523	41128	gene=IY08_00965	protein=acyl-phosphate glycerol 3-phosphate	protein_id=KGT45842.1
gene	164729	164830	41309	41410	gene=IY08_00975	protein=hypothetical protein	protein_id=KGT45843.1
gene	165022	165999	41602	42579	gene=IY08_00980	protein=LacI family transcriptional regulator	protein_id=KGT45844.1
gene	166160	166489	42740	43069	gene=IY08_00985	protein=translation initiation factor, aIF-2BI	protein_id=KGT45845.1
gene	166608	167444	43188	44024	gene=IY08_00990	protein=membrane protein YxkD	protein_id=KGT45846.1
gene	167583	167939	44163	44519	gene=IY08_00995	protein=ferrichrome ABC transporter permease	protein_id=KGT45847.1
gene	168505	168618	45085	45198	gene=IY08_01000	protein=iron ABC transporter permease	protein_id=KGT45848.1
gene	168678	169442	45258	46022	gene=IY08_01005	protein=DNAase	protein_id=KGT45849.1
gene	169559	171208	46139	47788	gene=IY08_01010	protein=hypothetical protein	protein_id=KGT45850.1
gene	171448	171978	48028	48558	gene=IY08_01015	protein=invasion protein	protein_id=KGT45851.1
gene	172146	172940	48726	49520	gene=IY08_01020	protein=galactose-1-phosphate uridylyltransferase	protein_id=KGT45852.1
gene	173077	173205	49657	49785	gene=IY08_01025	protein=Spore coat protein B	protein_id=KGT45853.1
gene	173627	173761	50207	50341	gene=IY08_01030	protein=hypothetical protein	protein_id=KGT45854.1
gene	173886	175766	50466	52346	gene=IY08_01035	protein=ABC transporter ATP-binding protein	protein_id=KGT45855.1
gene	176158	176355	52738	52935	gene=IY08_01040	protein=hypothetical protein	protein_id=KGT45856.1
gene	176981	178708	53561	55288	gene=IY08_01045	protein=ABC transporter substrate-binding protein	protein_id=KGT45857.1
gene	178812	179768	55392	56348	gene=IY08_01050	protein=diguanylate cyclase	protein_id=KGT45858.1
gene	179781	180701	56361	57281	gene=IY08_01055	protein=peptide ABC transporter permease	protein_id=KGT45859.1

gene	180712	181692	57292	58272	gene=IY08_01060	protein=peptide ABC transporter ATP-binding protein	protein_id=KGT45860.1
gene	181689	182654	58269	59234	gene=IY08_01065	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT45861.1
gene	182689	183561	59269	60141	gene=IY08_01070	protein=HAD family hydrolase	protein_id=KGT45862.1
gene	184002	184109	60582	60689	gene=IY08_01080	protein=fatty acid desaturase	protein_id=KGT45863.1
gene	184153	184260	60733	60840	gene=IY08_01085	protein=fatty acid desaturase	protein_id=KGT45864.1
gene	184400	184507	60980	61087	gene=IY08_01095	protein=fatty acid desaturase	protein_id=KGT45884.1
gene	184542	184661	61122	61241	gene=IY08_01100	protein=fatty acid desaturase	protein_id=KGT45865.1
gene	185055	186173	61635	62753	gene=IY08_01105	protein=4-hydroxyphenylpyruvate dioxygenase	protein_id=KGT45866.1
gene	186240	187196	62820	63776	gene=IY08_01110	protein=fumarylacetoacetase	protein_id=KGT45867.1
gene	187162	188334	63742	64914	gene=IY08_01115	protein=homogentisate 1,2-dioxygenase	protein_id=KGT45868.1
gene	188567	189982	65147	66562	gene=IY08_01120	protein=amino acid permease	protein_id=KGT45869.1
gene	190091	191362	66671	67942	gene=IY08_01125	protein=MFS transporter	protein_id=KGT45870.1
gene	191591	192676	68171	69256	gene=ddl	protein=D-alanine--D-alanine ligase	protein_id=KGT45871.1
gene	192739	194115	69319	70695	gene=IY08_01135	protein=UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	protein_id=KGT45872.1
gene	194421	196022	71001	72602	gene=IY08_01140	protein=DEAD/DEAH box helicase	protein_id=KGT45873.1
gene	196118	197080	72698	73660	gene=IY08_01145	protein=UV damage repair endonuclease UvdE	protein_id=KGT45874.1
gene	197073	197645	73653	74225	gene=IY08_01150	protein=rhomboid family protein	protein_id=KGT45875.1
gene	197739	198098	74319	74678	gene=IY08_01155	protein=4'-phosphopantetheinyl transferase	protein_id=KGT45876.1
gene	198255	199205	74835	75785	gene=IY08_01160	protein=sporulation protein	protein_id=KGT45877.1
gene	199323	200492	75903	77072	gene=IY08_01165	protein=alanine racemase	protein_id=KGT45878.1
gene	200801	201088	77381	77668	gene=IY08_01170	protein=antitoxin endoai	protein_id=KGT45879.1
gene	201093	201443	77673	78023	gene=IY08_01175	protein=PemK family transcriptional regulator	protein_id=KGT45880.1
gene	201511	203679	78091	80259	gene=IY08_01180	protein=hypothetical protein	protein_id=KGT45881.1
gene	203737	203853	80317	80433	gene=IY08_01185	protein=hypothetical protein	protein_id=KGT45882.1
gene	204049	204507	80629	81087	gene=IY08_01190	protein=hypothetical protein	protein_id=KGT45883.1
gene	204621	204695	81201	81275	tRNA		
scaffold5							
gene	204721	204921	1	201	gene=IY08_01200	protein=transposase	protein_id=KGT45785.1
gene	205268	205864	548	1144	gene=IY08_01205	protein=ABC transporter permease	protein_id=KGT45786.1
gene	206164	206436	1444	1716	pseudo		

gene	206831	207109	2111	2389	gene=IY08_01220	protein=AbrB family transcriptional regulator	protein_id=KGT45787.1
gene	207536	207775	2816	3055	gene=IY08_01225	protein=transcriptional regulator	protein_id=KGT45788.1
gene	208755	209065	4035	4345	pseudo		
gene	209535	210095	4815	5375	gene=IY08_01235	protein=spore coat protein	protein_id=KGT45789.1
gene	210960	211346	6240	6626	gene=IY08_01250	protein=hypothetical protein	protein_id=KGT45790.1
gene	211520	211792	6800	7072	gene=IY08_01255	protein=DNA-binding protein	protein_id=KGT45791.1
gene	212066	213535	7346	8815	gene=IY08_01265	protein=glutamate decarboxylase	protein_id=KGT45792.1
gene	214854	215258	10134	10538	gene=IY08_01270	protein=hypothetical protein	protein_id=KGT45793.1
gene	215510	216007	10790	11287	pseudo		
gene	216545	216894	11825	12174	pseudo		
gene	216916	217428	12196	12708	gene=IY08_01285	protein=hypothetical protein	protein_id=KGT45794.1
gene	217647	218519	12927	13799	gene=IY08_01290	protein=hypothetical protein	protein_id=KGT45795.1
gene	219043	219789	14323	15069	gene=IY08_01300	protein=hypothetical protein	protein_id=KGT45796.1
gene	220083	220508	15363	15788	gene=IY08_01305	protein=hypothetical protein	protein_id=KGT45797.1
gene	220719	221099	15999	16379	pseudo		
gene	221638	221947	16918	17227	pseudo		
gene	222244	223890	17524	19170	gene=IY08_01320	protein=cell wall hydrolase	protein_id=KGT45798.1
gene	225524	227137	20804	22417	gene=IY08_01325	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT45799.1
gene	227388	228064	22668	23344	pseudo		
gene	230190	230591	25470	25871	gene=IY08_01345	protein=beta-lactamase repressor	protein_id=KGT45800.1
gene	230881	232064	26161	27344	gene=IY08_01355	protein=beta-lactamase regulatory protein	partial=3'
scaffold6							
gene	232082	232158	2	78	tRNA		
gene	232162	232237	82	157	tRNA		
gene	232412	232885	332	805	gene=IY08_01370	protein=ATP-binding protein	protein_id=KGT45771.1
gene	232866	233558	786	1478	gene=IY08_01375	protein=hypothetical protein	protein_id=KGT45772.1
gene	233572	234015	1492	1935	gene=IY08_01380	protein=alanine acetyltransferase	protein_id=KGT45773.1
gene	234015	235031	1935	2951	gene=IY08_01385	protein=O-sialoglycoprotein endopeptidase	protein_id=KGT45774.1
gene	235516	237495	3436	5415	gene=IY08_01390	protein=ABC transporter ATP-binding protein	protein_id=KGT45775.1
gene	237629	238258	5549	6178	gene=IY08_01395	protein=redox-sensing transcriptional repressor Rex	protein_id=KGT45776.1
gene	238288	238479	6208	6399	gene=IY08_01400	protein=lipoprotein	protein_id=KGT45777.1

gene	238476	239225	6396	7145	gene=IY08_01405	protein=peptidase	protein_id=KGT45778.1
gene	239617	239901	7537	7821	gene=IY08_01410	protein=chaperonin	protein_id=KGT45779.1
gene	239940	241574	7860	9494	gene=groEL	protein=molecular chaperone GroEL	protein_id=KGT45780.1
gene	241972	243519	9892	11439	gene=IY08_01420	protein=GMP synthase	protein_id=KGT45781.1
gene	243905	245230	11825	13150	gene=IY08_01425	protein=guanine permease	protein_id=KGT45782.1
gene	245374	246075	13294	13995	gene=IY08_01430	protein=DeoR family transcriptional regulator	protein_id=KGT45783.1
gene	246059	247564	13979	15484	gene=IY08_01435	protein=histidine kinase	protein_id=KGT45784.1
scaffold7							
gene	247921	247954	1	34	5s rRNA		
gene	248742	249227	822	1307	gene=IY08_01445	protein=N5-carboxyaminoimidazole ribonucleotide mutase	protein_id=KGT45572.1
gene	249224	250375	1304	2455	gene=IY08_01450	protein=phosphoribosylaminoimidazole carboxylase	protein_id=KGT45573.1
gene	250372	251679	2452	3759	gene=IY08_01455	protein=adenylosuccinate lyase	protein_id=KGT45574.1
gene	251768	252487	3848	4567	gene=IY08_01460	protein=phosphoribosylaminoimidazole-succinocarboxamide synthase	protein_id=KGT45575.1
gene	252480	252734	4560	4814	gene=IY08_01465	protein=phosphoribosylformylglycinamide synthase	protein_id=KGT45576.1
gene	252731	253414	4811	5494	gene=IY08_01470	protein=phosphoribosylformylglycinamide synthase	protein_id=KGT45577.1
gene	253398	255617	5478	7697	gene=IY08_01475	protein=phosphoribosylformylglycinamide synthase	protein_id=KGT45578.1
gene	255602	257017	7682	9097	gene=IY08_01480	protein=amidophosphoribosyltransferase	protein_id=KGT45579.1
gene	257123	258163	9203	10243	gene=IY08_01485	protein=phosphoribosylaminoimidazole synthetase	protein_id=KGT45580.1
gene	258160	258747	10240	10827	gene=IY08_01490	protein=phosphoribosylglycinamide formyltransferase	protein_id=KGT45581.1
gene	258772	260307	10852	12387	gene=purH	protein=phosphoribosylaminoimidazolecarboxamide formyltransferase	protein_id=KGT45582.1
gene	260572	261843	12652	13923	gene=IY08_01500	protein=phosphoribosylamine--glycine ligase	protein_id=KGT45583.1
gene	261880	262044	13960	14124	gene=IY08_01505	protein=ribbon-helix-helix domain protein	protein_id=KGT45584.1
gene	262060	262905	14140	14985	gene=IY08_01510	protein=membrane protein	protein_id=KGT45585.1
gene	263125	263502	15205	15582	gene=IY08_01515	protein=MarR family transcriptional regulator	protein_id=KGT45586.1
gene	263661	263774	15741	15854	gene=IY08_01525	protein=hypothetical protein	protein_id=KGT45770.1
gene	263840	264529	15920	16609	gene=IY08_01530	protein=heptaprenylglyceryl phosphate synthase	protein_id=KGT45587.1
gene	264542	266791	16622	18871	gene=IY08_01535	protein=ATP-dependent DNA helicase PcrA	protein_id=KGT45588.1
gene	266807	268816	18887	20896	gene=ligA	protein=NAD-dependent DNA ligase LigA	protein_id=KGT45589.1
gene	268833	270029	20913	22109	gene=IY08_01545	protein=hypothetical protein	protein_id=KGT45590.1

gene	270126	270896	22206	22976	gene=IY08_01550	protein=membrane protein	protein_id=KGT45591.1
gene	271050	272597	23130	24677	gene=IY08_01555	protein=1-pyrroline-5-carboxylate dehydrogenase	protein_id=KGT45592.1
gene	272868	273413	24948	25493	gene=IY08_01560	protein=isochorismatase	protein_id=KGT45593.1
gene	273886	274905	25966	26985	gene=IY08_01565	protein=phosphate ABC transporter ATP-binding protein	protein_id=KGT45594.1
gene	274895	275560	26975	27640	gene=IY08_01570	protein=ABC transporter permease	protein_id=KGT45595.1
gene	275582	276436	27662	28516	gene=IY08_01575	protein=methionine ABC transporter substrate-binding	protein_id=KGT45596.1
gene	276601	277068	28681	29148	gene=IY08_01580	protein=hypothetical protein	protein_id=KGT45597.1
gene	277130	277321	29210	29401	gene=IY08_01585	protein=hypothetical protein	protein_id=KGT45598.1
gene	277314	278492	29394	30572	gene=IY08_01590	protein=arsenic ABC transporter ATPase	protein_id=KGT45599.1
gene	278572	279054	30652	31134	gene=IY08_01595	protein=MarR family transcriptional regulator	protein_id=KGT45600.1
gene	279286	279522	31366	31602	gene=IY08_01600	protein=hypothetical protein	protein_id=KGT45601.1
gene	279664	279954	31744	32034	gene=IY08_01605	protein=glutamyl-tRNA amidotransferase	protein_id=KGT45602.1
gene	279970	281427	32050	33507	gene=gatA	protein=glutamyl-tRNA amidotransferase	protein_id=KGT45603.1
gene	281442	282869	33522	34949	gene=IY08_01615	protein=glutamyl-tRNA amidotransferase	protein_id=KGT45604.1
gene	283428	284333	35508	36413	gene=IY08_01620	protein=lipid kinase	protein_id=KGT45605.1
gene	285111	286241	37191	38321	gene=IY08_01630	protein=transposase	protein_id=KGT45606.1
gene	286389	287132	38469	39212	gene=IY08_01635	protein=haloacid dehalogenase	protein_id=KGT45607.1
gene	287287	288651	39367	40731	gene=IY08_01640	protein=4-aminobutyrate aminotransferase	protein_id=KGT45608.1
gene	288767	290134	40847	42214	gene=IY08_01645	protein=RNA polymerase subunit sigma-54	protein_id=KGT45609.1
gene	290127	291578	42207	43658	gene=gabD	protein=succinate-semialdehyde dehydrogenase	protein_id=KGT45610.1
gene	291626	291949	43706	44029	gene=IY08_01655	protein=DNA mismatch repair protein MutS	protein_id=KGT45611.1
gene	292082	292573	44162	44653	gene=IY08_01660	protein=hypothetical protein	protein_id=KGT45612.1
gene	292619	293848	44699	45928	gene=IY08_01665	protein=peptidase M29	protein_id=KGT45613.1
gene	293965	295047	46045	47127	gene=IY08_01670	protein=polysaccharide deacetylase	protein_id=KGT45614.1
gene	295584	296291	47664	48371	gene=IY08_01680	protein=hypothetical protein	protein_id=KGT45615.1
gene	296337	297533	48417	49613	gene=IY08_01685	protein=pyrimidine nucleoside transporter NupC	protein_id=KGT45616.1
gene	297959	299335	50039	51415	gene=IY08_01690	protein=RNA methyltransferase	protein_id=KGT45617.1
gene	299497	300486	51577	52566	gene=IY08_01695	protein=tRNA-dihydrouridine synthase	protein_id=KGT45618.1
gene	300838	301356	52918	53436	gene=IY08_01700	protein=cytoplasmic protein	protein_id=KGT45619.1
gene	301451	302158	53531	54238	gene=IY08_01705	protein=zinc protease	protein_id=KGT45620.1
gene	302399	303094	54479	55174	gene=IY08_01710	protein=benzoate transporter	protein_id=KGT45621.1

gene	303109	304218	55189	56298	gene=IY08_01715	protein=mandelate racemase	protein_id=KGT45622.1
gene	304312	305583	56392	57663	gene=IY08_01720	protein=transcriptional regulator	protein_id=KGT45623.1
gene	305572	306993	57652	59073	gene=IY08_01725	protein=sodium:proton antiporter	protein_id=KGT45624.1
gene	307287	308402	59367	60482	gene=IY08_01730	protein=amidohydrolase	protein_id=KGT45625.1
gene	308637	309242	60717	61322	gene=IY08_01735	protein=SAM-dependent methyltransferase	protein_id=KGT45626.1
gene	309276	310802	61356	62882	gene=IY08_01740	protein=NADH dehydrogenase	protein_id=KGT45627.1
gene	310817	311380	62897	63460	gene=IY08_01745	protein=alkyl hydroperoxide reductase	protein_id=KGT45628.1
gene	311972	313201	64052	65281	gene=IY08_01750	protein=5-methylthioribose kinase	protein_id=KGT45629.1
gene	313211	314257	65291	66337	gene=IY08_01755	protein=methylthioribose-1-phosphate isomerase	protein_id=KGT45630.1
gene	314311	314952	66391	67032	gene=IY08_01760	protein=fucose phosphate aldolase	protein_id=KGT45631.1
gene	314997	316004	67077	68084	gene=IY08_01765	protein=iron ABC transporter permease	protein_id=KGT45632.1
gene	316001	317041	68081	69121	gene=IY08_01770	protein=iron ABC transporter	protein_id=KGT45633.1
gene	317090	318007	69170	70087	gene=IY08_01775	protein=ABC transporter substrate-binding protein	protein_id=KGT45634.1
gene	318050	318316	70130	70396	gene=IY08_01780	protein=hypothetical protein	protein_id=KGT45635.1
gene	318341	319390	70421	71470	gene=IY08_01785	protein=thioredoxin reductase	protein_id=KGT45636.1
gene	319433	319630	71513	71710	gene=IY08_01790	protein=hypothetical protein	protein_id=KGT45637.1
gene	319586	319954	71666	72034	gene=IY08_01795	protein=hypothetical protein	protein_id=KGT45638.1
gene	320145	320375	72225	72455	gene=IY08_01800	protein=hypothetical protein	protein_id=KGT45639.1
gene	320611	321126	72691	73206	gene=IY08_01805	protein=spore coat protein	protein_id=KGT45640.1
gene	321147	321596	73227	73676	gene=IY08_01810	protein=spore coat protein	protein_id=KGT45641.1
gene	321758	322426	73838	74506	gene=IY08_01815	protein=hypothetical protein	protein_id=KGT45642.1
gene	322666	323931	74746	76011	gene=IY08_01820	protein=S-adenosylmethionine decarboxylase related	protein_id=KGT45643.1
gene	324069	325295	76149	77375	gene=IY08_01830	protein=sporulation kinase	protein_id=KGT45644.1
gene	325524	325904	77604	77984	gene=IY08_01835	protein=hypothetical protein	protein_id=KGT45645.1
gene	325932	326564	78012	78644	gene=IY08_01840	protein=metal-dependent hydrolase	protein_id=KGT45646.1
gene	326911	328020	78991	80100	gene=IY08_01845	protein=hypothetical protein	protein_id=KGT45647.1
gene	328132	328914	80212	80994	gene=IY08_01850	protein=hypothetical protein	protein_id=KGT45648.1
gene	328928	330229	81008	82309	gene=IY08_01855	protein=MFS transporter	protein_id=KGT45649.1
gene	330373	331899	82453	83979	gene=IY08_01860	protein=(2Fe-2S)-binding protein	protein_id=KGT45650.1
gene	332481	333566	84561	85646	gene=IY08_01865	protein=fatty acid desaturase	protein_id=KGT45651.1
gene	333620	334312	85700	86392	gene=IY08_01870	protein=cystine transporter permease	protein_id=KGT45652.1

gene	334419	335213	86499	87293	gene=IY08_01875	protein=ABC transporter substrate-binding protein	protein_id=KGT45653.1
gene	335336	336058	87416	88138	gene=IY08_01880	protein=amino acid ABC transporter ATPase	protein_id=KGT45654.1
gene	336269	337561	88349	89641	gene=IY08_01885	protein=chemotaxis protein	protein_id=KGT45655.1
gene	337708	338157	89788	90237	gene=IY08_01890	protein=ArgR family transcriptional regulator	protein_id=KGT45656.1
gene	338426	339658	90506	91738	gene=IY08_01895	protein=arginine deiminase	protein_id=KGT45657.1
gene	339689	340687	91769	92767	gene=IY08_01900	protein=ornithine carbamoyltransferase	protein_id=KGT45658.1
gene	340787	342202	92867	94282	gene=IY08_01905	protein=amino acid APC transporter	protein_id=KGT45659.1
gene	342240	343202	94320	95282	gene=IY08_01910	protein=carbamate kinase	protein_id=KGT45660.1
gene	343404	344093	95484	96173	gene=IY08_01915	protein=Crp/Fnr family transcriptional regulator	protein_id=KGT45661.1
gene	344250	344933	96330	97013	gene=IY08_01920	protein=hypothetical protein	protein_id=KGT45662.1
gene	345058	345675	97138	97755	pseudo		
gene	345749	347413	97829	99493	gene=IY08_01930	protein=oligo-1,6-glucosidase	protein_id=KGT45663.1
gene	347615	349252	99695	101332	gene=IY08_01935	protein=PTS system transporter subunit IICB	protein_id=KGT45664.1
gene	349257	350048	101337	102128	gene=IY08_01940	protein=endonuclease	protein_id=KGT45665.1
gene	350353	353214	102433	105294	gene=IY08_01945	protein=phage infection protein	protein_id=KGT45666.1
gene	353255	355444	105335	107524	gene=IY08_01950	protein=DNA topoisomerase III	protein_id=KGT45667.1
gene	355852	356661	107932	108741	gene=IY08_01955	protein=hydroxyethylthiazole kinase	protein_id=KGT45668.1
gene	356677	357336	108757	109416	gene=thiE	protein=thiamine-phosphate pyrophosphorylase	protein_id=KGT45669.1
gene	357551	358864	109631	110944	gene=IY08_01965	protein=C4-dicarboxylate ABC transporter	protein_id=KGT45670.1
gene	359367	361109	111447	113189	gene=IY08_01970	protein=chemotaxis protein	protein_id=KGT45671.1
gene	361242	364823	113322	116903	gene=IY08_01975	protein=peptide synthetase	protein_id=KGT45672.1
gene	365079	365399	117159	117479	gene=IY08_01980	protein=hypothetical protein	protein_id=KGT45673.1
gene	365371	366144	117451	118224	gene=IY08_01985	protein=ABC transporter permease	protein_id=KGT45674.1
gene	366141	367139	118221	119219	gene=IY08_01990	protein=ABC transporter substrate-binding protein	protein_id=KGT45675.1
gene	367136	367885	119216	119965	gene=IY08_01995	protein=nitrate ABC transporter ATP-binding protein	protein_id=KGT45676.1
gene	368523	370547	120603	122627	gene=IY08_02000	protein=chitinase	protein_id=KGT45677.1
gene	370919	371290	122999	123370	gene=IY08_02005	protein=molecular chaperone DnaJ	protein_id=KGT45678.1
gene	371301	371615	123381	123695	gene=IY08_02010	protein=thioredoxin	protein_id=KGT45679.1
gene	371629	371874	123709	123954	gene=IY08_02015	protein=methanol dehydrogenase	protein_id=KGT45680.1
gene	371999	372142	124079	124222	gene=IY08_02020	protein=histidine kinase	protein_id=KGT45681.1
gene	372223	372804	124303	124884	gene=IY08_02025	protein=TetR family transcriptional regulator	protein_id=KGT45682.1

gene	372871	374103	124951	126183	gene=IY08_02030	protein=MFS transporter	protein_id=KGT45683.1
gene	374217	374411	126297	126491	gene=IY08_02035	protein=DNA-binding protein	protein_id=KGT45684.1
gene	374481	375764	126561	127844	gene=IY08_02040	protein=MFS transporter	protein_id=KGT45685.1
gene	375873	377186	127953	129266	gene=IY08_02045	protein=phosphodiesterase	protein_id=KGT45686.1
gene	377341	377634	129421	129714	gene=IY08_02050	protein=membrane protein	protein_id=KGT45687.1
gene	377981	379411	130061	131491	gene=IY08_02055	protein=proline--tRNA ligase	protein_id=KGT45688.1
gene	379528	380373	131608	132453	gene=IY08_02060	protein=cell wall anchor protein	protein_id=KGT45689.1
gene	380572	381450	132652	133530	gene=IY08_02065	protein=ROK family transcriptional regulator	protein_id=KGT45690.1
gene	381579	382175	133659	134255	gene=IY08_02070	protein=stress protein	protein_id=KGT45691.1
gene	382198	382782	134278	134862	gene=IY08_02075	protein=chemical-damaging agent resistance protein C	protein_id=KGT45692.1
gene	382868	383446	134948	135526	gene=IY08_02080	protein=chemical-damaging agent resistance protein C	protein_id=KGT45693.1
gene	383519	384310	135599	136390	gene=IY08_02085	protein=membrane protein	protein_id=KGT45694.1
gene	384420	386051	136500	138131	gene=IY08_02090	protein=hypothetical protein	protein_id=KGT45695.1
gene	386070	387152	138150	139232	gene=IY08_02095	protein=hypothetical protein	protein_id=KGT45696.1
gene	387188	389854	139268	141934	gene=IY08_02100	protein=ATPase	protein_id=KGT45697.1
gene	390047	390271	142127	142351	gene=IY08_02105	protein=hypothetical protein	protein_id=KGT45698.1
gene	390446	390910	142526	142990	gene=IY08_02110	protein=phosphotyrosine protein phosphatase	protein_id=KGT45699.1
gene	390964	391479	143044	143559	gene=IY08_02115	protein=hypothetical protein	protein_id=KGT45700.1
gene	391486	392352	143566	144432	gene=IY08_02120	protein=ribonuclease BN	protein_id=KGT45701.1
gene	392540	394465	144620	146545	gene=IY08_02130	protein=ATPase	protein_id=KGT45702.1
gene	394737	395687	146817	147767	gene=IY08_02135	protein=transporter	protein_id=KGT45703.1
gene	395808	396488	147888	148568	gene=IY08_02140	protein=hypothetical protein	protein_id=KGT45704.1
gene	396666	397202	148746	149282	gene=IY08_02145	protein=signal peptidase	protein_id=KGT45705.1
gene	397241	400003	149321	152083	gene=IY08_02150	protein=GTP-binding protein	protein_id=KGT45706.1
gene	400491	401090	152571	153170	gene=IY08_02155	protein=alkaline phosphatase	protein_id=KGT45707.1
gene	401101	401529	153181	153609	gene=IY08_02160	protein=membrane protein	protein_id=KGT45708.1
gene	401739	401885	153819	153965	gene=IY08_02165	protein=transporter	protein_id=KGT45709.1
gene	402041	402457	154121	154537	gene=IY08_02170	protein=general stress protein	protein_id=KGT45710.1
gene	402637	403692	154717	155772	gene=IY08_02175	protein=cation transporter	protein_id=KGT45711.1
gene	403772	404569	155852	156649	gene=IY08_02180	protein=hypothetical protein	protein_id=KGT45712.1
gene	404605	405732	156685	157812	gene=IY08_02185	protein=hypothetical protein	protein_id=KGT45713.1

gene	405946	406128	158026	158208	gene=IY08_02190	protein=hypothetical protein	protein_id=KGT45714.1
gene	406331	407851	158411	159931	gene=IY08_02195	protein=fumarate hydratase	protein_id=KGT45715.1
gene	407979	408761	160059	160841	gene=IY08_02200	protein=polysaccharide deacetylase	protein_id=KGT45716.1
gene	408821	409684	160901	161764	gene=IY08_02205	protein=DNA-3-methyladenine glycosylase	protein_id=KGT45717.1
gene	409695	411074	161775	163154	gene=IY08_02210	protein=RNA methyltransferase	protein_id=KGT45718.1
gene	411323	412216	163403	164296	gene=IY08_02215	protein=S-layer protein	protein_id=KGT45719.1
gene	412331	413068	164411	165148	gene=IY08_02220	protein=tRNA pseudouridine synthase A	protein_id=KGT45720.1
gene	413113	413316	165193	165396	gene=IY08_02225	protein=hypothetical protein	protein_id=KGT45721.1
gene	413400	414803	165480	166883	gene=IY08_02230	protein=ATPase AAA	protein_id=KGT45722.1
gene	415097	415351	167177	167431	gene=IY08_02235	protein=hypothetical protein	protein_id=KGT45723.1
gene	415458	416879	167538	168959	gene=IY08_02240	protein=amino acid permease	protein_id=KGT45724.1
gene	416975	418249	169055	170329	gene=IY08_02245	protein=acetylornithine deacetylase	protein_id=KGT45725.1
gene	418349	419002	170429	171082	gene=IY08_02250	protein=DNA-binding protein	protein_id=KGT45726.1
gene	419133	419744	171213	171824	gene=IY08_02255	protein=membrane protein	protein_id=KGT45727.1
gene	419859	420017	171939	172097	gene=IY08_02260	protein=hypothetical protein	protein_id=KGT45728.1
gene	420040	420381	172120	172461	gene=IY08_02265	protein=hypothetical protein	protein_id=KGT45729.1
gene	420420	420571	172500	172651	pseudo		
gene	420556	421485	172636	173565	gene=IY08_02275	protein=glutaminase	protein_id=KGT45730.1
gene	421811	423313	173891	175393	gene=IY08_02280	protein=PTS N-acetylglucosamine transporter subunit IIB	protein_id=KGT45731.1
gene	423567	424814	175647	176894	gene=IY08_02285	protein=penicillin-binding protein	protein_id=KGT45732.1
gene	424970	425371	177050	177451	gene=IY08_02290	protein=hypothetical protein	protein_id=KGT45733.1
gene	425388	425582	177468	177662	gene=IY08_02295	protein=hypothetical protein	protein_id=KGT45734.1
gene	425596	427140	177676	179220	gene=IY08_02300	protein=glycosyl transferase	protein_id=KGT45735.1
gene	427133	428374	179213	180454	gene=IY08_02305	protein=UDP-N-acetyl-D-mannosamine dehydrogenase	protein_id=KGT45736.1
gene	428371	429336	180451	181416	gene=IY08_02310	protein=NAD-dependent dehydratase	protein_id=KGT45737.1
gene	429329	430873	181409	182953	gene=IY08_02315	protein=glycosyl transferase	protein_id=KGT45738.1
gene	430842	431063	182922	183143	gene=IY08_02320	protein=hypothetical protein	protein_id=KGT45739.1
gene	431216	433465	183296	185545	gene=IY08_02325	protein=formate acetyltransferase	protein_id=KGT45740.1
gene	433535	434266	185615	186346	gene=IY08_02330	protein=pyruvate formate lyase-activating protein	protein_id=KGT45741.1
gene	434679	435845	186759	187925	gene=IY08_02335	protein=diacylglycerol glucosyltransferase	protein_id=KGT45742.1
gene	436214	436333	188294	188413	gene=IY08_02340	protein=hypothetical protein	protein_id=KGT45743.1

gene	436443	437000	188523	189080	gene=IY08_02345	protein=alanine acetyltransferase	protein_id=KGT45744.1
gene	437242	438372	189322	190452	gene=IY08_02350	protein=amidohydrolase	protein_id=KGT45745.1
gene	438512	439417	190592	191497	gene=IY08_02355	protein=multidrug MFS transporter	protein_id=KGT45746.1
gene	439499	440311	191579	192391	gene=IY08_02360	protein=recombinase RecX	protein_id=KGT45747.1
gene	440322	440639	192402	192719	gene=IY08_02365	protein=hypothetical protein	protein_id=KGT45748.1
gene	440704	440856	192784	192936	gene=IY08_02370	protein=hypothetical protein	protein_id=KGT45749.1
gene	440894	441052	192974	193132	gene=sspK	protein=acid-soluble spore protein K	protein_id=KGT45750.1
gene	441175	441441	193255	193521	gene=IY08_02380	protein=hypothetical protein	protein_id=KGT45751.1
gene	441466	442446	193546	194526	gene=IY08_02385	protein=membrane protein	protein_id=KGT45752.1
gene	442596	443693	194676	195773	gene=IY08_02390	protein=DNA glycosylase	protein_id=KGT45753.1
gene	443728	443952	195808	196032	gene=IY08_02395	protein=hypothetical protein	protein_id=KGT45754.1
gene	444078	444359	196158	196439	gene=IY08_02400	protein=spore protein	protein_id=KGT45755.1
gene	444548	444808	196628	196888	gene=IY08_02405	protein=stress-induced protein	protein_id=KGT45756.1
gene	445081	445611	197161	197691	gene=IY08_02410	protein=hypothetical protein	protein_id=KGT45757.1
gene	445666	447426	197746	199506	gene=IY08_02415	protein=multidrug ABC transporter ATP-binding protein	protein_id=KGT45758.1
gene	447441	448529	199521	200609	gene=IY08_02420	protein=membrane protein	protein_id=KGT45759.1
gene	448886	453322	200966	205402	gene=IY08_02425	protein=glutamate synthase	protein_id=KGT45760.1
gene	453521	454819	205601	206899	gene=IY08_02430	protein=glutamate-1-semialdehyde aminotransferase	protein_id=KGT45761.1
gene	454947	455960	207027	208040	gene=IY08_02435	protein=daunorubicin ABC transporter ATP-binding	protein_id=KGT45762.1
gene	455953	456744	208033	208824	gene=IY08_02440	protein=daunorubicin ABC transporter permease	protein_id=KGT45763.1
gene	456749	457534	208829	209614	gene=IY08_02445	protein=ABC transporter permease	protein_id=KGT45764.1
gene	457607	458011	209687	210091	gene=IY08_02450	protein=transporter	protein_id=KGT45765.1
gene	458056	458511	210136	210591	gene=IY08_02455	protein=peroxiredoxin	protein_id=KGT45766.1
gene	458806	459240	210886	211320	gene=IY08_02460	protein=Fur family transcriptional regulator	protein_id=KGT45767.1
gene	459411	459830	211491	211910	gene=IY08_02465	protein=GCN5 family acetyltransferase	protein_id=KGT45768.1
gene	459936	460292	212016	212372	gene=IY08_02470	protein=hypothetical protein	protein_id=KGT45769.1
scaffold8							
gene	460743	460826	3	86	tRNA		
gene	460834	460907	94	167	tRNA		
gene	460928	461003	188	263	tRNA		
gene	461067	461141	327	401	tRNA		

gene	461147	461221	407	481	tRNA		
gene	461235	461305	495	565	tRNA		
gene	461316	461400	576	660	tRNA		
gene	461515	461835	775	1095	gene=IY08_02510	protein=hypothetical protein	protein_id=KGT45480.1
gene	462186	462905	1446	2165	gene=IY08_02515	protein=hypothetical protein	protein_id=KGT45481.1
gene	463051	463512	2311	2772	gene=IY08_02520	protein=DNA mismatch repair protein MutT	protein_id=KGT45482.1
gene	464005	464781	3265	4041	gene=IY08_02525	protein=peptidoglycan transglycosylase	protein_id=KGT45483.1
gene	464969	465619	4229	4879	gene=IY08_02530	protein=disulfide bond formation protein DsbD	protein_id=KGT45484.1
gene	465735	465808	4995	5068	tRNA		
gene	466008	467150	5268	6410	gene=IY08_02540	protein=iron-sulfur cluster-binding protein	protein_id=KGT45485.1
gene	467195	468082	6455	7342	gene=IY08_02545	protein=hypothetical protein	protein_id=KGT45486.1
gene	468141	468629	7401	7889	gene=IY08_02550	protein=tRNA methyltransferase	protein_id=KGT45487.1
gene	468757	470826	8017	10086	gene=IY08_02555	protein=diguanylate cyclase	protein_id=KGT45488.1
gene	470849	470944	10109	10204	gene=IY08_02560	protein=hypothetical protein	protein_id=KGT45489.1
gene	471211	473106	10471	12366	gene=IY08_02565	protein=protein prkA	protein_id=KGT45490.1
gene	473180	473329	12440	12589	gene=IY08_02570	protein=hypothetical protein	protein_id=KGT45491.1
gene	473559	474734	12819	13994	gene=IY08_02575	protein=stress response protein	protein_id=KGT45492.1
gene	474863	477535	14123	16795	gene=IY08_02580	protein=internalin	protein_id=KGT45493.1
gene	477697	478565	16957	17825	pseudo		
gene	478627	480177	17887	19437	gene=IY08_02590	protein=glycine/betaine ABC transporter	protein_id=KGT45494.1
gene	480424	483321	19684	22581	gene=IY08_02595	protein=collagenase	protein_id=KGT45495.1
gene	483569	484117	22829	23377	gene=IY08_02600	protein=phosphate ABC transporter permease	protein_id=KGT45496.1
gene	484130	485704	23390	24964	gene=IY08_02605	protein=flotillin	protein_id=KGT45497.1
gene	485954	487930	25214	27190	gene=IY08_02610	protein=chemotaxis protein	protein_id=KGT45498.1
gene	488088	489689	27348	28949	gene=IY08_02615	protein=histidine kinase	protein_id=KGT45499.1
gene	489692	490384	28952	29644	gene=IY08_02620	protein=chemotaxis protein CheY	protein_id=KGT45500.1
gene	490429	491733	29689	30993	gene=IY08_02625	protein=citrate transporter	protein_id=KGT45501.1
gene	491988	492242	31248	31502	gene=IY08_02630	protein=hypothetical protein	protein_id=KGT45502.1
gene	492378	492881	31638	32141	gene=IY08_02635	protein=lipoprotein	protein_id=KGT45503.1
gene	493566	494189	32826	33449	gene=IY08_02640	protein=ankyrin	protein_id=KGT45504.1
gene	494344	494607	33604	33867	gene=IY08_02645	protein=hypothetical protein	protein_id=KGT45505.1

gene	494915	495481	34175	34741	gene=IY08_02650	protein=transcriptional regulator	protein_id=KGT45506.1
gene	495478	496575	34738	35835	gene=IY08_02655	protein=glycerol-3-phosphate ABC transporter ATP-binding protein	protein_id=KGT45507.1
gene	496575	497507	35835	36767	gene=IY08_02660	protein=glycerol-3-phosphate ABC transporter permease	protein_id=KGT45508.1
gene	497504	498325	36764	37585	gene=IY08_02665	protein=glycerol-3-phosphate ABC transporter permease	protein_id=KGT45509.1
gene	498347	499723	37607	38983	gene=IY08_02670	protein=glycerol-3-phosphate ABC transporter substrate-binding protein	protein_id=KGT45510.1
gene	500177	500881	39437	40141	gene=IY08_02680	protein=serine/threonine protein phosphatase	protein_id=KGT45511.1
gene	501074	501745	40334	41005	gene=IY08_02685	protein=response regulator	protein_id=KGT45512.1
gene	501757	502992	41017	42252	gene=IY08_02690	protein=histidine kinase	protein_id=KGT45513.1
gene	503226	504047	42486	43307	gene=IY08_02695	protein=transporter	protein_id=KGT45514.1
gene	504061	504810	43321	44070	gene=IY08_02700	protein=hypothetical protein	protein_id=KGT45515.1
gene	505063	507045	44323	46305	gene=IY08_02705	protein=chemotaxis protein	protein_id=KGT45516.1
gene	507124	508728	46384	47988	gene=IY08_02710	protein=histidine kinase	protein_id=KGT45517.1
gene	508725	509432	47985	48692	gene=IY08_02715	protein=response regulator	protein_id=KGT45518.1
gene	509555	510901	48815	50161	gene=IY08_02720	protein=malate permease	protein_id=KGT45519.1
gene	510961	512160	50221	51420	gene=IY08_02725	protein=malate dehydrogenase	protein_id=KGT45520.1
gene	512453	512977	51713	52237	gene=IY08_02735	protein=lipoprotein	protein_id=KGT45521.1
gene	513165	514091	52425	53351	gene=IY08_02740	protein=membrane protein	protein_id=KGT45522.1
gene	514212	515612	53472	54872	gene=IY08_02745	protein=GntR family transcriptional regulator	protein_id=KGT45523.1
gene	515645	516157	54905	55417	gene=IY08_02750	protein=acetyltransferase	protein_id=KGT45524.1
gene	516303	517757	55563	57017	gene=IY08_02755	protein=histidine kinase	protein_id=KGT45525.1
gene	517823	518494	57083	57754	gene=IY08_02760	protein=XRE family transcriptional regulator	protein_id=KGT45526.1
gene	518824	518946	58084	58206	gene=IY08_02765	protein=hypothetical protein	protein_id=KGT45527.1
gene	519455	519961	58715	59221	gene=IY08_02780	protein=acetyltransferase	protein_id=KGT45528.1
gene	520189	520995	59449	60255	gene=IY08_02785	protein=formate dehydrogenase	protein_id=KGT45529.1
gene	521296	524232	60556	63492	gene=IY08_02790	protein=oxidoreductase	protein_id=KGT45530.1
gene	524245	524727	63505	63987	gene=IY08_02795	protein=hypothetical protein	protein_id=KGT45531.1
gene	524883	526754	64143	66014	gene=IY08_02800	protein=glycerophosphodiester phosphodiesterase	protein_id=KGT45532.1
gene	527122	528255	66382	67515	gene=IY08_02805	protein=alanine dehydrogenase	protein_id=KGT45533.1
gene	528359	529774	67619	69034	gene=IY08_02810	protein=amino acid permease	protein_id=KGT45534.1

gene	529906	530460	69166	69720	gene=IY08_02815	protein=hypothetical protein	protein_id=KGT45535.1
gene	530667	531044	69927	70304	gene=IY08_02820	protein=ArsR family transcriptional regulator	protein_id=KGT45536.1
gene	531068	533434	70328	72694	gene=IY08_02825	protein=cadmium transporter	protein_id=KGT45537.1
gene	533637	535100	72897	74360	gene=IY08_02830	protein=nicotinate phosphoribosyltransferase	protein_id=KGT45538.1
gene	535300	536571	74560	75831	gene=IY08_02835	protein=transcriptional regulator	protein_id=KGT45539.1
gene	536866	538566	76126	77826	gene=IY08_02845	protein=bacillolysin	protein_id=KGT45540.1
gene	538630	539178	77890	78438	gene=IY08_02850	protein=hypothetical protein	protein_id=KGT45541.1
gene	539577	540095	78837	79355	gene=IY08_02855	protein=lipoprotein	protein_id=KGT45542.1
gene	540112	540384	79372	79644	gene=IY08_02860	protein=hypothetical protein	protein_id=KGT45543.1
gene	540427	541689	79687	80949	gene=IY08_02865	protein=vancomycin resistance protein	protein_id=KGT45544.1
gene	541924	542940	81184	82200	gene=IY08_02870	protein=LytR family transcriptional regulator	protein_id=KGT45545.1
gene	543275	544453	82535	83713	gene=IY08_02875	protein=pyrimidine nucleoside transporter NupC	protein_id=KGT45546.1
gene	544545	544931	83805	84191	gene=IY08_02880	protein=hypothetical protein	protein_id=KGT45547.1
gene	545040	546338	84300	85598	gene=IY08_02885	protein=membrane protein	protein_id=KGT45548.1
gene	546512	547945	85772	87205	gene=aspA	protein=aspartate ammonia-lyase	protein_id=KGT45549.1
gene	547985	549604	87245	88864	gene=IY08_02895	protein=L-lactate permease	protein_id=KGT45550.1
gene	550422	550709	89682	89969	gene=IY08_02900	protein=ArsR family transcriptional regulator	protein_id=KGT45551.1
gene	550901	551080	90161	90340	gene=sspH	protein=acid-soluble spore protein H	protein_id=KGT45552.1
gene	551118	552467	90378	91727	gene=IY08_02910	protein=MFS transporter	protein_id=KGT45553.1
gene	552848	553816	92108	93076	gene=IY08_02915	protein=iron siderophore-binding protein	protein_id=KGT45554.1
gene	553989	554993	93249	94253	gene=IY08_02920	protein=iron ABC transporter	protein_id=KGT45555.1
gene	554990	556048	94250	95308	gene=IY08_02925	protein=iron ABC transporter permease	protein_id=KGT45556.1
gene	556061	556882	95321	96142	gene=IY08_02930	protein=ABC transporter	protein_id=KGT45557.1
gene	556910	557641	96170	96901	gene=IY08_02935	protein=methyltransferase	protein_id=KGT45558.1
gene	557855	559045	97115	98305	gene=IY08_02940	protein=2-amino-3-ketobutyrate CoA ligase	protein_id=KGT45559.1
gene	559090	560055	98350	99315	gene=IY08_02945	protein=UDP-glucose 4-epimerase	protein_id=KGT45560.1
gene	560115	560537	99375	99797	gene=IY08_02950	protein=DNA mismatch repair protein MutT	protein_id=KGT45561.1
gene	560575	562458	99835	101718	gene=IY08_02955	protein=von Willebrand factor A	protein_id=KGT45562.1
gene	562462	563355	101722	102615	gene=IY08_02960	protein=hypothetical protein	protein_id=KGT45563.1
gene	563483	565012	102743	104272	gene=IY08_02965	protein=cardiolipin synthetase	protein_id=KGT45564.1
gene	565227	565583	104487	104843	gene=IY08_02970	protein=cobalt transporter	protein_id=KGT45565.1

gene	566064	567767	105324	107027	gene=IY08_02975	protein=diguanylate cyclase	protein_id=KGT45566.1
gene	567799	569196	107059	108456	gene=IY08_02980	protein=arginine:ornithine antiporter	protein_id=KGT45567.1
gene	569649	570359	108909	109619	gene=IY08_02985	protein=GntR family transcriptional regulator	protein_id=KGT45568.1
gene	570501	571928	109761	111188	gene=IY08_02990	protein=trehalose permease IIC protein	protein_id=KGT45569.1
gene	571942	573603	111202	112863	gene=IY08_02995	protein=trehalose-6-phosphate hydrolase	protein_id=KGT45570.1
gene	573637	574585	112897	113845	gene=IY08_03000	protein=spore germination protein GerK	frame=2
gene	574780	575886	114040	115146	gene=IY08_03010	protein=spore germination protein GerK	protein_id=KGT45400.1
gene	575867	577369	115127	116629	gene=IY08_03015	protein=spore germination protein GerK	protein_id=KGT45401.1
gene	577558	578529	116818	117789	gene=IY08_03020	protein=aminoglycoside phosphotransferase	protein_id=KGT45402.1
gene	578689	580149	117949	119409	gene=IY08_03025	protein=sodium:alanine symporter	protein_id=KGT45403.1
gene	580094	580301	119354	119561	pseudo		
gene	580282	581013	119542	120273	gene=IY08_03035	protein=amino acid ABC transporter ATP-binding protein	protein_id=KGT45404.1
gene	581026	581856	120286	121116	gene=IY08_03040	protein=glutamine ABC transporter substrate-binding	protein_id=KGT45405.1
gene	581919	582575	121179	121835	gene=IY08_03045	protein=glutamine ABC transporter permease	protein_id=KGT45406.1
gene	582576	583220	121836	122480	gene=IY08_03050	protein=glutamine ABC transporter permease	protein_id=KGT45407.1
gene	583425	584852	122685	124112	gene=IY08_03055	protein=amino acid permease	protein_id=KGT45408.1
gene	584827	585204	124087	124464	gene=IY08_03060	protein=osmotically inducible protein C	protein_id=KGT45409.1
gene	585268	585702	124528	124962	gene=IY08_03065	protein=HIT family hydrolase	protein_id=KGT45410.1
gene	585724	586665	124984	125925	gene=IY08_03070	protein=DeoR family transcriptional regulator	protein_id=KGT45411.1
gene	586774	587295	126034	126555	gene=IY08_03075	protein=diacylglycerol kinase	protein_id=KGT45412.1
gene	587308	588699	126568	127959	gene=IY08_03080	protein=histidine kinase	protein_id=KGT45413.1
gene	588711	589388	127971	128648	gene=IY08_03085	protein=XRE family transcriptional regulator	protein_id=KGT45414.1
gene	589564	590811	128824	130071	gene=IY08_03090	protein=ArsR family transcriptional regulator	protein_id=KGT45415.1
gene	590967	592418	130227	131678	gene=IY08_03095	protein=sulfate transporter	protein_id=KGT45416.1
gene	592484	592906	131744	132166	gene=IY08_03100	protein=universal stress protein	protein_id=KGT45417.1
gene	593110	593226	132370	132486	gene=IY08_03105	protein=hypothetical protein	protein_id=KGT45418.1
gene	593345	594694	132605	133954	gene=glpT	protein=sn-glycerol-3-phosphate transporter	protein_id=KGT45419.1
gene	594964	595422	134224	134682	gene=IY08_03115	protein=MarR family transcriptional regulator	protein_id=KGT45420.1
gene	595442	597055	134702	136315	gene=IY08_03120	protein=MFS transporter	protein_id=KGT45421.1
gene	597193	598164	136453	137424	gene=IY08_03125	protein=ribose operon repressor	protein_id=KGT45422.1
gene	598178	599074	137438	138334	gene=IY08_03130	protein=ribokinase	protein_id=KGT45423.1

gene	599071	599466	138331	138726	gene=IY08_03135	protein=ribose pyranase	protein_id=KGT45424.1
gene	599485	600969	138745	140229	gene=IY08_03140	protein=sugar ABC transporter ATP-binding protein	protein_id=KGT45425.1
gene	600972	601907	140232	141167	gene=rbsC	protein=ribose ABC transporter permease	protein_id=KGT45426.1
gene	601922	602848	141182	142108	gene=IY08_03150	protein=D-ribose transporter subunit RbsB	protein_id=KGT45427.1
gene	602883	603530	142143	142790	gene=IY08_03155	protein=transaldolase	protein_id=KGT45428.1
gene	603914	606313	143174	145573	gene=IY08_03160	protein=peptidase M6	protein_id=KGT45429.1
gene	606640	606981	145900	146241	gene=IY08_03165	protein=hypothetical protein	protein_id=KGT45430.1
gene	607003	607332	146263	146592	gene=IY08_03170	protein=hypothetical protein	protein_id=KGT45431.1
gene	607349	608503	146609	147763	gene=IY08_03175	protein=bicyclomycin resistance protein	protein_id=KGT45432.1
gene	608729	609781	147989	149041	gene=IY08_03180	protein=butanediol dehydrogenase	protein_id=KGT45433.1
gene	609901	610245	149161	149505	gene=IY08_03185	protein=transporter	protein_id=KGT45434.1
gene	610499	611350	149759	150610	gene=IY08_03190	protein=phospholipase C	protein_id=KGT45435.1
gene	611427	612428	150687	151688	gene=IY08_03195	protein=phospholipase C	protein_id=KGT45436.1
gene	612536	613708	151796	152968	gene=IY08_03200	protein=amino acid aldolase	protein_id=KGT45437.1
gene	613696	615012	152956	154272	gene=IY08_03205	protein=FAD-binding oxidoreductase	protein_id=KGT45438.1
gene	615104	616255	154364	155515	gene=IY08_03210	protein=permease	protein_id=KGT45439.1
gene	616427	616630	155687	155890	gene=IY08_03215	protein=hypothetical protein	protein_id=KGT45440.1
gene	616759	617046	156019	156306	gene=IY08_03220	protein=hypothetical protein	protein_id=KGT45441.1
gene	617226	618038	156486	157298	gene=IY08_03225	protein=UDP pyrophosphate phosphatase	protein_id=KGT45442.1
gene	618175	619116	157435	158376	gene=IY08_03230	protein=chemotaxis protein	protein_id=KGT45443.1
gene	619337	620617	158597	159877	gene=IY08_03235	protein=cell wall-binding protein	protein_id=KGT45444.1
gene	620730	620948	159990	160208	gene=IY08_03240	protein=XRE family transcriptional regulator	protein_id=KGT45445.1
gene	620941	621414	160201	160674	gene=IY08_03245	protein=RNA dependent RNA polymerase	protein_id=KGT45446.1
gene	621532	622164	160792	161424	gene=IY08_03250	protein=peptidase	protein_id=KGT45447.1
gene	622304	623383	161564	162643	gene=IY08_03255	protein=ribosomal protein L5-like protein	protein_id=KGT45448.1
gene	623413	624798	162673	164058	gene=IY08_03260	protein=MFS transporter	protein_id=KGT45449.1
gene	625051	626352	164311	165612	gene=IY08_03270	protein=branched-chain amino acid transporter	protein_id=KGT45450.1
gene	626492	628213	165752	167473	gene=IY08_03275	protein=membrane protein	protein_id=KGT45451.1
gene	628249	629796	167509	169056	gene=IY08_03280	protein=DNA-binding protein	protein_id=KGT45452.1
gene	629978	631369	169238	170629	gene=IY08_03285	protein=D-alanine/D-serine/glycine permease	protein_id=KGT45453.1
gene	631651	632943	170911	172203	gene=IY08_03290	protein=guanine permease	protein_id=KGT45454.1

gene	633142	633345	172402	172605	gene=IY08_03295	protein=Cro/C1 family transcriptional regulator	protein_id=KGT45455.1
gene	633347	633775	172607	173035	gene=IY08_03300	protein=hypothetical protein	protein_id=KGT45456.1
gene	633815	634252	173075	173512	gene=IY08_03305	protein=acetyltransferase	protein_id=KGT45457.1
gene	634267	634488	173527	173748	gene=IY08_03310	protein=hypothetical protein	protein_id=KGT45458.1
gene	634577	636406	173837	175666	gene=IY08_03315	protein=sodium:proton antiporter	protein_id=KGT45459.1
gene	636627	636938	175887	176198	gene=IY08_03320	protein=quinol oxidase subunit 4	protein_id=KGT45460.1
gene	636939	637541	176199	176801	gene=IY08_03325	protein=cytochrome o ubiquinol oxidase subunit III	protein_id=KGT45461.1
gene	637555	639489	176815	178749	gene=IY08_03330	protein=quinol oxidase subunit 1	protein_id=KGT45462.1
gene	639523	640398	178783	179658	gene=IY08_03335	protein=quinol oxidase subunit 2	protein_id=KGT45463.1
gene	640681	642096	179941	181356	gene=IY08_03340	protein=amino acid permease	protein_id=KGT45464.1
gene	642471	643181	181731	182441	gene=IY08_03345	protein=hypothetical protein	protein_id=KGT45465.1
gene	643314	644489	182574	183749	gene=IY08_03350	protein=N-acyl-L-amino acid amidohydrolase	protein_id=KGT45466.1
gene	644491	644688	183751	183948	gene=IY08_03355	protein=permease	protein_id=KGT45467.1
gene	644685	646157	183945	185417	gene=IY08_03360	protein=sodium:solute symporter	protein_id=KGT45468.1
gene	646388	647857	185648	187117	gene=IY08_03365	protein=spore germination protein GerLA	protein_id=KGT45469.1
gene	647858	648982	187118	188242	gene=IY08_03370	protein=spore germination protein GerLB	protein_id=KGT45470.1
gene	648966	650132	188226	189392	gene=IY08_03375	protein=spore germination protein GerLC	protein_id=KGT45471.1
gene	650144	650281	189404	189541	gene=IY08_03380	protein=hypothetical protein	protein_id=KGT45472.1
gene	650343	651743	189603	191003	gene=IY08_03385	protein=iron transporter FeoB	protein_id=KGT45473.1
gene	651721	652443	190981	191703	gene=IY08_03390	protein=iron transporter FeoB	protein_id=KGT45474.1
gene	652440	652697	191700	191957	gene=IY08_03395	protein=iron transporter FeoA	protein_id=KGT45475.1
gene	653210	654109	192470	193369	gene=IY08_03400	protein=phosphate-binding protein	protein_id=KGT45476.1
gene	654180	655070	193440	194330	gene=IY08_03405	protein=phosphate ABC transporter permease	protein_id=KGT45477.1
gene	655073	655993	194333	195253	gene=IY08_03410	protein=phosphate ABC transporter permease	protein_id=KGT45478.1
gene	656224	659268	195484	198528	gene=IY08_03415	protein=multidrug transporter AcrB	protein_id=KGT45479.1
scaffold9							
gene	660008	660082	8	82	tRNA		
gene	660084	660155	84	155	tRNA		
gene	660285	660704	285	704	gene=IY08_03430	protein=inosine-5'-monophosphate dehydrogenase	protein_id=KGT45297.1
gene	661026	662177	1026	2177	gene=IY08_03435	protein=hypothetical protein	protein_id=KGT45298.1
gene	662248	662403	2248	2403	gene=IY08_03440	protein=hypothetical protein	protein_id=KGT45299.1

gene	662418	662750	2418	2750	gene=IY08_03445	protein=hypothetical protein	protein_id=KGT45300.1
gene	662756	663910	2756	3910	gene=IY08_03450	protein=peptidase M24	protein_id=KGT45301.1
gene	664541	665236	4541	5236	gene=IY08_03455	protein=thiaminase	protein_id=KGT45302.1
gene	665205	665954	5205	5954	gene=IY08_03460	protein=ABC transporter ATP-binding protein	protein_id=KGT45303.1
gene	665954	666706	5954	6706	gene=IY08_03465	protein=ABC transporter permease	protein_id=KGT45304.1
gene	666703	667704	6703	7704	gene=IY08_03470	protein=ABC transporter substrate-binding protein	protein_id=KGT45305.1
gene	667715	668335	7715	8335	gene=IY08_03475	protein=transcriptional regulator TenI	protein_id=KGT45306.1
gene	668328	669437	8328	9437	gene=IY08_03480	protein=glycine oxidase	protein_id=KGT45307.1
gene	669453	669656	9453	9656	gene=IY08_03485	protein=thiamine biosynthesis protein ThiS	protein_id=KGT45308.1
gene	669659	670429	9659	10429	gene=IY08_03490	protein=thiazole synthase	protein_id=KGT45309.1
gene	670422	671441	10422	11441	gene=IY08_03495	protein=thiamine biosynthesis protein MoeB	protein_id=KGT45310.1
gene	671457	672269	11457	12269	gene=IY08_03500	protein=phosphomethylpyrimidine kinase	protein_id=KGT45311.1
gene	672596	672982	12596	12982	gene=IY08_03505	protein=hypothetical protein	protein_id=KGT45312.1
gene	672996	673229	12996	13229	gene=IY08_03510	protein=hypothetical protein	protein_id=KGT45313.1
gene	673735	673839	13735	13839	gene=IY08_03515	protein=SipW-cognate class signal peptide	protein_id=KGT45314.1
gene	673836	673916	13836	13916	gene=IY08_03520	protein=potassium ABC transporter ATPase	protein_id=KGT45315.1
gene	673937	675604	13937	15604	gene=IY08_03525	protein=potassium ABC transporter ATPase	protein_id=KGT45316.1
gene	675618	677708	15618	17708	gene=IY08_03530	protein=potassium-transporting ATPase subunit B	protein_id=KGT45317.1
gene	677725	678306	17725	18306	gene=IY08_03535	protein=potassium-transporting ATPase subunit C	protein_id=KGT45318.1
gene	678372	679517	18372	19517	gene=IY08_03540	protein=histidine kinase	protein_id=KGT45319.1
gene	679542	680723	19542	20723	gene=IY08_03545	protein=MFS transporter	protein_id=KGT45320.1
gene	680864	681325	20864	21325	gene=IY08_03550	protein=MarR family transcriptional regulator	protein_id=KGT45321.1
gene	681454	682308	21454	22308	gene=IY08_03555	protein=serine protease	protein_id=KGT45322.1
gene	682505	682888	22505	22888	gene=IY08_03560	protein=hypothetical protein	protein_id=KGT45323.1
gene	682976	684049	22976	24049	gene=IY08_03565	protein=ABC transporter permease	protein_id=KGT45324.1
gene	684059	685291	24059	25291	gene=IY08_03570	protein=ABC transporter permease	protein_id=KGT45325.1
gene	685292	685942	25292	25942	gene=IY08_03575	protein=peptide ABC transporter ATP-binding protein	protein_id=KGT45326.1
gene	685975	686178	25975	26178	gene=IY08_03580	protein=hypothetical protein	protein_id=KGT45327.1
gene	686276	687577	26276	27577	gene=IY08_03585	protein=guanine permease	protein_id=KGT45328.1
gene	687780	688646	27780	28646	gene=IY08_03590	protein=dehydrogenase	protein_id=KGT45329.1
gene	688713	689474	28713	29474	gene=IY08_03595	protein=protein erfK/srfK	protein_id=KGT45330.1

gene	689578	689829	29578	29829	gene=IY08_03600	protein=membrane protein	protein_id=KGT45331.1
gene	689842	690783	29842	30783	gene=IY08_03605	protein=fructokinase	protein_id=KGT45332.1
gene	690780	692255	30780	32255	gene=IY08_03610	protein=glycosyl hydrolase family 32	protein_id=KGT45333.1
gene	692273	693649	32273	33649	gene=IY08_03615	protein=PTS system sucrose-specific transporter subunits	protein_id=KGT45334.1
gene	693785	694771	33785	34771	gene=IY08_03620	protein=LacI family transcriptional regulator	protein_id=KGT45335.1
gene	694889	695104	34889	35104	gene=IY08_03625	protein=disulfide formation protein C	protein_id=KGT45336.1
gene	695177	695632	35177	35632	gene=IY08_03630	protein=thioredoxin	protein_id=KGT45337.1
gene	695645	696064	35645	36064	gene=IY08_03635	protein=disulfide oxidoreductase	protein_id=KGT45338.1
gene	696230	696478	36230	36478	gene=IY08_03640	protein=hypothetical protein	protein_id=KGT45339.1
gene	696599	697111	36599	37111	gene=IY08_03645	protein=lipoprotein	protein_id=KGT45340.1
gene	697157	698266	37157	38266	gene=IY08_03650	protein=spore germination protein GerB	protein_id=KGT45341.1
gene	698283	699365	38283	39365	gene=IY08_03655	protein=spore germination protein GerC	protein_id=KGT45342.1
gene	699362	700879	39362	40879	gene=IY08_03660	protein=spore germination protein GerA	protein_id=KGT45343.1
gene	701005	701601	41005	41601	gene=IY08_03665	protein=hypothetical protein	protein_id=KGT45344.1
gene	701840	702400	41840	42400	gene=IY08_03670	protein=nitroreductase	protein_id=KGT45345.1
gene	702515	703933	42515	43933	gene=IY08_03675	protein=stage V sporulation protein R	protein_id=KGT45346.1
gene	704042	705313	44042	45313	gene=IY08_03680	protein=alkaline ceramidase	protein_id=KGT45347.1
gene	705488	706456	45488	46456	gene=IY08_03685	protein=peptidase	protein_id=KGT45348.1
gene	706829	708493	46829	48493	gene=IY08_03690	protein=CoA-disulfide reductase	protein_id=KGT45349.1
gene	708679	708942	48679	48942	gene=IY08_03695	protein=cytoplasmic protein	protein_id=KGT45350.1
gene	709031	709591	49031	49591	gene=IY08_03700	protein=hypothetical protein	protein_id=KGT45351.1
gene	709630	710760	49630	50760	gene=IY08_03705	protein=hypothetical protein	protein_id=KGT45352.1
gene	710799	711026	50799	51026	gene=IY08_03710	protein=hypothetical protein	protein_id=KGT45353.1
gene	711093	711437	51093	51437	gene=IY08_03715	protein=sulfurtransferase	protein_id=KGT45354.1
gene	711457	711822	51457	51822	gene=IY08_03720	protein=sulfurtransferase	protein_id=KGT45355.1
gene	711837	712133	51837	52133	gene=IY08_03725	protein=rhodanese domain protein	protein_id=KGT45356.1
gene	712206	712685	52206	52685	gene=IY08_03730	protein=hypothetical protein	protein_id=KGT45357.1
gene	712719	713483	52719	53483	gene=IY08_03735	protein=membrane protein	protein_id=KGT45358.1
gene	713553	713993	53553	53993	gene=IY08_03740	protein=hypothetical protein	protein_id=KGT45359.1
gene	714142	715341	54142	55341	gene=IY08_03745	protein=LytR family transcriptional regulator	protein_id=KGT45360.1
gene	715656	716651	55656	56651	gene=IY08_03750	protein=quinone oxidoreductase	protein_id=KGT45361.1

gene	716688	718343	56688	58343	gene=IY08_03755	protein=sodium:phosphate symporter	protein_id=KGT45362.1
gene	718695	719897	58695	59897	gene=IY08_03760	protein=MFS transporter	protein_id=KGT45363.1
gene	720217	721305	60217	61305	gene=IY08_03765	protein=outer surface protein	protein_id=KGT45364.1
gene	721382	723322	61382	63322	gene=IY08_03770	protein=PTS fructose transporter subunit IIA	protein_id=KGT45365.1
gene	723433	723753	63433	63753	gene=IY08_03775	protein=PTS cellobiose transporter subunit IIA	protein_id=KGT45366.1
gene	723755	724060	63755	64060	gene=IY08_03780	protein=PTS cellbiose transporter subunit IIB	protein_id=KGT45367.1
gene	724144	725454	64144	65454	gene=IY08_03785	protein=PTS cellbiose transporter subunit IIC	protein_id=KGT45368.1
gene	725430	725708	65430	65708	gene=IY08_03790	protein=hypothetical protein	protein_id=KGT45369.1
gene	725698	726783	65698	66783	gene=IY08_03795	protein=outer surface protein	protein_id=KGT45370.1
gene	726892	727815	66892	67815	gene=IY08_03800	protein=PBS lyase	protein_id=KGT45371.1
gene	727869	729239	67869	69239	gene=IY08_03805	protein=enterotoxin	protein_id=KGT45372.1
gene	729697	730875	69697	70875	gene=IY08_03810	protein=ABC transporter permease	protein_id=KGT45373.1
gene	730878	731552	70878	71552	gene=IY08_03815	protein=macrolide ABC transporter ATP-binding protein	protein_id=KGT45374.1
gene	731549	732652	71549	72652	gene=IY08_03820	protein=ABC transporter substrate-binding protein	protein_id=KGT45375.1
gene	732864	733598	72864	73598	gene=IY08_03825	protein=ABC transporter permease	protein_id=KGT45376.1
gene	733689	734555	73689	74555	gene=IY08_03830	protein=peptide ABC transporter permease	protein_id=KGT45377.1
gene	734557	735561	74557	75561	gene=IY08_03835	protein=peptide ABC transporter permease	protein_id=KGT45378.1
gene	735607	736923	75607	76923	gene=IY08_03840	protein=branched-chain amino acid transporter	protein_id=KGT45379.1
gene	737141	737710	77141	77710	gene=IY08_03845	protein=CotJC	protein_id=KGT45380.1
gene	737723	737986	77723	77986	gene=IY08_03850	protein=spore coat protein CotJB	protein_id=KGT45381.1
gene	737995	738210	77995	78210	gene=IY08_03855	protein=CotJA	protein_id=KGT45382.1
gene	738310	738672	78310	78672	gene=IY08_03860	protein=lactoylglutathione lyase	protein_id=KGT45383.1
gene	738687	739466	78687	79466	gene=IY08_03865	protein=hypothetical protein	protein_id=KGT45384.1
gene	739484	740296	79484	80296	gene=IY08_03870	protein=DNA repair protein	protein_id=KGT45385.1
gene	740635	740916	80635	80916	gene=IY08_03875	protein=membrane protein	protein_id=KGT45386.1
gene	740927	741532	80927	81532	gene=IY08_03880	protein=alkaline phosphatase	protein_id=KGT45387.1
gene	741631	741999	81631	81999	gene=IY08_03885	protein=hypothetical protein	protein_id=KGT45388.1
gene	742020	742364	82020	82364	gene=IY08_03890	protein=hypothetical protein	protein_id=KGT45389.1
gene	742421	742846	82421	82846	gene=IY08_03895	protein=group-specific protein	protein_id=KGT45390.1
gene	743199	745661	83199	85661	gene=IY08_03900	protein=acid phosphatase	protein_id=KGT45391.1
gene	745741	745944	85741	85944	gene=IY08_03905	protein=hypothetical protein	protein_id=KGT45392.1

gene	745957	746127	85957	86127	gene=IY08_03910	protein=RpiR family transcriptional regulator	protein_id=KGT45393.1
gene	746156	747559	86156	87559	gene=IY08_03915	protein=amino acid permease	protein_id=KGT45394.1
gene	747818	748945	87818	88945	gene=IY08_03920	protein=sodium:proton antiporter	protein_id=KGT45395.1
gene	749070	749384	89070	89384	gene=IY08_03925	protein=outer surface protein	protein_id=KGT45396.1
gene	749414	750277	89414	90277	gene=IY08_03930	protein=RpiR family transcriptional regulator	protein_id=KGT45397.1
gene	750588	751472	90588	91472	gene=murQ	protein=N-acetylmuramic acid-6-phosphate etherase	protein_id=KGT45398.1
gene	751515	751988	91515	91988	gene=IY08_03940	protein=PTS sugar transporter subunit IIC	partial=3'
gene	752028	752895	92028	92895	gene=IY08_03945	protein=PTS sugar transporter subunit IIC	frame=2
gene	752944	754017	92944	94017	gene=IY08_03950	protein=cell surface protein	protein_id=KGT45162.1
gene	754170	754574	94170	94574	gene=IY08_03955	protein=DoxX	protein_id=KGT45163.1
gene	754729	755130	94729	95130	gene=IY08_03960	protein=ketosteroid isomerase	protein_id=KGT45164.1
gene	755130	755615	95130	95615	gene=IY08_03965	protein=hypothetical protein	protein_id=KGT45165.1
gene	755650	756561	95650	96561	gene=IY08_03970	protein=transporter	protein_id=KGT45166.1
gene	756767	757261	96767	97261	gene=IY08_03975	protein=AsnC family transcriptional regulator	protein_id=KGT45167.1
gene	757390	757845	97390	97845	gene=IY08_03980	protein=acetyltransferase	protein_id=KGT45168.1
gene	757926	758696	97926	98696	gene=IY08_03985	protein=oxidoreductase	protein_id=KGT45169.1
gene	758831	759190	98831	99190	gene=IY08_03990	protein=MerR family transcriptional regulator	protein_id=KGT45170.1
gene	759603	759947	99603	99947	gene=IY08_03995	protein=ligand-binding protein SH3	protein_id=KGT45171.1
gene	759950	760264	99950	100264	gene=IY08_04000	protein=multidrug resistance protein SMR	protein_id=KGT45172.1
gene	760416	760994	100416	100994	gene=IY08_04005	protein=TetR family transcriptional regulator	protein_id=KGT45173.1
gene	761208	762410	101208	102410	gene=IY08_04010	protein=multidrug MFS transporter	protein_id=KGT45174.1
gene	763683	764063	103683	104063	gene=IY08_04015	protein=hypothetical protein	protein_id=KGT45175.1
gene	764550	765248	104550	105248	gene=IY08_04025	protein=DeoR family transcriptional regulator	protein_id=KGT45176.1
gene	765241	766326	105241	106326	gene=IY08_04030	protein=histidine kinase	protein_id=KGT45177.1
gene	766603	767703	106603	107703	gene=IY08_04035	protein=ABC transporter substrate-binding protein	protein_id=KGT45178.1
gene	767700	768374	107700	108374	gene=IY08_04040	protein=macrolide ABC transporter ATP-binding protein	protein_id=KGT45179.1
gene	768377	769555	108377	109555	gene=IY08_04045	protein=ABC transporter permease	protein_id=KGT45180.1
gene	769727	770497	109727	110497	gene=IY08_04050	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT45181.1
gene	770574	771941	110574	111941	gene=IY08_04055	protein=permease	protein_id=KGT45182.1
gene	772254	773261	112254	113261	gene=IY08_04060	protein=metallo-beta-lactamase	protein_id=KGT45183.1
gene	773536	773850	113536	113850	pseudo		

gene	773892	774230	113892	114230	gene=IY08_04070	protein=MarR family transcriptional regulator	protein_id=KGT45184.1
gene	774400	774939	114400	114939	gene=IY08_04075	protein=lipoprotein	protein_id=KGT45185.1
gene	774963	775511	114963	115511	gene=IY08_04080	protein=flavodoxin	protein_id=KGT45186.1
gene	775574	777313	115574	117313	gene=IY08_04085	protein=ABC transporter substrate-binding protein	protein_id=KGT45187.1
gene	777418	778674	117418	118674	gene=IY08_04090	protein=MFS transporter	protein_id=KGT45188.1
gene	778719	778922	118719	118922	gene=IY08_04095	protein=hypothetical protein	protein_id=KGT45189.1
gene	779248	779763	119248	119763	gene=IY08_04105	protein=cysteine protease	protein_id=KGT45190.1
gene	779787	781784	119787	121784	gene=IY08_04110	protein=catalase	protein_id=KGT45191.1
gene	781974	783173	121974	123173	gene=IY08_04115	protein=permease	protein_id=KGT45192.1
gene	783234	784658	123234	124658	gene=IY08_04120	protein=arginine:ornithine antiporter	protein_id=KGT45193.1
gene	785190	786020	125190	126020	gene=IY08_04125	protein=glutamate racemase	protein_id=KGT45194.1
gene	786131	787216	126131	127216	gene=IY08_04130	protein=hypothetical protein	protein_id=KGT45195.1
gene	787296	788735	127296	128735	gene=IY08_04135	protein=glyceraldehyde-3-phosphate dehydrogenase	protein_id=KGT45196.1
gene	788978	789082	128978	129082	gene=IY08_04140	protein=hypothetical protein	protein_id=KGT45197.1
gene	789332	791092	129332	131092	gene=IY08_04145	protein=multidrug ABC transporter ATP-binding protein	protein_id=KGT45198.1
gene	791089	793089	131089	133089	gene=IY08_04150	protein=multidrug ABC transporter permease	protein_id=KGT45199.1
gene	793362	794159	133362	134159	gene=IY08_04155	protein=L-cystine-binding protein TcyA	protein_id=KGT45200.1
gene	794146	794844	134146	134844	gene=IY08_04160	protein=cysteine ABC transporter permease	protein_id=KGT45201.1
gene	794873	795607	134873	135607	gene=IY08_04165	protein=arginine ABC transporter ATP-binding protein	protein_id=KGT45202.1
gene	795659	795862	135659	135862	gene=IY08_04170	protein=spore protein	protein_id=KGT45203.1
gene	796312	796557	136312	136557	gene=IY08_04175	protein=hypothetical protein	protein_id=KGT45204.1
gene	796577	798034	136577	138034	gene=IY08_04180	protein=hypothetical protein	protein_id=KGT45205.1
gene	798055	799107	138055	139107	gene=IY08_04185	protein=histidine kinase	protein_id=KGT45206.1
gene	799237	800373	139237	140373	gene=IY08_04190	protein=membrane protein	protein_id=KGT45207.1
gene	800516	800872	140516	140872	gene=IY08_04195	protein=hypothetical protein	protein_id=KGT45208.1
gene	801002	801607	141002	141607	gene=IY08_04200	protein=hypothetical protein	protein_id=KGT45209.1
gene	801629	802189	141629	142189	gene=IY08_04205	protein=hypothetical protein	protein_id=KGT45210.1
gene	802625	804313	142625	144313	gene=IY08_04210	protein=acetolactate synthase	protein_id=KGT45211.1
gene	804330	805088	144330	145088	gene=IY08_04215	protein=alpha-acetolactate decarboxylase	protein_id=KGT45212.1
gene	805150	805767	145150	145767	gene=IY08_04220	protein=3-methyladenine DNA glycosylase	protein_id=KGT45213.1
gene	805902	806774	145902	146774	gene=IY08_04225	protein=haloacid dehalogenase	protein_id=KGT45214.1

gene	807160	811113	147160	151113	gene=IY08_04230	protein=adhesin	protein_id=KGT45215.1
gene	811208	812911	151208	152911	gene=IY08_04235	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT45216.1
gene	813162	814652	153162	154652	gene=IY08_04240	protein=coproporphyrinogen III oxidase	protein_id=KGT45217.1
gene	814993	816549	154993	156549	gene=IY08_04245	protein=long-chain fatty acid--CoA ligase	protein_id=KGT45218.1
gene	817095	817292	157095	157292	gene=IY08_04250	protein=hypothetical protein	protein_id=KGT45219.1
gene	817427	817891	157427	157891	gene=IY08_04255	protein=hypothetical protein	protein_id=KGT45220.1
gene	818079	819548	158079	159548	gene=IY08_04260	protein=sulfate transporter	protein_id=KGT45221.1
gene	819883	821403	159883	161403	gene=IY08_04265	protein=polysaccharide biosynthesis protein	protein_id=KGT45222.1
gene	821547	822635	161547	162635	gene=IY08_04270	protein=CsaB protein	protein_id=KGT45223.1
gene	822782	824644	162782	164644	gene=IY08_04275	protein=glucosaminidase	protein_id=KGT45224.1
gene	824691	826085	164691	166085	gene=IY08_04280	protein=membrane protein	protein_id=KGT45225.1
gene	826410	827198	166410	167198	gene=IY08_04285	protein=enoyl-CoA hydratase	protein_id=KGT45226.1
gene	827308	827625	167308	167625	gene=IY08_04290	protein=hypothetical protein	protein_id=KGT45227.1
gene	827643	827969	167643	167969	gene=IY08_04295	protein=phosphoribosyl-ATP pyrophosphohydrolase	protein_id=KGT45228.1
gene	827991	828170	167991	168170	gene=IY08_04300	protein=hypothetical protein	protein_id=KGT45229.1
gene	828297	829346	168297	169346	gene=IY08_04305	protein=peptidase M42	protein_id=KGT45230.1
gene	829736	831343	169736	171343	gene=IY08_04310	protein=amidase	protein_id=KGT45231.1
gene	831497	832450	171497	172450	gene=IY08_04315	protein=RNA methyltransferase	protein_id=KGT45232.1
gene	832633	832779	172633	172779	gene=IY08_04320	protein=hypothetical protein	protein_id=KGT45233.1
gene	833073	834077	173073	174077	gene=IY08_04325	protein=proline racemase	protein_id=KGT45234.1
gene	834097	835074	174097	175074	gene=IY08_04330	protein=ornithine cyclodeaminase	protein_id=KGT45235.1
gene	835239	835577	175239	175577	gene=IY08_04335	protein=hypothetical protein	protein_id=KGT45236.1
gene	835838	836467	175838	176467	gene=IY08_04340	protein=hypothetical protein	protein_id=KGT45237.1
gene	836931	837551	176931	177551	gene=IY08_04345	protein=thioredoxin	protein_id=KGT45238.1
gene	837883	838704	177883	178704	gene=IY08_04350	protein=cytoplasmic protein	protein_id=KGT45239.1
gene	838709	839101	178709	179101	gene=IY08_04355	protein=ketosteroid isomerase	protein_id=KGT45240.1
gene	839253	839777	179253	179777	gene=IY08_04365	protein=pyruvate kinase	protein_id=KGT45241.1
gene	840604	841221	180604	181221	gene=IY08_04370	protein=bacteriocin ABC transporter ATP-binding protein	protein_id=KGT45242.1
gene	841224	843389	181224	183389	gene=IY08_04375	protein=membrane protein	protein_id=KGT45243.1
gene	843477	843881	183477	183881	gene=IY08_04380	protein=hypothetical protein	protein_id=KGT45244.1
gene	844561	844872	184561	184872	gene=IY08_04385	protein=ArsR family transcriptional regulator	protein_id=KGT45245.1

gene	845184	845627	185184	185627	gene=IY08_04390	protein=hypothetical protein	protein_id=KGT45246.1
gene	846688	846834	186688	186834	gene=IY08_04400	protein=cytoplasmic protein	protein_id=KGT45247.1
gene	847229	847525	187229	187525	gene=IY08_04405	protein=type VII secretion protein EsxA	protein_id=KGT45248.1
gene	847712	847987	187712	187987	gene=IY08_04410	protein=creatininase	protein_id=KGT45249.1
gene	848029	848391	188029	188391	gene=IY08_04415	protein=hypothetical protein	protein_id=KGT45250.1
gene	848388	848807	188388	188807	gene=IY08_04420	protein=hypothetical protein	protein_id=KGT45251.1
gene	849354	849692	189354	189692	gene=IY08_04425	protein=hypothetical protein	protein_id=KGT45252.1
gene	849694	849912	189694	189912	gene=IY08_04430	protein=hypothetical protein	protein_id=KGT45253.1
gene	850173	850421	190173	190421	gene=IY08_04435	protein=hypothetical protein	protein_id=KGT45254.1
gene	850914	851582	190914	191582	gene=IY08_04445	protein=membrane protein	protein_id=KGT45255.1
gene	851700	851891	191700	191891	gene=IY08_04450	protein=hypothetical protein	protein_id=KGT45256.1
gene	852021	852443	192021	192443	gene=IY08_04455	protein=hypothetical protein	protein_id=KGT45257.1
gene	852478	853050	192478	193050	gene=IY08_04460	protein=hypothetical protein	protein_id=KGT45258.1
gene	853191	853643	193191	193643	gene=IY08_04470	protein=SMI1 / KNR4 family protein	protein_id=KGT45259.1
gene	853662	854108	193662	194108	gene=IY08_04475	protein=SMI1/KNR4 family protein	protein_id=KGT45260.1
gene	854377	854634	194377	194634	gene=IY08_04480	protein=type IV secretion protein Rhs	protein_id=KGT45261.1
gene	854646	855035	194646	195035	gene=IY08_04485	protein=hypothetical protein	protein_id=KGT45262.1
gene	855300	855494	195300	195494	gene=IY08_04490	protein=hypothetical protein	protein_id=KGT45263.1
gene	855543	856214	195543	196214	gene=IY08_04495	protein=membrane protein	protein_id=KGT45264.1
gene	856347	856493	196347	196493	gene=IY08_04500	protein=cytoplasmic protein	protein_id=KGT45265.1
gene	856915	857211	196915	197211	gene=IY08_04505	protein=type VII secretion protein EsxA	protein_id=KGT45266.1
gene	857369	857632	197369	197632	gene=IY08_04510	protein=creatininase	protein_id=KGT45267.1
gene	857673	858035	197673	198035	gene=IY08_04515	protein=hypothetical protein	protein_id=KGT45268.1
gene	858032	859303	198032	199303	gene=IY08_04520	protein=hypothetical protein	protein_id=KGT45269.1
gene	859318	859527	199318	199527	gene=IY08_04525	protein=hypothetical protein	protein_id=KGT45270.1
gene	859529	859813	199529	199813	gene=IY08_04530	protein=hypothetical protein	protein_id=KGT45271.1
gene	859894	860274	199894	200274	gene=IY08_04535	protein=lipoprotein	protein_id=KGT45272.1
gene	860463	861248	200463	201248	gene=IY08_04540	protein=ABC transporter ATP-binding protein	protein_id=KGT45273.1
gene	861368	861472	201368	201472	gene=IY08_04545	protein=integrase	protein_id=KGT45274.1
gene	862164	862643	202164	202643	gene=IY08_04555	protein=hypothetical protein	protein_id=KGT45275.1
gene	863069	864391	203069	204391	gene=IY08_04560	protein=alpha-ketoglutarate transporter	protein_id=KGT45276.1

gene	864617	866206	204617	206206	gene=IY08_04565	protein=ATPase	protein_id=KGT45277.1
gene	866226	866903	206226	206903	gene=IY08_04570	protein=transcriptional regulator	protein_id=KGT45278.1
gene	866900	867868	206900	207868	gene=IY08_04575	protein=membrane protein	protein_id=KGT45279.1
gene	868094	868495	208094	208495	gene=IY08_04580	protein=DNA mismatch repair protein MutT	protein_id=KGT45280.1
gene	868610	871510	208610	211510	gene=IY08_04585	protein=helicase	protein_id=KGT45281.1
gene	871911	872771	211911	212771	gene=IY08_04590	protein=XRE family transcriptional regulator	protein_id=KGT45282.1
gene	872768	874054	212768	214054	gene=IY08_04595	protein=DNA helicase	protein_id=KGT45283.1
gene	874146	874931	214146	214931	gene=IY08_04600	protein=transcriptional regulator	protein_id=KGT45284.1
gene	875042	875809	215042	215809	gene=IY08_04605	protein=membrane protein	protein_id=KGT45285.1
gene	876042	878075	216042	218075	gene=IY08_04610	protein=Fis family transcriptional regulator	protein_id=KGT45286.1
gene	878403	879161	218403	219161	gene=IY08_04615	protein=glutamine amidotransferase	protein_id=KGT45287.1
gene	879314	880744	219314	220744	gene=IY08_04620	protein=C4-dicarboxylate ABC transporter permease	protein_id=KGT45288.1
gene	880972	881124	220972	221124	gene=IY08_04625	protein=hypothetical protein	protein_id=KGT45289.1
gene	881454	882029	221454	222029	gene=IY08_04630	protein=TetR family transcriptional regulator	protein_id=KGT45290.1
gene	882172	883647	222172	223647	gene=IY08_04635	protein=multidrug MFS transporter	protein_id=KGT45291.1
gene	884167	884727	224167	224727	gene=IY08_04645	protein=hypothetical protein	protein_id=KGT45292.1
gene	885409	885954	225409	225954	gene=IY08_04660	protein=alanine acetyltransferase	protein_id=KGT45293.1
gene	885935	886117	225935	226117	gene=IY08_04665	protein=hypothetical protein	protein_id=KGT45294.1
gene	886563	887078	226563	227078	gene=IY08_04670	protein=cell wall anchor protein	protein_id=KGT45295.1
gene	887135	887643	227135	227643	gene=IY08_04675	protein=peptidase	partial=3'
gene	888002	888280	228002	228280	gene=IY08_04685	protein=ArsR family transcriptional regulator	protein_id=KGT45153.1
gene	888929	889345	228929	229345	gene=IY08_04695	protein=hypothetical protein	protein_id=KGT45154.1
gene	889624	890352	229624	230352	gene=IY08_04700	protein=abortive infection protein	protein_id=KGT45155.1
gene	890875	891219	230875	231219	gene=IY08_04710	protein=hypothetical protein	protein_id=KGT45156.1
gene	891266	891589	231266	231589	gene=IY08_04715	protein=hypothetical protein	protein_id=KGT45157.1
gene	891586	891915	231586	231915	gene=IY08_04720	protein=hypothetical protein	protein_id=KGT45158.1
gene	892344	892727	232344	232727	gene=IY08_04725	protein=hypothetical protein	protein_id=KGT45159.1
gene	892729	893892	232729	233892	gene=IY08_04730	protein=hypothetical protein	protein_id=KGT45160.1
gene	894003	894333	234003	234333	gene=IY08_04735	protein=beta-lactamase	frame=2
gene	894410	894793	234410	234793	gene=IY08_04740	protein=beta-lactamase	protein_id=KGT45147.1
gene	894870	895253	234870	235253	gene=IY08_04745	protein=beta-lactamase	protein_id=KGT45148.1

gene	895469	896851	235469	236851	gene=IY08_04750	protein=hydrolase	protein_id=KGT45149.1
gene	898325	898975	238325	238975	gene=IY08_04760	protein=hypothetical protein	protein_id=KGT45150.1
gene	899842	900276	239842	240276	gene=IY08_04765	protein=sodium:proton symporter	protein_id=KGT45151.1
gene	900514	901187	240514	241187	gene=IY08_04770	protein=FMN-dependent NADH-azoreductase	partial=3'
gene	901801	901926	241801	241926	gene=IY08_04775	protein=hypothetical protein	protein_id=KGT45095.1
gene	902124	902384	242124	242384	gene=IY08_04780	protein=transporter	protein_id=KGT45096.1
gene	902723	904132	242723	244132	gene=IY08_04785	protein=carboxylic ester hydrolase	protein_id=KGT45097.1
gene	904305	904406	244305	244406	gene=IY08_04790	protein=hypothetical protein	protein_id=KGT45098.1
gene	904760	905026	244760	245026	gene=IY08_04800	protein=hypothetical protein	protein_id=KGT45099.1
gene	905409	905765	245409	245765	gene=IY08_04805	protein=MarR family transcriptional regulator	protein_id=KGT45100.1
gene	905930	906388	245930	246388	gene=IY08_04810	protein=MarR family transcriptional regulator	protein_id=KGT45101.1
gene	906432	906965	246432	246965	gene=IY08_04815	protein=CDP-diacylglycerol--serine O-	protein_id=KGT45102.1
gene	907005	907376	247005	247376	gene=IY08_04820	protein=ATP synthase subunit I	protein_id=KGT45103.1
gene	907670	908323	247670	248323	gene=IY08_04825	protein=membrane protein	protein_id=KGT45104.1
gene	908682	909320	248682	249320	gene=IY08_04830	protein=VanZ family protein	protein_id=KGT45105.1
gene	909420	910418	249420	250418	gene=IY08_04835	protein=DhaKLM operon coactivator DhaQ	protein_id=KGT45106.1
gene	910438	911004	250438	251004	gene=IY08_04840	protein=TetR family transcriptional regulator	protein_id=KGT45107.1
gene	911183	912934	251183	252934	gene=IY08_04845	protein=hypothetical protein	protein_id=KGT45108.1
gene	913164	913514	253164	253514	gene=IY08_04850	protein=antifungal polypeptide	protein_id=KGT45109.1
gene	913707	914258	253707	254258	gene=IY08_04855	protein=hypothetical protein	protein_id=KGT45110.1
gene	914551	914940	254551	254940	gene=IY08_04860	protein=hypothetical protein	protein_id=KGT45111.1
gene	915511	916401	255511	256401	gene=IY08_04865	protein=DNA-binding protein	protein_id=KGT45112.1
gene	917007	917171	257007	257171	gene=IY08_04875	protein=cell division protein	protein_id=KGT45113.1
gene	917651	919384	257651	259384	gene=IY08_04880	protein=S-layer protein	protein_id=KGT45114.1
gene	919536	920153	259536	260153	gene=IY08_04885	protein=hypothetical protein	protein_id=KGT45115.1
gene	920722	921699	260722	261699	gene=IY08_04890	protein=membrane protein	protein_id=KGT45116.1
gene	921703	922233	261703	262233	gene=IY08_04895	protein=RNA polymerase sigma factor SigX	protein_id=KGT45117.1
gene	923261	923674	263261	263674	gene=IY08_04905	protein=hypothetical protein	protein_id=KGT45118.1
gene	923757	924212	263757	264212	gene=IY08_04910	protein=lipoprotein	protein_id=KGT45119.1
gene	924426	924815	264426	264815	gene=IY08_04915	protein=general stress protein	protein_id=KGT45120.1
gene	924866	925066	264866	265066	gene=IY08_04920	protein=hypothetical protein	protein_id=KGT45121.1

gene	925142	925393	265142	265393	gene=IY08_04925	protein=membrane protein	protein_id=KGT45122.1
gene	925574	925774	265574	265774	gene=IY08_04930	protein=methyltransferase	protein_id=KGT45123.1
gene	925971	926309	265971	266309	gene=IY08_04935	protein=metal ABC transporter ATPase	protein_id=KGT45124.1
gene	926316	926798	266316	266798	gene=IY08_04940	protein=serine/threonine protein kinase	protein_id=KGT45125.1
gene	926764	927537	266764	267537	gene=IY08_04945	protein=RNA polymerase sigma factor SigB	protein_id=KGT45126.1
gene	927607	928047	267607	268047	gene=IY08_04950	protein=bacterioferritin	protein_id=KGT45127.1
gene	928223	929365	268223	269365	gene=IY08_04955	protein=response regulator	protein_id=KGT45128.1
gene	929549	930406	269549	270406	gene=IY08_04960	protein=chemotaxis protein CheR	protein_id=KGT45129.1
gene	930423	933113	270423	273113	gene=IY08_04965	protein=histidine kinase	protein_id=KGT45130.1
gene	933318	933569	273318	273569	gene=IY08_04970	protein=hypothetical protein	protein_id=KGT45131.1
gene	933806	933946	273806	273946	gene=IY08_04975	protein=hypothetical protein	protein_id=KGT45132.1
gene	933983	934513	273983	274513	gene=IY08_04980	protein=general stress protein	protein_id=KGT45133.1
gene	934652	934855	274652	274855	gene=IY08_04985	protein=hypothetical protein	protein_id=KGT45134.1
gene	934994	935305	274994	275305	gene=IY08_04990	protein=hypothetical protein	protein_id=KGT45135.1
gene	935969	936274	275969	276274	gene=IY08_05000	protein=hypothetical protein	protein_id=KGT45136.1
gene	936392	937384	276392	277384	gene=IY08_05005	protein=alcohol dehydrogenase	protein_id=KGT45137.1
gene	937534	938520	277534	278520	gene=IY08_05010	protein=choloylglycine hydrolase	protein_id=KGT45138.1
gene	938642	938782	278642	278782	gene=IY08_05015	protein=hypothetical protein	protein_id=KGT45139.1
gene	938936	939298	278936	279298	gene=IY08_05025	protein=hypothetical protein	protein_id=KGT45140.1
gene	939325	939510	279325	279510	gene=IY08_05030	protein=hypothetical protein	protein_id=KGT45141.1
gene	939719	940960	279719	280960	gene=IY08_05035	protein=DNA repair exonuclease	protein_id=KGT45142.1
gene	940957	943881	280957	283881	gene=IY08_05040	protein=DNA double-strand break repair Rad50 ATPase	protein_id=KGT45143.1
gene	943923	944867	283923	284867	gene=IY08_05045	protein=3'-5' exonuclease	protein_id=KGT45144.1
gene	945162	946589	285162	286589	gene=IY08_05050	protein=beta-lactamase	protein_id=KGT45145.1
gene	947249	947449	287249	287449	gene=IY08_05055	protein=hypothetical protein	protein_id=KGT45053.1
gene	947472	947660	287472	287660	gene=IY08_05060	protein=hypothetical protein	protein_id=KGT45054.1
gene	948282	949226	288282	289226	gene=IY08_05065	protein=glyoxalase	protein_id=KGT45055.1
gene	949282	950259	289282	290259	gene=IY08_05070	protein=glyoxalase	protein_id=KGT45056.1
gene	950515	951609	290515	291609	gene=IY08_05075	protein=histidine kinase	protein_id=KGT45057.1
gene	951609	951812	291609	291812	gene=IY08_05080	protein=aspartate phosphatase	protein_id=KGT45058.1
gene	952053	952925	292053	292925	gene=IY08_05085	protein=alpha/beta hydrolase	protein_id=KGT45059.1

gene	953004	953204	293004	293204	gene=IY08_05090	protein=SigE-dependent sporulation protein	protein_id=KGT45060.1
gene	953421	954272	293421	294272	gene=IY08_05095	protein=hypothetical protein	protein_id=KGT45061.1
gene	954546	955211	294546	295211	gene=IY08_05100	protein=hypothetical protein	protein_id=KGT45062.1
gene	955570	956763	295570	296763	gene=IY08_05110	protein=oxalate decarboxylase	protein_id=KGT45063.1
gene	957030	957479	297030	297479	gene=IY08_05115	protein=XRE family transcriptional regulator	protein_id=KGT45064.1
gene	957577	958137	297577	298137	gene=IY08_05120	protein=glycerol-3-phosphate responsive antiterminator	protein_id=KGT45065.1
gene	958364	959185	298364	299185	gene=IY08_05125	protein=glycerol transporter	protein_id=KGT45066.1
gene	959199	960689	299199	300689	gene=glpK	protein=glycerol kinase	protein_id=KGT45067.1
gene	960823	962505	300823	302505	gene=IY08_05135	protein=glycerol-3-phosphate dehydrogenase	protein_id=KGT45068.1
gene	962623	962955	302623	302955	gene=IY08_05140	protein=PadR family transcriptional regulator	protein_id=KGT45069.1
gene	962948	963721	302948	303721	gene=IY08_05145	protein=teicoplanin resistance protein VanZ	protein_id=KGT45070.1
gene	964050	964214	304050	304214	gene=IY08_05150	protein=hypothetical protein	protein_id=KGT45071.1
gene	964495	965028	304495	305028	gene=IY08_05155	protein=RNA polymerase factor sigma C	protein_id=KGT45072.1
gene	965033	965440	305033	305440	gene=lstR	protein=lineage-specific thermal regulator protein	protein_id=KGT45073.1
gene	965448	966713	305448	306713	gene=IY08_05165	protein=cell division protein FtsW	protein_id=KGT45074.1
gene	967109	967993	307109	307993	gene=IY08_05175	protein=ATPase	protein_id=KGT45075.1
gene	968091	970427	308091	310427	gene=IY08_05180	protein=helicase	protein_id=KGT45076.1
gene	970824	971693	310824	311693	gene=prsA	protein=peptidylprolyl isomerase	protein_id=KGT45077.1
gene	971813	972025	311813	312025	gene=IY08_05190	protein=hypothetical protein	protein_id=KGT45078.1
gene	972117	972311	312117	312311	gene=IY08_05195	protein=hypothetical protein	protein_id=KGT45079.1
gene	972427	972762	312427	312762	gene=IY08_05200	protein=wall-associated protein	protein_id=KGT45080.1
gene	972768	973325	312768	313325	gene=IY08_05205	protein=transcriptional regulator Hpr	protein_id=KGT45081.1
gene	973625	973987	313625	313987	gene=IY08_05210	protein=general stress protein	protein_id=KGT45082.1
gene	974167	974601	314167	314601	gene=IY08_05215	protein=protein hit	protein_id=KGT45083.1
gene	975164	975907	315164	315907	gene=IY08_05220	protein=multidrug ABC transporter ATP-binding protein	protein_id=KGT45084.1
gene	975900	977111	315900	317111	gene=IY08_05225	protein=ABC transporter permease	protein_id=KGT45085.1
gene	977125	977832	317125	317832	gene=IY08_05230	protein=ecsC	protein_id=KGT45086.1
gene	978172	978753	318172	318753	gene=IY08_05240	protein=TetR family transcriptional regulator	protein_id=KGT45087.1
gene	978756	978923	318756	318923	gene=IY08_05245	protein=hypothetical protein	protein_id=KGT45088.1
gene	979003	979479	319003	319479	gene=IY08_05250	protein=membrane protein	protein_id=KGT45089.1
gene	979472	980914	319472	320914	gene=IY08_05255	protein=membrane protein	protein_id=KGT45090.1

gene	981115	981768	321115	321768	gene=IY08_05260	protein=membrane protein	protein_id=KGT45091.1
gene	981993	982418	321993	322418	gene=IY08_05265	protein=hypothetical protein	protein_id=KGT45092.1
gene	982870	983424	322870	323424	gene=IY08_05270	protein=TetR family transcriptional regulator	protein_id=KGT45093.1
gene	983731	987681	323731	327681	gene=IY08_05275	protein=adhesin	partial=3'
gene	987745	989655	327745	329655	gene=IY08_05280	protein=adhesin	partial=5'
gene	990134	990871	330134	330871	gene=IY08_05285	protein=hypothetical protein	protein_id=KGT44938.1
gene	990868	991614	330868	331614	gene=IY08_05290	protein=3-oxoacyl-ACP reductase	protein_id=KGT44939.1
gene	991703	992644	331703	332644	gene=IY08_05295	protein=transporter	protein_id=KGT44940.1
gene	992875	993351	332875	333351	gene=IY08_05300	protein=membrane protein	protein_id=KGT44941.1
gene	993344	994759	333344	334759	gene=IY08_05305	protein=membrane protein	protein_id=KGT44942.1
gene	995065	995568	335065	335568	gene=IY08_05310	protein=histidine kinase	protein_id=KGT44943.1
gene	995696	997813	335696	337813	gene=IY08_05315	protein=penicillin-binding protein	protein_id=KGT44944.1
gene	997991	999037	337991	339037	gene=IY08_05320	protein=uroporphyrinogen decarboxylase	protein_id=KGT44945.1
gene	999052	999987	339052	339987	gene=IY08_05325	protein=ferrochelataase	protein_id=KGT44946.1
gene	1000007	1001428	340007	341428	gene=IY08_05330	protein=protoporphyrinogen oxidase	protein_id=KGT44947.1
gene	1001485	1002837	341485	342837	gene=IY08_05335	protein=hypothetical protein	protein_id=KGT44948.1
gene	1003079	1005445	343079	345445	gene=IY08_05340	protein=endonuclease	protein_id=KGT44949.1
gene	1005578	1005877	345578	345877	gene=IY08_05345	protein=hypothetical protein	protein_id=KGT44950.1
gene	1005931	1006776	345931	346776	gene=IY08_05350	protein=membrane protein	protein_id=KGT44951.1
gene	1007006	1007407	347006	347407	gene=IY08_05355	protein=beta-lactamase repressor	protein_id=KGT44952.1
gene	1007410	1009308	347410	349308	gene=IY08_05360	protein=methicillin resistance protein	protein_id=KGT44953.1
gene	1009522	1010094	349522	350094	gene=IY08_05365	protein=TetR family transcriptional regulator	protein_id=KGT44954.1
gene	1010311	1013646	350311	353646	gene=IY08_05370	protein=phage infection protein	protein_id=KGT44955.1
gene	1013790	1014002	353790	354002	gene=IY08_05375	protein=hypothetical protein	protein_id=KGT44956.1
gene	1014006	1014311	354006	354311	gene=IY08_05380	protein=transcriptional regulator	protein_id=KGT44957.1
gene	1014338	1014691	354338	354691	gene=IY08_05385	protein=PlcR-regulated protein PRP2	protein_id=KGT44958.1
gene	1014825	1015334	354825	355334	gene=IY08_05390	protein=acetyltransferase	protein_id=KGT44959.1
gene	1015529	1016542	355529	356542	gene=IY08_05395	protein=LacI family transcriptional regulator	protein_id=KGT44960.1
gene	1016582	1016710	356582	356710	gene=IY08_05400	protein=hypothetical protein	protein_id=KGT44961.1
gene	1016891	1017625	356891	357625	gene=IY08_05405	protein=hypothetical protein	protein_id=KGT44962.1
gene	1017635	1018624	357635	358624	gene=IY08_05410	protein=lipoate--protein ligase	protein_id=KGT44963.1

gene	1018885	1019313	358885	359313	gene=IY08_05415	protein=lipoprotein	protein_id=KGT44964.1
gene	1019475	1021007	359475	361007	gene=IY08_05420	protein=long-chain fatty acid--CoA ligase	protein_id=KGT44965.1
gene	1021175	1021351	361175	361351	gene=IY08_05425	protein=S-layer protein	protein_id=KGT44966.1
gene	1021526	1022581	361526	362581	gene=IY08_05430	protein=sulfate transporter subunit	protein_id=KGT44967.1
gene	1022614	1023441	362614	363441	gene=IY08_05435	protein=sulfate ABC transporter permease	protein_id=KGT44968.1
gene	1023453	1024310	363453	364310	gene=IY08_05440	protein=sulfate ABC transporter permease	protein_id=KGT44969.1
gene	1024322	1025395	364322	365395	gene=IY08_05445	protein=sulfate ABC transporter ATP-binding protein	protein_id=KGT44970.1
gene	1025437	1026447	365437	366447	gene=IY08_05450	protein=cytotoxin	protein_id=KGT44971.1
gene	1026739	1027845	366739	367845	gene=IY08_05460	protein=phosphoesterase	protein_id=KGT44972.1
gene	1027980	1028957	367980	368957	gene=IY08_05465	protein=hypothetical protein	protein_id=KGT44973.1
gene	1029001	1030125	369001	370125	gene=IY08_05470	protein=sigma-M negative effector	protein_id=KGT44974.1
gene	1030131	1030616	370131	370616	gene=IY08_05475	protein=RNA polymerase sigma factor	protein_id=KGT44975.1
gene	1030754	1031656	370754	371656	gene=IY08_05480	protein=AraC family transcriptional regulator	protein_id=KGT44976.1
gene	1032402	1034144	372402	374144	gene=IY08_05495	protein=histidine kinase	protein_id=KGT44977.1
gene	1034154	1034858	374154	374858	gene=IY08_05500	protein=transcriptional regulator	protein_id=KGT44978.1
gene	1034999	1035847	374999	375847	gene=IY08_05505	protein=CAAX protease	protein_id=KGT44979.1
gene	1035849	1036205	375849	376205	gene=IY08_05510	protein=hypothetical protein	protein_id=KGT44980.1
gene	1036237	1036536	376237	376536	gene=IY08_05515	protein=hypothetical protein	protein_id=KGT44981.1
gene	1036765	1038033	376765	378033	gene=IY08_05520	protein=peptidase M48	protein_id=KGT44982.1
gene	1038170	1039897	378170	379897	gene=IY08_05525	protein=chemotaxis protein	protein_id=KGT44983.1
gene	1040338	1040994	380338	380994	gene=IY08_05530	protein=S-layer protein	protein_id=KGT44984.1
gene	1041238	1041900	381238	381900	gene=IY08_05540	protein=S-layer protein	protein_id=KGT44985.1
gene	1042120	1043709	382120	383709	gene=IY08_05545	protein=malate synthase	protein_id=KGT44986.1
gene	1043733	1045010	383733	385010	gene=IY08_05550	protein=isocitrate lyase	protein_id=KGT44987.1
gene	1045120	1045911	385120	385911	gene=IY08_05555	protein=aminoglycoside phosphotransferase	protein_id=KGT44988.1
gene	1045931	1046425	385931	386425	gene=IY08_05560	protein=DNA helicase	protein_id=KGT44989.1
gene	1046709	1046912	386709	386912	gene=IY08_05565	protein=cold-shock protein	protein_id=KGT44990.1
gene	1047110	1047313	387110	387313	gene=IY08_05570	protein=hypothetical protein	protein_id=KGT44991.1
gene	1047662	1047847	387662	387847	gene=IY08_05575	protein=ATPase	protein_id=KGT44992.1
gene	1048132	1048713	388132	388713	gene=IY08_05585	protein=competence protein	protein_id=KGT44993.1
gene	1049050	1049643	389050	389643	gene=IY08_05590	protein=hypothetical protein	protein_id=KGT44994.1

gene	1049700	1050263	389700	390263	gene=IY08_05595	protein=signal peptidase	protein_id=KGT44995.1
gene	1050380	1053895	390380	393895	gene=IY08_05600	protein=ATP-dependent helicase	protein_id=KGT44996.1
gene	1053892	1057617	393892	397617	gene=IY08_05605	protein=ATP-dependent helicase	protein_id=KGT44997.1
gene	1057630	1057917	397630	397917	gene=IY08_05610	protein=hypothetical protein	protein_id=KGT44998.1
gene	1058055	1058270	398055	398270	gene=IY08_05615	protein=spore germination protein GerPF	protein_id=KGT44999.1
gene	1058313	1058699	398313	398699	gene=IY08_05620	protein=spore germination protein GerPE	protein_id=KGT45000.1
gene	1058715	1058909	398715	398909	gene=IY08_05625	protein=spore germination protein GerPD	protein_id=KGT45001.1
gene	1058916	1059530	398916	399530	gene=IY08_05630	protein=spore germination protein GerPC	protein_id=KGT45002.1
gene	1059598	1059804	399598	399804	gene=IY08_05635	protein=spore germination protein GerPB	protein_id=KGT45003.1
gene	1059819	1060040	399819	400040	gene=IY08_05640	protein=spore germination protein GerPA	protein_id=KGT45004.1
gene	1060137	1060316	400137	400316	gene=IY08_05645	protein=stage 0 sporulation protein	protein_id=KGT45005.1
gene	1060563	1061462	400563	401462	gene=IY08_05650	protein=hypothetical protein	protein_id=KGT45006.1
gene	1061498	1061782	401498	401782	gene=IY08_05655	protein=hypothetical protein	protein_id=KGT45007.1
gene	1061892	1063082	401892	403082	gene=rocD	protein=ornithine--oxo-acid aminotransferase	protein_id=KGT45008.1
gene	1063233	1063601	403233	403601	gene=IY08_05665	protein=hypothetical protein	protein_id=KGT45009.1
gene	1063657	1064211	403657	404211	gene=IY08_05670	protein=hypothetical protein	protein_id=KGT45010.1
gene	1064450	1066297	404450	406297	gene=IY08_05675	protein=asparagine synthase	protein_id=KGT45011.1
gene	1066485	1067444	406485	407444	gene=IY08_05680	protein=ferrochelatase	protein_id=KGT45012.1
gene	1067504	1068970	407504	408970	gene=IY08_05685	protein=catalase	protein_id=KGT45013.1
gene	1069235	1070467	409235	410467	gene=IY08_05690	protein=ammonia channel protein	protein_id=KGT45014.1
gene	1070687	1071982	410687	411982	gene=IY08_05700	protein=alpha-amylase	protein_id=KGT45015.1
gene	1072923	1073414	412923	413414	gene=IY08_05705	protein=hypothetical protein	protein_id=KGT45016.1
gene	1073645	1074499	413645	414499	gene=IY08_05710	protein=hypothetical protein	protein_id=KGT45017.1
gene	1074553	1075410	414553	415410	gene=prsA	protein=peptidylprolyl isomerase	protein_id=KGT45018.1
gene	1075540	1075671	415540	415671	gene=IY08_05720	protein=hypothetical protein	protein_id=KGT45019.1
gene	1075772	1076629	415772	416629	gene=IY08_05725	protein=membrane protein	protein_id=KGT45020.1
gene	1076655	1076852	416655	416852	gene=IY08_05730	protein=hypothetical protein	protein_id=KGT45021.1
gene	1076853	1076993	416853	416993	gene=IY08_05735	protein=competence protein	protein_id=KGT45022.1
gene	1077099	1077908	417099	417908	gene=IY08_05740	protein=haloacid dehalogenase	protein_id=KGT45023.1
gene	1078003	1078137	418003	418137	gene=IY08_05745	protein=hypothetical protein	protein_id=KGT45024.1
gene	1078399	1078578	418399	418578	gene=IY08_05750	protein=hypothetical protein	protein_id=KGT45025.1

gene	1078788	1081388	418788	421388	gene=IY08_05755	protein=protein disaggregation chaperone	protein_id=KGT45026.1
gene	1081428	1081610	421428	421610	gene=IY08_05760	protein=DeoR family transcriptional regulator	protein_id=KGT45027.1
gene	1081767	1082501	421767	422501	gene=IY08_05765	protein=hydrolase	protein_id=KGT45028.1
gene	1082531	1083403	422531	423403	gene=IY08_05770	protein=UDP-glucose 4-epimerase	protein_id=KGT45029.1
gene	1083458	1083634	423458	423634	gene=IY08_05775	protein=competence protein ComG	protein_id=KGT45030.1
gene	1083855	1084787	423855	424787	gene=IY08_05780	protein=3-oxoacyl-ACP synthase	protein_id=KGT45031.1
gene	1084819	1086057	424819	426057	gene=IY08_05785	protein=3-oxoacyl-ACP synthase	protein_id=KGT45032.1
gene	1086164	1086952	426164	426952	gene=IY08_05790	protein=cytoplasmic protein	protein_id=KGT45033.1
gene	1087096	1087842	427096	427842	gene=IY08_05795	protein=hypothetical protein	protein_id=KGT45034.1
gene	1087865	1088047	427865	428047	gene=IY08_05800	protein=MerR family transcriptional regulator	protein_id=KGT45035.1
gene	1088122	1089111	428122	429111	gene=IY08_05805	protein=tryptophanyl-tRNA synthetase	protein_id=KGT45036.1
gene	1089510	1089890	429510	429890	gene=IY08_05810	protein=transporter	protein_id=KGT45037.1
gene	1090210	1091865	430210	431865	gene=IY08_05815	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT45038.1
gene	1091994	1092923	431994	432923	gene=IY08_05820	protein=peptide ABC transporter permease	protein_id=KGT45039.1
gene	1092920	1093936	432920	433936	gene=IY08_05825	protein=peptide ABC transporter permease	protein_id=KGT45040.1
gene	1093955	1094998	433955	434998	gene=IY08_05830	protein=peptide ABC transporter ATP-binding protein	protein_id=KGT45041.1
gene	1094991	1095926	434991	435926	gene=IY08_05835	protein=peptide ABC transporter ATP-binding protein	protein_id=KGT45042.1
gene	1096070	1097515	436070	437515	gene=IY08_05840	protein=multidrug transporter MatE	protein_id=KGT45043.1
gene	1097868	1099514	437868	439514	gene=IY08_05845	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT45044.1
gene	1099544	1099747	439544	439747	gene=IY08_05850	protein=hypothetical protein	protein_id=KGT45045.1
gene	1100068	1100226	440068	440226	gene=IY08_05855	protein=hypothetical protein	protein_id=KGT45046.1
gene	1100341	1100736	440341	440736	gene=IY08_05860	protein=ArsR family transcriptional regulator	protein_id=KGT45047.1
gene	1100786	1101460	440786	441460	gene=IY08_05865	protein=membrane protein	protein_id=KGT45048.1
gene	1101806	1102489	441806	442489	gene=IY08_05870	protein=adaptor protein	protein_id=KGT45049.1
gene	1102562	1104106	442562	444106	gene=IY08_05875	protein=cardiolipin synthetase	protein_id=KGT45050.1
gene	1104187	1105431	444187	445431	gene=IY08_05880	protein=competence protein	protein_id=KGT45051.1
gene	1105483	1107309	445483	447309	gene=IY08_05885	protein=oligopeptidase PepB	protein_id=KGT45052.1
gene	1107482	1107655	447482	447655	gene=IY08_05890	protein=hypothetical protein	protein_id=KGT44756.1
gene	1107885	1108778	447885	448778	gene=IY08_05895	protein=hypothetical protein	protein_id=KGT44757.1
gene	1108778	1109176	448778	449176	gene=IY08_05900	protein=globin	protein_id=KGT44758.1
gene	1109345	1109923	449345	449923	gene=IY08_05905	protein=hypothetical protein	protein_id=KGT44759.1

gene	1110068	1110439	450068	450439	gene=IY08_05910	protein=hypothetical protein	protein_id=KGT44760.1
gene	1110470	1111108	450470	451108	gene=IY08_05915	protein=GTP pyrophosphokinase	protein_id=KGT44761.1
gene	1111127	1111924	451127	451924	gene=ppnK	protein=inorganic polyphosphate kinase	protein_id=KGT44762.1
gene	1111939	1112832	451939	452832	gene=IY08_05925	protein=pseudouridine synthase	protein_id=KGT44763.1
gene	1112881	1114269	452881	454269	gene=IY08_05930	protein=peptidase G2	protein_id=KGT44764.1
gene	1114393	1115133	454393	455133	gene=IY08_05935	protein=bis(5'-nucleosyl)-tetrphosphatase	protein_id=KGT44765.1
gene	1115210	1116370	455210	456370	gene=IY08_05940	protein=cell division protein FtsW	protein_id=KGT44766.1
gene	1116609	1117535	456609	457535	gene=IY08_05945	protein=glycosyl transferase family 2	protein_id=KGT44767.1
gene	1117549	1118301	457549	458301	gene=IY08_05950	protein=methyltransferase	protein_id=KGT44768.1
gene	1118485	1119330	458485	459330	gene=IY08_05955	protein=macrocin-O-methyltransferase	protein_id=KGT44769.1
gene	1119453	1120313	459453	460313	gene=IY08_05960	protein=triple helix repeat-containing collagen	protein_id=KGT44770.1
gene	1120479	1121576	460479	461576	gene=IY08_05965	protein=beta 1,4 glucosyltransferase	protein_id=KGT44771.1
gene	1121789	1122478	461789	462478	gene=IY08_05970	protein=SAM-dependent methyltransferase	protein_id=KGT44772.1
gene	1122475	1123161	462475	463161	gene=IY08_05975	protein=streptomycin biosynthesis protein StrF	protein_id=KGT44773.1
gene	1123176	1123856	463176	463856	gene=IY08_05980	protein=streptomycin biosynthesis protein StrF	protein_id=KGT44774.1
gene	1123871	1124608	463871	464608	gene=IY08_05985	protein=spore coat protein	protein_id=KGT44775.1
gene	1124617	1125162	464617	465162	gene=IY08_05990	protein=dTDP-4-dehydorrhamnose 3,5-epimerase	protein_id=KGT44776.1
gene	1125178	1126149	465178	466149	gene=IY08_05995	protein=dTDP-glucose 4,6-dehydratase	protein_id=KGT44777.1
gene	1126162	1127016	466162	467016	gene=IY08_06000	protein=spore coat protein	protein_id=KGT44778.1
gene	1127125	1127895	467125	467895	gene=IY08_06005	protein=enoyl-ACP reductase	protein_id=KGT44779.1
gene	1128058	1128579	468058	468579	gene=IY08_06010	protein=Signal recognition particle receptor protein FtsY	protein_id=KGT44780.1
gene	1128628	1129092	468628	469092	gene=IY08_06015	protein=spore coat protein	protein_id=KGT44781.1
gene	1129218	1129577	469218	469577	gene=IY08_06020	protein=membrane protein	protein_id=KGT44782.1
gene	1129679	1129864	469679	469864	gene=IY08_06025	protein=cytochrome C oxidase subunit III	protein_id=KGT44783.1
gene	1129940	1130443	469940	470443	gene=IY08_06030	protein=membrane protein	protein_id=KGT44784.1
gene	1130611	1131078	470611	471078	gene=IY08_06035	protein=spore coat protein	protein_id=KGT44785.1
gene	1131222	1133288	471222	473288	gene=IY08_06040	protein=ATP-dependent DNA helicase	protein_id=KGT44786.1
gene	1133389	1133811	473389	473811	gene=IY08_06045	protein=acetyltransferase	protein_id=KGT44787.1
gene	1133813	1134331	473813	474331	gene=IY08_06050	protein=hypothetical protein	protein_id=KGT44788.1
gene	1134425	1135156	474425	475156	gene=IY08_06055	protein=hypothetical protein	protein_id=KGT44789.1
gene	1135360	1136271	475360	476271	gene=IY08_06060	protein=multidrug transporter	protein_id=KGT44790.1

gene	1136348	1136674	476348	476674	gene=IY08_06065	protein=cyclic nucleotide-binding protein	protein_id=KGT44791.1
gene	1136699	1137097	476699	477097	gene=IY08_06070	protein=hypothetical protein	protein_id=KGT44792.1
gene	1137253	1138731	477253	478731	gene=IY08_06075	protein=proline:sodium symporter PutP	protein_id=KGT44793.1
gene	1139170	1139358	479170	479358	gene=IY08_06080	protein=hypothetical protein	protein_id=KGT44794.1
gene	1139762	1141180	479762	481180	gene=IY08_06085	protein=anthranilate synthase subunit I	protein_id=KGT44795.1
gene	1141177	1141764	481177	481764	gene=IY08_06090	protein=anthranilate synthase	protein_id=KGT44796.1
gene	1141761	1142786	481761	482786	gene=IY08_06095	protein=anthranilate phosphoribosyltransferase	protein_id=KGT44797.1
gene	1142788	1143549	482788	483549	gene=IY08_06100	protein=indole-3-glycerol phosphate synthase	protein_id=KGT44798.1
gene	1143546	1144160	483546	484160	gene=IY08_06105	protein=N-(5'-phosphoribosyl)anthranilate isomerase	protein_id=KGT44799.1
gene	1144157	1145350	484157	485350	gene=IY08_06110	protein=tryptophan synthase subunit beta	protein_id=KGT44800.1
gene	1145354	1146130	485354	486130	gene=IY08_06115	protein=tryptophan synthase subunit alpha	protein_id=KGT44801.1
gene	1146204	1146563	486204	486563	gene=IY08_06120	protein=hypothetical protein	protein_id=KGT44802.1
gene	1146678	1148177	486678	488177	gene=IY08_06125	protein=lactate permease	protein_id=KGT44803.1
gene	1148268	1148951	488268	488951	gene=IY08_06130	protein=hypothetical protein	protein_id=KGT44804.1
gene	1148966	1149799	488966	489799	gene=IY08_06135	protein=membrane protein	protein_id=KGT44805.1
gene	1149996	1150781	489996	490781	gene=IY08_06140	protein=hypothetical protein	protein_id=KGT44806.1
gene	1150801	1152036	490801	492036	gene=IY08_06145	protein=hypothetical protein	protein_id=KGT44807.1
gene	1152083	1152505	492083	492505	gene=IY08_06150	protein=hypothetical protein	protein_id=KGT44808.1
gene	1152705	1154039	492705	494039	gene=IY08_06155	protein=NADH dehydrogenase	protein_id=KGT44809.1
gene	1154199	1154609	494199	494609	gene=IY08_06160	protein=hypothetical protein	protein_id=KGT44810.1
gene	1154640	1156181	494640	496181	gene=IY08_06165	protein=NADH oxidase	protein_id=KGT44811.1
gene	1156197	1158146	496197	498146	gene=IY08_06170	protein=bacteriocin biosynthesis protein SagD	protein_id=KGT44812.1
gene	1158143	1160062	498143	500062	gene=IY08_06175	protein=bacteriocin maturation protein	protein_id=KGT44813.1
gene	1160186	1161448	500186	501448	gene=IY08_06180	protein=dihydrolipoamide succinyltransferase	protein_id=KGT44814.1
gene	1161582	1164449	501582	504449	gene=IY08_06185	protein=2-oxoglutarate dehydrogenase	protein_id=KGT44815.1
gene	1165278	1165460	505278	505460	gene=IY08_06195	protein=hypothetical protein	protein_id=KGT44816.1
gene	1165593	1165955	505593	505955	gene=IY08_06200	protein=hypothetical protein	protein_id=KGT44817.1
gene	1165972	1166225	505972	506225	pseudo		
gene	1166307	1166852	506307	506852	gene=IY08_06215	protein=hypothetical protein	protein_id=KGT44818.1
gene	1167011	1167607	507011	507607	gene=IY08_06220	protein=hypothetical protein	protein_id=KGT44819.1
gene	1168485	1169384	508485	509384	gene=IY08_06225	protein=sodium ABC transporter ATP-binding protein	protein_id=KGT44820.1

gene	1169377	1170618	509377	510618	gene=IY08_06230	protein=sodium export permease	protein_id=KGT44821.1
gene	1170932	1171004	510932	511004	tRNA		
gene	1171275	1171739	511275	511739	gene=IY08_06240	protein=signal peptide protein	protein_id=KGT44822.1
gene	1172329	1172550	512329	512550	gene=IY08_06245	protein=hypothetical protein	protein_id=KGT44823.1
gene	1172958	1173185	512958	513185	gene=IY08_06250	protein=hypothetical protein	protein_id=KGT44824.1
gene	1173337	1174623	513337	514623	gene=IY08_06255	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT44825.1
gene	1174814	1175383	514814	515383	gene=IY08_06260	protein=signal peptidase	protein_id=KGT44826.1
gene	1175444	1176031	515444	516031	gene=IY08_06265	protein=cell division protein FtsN	protein_id=KGT44827.1
gene	1176166	1176972	516166	516972	gene=IY08_06270	protein=erpL protein	protein_id=KGT44828.1
gene	1177360	1177953	517360	517953	gene=IY08_06275	protein=cell division protein FtsN	protein_id=KGT44829.1
gene	1178026	1178349	518026	518349	gene=IY08_06280	protein=transcriptional regulator	protein_id=KGT44830.1
gene	1178429	1178563	518429	518563	gene=IY08_06285	protein=SinI anti-repressor domain-containing protein	protein_id=KGT44831.1
gene	1178906	1181296	518906	521296	gene=IY08_06290	protein=peptidase M6	protein_id=KGT44832.1
gene	1181468	1182835	521468	522835	gene=IY08_06295	protein=aldehyde dehydrogenase	protein_id=KGT44833.1
gene	1183075	1184058	523075	524058	gene=IY08_06300	protein=spermidine/putrescine ABC transporter ATP-binding protein	protein_id=KGT44834.1
gene	1184055	1184903	524055	524903	gene=IY08_06305	protein=ABC transporter permease	protein_id=KGT44835.1
gene	1184910	1185710	524910	525710	gene=IY08_06310	protein=spermidine/putrescine ABC transporter permease	protein_id=KGT44836.1
gene	1185749	1186798	525749	526798	gene=IY08_06315	protein=spermidine/putrescine ABC transporter substrate-binding protein	protein_id=KGT44837.1
gene	1186858	1187505	526858	527505	gene=IY08_06320	protein=phosphoesterase	protein_id=KGT44838.1
gene	1187616	1189808	527616	529808	gene=IY08_06325	protein=membrane protein	protein_id=KGT44839.1
gene	1189910	1190326	529910	530326	gene=IY08_06330	protein=histidinol dehydrogenase	protein_id=KGT44840.1
gene	1190427	1191350	530427	531350	gene=IY08_06335	protein=pseudouridine synthase	protein_id=KGT44841.1
gene	1191442	1192047	531442	532047	gene=IY08_06340	protein=membrane protein	protein_id=KGT44842.1
gene	1192085	1192912	532085	532912	gene=IY08_06345	protein=serine protease	protein_id=KGT44843.1
gene	1193378	1194706	533378	534706	gene=IY08_06350	protein=glycolate oxidase	protein_id=KGT44844.1
gene	1194703	1196115	534703	536115	gene=IY08_06355	protein=FAD-binding protein	protein_id=KGT44845.1
gene	1196233	1197348	536233	537348	gene=IY08_06360	protein=carbohydrate diacid regulator	protein_id=KGT44846.1
gene	1197485	1198459	537485	538459	gene=IY08_06365	protein=40-residue YVTN family beta-propeller	protein_id=KGT44847.1
gene	1198452	1199123	538452	539123	gene=IY08_06370	protein=transcriptional regulator	protein_id=KGT44848.1

gene	1199127	1200527	539127	540527	gene=IY08_06375	protein=histidine kinase	protein_id=KGT44849.1
gene	1200943	1201599	540943	541599	gene=IY08_06380	protein=GntR family transcriptional regulator	protein_id=KGT44850.1
gene	1201768	1202487	541768	542487	gene=IY08_06385	protein=Fe-S oxidoreductase	protein_id=KGT44851.1
gene	1202504	1203925	542504	543925	gene=IY08_06390	protein=amino acid dehydrogenase	protein_id=KGT44852.1
gene	1203925	1204635	543925	544635	gene=IY08_06395	protein=lactate utilization protein C	protein_id=KGT44853.1
gene	1204748	1205470	544748	545470	gene=IY08_06400	protein=peptidase A24	protein_id=KGT44854.1
gene	1205498	1205797	545498	545797	gene=IY08_06405	protein=hypothetical protein	protein_id=KGT44855.1
gene	1205825	1206676	545825	546676	gene=IY08_06410	protein=transporter	protein_id=KGT44856.1
gene	1206879	1207673	546879	547673	gene=IY08_06415	protein=membrane protein	protein_id=KGT44857.1
gene	1207968	1209287	547968	549287	gene=IY08_06420	protein=potassium transporter TrkH	protein_id=KGT44858.1
gene	1209402	1209587	549402	549587	gene=IY08_06425	protein=spore protein	protein_id=KGT44859.1
gene	1209735	1210178	549735	550178	gene=IY08_06430	protein=3-hydroxybutyryl-CoA dehydratase	protein_id=KGT44860.1
gene	1210280	1210804	550280	550804	gene=IY08_06435	protein=DNA recombinase	protein_id=KGT44861.1
gene	1210847	1211299	550847	551299	gene=IY08_06440	protein=PadR family transcriptional regulator	protein_id=KGT44862.1
gene	1211498	1211980	551498	551980	gene=IY08_06445	protein=PhaR protein	protein_id=KGT44863.1
gene	1212131	1212874	552131	552874	gene=IY08_06450	protein=3-oxoacyl-ACP synthase	protein_id=KGT44864.1
gene	1212958	1214043	552958	554043	gene=IY08_06455	protein=poly(R)-hydroxyalkanoic acid synthase	protein_id=KGT44865.1
gene	1214139	1215332	554139	555332	gene=IY08_06460	protein=oxidoreductase	protein_id=KGT44866.1
gene	1215356	1216705	555356	556705	gene=IY08_06465	protein=ATP synthase	protein_id=KGT44867.1
gene	1216744	1217079	556744	557079	gene=IY08_06470	protein=hypothetical protein	protein_id=KGT44868.1
gene	1217228	1217380	557228	557380	gene=IY08_06475	protein=stage 0 sporulation regulatory protein	protein_id=KGT44869.1
gene	1217609	1218685	557609	558685	gene=IY08_06480	protein=iron ABC transporter substrate-binding protein	protein_id=KGT44870.1
gene	1218706	1219707	558706	559707	gene=IY08_06485	protein=phosphonate ABC transporter ATP-binding protein	protein_id=KGT44871.1
gene	1219708	1221465	559708	561465	gene=IY08_06490	protein=phosphonate ABC transporter permease	protein_id=KGT44872.1
gene	1221487	1222281	561487	562281	gene=IY08_06495	protein=phosphonoacetaldehyde hydrolase	protein_id=KGT44873.1
gene	1222297	1223394	562297	563394	gene=IY08_06500	protein=2-aminoethylphosphonate--pyruvate	protein_id=KGT44874.1
gene	1223391	1224575	563391	564575	gene=IY08_06505	protein=saccharopine dehydrogenase	protein_id=KGT44875.1
gene	1224616	1225398	564616	565398	gene=IY08_06510	protein=cytochrome C	protein_id=KGT44876.1
gene	1225568	1225687	565568	565687	gene=IY08_06515	protein=hypothetical protein	protein_id=KGT44877.1
gene	1225820	1228120	565820	568120	gene=IY08_06520	protein=internalin	protein_id=KGT44878.1
gene	1228450	1229079	568450	569079	gene=IY08_06525	protein=hypothetical protein	protein_id=KGT44879.1

gene	1229206	1229829	569206	569829	gene=IY08_06530	protein=CBS domain-containing protein	protein_id=KGT44880.1
gene	1230003	1230773	570003	570773	gene=IY08_06535	protein=dihydroorotate dehydrogenase	protein_id=KGT44881.1
gene	1231250	1231531	571250	571531	gene=IY08_06540	protein=stage 0 sporulation protein	protein_id=KGT44882.1
gene	1231561	1233057	571561	573057	gene=IY08_06545	protein=histidine kinase	protein_id=KGT44883.1
gene	1233253	1233699	573253	573699	gene=IY08_06550	protein=MarR family transcriptional regulator	protein_id=KGT44884.1
gene	1233856	1235550	573856	575550	gene=IY08_06555	protein=oligoendopeptidase F	protein_id=KGT44885.1
gene	1235688	1236221	575688	576221	gene=IY08_06560	protein=Putrescine importer	protein_id=KGT44886.1
gene	1236323	1236439	576323	576439	gene=IY08_06570	protein=glutamate dehydrogenase	protein_id=KGT44887.1
gene	1236451	1237659	576451	577659	gene=IY08_06575	protein=sporulation kinase	protein_id=KGT44888.1
gene	1238003	1238665	578003	578665	gene=IY08_06580	protein=7-cyano-7-deazaguanine synthase	protein_id=KGT44889.1
gene	1238665	1239156	578665	579156	gene=IY08_06585	protein=6-pyruvoyl tetrahydrobiopterin synthase	protein_id=KGT44890.1
gene	1239149	1239865	579149	579865	gene=IY08_06590	protein=7-carboxy-7-deazaguanine synthase	protein_id=KGT44891.1
gene	1239884	1240381	579884	580381	gene=IY08_06595	protein=7-cyano-7-deazaguanine reductase	protein_id=KGT44892.1
gene	1240430	1240615	580430	580615	gene=IY08_06600	protein=hypothetical protein	protein_id=KGT44893.1
gene	1240698	1240772	580698	580772	gene=IY08_06605	protein=hypothetical protein	protein_id=KGT44894.1
gene	1240876	1241031	580876	581031	gene=IY08_06610	protein=ABC transporter permease	protein_id=KGT44895.1
gene	1241120	1241722	581120	581722	gene=IY08_06615	protein=phosphoglycerate mutase	protein_id=KGT44896.1
gene	1241758	1242336	581758	582336	gene=IY08_06620	protein=acetyltransferase	protein_id=KGT44897.1
gene	1242671	1242865	582671	582865	gene=IY08_06625	protein=abortive phage infection protein	protein_id=KGT44898.1
gene	1242965	1243282	582965	583282	gene=IY08_06630	protein=hypothetical protein	protein_id=KGT44899.1
gene	1243450	1243695	583450	583695	gene=IY08_06635	protein=hypothetical protein	protein_id=KGT44900.1
gene	1243760	1244119	583760	584119	gene=IY08_06640	protein=ribonucleotide reductase stimulatory protein	protein_id=KGT44901.1
gene	1244106	1246190	584106	586190	gene=IY08_06645	protein=ribonucleotide-diphosphate reductase subunit alpha	protein_id=KGT44902.1
gene	1247113	1247886	587113	587886	gene=IY08_06655	protein=nuclease	protein_id=KGT44903.1
gene	1248628	1249008	588628	589008	gene=IY08_06665	protein=GntR family transcriptional regulator	protein_id=KGT44904.1
gene	1249005	1249703	589005	589703	gene=IY08_06670	protein=ABC transporter	protein_id=KGT44905.1
gene	1249700	1250491	589700	590491	gene=IY08_06675	protein=ABC transporter permease	protein_id=KGT44906.1
gene	1250506	1251408	590506	591408	gene=IY08_06680	protein=ABC transporter ATP-binding protein	protein_id=KGT44907.1
gene	1251408	1252184	591408	592184	gene=IY08_06685	protein=ABC transporter permease	protein_id=KGT44908.1
gene	1252432	1253445	592432	593445	gene=IY08_06690	protein=AbrB family transcriptional regulator	protein_id=KGT44909.1
gene	1253475	1253657	593475	593657	gene=IY08_06695	protein=hypothetical protein	protein_id=KGT44910.1

gene	1253758	1254210	593758	594210	gene=IY08_06700	protein=AsnC family transcriptional regulator	protein_id=KGT44911.1
gene	1254337	1254747	594337	594747	gene=IY08_06705	protein=alkylhydroperoxidase	protein_id=KGT44912.1
gene	1254758	1255312	594758	595312	gene=IY08_06710	protein=isochorismatase	protein_id=KGT44913.1
gene	1255399	1255797	595399	595797	gene=IY08_06715	protein=SSEB protein	protein_id=KGT44914.1
gene	1255825	1256745	595825	596745	gene=IY08_06720	protein=peptidase U61 LD-carboxypeptidase A	protein_id=KGT44915.1
gene	1256861	1257949	596861	597949	gene=IY08_06725	protein=nitronate monooxygenase	protein_id=KGT44916.1
gene	1257971	1259146	597971	599146	gene=IY08_06730	protein=alanine transporter	protein_id=KGT44917.1
gene	1259143	1259382	599143	599382	gene=IY08_06735	protein=alanine-phosphoribitol ligase	protein_id=KGT44918.1
gene	1259451	1260626	599451	600626	gene=IY08_06740	protein=alanine transporter	protein_id=KGT44919.1
gene	1260623	1262137	600623	602137	gene=IY08_06745	protein=alanine-phosphoribitol ligase	protein_id=KGT44920.1
gene	1262150	1262296	602150	602296	gene=IY08_06750	protein=cytochrome C553	protein_id=KGT44921.1
gene	1262634	1263803	602634	603803	gene=IY08_06755	protein=N-acyl-L-amino acid amidohydrolase	protein_id=KGT44922.1
gene	1264028	1264210	604028	604210	gene=IY08_06760	protein=hypothetical protein	protein_id=KGT44923.1
gene	1264203	1264649	604203	604649	gene=IY08_06765	protein=flavodoxin	protein_id=KGT44924.1
gene	1264674	1265447	604674	605447	gene=IY08_06770	protein=hypothetical protein	protein_id=KGT44925.1
gene	1265546	1265707	605546	605707	gene=IY08_06775	protein=branched-chain amino acid aminotransferase	protein_id=KGT44926.1
gene	1265839	1266357	605839	606357	gene=IY08_06780	protein=biotin transporter BioY	protein_id=KGT44927.1
gene	1266441	1266590	606441	606590	gene=IY08_06785	protein=ketol-acid reductoisomerase	protein_id=KGT44928.1
gene	1266609	1266782	606609	606782	gene=IY08_06790	protein=2-isopropylmalate synthase	protein_id=KGT44929.1
gene	1266859	1268217	606859	608217	gene=IY08_06795	protein=multidrug transporter MatE	protein_id=KGT44930.1
gene	1268404	1269195	608404	609195	gene=IY08_06800	protein=UDP pyrophosphate phosphatase	protein_id=KGT44931.1
gene	1269225	1269779	609225	609779	gene=IY08_06805	protein=thioredoxin	protein_id=KGT44932.1
gene	1269846	1270277	609846	610277	gene=IY08_06810	protein=hypothetical protein	protein_id=KGT44933.1
gene	1270438	1270857	610438	610857	gene=IY08_06815	protein=MarR family transcriptional regulator	protein_id=KGT44934.1
gene	1271012	1271167	611012	611167	gene=IY08_06820	protein=imidazoleglycerol-phosphate dehydratase	protein_id=KGT44935.1
gene	1271190	1272425	611190	612425	gene=IY08_06825	protein=sodium:dicarboxylate symporter	protein_id=KGT44936.1
gene	1273705	1275048	613705	615048	gene=IY08_06830	protein=Ktr system potassium transporter B	protein_id=KGT44537.1
gene	1275084	1275458	615084	615458	gene=IY08_06835	protein=imidazole glycerol phosphate synthase	protein_id=KGT44538.1
gene	1275707	1276114	615707	616114	gene=IY08_06840	protein=spore protein	protein_id=KGT44539.1
gene	1276223	1276312	616223	616312	gene=IY08_06845	protein=phosphoribosyl-ATP pyrophosphatase	protein_id=KGT44540.1
gene	1276365	1276481	616365	616481	gene=IY08_06850	protein=hypothetical protein	protein_id=KGT44541.1

gene	1276665	1276904	616665	616904	gene=IY08_06855	protein=hypothetical protein	protein_id=KGT44542.1
gene	1276991	1277230	616991	617230	gene=IY08_06860	protein=hypothetical protein	protein_id=KGT44543.1
gene	1277290	1277460	617290	617460	gene=IY08_06865	protein=hypothetical protein	protein_id=KGT44544.1
gene	1277645	1278541	617645	618541	gene=IY08_06870	protein=branched-chain amino acid aminotransferase	protein_id=KGT44545.1
gene	1278857	1280557	618857	620557	gene=IY08_06875	protein=acetolactate synthase catalytic subunit	protein_id=KGT44546.1
gene	1280554	1281063	620554	621063	gene=IY08_06880	protein=acetolactate synthase	protein_id=KGT44547.1
gene	1281090	1282100	621090	622100	gene=IY08_06885	protein=ketol-acid reductoisomerase	protein_id=KGT44548.1
gene	1282102	1283622	622102	623622	gene=IY08_06890	protein=2-isopropylmalate synthase	protein_id=KGT44549.1
gene	1283700	1284764	623700	624764	gene=IY08_06895	protein=3-isopropylmalate dehydrogenase	protein_id=KGT44550.1
gene	1284764	1286158	624764	626158	gene=IY08_06900	protein=isopropylmalate isomerase	protein_id=KGT44551.1
gene	1286136	1286717	626136	626717	gene=leuD	protein=isopropylmalate isomerase	protein_id=KGT44552.1
gene	1287027	1288289	627027	628289	gene=IY08_06910	protein=ATP phosphoribosyltransferase	protein_id=KGT44553.1
gene	1288265	1288900	628265	628900	gene=IY08_06915	protein=ATP phosphoribosyltransferase	protein_id=KGT44554.1
gene	1288912	1290201	628912	630201	gene=IY08_06920	protein=histidinol dehydrogenase	protein_id=KGT44555.1
gene	1290201	1290785	630201	630785	gene=hisB	protein=imidazoleglycerol-phosphate dehydratase	protein_id=KGT44556.1
gene	1290786	1291415	630786	631415	gene=IY08_06930	protein=imidazole glycerol phosphate synthase subunit	protein_id=KGT44557.1
gene	1291388	1292107	631388	632107	gene=IY08_06935	protein=1-(5-phosphoribosyl)-5-	(5-phosphoribosylamino)m
gene	1292101	1292859	632101	632859	gene=IY08_06940	protein=imidazole glycerol phosphate synthase	protein_id=KGT44559.1
gene	1292856	1293161	632856	633161	gene=IY08_06945	protein=phosphoribosyl-AMP cyclohydrolase	protein_id=KGT44560.1
gene	1293172	1293495	633172	633495	gene=IY08_06950	protein=phosphoribosyl-ATP pyrophosphatase	protein_id=KGT44561.1
gene	1293508	1294524	633508	634524	gene=IY08_06955	protein=histidinol phosphatase	protein_id=KGT44562.1
gene	1294593	1294760	634593	634760	gene=IY08_06960	protein=hypothetical protein	protein_id=KGT44563.1
gene	1294905	1295876	634905	635876	gene=IY08_06965	protein=2-hydroxyacid dehydrogenase	protein_id=KGT44564.1
gene	1295907	1296608	635907	636608	gene=IY08_06970	protein=CDP-diacylglycerol--serine O-	protein_id=KGT44565.1
gene	1296797	1298683	636797	638683	gene=IY08_06975	protein=hypothetical protein	protein_id=KGT44566.1
gene	1298938	1299333	638938	639333	gene=IY08_06980	protein=hypothetical protein	protein_id=KGT44567.1
gene	1299785	1301101	639785	641101	gene=IY08_06985	protein=diaminopimelate decarboxylase	protein_id=KGT44568.1
gene	1301398	1301541	641398	641541	gene=IY08_06990	protein=hypothetical protein	protein_id=KGT44569.1
gene	1301629	1302333	641629	642333	gene=IY08_06995	protein=phosphoadenosine phosphosulfate reductase	protein_id=KGT44570.1
gene	1302373	1303509	642373	643509	gene=sat	protein=sulfate adenylyltransferase	protein_id=KGT44571.1
gene	1303522	1304115	643522	644115	gene=IY08_07005	protein=adenylylsulfate kinase	protein_id=KGT44572.1

gene	1304127	1305749	644127	645749	gene=IY08_07010	protein=ferredoxin--nitrite reductase	protein_id=KGT44573.1
gene	1305760	1305960	645760	645960	gene=IY08_07015	protein=hypothetical protein	protein_id=KGT44574.1
gene	1306045	1306821	646045	646821	gene=IY08_07020	protein=uroporphyrin-III methyltransferase	protein_id=KGT44575.1
gene	1306823	1307578	646823	647578	gene=IY08_07025	protein=cobalamin biosynthesis protein CbiX	protein_id=KGT44576.1
gene	1307553	1308167	647553	648167	gene=IY08_07030	protein=precorrin-2 dehydrogenase	protein_id=KGT44577.1
gene	1308287	1308430	648287	648430	gene=IY08_07035	protein=hypothetical protein	protein_id=KGT44578.1
gene	1308592	1309947	648592	649947	gene=IY08_07040	protein=hypothetical protein	protein_id=KGT44579.1
gene	1310241	1311515	650241	651515	gene=IY08_07050	protein=peptidase M24	protein_id=KGT44580.1
gene	1312011	1313285	652011	653285	gene=IY08_07055	protein=glutamate:protein symporter	protein_id=KGT44581.1
gene	1313354	1313872	653354	653872	gene=IY08_07060	protein=hypothetical protein	protein_id=KGT44582.1
gene	1314193	1315509	654193	655509	gene=IY08_07065	protein=sodium:proton antiporter	protein_id=KGT44583.1
gene	1315691	1316047	655691	656047	gene=IY08_07070	protein=flagellar basal body rod protein	protein_id=KGT44584.1
gene	1316095	1316757	656095	656757	gene=IY08_07075	protein=phage-shock protein	protein_id=KGT44585.1
gene	1316864	1317604	656864	657604	gene=IY08_07080	protein=transporter	protein_id=KGT44586.1
gene	1317604	1318659	657604	658659	gene=IY08_07085	protein=histidine kinase	protein_id=KGT44587.1
gene	1318656	1319288	658656	659288	gene=IY08_07090	protein=LuxR family transcriptional regulator	protein_id=KGT44588.1
gene	1319537	1319800	659537	659800	gene=IY08_07095	protein=hypothetical protein	protein_id=KGT44589.1
gene	1319825	1321180	659825	661180	gene=IY08_07100	protein=branched-chain amino acid transporter	protein_id=KGT44590.1
gene	1321766	1321975	661766	661975	gene=IY08_07105	protein=hypothetical protein	protein_id=KGT44591.1
gene	1322016	1322792	662016	662792	gene=IY08_07110	protein=SAM-dependent methyltransferase	protein_id=KGT44592.1
gene	1322901	1323755	662901	663755	gene=IY08_07115	protein=ribosomal protein L5 domain protein	protein_id=KGT44593.1
gene	1323863	1324060	663863	664060	gene=IY08_07120	protein=hypothetical protein	protein_id=KGT44594.1
gene	1324211	1325308	664211	665308	gene=IY08_07125	protein=membrane protein	protein_id=KGT44595.1
gene	1325423	1325941	665423	665941	gene=IY08_07130	protein=hypothetical protein	protein_id=KGT44596.1
gene	1326101	1327309	666101	667309	gene=IY08_07135	protein=dihydropteridine reductase	protein_id=KGT44597.1
gene	1327327	1327839	667327	667839	gene=IY08_07140	protein=Crp/Fnr family transcriptional regulator	protein_id=KGT44598.1
gene	1328010	1328237	668010	668237	gene=IY08_07145	protein=hypothetical protein	protein_id=KGT44599.1
gene	1328223	1328354	668223	668354	gene=IY08_07150	protein=hypothetical protein	protein_id=KGT44600.1
gene	1328531	1329331	668531	669331	gene=IY08_07155	protein=membrane protein	protein_id=KGT44601.1
gene	1329449	1330447	669449	670447	gene=IY08_07160	protein=inorganic phosphate transporter	protein_id=KGT44602.1
gene	1330459	1331079	670459	671079	gene=IY08_07165	protein=hypothetical protein	protein_id=KGT44603.1

gene	1331391	1333433	671391	673433	gene=IY08_07170	protein=peptidase	protein_id=KGT44604.1
gene	1333529	1333957	673529	673957	gene=IY08_07175	protein=hypothetical protein	protein_id=KGT44605.1
gene	1334174	1334443	674174	674443	gene=IY08_07180	protein=flagellar hook-length control protein FliK	protein_id=KGT44606.1
gene	1334666	1335937	674666	675937	gene=IY08_07185	protein=sporulation kinase	protein_id=KGT44607.1
gene	1336076	1336921	676076	676921	gene=IY08_07190	protein=hypothetical protein	protein_id=KGT44608.1
gene	1337137	1337331	677137	677331	gene=IY08_07200	protein=hypothetical protein	protein_id=KGT44609.1
gene	1337453	1337983	677453	677983	gene=IY08_07205	protein=integrase	protein_id=KGT44610.1
gene	1338091	1339905	678091	679905	gene=IY08_07210	protein=histidine kinase	protein_id=KGT44611.1
gene	1340214	1340921	680214	680921	gene=IY08_07215	protein=purine nucleoside phosphorylase DeoD-type	protein_id=KGT44612.1
gene	1341099	1341887	681099	681887	gene=IY08_07220	protein=hypothetical protein	protein_id=KGT44613.1
gene	1341892	1344471	681892	684471	gene=IY08_07225	protein=lysylcardiolipin synthase / lysyltransferase	protein_id=KGT44614.1
gene	1344653	1345042	684653	685042	gene=IY08_07230	protein=hypothetical protein	protein_id=KGT44615.1
gene	1345064	1345555	685064	685555	gene=IY08_07235	protein=hypothetical protein	protein_id=KGT44616.1
gene	1345661	1346575	685661	686575	gene=IY08_07240	protein=superoxide dismutase	protein_id=KGT44617.1
gene	1346688	1347812	686688	687812	gene=IY08_07245	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT44618.1
gene	1347805	1348401	687805	688401	gene=IY08_07250	protein=spore maturation protein	protein_id=KGT44619.1
gene	1348398	1348928	688398	688928	gene=IY08_07255	protein=spore maturation protein	protein_id=KGT44620.1
gene	1349218	1349946	689218	689946	gene=IY08_07260	protein=pseudouridine synthase	protein_id=KGT44621.1
gene	1350053	1350574	690053	690574	gene=IY08_07265	protein=thiol-disulfide oxidoreductase	protein_id=KGT44622.1
gene	1350696	1352321	690696	692321	gene=IY08_07270	protein=cytochrome C biogenesis protein	protein_id=KGT44623.1
gene	1352336	1353493	692336	693493	gene=IY08_07275	protein=cytochrome C biogenesis protein	protein_id=KGT44624.1
gene	1353797	1354513	693797	694513	gene=IY08_07280	protein=transcriptional regulator	protein_id=KGT44625.1
gene	1354546	1356288	694546	696288	gene=IY08_07285	protein=histidine kinase	protein_id=KGT44626.1
gene	1356425	1357006	696425	697006	gene=IY08_07290	protein=ATP:cob(I)alamin adenosyltransferase	protein_id=KGT44627.1
gene	1357092	1357706	697092	697706	gene=IY08_07295	protein=peptidase M23	protein_id=KGT44628.1
gene	1357871	1358557	697871	698557	gene=IY08_07300	protein=hypothetical protein	protein_id=KGT44629.1
gene	1359108	1359686	699108	699686	gene=IY08_07305	protein=riboflavin transporter FmnP	protein_id=KGT44630.1
gene	1359808	1360056	699808	700056	gene=IY08_07310	protein=ferredoxin	protein_id=KGT44631.1
gene	1360355	1361416	700355	701416	gene=IY08_07315	protein=ATP-dependent DNA helicase RecQ	protein_id=KGT44632.1
gene	1361406	1362935	701406	702935	gene=IY08_07320	protein=ATP-dependent DNA helicase RecQ	protein_id=KGT44633.1
gene	1362935	1363498	702935	703498	gene=IY08_07325	protein=CAAX protease	protein_id=KGT44634.1

gene	1363521	1364000	703521	704000	gene=IY08_07330	protein=peptidase M23B	protein_id=KGT44635.1
gene	1364068	1364844	704068	704844	gene=IY08_07335	protein=metallophosphoesterase	protein_id=KGT44636.1
gene	1364844	1365719	704844	705719	gene=IY08_07340	protein=MerR family transcriptional regulator	protein_id=KGT44637.1
gene	1365797	1366405	705797	706405	gene=IY08_07345	protein=adaptor protein	protein_id=KGT44638.1
gene	1366717	1368003	706717	708003	gene=IY08_07350	protein=glutamate dehydrogenase	protein_id=KGT44639.1
gene	1368084	1368293	708084	708293	gene=IY08_07355	protein=hypothetical protein	protein_id=KGT44640.1
gene	1368387	1368623	708387	708623	gene=IY08_07360	protein=hypothetical protein	protein_id=KGT44641.1
gene	1368703	1369233	708703	709233	gene=IY08_07365	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT44642.1
gene	1369342	1370322	709342	710322	gene=IY08_07370	protein=hypothetical protein	protein_id=KGT44643.1
gene	1370358	1371290	710358	711290	gene=IY08_07375	protein=asparaginase	protein_id=KGT44644.1
gene	1371513	1371686	711513	711686	gene=IY08_07380	protein=hypothetical protein	protein_id=KGT44645.1
gene	1371816	1372493	711816	712493	gene=IY08_07385	protein=cytidylate kinase	protein_id=KGT44646.1
gene	1372828	1373976	712828	713976	gene=IY08_07390	protein=30S ribosomal protein S1	protein_id=KGT44647.1
gene	1373989	1375038	713989	715038	gene=IY08_07395	protein=isopentenyl pyrophosphate isomerase	protein_id=KGT44648.1
gene	1375345	1375479	715345	715479	gene=IY08_07400	protein=hypothetical protein	protein_id=KGT44649.1
gene	1375597	1376208	715597	716208	gene=IY08_07405	protein=membrane protein	protein_id=KGT44650.1
gene	1376201	1377094	716201	717094	gene=IY08_07410	protein=membrane protein	protein_id=KGT44651.1
gene	1377091	1377276	717091	717276	gene=IY08_07415	protein=hypothetical protein	protein_id=KGT44652.1
gene	1377401	1378711	717401	718711	gene=engA	protein=GTP-binding protein Der	protein_id=KGT44653.1
gene	1378730	1379752	718730	719752	gene=IY08_07425	protein=glycerol-3-phosphate dehydrogenase	protein_id=KGT44654.1
gene	1379869	1380120	719869	720120	gene=IY08_07430	protein=ATP synthase	protein_id=KGT44655.1
gene	1380388	1380591	720388	720591	gene=IY08_07435	protein=hypothetical protein	protein_id=KGT44656.1
gene	1380655	1381365	720655	721365	gene=IY08_07440	protein=hypothetical protein	protein_id=KGT44657.1
gene	1381611	1383089	721611	723089	gene=IY08_07445	protein=stage IV sporulation protein A	protein_id=KGT44658.1
gene	1383388	1383660	723388	723660	gene=IY08_07450	protein=DNA-binding protein	protein_id=KGT44659.1
gene	1384533	1385267	724533	725267	gene=IY08_07460	protein=heptaprenyl diphosphate synthase	protein_id=KGT44660.1
gene	1385306	1386019	725306	726019	gene=IY08_07465	protein=ubiquinone biosynthesis methyltransferase UbiE	protein_id=KGT44661.1
gene	1386051	1387013	726051	727013	gene=IY08_07470	protein=heptaprenyl diphosphate synthase	protein_id=KGT44662.1
gene	1387138	1387584	727138	727584	gene=IY08_07475	protein=nucleoside diphosphate kinase	protein_id=KGT44663.1
gene	1387849	1389021	727849	729021	gene=IY08_07480	protein=chorismate synthase	protein_id=KGT44664.1
gene	1389021	1390106	729021	730106	gene=IY08_07485	protein=3-dehydroquinate synthase	protein_id=KGT44665.1

gene	1390239	1391351	730239	731351	gene=IY08_07490	protein=histidinol-phosphate aminotransferase	protein_id=KGT44666.1
gene	1391680	1392942	731680	732942	gene=IY08_07495	protein=TPR repeat-containing protein	protein_id=KGT44667.1
gene	1393016	1393552	733016	733552	gene=IY08_07500	protein=hypothetical protein	protein_id=KGT44668.1
gene	1393707	1394168	733707	734168	gene=IY08_07505	protein=hypothetical protein	protein_id=KGT44669.1
gene	1394306	1394818	734306	734818	gene=IY08_07510	protein=menaquinol-cytochrome C reductase	protein_id=KGT44670.1
gene	1394819	1395493	734819	735493	gene=IY08_07515	protein=cytochrome b6	protein_id=KGT44671.1
gene	1395537	1396304	735537	736304	gene=IY08_07520	protein=cytochrome Cbb3	protein_id=KGT44672.1
gene	1396441	1397013	736441	737013	gene=IY08_07525	protein=membrane protein	protein_id=KGT44673.1
gene	1397039	1397725	737039	737725	gene=IY08_07530	protein=membrane protein	protein_id=KGT44674.1
gene	1397833	1398621	737833	738621	gene=IY08_07535	protein=sporulation protein	protein_id=KGT44675.1
gene	1398726	1399406	738726	739406	gene=IY08_07540	protein=flagellar biosynthesis anti-sigma factor FlgM	protein_id=KGT44676.1
gene	1399509	1400150	739509	740150	gene=IY08_07545	protein=uracil-DNA glycosylase	protein_id=KGT44677.1
gene	1400179	1401060	740179	741060	gene=IY08_07550	protein=membrane protein	protein_id=KGT44678.1
gene	1401268	1401462	741268	741462	gene=IY08_07555	protein=hypothetical protein	protein_id=KGT44679.1
gene	1401511	1401882	741511	741882	gene=IY08_07560	protein=nucleotide pyrophosphohydrolase	protein_id=KGT44680.1
gene	1401882	1402682	741882	742682	gene=IY08_07565	protein=dihydrodipicolinate reductase	protein_id=KGT44681.1
gene	1402697	1403092	742697	743092	gene=IY08_07570	protein=methylglyoxal synthase	protein_id=KGT44682.1
gene	1403104	1403808	743104	743808	gene=IY08_07575	protein=deacetylase	protein_id=KGT44683.1
gene	1403805	1404950	743805	744950	gene=IY08_07580	protein=N-acetyl-alpha-D-glucosaminyl L-malate synthase	protein_id=KGT44684.1
gene	1404937	1406130	744937	746130	gene=IY08_07585	protein=tRNA CCA-pyrophosphorylase	protein_id=KGT44685.1
gene	1406115	1407095	746115	747095	gene=IY08_07590	protein=biotin--acetyl-CoA-carboxylase ligase	protein_id=KGT44686.1
gene	1407223	1407612	747223	747612	gene=IY08_07595	protein=cytochrome B561	protein_id=KGT44687.1
gene	1408096	1408932	748096	748932	gene=IY08_07605	protein=3-methyl-2-oxobutanoate	protein_id=KGT44688.1
gene	1408932	1409780	748932	749780	gene=IY08_07610	protein=pantoate--beta-alanine ligase	protein_id=KGT44689.1
gene	1409793	1410176	749793	750176	gene=IY08_07615	protein=aspartate decarboxylase	protein_id=KGT44690.1
gene	1410308	1413112	750308	753112	gene=IY08_07620	protein=ATP-dependent DNA helicase	protein_id=KGT44691.1
gene	1413363	1413533	753363	753533	gene=IY08_07625	protein=hypothetical protein	protein_id=KGT44692.1
gene	1413541	1414044	753541	754044	gene=IY08_07630	protein=peptidase M4	protein_id=KGT44693.1
gene	1414063	1415250	754063	755250	gene=IY08_07635	protein=aspartate aminotransferase	protein_id=KGT44694.1
gene	1415371	1416078	755371	756078	gene=IY08_07640	protein=DNA replication protein DnaD	protein_id=KGT44695.1
gene	1416094	1416741	756094	756741	gene=IY08_07645	protein=endonuclease III	protein_id=KGT44696.1

gene	1416745	1417248	756745	757248	gene=IY08_07650	protein=GTPase	protein_id=KGT44697.1
gene	1417290	1419989	757290	759989	gene=IY08_07655	protein=penicillin-binding protein	protein_id=KGT44698.1
gene	1420056	1420658	760056	760658	gene=IY08_07660	protein=Holliday junction resolvase	protein_id=KGT44699.1
gene	1420762	1421787	760762	761787	gene=IY08_07665	protein=hypothetical protein	protein_id=KGT44700.1
gene	1422204	1422446	762204	762446	gene=IY08_07675	protein=hypothetical protein	protein_id=KGT44701.1
gene	1422462	1422806	762462	762806	gene=IY08_07680	protein=hypothetical protein	protein_id=KGT44702.1
gene	1422833	1423024	762833	763024	gene=IY08_07685	protein=hypothetical protein	protein_id=KGT44703.1
gene	1423202	1423738	763202	763738	gene=IY08_07690	protein=spore coat protein	protein_id=KGT44704.1
gene	1423893	1424321	763893	764321	gene=IY08_07695	protein=spore coat protein	protein_id=KGT44705.1
gene	1424378	1424932	764378	764932	gene=IY08_07700	protein=hypothetical protein	protein_id=KGT44706.1
gene	1425031	1425366	765031	765366	gene=IY08_07705	protein=cell division protein GpsB	protein_id=KGT44707.1
gene	1425449	1425854	765449	765854	ncRNA		
gene	1426024	1427163	766024	767163	gene=IY08_07710	protein=RNA methyltransferase	protein_id=KGT44708.1
gene	1427225	1427407	767225	767407	gene=IY08_07715	protein=hypothetical protein	protein_id=KGT44709.1
gene	1427546	1429483	767546	769483	gene=IY08_07720	protein=ATP-dependent helicase	protein_id=KGT44710.1
gene	1429585	1431102	769585	771102	gene=IY08_07725	protein=peptidase M32	protein_id=KGT44711.1
gene	1431151	1431624	771151	771624	gene=IY08_07730	protein=acetyltransferase	protein_id=KGT44712.1
gene	1431782	1432528	771782	772528	gene=IY08_07735	protein=methionine aminopeptidase	protein_id=KGT44713.1
gene	1432855	1433448	772855	773448	gene=IY08_07740	protein=xanthine phosphoribosyltransferase	protein_id=KGT44714.1
gene	1433452	1434774	773452	774774	gene=IY08_07745	protein=xanthine permease	protein_id=KGT44715.1
gene	1434790	1435953	774790	775953	gene=IY08_07750	protein=membrane protein	protein_id=KGT44716.1
gene	1436502	1440161	776502	780161	gene=IY08_07760	protein=GTPase	protein_id=KGT44717.1
gene	1440165	1440419	780165	780419	gene=IY08_07765	protein=hypothetical protein	protein_id=KGT44718.1
gene	1440492	1440959	780492	780959	gene=IY08_07770	protein=acetyltransferase	protein_id=KGT44719.1
gene	1440980	1441252	780980	781252	gene=IY08_07775	protein=hypothetical protein	protein_id=KGT44720.1
gene	1441255	1442088	781255	782088	gene=IY08_07780	protein=3-mercaptopyruvate sulfurtransferase	protein_id=KGT44721.1
gene	1442647	1443096	782647	783096	gene=IY08_07785	protein=hypothetical protein	protein_id=KGT44722.1
gene	1443180	1443491	783180	783491	gene=IY08_07790	protein=lipoprotein	protein_id=KGT44723.1
gene	1443495	1444733	783495	784733	gene=IY08_07795	protein=glutathionylspermidine synthase	protein_id=KGT44724.1
gene	1444726	1445112	784726	785112	gene=IY08_07800	protein=cell surface protein	protein_id=KGT44725.1
gene	1445827	1446552	785827	786552	gene=IY08_07805	protein=magnesium transporter	protein_id=KGT44726.1

gene	1446685	1447551	786685	787551	gene=IY08_07810	protein=5'-3' exonuclease	protein_id=KGT44727.1
gene	1447907	1448047	787907	788047	gene=IY08_07815	protein=hypothetical protein	protein_id=KGT44728.1
gene	1448376	1449569	788376	789569	gene=IY08_07820	protein=acetyltransferase	protein_id=KGT44729.1
gene	1449570	1450313	789570	790313	gene=IY08_07825	protein=capsule biosynthesis protein CapK	protein_id=KGT44730.1
gene	1450300	1450920	790300	790920	gene=IY08_07830	protein=tyrosine protein kinase	protein_id=KGT44731.1
gene	1450939	1451577	790939	791577	gene=IY08_07835	protein=capsular biosynthesis protein	protein_id=KGT44732.1
gene	1451634	1453070	791634	793070	gene=IY08_07840	protein=sugar translocase	protein_id=KGT44733.1
gene	1453074	1454288	793074	794288	gene=IY08_07845	protein=polysaccharide polymerase	protein_id=KGT44734.1
gene	1454263	1455063	794263	795063	gene=IY08_07850	protein=glycosyl transferase	protein_id=KGT44735.1
gene	1455060	1456112	795060	796112	gene=IY08_07855	protein=mannosyl transferase	protein_id=KGT44736.1
gene	1456205	1457752	796205	797752	gene=IY08_07860	protein=hypothetical protein	protein_id=KGT44737.1
gene	1457865	1472897	797865	812897	gene=IY08_07865	protein=cell surface protein	protein_id=KGT44738.1
gene	1473020	1473880	813020	813880	gene=IY08_07870	protein=acetyltransferase	protein_id=KGT44739.1
gene	1473922	1474482	813922	814482	gene=IY08_07875	protein=isochorismatase	protein_id=KGT44740.1
gene	1474665	1474925	814665	814925	gene=IY08_07880	protein=hypothetical protein	protein_id=KGT44741.1
gene	1474928	1475833	814928	815833	gene=IY08_07885	protein=membrane protein	protein_id=KGT44742.1
gene	1475847	1476233	815847	816233	gene=rnhA	protein=ribonuclease H	protein_id=KGT44743.1
gene	1476303	1477175	816303	817175	gene=IY08_07895	protein=LACX protein	protein_id=KGT44744.1
gene	1477358	1477843	817358	817843	gene=IY08_07900	protein=membrane protein	protein_id=KGT44745.1
gene	1477995	1478654	817995	818654	gene=IY08_07905	protein=hypothetical protein	protein_id=KGT44746.1
gene	1478667	1478843	818667	818843	gene=IY08_07910	protein=hypothetical protein	protein_id=KGT44747.1
gene	1478877	1479125	818877	819125	gene=IY08_07915	protein=hypothetical protein	protein_id=KGT44748.1
gene	1479245	1479442	819245	819442	gene=IY08_07920	protein=cold-shock protein	protein_id=KGT44749.1
gene	1479705	1480433	819705	820433	gene=IY08_07925	protein=YqcI/YcgG family protein	protein_id=KGT44750.1
gene	1480559	1481191	820559	821191	gene=IY08_07930	protein=amino acid transporter	protein_id=KGT44751.1
gene	1481211	1481504	821211	821504	gene=IY08_07935	protein=cytoplasmic protein	protein_id=KGT44752.1
gene	1481583	1482212	821583	822212	gene=IY08_07940	protein=fatty acid hydroxylase	protein_id=KGT44753.1
gene	1482435	1482776	822435	822776	gene=IY08_07945	protein=membrane protein	protein_id=KGT44754.1
gene	1482833	1483757	822833	823757	gene=IY08_07950	protein=symporter	partial=3'
gene	1483827	1484360	823827	824360	gene=IY08_07960	protein=symporter	partial=5'
gene	1484549	1485901	824549	825901	gene=IY08_07965	protein=aminotransferase	protein_id=KGT44496.1

gene	1485985	1486263	825985	826263	gene=IY08_07970	protein=hypothetical protein	protein_id=KGT44497.1
gene	1486327	1487490	826327	827490	gene=IY08_07975	protein=sodium:proton antiporter	protein_id=KGT44498.1
gene	1487824	1489497	827824	829497	gene=IY08_07980	protein=ribonuclease J	protein_id=KGT44499.1
gene	1489591	1490436	829591	830436	gene=IY08_07985	protein=MerR family transcriptional regulator	protein_id=KGT44500.1
gene	1490569	1491924	830569	831924	gene=IY08_07990	protein=multidrug transporter MatE	protein_id=KGT44501.1
gene	1491959	1492624	831959	832624	gene=IY08_07995	protein=membrane protein	protein_id=KGT44502.1
gene	1492786	1493364	832786	833364	gene=IY08_08000	protein=cytoplasmic protein	protein_id=KGT44503.1
gene	1493512	1493829	833512	833829	gene=IY08_08005	protein=membrane protein	protein_id=KGT44504.1
gene	1493979	1494713	833979	834713	gene=IY08_08010	protein=NADPH-dependent oxidoreductase	protein_id=KGT44505.1
gene	1495090	1495815	835090	835815	gene=IY08_08015	protein=membrane protein	protein_id=KGT44506.1
gene	1496037	1497236	836037	837236	gene=IY08_08020	protein=macrolide transporter	protein_id=KGT44507.1
gene	1497244	1497711	837244	837711	gene=IY08_08025	protein=glyoxalase	protein_id=KGT44508.1
gene	1497879	1497998	837879	837998	gene=IY08_08030	protein=hypothetical protein	protein_id=KGT44509.1
gene	1498231	1498449	838231	838449	gene=IY08_08035	protein=stage 0 sporulation regulatory protein	protein_id=KGT44510.1
gene	1498503	1498691	838503	838691	gene=IY08_08040	protein=Fe-S cluster assembly protein HesB	protein_id=KGT44511.1
gene	1498719	1499321	838719	839321	gene=IY08_08045	protein=HAD family hydrolase	protein_id=KGT44512.1
gene	1499494	1500327	839494	840327	gene=IY08_08050	protein=flagellar motor protein MotP	protein_id=KGT44513.1
gene	1500347	1501024	840347	841024	gene=IY08_08055	protein=flagellar motor protein MotS	protein_id=KGT44514.1
gene	1501175	1501543	841175	841543	gene=IY08_08060	protein=chemotaxis protein CheY	protein_id=KGT44515.1
gene	1501673	1503691	841673	843691	gene=IY08_08065	protein=chemotaxis protein CheA	protein_id=KGT44516.1
gene	1503861	1505498	843861	845498	gene=IY08_08070	protein=flagellar motor switch protein	protein_id=KGT44517.1
gene	1505528	1506904	845528	846904	gene=IY08_08075	protein=transglycosylase	protein_id=KGT44518.1
gene	1506932	1507648	846932	847648	gene=IY08_08080	protein=hypothetical protein	protein_id=KGT44519.1
gene	1507680	1508462	847680	848462	gene=IY08_08085	protein=chemotaxis protein CheR	protein_id=KGT44520.1
gene	1508502	1508999	848502	848999	gene=IY08_08090	protein=flagellar motor switch protein FliG	protein_id=KGT44521.1
gene	1509143	1509607	849143	849607	gene=IY08_08095	protein=UDP-N-acetylenolpyruvoylglucosamine reductase	protein_id=KGT44522.1
gene	1509623	1510075	849623	850075	gene=IY08_08100	protein=hypothetical protein	protein_id=KGT44523.1
gene	1510093	1511391	850093	851391	gene=flgK	protein=flagellar hook protein FlgK	protein_id=KGT44524.1
gene	1511433	1512296	851433	852296	gene=flgL	protein=flagellar hook protein FlgL	protein_id=KGT44525.1
gene	1512316	1513698	852316	853698	gene=fliD	protein=flagellar capping protein	protein_id=KGT44526.1
gene	1513721	1514089	853721	854089	gene=IY08_08120	protein=flagellar biosynthesis protein FliS	protein_id=KGT44527.1

gene	1514079	1514351	854079	854351	gene=IY08_08125	protein=flagellar basal body rod protein FlgG	protein_id=KGT44528.1
gene	1514712	1515119	854712	855119	gene=flgB	protein=flagellar basal body rod protein FlgB	protein_id=KGT44529.1
gene	1515141	1515554	855141	855554	gene=IY08_08135	protein=flagellar basal body rod protein FlgC	protein_id=KGT44530.1
gene	1515571	1515870	855571	855870	gene=fliE	protein=flagellar hook-basal body protein FliE	protein_id=KGT44531.1
gene	1515893	1517467	855893	857467	gene=IY08_08145	protein=flagellar M-ring protein FliF	protein_id=KGT44532.1
gene	1517481	1518485	857481	858485	gene=IY08_08150	protein=flagellar motor switch protein FliG	protein_id=KGT44533.1
gene	1518472	1519161	858472	859161	gene=fliH	protein=flagellar assembly protein H	protein_id=KGT44534.1
gene	1519158	1520462	859158	860462	gene=fliI	protein=ATP synthase	protein_id=KGT44535.1
gene	1520615	1520754	860615	860754	gene=IY08_08165	protein=cytoplasmic protein	partial=3'
gene	1520790	1521017	860790	861017	gene=IY08_08170	protein=cytoplasmic protein	partial=5'
gene	1521028	1522137	861028	862137	gene=IY08_08175	protein=hypothetical protein	protein_id=KGT44476.1
gene	1522141	1522719	862141	862719	gene=flgD	protein=flagellar basal body rod modification protein	protein_id=KGT44477.1
gene	1522736	1523959	862736	863959	gene=IY08_08185	protein=flagellar hook protein FlgE	protein_id=KGT44478.1
gene	1524009	1524344	864009	864344	gene=IY08_08190	protein=hypothetical protein	protein_id=KGT44479.1
gene	1524559	1525044	864559	865044	gene=IY08_08195	protein=LysR family transcriptional regulator	protein_id=KGT44480.1
gene	1525168	1526076	865168	866076	gene=IY08_08200	protein=chemotaxis protein CheV	protein_id=KGT44481.1
gene	1526818	1527765	866818	867765	gene=IY08_08205	protein=motility gene repressor MogR	protein_id=KGT44482.1
gene	1527861	1528661	867861	868661	gene=IY08_08210	protein=flagellin	protein_id=KGT44483.1
gene	1528913	1530007	868913	870007	gene=IY08_08215	protein=flagellin	protein_id=KGT44484.1
gene	1530265	1531050	870265	871050	gene=IY08_08220	protein=lytic transglycosylase	protein_id=KGT44485.1
gene	1531113	1531337	871113	871337	gene=IY08_08225	protein=flagellar motor switch protein	protein_id=KGT44486.1
gene	1531352	1532338	871352	872338	gene=IY08_08230	protein=flagellar motor switch protein FliM	protein_id=KGT44487.1
gene	1532349	1532708	872349	872708	gene=IY08_08235	protein=flagellar motor switch protein	protein_id=KGT44488.1
gene	1532721	1533041	872721	873041	gene=IY08_08240	protein=flagellar motor switch protein FliN	protein_id=KGT44489.1
gene	1533038	1533796	873038	873796	gene=IY08_08245	protein=flagellar biosynthesis protein flip	protein_id=KGT44490.1
gene	1533830	1534105	873830	874105	gene=IY08_08250	protein=flagellar biosynthesis protein FliQ	protein_id=KGT44491.1
gene	1534121	1534882	874121	874882	gene=IY08_08255	protein=flagellar biosynthesis protein FliR	protein_id=KGT44492.1
gene	1534893	1535939	874893	875939	gene=IY08_08260	protein=flagellar biosynthesis protein FlhB	protein_id=KGT44493.1
gene	1536104	1537228	876104	877228	gene=IY08_08265	protein=flagellar biosynthesis protein FlhA	partial=3'
gene	1537285	1538065	877285	878065	gene=IY08_08270	protein=flagellar biosynthesis protein FlhA	frame=2
gene	1538080	1539399	878080	879399	gene=flhF	protein=flagellar biosynthesis regulator FlhF	protein_id=KGT44401.1

gene	1539472	1540215	879472	880215	gene=flgG	protein=flagellar basal body rod protein FlgG	protein_id=KGT44402.1
gene	1540333	1541043	880333	881043	gene=IY08_08285	protein=alanyl tRNA synthetase	protein_id=KGT44403.1
gene	1541061	1541897	881061	881897	gene=IY08_08290	protein=transcriptional regulator	protein_id=KGT44404.1
gene	1541890	1542615	881890	882615	gene=IY08_08295	protein=branched-chain amino acid ABC transporter	protein_id=KGT44405.1
gene	1542606	1542917	882606	882917	gene=IY08_08300	protein=branched-chain amino acid ABC transporter	protein_id=KGT44406.1
gene	1542980	1543150	882980	883150	gene=IY08_08305	protein=hypothetical protein	protein_id=KGT44407.1
gene	1543176	1543535	883176	883535	gene=IY08_08310	protein=hypothetical protein	protein_id=KGT44408.1
gene	1543651	1544235	883651	884235	gene=IY08_08315	protein=DeoR family transcriptional regulator	protein_id=KGT44409.1
gene	1544238	1544573	884238	884573	gene=IY08_08320	protein=JEMB protein	protein_id=KGT44410.1
gene	1544758	1544937	884758	884937	gene=IY08_08325	protein=spore protein	protein_id=KGT44411.1
gene	1545004	1546218	885004	886218	gene=IY08_08330	protein=DNA-binding protein	protein_id=KGT44412.1
gene	1546338	1547606	886338	887606	gene=IY08_08335	protein=permease	protein_id=KGT44413.1
gene	1547725	1548249	887725	888249	gene=IY08_08340	protein=lipoprotein	protein_id=KGT44414.1
gene	1548290	1549183	888290	889183	gene=IY08_08345	protein=LysR family transcriptional regulator	protein_id=KGT44415.1
gene	1549346	1550338	889346	890338	gene=IY08_08350	protein=ABC transporter ATP-binding protein	protein_id=KGT44416.1
gene	1550316	1551341	890316	891341	gene=IY08_08355	protein=ABC transporter substrate-binding protein	protein_id=KGT44417.1
gene	1551354	1553024	891354	893024	gene=IY08_08360	protein=ABC transporter permease	protein_id=KGT44418.1
gene	1553021	1554283	893021	894283	gene=IY08_08365	protein=metallo-beta-lactamase	protein_id=KGT44419.1
gene	1554304	1555137	894304	895137	gene=IY08_08370	protein=hypothetical protein	protein_id=KGT44420.1
gene	1555192	1555614	895192	895614	gene=IY08_08375	protein=hypothetical protein	protein_id=KGT44421.1
gene	1555838	1555999	895838	895999	gene=IY08_08380	protein=peptidase	protein_id=KGT44422.1
gene	1556177	1557268	896177	897268	gene=IY08_08385	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT44423.1
gene	1557385	1557960	897385	897960	gene=IY08_08390	protein=phosphoglycerate mutase	protein_id=KGT44424.1
gene	1558050	1558421	898050	898421	gene=IY08_08395	protein=hypothetical protein	protein_id=KGT44425.1
gene	1558461	1559372	898461	899372	gene=IY08_08400	protein=alpha/beta hydrolase	protein_id=KGT44426.1
gene	1559333	1559662	899333	899662	gene=IY08_08405	protein=sodium:proton antiporter	protein_id=KGT44427.1
gene	1559646	1560056	899646	900056	gene=IY08_08410	protein=MarR family transcriptional regulator	protein_id=KGT44428.1
gene	1560179	1561006	900179	901006	gene=IY08_08415	protein=hypothetical protein	protein_id=KGT44429.1
gene	1561049	1562872	901049	902872	gene=IY08_08420	protein=asparagine synthase	protein_id=KGT44430.1
gene	1563134	1563700	903134	903700	gene=IY08_08425	protein=RNA polymerase factor sigma-70	protein_id=KGT44431.1
gene	1563697	1564803	903697	904803	gene=IY08_08430	protein=ECF-type sigma factor negative effector	protein_id=KGT44432.1

gene	1564843	1565916	904843	905916	gene=IY08_08435	protein=glycosyl hydrolase	protein_id=KGT44433.1
gene	1566128	1567027	906128	907027	gene=IY08_08440	protein=cation transporter	protein_id=KGT44434.1
gene	1567221	1567391	907221	907391	gene=IY08_08445	protein=histidine kinase	protein_id=KGT44435.1
gene	1567448	1568119	907448	908119	gene=IY08_08450	protein=GntR family transcriptional regulator	protein_id=KGT44436.1
gene	1568136	1569101	908136	909101	gene=IY08_08455	protein=transporter	protein_id=KGT44437.1
gene	1569237	1569548	909237	909548	gene=IY08_08460	protein=multidrug ABC transporter permease	protein_id=KGT44438.1
gene	1569584	1570771	909584	910771	gene=IY08_08465	protein=cobalamin biosynthesis protein CobW	protein_id=KGT44439.1
gene	1570955	1571932	910955	911932	gene=IY08_08470	protein=membrane protein	protein_id=KGT44440.1
gene	1571946	1572830	911946	912830	gene=IY08_08475	protein=hypothetical protein	protein_id=KGT44441.1
gene	1572943	1573602	912943	913602	gene=IY08_08480	protein=hypothetical protein	protein_id=KGT44442.1
gene	1574065	1575468	914065	915468	gene=IY08_08485	protein=antiporter	protein_id=KGT44443.1
gene	1575509	1575889	915509	915889	gene=IY08_08490	protein=MerR family transcriptional regulator	protein_id=KGT44444.1
gene	1575906	1576616	915906	916616	gene=IY08_08495	protein=short-chain dehydrogenase	protein_id=KGT44445.1
gene	1576808	1578196	916808	918196	gene=IY08_08500	protein=fumarate hydratase	protein_id=KGT44446.1
gene	1578292	1578714	918292	918714	gene=IY08_08505	protein=hypothetical protein	protein_id=KGT44447.1
gene	1578878	1579039	918878	919039	gene=IY08_08510	protein=hypothetical protein	protein_id=KGT44448.1
gene	1579405	1580169	919405	920169	gene=IY08_08515	protein=transcriptional regulator	protein_id=KGT44449.1
gene	1580267	1581676	920267	921676	gene=IY08_08520	protein=multidrug transporter MatE	protein_id=KGT44450.1
gene	1581733	1582431	921733	922431	gene=IY08_08525	protein=peptidase	protein_id=KGT44451.1
gene	1582824	1583219	922824	923219	gene=IY08_08530	protein=hypothetical protein	protein_id=KGT44452.1
gene	1583330	1583746	923330	923746	gene=IY08_08535	protein=transcriptional regulator	protein_id=KGT44453.1
gene	1583748	1584560	923748	924560	gene=IY08_08540	protein=cell surface protein	protein_id=KGT44454.1
gene	1584614	1585333	924614	925333	pseudo		
gene	1585346	1585900	925346	925900	gene=IY08_08550	protein=thiol:disulfide interchange protein	protein_id=KGT44455.1
gene	1585918	1586598	925918	926598	gene=IY08_08555	protein=diacylglycerol transferase	protein_id=KGT44456.1
gene	1586839	1587933	926839	927933	gene=IY08_08565	protein=histidine kinase	protein_id=KGT44457.1
gene	1588077	1588253	928077	928253	gene=IY08_08570	protein=ATPase	protein_id=KGT44458.1
gene	1588293	1588838	928293	928838	gene=IY08_08575	protein=DNA-binding protein	protein_id=KGT44459.1
gene	1588989	1590320	928989	930320	gene=IY08_08580	protein=serine ammonia-lyase	protein_id=KGT44460.1
gene	1590475	1591722	930475	931722	gene=IY08_08585	protein=hypothetical protein	protein_id=KGT44461.1
gene	1591753	1592709	931753	932709	gene=IY08_08590	protein=exosporium protein E	protein_id=KGT44462.1

gene	1592706	1593776	932706	933776	gene=IY08_08595	protein=multi-TM2 domain-containing protein	protein_id=KGT44463.1
gene	1593769	1594212	933769	934212	gene=IY08_08600	protein=hypothetical protein	protein_id=KGT44464.1
gene	1594209	1594547	934209	934547	gene=IY08_08605	protein=RNA polymerase sigma factor SigW	protein_id=KGT44465.1
gene	1594939	1595613	934939	935613	gene=IY08_08610	protein=LuxR family transcriptional regulator	protein_id=KGT44466.1
gene	1595618	1596718	935618	936718	gene=IY08_08615	protein=histidine kinase	protein_id=KGT44467.1
gene	1596855	1597793	936855	937793	gene=IY08_08620	protein=antibiotic ABC transporter ATP-binding protein	protein_id=KGT44468.1
gene	1597831	1598940	937831	938940	gene=IY08_08625	protein=ABC transporter permease	protein_id=KGT44469.1
gene	1598942	1600087	938942	940087	gene=IY08_08630	protein=ABC transporter permease	protein_id=KGT44470.1
gene	1600132	1601070	940132	941070	gene=IY08_08635	protein=acetyltransferase	protein_id=KGT44471.1
gene	1601188	1602399	941188	942399	gene=IY08_08640	protein=cardiolipin synthetase	protein_id=KGT44472.1
gene	1602453	1603196	942453	943196	gene=pyrH	protein=uridylate kinase	protein_id=KGT44473.1
gene	1603573	1604597	943573	944597	gene=IY08_08650	protein=glutamate:protein symporter	protein_id=KGT44474.1
gene	1604650	1604874	944650	944874	gene=IY08_08655	protein=glutamate:protein symporter	protein_id=KGT44398.1
gene	1604899	1605048	944899	945048	gene=IY08_08660	protein=AnsB (L-aspartase AnsB)	protein_id=KGT44399.1
gene	1605059	1605600	945059	945600	gene=aspA	protein=aspartate ammonia-lyase	protein_id=KGT44397.1]
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gene	1605601	1605991	1	391	gene=aspA	protein=aspartate ammonia-lyase	protein_id=KGT44374.1]
gene	1606067	1607779	467	2179	gene=IY08_08675	protein=malate dehydrogenase	protein_id=KGT44375.1
gene	1607852	1609141	2252	3541	gene=IY08_08680	protein=histidine kinase	protein_id=KGT44376.1
gene	1609144	1610076	3544	4476	gene=IY08_08685	protein=transcriptional regulator	protein_id=KGT44377.1
gene	1610195	1613389	4595	7789	gene=IY08_08695	protein=helicase SNF	protein_id=KGT44378.1
gene	1613488	1613622	7888	8022	gene=IY08_08700	protein=hypothetical protein	protein_id=KGT44379.1
gene	1613724	1613897	8124	8297	gene=IY08_08705	protein=hypothetical protein	protein_id=KGT44380.1
gene	1614146	1614340	8546	8740	gene=IY08_08710	protein=hypothetical protein	protein_id=KGT44381.1
gene	1614358	1615341	8758	9741	gene=IY08_08715	protein=asparagine synthase	protein_id=KGT44382.1
gene	1615400	1615852	9800	10252	gene=IY08_08720	protein=glyoxalase	protein_id=KGT44383.1
gene	1616079	1617308	10479	11708	gene=IY08_08725	protein=aspartate kinase	protein_id=KGT44384.1
gene	1617431	1617618	11831	12018	pseudo		
gene	1617890	1618798	12290	13198	gene=IY08_08735	protein=membrane protein	protein_id=KGT44385.1
gene	1618803	1619414	13203	13814	gene=IY08_08740	protein=hypothetical protein	protein_id=KGT44386.1
gene	1619420	1621045	13820	15445	gene=IY08_08745	protein=membrane protein	protein_id=KGT44387.1

gene	1621074	1621559	15474	15959	gene=IY08_08750	protein=DNA mismatch repair protein MutT	protein_id=KGT44388.1
gene	1621697	1622959	16097	17359	gene=IY08_08755	protein=tetracycline resistance protein	protein_id=KGT44389.1
gene	1622982	1623135	17382	17535	pseudo		
gene	1623155	1623619	17555	18019	gene=IY08_08765	protein=hypothetical protein	protein_id=KGT44390.1
gene	1624023	1624826	18423	19226	gene=IY08_08770	protein=UDP-galactose-lipid carrier transferase	protein_id=KGT44391.1
gene	1624979	1625518	19379	19918	gene=IY08_08775	protein=PadR family transcriptional regulator	protein_id=KGT44392.1
gene	1625555	1627303	19955	21703	gene=IY08_08780	protein=MFS transporter	protein_id=KGT44393.1
gene	1627512	1628786	21912	23186	gene=IY08_08785	protein=MFS transporter	protein_id=KGT44394.1
gene	1630048	1631307	24448	25707	gene=IY08_08795	protein=GTP-binding protein	protein_id=KGT44395.1
gene	1631519	1631857	25919	26257	gene=IY08_08800	protein=hypothetical protein	protein_id=KGT44396.1
gene	1631930	1632736	26330	27136	gene=IY08_08805	protein=Fosmidomycin resistance protein	protein_id=KGT44229.1
gene	1632747	1633664	27147	28064	gene=IY08_08810	protein=cysteine synthase	protein_id=KGT44230.1
gene	1633743	1634255	28143	28655	gene=IY08_08815	protein=acetyltransferase	protein_id=KGT44231.1
gene	1634348	1635175	28748	29575	gene=IY08_08820	protein=cytoplasmic protein	protein_id=KGT44232.1
gene	1635199	1635774	29599	30174	gene=IY08_08825	protein=hypothetical protein	protein_id=KGT44233.1
gene	1636540	1637877	30940	32277	gene=IY08_08830	protein=hypothetical protein	protein_id=KGT44234.1
gene	1637915	1638619	32315	33019	gene=IY08_08835	protein=polysaccharide deacetylase	protein_id=KGT44235.1
gene	1638946	1639209	33346	33609	gene=IY08_08845	protein=hypothetical protein	protein_id=KGT44236.1
gene	1639370	1640056	33770	34456	gene=IY08_08850	protein=membrane protein	protein_id=KGT44237.1
gene	1640167	1640808	34567	35208	gene=IY08_08855	protein=ferrous iron transporter A	protein_id=KGT44238.1
gene	1640951	1641304	35351	35704	gene=IY08_08860	protein=hypothetical protein	protein_id=KGT44239.1
gene	1641527	1641727	35927	36127	gene=IY08_08865	protein=hypothetical protein	protein_id=KGT44240.1
gene	1641891	1642427	36291	36827	gene=IY08_08875	protein=methionine sulfoxide reductase A	protein_id=KGT44241.1
gene	1642518	1643276	36918	37676	gene=IY08_08880	protein=short-chain dehydrogenase	protein_id=KGT44242.1
gene	1644211	1645110	38611	39510	gene=IY08_08885	protein=branched-chain amino acid aminotransferase	protein_id=KGT44243.1
gene	1645133	1646848	39533	41248	gene=IY08_08890	protein=acetolactate synthase catalytic subunit	protein_id=KGT44244.1
gene	1646845	1647075	41245	41475	gene=IY08_08895	protein=acetolactate synthase 1 regulatory subunit	protein_id=KGT44245.1
gene	1647090	1648097	41490	42497	gene=IY08_08900	protein=ketol-acid reductoisomerase	protein_id=KGT44246.1
gene	1648144	1649817	42544	44217	gene=IY08_08905	protein=dihydroxy-acid dehydratase	protein_id=KGT44247.1
gene	1649849	1651111	44249	45511	gene=IY08_08910	protein=threonine dehydratase	protein_id=KGT44248.1
gene	1651192	1651419	45592	45819	gene=IY08_08915	protein=hypothetical protein	protein_id=KGT44249.1

gene	1651472	1652575	45872	46975	gene=IY08_08920	protein=capsular biosynthesis protein	protein_id=KGT44250.1
gene	1652780	1653496	47180	47896	gene=IY08_08925	protein=membrane protein	protein_id=KGT44251.1
gene	1653515	1654375	47915	48775	gene=IY08_08930	protein=acetyltransferase	protein_id=KGT44252.1
gene	1654543	1655757	48943	50157	gene=IY08_08935	protein=MFS transporter	protein_id=KGT44253.1
gene	1655811	1656572	50211	50972	gene=IY08_08940	protein=MFS transporter	protein_id=KGT44254.1
gene	1656785	1657708	51185	52108	gene=IY08_08945	protein=alpha/beta hydrolase	protein_id=KGT44255.1
gene	1658003	1658647	52403	53047	gene=IY08_08950	protein=LytR family transcriptional regulator	protein_id=KGT44256.1
gene	1658775	1660289	53175	54689	gene=IY08_08955	protein=acetyl-CoA hydrolase	protein_id=KGT44257.1
gene	1660515	1660958	54915	55358	gene=IY08_08960	protein=acetyltransferase	protein_id=KGT44258.1
gene	1660986	1661345	55386	55745	pseudo		
gene	1661399	1662724	55799	57124	gene=IY08_08970	protein=5-methylthioadenosine deaminase	protein_id=KGT44259.1
gene	1662878	1664506	57278	58906	gene=IY08_08975	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT44260.1
gene	1664558	1665088	58958	59488	gene=IY08_08980	protein=acetyltransferase	protein_id=KGT44261.1
gene	1665285	1666580	59685	60980	gene=IY08_08985	protein=manganese transport protein MntH	protein_id=KGT44262.1
gene	1667059	1668018	61459	62418	gene=IY08_08990	protein=sulfurtransferase	protein_id=KGT44263.1
gene	1668229	1669704	62629	64104	gene=IY08_08995	protein=hypothetical protein	protein_id=KGT44264.1
gene	1669880	1670824	64280	65224	gene=IY08_09000	protein=2-dehydropantoate 2-reductase	protein_id=KGT44265.1
gene	1670889	1671017	65289	65417	gene=IY08_09005	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT44266.1
gene	1671449	1673275	65849	67675	gene=IY08_09010	protein=amino acid permease	protein_id=KGT44267.1
gene	1673873	1675033	68273	69433	gene=IY08_09015	protein=enterotoxin	protein_id=KGT44268.1
gene	1675072	1676280	69472	70680	gene=IY08_09020	protein=enterotoxin	protein_id=KGT44269.1
gene	1676388	1677467	70788	71867	gene=IY08_09025	protein=enterotoxin	protein_id=KGT44270.1
gene	1677701	1678327	72101	72727	gene=IY08_09030	protein=amino acid transporter LysE	protein_id=KGT44271.1
gene	1678452	1678763	72852	73163	gene=IY08_09035	protein=hypothetical protein	protein_id=KGT44272.1
gene	1678855	1679508	73255	73908	gene=IY08_09040	protein=CAAX protease	protein_id=KGT44273.1
gene	1680149	1680739	74549	75139	gene=IY08_09045	protein=TetR family transcriptional regulator	protein_id=KGT44274.1
gene	1681030	1682196	75430	76596	gene=IY08_09050	protein=hypothetical protein	protein_id=KGT44275.1
gene	1682574	1683521	76974	77921	gene=IY08_09055	protein=RNA polymerase sigma70	protein_id=KGT44276.1
gene	1683627	1683848	78027	78248	gene=IY08_09060	protein=hypothetical protein	protein_id=KGT44277.1
gene	1683826	1684497	78226	78897	gene=IY08_09065	protein=deoxyribose-phosphate aldolase	protein_id=KGT44278.1
gene	1684600	1685781	79000	80181	gene=IY08_09070	protein=pyrimidine nucleoside transporter NupC	protein_id=KGT44279.1

gene	1685818	1687119	80218	81519	gene=deoA	protein=thymidine phosphorylase	protein_id=KGT44280.1
gene	1687153	1687548	81553	81948	gene=IY08_09080	protein=cytidine deaminase	protein_id=KGT44281.1
gene	1687695	1688090	82095	82490	gene=IY08_09085	protein=membrane protein	protein_id=KGT44282.1
gene	1688108	1688587	82508	82987	gene=IY08_09090	protein=membrane protein	protein_id=KGT44283.1
gene	1688635	1688865	83035	83265	gene=IY08_09095	protein=hypothetical protein	protein_id=KGT44284.1
gene	1689055	1690338	83455	84738	gene=IY08_09100	protein=Xaa-Pro aminopeptidase	protein_id=KGT44285.1
gene	1690433	1691068	84833	85468	gene=IY08_09105	protein=quinolone resistance protein	protein_id=KGT44286.1
gene	1691431	1693071	85831	87471	gene=IY08_09110	protein=copper oxidase	protein_id=KGT44287.1
gene	1693123	1693668	87523	88068	gene=IY08_09115	protein=membrane protein	protein_id=KGT44288.1
gene	1693991	1696135	88391	90535	gene=IY08_09120	protein=DNA topoisomerase III	protein_id=KGT44289.1
gene	1696340	1697587	90740	91987	gene=IY08_09125	protein=membrane protein	protein_id=KGT44290.1
gene	1697775	1698740	92175	93140	gene=IY08_09130	protein=arsenic resistance protein	protein_id=KGT44291.1
gene	1699033	1699725	93433	94125	gene=IY08_09135	protein=FMN-dependent NADH-azoreductase	protein_id=KGT44292.1
gene	1699964	1701322	94364	95722	gene=IY08_09140	protein=branched-chain amino acid transporter	protein_id=KGT44293.1
gene	1701406	1701825	95806	96225	gene=IY08_09145	protein=glyoxalase	protein_id=KGT44294.1
gene	1702154	1703803	96554	98203	gene=IY08_09150	protein=copper resistance protein	protein_id=KGT44295.1
gene	1703838	1704458	98238	98858	gene=IY08_09155	protein=hypothetical protein	protein_id=KGT44296.1
gene	1704501	1705406	98901	99806	gene=IY08_09160	protein=transporter	protein_id=KGT44297.1
gene	1705504	1706373	99904	100773	gene=IY08_09165	protein=LysR family transcriptional regulator	protein_id=KGT44298.1
gene	1706494	1706925	100894	101325	gene=IY08_09170	protein=Rrf2 family transcriptional regulator	protein_id=KGT44299.1
gene	1706996	1707646	101396	102046	gene=IY08_09175	protein=hypothetical protein	protein_id=KGT44300.1
gene	1707704	1708306	102104	102706	gene=IY08_09180	protein=nitroreductase	protein_id=KGT44301.1
gene	1708433	1708564	102833	102964	gene=IY08_09185	protein=DNA mismatch repair protein MutT	protein_id=KGT44302.1
gene	1708738	1708922	103138	103322	pseudo		
gene	1709059	1710081	103459	104481	gene=IY08_09195	protein=membrane protein	protein_id=KGT44303.1
gene	1710240	1710869	104640	105269	pseudo		
gene	1711963	1713270	106363	107670	gene=IY08_09205	protein=hypothetical protein	protein_id=KGT44304.1
gene	1713303	1721135	107703	115535	gene=IY08_09210	protein=hypothetical protein	protein_id=KGT44305.1
gene	1721132	1724509	115532	118909	gene=IY08_09215	protein=hypothetical protein	protein_id=KGT44306.1
gene	1724536	1728594	118936	122994	gene=IY08_09220	protein=hypothetical protein	protein_id=KGT44307.1
gene	1728690	1733612	123090	128012	gene=IY08_09225	protein=hypothetical protein	protein_id=KGT44308.1

gene	1733909	1734586	128309	128986	gene=IY08_09230	protein=hypothetical protein	protein_id=KGT44309.1
gene	1735200	1736144	129600	130544	gene=IY08_09245	protein=lactate dehydrogenase	protein_id=KGT44310.1
gene	1736345	1737781	130745	132181	gene=IY08_09250	protein=amine oxidase	protein_id=KGT44311.1
gene	1737888	1738811	132288	133211	gene=IY08_09255	protein=cobalamin biosynthesis protein	protein_id=KGT44312.1
gene	1739075	1740292	133475	134692	gene=IY08_09260	protein=ABC transporter permease	protein_id=KGT44313.1
gene	1740383	1741156	134783	135556	gene=IY08_09265	protein=branched-chain amino acid ABC transporter substrate-binding protein	protein_id=KGT44314.1
gene	1741134	1741835	135534	136235	gene=IY08_09270	protein=branched-chain amino acid ABC transporter ATP-binding protein	protein_id=KGT44315.1
gene	1741857	1742717	136257	137117	gene=IY08_09275	protein=ABC transporter permease	protein_id=KGT44316.1
gene	1742767	1743720	137167	138120	gene=IY08_09280	protein=branched-chain amino acid ABC transporter	protein_id=KGT44317.1
gene	1743782	1744570	138182	138970	gene=IY08_09285	protein=LysR family transcriptional regulator	protein_id=KGT44318.1
gene	1744691	1745239	139091	139639	gene=IY08_09290	protein=Petrobactin biosynthesis protein AsbA	protein_id=KGT44319.1
gene	1745282	1745710	139682	140110	gene=IY08_09295	protein=4-oxalocrotonate tautomerase	protein_id=KGT44320.1
gene	1745691	1746014	140091	140414	gene=IY08_09300	protein=carboxymuconolactone decarboxylase	protein_id=KGT44321.1
gene	1746168	1746611	140568	141011	gene=IY08_09305	protein=MarR family transcriptional regulator	protein_id=KGT44322.1
gene	1746731	1747786	141131	142186	gene=IY08_09310	protein=Luciferase	protein_id=KGT44323.1
gene	1748380	1749783	142780	144183	gene=IY08_09315	protein=cytochrome D ubiquinol oxidase subunit I	protein_id=KGT44324.1
gene	1749770	1750786	144170	145186	gene=IY08_09320	protein=nitrate reductase	protein_id=KGT44325.1
gene	1750786	1752507	145186	146907	gene=IY08_09325	protein=ATP-binding/permease CydC	protein_id=KGT44326.1
gene	1752504	1754228	146904	148628	gene=IY08_09330	protein=ABC transporter ATP-binding protein	protein_id=KGT44327.1
gene	1754362	1755510	148762	149910	gene=IY08_09335	protein=hypothetical protein	protein_id=KGT44328.1
gene	1755618	1758179	150018	152579	gene=IY08_09340	protein=glycosyl transferase family 2	protein_id=KGT44329.1
gene	1758199	1759329	152599	153729	gene=IY08_09345	protein=aminotransferase DegT	protein_id=KGT44330.1
gene	1759322	1759888	153722	154288	gene=IY08_09350	protein=galactoside O-acetyltransferase	protein_id=KGT44331.1
gene	1760073	1760294	154473	154694	gene=IY08_09355	protein=hypothetical protein	protein_id=KGT44332.1
gene	1760385	1760831	154785	155231	gene=IY08_09360	protein=lipoprotein	protein_id=KGT44333.1
gene	1760867	1761205	155267	155605	gene=IY08_09365	protein=multidrug ABC transporter	protein_id=KGT44334.1
gene	1761198	1761539	155598	155939	gene=IY08_09370	protein=hypothetical protein	protein_id=KGT44335.1
gene	1761687	1762688	156087	157088	gene=IY08_09375	protein=peptidase S66	protein_id=KGT44336.1
gene	1762948	1763901	157348	158301	gene=IY08_09380	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT44337.1

gene	1764148	1764750	158548	159150	gene=IY08_09385	protein=nitroreductase	protein_id=KGT44338.1
gene	1764793	1764963	159193	159363	gene=IY08_09390	protein=DNA mismatch repair protein MutT	protein_id=KGT44339.1
gene	1765706	1766986	160106	161386	gene=IY08_09400	protein=peptidase P60	protein_id=KGT44340.1
gene	1767086	1767850	161486	162250	gene=IY08_09405	protein=alpha/beta hydrolase	protein_id=KGT44341.1
gene	1768091	1769851	162491	164251	gene=IY08_09410	protein=multidrug ABC transporter permease	protein_id=KGT44342.1
gene	1769928	1770614	164328	165014	gene=IY08_09415	protein=heme response regulator HssR	protein_id=KGT44343.1
gene	1770611	1771684	165011	166084	gene=IY08_09420	protein=membrane protein	protein_id=KGT44344.1
gene	1771974	1772687	166374	167087	gene=fabG	protein=3-ketoacyl-ACP reductase	protein_id=KGT44345.1
gene	1772978	1773850	167378	168250	gene=IY08_09430	protein=aminoglycoside adenylyltransferase	protein_id=KGT44346.1
gene	1773971	1774798	168371	169198	gene=IY08_09435	protein=polysaccharide deacetylase	protein_id=KGT44347.1
gene	1774869	1775207	169269	169607	gene=IY08_09440	protein=membrane protein	protein_id=KGT44348.1
gene	1775254	1775862	169654	170262	gene=IY08_09445	protein=DNA mismatch repair protein MutT	protein_id=KGT44349.1
gene	1775944	1776582	170344	170982	gene=IY08_09450	protein=phosphohydrolase	protein_id=KGT44350.1
gene	1777352	1778647	171752	173047	gene=IY08_09460	protein=homoserine dehydrogenase	protein_id=KGT44351.1
gene	1778640	1779698	173040	174098	gene=IY08_09465	protein=threonine synthase	protein_id=KGT44352.1
gene	1779695	1780588	174095	174988	gene=IY08_09470	protein=serine kinase	protein_id=KGT44353.1
gene	1780720	1780929	175120	175329	gene=IY08_09475	protein=phage capsid protein	protein_id=KGT44354.1
gene	1781137	1783440	175537	177840	gene=IY08_09480	protein=lipoprotein	protein_id=KGT44355.1
gene	1783761	1784762	178161	179162	gene=IY08_09485	protein=LytR family transcriptional regulator	protein_id=KGT44356.1
gene	1784927	1786174	179327	180574	gene=IY08_09490	protein=lipoprotein	protein_id=KGT44357.1
gene	1786187	1786876	180587	181276	gene=IY08_09495	protein=regulator	protein_id=KGT44358.1
gene	1786873	1788231	181273	182631	gene=IY08_09500	protein=histidine kinase	protein_id=KGT44359.1
gene	1788333	1789154	182733	183554	gene=IY08_09505	protein=peptidoglycan N-acetylglucosamine deacetylase	protein_id=KGT44360.1
gene	1789169	1789825	183569	184225	gene=IY08_09510	protein=lipoprotein	protein_id=KGT44361.1
gene	1789985	1790665	184385	185065	gene=IY08_09515	protein=methyltransferase	protein_id=KGT44362.1
gene	1790761	1791285	185161	185685	gene=IY08_09520	protein=acetyltransferase	protein_id=KGT44363.1
gene	1791584	1793392	185984	187792	gene=IY08_09525	protein=IucA/IucC family siderophore biosynthesis protein	protein_id=KGT44364.1
gene	1793453	1795291	187853	189691	gene=IY08_09530	protein=siderophore biosynthesis protein	protein_id=KGT44365.1
gene	1795278	1796516	189678	190916	gene=IY08_09535	protein=acyl-CoA synthetase	protein_id=KGT44366.1
gene	1796513	1796779	190913	191179	gene=IY08_09540	protein=acyl carrier protein	protein_id=KGT44367.1
gene	1796803	1797786	191203	192186	gene=IY08_09545	protein=Petrobactin biosynthesis protein AsbE	protein_id=KGT44368.1

gene	1797824	1798666	192224	193066	gene=IY08_09550	protein=3-dehydroshikimate dehydratase	protein_id=KGT44369.1
gene	1798791	1798997	193191	193397	gene=IY08_09555	protein=spore protein	protein_id=KGT44370.1
gene	1799165	1800463	193565	194863	gene=IY08_09560	protein=MFS transporter	protein_id=KGT44371.1
gene	1800517	1801131	194917	195531	gene=IY08_09565	protein=LysE family L-lysine exporter	protein_id=KGT44372.1
gene	1801250	1802193	195650	196593	gene=IY08_09570	protein=GntR family transcriptional regulator	protein_id=KGT44373.1
gene	1802204	1802692	196604	197092	gene=IY08_09575	protein=GntR family transcriptional regulator	protein_id=KGT44165.1
gene	1802705	1802872	197105	197272	gene=IY08_09580	protein=hypothetical protein	protein_id=KGT44166.1
gene	1802986	1803951	197386	198351	gene=IY08_09585	protein=phospholipase	protein_id=KGT44167.1
gene	1804038	1804184	198438	198584	gene=IY08_09590	protein=Luciferase	protein_id=KGT44168.1
gene	1804408	1805160	198808	199560	gene=IY08_09595	protein=cytoplasmic protein	protein_id=KGT44169.1
gene	1805310	1806470	199710	200870	gene=IY08_09600	protein=peptidase	protein_id=KGT44170.1
gene	1806576	1806773	200976	201173	gene=IY08_09605	protein=DNA mismatch repair protein MutT	protein_id=KGT44171.1
gene	1806806	1807267	201206	201667	gene=IY08_09610	protein=NTP pyrophosphohydrolase	protein_id=KGT44172.1
gene	1807317	1808135	201717	202535	gene=IY08_09615	protein=NAD synthetase	protein_id=KGT44173.1
gene	1808410	1810290	202810	204690	gene=IY08_09620	protein=ABC transporter permease	protein_id=KGT44174.1
gene	1810406	1810693	204806	205093	gene=IY08_09625	protein=transition state regulator Abh	protein_id=KGT44175.1
gene	1810968	1811915	205368	206315	gene=IY08_09630	protein=serine protease	protein_id=KGT44176.1
gene	1811957	1812265	206357	206665	gene=IY08_09635	protein=ArsR family transcriptional regulator	protein_id=KGT44177.1
gene	1812372	1813307	206772	207707	gene=IY08_09640	protein=oxidoreductase	protein_id=KGT44178.1
gene	1813355	1814530	207755	208930	gene=IY08_09645	protein=MFS transporter	protein_id=KGT44179.1
gene	1814579	1814785	208979	209185	gene=IY08_09650	protein=hypothetical protein	protein_id=KGT44180.1
gene	1814825	1815049	209225	209449	gene=IY08_09655	protein=hypothetical protein	protein_id=KGT44181.1
gene	1815134	1815481	209534	209881	gene=IY08_09660	protein=hypothetical protein	protein_id=KGT44182.1
gene	1815678	1816180	210078	210580	pseudo		
gene	1816363	1817415	210763	211815	gene=IY08_09670	protein=GTPase RsgA	protein_id=KGT44183.1
gene	1817616	1819598	212016	213998	gene=IY08_09675	protein=chemotaxis protein	protein_id=KGT44184.1
gene	1819663	1819824	214063	214224	gene=IY08_09680	protein=hypothetical protein	protein_id=KGT44185.1
gene	1819795	1820100	214195	214500	gene=IY08_09685	protein=hypothetical protein	protein_id=KGT44186.1
gene	1820423	1820788	214823	215188	gene=IY08_09690	protein=hypothetical protein	protein_id=KGT44187.1
gene	1820823	1821863	215223	216263	gene=IY08_09695	protein=membrane protein	protein_id=KGT44188.1
gene	1822104	1822547	216504	216947	gene=IY08_09700	protein=general stress protein	protein_id=KGT44189.1

gene	1822650	1823105	217050	217505	gene=IY08_09705	protein=hypothetical protein	protein_id=KGT44190.1
gene	1823320	1824264	217720	218664	gene=IY08_09710	protein=alpha/beta hydrolase	protein_id=KGT44191.1
gene	1824309	1825310	218709	219710	gene=IY08_09715	protein=hypothetical protein	protein_id=KGT44192.1
gene	1825415	1825606	219815	220006	gene=IY08_09720	protein=membrane protein	protein_id=KGT44193.1
gene	1825784	1827247	220184	221647	gene=IY08_09725	protein=amine oxidase	protein_id=KGT44194.1
gene	1827332	1827916	221732	222316	gene=IY08_09730	protein=acetyltransferase	protein_id=KGT44195.1
gene	1827941	1828843	222341	223243	gene=IY08_09735	protein=oxidoreductase	protein_id=KGT44196.1
gene	1829105	1830574	223505	224974	gene=IY08_09740	protein=transposase	protein_id=KGT44197.1
gene	1830672	1831622	225072	226022	gene=IY08_09745	protein=cobalamin biosynthesis protein CobW	protein_id=KGT44198.1
gene	1831735	1832205	226135	226605	gene=IY08_09750	protein=spermidine acetyltransferase	protein_id=KGT44199.1
gene	1832344	1833294	226744	227694	gene=IY08_09755	protein=adhesin	protein_id=KGT44200.1
gene	1833561	1833710	227961	228110	gene=IY08_09760	protein=hypothetical protein	protein_id=KGT44201.1
gene	1833826	1834485	228226	228885	gene=IY08_09765	protein=oxidoreductase	protein_id=KGT44202.1
gene	1834515	1835552	228915	229952	gene=IY08_09770	protein=NADPH dehydrogenase	protein_id=KGT44203.1
gene	1835686	1836138	230086	230538	gene=IY08_09775	protein=cysteine methyltransferase	protein_id=KGT44204.1
gene	1836164	1837150	230564	231550	gene=IY08_09780	protein=group-specific protein	protein_id=KGT44205.1
gene	1837235	1838896	231635	233296	gene=IY08_09785	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT44206.1
gene	1838956	1839372	233356	233772	gene=IY08_09790	protein=fosfomycin resistance protein FosB	protein_id=KGT44207.1
gene	1839386	1839931	233786	234331	gene=IY08_09795	protein=short-chain dehydrogenase	protein_id=KGT44208.1
gene	1839945	1840556	234345	234956	gene=IY08_09800	protein=phosphatase	protein_id=KGT44209.1
gene	1840602	1841180	235002	235580	gene=IY08_09805	protein=Spore coat protein G	protein_id=KGT44210.1
gene	1841362	1842438	235762	236838	gene=IY08_09810	protein=spore coat protein	protein_id=KGT44211.1
gene	1842543	1843160	236943	237560	gene=IY08_09815	protein=ADP-ribose pyrophosphatase	protein_id=KGT44212.1
gene	1843265	1843867	237665	238267	gene=IY08_09820	protein=membrane protein	protein_id=KGT44213.1
gene	1843965	1845344	238365	239744	gene=IY08_09825	protein=transporter	protein_id=KGT44214.1
gene	1845677	1846618	240077	241018	gene=IY08_09830	protein=magnesium transporter	protein_id=KGT44215.1
gene	1846817	1847713	241217	242113	gene=IY08_09835	protein=membrane protein	protein_id=KGT44216.1
gene	1847717	1848586	242117	242986	gene=IY08_09840	protein=hypothetical protein	protein_id=KGT44217.1
gene	1848706	1849212	243106	243612	gene=IY08_09845	protein=acyl-CoA hydrolase	protein_id=KGT44218.1
gene	1849586	1850770	243986	245170	gene=IY08_09855	protein=cardiolipin synthetase	protein_id=KGT44219.1
gene	1850802	1851260	245202	245660	gene=IY08_09860	protein=spore coat protein	protein_id=KGT44220.1

gene	1851486	1851665	245886	246065	gene=IY08_09865	protein=hypothetical protein	protein_id=KGT44221.1
gene	1851767	1852390	246167	246790	gene=IY08_09870	protein=hypothetical protein	protein_id=KGT44222.1
gene	1852415	1852897	246815	247297	gene=IY08_09875	protein=membrane protein	protein_id=KGT44223.1
gene	1852899	1854206	247299	248606	gene=IY08_09880	protein=membrane protein	protein_id=KGT44224.1
gene	1854415	1855284	248815	249684	gene=IY08_09885	protein=membrane protein	protein_id=KGT44225.1
gene	1855541	1856188	249941	250588	gene=IY08_09890	protein=CBS domain-containing protein	protein_id=KGT44226.1
gene	1856381	1856887	250781	251287	gene=IY08_09900	protein=transposase	protein_id=KGT44227.1
gene	1856968	1857726	251368	252126	gene=IY08_09905	protein=integrase	protein_id=KGT44228.1
scaffold11							
gene	1858514	1859860	554	1900	gene=IY08_09915	protein=branched-chain amino acid transporter	protein_id=KGT44134.1
gene	1859926	1860255	1966	2295	gene=IY08_09920	protein=tRNA-binding protein	protein_id=KGT44135.1
gene	1860236	1860802	2276	2842	gene=IY08_09925	protein=hypothetical protein	protein_id=KGT44136.1
gene	1860775	1861080	2815	3120	gene=IY08_09930	protein=permease	protein_id=KGT44137.1
gene	1861085	1861381	3125	3421	gene=IY08_09935	protein=hypothetical protein	protein_id=KGT44138.1
gene	1861470	1862624	3510	4664	gene=IY08_09940	protein=stage II sporulation protein P	protein_id=KGT44139.1
gene	1862881	1863378	4921	5418	gene=IY08_09945	protein=GCN5 family acetyltransferase	protein_id=KGT44140.1
gene	1863390	1864130	5430	6170	gene=IY08_09950	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT44141.1
gene	1864154	1864600	6194	6640	gene=IY08_09955	protein=DNA mismatch repair protein MutT	protein_id=KGT44142.1
gene	1864817	1866034	6857	8074	gene=IY08_09960	protein=macrolide transporter	protein_id=KGT44143.1
gene	1866309	1866737	8349	8777	gene=IY08_09965	protein=hypothetical protein	protein_id=KGT44144.1
gene	1866740	1867708	8780	9748	gene=IY08_09970	protein=peptidase	protein_id=KGT44145.1
gene	1867778	1868932	9818	10972	gene=IY08_09975	protein=stage II sporulation protein P	protein_id=KGT44146.1
gene	1869022	1869612	11062	11652	gene=IY08_09980	protein=phosphoglycerate mutase	protein_id=KGT44147.1
gene	1869619	1870395	11659	12435	gene=IY08_09985	protein=HAD family hydrolase	protein_id=KGT44148.1
gene	1870426	1870897	12466	12937	pseudo		
gene	1870913	1871374	12953	13414	gene=IY08_09995	protein=hypothetical protein	protein_id=KGT44149.1
gene	1871546	1872721	13586	14761	gene=IY08_10000	protein=alanine racemase	protein_id=KGT44150.1
gene	1873014	1873883	15054	15923	gene=IY08_10005	protein=acetyltransferase	protein_id=KGT44151.1
gene	1874448	1875656	16488	17696	gene=IY08_10010	protein=glycosyl transferase	protein_id=KGT44152.1
gene	1875837	1876682	17877	18722	gene=IY08_10015	protein=membrane protein	protein_id=KGT44153.1
gene	1876771	1878186	18811	20226	gene=IY08_10020	protein=GntR family transcriptional regulator	protein_id=KGT44154.1

gene	1878316	1878738	20356	20778	gene=IY08_10025	protein=acetyltransferase	protein_id=KGT44155.1
gene	1878912	1880039	20952	22079	gene=IY08_10030	protein=serine/threonine protein phosphatase	protein_id=KGT44156.1
gene	1880060	1880686	22100	22726	gene=IY08_10035	protein=membrane protein	protein_id=KGT44157.1
gene	1880823	1881389	22863	23429	gene=IY08_10040	protein=acetyltransferase	protein_id=KGT44158.1
gene	1881396	1881956	23436	23996	gene=IY08_10045	protein=hypothetical protein	protein_id=KGT44159.1
gene	1881953	1882438	23993	24478	gene=IY08_10050	protein=GNAT family acetyltransferase	protein_id=KGT44160.1
gene	1882451	1882816	24491	24856	gene=IY08_10055	protein=cupin	protein_id=KGT44161.1
gene	1882819	1883247	24859	25287	gene=IY08_10060	protein=acetyltransferase	protein_id=KGT44162.1
gene	1883541	1883837	25581	25877	gene=IY08_10065	protein=type VII secretion protein EsxA	protein_id=KGT44163.1
gene	1883991	>1885777	26031	27817	gene=IY08_10070	protein=type VII secretion protein	protein_id=KGT44164.1
gene	1887614	1888117	28078	29682	gene=IY08_10075	protein=type VII secretion protein	protein_id=KGT44070.1
gene	1888122	1888373	29654	30157	gene=IY08_10080	protein=type VII secretion protein	protein_id=KGT44071.1
gene	1888447	1889646	30162	30413	gene=IY08_10085	protein=hypothetical protein	protein_id=KGT44072.1
gene	1889686	1894191	30487	31686	gene=IY08_10090	protein=membrane protein	protein_id=KGT44073.1
gene	1894188	1895009	31726	36231	gene=IY08_10095	protein=cell division protein FtsK	protein_id=KGT44074.1
gene	1895027	1896490	36228	37049	gene=IY08_10100	protein=hypothetical protein	protein_id=KGT44075.1
gene	1896517	1896777	37067	38530	gene=IY08_10105	protein=lipase	protein_id=KGT44076.1
gene	1896779	1897096	38557	38817	gene=IY08_10110	protein=hypothetical protein	protein_id=KGT44077.1
gene	1897442	1897702	38819	39136	gene=IY08_10115	protein=cytoplasmic protein	protein_id=KGT44078.1
gene	1897715	1898353	39482	39742	gene=IY08_10120	protein=hypothetical protein	protein_id=KGT44079.1
gene	1898791	1899573	39755	40393	gene=IY08_10125	protein=hypothetical protein	protein_id=KGT44080.1
gene	1899635	1900429	40831	41613	gene=IY08_10130	protein=hypothetical protein	protein_id=KGT44081.1
gene	1900457	1901254	41675	42469	gene=IY08_10135	protein=hypothetical protein	protein_id=KGT44082.1
gene	1901349	1901626	42497	43294	gene=IY08_10140	protein=hypothetical protein	protein_id=KGT44083.1
gene	1901718	1902256	43389	43666	pseudo		
gene	1902319	1903089	43758	44296	pseudo		
gene	1903151	1903921	44359	45129	gene=IY08_10155	protein=hypothetical protein	protein_id=KGT44084.1
gene	1904127	1904903	45191	45961	gene=IY08_10160	protein=hypothetical protein	protein_id=KGT44085.1
gene	1905056	1905853	46167	46943	gene=IY08_10165	protein=hypothetical protein	protein_id=KGT44086.1
gene	1906137	1906922	47096	47893	gene=IY08_10170	protein=hypothetical protein	protein_id=KGT44087.1
gene	1907054	1907479	48177	48962	gene=IY08_10175	protein=acetyltransferase	protein_id=KGT44088.1

gene	1907640	1908416	49094	49519	gene=IY08_10180	protein=spore protein	protein_id=KGT44089.1
gene	1908468	1908788	49680	50456	gene=IY08_10185	protein=oxalate:formate antiporter	protein_id=KGT44090.1
gene	1908858	1909070	50508	50828	gene=IY08_10190	protein=hypothetical protein	protein_id=KGT44091.1
gene	1909100	1909438	50898	51110	gene=IY08_10195	protein=hypothetical protein	protein_id=KGT44092.1
gene	1909774	1910454	51140	51478	gene=IY08_10200	protein=permease	protein_id=KGT44093.1
gene	1910549	1912237	51814	52494	gene=IY08_10205	protein=methyltransferase	protein_id=KGT44094.1
gene	1912328	1912855	52589	54277	gene=IY08_10210	protein=formate--tetrahydrofolate ligase	protein_id=KGT44095.1
gene	1912875	1914044	54368	54895	gene=IY08_10215	protein=hypothetical protein	protein_id=KGT44096.1
gene	1914262	1915071	54915	56084	gene=IY08_10220	protein=RNA helicase	protein_id=KGT44097.1
gene	1915127	1915510	56302	57111	gene=IY08_10225	protein=hypothetical protein	protein_id=KGT44098.1
gene	1915556	1916194	57167	57550	gene=IY08_10230	protein=glyoxalase	protein_id=KGT44099.1
gene	1916236	1917210	57596	58234	gene=IY08_10235	protein=hydrolase	protein_id=KGT44100.1
gene	1917417	1917995	58276	59250	gene=IY08_10240	protein=quinone oxidoreductase	protein_id=KGT44101.1
gene	1917992	1918672	59457	60035	gene=IY08_10245	protein=RNA polymerase sigma factor	protein_id=KGT44102.1
gene	1918729	1919163	60032	60712	gene=IY08_10250	protein=ECF-type sigma factor negative effector	protein_id=KGT44103.1
gene	1919249	1920220	60769	61203	gene=IY08_10255	protein=membrane protein	protein_id=KGT44104.1
gene	1920316	1920525	61289	62260	gene=IY08_10260	protein=beta-lactamase	protein_id=KGT44105.1
gene	1920749	1921231	62356	62565	gene=IY08_10265	protein=hypothetical protein	protein_id=KGT44106.1
gene	1921315	1923543	62789	63271	gene=IY08_10270	protein=glutathione peroxidase	protein_id=KGT44107.1
gene	1923540	1924754	63355	65583	gene=IY08_10275	protein=protease	protein_id=KGT44108.1
gene	1924754	1925716	65580	66794	gene=IY08_10280	protein=hypothetical protein	protein_id=KGT44109.1
gene	1926116	1926457	66794	67756	gene=IY08_10285	protein=ATPase AAA	protein_id=KGT44110.1
gene	1926574	1927074	68156	68497	gene=IY08_10290	protein=hypothetical protein	protein_id=KGT44111.1
gene	1927552	1931235	68614	69114	gene=IY08_10295	protein=hypothetical protein	protein_id=KGT44112.1
gene	1931225	1932700	69592	73275	gene=narZ	protein=nitrate reductase	protein_id=KGT44113.1
gene	1932720	1933250	73265	74740	gene=narH	protein=nitrate reductase	protein_id=KGT44114.1
gene	1933268	1933957	74760	75290	gene=IY08_10310	protein=nitrate reductase	protein_id=KGT44115.1
gene	1934094	1934786	75308	75997	gene=IY08_10315	protein=nitrate reductase	protein_id=KGT44116.1
gene	1935064	1936077	76134	76826	gene=IY08_10320	protein=Crp/Fnr family transcriptional regulator	protein_id=KGT44117.1
gene	1936095	1937108	77104	78117	gene=IY08_10325	protein=molybdenum cofactor biosynthesis protein A	protein_id=KGT44118.1
gene	1937152	1938441	78135	79148	gene=IY08_10330	protein=thiamine biosynthesis protein MoeB	protein_id=KGT44119.1

gene	1938486	1938956	79192	80481	gene=IY08_10335	protein=molybdopterin molybdenumtransferase	protein_id=KGT44120.1
gene	1938953	1939186	80526	80996	gene=IY08_10340	protein=molybdopterin (MPT) converting factor, subunit 2	protein_id=KGT44121.1
gene	1939267	1940436	80993	81226	gene=IY08_10345	protein=molybdenum cofactor biosynthesis protein MoaD	protein_id=KGT44122.1
gene	1940714	1940848	81307	82476	gene=IY08_10350	protein=MFS transporter	protein_id=KGT44123.1
gene	1941108	1942025	82754	82888	gene=IY08_10355	protein=hypothetical protein	protein_id=KGT44124.1
gene	1942349	1942726	83148	84065	gene=IY08_10360	protein=transporter	protein_id=KGT44125.1
gene	1942917	1943390	84389	84766	gene=IY08_10365	protein=hypothetical protein	protein_id=KGT44126.1
gene	1943383	1944093	84957	85430	gene=IY08_10370	protein=precorrin-2 dehydrogenase	protein_id=KGT44127.1
gene	1944090	1945514	85423	86133	gene=IY08_10375	protein=cobalamin biosynthesis protein CbiX	protein_id=KGT44128.1
gene	1945573	1945890	86130	87554	gene=IY08_10380	protein=uroporphyrinogen-III synthase	protein_id=KGT44129.1
gene	1945906	1948314	87613	87930	gene=IY08_10385	protein=nitrite reductase	protein_id=KGT44130.1
gene	1948523	1949230	87946	90354	gene=IY08_10390	protein=nitrite reductase	protein_id=KGT44131.1
gene	1949433	>1949614	90563	91270	gene=IY08_10395	protein=regulator of cell morphogenesis and NO signaling, scdA family (2 C-terminal HHE domains)	protein_id=KGT44132.1
gene	1950529	1950681	91473	91654	gene=IY08_10400	protein=calcium-binding protein	protein_id=KGT44133.1]
gene	1950900	1951109	91774	92360	gene=IY08_10405	protein=calcium-binding protein	protein_id=KGT43928.1
gene	1951206	1952045	92569	92721	gene=IY08_10410	protein=exosporium protein G	protein_id=KGT43929.1
gene	1952599	1954200	92940	93149	gene=IY08_10415	protein=hypothetical protein	protein_id=KGT43930.1
gene	1954353	1954901	93246	94085	gene=IY08_10420	protein=acetyltransferase	protein_id=KGT43931.1
gene	1955511	1955786	94639	96240	gene=IY08_10425	protein=hypothetical protein	protein_id=KGT43932.1
gene	1956096	1956383	96393	96941	gene=IY08_10430	protein=preprotein translocase	protein_id=KGT43933.1
gene	1956518	1956955	97551	97826	gene=IY08_10435	protein=stage V sporulation protein S	protein_id=KGT43934.1
gene	1957021	1957872	98136	98423	gene=IY08_10440	protein=hypothetical protein	protein_id=KGT43935.1
gene	1958243	1958896	98558	98995	gene=IY08_10445	protein=tranposase	protein_id=KGT43936.1
gene	1959216	1960352	99061	99912	gene=IY08_10450	protein=transposase	protein_id=KGT43937.1
gene	1960349	1960564	100283	100936	gene=IY08_10460	protein=hypothetical protein	protein_id=KGT43938.1
gene	1960987	1961679	101256	102392	gene=IY08_10465	protein=aspartate phosphatase	protein_id=KGT43939.1
gene	1961789	1962436	102389	102604	gene=IY08_10470	protein=hypothetical protein	protein_id=KGT43940.1
gene	1962433	1964328	103027	103719	gene=IY08_10475	protein=hypothetical protein	protein_id=KGT43941.1
gene	1964404	1965135	103829	104476	gene=IY08_10480	protein=phosphohydrolase	protein_id=KGT43942.1
gene	1965241	1965495	104473	106368	gene=IY08_10485	protein=multidrug ABC transporter ATP-binding protein	protein_id=KGT43943.1

gene	1965657	1965992	106444	107175	gene=IY08_10490	protein=membrane protein	protein_id=KGT43944.1
gene	1966332	1966892	107281	107535	gene=IY08_10495	protein=hypothetical protein	protein_id=KGT43945.1
gene	1967310	1968437	107697	108032	gene=IY08_10500	protein=single-stranded DNA-binding protein	protein_id=KGT43946.1
gene	1968441	1968824	108372	108932	gene=IY08_10510	protein=shikimate kinase	protein_id=KGT43947.1
gene	1968908	1969342	109350	110477	gene=IY08_10515	protein=PBS lyase	protein_id=KGT43948.1
gene	1969392	1970168	110481	110864	gene=IY08_10520	protein=thioredoxin	protein_id=KGT43949.1
gene	1970469	1972157	110948	111382	gene=IY08_10525	protein=hypothetical protein	protein_id=KGT43950.1
gene	1972270	1972599	111432	112208	gene=IY08_10530	protein=protein-L-IsoD(D-D) O-methyltransferase	protein_id=KGT43951.1
gene	1972629	1972847	112509	114197	gene=IY08_10535	protein=arginine--tRNA ligase	protein_id=KGT43952.1
gene	1972941	1973450	114310	114639	gene=IY08_10540	protein=hypothetical protein	protein_id=KGT43953.1
gene	1973828	1978030	114669	114887	gene=IY08_10545	protein=hypothetical protein	protein_id=KGT43954.1
gene	1978417	1981518	114981	115490	pseudo		
gene	1981570	1982655	115868	120070	gene=IY08_10555	protein=TPR repeat-containing protein	protein_id=KGT43955.1
gene	1982657	1983241	120457	123558	gene=IY08_10560	protein=isoleucyl-tRNA synthetase	protein_id=KGT43956.1
gene	1983573	1985084	123610	124695	gene=IY08_10565	protein=membrane protein	protein_id=KGT43957.1
gene	1985192	1985671	124697	125281	gene=IY08_10570	protein=TetR family transcriptional regulator	protein_id=KGT43958.1
gene	1986213	1987511	125613	127124	gene=IY08_10575	protein=peptidase M36	protein_id=KGT43959.1
gene	1988084	1989424	127232	127711	gene=IY08_10580	protein=hypothetical protein	protein_id=KGT43960.1
gene	1989499	1990374	128253	129551	gene=IY08_10585	protein=aspartyl-tRNA synthetase	protein_id=KGT43961.1
gene	1990411	1990986	130124	131464	gene=IY08_10590	protein=hypothetical protein	protein_id=KGT43962.1
gene	1991011	1991808	131539	132414	gene=IY08_10595	protein=alpha/beta hydrolase	protein_id=KGT43963.1
gene	1991999	1992664	132451	133026	gene=IY08_10600	protein=hypothetical protein	protein_id=KGT43964.1
gene	1992869	1994308	133051	133848	gene=IY08_10605	protein=membrane protein	protein_id=KGT43965.1
gene	1994388	1995590	134039	134704	gene=IY08_10610	protein=5'-nucleotidase	protein_id=KGT43966.1
gene	1995762	1996457	134909	136348	gene=IY08_10615	protein=transporter	protein_id=KGT43967.1
gene	1996546	1997019	136428	137630	gene=IY08_10620	protein=alcohol dehydrogenase	protein_id=KGT43968.1
gene	1997016	1997456	137802	138497	gene=IY08_10625	protein=aspartate racemase	protein_id=KGT43969.1
gene	1997631	1998116	138586	139059	gene=IY08_10630	protein=transcriptional regulator	protein_id=KGT43970.1
gene	1998127	1998345	139056	139496	gene=IY08_10635	protein=acetyltransferase	protein_id=KGT43971.1
gene	1998587	1999114	139671	140156	gene=IY08_10640	protein=membrane protein	protein_id=KGT43972.1
gene	1999145	1999576	140167	140385	gene=IY08_10645	protein=XRE family transcriptional regulator	protein_id=KGT43973.1

gene	1999730	2000439	140627	141154	gene=IY08_10650	protein=hypothetical protein	protein_id=KGT43974.1
gene	2000432	2001646	141185	141616	gene=IY08_10655	protein=GCN5 family acetyltransferase	protein_id=KGT43975.1
gene	2001914	2002501	141770	142479	pseudo		
gene	2002606	2003241	142472	143686	gene=IY08_10665	protein=ABC transporter permease	protein_id=KGT43976.1
gene	2003243	2003629	143954	144541	gene=IY08_10670	protein=cell division protein FtsK	protein_id=KGT43977.1
gene	2003641	2004573	144646	145281	gene=IY08_10675	protein=HAD family hydrolase	protein_id=KGT43978.1
gene	2004624	2006081	145283	145669	gene=IY08_10680	protein=hypothetical protein	protein_id=KGT43979.1
gene	2006280	2007236	145681	146613	gene=IY08_10685	protein=aminoglycoside phosphotransferase	protein_id=KGT43980.1
gene	2007256	2007744	146664	148121	gene=IY08_10690	protein=penicillin-binding protein	protein_id=KGT43981.1
gene	2007900	2009885	148320	149276	gene=IY08_10695	protein=thymidylate synthase	protein_id=KGT43982.1
gene	2010127	2010762	149296	149784	gene=IY08_10700	protein=dihydrofolate reductase	protein_id=KGT43983.1
gene	2010873	2011592	149940	151925	gene=IY08_10705	protein=MecA protein	protein_id=KGT43984.1
gene	2011634	2012290	152167	152802	gene=IY08_10710	protein=FMN-dependent NADH-azoreductase	protein_id=KGT43985.1
gene	2012504	2012689	152913	153632	gene=IY08_10715	protein=acyl-phosphate glycerol 3-phosphate	protein_id=KGT43986.1
gene	2012732	2013472	153674	154330	gene=IY08_10720	protein=hemolysin D	protein_id=KGT43987.1
gene	2013802	2014053	154544	154729	gene=tatA	protein=preprotein translocase subunit SecA	protein_id=KGT43988.1
gene	2014208	2015050	154772	155512	gene=IY08_10730	protein=preprotein translocase subunit TatC	protein_id=KGT43989.1
gene	2015380	2016354	155842	156093	gene=IY08_10735	protein=hypothetical protein	protein_id=KGT43990.1
gene	2016690	2017277	156248	157090	gene=IY08_10740	protein=DegV domain-containing protein	protein_id=KGT43991.1
gene	2017313	2017774	157420	158394	gene=IY08_10745	protein=membrane protein	protein_id=KGT43992.1
gene	2017992	2019893	158730	159317	gene=IY08_10750	protein=cysteine ABC transporter ATP-binding protein	protein_id=KGT43993.1
gene	2019987	2020346	159353	159814	gene=IY08_10755	protein=molecular chaperone Hsp20	protein_id=KGT43994.1
gene	2020398	2020727	160032	161933	gene=IY08_10760	protein=asparagine synthase	protein_id=KGT43995.1
gene	2020830	2021801	162027	162386	gene=IY08_10765	protein=acetyltransferase	protein_id=KGT43996.1
gene	2022041	2023003	162438	162767	gene=IY08_10770	protein=hypothetical protein	protein_id=KGT43997.1
gene	2023130	2024005	162870	163841	gene=IY08_10775	protein=sporulation protein	protein_id=KGT43998.1
gene	2024104	2024751	164081	165043	gene=IY08_10780	protein=iron(III) dicitrate-binding protein	protein_id=KGT43999.1
gene	2025010	2025498	165170	166045	gene=IY08_10785	protein=D-amino acid aminotransferase	protein_id=KGT44000.1
gene	2025624	2025818	166144	166791	gene=IY08_10790	protein=NAD(P)H nitroreductase	protein_id=KGT44001.1
gene	2025930	2026478	167050	167538	gene=IY08_10795	protein=lipoprotein	protein_id=KGT44002.1
gene	2026829	2027266	167664	167858	gene=IY08_10800	protein=hypothetical protein	protein_id=KGT44003.1

gene	2027559	2028452	167970	168518	gene=IY08_10805	protein=isochorismatase	protein_id=KGT44004.1
gene	2028610	2029728	168869	169306	gene=IY08_10810	protein=molecular chaperone Hsp20	protein_id=KGT44005.1
gene	2029743	2030384	169599	170492	gene=IY08_10815	protein=mechanosensitive ion channel protein	protein_id=KGT44006.1
gene	2030589	2031443	170650	171768	gene=IY08_10820	protein=histidine kinase	protein_id=KGT44007.1
gene	2031606	2032463	171783	172424	gene=IY08_10825	protein=LuxR family transcriptional regulator	protein_id=KGT44008.1
gene	2032757	2033794	172629	173483	gene=IY08_10830	protein=RpiR family transcriptional regulator	protein_id=KGT44009.1
gene	2033944	2034963	173646	174503	gene=IY08_10835	protein=phenazine biosynthesis protein PhzF	protein_id=KGT44010.1
gene	2034960	2035862	174797	175834	gene=adhP	protein=ethanol-active dehydrogenase/acetaldehyde-active reductase	protein_id=KGT44011.1
gene	2036426	2037964	175984	177003	gene=IY08_10845	protein=peptide ABC transporter permease	protein_id=KGT44012.1
gene	2037979	2039328	177000	177902	gene=IY08_10850	protein=membrane protein	protein_id=KGT44013.1
gene	2039347	2040243	178466	180004	gene=IY08_10855	protein=gluconokinase	protein_id=KGT44014.1
gene	2040577	2041797	180019	181368	gene=IY08_10860	protein=permease DsdX	protein_id=KGT44015.1
gene	2041832	2042986	181387	182283	gene=IY08_10865	protein=6-phosphogluconate dehydrogenase	protein_id=KGT44016.1
gene	2043131	2043667	182617	183837	gene=IY08_10870	protein=glycosyl transferase	protein_id=KGT44017.1
gene	2043669	2044898	183872	185026	gene=IY08_10875	protein=DNA-binding protein	protein_id=KGT44018.1
gene	2044963	2045520	185171	185707	gene=IY08_10880	protein=NADH-ubiquinone oxidoreductase	protein_id=KGT44019.1
gene	2045621	2046568	185709	186938	gene=IY08_10885	protein=MFS transporter	protein_id=KGT44020.1
gene	2046572	2048083	187003	187560	gene=IY08_10890	protein=cytoplasmic protein	protein_id=KGT44021.1
gene	2048297	2049724	187661	188608	gene=IY08_10895	protein=glycine/betaine ABC transporter ATP-binding	protein_id=KGT44022.1
gene	2049802	2050062	188612	190123	gene=IY08_10900	protein=glycine/betaine ABC transporter permease	protein_id=KGT44023.1
gene	2050168	2051985	190337	191764	gene=IY08_10905	protein=amino acid APC transporter	protein_id=KGT44024.1
gene	2051975	2053825	191842	192102	gene=IY08_10910	protein=LemA domain protein	protein_id=KGT44025.1
gene	2054102	2054698	192208	194025	gene=IY08_10915	protein=hypothetical protein	protein_id=KGT44026.1
gene	2054795	2055337	194015	195865	gene=IY08_10920	protein=hypothetical protein	protein_id=KGT44027.1
gene	2055692	2057047	196142	196738	gene=IY08_10925	protein=hypothetical protein	protein_id=KGT44028.1
gene	2057180	2058604	196835	197377	gene=racA	protein=chromosome segregation protein	protein_id=KGT44029.1
gene	2058707	2059099	197732	199087	gene=IY08_10935	protein=membrane protein	protein_id=KGT44030.1
gene	2059349	2060467	199220	200644	gene=IY08_10940	protein=aldehyde dehydrogenase	protein_id=KGT44031.1
gene	2060501	2061250	200747	201139	gene=IY08_10945	protein=hypothetical protein	protein_id=KGT44032.1
gene	2062204	2063514	201389	202507	gene=IY08_10950	protein=histidine kinase	protein_id=KGT44033.1

gene	2063511	2064209	202541	203290	gene=IY08_10955	protein=hypothetical protein	protein_id=KGT44034.1
gene	2064194	2064856	204244	205554	gene=IY08_10960	protein=hypothetical protein	protein_id=KGT44035.1
gene	2064872	2066140	205551	206249	gene=IY08_10965	protein=CoA-transferase	protein_id=KGT44036.1
gene	2066137	2067036	206234	206896	gene=IY08_10970	protein=CoA-transferase	protein_id=KGT44037.1
gene	2067206	2068585	206912	208180	gene=IY08_10975	protein=acetylornithine deacetylase	protein_id=KGT44038.1
gene	2068796	2070217	208177	209076	gene=IY08_10980	protein=beta-lysine acetyltransferase	protein_id=KGT44039.1
gene	2070214	2070486	209246	210625	gene=IY08_10985	protein=ATPase AAA	protein_id=KGT44040.1
gene	2070559	2070774	210836	212257	gene=IY08_10990	protein=lysine 2,3-aminomutase	protein_id=KGT44041.1
gene	2071025	2071687	212254	212526	gene=IY08_10995	protein=hypothetical protein	protein_id=KGT44042.1
gene	2071692	2071847	212599	212814	gene=IY08_11000	protein=hypothetical protein	protein_id=KGT44043.1
gene	2071997	2072176	213065	213727	gene=IY08_11005	protein=hypothetical protein	protein_id=KGT44044.1
gene	2072287	2072469	213732	213887	gene=IY08_11010	protein=hypothetical protein	protein_id=KGT44045.1
gene	2072469	2073290	214037	214216	gene=IY08_11015	protein=hypothetical protein	protein_id=KGT44046.1
gene	2073272	2074027	214327	214509	gene=IY08_11020	protein=hypothetical protein	protein_id=KGT44047.1
gene	2074099	2074740	214509	215330	gene=IY08_11025	protein=serine/threonine protein kinase	protein_id=KGT44048.1
gene	2074730	2075611	215312	216067	gene=IY08_11030	protein=sporulation protein SpoOM	protein_id=KGT44049.1
gene	2075965	2076279	216139	216780	gene=IY08_11035	protein=phosphoesterase	protein_id=KGT44050.1
gene	2077092	2077331	216770	217651	gene=IY08_11040	protein=transporter	protein_id=KGT44051.1
gene	2077596	2077871	218005	218319	gene=IY08_11045	protein=thioredoxin	protein_id=KGT44052.1
gene	2078014	2078265	219132	219371	gene=IY08_11055	protein=hypothetical protein	protein_id=KGT44053.1
gene	2078403	2078939	219636	219911	gene=IY08_11060	protein=hypothetical protein	protein_id=KGT44054.1
gene	2079636	2079830	220054	220305	gene=IY08_11065	protein=alpha/beta hydrolase	protein_id=KGT44055.1
gene	2080492	2081496	220443	220979	gene=IY08_11070	protein=ABC transporter permease	protein_id=KGT44056.1
gene	2081689	2082540	221676	221870	gene=IY08_11075	protein=hypothetical protein	protein_id=KGT44057.1
gene	2082944	2083162	222532	223536	gene=IY08_11085	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT44058.1
gene	2083412	2083642	223729	224580	gene=prsA	protein=peptidylprolyl isomerase	protein_id=KGT44059.1
gene	2084131	2084466	224984	225202	gene=IY08_11095	protein=hypothetical protein	protein_id=KGT44060.1
gene	2084675	2084890	225452	225682	gene=IY08_11100	protein=hypothetical protein	protein_id=KGT44061.1
gene	2085098	2085433	226171	226506	gene=IY08_11110	protein=hypothetical protein	protein_id=KGT44062.1
gene	2085478	2085679	226715	226930	gene=IY08_11115	protein=spore germination protein GerPF	protein_id=KGT44063.1
gene	2085822	2086529	227138	227473	gene=IY08_11120	protein=hypothetical protein	protein_id=KGT44064.1

gene	2086669	2087322	227518	227719	pseudo		
gene	2087437	2087649	227862	228569	gene=IY08_11130	protein=short-chain dehydrogenase	protein_id=KGT44065.1
gene	2087717	2087926	228709	229362	gene=IY08_11135	protein=AraC family transcriptional regulator	protein_id=KGT44066.1
gene	2088393	>2090645	229477	229689	gene=IY08_11140	protein=hemolysin BL lytic component L2	protein_id=KGT44067.1
gene	2091307	2091588	229757	229966	gene=IY08_11145	protein=hypothetical protein	protein_id=KGT44068.1
gene	2091824	2092099	230433	232685	gene=IY08_11150	protein=penicillin-binding protein	partial=3'
gene	2092115	2092405	233347	233628	gene=IY08_11160	protein=hypothetical protein	protein_id=KGT43804.1
gene	2092801	2093922	233864	234139	gene=IY08_11165	protein=MFS transporter	protein_id=KGT43805.1
gene	2094021	2095457	234155	234445	gene=IY08_11170	protein=cytoplasmic protein	protein_id=KGT43806.1
gene	2095476	2096384	234841	235962	gene=IY08_11175	protein=citrate synthase 3	protein_id=KGT43807.1
gene	2096537	2098246	236061	237497	gene=prpD	protein=2-methylcitrate dehydratase	protein_id=KGT43808.1
gene	2098263	2099153	237516	238424	gene=IY08_11185	protein=methylisocitrate lyase	protein_id=KGT43809.1
gene	2099176	2100636	238577	240286	gene=IY08_11190	protein=acyl-CoA dehydrogenase	protein_id=KGT43810.1
gene	2100707	2101339	240303	241193	gene=IY08_11195	protein=3-hydroxyisobutyrate dehydrogenase	protein_id=KGT43811.1
gene	2101592	2102647	241216	242676	gene=IY08_11200	protein=methylmalonate-semialdehyde dehydrogenase	protein_id=KGT43812.1
gene	2102977	2103234	242747	243379	gene=IY08_11205	protein=lysine transporter LysE	protein_id=KGT43813.1
gene	2103419	2103658	243632	244687	gene=IY08_11210	protein=3-hydroxyisobutyryl-CoA hydrolase	protein_id=KGT43814.1
gene	2103674	2104831	245017	245274	gene=IY08_11215	protein=hypothetical protein	protein_id=KGT43815.1
gene	2104828	2107917	245459	245698	gene=IY08_11220	protein=hypothetical protein	protein_id=KGT43816.1
gene	2108025	2108198	245714	246871	gene=IY08_11225	protein=DNA repair exonuclease	protein_id=KGT43817.1
gene	2108534	2108833	246868	249957	gene=IY08_11230	protein=exonuclease	protein_id=KGT43818.1
gene	2108892	2109077	250065	250238	gene=IY08_11235	protein=membrane protein	protein_id=KGT43819.1
gene	2109290	2109436	250574	250873	gene=IY08_11240	protein=ArsR family transcriptional regulator	protein_id=KGT43820.1
gene	2109433	2110635	250932	251117	gene=IY08_11245	protein=hypothetical protein	protein_id=KGT43821.1
gene	2111263	2112048	251330	251476	gene=IY08_11250	protein=hypothetical protein	protein_id=KGT43822.1
gene	2112074	2113273	251473	252675	gene=IY08_11255	protein=membrane protein	protein_id=KGT43823.1
gene	2113286	2114902	253303	254088	gene=IY08_11260	protein=2,3-dihydroxybenzoate-2,3-dehydrogenase	protein_id=KGT43824.1
gene	2114927	2115820	254114	255313	gene=IY08_11265	protein=isochorismate synthase	protein_id=KGT43825.1
gene	2115854	2123011	255326	256942	gene=entE	protein=enterobactin synthase subunit E	protein_id=KGT43826.1
gene	2123008	2123232	256967	257860	gene=IY08_11275	protein=Isochorismatase	protein_id=KGT43827.1
gene	2123232	2124662	257894	265051	gene=IY08_11280	protein=diguanylate cyclase	protein_id=KGT43828.1

gene	2124720	2125469	265048	265272	gene=IY08_11285	protein=antibiotic transporter	protein_id=KGT43829.1
gene	2125495	2126037	265272	266702	gene=IY08_11290	protein=DSBA oxidoreductase	protein_id=KGT43830.1
gene	2126078	2126350	266760	267509	gene=IY08_11295	protein=4'-phosphopantetheinyl transferase	protein_id=KGT43831.1
gene	2126555	2127319	267535	268077	gene=IY08_11300	protein=cold-shock protein	protein_id=KGT43832.1
gene	2127337	2127861	268118	268390	gene=IY08_11305	protein=DNA-binding protein	protein_id=KGT43833.1
gene	2127953	2129146	268595	269359	gene=IY08_11310	protein=serine hydroxymethyltransferase	protein_id=KGT43834.1
gene	2129378	2130745	269377	269901	gene=IY08_11315	protein=diguanylate cyclase	protein_id=KGT43835.1
gene	2131183	2131758	269993	271186	gene=IY08_11320	protein=alkaline serine protease	protein_id=KGT43836.1
gene	2131927	2132253	271418	272785	gene=IY08_11325	protein=transporter	protein_id=KGT43837.1
gene	2132457	2133077	273223	273798	gene=IY08_11330	protein=hypothetical protein	protein_id=KGT43838.1
gene	2133263	2133970	273967	274293	gene=IY08_11335	protein=hypothetical protein	protein_id=KGT43839.1
gene	2134621	2136543	274497	275117	gene=IY08_11340	protein=antibiotic biosynthesis monooxygenase	protein_id=KGT43840.1
gene	2136793	2137560	275303	276010	gene=IY08_11345	protein=pseudouridine synthase	protein_id=KGT43841.1
gene	2137572	2139452	276661	278583	gene=IY08_11350	protein=threonine--tRNA ligase	protein_id=KGT43842.1
gene	2139724	2140755	278833	279600	gene=IY08_11355	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT43843.1
gene	2140975	2141675	279612	281492	gene=IY08_11360	protein=ABC transporter permease	protein_id=KGT43844.1
gene	2141795	2142661	281764	282795	gene=IY08_11365	protein=alpha/beta hydrolase	protein_id=KGT43845.1
gene	2142663	2143664	283015	283715	pseudo		
gene	2143710	2145410	283835	284701	gene=IY08_11375	protein=peptide ABC transporter permease	protein_id=KGT43846.1
gene	2145546	2146283	284703	285704	pseudo		
gene	2146439	2147305	285750	287450	gene=IY08_11385	protein=pyruvate oxidase	protein_id=KGT43847.1
gene	2147452	2148393	287586	288323	gene=IY08_11390	protein=zinc uptake transporter	protein_id=KGT43848.1
gene	2148427	2149029	288479	289345	gene=IY08_11395	protein=Zn-dependent hydrolase	protein_id=KGT43849.1
gene	2149237	2149722	289492	290433	gene=IY08_11400	protein=ABC transporter substrate-binding protein	protein_id=KGT43850.1
gene	2149896	2150321	290467	291069	gene=IY08_11405	protein=hypothetical protein	protein_id=KGT43851.1
gene	2150340	2151035	291277	291762	gene=IY08_11410	protein=hypothetical protein	protein_id=KGT43852.1
gene	2151052	2151522	291936	292361	gene=IY08_11415	protein=membrane protein	protein_id=KGT43853.1
gene	2152138	2152545	292380	293075	gene=IY08_11420	protein=catabolite gene activator protein	protein_id=KGT43854.1
gene	2152662	2153315	293092	293562	gene=IY08_11425	protein=membrane protein	protein_id=KGT43855.1
gene	2153438	2154061	294178	294585	gene=IY08_11430	protein=acetyltransferase	protein_id=KGT43856.1
gene	2154183	2156414	294702	295355	gene=IY08_11435	protein=hydrolase	protein_id=KGT43857.1

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gene	2156845	2157495	296223	298454	gene=IY08_11445	protein=membrane protein	protein_id=KGT43859.1
gene	2157824	2158348	298502	298684	gene=IY08_11450	protein=hypothetical protein	protein_id=KGT43860.1
gene	2158404	2159330	298885	299535	gene=IY08_11455	protein=chloramphenicol acetyltransferase	protein_id=KGT43861.1
gene	2159490	2159999	299864	300388	gene=IY08_11460	protein=acetyltransferase	protein_id=KGT43862.1
gene	2160025	2160912	300444	301370	gene=IY08_11465	protein=acetyltransferase	protein_id=KGT43863.1
gene	2161083	2161643	301530	302039	gene=IY08_11470	protein=acetyltransferase	protein_id=KGT43864.1
gene	2161677	2162624	302065	302952	gene=IY08_11475	protein=membrane protein	protein_id=KGT43865.1
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gene	2163122	2164513	303717	304664	gene=IY08_11485	protein=hypothetical protein	protein_id=KGT43867.1
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gene	2166021	2166206	306609	307157	gene=IY08_11500	protein=hypothetical protein	protein_id=KGT43870.1
gene	2166293	2166496	307466	308017	gene=IY08_11505	protein=acetyltransferase	protein_id=KGT43871.1
gene	2166889	2167785	308061	308246	gene=IY08_11510	protein=cold-shock protein	protein_id=KGT43872.1
gene	2167803	2168444	308333	308536	gene=IY08_11515	protein=cold-shock protein	protein_id=KGT43873.1
gene	2168702	2169307	308929	309825	gene=IY08_11520	protein=CAAX protease	protein_id=KGT43874.1
gene	2169378	2170244	309843	310484	gene=IY08_11525	protein=chloramphenicol acetyltransferase	protein_id=KGT43875.1
gene	2170374	2171417	310742	311347	gene=IY08_11530	protein=CTP synthase	protein_id=KGT43876.1
gene	2171547	2171978	311418	312284	gene=IY08_11535	protein=LysR family transcriptional regulator	protein_id=KGT43877.1
gene	2172287	2172550	312414	313457	gene=IY08_11540	protein=aspartate-semialdehyde dehydrogenase	protein_id=KGT43878.1
gene	2172647	2173549	313587	314018	gene=IY08_11545	protein=hypothetical protein	protein_id=KGT43879.1
gene	2173706	2174395	314327	314590	gene=IY08_11550	protein=hypothetical protein	protein_id=KGT43880.1
gene	2174654	2175541	314687	315589	gene=IY08_11555	protein=LysR family transcriptional regulator	protein_id=KGT43881.1
gene	2175575	2176171	315746	316435	gene=IY08_11560	protein=cytoplasmic protein	protein_id=KGT43882.1
gene	2176393	2178147	316694	317581	gene=IY08_11565	protein=acetyltransferase	protein_id=KGT43883.1
gene	2178140	2179936	317615	318211	gene=IY08_11570	protein=hypothetical protein	protein_id=KGT43884.1
gene	2180005	2180148	318433	320187	gene=IY08_11575	protein=multidrug ABC transporter ATP-binding protein	protein_id=KGT43885.1
gene	2180573	2181076	320180	321976	gene=IY08_11580	protein=multidrug ABC transporter ATP-binding protein	protein_id=KGT43886.1
gene	2181462	2181746	322045	322188	gene=IY08_11585	protein=integrase	protein_id=KGT43887.1
gene	2181997	2182269	322613	323116	gene=IY08_11590	protein=membrane protein	protein_id=KGT43888.1

gene	2182655	2183443	323502	323786	gene=IY08_11595	protein=hypothetical protein	protein_id=KGT43889.1
gene	2183872	2184504	324037	324309	gene=IY08_11600	protein=hypothetical protein	protein_id=KGT43890.1
gene	2184720	2185685	324695	325483	gene=IY08_11605	protein=hypothetical protein	protein_id=KGT43891.1
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gene	2188104	2188736	326760	327725	gene=IY08_11615	protein=triple helix repeat-containing collagen	protein_id=KGT43893.1
gene	2188966	2189271	328283	329578	gene=IY08_11620	protein=spore surface glycoprotein BclB	protein_id=KGT43894.1
gene	2189365	2190675	330144	330776	gene=IY08_11625	protein=cupin	protein_id=KGT43895.1
gene	2190653	2191522	331006	331311	gene=IY08_11630	protein=hypothetical protein	protein_id=KGT43896.1
gene	2191556	2191714	331405	332715	gene=IY08_11635	protein=dehydrogenase	protein_id=KGT43897.1
gene	2192020	2192613	332693	333562	gene=IY08_11640	protein=RNA polymerase sigma factor SigJ	protein_id=KGT43898.1
gene	2192927	2194039	333596	333754	gene=IY08_11645	protein=phosphoesterase	protein_id=KGT43899.1
gene	2194064	2194897	334060	334653	gene=IY08_11650	protein=methyltransferase	protein_id=KGT43900.1
gene	2194956	2196515	334967	336079	gene=IY08_11655	protein=Tellurite resistance protein	protein_id=KGT43901.1
gene	2196743	2197048	336104	336937	gene=IY08_11660	protein=hypothetical protein	protein_id=KGT43902.1
gene	2197060	2198343	336996	338555	gene=IY08_11665	protein=hypothetical protein	protein_id=KGT43903.1
gene	2198422	2198688	338783	339088	gene=IY08_11670	protein=PTS cellobiose transporter subunit IIB	protein_id=KGT43904.1
gene	2198711	2199883	339100	340383	gene=IY08_11675	protein=PTS lactose transporter subunit IIC	protein_id=KGT43905.1
gene	2199880	2200773	340462	340728	gene=IY08_11680	protein=hypothetical protein	protein_id=KGT43906.1
gene	2200912	2201460	340751	341923	gene=IY08_11685	protein=anhydro-N-acetylmuramic acid kinase	protein_id=KGT43907.1
gene	2201531	2203114	341920	342813	gene=IY08_11690	protein=ATPase	protein_id=KGT43908.1
gene	2203189	2204190	342952	343500	gene=IY08_11695	protein=glycerol-3-phosphate acyltransferase	protein_id=KGT43909.1
gene	2204422	2204892	343571	345154	gene=IY08_11700	protein=acetyltransferase	protein_id=KGT43910.1
gene	2205036	2206271	345229	346230	gene=IY08_11705	protein=threonine dehydratase	protein_id=KGT43911.1
gene	2206493	2206822	346462	346932	gene=IY08_11710	protein=MarR family transcriptional regulator	protein_id=KGT43912.1
gene	2207070	2207756	347076	348311	gene=IY08_11715	protein=MFS transporter	protein_id=KGT43913.1
gene	2208129	2209505	348533	348862	gene=IY08_11720	protein=hypothetical protein	protein_id=KGT43914.1
gene	2210859	2211071	349110	349796	gene=IY08_11725	protein=metal-dependent hydrolase	protein_id=KGT43915.1
gene	2211414	2212049	350169	351545	gene=IY08_11735	protein=RNA helicase	protein_id=KGT43916.1
gene	2212114	2213358	352899	353111	gene=IY08_11750	protein=hypothetical protein	protein_id=KGT43917.1
gene	2213700	2214014	353454	354089	gene=IY08_11755	protein=TetR family transcriptional regulator	protein_id=KGT43918.1
gene	2214142	2214375	354154	355398	gene=IY08_11760	protein=ABC transporter permease	protein_id=KGT43919.1

gene	2215255	2215959	355740	356054	gene=IY08_11765	protein=ABC transporter permease	protein_id=KGT43920.1
gene	2216871	2217581	356182	356415	gene=IY08_11770	protein=hypothetical protein	protein_id=KGT43921.1
gene	2218354	2218662	357295	357999	gene=IY08_11775	protein=triple helix repeat-containing collagen	protein_id=KGT43922.1
gene	2218880	2219077	358911	359621	gene=IY08_11780	protein=hypothetical protein	protein_id=KGT43923.1
gene	2219196	2219366	360394	360702	gene=IY08_11790	protein=hypothetical protein	protein_id=KGT43924.1
gene	2219394	2219866	360920	361117	gene=IY08_11800	protein=zinc finger protein 100	protein_id=KGT43925.1
gene	2219866	2220408	361236	361406	gene=IY08_11805	protein=phage protein	protein_id=KGT43926.1
gene	1886038	1887642	361434	361906	pseudo		
gene	1949734	1950320	361906	362448	gene=IY08_11815	protein=integrase	protein_id=KGT43927.1
scaffold12							
gene	2221004	2221420	404	820	gene=IY08_11820	protein=methyltransferase	protein_id=KGT43773.1
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gene	2224549	2226228	3949	5628	gene=IY08_11850	protein=hypothetical protein	protein_id=KGT43776.1
gene	2227299	2228000	6699	7400	gene=IY08_11855	protein=hypothetical protein	protein_id=KGT43777.1
gene	2228127	2229011	7527	8411	gene=IY08_11860	protein=hypothetical protein	protein_id=KGT43778.1
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gene	2230764	2231474	10164	10874	gene=IY08_11875	protein=methyltransferase	protein_id=KGT43780.1
gene	2231592	2231999	10992	11399	gene=IY08_11880	protein=3-demethylubiquinone-9 3-methyltransferase	protein_id=KGT43781.1
gene	2232559	2234244	11959	13644	gene=IY08_11890	protein=indolepyruvate decarboxylase	protein_id=KGT43782.1
gene	2234352	2234834	13752	14234	gene=IY08_11895	protein=MarR family transcriptional regulator	protein_id=KGT43783.1
gene	2235001	2235738	14401	15138	gene=gpmA	protein=phosphoglyceromutase	protein_id=KGT43784.1
gene	2235976	2236713	15376	16113	gene=IY08_11905	protein=stage II sporulation protein SB	protein_id=KGT43785.1
gene	2236826	2236954	16226	16354	gene=IY08_11910	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT43786.1
gene	2237027	2237203	16427	16603	gene=IY08_11915	protein=stage III sporulation protein AA	protein_id=KGT43787.1
gene	2237222	2237611	16622	17011	gene=IY08_11920	protein=cytoplasmic protein	protein_id=KGT43788.1
gene	2237823	2239292	17223	18692	gene=IY08_11925	protein=aminoacyl-histidine dipeptidase	protein_id=KGT43789.1
gene	2239538	2240347	18938	19747	gene=IY08_11930	protein=hypothetical protein	protein_id=KGT43790.1
gene	2240373	2240975	19773	20375	gene=IY08_11935	protein=hypothetical protein	protein_id=KGT43791.1
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gene	2242863	2243141	22263	22541	gene=IY08_11950	protein=transition state regulator Abh	protein_id=KGT43794.1
gene	2243661	2244911	23061	24311	gene=IY08_11955	protein=hypothetical protein	protein_id=KGT43795.1
gene	2244979	2245737	24379	25137	gene=IY08_11960	protein=hypothetical protein	protein_id=KGT43796.1
gene	2245991	2246650	25391	26050	gene=IY08_11965	protein=chloramphenicol acetyltransferase	protein_id=KGT43797.1
gene	2246982	2248295	26382	27695	gene=IY08_11970	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT43798.1
gene	2248716	2249306	28116	28706	gene=IY08_11975	protein=lipase	protein_id=KGT43799.1
gene	2250374	2251627	29774	31027	gene=IY08_11980	protein=MFS transporter	protein_id=KGT43800.1
gene	2251641	2256197	31041	35597	gene=IY08_11985	protein=peptide synthetase	protein_id=KGT43801.1
gene	2256200	2262670	35600	42070	gene=IY08_11990	protein=peptide synthetase	protein_id=KGT43802.1
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gene	2264209	2277562	43609	56962	gene=IY08_12000	protein=thioester reductase	protein_id=KGT43706.1]
gene	2277884	2278588	57284	57988	gene=IY08_12005	protein=4'-phosphopantetheinyl transferase	protein_id=KGT43707.1
gene	2278575	2279297	57975	58697	gene=IY08_12010	protein=thioesterase	protein_id=KGT43708.1
gene	2279417	2279499	58817	58899	tRNA		
gene	2279638	2279710	59038	59110	tRNA		
gene	2281161	2281745	60561	61145	gene=IY08_12025	protein=succinoglycan biosynthesis protein	protein_id=KGT43709.1
gene	2282243	2282890	61643	62290	gene=IY08_12030	protein=antigen	protein_id=KGT43710.1
gene	2283193	2283699	62593	63099	gene=IY08_12035	protein=acetyltransferase	protein_id=KGT43711.1
gene	2284066	2284251	63466	63651	gene=IY08_12040	protein=hypothetical protein	protein_id=KGT43712.1
gene	2285198	2286616	64598	66016	gene=IY08_12050	protein=glucosaminidase	protein_id=KGT43713.1
gene	2287613	2287945	67013	67345	gene=IY08_12055	protein=hypothetical protein	protein_id=KGT43714.1
gene	2288062	2288574	67462	67974	gene=IY08_12060	protein=protein kinase	protein_id=KGT43715.1
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gene	2292950	2293840	72350	73240	gene=IY08_12085	protein=serine dehydratase	protein_id=KGT43720.1
gene	2294131	2295450	73531	74850	gene=IY08_12090	protein=septum formation initiator	protein_id=KGT43721.1
gene	2295739	2295963	75139	75363	gene=IY08_12095	protein=hypothetical protein	protein_id=KGT43722.1
gene	2296252	2296425	75652	75825	gene=IY08_12100	protein=asparagine synthase	protein_id=KGT43723.1

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gene	2300773	2301894	80173	81294	gene=IY08_12125	protein=cell division protein FtsW	protein_id=KGT43727.1
gene	2303212	2304540	82612	83940	gene=IY08_12130	protein=magnesium transporter	protein_id=KGT43728.1
gene	2304698	2305795	84098	85195	gene=IY08_12135	protein=branched-chain amino acid ABC transporter	protein_id=KGT43729.1
gene	2306075	2308042	85475	87442	gene=IY08_12140	protein=MecA protein	protein_id=KGT43730.1
gene	2308448	2308981	87848	88381	gene=IY08_12145	protein=RNA polymerase subunit sigma-24	protein_id=KGT43731.1
gene	2308971	2309798	88371	89198	gene=IY08_12150	protein=ECF-type sigma factor negative effector	protein_id=KGT43732.1
gene	2309813	2311570	89213	90970	gene=IY08_12155	protein=penicillin-binding protein	protein_id=KGT43733.1
gene	2311955	2314087	91355	93487	gene=IY08_12160	protein=penicillin-binding protein	protein_id=KGT43734.1
gene	2314306	2315232	93706	94632	gene=IY08_12165	protein=beta-lactamase	protein_id=KGT43735.1
gene	2315490	2316332	94890	95732	gene=IY08_12170	protein=phosphoesterase	protein_id=KGT43736.1
gene	2316547	2316798	95947	96198	gene=IY08_12175	protein=hypothetical protein	protein_id=KGT43737.1
gene	2316982	2317707	96382	97107	gene=IY08_12180	protein=ABC transporter ATP-binding protein	protein_id=KGT43738.1
gene	2317704	2318723	97104	98123	gene=IY08_12185	protein=ABC transporter permease	protein_id=KGT43739.1
gene	2318748	2319401	98148	98801	gene=IY08_12190	protein=TetR family transcriptional regulator	protein_id=KGT43740.1
gene	2319524	2319823	98924	99223	gene=IY08_12195	protein=GNAT family acetyltransferase	protein_id=KGT43741.1
gene	2320057	2321025	99457	100425	gene=IY08_12200	protein=cytoplasmic protein	protein_id=KGT43742.1
gene	2321242	2322387	100642	101787	gene=IY08_12205	protein=acyl-CoA dehydrogenase	protein_id=KGT43743.1
gene	2322403	2323740	101803	103140	gene=IY08_12210	protein=biotin carboxylase	protein_id=KGT43744.1
gene	2323767	2323982	103167	103382	gene=IY08_12215	protein=acetyl-CoA carboxylase	protein_id=KGT43745.1
gene	2324004	2324915	103404	104315	gene=IY08_12220	protein=hydroxymethylglutaryl-CoA lyase	protein_id=KGT43746.1
gene	2324920	2325708	104320	105108	gene=IY08_12225	protein=enoyl-CoA hydratase	protein_id=KGT43747.1
gene	2325711	2327252	105111	106652	gene=IY08_12230	protein=carboxylase	protein_id=KGT43748.1
gene	2327302	2329242	106702	108642	gene=IY08_12235	protein=AMP-dependent synthetase	protein_id=KGT43749.1
gene	2329564	2329896	108964	109296	gene=IY08_12240	protein=hypothetical protein	protein_id=KGT43750.1
gene	2330493	2330849	109893	110249	gene=IY08_12245	protein=hypothetical protein	protein_id=KGT43751.1
gene	2330955	2331488	110355	110888	gene=IY08_12250	protein=aminoglycoside adenylyltransferase	protein_id=KGT43752.1
gene	2331543	2332103	110943	111503	gene=IY08_12255	protein=hypothetical protein	protein_id=KGT43753.1

gene	2332096	2332836	111496	112236	gene=IY08_12260	protein=hydrolase	protein_id=KGT43754.1
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gene	2333355	2333492	112755	112892	gene=IY08_12270	protein=hypothetical protein	protein_id=KGT43755.1
gene	2333828	2334844	113228	114244	gene=IY08_12275	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT43756.1
gene	2335021	2336178	114421	115578	gene=IY08_12280	protein=histidine kinase	protein_id=KGT43757.1
gene	2336168	2336863	115568	116263	gene=IY08_12285	protein=PhoB family transcriptional regulator	protein_id=KGT43758.1
gene	2337056	2337664	116456	117064	gene=IY08_12290	protein=HAD family hydrolase	protein_id=KGT43759.1
gene	2337678	2338049	117078	117449	pseudo		
gene	2338221	2338325	117621	117725	gene=IY08_12300	protein=hypothetical protein	protein_id=KGT43772.1
gene	2338349	2339086	117749	118486	gene=IY08_12305	protein=S-adenosylhomocysteine nucleosidase	protein_id=KGT43760.1
gene	2339230	2340078	118630	119478	gene=IY08_12310	protein=acetyltransferase	protein_id=KGT43761.1
gene	2340270	2340644	119670	120044	gene=IY08_12315	protein=hypothetical protein	protein_id=KGT43762.1
gene	2340820	2343501	120220	122901	gene=IY08_12320	protein=peptidase M4	protein_id=KGT43763.1
gene	2343834	2345060	123234	124460	gene=IY08_12325	protein=AraC family transcriptional regulator	protein_id=KGT43764.1
gene	2345622	2347313	125022	126713	gene=IY08_12330	protein=adhesin	protein_id=KGT43765.1
gene	2347356	2348204	126756	127604	gene=IY08_12335	protein=sortase	protein_id=KGT43766.1
gene	2348353	2350590	127753	129990	gene=IY08_12340	protein=collagen-binding protein	protein_id=KGT43767.1
gene	2350747	2351309	130147	130709	pseudo		
gene	2351550	2352029	130950	131429	gene=IY08_12350	protein=activator of Hsp90 ATPase 1 family protein	protein_id=KGT43768.1
gene	2352109	2355279	131509	134679	gene=IY08_12355	protein=excinuclease ABC subunit A	protein_id=KGT43769.1
gene	2355673	2356014	135073	135414	gene=IY08_12360	protein=PadR family transcriptional regulator	protein_id=KGT43770.1
gene	2356011	2356542	135411	135942	pseudo		
gene	2356523	2357478	135923	136878	gene=IY08_12370	protein=penicillin-binding protein	partial=3'
gene	2357561	2357977	136961	137377	gene=IY08_12375	protein=hypothetical protein	protein_id=KGT43663.1
gene	2358093	2358905	137493	138305	gene=IY08_12380	protein=MerR family transcriptional regulator	protein_id=KGT43664.1
gene	2358976	2360202	138376	139602	gene=IY08_12385	protein=macrolide transporter	protein_id=KGT43665.1
gene	2360940	2361692	140340	141092	gene=IY08_12395	protein=SAM-dependent methyltransferase	protein_id=KGT43666.1
gene	2361821	2362654	141221	142054	gene=IY08_12400	protein=lipase	protein_id=KGT43667.1
gene	2362772	2363566	142172	142966	gene=IY08_12405	protein=glyoxalase	protein_id=KGT43668.1
gene	2363683	2364381	143083	143781	pseudo		
gene	2364460	2365407	143860	144807	gene=IY08_12415	protein=protein kinase	protein_id=KGT43669.1

gene	2365949	2366677	145349	146077	gene=IY08_12420	protein=AraC family transcriptional regulator	protein_id=KGT43670.1
gene	2366692	2368383	146092	147783	gene=IY08_12425	protein=oligoendopeptidase F	protein_id=KGT43671.1
gene	2368554	2369147	147954	148547	gene=IY08_12430	protein=lipoprotein	protein_id=KGT43672.1
gene	2369218	2370597	148618	149997	gene=IY08_12435	protein=GntR family transcriptional regulator	protein_id=KGT43673.1
gene	2370770	2371012	150170	150412	gene=IY08_12440	protein=transposase	protein_id=KGT43674.1
gene	2371076	2372038	150476	151438	gene=IY08_12445	protein=DeoR family transcriptional regulator	protein_id=KGT43675.1
gene	2372113	2372742	151513	152142	gene=IY08_12450	protein=glutamine amidotransferase	protein_id=KGT43676.1
gene	2373114	2373317	152514	152717	gene=IY08_12455	protein=hypothetical protein	protein_id=KGT43677.1
gene	2373346	2373588	152746	152988	gene=IY08_12460	protein=hypothetical protein	protein_id=KGT43678.1
gene	2373698	2374619	153098	154019	pseudo		
gene	2374820	2374987	154220	154387	gene=IY08_12470	protein=DOD family homing endonuclease	protein_id=KGT43679.1
gene	2375179	2375676	154579	155076	gene=IY08_12475	protein=membrane protein	protein_id=KGT43680.1
gene	2375911	2376540	155311	155940	gene=IY08_12480	protein=methyltransferase	protein_id=KGT43681.1
gene	2376794	2377495	156194	156895	gene=IY08_12485	protein=methyltransferase	protein_id=KGT43682.1
gene	2377492	2378394	156892	157794	gene=IY08_12490	protein=SMP-30/gluconolactonase/LRE domain protein	protein_id=KGT43683.1
gene	2378539	2378709	157939	158109	gene=IY08_12495	protein=hypothetical protein	protein_id=KGT43684.1
gene	2379121	2380674	158521	160074	gene=IY08_12500	protein=lysyl-tRNA synthetase	protein_id=KGT43685.1
gene	2380734	2381162	160134	160562	gene=IY08_12505	protein=cell wall hydrolase	protein_id=KGT43686.1
gene	2381313	2382227	160713	161627	pseudo		
gene	2382354	2383061	161754	162461	gene=IY08_12515	protein=transcriptional regulator	protein_id=KGT43687.1
gene	2383058	2384041	162458	163441	gene=IY08_12520	protein=membrane protein	protein_id=KGT43688.1
gene	2384482	2386110	163882	165510	gene=IY08_12525	protein=elongation factor 3	protein_id=KGT43689.1
gene	2386131	2386715	165531	166115	gene=IY08_12530	protein=acetyltransferase	protein_id=KGT43690.1
gene	2386972	2387742	166372	167142	gene=IY08_12535	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT43691.1
gene	2387717	2389648	167117	169048	gene=IY08_12540	protein=ABC transporter permease	protein_id=KGT43692.1
gene	2389717	2390385	169117	169785	gene=IY08_12545	protein=hypothetical protein	protein_id=KGT43693.1
gene	2390462	2390803	169862	170203	gene=IY08_12550	protein=hypothetical protein	protein_id=KGT43694.1
gene	2391084	2392325	170484	171725	gene=IY08_12555	protein=lipase	protein_id=KGT43695.1
gene	2392413	2393438	171813	172838	gene=IY08_12560	protein=homoserine dehydrogenase	protein_id=KGT43696.1
gene	2393528	2394976	172928	174376	gene=IY08_12565	protein=GntR family transcriptional regulator	protein_id=KGT43697.1
gene	2394981	2395895	174381	175295	gene=IY08_12570	protein=D-alanine--D-alanine ligase	protein_id=KGT43698.1

gene	2396202	2396891	175602	176291	gene=IY08_12575	protein=thiaminase	protein_id=KGT43699.1
gene	2397289	2397552	176689	176952	gene=IY08_12580	protein=hypothetical protein	protein_id=KGT43700.1
gene	2398115	2398408	177515	177808	gene=IY08_12585	protein=sporulation lipoprotein YhcN/YlaJ	protein_id=KGT43701.1
gene	2398810	2399271	178210	178671	gene=IY08_12590	protein=nucleoside 2-deoxyribosyltransferase	protein_id=KGT43702.1
gene	2399623	2399918	179023	179318	pseudo		
gene	2400593	2401294	179993	180694	gene=IY08_12615	protein=hypothetical protein	protein_id=KGT43703.1
gene	2401333	2402442	180733	181842	gene=IY08_12620	protein=integrase	protein_id=KGT43704.1
gene	2402734	2402865	182134	182265	gene=IY08_12625	protein=exosporium leader peptide	protein_id=KGT43705.1
gene	2402913	2404016	182313	183416	gene=IY08_12630	protein=collagen triple helix repeat protein	protein_id=KGT43644.1
gene	2404581	2405732	183981	185132	gene=IY08_12635	protein=hypothetical protein	protein_id=KGT43645.1
gene	2405770	2405916	185170	185316	gene=IY08_12640	protein=complement C1q protein	protein_id=KGT43646.1
gene	2406241	2406594	185641	185994	gene=IY08_12650	protein=XRE family transcriptional regulator	protein_id=KGT43647.1
gene	2406795	2406986	186195	186386	gene=IY08_12655	protein=XRE family transcriptional regulator	protein_id=KGT43648.1
gene	2407043	2407309	186443	186709	gene=IY08_12660	protein=DNA-binding protein	protein_id=KGT43649.1
gene	2407309	2407473	186709	186873	gene=IY08_12665	protein=phage protein	protein_id=KGT43650.1
gene	2407531	2408586	186931	187986	gene=IY08_12670	protein=primosomal replication protein N	protein_id=KGT43651.1
gene	2408590	2408868	187990	188268	gene=IY08_12675	protein=AbrB family transcriptional regulator	protein_id=KGT43652.1
gene	2408861	2409220	188261	188620	gene=IY08_12680	protein=cell division protein SepF	protein_id=KGT43653.1
gene	2409239	2409406	188639	188806	gene=IY08_12685	protein=phage protein	protein_id=KGT43654.1
gene	2409432	2409683	188832	189083	gene=IY08_12690	protein=hypothetical protein	protein_id=KGT43655.1
gene	2409703	2410185	189103	189585	gene=IY08_12695	protein=nucleotide pyrophosphohydrolase	protein_id=KGT43656.1
gene	2410426	2411787	189826	191187	gene=IY08_12700	protein=hypothetical protein	protein_id=KGT43657.1
gene	2412565	2412864	191965	192264	gene=IY08_12705	protein=hypothetical protein	protein_id=KGT43658.1
gene	2412949	2413404	192349	192804	gene=IY08_12710	protein=MarR family transcriptional regulator	protein_id=KGT43659.1
gene	2413794	2415092	193194	194492	gene=IY08_12715	protein=hypothetical protein	protein_id=KGT43660.1
gene	2415635	2415832	195035	195232	gene=IY08_12720	protein=hypothetical protein	protein_id=KGT43661.1
gene	2415993	2416175	195393	195575	gene=IY08_12725	protein=hypothetical protein	protein_id=KGT43662.1
scaffold13							
gene	2416526	2416723	206	403	gene=IY08_12730	protein=zinc finger protein 100	protein_id=KGT43556.1
gene	2416840	2417001	520	681	gene=IY08_12735	protein=phage protein	protein_id=KGT43557.1
gene	2417029	2417511	709	1191	gene=IY08_12740	protein=ArpU family transcriptional regulator	protein_id=KGT43558.1

gene	2417511	2418053	1191	1733	gene=IY08_12745	protein=integrase	protein_id=KGT43559.1
gene	2418268	2419218	1948	2898	gene=IY08_12750	protein=nucleoside hydrolase	protein_id=KGT43560.1
gene	2419682	2420068	3362	3748	gene=IY08_12755	protein=hypothetical protein	protein_id=KGT43561.1
gene	2420912	2421346	4592	5026	gene=IY08_12765	protein=hypothetical protein	protein_id=KGT43562.1
gene	2421641	2421853	5321	5533	gene=IY08_12775	protein=phage protein	protein_id=KGT43563.1
gene	2421989	2422276	5669	5956	gene=IY08_12780	protein=transglycosylase	protein_id=KGT43564.1
gene	2422257	2422631	5937	6311	gene=IY08_12785	protein=hypothetical protein	protein_id=KGT43565.1
gene	2422637	2423014	6317	6694	gene=IY08_12790	protein=HNH endonuclease	protein_id=KGT43566.1
gene	2423152	2423652	6832	7332	gene=IY08_12795	protein=terminase	protein_id=KGT43567.1
gene	2423649	2425343	7329	9023	gene=IY08_12800	protein=terminase	protein_id=KGT43568.1
gene	2425532	2426785	9212	10465	gene=IY08_12810	protein=portal protein	protein_id=KGT43569.1
gene	2426772	2427482	10452	11162	gene=IY08_12815	protein=peptidase	protein_id=KGT43570.1
gene	2427519	2428691	11199	12371	gene=IY08_12820	protein=phage portal protein	protein_id=KGT43571.1
gene	2428712	2428999	12392	12679	gene=IY08_12825	protein=DNA-packaging protein	protein_id=KGT43572.1
gene	2428986	2429309	12666	12989	gene=IY08_12830	protein=head-tail adaptor protein	protein_id=KGT43573.1
gene	2429302	2429736	12982	13416	gene=IY08_12835	protein=HK97 family phage protein	protein_id=KGT43574.1
gene	2429733	2430092	13413	13772	gene=IY08_12840	protein=hypothetical protein	protein_id=KGT43575.1
gene	2430093	2430698	13773	14378	gene=IY08_12845	protein=tail protein	protein_id=KGT43576.1
gene	2430748	2431065	14428	14745	gene=IY08_12850	protein=hypothetical protein	protein_id=KGT43577.1
gene	2431287	2432603	14967	16283	gene=IY08_12860	protein=tail protein	protein_id=KGT43578.1
gene	2432784	2435402	16464	19082	gene=IY08_12865	protein=tail protein	protein_id=KGT43579.1
gene	2435417	2436898	19097	20578	gene=IY08_12870	protein=phage tail protein	protein_id=KGT43580.1
gene	2436895	2440977	20575	24657	gene=IY08_12875	protein=phage minor structural protein	protein_id=KGT43581.1
gene	2441015	2441251	24695	24931	gene=IY08_12880	protein=hypothetical protein	protein_id=KGT43582.1
gene	2441251	2441490	24931	25170	gene=IY08_12885	protein=holin	protein_id=KGT43583.1
gene	2441487	2442551	25167	26231	gene=IY08_12890	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT43584.1
gene	2442593	2443432	26273	27112	gene=IY08_12895	protein=triple helix repeat-containing collagen	protein_id=KGT43585.1
gene	2443557	2443730	27237	27410	gene=IY08_12900	protein=asparagine synthase	protein_id=KGT43586.1
gene	2444113	2445795	27793	29475	gene=IY08_12905	protein=hypothetical protein	protein_id=KGT43587.1
gene	2446003	2446770	29683	30450	gene=IY08_12910	protein=hypothetical protein	protein_id=KGT43588.1
gene	2446910	2447326	30590	31006	gene=IY08_12915	protein=membrane protein	protein_id=KGT43589.1

gene	2447447	2447650	31127	31330	gene=IY08_12920	protein=hypothetical protein	protein_id=KGT43590.1
gene	2447979	2448191	31659	31871	gene=IY08_12925	protein=membrane protein	protein_id=KGT43591.1
gene	2448400	2449404	32080	33084	gene=IY08_12930	protein=hypothetical protein	protein_id=KGT43592.1
gene	2449550	2449954	33230	33634	gene=IY08_12935	protein=hypothetical protein	protein_id=KGT43593.1
gene	2450115	2451350	33795	35030	gene=IY08_12940	protein=cytochrome P450	protein_id=KGT43594.1
gene	2451618	2452901	35298	36581	gene=IY08_12945	protein=MFS transporter	protein_id=KGT43595.1
gene	2452891	2453523	36571	37203	gene=IY08_12950	protein=acetyltransferase	protein_id=KGT43596.1
gene	2453594	2453749	37274	37429	gene=IY08_12955	protein=hypothetical protein	protein_id=KGT43597.1
gene	2453852	2454349	37532	38029	gene=IY08_12960	protein=PadR family transcriptional regulator	protein_id=KGT43598.1
gene	2454490	2455704	38170	39384	gene=IY08_12965	protein=cytochrome P450	protein_id=KGT43599.1
gene	2455813	2456391	39493	40071	gene=IY08_12970	protein=cysteine dioxygenase	protein_id=KGT43600.1
gene	2456567	2457418	40247	41098	gene=IY08_12975	protein=HAD family hydrolase	protein_id=KGT43601.1
gene	2457870	2459657	41550	43337	gene=IY08_12980	protein=histidine kinase	protein_id=KGT43602.1
gene	2459892	2462018	43572	45698	gene=IY08_12985	protein=penicillin-binding protein	protein_id=KGT43603.1
gene	2462095	2462625	45775	46305	gene=IY08_12990	protein=signal peptidase	protein_id=KGT43604.1
gene	2462885	2464072	46565	47752	gene=IY08_12995	protein=UDP-glucosyltransferase	protein_id=KGT43605.1
gene	2464167	2464847	47847	48527	gene=IY08_13000	protein=aspartate racemase	protein_id=KGT43606.1
gene	2465258	2465806	48938	49486	gene=IY08_13005	protein=hypothetical protein	protein_id=KGT43607.1
gene	2465817	2467517	49497	51197	gene=IY08_13010	protein=ABC transporter ATP-binding protein	protein_id=KGT43608.1
gene	2467510	2468310	51190	51990	gene=IY08_13015	protein=cobalamin biosynthesis protein CbiQ	protein_id=KGT43609.1
gene	2468656	2469915	52336	53595	gene=IY08_13025	protein=histidine kinase	protein_id=KGT43610.1
gene	2470132	2470335	53812	54015	gene=IY08_13030	protein=transposase	protein_id=KGT43611.1
gene	2470770	2471633	54450	55313	gene=IY08_13035	protein=hypothetical protein	protein_id=KGT43612.1
gene	2472058	2474172	55738	57852	gene=IY08_13040	protein=40-residue YVTN family beta-propeller	protein_id=KGT43613.1
gene	2474739	2475203	58419	58883	gene=IY08_13045	protein=hypothetical protein	protein_id=KGT43614.1
gene	2476338	2477066	60018	60746	gene=IY08_13050	protein=hypothetical protein	protein_id=KGT43615.1
gene	2477417	2477883	61097	61563	pseudo		
gene	2479932	2481731	63612	65411	gene=IY08_13060	protein=reverse transcriptase	protein_id=KGT43616.1
gene	2482159	2482329	65839	66009	pseudo		
gene	2483713	2484594	67393	68274	gene=IY08_13085	protein=serine/threonine protein kinase	protein_id=KGT43617.1
gene	2484722	2485228	68402	68908	gene=IY08_13090	protein=glutamate-rich protein GrpB	protein_id=KGT43618.1

gene	2485400	2486389	69080	70069	gene=IY08_13095	protein=alcohol dehydrogenase	protein_id=KGT43619.1
gene	2486637	2487236	70317	70916	gene=IY08_13100	protein=phosphoesterase	protein_id=KGT43620.1
gene	2487526	2489664	71206	73344	gene=IY08_13105	protein=dihydropteridine reductase	protein_id=KGT43621.1
gene	2489854	2490450	73534	74130	gene=IY08_13110	protein=TetR family transcriptional regulator	protein_id=KGT43622.1
gene	2490535	2491356	74215	75036	gene=IY08_13115	protein=oxidoreductase	protein_id=KGT43623.1
gene	2491736	2492968	75416	76648	gene=IY08_13120	protein=permease	protein_id=KGT43624.1
gene	2493231	2494256	76911	77936	gene=IY08_13125	protein=penicillin-binding protein	protein_id=KGT43625.1
gene	2494933	2495388	78613	79068	gene=IY08_13135	protein=membrane protein	protein_id=KGT43626.1
gene	2495468	2495974	79148	79654	gene=IY08_13140	protein=ABC transporter	protein_id=KGT43627.1
gene	2496174	2496980	79854	80660	gene=IY08_13145	protein=alanine aminotransferase	protein_id=KGT43628.1
gene	2497227	2497721	80907	81401	gene=IY08_13150	protein=XRE family transcriptional regulator	protein_id=KGT43629.1
gene	2497735	2498109	81415	81789	gene=IY08_13155	protein=ammonia permease	protein_id=KGT43630.1
gene	2498670	2499095	82350	82775	gene=IY08_13160	protein=hypothetical protein	protein_id=KGT43631.1
gene	2499613	2500836	83293	84516	gene=IY08_13165	protein=methyltransferase	protein_id=KGT43632.1
gene	2500949	2502244	84629	85924	gene=IY08_13170	protein=permease	protein_id=KGT43633.1
gene	2502508	2503305	86188	86985	gene=IY08_13175	protein=MerR family transcriptional regulator	protein_id=KGT43634.1
gene	2503328	2503972	87008	87652	gene=IY08_13180	protein=membrane protein	protein_id=KGT43635.1
gene	2504022	2504723	87702	88403	gene=IY08_13185	protein=hypothetical protein	protein_id=KGT43636.1
gene	2505234	2506034	88914	89714	gene=IY08_13195	protein=acetyltransferase	protein_id=KGT43637.1
gene	2506080	2506958	89760	90638	gene=IY08_13200	protein=glycerophosphodiester phosphodiesterase	protein_id=KGT43638.1
gene	2507245	2508090	90925	91770	gene=IY08_13205	protein=peptidase M15	protein_id=KGT43639.1
gene	2508224	2508685	91904	92365	gene=IY08_13210	protein=alcohol dehydrogenase	protein_id=KGT43640.1
gene	2508860	2509390	92540	93070	gene=IY08_13215	protein=alpha/beta hydrolase	protein_id=KGT43641.1
gene	2509436	2510869	93116	94549	gene=IY08_13220	protein=GntR family transcriptional regulator	protein_id=KGT43642.1
gene	2511022	2511405	94702	95085	gene=IY08_13225	protein=membrane protein	protein_id=KGT43643.1
gene	2511432	2511956	95112	95636	gene=IY08_13230	protein=membrane protein	protein_id=KGT43478.1
gene	2512095	2513456	95775	97136	gene=IY08_13235	protein=chitosanase	protein_id=KGT43479.1
gene	2513619	2514542	97299	98222	gene=IY08_13240	protein=nucleoside hydrolase	protein_id=KGT43480.1
gene	2514619	2515077	98299	98757	gene=IY08_13245	protein=GCN5 family acetyltransferase	protein_id=KGT43481.1
gene	2515107	2515454	98787	99134	gene=IY08_13250	protein=cytochrome C biogenesis protein	protein_id=KGT43482.1
gene	2515471	2515917	99151	99597	gene=IY08_13255	protein=DNA mismatch repair protein MutT	protein_id=KGT43483.1

gene	2516117	2516365	99797	100045	gene=IY08_13260	protein=sporulation protein	protein_id=KGT43484.1
gene	2516466	2517482	100146	101162	gene=IY08_13265	protein=penicillin-binding protein	protein_id=KGT43485.1
gene	2517514	2517657	101194	101337	gene=IY08_13270	protein=Spore cortex-lytic enzyme	protein_id=KGT43486.1
gene	2517937	2519145	101617	102825	gene=IY08_13275	protein=membrane protein	protein_id=KGT43487.1
gene	2519276	2519701	102956	103381	gene=IY08_13280	protein=acetyltransferase	protein_id=KGT43488.1
gene	2519910	2520353	103590	104033	gene=IY08_13285	protein=DNA mismatch repair protein MutT	protein_id=KGT43489.1
gene	2520384	2521514	104064	105194	gene=IY08_13290	protein=DNA polymerase III subunit beta	protein_id=KGT43490.1
gene	2521734	2522657	105414	106337	gene=IY08_13295	protein=hypothetical protein	protein_id=KGT43491.1
gene	2522721	2523683	106401	107363	gene=IY08_13300	protein=membrane protein	protein_id=KGT43492.1
gene	2523980	2524957	107660	108637	gene=IY08_13305	protein=endonuclease	protein_id=KGT43493.1
gene	2525574	2525969	109254	109649	gene=IY08_13315	protein=endoribonuclease L-PSP	protein_id=KGT43494.1
gene	2526677	2527492	110357	111172	gene=IY08_13320	protein=cytoplasmic protein	protein_id=KGT43495.1
gene	2527571	2527978	111251	111658	gene=IY08_13325	protein=enterochelin esterase	protein_id=KGT43496.1
gene	2528070	2529128	111750	112808	gene=IY08_13330	protein=esterase	protein_id=KGT43497.1
gene	2529218	2529583	112898	113263	gene=IY08_13335	protein=hypothetical protein	protein_id=KGT43498.1
gene	2529865	2530236	113545	113916	gene=IY08_13340	protein=hypothetical protein	protein_id=KGT43499.1
gene	2530249	2531100	113929	114780	gene=IY08_13345	protein=patatin	protein_id=KGT43500.1
gene	2531280	2531657	114960	115337	gene=IY08_13350	protein=cytoplasmic protein	protein_id=KGT43501.1
gene	2531778	2532251	115458	115931	gene=IY08_13355	protein=acetyltransferase	protein_id=KGT43502.1
gene	2532253	2532774	115933	116454	gene=IY08_13360	protein=metal-dependent hydrolase	protein_id=KGT43503.1
gene	2532791	2533318	116471	116998	gene=IY08_13365	protein=acetyltransferase	protein_id=KGT43504.1
gene	2533382	2534704	117062	118384	gene=IY08_13370	protein=glutamate synthase	protein_id=KGT43505.1
gene	2534787	2535566	118467	119246	gene=IY08_13375	protein=UDP pyrophosphate phosphatase	protein_id=KGT43506.1
gene	2535699	2535905	119379	119585	gene=IY08_13380	protein=hypothetical protein	protein_id=KGT43507.1
gene	2535963	2536343	119643	120023	gene=IY08_13385	protein=hypothetical protein	protein_id=KGT43508.1
gene	2536421	2536984	120101	120664	gene=IY08_13390	protein=GNAT family acetyltransferase	protein_id=KGT43509.1
gene	2537017	2537589	120697	121269	gene=IY08_13395	protein=membrane protein	protein_id=KGT43510.1
gene	2537793	2539223	121473	122903	gene=IY08_13400	protein=glucose dehydrogenase	protein_id=KGT43511.1
gene	2539360	2539617	123040	123297	gene=IY08_13405	protein=hypothetical protein	protein_id=KGT43512.1
gene	2539709	2539888	123389	123568	gene=IY08_13410	protein=hypothetical protein	protein_id=KGT43513.1
gene	2540082	2540741	123762	124421	gene=IY08_13415	protein=serine/threonine protein kinase	protein_id=KGT43514.1

gene	2540934	2541374	124614	125054	gene=IY08_13420	protein=cytochrome C biogenesis protein CcdA	protein_id=KGT43515.1
gene	2541591	2542706	125271	126386	gene=IY08_13425	protein=oxidoreductase	protein_id=KGT43516.1
gene	2542833	2543486	126513	127166	gene=IY08_13430	protein=hypothetical protein	protein_id=KGT43517.1
gene	2543831	2544598	127511	128278	gene=IY08_13440	protein=acetyltransferase	protein_id=KGT43518.1
gene	2544789	2545292	128469	128972	gene=IY08_13445	protein=MepB	protein_id=KGT43519.1
gene	2545401	2545769	129081	129449	gene=IY08_13450	protein=cytoplasmic protein	protein_id=KGT43520.1
gene	2545975	2546667	129655	130347	gene=IY08_13455	protein=2-haloalkanoic acid dehalogenase	protein_id=KGT43521.1
gene	2547114	2547779	130794	131459	gene=IY08_13460	protein=transcriptional regulator	protein_id=KGT43522.1
gene	2547772	2549244	131452	132924	gene=IY08_13465	protein=histidine kinase	protein_id=KGT43523.1
gene	2549573	2550109	133253	133789	gene=IY08_13470	protein=damage-inducible protein DinB	protein_id=KGT43524.1
gene	2550311	2550493	133991	134173	gene=IY08_13475	protein=hypothetical protein	protein_id=KGT43525.1
gene	2550786	2551463	134466	135143	gene=IY08_13480	protein=ABC transporter	protein_id=KGT43526.1
gene	2551475	2552905	135155	136585	gene=IY08_13485	protein=permease	protein_id=KGT43527.1
gene	2553460	2554461	137140	138141	gene=IY08_13490	protein=hypothetical protein	protein_id=KGT43528.1
gene	2555093	2556049	138773	139729	gene=IY08_13495	protein=lipase	protein_id=KGT43529.1
gene	2556161	2557615	139841	141295	gene=IY08_13500	protein=2,4-diaminobutyrate decarboxylase	protein_id=KGT43530.1
gene	2557671	2564687	141351	148367	gene=IY08_13505	protein=AMP-binding protein	protein_id=KGT43531.1
gene	2564720	2565697	148400	149377	gene=IY08_13510	protein=dehydrogenase	protein_id=KGT43532.1
gene	2566569	2569127	150249	152807	gene=IY08_13515	protein=pullulanase	protein_id=KGT43533.1
gene	2569604	2571307	153284	154987	gene=IY08_13520	protein=bacillolysin	protein_id=KGT43534.1
gene	2571648	2573600	155328	157280	gene=IY08_13525	protein=2', 3'-cyclic nucleotide 2'-phosphodiesterase	protein_id=KGT43535.1
gene	2574137	2574652	157817	158332	gene=IY08_13530	protein=PadR family transcriptional regulator	protein_id=KGT43536.1
gene	2574781	2575257	158461	158937	gene=IY08_13535	protein=AraC family transcriptional regulator	protein_id=KGT43537.1
gene	2575812	2577116	159492	160796	gene=IY08_13540	protein=preprotein translocase subunit SecY	protein_id=KGT43538.1
gene	2577202	2578119	160882	161799	gene=IY08_13545	protein=transporter	protein_id=KGT43539.1
gene	2578268	2579701	161948	163381	gene=IY08_13550	protein=GntR family transcriptional regulator	protein_id=KGT43540.1
gene	2579769	2579870	163449	163550	gene=IY08_13555	protein=oxidoreductase	protein_id=KGT43541.1
gene	2580187	2581041	163867	164721	gene=IY08_13560	protein=acetyltransferase	protein_id=KGT43542.1
gene	2581156	2581491	164836	165171	gene=IY08_13565	protein=hypothetical protein	protein_id=KGT43543.1
gene	2581503	2582672	165183	166352	gene=IY08_13570	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT43544.1
gene	2582882	2583286	166562	166966	gene=IY08_13575	protein=hypothetical protein	protein_id=KGT43545.1

gene	2583331	2583867	167011	167547	gene=IY08_13580	protein=cytoplasmic protein	protein_id=KGT43546.1
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gene	2584268	2584765	167948	168445	gene=IY08_13590	protein=acetyltransferase	protein_id=KGT43548.1
gene	2584792	2585148	168472	168828	gene=IY08_13595	protein=hypothetical protein	protein_id=KGT43549.1
gene	2585255	2585851	168935	169531	gene=IY08_13600	protein=hypothetical protein	protein_id=KGT43550.1
gene	2585878	2587218	169558	170898	gene=IY08_13605	protein=sporulation protein	protein_id=KGT43551.1
gene	2587234	2588013	170914	171693	gene=IY08_13610	protein=hydrolase	protein_id=KGT43552.1
gene	2588159	2588491	171839	172171	gene=IY08_13615	protein=hypothetical protein	protein_id=KGT43553.1
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gene	2589278	2590202	172958	173882	gene=IY08_13625	protein=6-aminohexanoate hydrolase	protein_id=KGT43555.1]
gene	2590340	2591179	174020	174859	gene=IY08_13630	protein=tryptophan 2,3-dioxygenase	protein_id=KGT43444.1
gene	2591212	2591841	174892	175521	gene=IY08_13635	protein=kynurenine formamidase	protein_id=KGT43445.1
gene	2591844	2593130	175524	176810	gene=IY08_13640	protein=kynureninase	protein_id=KGT43446.1
gene	2593290	2593901	176970	177581	gene=IY08_13645	protein=TetR family transcriptional regulator	protein_id=KGT43447.1
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gene	2594471	2595274	178151	178954	pseudo		
gene	2595302	2595760	178982	179440	gene=IY08_13660	protein=3-isopropylmalate dehydrogenase	protein_id=KGT43449.1
gene	2595910	2596149	179590	179829	gene=IY08_13665	protein=hypothetical protein	protein_id=KGT43450.1
gene	2596286	2596543	179966	180223	gene=IY08_13670	protein=hypothetical protein	protein_id=KGT43451.1
gene	2596656	2598506	180336	182186	gene=IY08_13675	protein=acetoin dehydrogenase	protein_id=KGT43452.1
gene	2598629	2598796	182309	182476	gene=IY08_13680	protein=membrane protein	protein_id=KGT43453.1
gene	2598820	2599158	182500	182838	gene=IY08_13685	protein=cytoplasmic protein	protein_id=KGT43454.1
gene	2599131	2599727	182811	183407	gene=IY08_13690	protein=GNAT family acetyltransferase	protein_id=KGT43455.1
gene	2599724	2600509	183404	184189	gene=IY08_13695	protein=cytochrome C	protein_id=KGT43456.1
gene	2600760	2601257	184440	184937	gene=IY08_13700	protein=lipoprotein	protein_id=KGT43457.1
gene	2601323	2601922	185003	185602	gene=IY08_13705	protein=methyltransferase	protein_id=KGT43458.1
gene	2602012	2602413	185692	186093	gene=IY08_13710	protein=Rrf2 family transcriptional regulator	protein_id=KGT43459.1
gene	2602499	2603089	186179	186769	gene=IY08_13715	protein=hypothetical protein	protein_id=KGT43460.1
gene	2603344	2603937	187024	187617	gene=IY08_13720	protein=hypothetical protein	protein_id=KGT43461.1
gene	2604023	2605402	187703	189082	gene=acoL	protein=dihydrolipoamide dehydrogenase	protein_id=KGT43462.1

gene	2605418	2606617	189098	190297	gene=IY08_13730	protein=branched-chain alpha-keto acid dehydrogenase subunit E2	protein_id=KGT43463.1
gene	2606645	2607679	190325	191359	gene=IY08_13735	protein=pyruvate dehydrogenase	protein_id=KGT43464.1
gene	2607697	2608695	191377	192375	gene=IY08_13740	protein=acetoin:2,6-dichlorophenolindophenol oxidoreductase subunit alpha	protein_id=KGT43465.1
gene	2608865	2609344	192545	193024	gene=IY08_13750	protein=DltD domain-containing protein	protein_id=KGT43466.1
gene	2609510	2610355	193190	194035	gene=IY08_13755	protein=short-chain dehydrogenase	protein_id=KGT43467.1
gene	2610396	2610905	194076	194585	gene=IY08_13760	protein=glutamate-rich protein grpB	protein_id=KGT43468.1
gene	2610960	2611397	194640	195077	gene=IY08_13765	protein=DNA mismatch repair protein MutT	protein_id=KGT43469.1
gene	2611426	2611737	195106	195417	gene=IY08_13770	protein=capsular biosynthesis protein CpsH	protein_id=KGT43470.1
gene	2611818	2612594	195498	196274	gene=IY08_13775	protein=protein phosphatase	protein_id=KGT43471.1
gene	2612626	2613111	196306	196791	gene=IY08_13780	protein=HIT family hydrolase	protein_id=KGT43472.1
gene	2613218	2613385	196898	197065	gene=IY08_13785	protein=septum formation initiator	protein_id=KGT43473.1
gene	2613603	2613839	197283	197519	gene=IY08_13790	protein=hypothetical protein	protein_id=KGT43474.1
gene	2613893	2614729	197573	198409	gene=IY08_13795	protein=glycine/betaine ABC transporter	protein_id=KGT43475.1
gene	2614722	2615927	198402	199607	gene=IY08_13800	protein=glycine/betaine ABC transporter ATP-binding	protein_id=KGT43476.1
gene	2616099	2616583	199779	200263	gene=IY08_13805	protein=glycine/betaine ABC transporter	protein_id=KGT43477.1
gene	2616668	2616969	200348	200649	gene=IY08_13810	protein=glycine/betaine ABC transporter	protein_id=KGT43267.1]
gene	2617016	2617597	200696	201277	gene=IY08_13815	protein=Clp protease	protein_id=KGT43268.1
gene	2617619	2618305	201299	201985	gene=IY08_13820	protein=RNA polymerase factor sigma-70	protein_id=KGT43269.1
gene	2618448	2618768	202128	202448	gene=IY08_13825	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT43270.1
gene	2618773	2619435	202453	203115	gene=IY08_13830	protein=ribose 5-phosphate isomerase	protein_id=KGT43271.1
gene	2619550	2619984	203230	203664	gene=IY08_13835	protein=hypothetical protein	protein_id=KGT43272.1
gene	2620111	2621478	203791	205158	gene=IY08_13840	protein=chitin-binding protein	protein_id=KGT43273.1
gene	2621932	2623125	205612	206805	gene=IY08_13845	protein=glycosyl transferase family 1	protein_id=KGT43274.1
gene	2623217	2623897	206897	207577	gene=IY08_13850	protein=cytoplasmic protein	protein_id=KGT43275.1
gene	2624059	2624562	207739	208242	gene=IY08_13855	protein=topology modulation protein	protein_id=KGT43276.1
gene	2624559	2625488	208239	209168	gene=IY08_13860	protein=aminoglycoside phosphotransferase	protein_id=KGT43277.1
gene	2625513	2625899	209193	209579	gene=IY08_13865	protein=membrane protein	protein_id=KGT43278.1
gene	2625965	2626672	209645	210352	gene=IY08_13870	protein=ubiquinone biosynthesis methyltransferase UbiE	protein_id=KGT43279.1
gene	2626694	2627047	210374	210727	gene=IY08_13875	protein=cytoplasmic protein	protein_id=KGT43280.1

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gene	2627503	2627919	211183	211599	gene=IY08_13885	protein=acetyltransferase	protein_id=KGT43282.1
gene	2627948	2628319	211628	211999	gene=IY08_13890	protein=hypothetical protein	protein_id=KGT43283.1
gene	2628316	2629092	211996	212772	gene=IY08_13895	protein=membrane protein	protein_id=KGT43284.1
gene	2629219	2629731	212899	213411	gene=IY08_13900	protein=phosphinothricin acetyltransferase	protein_id=KGT43285.1
gene	2629812	2630813	213492	214493	gene=IY08_13905	protein=membrane protein	protein_id=KGT43286.1
gene	2630800	2631144	214480	214824	gene=IY08_13910	protein=PadR family transcriptional regulator	protein_id=KGT43287.1
gene	2632022	2632750	215702	216430	gene=IY08_13925	protein=hypothetical protein	protein_id=KGT43288.1
gene	2632867	2634942	216547	218622	gene=IY08_13930	protein=helicase UvrD	protein_id=KGT43289.1
gene	2635164	2635576	218844	219256	pseudo		
gene	2635631	2636011	219311	219691	gene=IY08_13940	protein=branched-chain alpha-keto acid dehydrogenase	protein_id=KGT43290.1
gene	2636037	2638154	219717	221834	gene=IY08_13945	protein=ATP-dependent DNA helicase	protein_id=KGT43291.1
gene	2638430	2638591	222110	222271	gene=IY08_13950	protein=hypothetical protein	protein_id=KGT43292.1
gene	2639278	2639901	222958	223581	gene=IY08_13955	protein=acetylglutamate kinase	protein_id=KGT43293.1
gene	2640066	2640422	223746	224102	gene=IY08_13960	protein=cytoplasmic protein	protein_id=KGT43294.1
gene	2640558	2641010	224238	224690	gene=IY08_13965	protein=hypothetical protein	protein_id=KGT43295.1
gene	2641412	2642146	225092	225826	gene=IY08_13975	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT43296.1
gene	2642436	2642885	226116	226565	gene=IY08_13980	protein=hypothetical protein	protein_id=KGT43297.1
gene	2643127	2643315	226807	226995	gene=IY08_13985	protein=hypothetical protein	protein_id=KGT43298.1
gene	2643634	2644563	227314	228243	gene=IY08_13990	protein=inorganic pyrophosphatase	protein_id=KGT43299.1
gene	2644724	2645389	228404	229069	gene=IY08_13995	protein=chitin-binding protein	protein_id=KGT43300.1
gene	2645636	2646139	229316	229819	gene=IY08_14000	protein=GCN5 family acetyltransferase	protein_id=KGT43301.1
gene	2646246	2646887	229926	230567	gene=IY08_14005	protein=phosphohydrolase	protein_id=KGT43302.1
gene	2647145	2647510	230825	231190	gene=IY08_14010	protein=alkylhydroperoxidase	protein_id=KGT43303.1
gene	2647610	2649100	231290	232780	gene=IY08_14015	protein=sodium:alanine symporter	protein_id=KGT43304.1
gene	2649231	2650715	232911	234395	gene=IY08_14020	protein=betaine-aldehyde dehydrogenase	protein_id=KGT43305.1
gene	2650733	2651629	234413	235309	gene=IY08_14025	protein=dihydrodipicolinate synthase	protein_id=KGT43306.1
gene	2651652	2652593	235332	236273	gene=IY08_14030	protein=proline racemase	protein_id=KGT43307.1
gene	2652590	2653627	236270	237307	gene=IY08_14035	protein=proline racemase	protein_id=KGT43308.1
gene	2653624	2654799	237304	238479	gene=IY08_14040	protein=glycine oxidase	protein_id=KGT43309.1
gene	2654980	2656641	238660	240321	gene=IY08_14045	protein=histidine kinase	protein_id=KGT43310.1

gene	2656751	2657023	240431	240703	gene=IY08_14050	protein=pyridine nucleotide-disulfide oxidoreductase	protein_id=KGT43311.1
gene	2657020	2657352	240700	241032	gene=IY08_14055	protein=(2Fe-2S)-binding protein	protein_id=KGT43312.1
gene	2657349	2658593	241029	242273	gene=IY08_14060	protein=sarcosine oxidase subunit alpha	protein_id=KGT43313.1
gene	2658651	2659373	242331	243053	gene=IY08_14065	protein=hypothetical protein	protein_id=KGT43314.1
gene	2659530	2659838	243210	243518	gene=IY08_14070	protein=hypothetical protein	protein_id=KGT43315.1
gene	2659826	2660275	243506	243955	gene=IY08_14075	protein=hypothetical protein	protein_id=KGT43316.1
gene	2660534	2661298	244214	244978	gene=IY08_14080	protein=hypothetical protein	protein_id=KGT43317.1
gene	2661504	2662004	245184	245684	gene=IY08_14085	protein=acetyltransferase	protein_id=KGT43318.1
gene	2662041	2663156	245721	246836	gene=IY08_14090	protein=metal-dependent phosphohydrolase	protein_id=KGT43319.1
gene	2663434	2664039	247114	247719	gene=IY08_14095	protein=membrane protein	protein_id=KGT43320.1
gene	2664208	2664432	247888	248112	gene=IY08_14100	protein=hypothetical protein	protein_id=KGT43321.1
gene	2664473	2665654	248153	249334	gene=IY08_14105	protein=alanine transporter	protein_id=KGT43322.1
gene	2665923	2666450	249603	250130	gene=IY08_14110	protein=acetyltransferase	protein_id=KGT43323.1
gene	2666572	2668194	250252	251874	gene=IY08_14115	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT43324.1
gene	2668214	2669215	251894	252895	gene=IY08_14120	protein=peptidase P60	protein_id=KGT43325.1
gene	2669256	2670317	252936	253997	gene=IY08_14125	protein=mandelate racemase	protein_id=KGT43326.1
gene	2670504	2670830	254184	254510	gene=IY08_14130	protein=hypothetical protein	protein_id=KGT43327.1
gene	2671126	2671482	254806	255162	gene=IY08_14135	protein=cell division protein DIVIC	protein_id=KGT43328.1
gene	2671767	2672693	255447	256373	gene=IY08_14140	protein=oxidoreductase	protein_id=KGT43329.1
gene	2672713	2673309	256393	256989	gene=IY08_14145	protein=AraC family transcriptional regulator	protein_id=KGT43330.1
gene	2673306	2673797	256986	257477	gene=IY08_14150	protein=ankyrin	protein_id=KGT43331.1
gene	2674335	2674565	258015	258245	gene=IY08_14155	protein=hypothetical protein	protein_id=KGT43332.1
gene	2674936	2675199	258616	258879	gene=IY08_14160	protein=hypothetical protein	protein_id=KGT43333.1
gene	2675343	2675903	259023	259583	gene=IY08_14165	protein=shikimate kinase	protein_id=KGT43334.1
gene	2676005	2676766	259685	260446	gene=IY08_14170	protein=methyltransferase	protein_id=KGT43335.1
gene	2676994	2678733	260674	262413	gene=IY08_14175	protein=x-prolyl-dipeptidyl aminopeptidase	protein_id=KGT43336.1
gene	2679055	2679897	262735	263577	gene=prsA	protein=peptidylprolyl isomerase	protein_id=KGT43337.1
gene	2680087	2681463	263767	265143	gene=IY08_14185	protein=histidine kinase	protein_id=KGT43338.1
gene	2681456	2682103	265136	265783	gene=IY08_14190	protein=regulator	protein_id=KGT43339.1
gene	2682225	2682641	265905	266321	gene=IY08_14195	protein=hypothetical protein	protein_id=KGT43340.1
gene	2682838	2683284	266518	266964	gene=IY08_14200	protein=GNAT family acetyltransferase	protein_id=KGT43341.1

gene	2683545	2684249	267225	267929	gene=IY08_14205	protein=alpha/beta hydrolase	protein_id=KGT43342.1
gene	2684304	2684963	267984	268643	gene=IY08_14210	protein=MTA/SAH nucleosidase	protein_id=KGT43343.1
gene	2684966	2685679	268646	269359	gene=IY08_14215	protein=5'-methylthioadenosine nucleosidase	protein_id=KGT43344.1
gene	2685697	2686446	269377	270126	gene=IY08_14220	protein=acetylglucosaminyl diphospho-UDP acetyl-beta-D-mannosaminyltransferase	protein_id=KGT43345.1
gene	2686459	2688042	270139	271722	gene=IY08_14225	protein=oligoendopeptidase F	protein_id=KGT43346.1
gene	2688330	2689190	272010	272870	gene=IY08_14230	protein=DegV family EDD domain-containing protein	protein_id=KGT43347.1
gene	2689669	2690121	273349	273801	gene=IY08_14235	protein=spore coat protein	protein_id=KGT43348.1
gene	2690136	2690336	273816	274016	gene=IY08_14240	protein=spore coat protein	protein_id=KGT43349.1
gene	2690710	2691195	274390	274875	gene=IY08_14245	protein=spore coat protein	protein_id=KGT43350.1
gene	2691781	2692551	275461	276231	gene=IY08_14250	protein=GCN5 family acetyltransferase	protein_id=KGT43351.1
gene	2692961	2693197	276641	276877	gene=IY08_14265	protein=hypothetical protein	protein_id=KGT43352.1
gene	2693450	2693770	277130	277450	gene=IY08_14270	protein=hypothetical protein	protein_id=KGT43353.1
gene	2693825	2695357	277505	279037	gene=IY08_14275	protein=major facilitator transporter	protein_id=KGT43354.1
gene	2695382	2696089	279062	279769	gene=IY08_14280	protein=cytoplasmic protein	protein_id=KGT43355.1
gene	2696108	2696818	279788	280498	gene=IY08_14285	protein=cytoplasmic protein	protein_id=KGT43356.1
gene	2696832	2697455	280512	281135	gene=IY08_14290	protein=hypothetical protein	protein_id=KGT43357.1
gene	2697615	2699351	281295	283031	gene=IY08_14295	protein=peptide-binding protein	protein_id=KGT43358.1
gene	2699453	2700667	283133	284347	gene=IY08_14300	protein=MFS transporter	protein_id=KGT43359.1
gene	2700838	2701509	284518	285189	gene=IY08_14305	protein=lipoprotein	protein_id=KGT43360.1
gene	2701844	2701990	285524	285670	gene=IY08_14310	protein=chorismate mutase	protein_id=KGT43361.1
gene	2702307	2702702	285987	286382	gene=IY08_14315	protein=cytosolic protein	protein_id=KGT43362.1
gene	2702780	2703022	286460	286702	gene=IY08_14320	protein=membrane protein	protein_id=KGT43363.1
gene	2703202	2704167	286882	287847	gene=IY08_14325	protein=nucleoside hydrolase	protein_id=KGT43364.1
gene	2704245	2704433	287925	288113	gene=IY08_14330	protein=hypothetical protein	protein_id=KGT43365.1
gene	2704503	2705288	288183	288968	gene=IY08_14335	protein=SAM-dependent methyltransferase	protein_id=KGT43366.1
gene	2705486	2705854	289166	289534	gene=IY08_14340	protein=hypothetical protein	protein_id=KGT43367.1
gene	2706006	2706122	289686	289802	gene=IY08_14345	protein=cell wall assembly protein	protein_id=KGT43368.1
gene	2706653	2707087	290333	290767	gene=IY08_14355	protein=exosporium protein C	protein_id=KGT43369.1
gene	2707382	2708584	291062	292264	gene=IY08_14360	protein=macrolide transporter	protein_id=KGT43370.1
gene	2708738	2709037	292418	292717	gene=IY08_14365	protein=hypothetical protein	protein_id=KGT43371.1

gene	2709207	2709569	292887	293249	gene=IY08_14370	protein=lipoprotein	protein_id=KGT43372.1
gene	2709912	2711111	293592	294791	gene=IY08_14375	protein=aminotransferase	protein_id=KGT43373.1
gene	2711168	2711566	294848	295246	gene=IY08_14380	protein=hypothetical protein	protein_id=KGT43374.1
gene	2711651	2712472	295331	296152	gene=IY08_14385	protein=pantothenate kinase	protein_id=KGT43375.1
gene	2712487	2712996	296167	296676	gene=IY08_14390	protein=2'-5' RNA ligase	protein_id=KGT43376.1
gene	2713115	2713594	296795	297274	gene=IY08_14395	protein=cobalamin biosynthesis protein CbiX	protein_id=KGT43377.1
gene	2713634	2714305	297314	297985	gene=IY08_14400	protein=ABC transporter permease	protein_id=KGT43378.1
gene	2714302	2715174	297982	298854	gene=IY08_14405	protein=ABC transporter ATP-binding protein	protein_id=KGT43379.1
gene	2715171	2715551	298851	299231	gene=IY08_14410	protein=transcriptional regulator	protein_id=KGT43380.1
gene	2715676	2716164	299356	299844	gene=IY08_14415	protein=hypothetical protein	protein_id=KGT43381.1
gene	2716178	2716771	299858	300451	gene=IY08_14420	protein=hypothetical protein	protein_id=KGT43382.1
gene	2716950	2717048	300630	300728	gene=IY08_14425	protein=hypothetical protein	protein_id=KGT43383.1
gene	2717213	2717353	300893	301033	gene=IY08_14430	protein=carbohydrate kinase	protein_id=KGT43384.1
gene	2717381	2717524	301061	301204	gene=IY08_14435	protein=polyketide synthase	protein_id=KGT43385.1
gene	2717553	2717696	301233	301376	gene=IY08_14440	protein=sporulation protein	protein_id=KGT43386.1
gene	2717825	2717965	301505	301645	gene=IY08_14445	protein=sporulation protein	protein_id=KGT43387.1
gene	2718018	2718158	301698	301838	gene=IY08_14450	protein=sporulation protein	protein_id=KGT43388.1
gene	2718186	2718326	301866	302006	gene=IY08_14455	protein=sporulation protein	protein_id=KGT43389.1
gene	2718567	2719652	302247	303332	gene=IY08_14460	protein=permease	protein_id=KGT43390.1
gene	2719802	2720623	303482	304303	gene=IY08_14465	protein=hypothetical protein	protein_id=KGT43391.1
gene	2720852	2720944	304532	304624	gene=IY08_14470	protein=hypothetical protein	protein_id=KGT43392.1
gene	2721140	2722252	304820	305932	gene=IY08_14475	protein=alkanesulfonate monooxygenase	protein_id=KGT43393.1
gene	2722329	2723177	306009	306857	gene=IY08_14480	protein=sulfonate ABC transporter permease	protein_id=KGT43394.1
gene	2723194	2724180	306874	307860	gene=IY08_14485	protein=sulfonate ABC transporter substrate-binding	protein_id=KGT43395.1
gene	2724198	2724953	307878	308633	gene=IY08_14490	protein=sulfonate ABC transporter ATP-binding protein	protein_id=KGT43396.1
gene	2725404	2725913	309084	309593	gene=IY08_14495	protein=hypothetical protein	protein_id=KGT43397.1
gene	2726119	2727159	309799	310839	gene=IY08_14505	protein=membrane protein	protein_id=KGT43398.1
gene	2727172	2727645	310852	311325	gene=IY08_14510	protein=TPR repeat-containing protein	protein_id=KGT43399.1
gene	2727787	2728476	311467	312156	gene=IY08_14515	protein=hypothetical protein	protein_id=KGT43400.1
gene	2728492	2729295	312172	312975	gene=IY08_14520	protein=aminoglycoside 3-N-acetyltransferase	protein_id=KGT43401.1
gene	2729546	2730793	313226	314473	gene=IY08_14525	protein=glutathionylspermidine synthase	protein_id=KGT43402.1

gene	2730814	2731422	314494	315102	gene=IY08_14530	protein=lipoprotein	protein_id=KGT43403.1
gene	2731535	2731936	315215	315616	gene=IY08_14535	protein=acetyltransferase	protein_id=KGT43404.1
gene	2731993	2732931	315673	316611	gene=IY08_14540	protein=membrane protein	protein_id=KGT43405.1
gene	2733334	2733858	317014	317538	gene=IY08_14545	protein=hypothetical protein	protein_id=KGT43406.1
gene	2733874	2734374	317554	318054	gene=IY08_14550	protein=acetyltransferase	protein_id=KGT43407.1
gene	2734415	2734951	318095	318631	gene=IY08_14555	protein=acetyltransferase	protein_id=KGT43408.1
gene	2734967	2735668	318647	319348	gene=IY08_14560	protein=nucleotidyltransferase	protein_id=KGT43409.1
gene	2735690	2736367	319370	320047	gene=IY08_14565	protein=DNA alkylation repair protein	protein_id=KGT43410.1
gene	2736517	2736759	320197	320439	pseudo		
gene	2736935	2737324	320615	321004	gene=IY08_14575	protein=hypothetical protein	protein_id=KGT43411.1
gene	2737906	2738733	321586	322413	gene=IY08_14585	protein=peptidoglycan N-acetylglucosamine deacetylase	protein_id=KGT43412.1
gene	2739115	2739789	322795	323469	gene=IY08_14590	protein=membrane protein	protein_id=KGT43413.1
gene	2739842	2741815	323522	325495	gene=IY08_14595	protein=glycerol phosphate lipoteichoic acid synthase	protein_id=KGT43414.1
gene	2742344	2743969	326024	327649	gene=IY08_14605	protein=ABC transporter ATP-binding protein	protein_id=KGT43415.1
gene	2744282	2747398	327962	331078	gene=IY08_14615	protein=membrane protein	protein_id=KGT43416.1
gene	2747545	2748111	331225	331791	gene=IY08_14620	protein=TetR family transcriptional regulator	protein_id=KGT43417.1
gene	2748379	2749539	332059	333219	gene=IY08_14630	protein=acetyltransferase	protein_id=KGT43418.1
gene	2749664	2750953	333344	334633	gene=IY08_14635	protein=3-phosphoshikimate 1-carboxyvinyltransferase	protein_id=KGT43419.1
gene	2750971	2752071	334651	335751	gene=IY08_14640	protein=prephenate dehydrogenase	protein_id=KGT43420.1
gene	2752064	2753164	335744	336844	gene=IY08_14645	protein=histidinol-phosphate aminotransferase	protein_id=KGT43421.1
gene	2753183	2754355	336863	338035	gene=IY08_14650	protein=chorismate synthase	protein_id=KGT43422.1
gene	2754638	2755714	338318	339394	gene=IY08_14655	protein=chorismate mutase	protein_id=KGT43423.1
gene	2756542	2760024	340222	343704	gene=IY08_14660	protein=reticulocyte-binding protein	protein_id=KGT43424.1
gene	2760206	2760643	343886	344323	gene=IY08_14665	protein=membrane protein	protein_id=KGT43425.1
gene	2760794	2761324	344474	345004	gene=IY08_14670	protein=isochorismatase	protein_id=KGT43426.1
gene	2761359	2761895	345039	345575	gene=IY08_14675	protein=2-aminoglycoside phosphotransferase	protein_id=KGT43427.1
gene	2761908	2762213	345588	345893	gene=IY08_14680	protein=hypothetical protein	protein_id=KGT43428.1
gene	2762315	2762839	345995	346519	gene=IY08_14685	protein=hypothetical protein	protein_id=KGT43429.1
gene	2762858	2763532	346538	347212	gene=IY08_14690	protein=hypothetical protein	protein_id=KGT43430.1
gene	2763585	2764007	347265	347687	gene=IY08_14695	protein=1,3-beta-glucan synthase regulator	protein_id=KGT43431.1
gene	2764325	2765647	348005	349327	gene=IY08_14700	protein=enterotoxin	protein_id=KGT43432.1

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gene	2766533	2766913	350213	350593	gene=IY08_14710	protein=hypothetical protein	protein_id=KGT43434.1
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gene	2767597	2768079	351277	351759	gene=IY08_14720	protein=hypothetical protein	protein_id=KGT43435.1
gene	2768221	2768568	351901	352248	gene=IY08_14725	protein=short-chain dehydrogenase	protein_id=KGT43436.1
gene	2768702	2769748	352382	353428	gene=IY08_14730	protein=hypothetical protein	protein_id=KGT43437.1
gene	2770129	2771631	353809	355311	gene=IY08_14735	protein=malate:quinone oxidoreductase	protein_id=KGT43438.1
gene	2771679	2772722	355359	356402	gene=IY08_14740	protein=autoinducer 2-binding protein lsrB	protein_id=KGT43439.1
gene	2772719	2773708	356399	357388	gene=IY08_14745	protein=autoinducer 2 import system permease LsrD	protein_id=KGT43440.1
gene	2773705	2774658	357385	358338	gene=IY08_14750	protein=sugar ABC transporter permease	protein_id=KGT43441.1
gene	2774655	2776172	358335	359852	gene=IY08_14755	protein=sugar ABC transporter ATP-binding protein	protein_id=KGT43442.1
gene	2776370	2776800	360050	360480	gene=IY08_14760	protein=aminotransferase	protein_id=KGT43443.1
gene	2776891	2777313	360571	360993	gene=IY08_14765	protein=aminotransferase	protein_id=KGT43146.1
gene	2777313	2778875	360993	362555	gene=IY08_14770	protein=autoinducer kinase	protein_id=KGT43147.1
gene	2778901	2779263	362581	362943	gene=IY08_14775	protein=cupin	protein_id=KGT43148.1
gene	2779270	2780052	362950	363732	gene=IY08_14780	protein=aldolase	protein_id=KGT43149.1
gene	2780162	2780579	363842	364259	pseudo		
gene	2780783	2781487	364463	365167	gene=IY08_14790	protein=DNA polymerase subunit beta	protein_id=KGT43150.1
gene	2781557	2781883	365237	365563	gene=IY08_14795	protein=antibiotic biosynthesis monooxygenase	protein_id=KGT43151.1
gene	2781980	2783194	365660	366874	gene=IY08_14800	protein=permease	protein_id=KGT43152.1
gene	2783252	2784295	366932	367975	gene=IY08_14805	protein=ArsR family transcriptional regulator	protein_id=KGT43153.1
gene	2784599	2785090	368279	368770	gene=IY08_14810	protein=hypothetical protein	protein_id=KGT43154.1
gene	2785304	2786497	368984	370177	gene=IY08_14815	protein=nucleoside permease	protein_id=KGT43155.1
gene	2786547	2787794	370227	371474	gene=IY08_14820	protein=gamma-glutamyl phosphate reductase	protein_id=KGT43156.1
gene	2787811	2788914	371491	372594	gene=IY08_14825	protein=gamma-glutamyl kinase	protein_id=KGT43157.1
gene	2789605	2790423	373285	374103	gene=IY08_14830	protein=pyrroline-5-carboxylate reductase	protein_id=KGT43158.1
gene	2790561	2792201	374241	375881	gene=IY08_14835	protein=hypothetical protein	protein_id=KGT43159.1
gene	2792276	2793025	375956	376705	gene=IY08_14840	protein=IclR family transcriptional regulator	protein_id=KGT43160.1
gene	2793293	2794717	376973	378397	gene=IY08_14845	protein=amino acid permease	protein_id=KGT43161.1
gene	2795015	2795473	378695	379153	gene=IY08_14850	protein=fosmidomycin resistance protein	protein_id=KGT43162.1
gene	2795722	2796753	379402	380433	gene=IY08_14855	protein=fatty acid desaturase	protein_id=KGT43163.1

gene	2797062	2799449	380742	383129	gene=IY08_14860	protein=peptidase M6	protein_id=KGT43164.1
gene	2799739	2800569	383419	384249	gene=IY08_14865	protein=vancomycin resistance protein	protein_id=KGT43165.1
gene	2801042	2802715	384722	386395	gene=IY08_14870	protein=alkaline phosphatase	protein_id=KGT43166.1
gene	2803009	2803491	386689	387171	gene=IY08_14875	protein=membrane protein	protein_id=KGT43167.1
gene	2803502	2803717	387182	387397	gene=IY08_14880	protein=XRE family transcriptional regulator	protein_id=KGT43168.1
gene	2803758	2804069	387438	387749	gene=IY08_14885	protein=hypothetical protein	protein_id=KGT43169.1
gene	2804367	2804945	388047	388625	gene=IY08_14890	protein=phosphoglycolate phosphatase	protein_id=KGT43170.1
gene	2804969	2805550	388649	389230	gene=IY08_14895	protein=uridine kinase	protein_id=KGT43171.1
gene	2805550	2806092	389230	389772	gene=IY08_14900	protein=acetyltransferase	protein_id=KGT43172.1
gene	2806107	2806490	389787	390170	gene=IY08_14905	protein=glyoxalase	protein_id=KGT43173.1
gene	2806772	2807017	390452	390697	gene=IY08_14915	protein=DNA alkylation repair protein	protein_id=KGT43174.1
gene	2807564	2808091	391244	391771	gene=IY08_14920	protein=Signal peptidase I	protein_id=KGT43175.1
gene	2808099	2808416	391779	392096	gene=IY08_14925	protein=PadR family transcriptional regulator	protein_id=KGT43176.1
gene	2808623	2809552	392303	393232	gene=IY08_14930	protein=magnesium chelatase	protein_id=KGT43177.1
gene	2809549	2810715	393229	394395	gene=IY08_14935	protein=hypothetical protein	protein_id=KGT43178.1
gene	2810687	2811796	394367	395476	gene=IY08_14940	protein=hypothetical protein	protein_id=KGT43179.1
gene	2811853	2813310	395533	396990	gene=IY08_14945	protein=MFS transporter	protein_id=KGT43180.1
gene	2813714	2813974	397394	397654	gene=IY08_14950	protein=hypothetical protein	protein_id=KGT43181.1
gene	2814062	2815558	397742	399238	gene=IY08_14955	protein=glycosyl transferase	protein_id=KGT43182.1
gene	2815701	2815943	399381	399623	gene=IY08_14960	protein=hypothetical protein	protein_id=KGT43183.1
gene	2816054	2816245	399734	399925	gene=IY08_14965	protein=hypothetical protein	protein_id=KGT43184.1
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gene	2818876	2820393	402556	404073	gene=IY08_14980	protein=glycosyl transferase	protein_id=KGT43185.1
gene	2820616	2821638	404296	405318	gene=IY08_14985	protein=hypothetical protein	protein_id=KGT43186.1
gene	2821911	2823128	405591	406808	gene=IY08_14990	protein=acetylornithine aminotransferase	protein_id=KGT43187.1
gene	2823393	2824772	407073	408452	gene=IY08_14995	protein=catalase	protein_id=KGT43188.1
gene	2824991	2827627	408671	411307	gene=IY08_15000	protein=collagenase	protein_id=KGT43189.1
gene	2828118	2828630	411798	412310	gene=IY08_15005	protein=hypothetical protein	protein_id=KGT43190.1
gene	2828744	2830498	412424	414178	gene=IY08_15010	protein=adenine deaminase	protein_id=KGT43191.1
gene	2830850	2832016	414530	415696	gene=IY08_15015	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT43192.1
gene	2832275	2832781	415955	416461	gene=IY08_15020	protein=hypothetical protein	protein_id=KGT43193.1

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gene	2833720	2834829	417400	418509	gene=IY08_15030	protein=hypothetical protein	protein_id=KGT43195.1
gene	2834826	2835758	418506	419438	gene=IY08_15035	protein=ATPase AAA	protein_id=KGT43196.1
gene	2835969	2836574	419649	420254	gene=IY08_15040	protein=hypothetical protein	protein_id=KGT43197.1
gene	2837004	2837501	420684	421181	gene=IY08_15045	protein=hypothetical protein	protein_id=KGT43198.1
gene	2837507	2837989	421187	421669	gene=IY08_15050	protein=sugar-binding protein	protein_id=KGT43199.1
gene	2838374	2839105	422054	422785	gene=IY08_15055	protein=hypothetical protein	protein_id=KGT43200.1
gene	2839123	2839767	422803	423447	gene=IY08_15060	protein=hypothetical protein	protein_id=KGT43201.1
gene	2840170	2840604	423850	424284	gene=IY08_15065	protein=hypothetical protein	protein_id=KGT43202.1
gene	2840606	2842329	424286	426009	pseudo		
gene	2842326	2842688	426006	426368	gene=IY08_15075	protein=hypothetical protein	protein_id=KGT43203.1
gene	2842729	2843004	426409	426684	gene=IY08_15080	protein=creatininase	protein_id=KGT43204.1
gene	2843217	2843510	426897	427190	gene=IY08_15085	protein=monooxygenase	protein_id=KGT43205.1
gene	2843557	2844195	427237	427875	gene=IY08_15090	protein=NAD(P)H nitroreductase	protein_id=KGT43206.1
gene	2844214	2844642	427894	428322	gene=IY08_15095	protein=MarR family transcriptional regulator	protein_id=KGT43207.1
gene	2844908	2846851	428588	430531	gene=IY08_15100	protein=tetracycline resistance protein	protein_id=KGT43208.1
gene	2846897	2847541	430577	431221	gene=IY08_15105	protein=hypothetical protein	protein_id=KGT43209.1
gene	2847563	2848030	431243	431710	gene=IY08_15110	protein=DNA mismatch repair protein MutT	protein_id=KGT43210.1
gene	2848225	2849016	431905	432696	gene=IY08_15115	protein=WGR domain family protein	protein_id=KGT43211.1
gene	2849081	2849512	432761	433192	gene=IY08_15120	protein=cell wall assembly protein	protein_id=KGT43212.1
gene	2849565	2850590	433245	434270	gene=IY08_15125	protein=NAD-dependent dehydratase	protein_id=KGT43213.1
gene	2850757	2851427	434437	435107	pseudo		
gene	2851427	2852689	435107	436369	gene=IY08_15135	protein=ABC transporter permease	protein_id=KGT43214.1
gene	2852695	2853780	436375	437460	gene=IY08_15140	protein=ABC transporter permease	protein_id=KGT43215.1
gene	2853846	2854214	437526	437894	gene=IY08_15145	protein=hypothetical protein	protein_id=KGT43216.1
gene	2854421	2855368	438101	439048	gene=IY08_15150	protein=6-aminohexanoate hydrolase	protein_id=KGT43217.1
gene	2855393	2856271	439073	439951	gene=IY08_15155	protein=AraC family transcriptional regulator	protein_id=KGT43218.1
gene	2856438	2856947	440118	440627	gene=IY08_15160	protein=cytosine deaminase	protein_id=KGT43219.1
gene	2857103	2857573	440783	441253	gene=IY08_15165	protein=acetyltransferase	protein_id=KGT43220.1
gene	2857591	2857998	441271	441678	gene=IY08_15170	protein=hypothetical protein	protein_id=KGT43221.1
gene	2858093	2858545	441773	442225	gene=IY08_15175	protein=DNA mismatch repair protein MutT	protein_id=KGT43222.1

gene	2858579	2859490	442259	443170	gene=IY08_15180	protein=membrane protein	protein_id=KGT43223.1
gene	2859616	2861058	443296	444738	gene=IY08_15185	protein=GntR family transcriptional regulator	protein_id=KGT43224.1
gene	2861288	2861728	444968	445408	gene=IY08_15190	protein=hypothetical protein	protein_id=KGT43225.1
gene	2861815	2862129	445495	445809	gene=IY08_15195	protein=hypothetical protein	protein_id=KGT43226.1
gene	2862210	2863034	445890	446714	gene=IY08_15200	protein=membrane protein	protein_id=KGT43227.1
gene	2863127	2863588	446807	447268	gene=IY08_15205	protein=hypothetical protein	protein_id=KGT43228.1
gene	2863616	2864284	447296	447964	gene=IY08_15210	protein=uridine kinase	protein_id=KGT43229.1
gene	2864455	2865198	448135	448878	gene=IY08_15215	protein=serine/threonine protein phosphatase	protein_id=KGT43230.1
gene	2865212	2866138	448892	449818	gene=IY08_15220	protein=aminoglycoside phosphotransferase	protein_id=KGT43231.1
gene	2866153	2866950	449833	450630	gene=IY08_15225	protein=hypothetical protein	protein_id=KGT43232.1
gene	2867156	2868058	450836	451738	gene=IY08_15230	protein=membrane protein	protein_id=KGT43233.1
gene	2868096	2868545	451776	452225	gene=IY08_15235	protein=acetyltransferase	protein_id=KGT43234.1
gene	2869176	2870642	452856	454322	gene=IY08_15240	protein=gamma-aminobutyrate permease	protein_id=KGT43235.1
gene	2870756	2871061	454436	454741	gene=IY08_15245	protein=Fe-S cluster assembly protein HesB	protein_id=KGT43236.1
gene	2871095	2871865	454775	455545	gene=IY08_15250	protein=DNA alkylation repair protein	protein_id=KGT43237.1
gene	2871975	2872955	455655	456635	gene=IY08_15255	protein=hypothetical protein	protein_id=KGT43238.1
gene	2873170	2873451	456850	457131	gene=IY08_15260	protein=hypothetical protein	protein_id=KGT43239.1
gene	2873757	2874518	457437	458198	gene=IY08_15265	protein=SAM-dependent methyltransferase	protein_id=KGT43240.1
gene	2874699	2875223	458379	458903	gene=IY08_15275	protein=DNA mismatch repair protein MutT	protein_id=KGT43241.1
gene	2875493	2876005	459173	459685	gene=IY08_15280	protein=cephalosporin hydroxylase	protein_id=KGT43242.1
gene	2876040	2876561	459720	460241	gene=IY08_15285	protein=signal peptidase	protein_id=KGT43243.1
gene	2876643	2878796	460323	462476	gene=IY08_15290	protein=penicillin-binding protein	protein_id=KGT43244.1
gene	2879031	2879759	462711	463439	gene=IY08_15295	protein=NAD-dependent deacetylase	protein_id=KGT43245.1
gene	2879835	2880482	463515	464162	gene=IY08_15300	protein=pyrrolidone-carboxylate peptidase	protein_id=KGT43246.1
gene	2880499	2881461	464179	465141	gene=IY08_15305	protein=permease	protein_id=KGT43247.1
gene	2881463	2882158	465143	465838	gene=IY08_15310	protein=membrane protein	protein_id=KGT43248.1
gene	2882181	2882942	465861	466622	gene=IY08_15315	protein=LamB/YcsF family protein	protein_id=KGT43249.1
gene	2882955	2883950	466635	467630	gene=IY08_15320	protein=KipI antagonist	protein_id=KGT43250.1
gene	2883941	2884654	467621	468334	gene=IY08_15325	protein=kinase	protein_id=KGT43251.1
gene	2884669	2885421	468349	469101	gene=IY08_15330	protein=IclR family transcriptional regulator	protein_id=KGT43252.1
gene	2885577	2886128	469257	469808	gene=IY08_15335	protein=signal peptidase I	protein_id=KGT43253.1

gene	2886152	2886829	469832	470509	gene=IY08_15340	protein=copper homeostasis protein	protein_id=KGT43254.1
gene	2887028	2887735	470708	471415	gene=IY08_15350	protein=ArsR family transcriptional regulator	protein_id=KGT43255.1
gene	2887805	2888275	471485	471955	gene=IY08_15355	protein=hypothetical protein	protein_id=KGT43256.1
gene	2888491	2889639	472171	473319	gene=IY08_15360	protein=acyl-CoA dehydrogenase	protein_id=KGT43257.1
gene	2889794	2890426	473474	474106	gene=IY08_15365	protein=multidrug MFS transporter	protein_id=KGT43258.1
gene	2890756	2891343	474436	475023	gene=IY08_15370	protein=GNAT family acetyltransferase	protein_id=KGT43259.1
gene	2891733	2893061	475413	476741	gene=IY08_15380	protein=histidine transporter	protein_id=KGT43260.1
gene	2893173	2894051	476853	477731	gene=IY08_15385	protein=acetyltransferase	protein_id=KGT43261.1
gene	2894052	2894567	477732	478247	gene=IY08_15390	protein=acetyltransferase	protein_id=KGT43262.1
gene	2894594	2895055	478274	478735	gene=IY08_15395	protein=prophage protein	protein_id=KGT43263.1
gene	2895287	2895721	478967	479401	gene=IY08_15400	protein=hypothetical protein	protein_id=KGT43264.1
gene	2895993	2896499	479673	480179	gene=IY08_15405	protein=acetyltransferase	protein_id=KGT43265.1
scaffold14							
gene	2898101	2898598	1241	1738	gene=IY08_15425	protein=hypothetical protein	protein_id=KGT43094.1
gene	2898697	2899755	1837	2895	gene=IY08_15430	protein=histidine kinase	protein_id=KGT43095.1
gene	2899752	2900465	2892	3605	gene=IY08_15435	protein=PhoP family transcriptional regulator	protein_id=KGT43096.1
gene	2900835	2903051	3975	6191	gene=IY08_15440	protein=hypothetical protein	protein_id=KGT43097.1
gene	2903327	2905732	6467	8872	gene=IY08_15445	protein=sporulation kinase	protein_id=KGT43098.1
gene	2906426	2907826	9566	10966	gene=IY08_15450	protein=hemolysin BL-binding component precursor	protein_id=KGT43099.1
gene	2908202	2909329	11342	12469	gene=IY08_15455	protein=hemolysin	protein_id=KGT43100.1
gene	2909366	2910586	12506	13726	gene=IY08_15460	protein=hemolysin BL lytic component L1	protein_id=KGT43101.1
gene	2910648	2911967	13788	15107	gene=IY08_15465	protein=hemolysin BL lytic component L2	protein_id=KGT43102.1
gene	2913620	2914849	16760	17989	gene=IY08_15470	protein=AraC family transcriptional regulator	protein_id=KGT43103.1
gene	2916153	2916383	19293	19523	pseudo		
gene	2916550	2917191	19690	20331	gene=IY08_15480	protein=excinuclease ABC subunit C	protein_id=KGT43104.1
gene	2917357	2918772	20497	21912	gene=IY08_15485	protein=amino acid permease	protein_id=KGT43105.1
gene	2918906	2919724	22046	22864	gene=IY08_15490	protein=pyrroline-5-carboxylate reductase	protein_id=KGT43106.1
gene	2920049	2921242	23189	24382	gene=IY08_15495	protein=spore germination protein GerC	protein_id=KGT43107.1
gene	2921239	2922330	24379	25470	gene=IY08_15500	protein=spore germination protein	protein_id=KGT43108.1
gene	2922357	2923931	25497	27071	gene=IY08_15505	protein=spore germination protein	protein_id=KGT43109.1
gene	2924583	2925527	27723	28667	gene=IY08_15515	protein=transcriptional regulator	protein_id=KGT43110.1

gene	2925532	2926848	28672	29988	gene=IY08_15520	protein=histidine kinase	protein_id=KGT43111.1
gene	2927082	2928062	30222	31202	gene=IY08_15525	protein=glutaminase	protein_id=KGT43112.1
gene	2928187	2929611	31327	32751	gene=IY08_15535	protein=sodium:alanine symporter	protein_id=KGT43113.1
gene	2930570	2931721	33710	34861	gene=IY08_15540	protein=arsenic transporter	protein_id=KGT43114.1
gene	2932096	2933253	35236	36393	gene=IY08_15550	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT43115.1
gene	2933839	2935170	36979	38310	gene=IY08_15555	protein=erythromycin esterase	protein_id=KGT43116.1
gene	2935693	2937282	38833	40422	gene=IY08_15560	protein=5'-nucleotidase	protein_id=KGT43117.1
gene	2937668	2938504	40808	41644	gene=IY08_15565	protein=bromoperoxidase	protein_id=KGT43118.1
gene	2939007	2939651	42147	42791	gene=IY08_15570	protein=hypothetical protein	protein_id=KGT43119.1
gene	2939962	2940606	43102	43746	gene=IY08_15580	protein=hydrolase	protein_id=KGT43120.1
gene	2940603	2941196	43743	44336	gene=IY08_15585	protein=hypothetical protein	protein_id=KGT43121.1
gene	2941210	2943045	44350	46185	gene=IY08_15590	protein=amidohydrolase	protein_id=KGT43122.1
gene	2943351	2944229	46491	47369	gene=IY08_15595	protein=LysR family transcriptional regulator	protein_id=KGT43123.1
gene	2944449	2944892	47589	48032	gene=IY08_15600	protein=transcriptional regulator	protein_id=KGT43124.1
gene	2945454	2945825	48594	48965	gene=IY08_15605	protein=hypothetical protein	protein_id=KGT43125.1
gene	2945886	2946554	49026	49694	gene=IY08_15610	protein=hypothetical protein	protein_id=KGT43126.1
gene	2947076	2948026	50216	51166	gene=IY08_15620	protein=magnesium transporter	protein_id=KGT43127.1
gene	2948332	2949357	51472	52497	gene=IY08_15625	protein=ATP synthase F0F1 subunit alpha	protein_id=KGT43128.1
gene	2949393	2949794	52533	52934	gene=IY08_15630	protein=peptidase U61 LD-carboxypeptidase A	protein_id=KGT43129.1
gene	2949880	2950266	53020	53406	gene=IY08_15635	protein=general stress protein	protein_id=KGT43130.1
gene	2950603	2952141	53743	55281	gene=IY08_15640	protein=hydrolase	protein_id=KGT43131.1
gene	2952715	2953080	55855	56220	gene=IY08_15645	protein=hypothetical protein	protein_id=KGT43132.1
gene	2953168	2953878	56308	57018	gene=IY08_15650	protein=carboxymethylenebutenolidase	protein_id=KGT43133.1
gene	2953982	2954437	57122	57577	gene=IY08_15655	protein=membrane protein	protein_id=KGT43134.1
gene	2954549	2955979	57689	59119	gene=IY08_15660	protein=deoxyribodipyrimidine photolyase	protein_id=KGT43135.1
gene	2956052	2956873	59192	60013	gene=IY08_15665	protein=NmrA family transcriptional regulator	protein_id=KGT43136.1
gene	2956879	2957304	60019	60444	gene=IY08_15670	protein=transcriptional regulator	protein_id=KGT43137.1
gene	2957615	2957899	60755	61039	gene=IY08_15675	protein=hypothetical protein	protein_id=KGT43138.1
gene	2957941	2959401	61081	62541	gene=IY08_15680	protein=histidine kinase	protein_id=KGT43139.1
gene	2959398	2960084	62538	63224	gene=IY08_15685	protein=DeoR family transcriptional regulator	protein_id=KGT43140.1
gene	2960619	2961200	63759	64340	gene=IY08_15690	protein=PadR family transcriptional regulator	protein_id=KGT43141.1

gene	2961277	2962800	64417	65940	gene=IY08_15695	protein=major facilitator transporter	protein_id=KGT43142.1
gene	2963026	2964243	66166	67383	gene=IY08_15700	protein=FAD-dependent oxidoreductase	protein_id=KGT43143.1
gene	2964418	2965443	67558	68583	gene=IY08_15705	protein=acetyl esterase	protein_id=KGT43144.1
gene	2965701	2966222	68841	69362	gene=IY08_15710	protein=carbonic anhydrase	protein_id=KGT43145.1
gene	2966558	2968890	69698	72030	gene=IY08_15720	protein=hypothetical protein	protein_id=KGT43089.1
gene	2968932	2970464	72072	73604	gene=IY08_15725	protein=NADH dehydrogenase	protein_id=KGT43090.1
gene	2971072	2971434	74212	74574	gene=IY08_15730	protein=hypothetical protein	protein_id=KGT43091.1
gene	2971788	2972876	74928	76016	gene=IY08_15735	protein=membrane protein	protein_id=KGT43092.1
gene	2972904	2974091	76044	77231	gene=IY08_15740	protein=spore germination protein	protein_id=KGT43093.1
gene	2974330	2975687	77470	78827	gene=IY08_15750	protein=spore germination protein GerA	protein_id=KGT43074.1
gene	2976033	2976875	79173	80015	gene=IY08_15755	protein=peptidoglycan N-acetylglucosamine deacetylase	protein_id=KGT43075.1
gene	2977271	2977828	80411	80968	gene=IY08_15760	protein=streptothricin acetyltransferase	protein_id=KGT43076.1
gene	2977927	2978838	81067	81978	gene=IY08_15765	protein=1,4-dihydroxy-2-naphthoate octaprenyltransferase	protein_id=KGT43077.1
gene	2979118	2979522	82258	82662	gene=IY08_15770	protein=arsenate reductase	protein_id=KGT43078.1
gene	2979549	2980589	82689	83729	gene=IY08_15775	protein=arsenic resistance protein ArsB	protein_id=KGT43079.1
gene	2980608	2981045	83748	84185	gene=IY08_15780	protein=hypothetical protein	protein_id=KGT43080.1
gene	2981106	2981411	84246	84551	gene=IY08_15785	protein=ArsR family transcriptional regulator	protein_id=KGT43081.1
gene	2981526	2981669	84666	84809	gene=IY08_15790	protein=hypothetical protein	protein_id=KGT43082.1
gene	2981943	2982452	85083	85592	gene=IY08_15795	protein=squalene-hopene cyclase	protein_id=KGT43083.1
gene	2983116	2983850	86256	86990	gene=IY08_15800	protein=membrane protein	protein_id=KGT43084.1
gene	2983890	2984684	87030	87824	gene=IY08_15805	protein=ABC transporter permease	protein_id=KGT43085.1
gene	2984681	2985379	87821	88519	gene=IY08_15810	protein=ABC transporter	protein_id=KGT43086.1
gene	2985376	2985756	88516	88896	gene=IY08_15815	protein=GntR family transcriptional regulator	protein_id=KGT43087.1
gene	2986628	2987134	89768	90274	gene=IY08_15820	protein=hypothetical protein	protein_id=KGT43088.1
gene	2987432	2987811	90572	90951	pseudo		
gene	2988579	2990465	91719	93605	gene=IY08_15835	protein=beta-lactamase regulatory protein	protein_id=KGT43057.1
gene	2990465	2990866	93605	94006	gene=IY08_15840	protein=beta-lactamase repressor	protein_id=KGT43058.1
gene	2991363	2993105	94503	96245	gene=IY08_15845	protein=chemotaxis protein	protein_id=KGT43059.1
gene	2993332	2994153	96472	97293	gene=IY08_15850	protein=peptidoglycan N-acetylglucosamine deacetylase	protein_id=KGT43060.1
gene	2994288	2994791	97428	97931	gene=IY08_15855	protein=hypothetical protein	protein_id=KGT43061.1
gene	2995454	2996008	98594	99148	gene=IY08_15865	protein=MerR family transcriptional regulator	protein_id=KGT43062.1

gene	2996157	2997584	99297	100724	gene=IY08_15870	protein=glucosaminidase	protein_id=KGT43063.1
gene	2998244	2999893	101384	103033	gene=IY08_15875	protein=S-layer protein	protein_id=KGT43064.1
gene	3001040	3002113	104180	105253	gene=IY08_15880	protein=hypothetical protein	protein_id=KGT43065.1
gene	3002397	3003557	105537	106697	gene=IY08_15885	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT43066.1
gene	3004456	3005136	107596	108276	gene=IY08_15890	protein=hypothetical protein	protein_id=KGT43067.1
gene	3005466	3007409	108606	110549	gene=IY08_15895	protein=ABC transporter permease	protein_id=KGT43068.1
gene	3007384	3008154	110524	111294	gene=IY08_15900	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT43069.1
gene	3008987	3009937	112127	113077	gene=IY08_15910	protein=beta-lactamase	protein_id=KGT43070.1
gene	3011499	3013460	114639	116600	gene=IY08_15915	protein=chitin-binding protein	protein_id=KGT43071.1
gene	3013958	3014443	117098	117583	gene=IY08_15920	protein=hypothetical protein	protein_id=KGT43072.1
gene	3014704	3015468	117844	118608	gene=IY08_15925	protein=short-chain dehydrogenase	protein_id=KGT43073.1
scaffold15							
gene	3016201	3016467	1	267	gene=IY08_15935	protein=transposase	protein_id=KGT43051.1
gene	3016677	3016838	477	638	gene=IY08_15940	protein=stage 0 sporulation regulatory protein	protein_id=KGT43052.1
gene	3017459	3018001	1259	1801	gene=IY08_15945	protein=stress protein	protein_id=KGT43053.1
gene	3018668	3018907	2468	2707	gene=IY08_15950	protein=DSBA oxidoreductase	protein_id=KGT43054.1
gene	3019200	3020027	3000	3827	gene=IY08_15955	protein=AraC family transcriptional regulator	protein_id=KGT43055.1
gene	3020286	3021156	4086	4956	pseudo		
gene	3021293	3021779	5093	5579	gene=IY08_15965	protein=beta-lactamase regulatory protein	protein_id=KGT43056.1]
gene	3021852	3023059	5652	6859	gene=IY08_15970	protein=beta-lactamase regulatory protein	protein_id=KGT43048.1
gene	3023203	3023604	7003	7404	gene=IY08_15975	protein=beta-lactamase repressor	protein_id=KGT43049.1
gene	3023972	3024162	7772	7962	gene=IY08_15980	protein=transposase	protein_id=KGT43050.1
gene	3024249	3025131	8049	8931	pseudo		
gene	3028005	3028544	11805	12344	gene=IY08_15995	protein=hypothetical protein	protein_id=KGT42725.1
gene	3028957	3029649	12757	13449	gene=IY08_16000	protein=transcriptional regulator	protein_id=KGT42726.1
gene	3029646	3030641	13446	14441	gene=IY08_16005	protein=histidine kinase	protein_id=KGT42727.1
gene	3030757	3031518	14557	15318	gene=IY08_16010	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT42728.1
gene	3031508	3033355	15308	17155	gene=IY08_16015	protein=ABC transporter permease	protein_id=KGT42729.1
gene	3033578	3034288	17378	18088	gene=IY08_16020	protein=conjugal transfer protein TraX	protein_id=KGT42730.1
gene	3034736	3036592	18536	20392	gene=IY08_16025	protein=MxaA domain-containing protein	protein_id=KGT42731.1
gene	3036652	3037218	20452	21018	gene=IY08_16030	protein=TetR family transcriptional regulator	protein_id=KGT42732.1

gene	3037554	3038318	21354	22118	gene=IY08_16035	protein=short-chain dehydrogenase	protein_id=KGT42733.1
gene	3038486	3038926	22286	22726	gene=IY08_16040	protein=AsnC family transcriptional regulator	protein_id=KGT42734.1
gene	3039098	3040303	22898	24103	gene=IY08_16045	protein=amidohydrolase	protein_id=KGT42735.1
gene	3040570	3042879	24370	26679	gene=IY08_16050	protein=disulfide oxidoreductase	protein_id=KGT42736.1
gene	3042991	3043383	26791	27183	gene=IY08_16055	protein=glyoxalase	protein_id=KGT42737.1
gene	3043519	3043843	27319	27643	pseudo		
gene	3044160	3046235	27960	30035	gene=IY08_16065	protein=beta-lactamase	protein_id=KGT42738.1
gene	3047154	3047459	30954	31259	gene=IY08_16075	protein=monooxygenase	protein_id=KGT42739.1
gene	3047655	3048008	31455	31808	gene=IY08_16080	protein=hypothetical protein	protein_id=KGT42740.1
gene	3048335	3048754	32135	32554	gene=IY08_16085	protein=MarR family transcriptional regulator	protein_id=KGT42741.1
gene	3049232	3049618	33032	33418	gene=IY08_16090	protein=cytoplasmic protein	protein_id=KGT42742.1
gene	3050037	3050198	33837	33998	gene=IY08_16095	protein=membrane protein	protein_id=KGT42743.1
gene	3050493	3050708	34293	34508	gene=IY08_16100	protein=hypothetical protein	protein_id=KGT42744.1
gene	3051051	3052496	34851	36296	gene=IY08_16105	protein=ErfK/YbiS/YcfS/YnhG family protein	protein_id=KGT42745.1
gene	3053120	3053998	36920	37798	gene=IY08_16115	protein=CAAX protease	protein_id=KGT42746.1
gene	3054359	3055696	38159	39496	gene=IY08_16120	protein=erythromycin esterase	protein_id=KGT42747.1
gene	3056053	3056631	39853	40431	gene=IY08_16125	protein=luciferase	protein_id=KGT42748.1
gene	3056746	3058533	40546	42333	gene=IY08_16130	protein=histidine kinase	protein_id=KGT42749.1
gene	3059050	3059436	42850	43236	gene=IY08_16135	protein=hypothetical protein	protein_id=KGT42750.1
gene	3059512	3060462	43312	44262	gene=IY08_16140	protein=beta-lactamase	protein_id=KGT42751.1
gene	3060768	3061196	44568	44996	gene=IY08_16145	protein=hypothetical protein	protein_id=KGT42752.1
gene	3061870	3063981	45670	47781	gene=IY08_16150	protein=cytoplasmic protein	protein_id=KGT42753.1
gene	3064193	3067390	47993	51190	gene=IY08_16155	protein=NADPH--cytochrome P450 reductase	protein_id=KGT42754.1
gene	3067924	3069402	51724	53202	gene=IY08_16160	protein=MFS transporter	protein_id=KGT42755.1
gene	3069799	3070395	53599	54195	gene=IY08_16165	protein=hypothetical protein	protein_id=KGT42756.1
gene	3070479	3071474	54279	55274	gene=IY08_16170	protein=cytochrome C biogenesis protein CcmE	protein_id=KGT42757.1
gene	3071831	3073063	55631	56863	gene=IY08_16175	protein=metallophosphoesterase	protein_id=KGT42758.1
gene	3073390	3074349	57190	58149	gene=IY08_16180	protein=RTCB protein	protein_id=KGT42759.1
gene	3074632	3074850	58432	58650	gene=IY08_16185	protein=hypothetical protein	protein_id=KGT42760.1
gene	3074994	3075908	58794	59708	gene=IY08_16190	protein=SAM-dependent methyltransferase	protein_id=KGT42761.1
gene	3076130	3076720	59930	60520	gene=IY08_16195	protein=CRISPR-associated protein Cas2	protein_id=KGT42762.1

gene	3076861	3077973	60661	61773	gene=IY08_16200	protein=cell wall anchor protein	protein_id=KGT42763.1
gene	3078038	3078709	61838	62509	gene=IY08_16205	protein=hemin ABC transporter ATP-binding protein	protein_id=KGT42764.1
gene	3078709	3079773	62509	63573	gene=IY08_16210	protein=ABC transporter permease	protein_id=KGT42765.1
gene	3079959	3080582	63759	64382	gene=IY08_16215	protein=ArsR family transcriptional regulator	protein_id=KGT42766.1
gene	3080652	3081911	64452	65711	gene=IY08_16220	protein=MFS transporter	protein_id=KGT42767.1
gene	3082063	3082533	65863	66333	gene=IY08_16225	protein=hypothetical protein	protein_id=KGT42768.1
gene	3082737	3084113	66537	67913	gene=IY08_16230	protein=membrane protein	protein_id=KGT42769.1
gene	3084115	3084792	67915	68592	gene=IY08_16235	protein=heme response regulator HssR	protein_id=KGT42770.1
gene	3084873	3085541	68673	69341	pseudo		
gene	3085656	3086108	69456	69908	gene=IY08_16245	protein=MarR family transcriptional regulator	protein_id=KGT42771.1
gene	3086134	3086652	69934	70452	gene=IY08_16250	protein=GNAT family acetyltransferase	protein_id=KGT42772.1
gene	3086675	3087298	70475	71098	gene=IY08_16255	protein=protease	protein_id=KGT42773.1
gene	3087493	3088332	71293	72132	gene=IY08_16260	protein=membrane protein YxkD	protein_id=KGT42774.1
gene	3088664	3089305	72464	73105	gene=IY08_16265	protein=ATP F0F1 synthase subunit alpha	protein_id=KGT42775.1
gene	3089752	3090234	73552	74034	gene=IY08_16270	protein=hypothetical protein	protein_id=KGT42776.1
gene	3091093	3091503	74893	75303	gene=IY08_16275	protein=PbsX family transcriptional regulator	protein_id=KGT42777.1
gene	3091931	3092440	75731	76240	gene=IY08_16280	protein=hypothetical protein	protein_id=KGT42778.1
gene	3092582	3093829	76382	77629	gene=IY08_16285	protein=hypothetical protein	protein_id=KGT42779.1
gene	3093843	3095015	77643	78815	gene=IY08_16290	protein=3-phosphoglycerate dehydrogenase	protein_id=KGT42780.1
gene	3095028	3096110	78828	79910	gene=IY08_16295	protein=MFS transporter	protein_id=KGT42781.1
gene	3096320	3096511	80120	80311	gene=IY08_16300	protein=GNAT family acetyltransferase	protein_id=KGT42782.1
gene	3096601	3097668	80401	81468	gene=IY08_16305	protein=hypothetical protein	protein_id=KGT42783.1
gene	3097842	3098630	81642	82430	gene=IY08_16310	protein=hypothetical protein	protein_id=KGT42784.1
gene	3098712	3099077	82512	82877	gene=IY08_16315	protein=hypothetical protein	protein_id=KGT42785.1
gene	3099364	3101754	83164	85554	gene=IY08_16320	protein=beta-lactam antibiotic acylase	protein_id=KGT42786.1
gene	3101830	3102594	85630	86394	gene=IY08_16325	protein=XRE family transcriptional regulator	protein_id=KGT42787.1
gene	3103062	3104882	86862	88682	gene=IY08_16330	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT42788.1
gene	3105218	3105676	89018	89476	gene=IY08_16335	protein=lipoprotein	protein_id=KGT42789.1
gene	3105832	3106788	89632	90588	gene=IY08_16340	protein=membrane protein	protein_id=KGT42790.1
gene	3106845	3107174	90645	90974	gene=IY08_16345	protein=hypothetical protein	protein_id=KGT42791.1
gene	3107276	3107614	91076	91414	gene=IY08_16350	protein=hypothetical protein	protein_id=KGT42792.1

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gene	3108202	3108690	92002	92490	gene=IY08_16360	protein=cytoplasmic protein	protein_id=KGT42794.1
gene	3108895	3109602	92695	93402	gene=IY08_16365	protein=DNA alkylation repair protein	protein_id=KGT42795.1
gene	3109691	3110158	93491	93958	gene=IY08_16370	protein=cytoplasmic protein	protein_id=KGT42796.1
gene	3110225	3110653	94025	94453	gene=IY08_16375	protein=SMI1/KNR4 family protein	protein_id=KGT42797.1
gene	3110718	3111107	94518	94907	gene=IY08_16380	protein=hypothetical protein	protein_id=KGT42798.1
gene	3111680	3112231	95480	96031	gene=IY08_16390	protein=hypothetical protein	protein_id=KGT42799.1
gene	3112336	3112890	96136	96690	pseudo		
gene	3112915	3113112	96715	96912	gene=IY08_16400	protein=hypothetical protein	protein_id=KGT42800.1
gene	3113377	3114189	97177	97989	gene=IY08_16405	protein=membrane protein	protein_id=KGT42801.1
gene	3114297	3114575	98097	98375	gene=IY08_16410	protein=hypothetical protein	protein_id=KGT42802.1
gene	3115237	3115854	99037	99654	gene=IY08_16415	protein=cytoplasmic protein	protein_id=KGT42803.1
gene	3116124	3116357	99924	100157	gene=IY08_16420	protein=hypothetical protein	protein_id=KGT42804.1
gene	3116441	3116857	100241	100657	gene=IY08_16425	protein=SMI1/KNR4 family protein	protein_id=KGT42805.1
gene	3117014	3117472	100814	101272	gene=IY08_16430	protein=morn repeat protein	protein_id=KGT42806.1
gene	3117757	3118140	101557	101940	gene=IY08_16435	protein=hypothetical protein	protein_id=KGT42807.1
gene	3118153	3119313	101953	103113	gene=IY08_16440	protein=cytoplasmic protein	protein_id=KGT42808.1
gene	3119372	3119755	103172	103555	gene=IY08_16445	protein=beta-lactamase	protein_id=KGT42809.1
gene	3119818	3120201	103618	104001	gene=IY08_16450	protein=beta-lactamase	protein_id=KGT42810.1
gene	3120452	3120808	104252	104608	gene=IY08_16455	protein=hypothetical protein	protein_id=KGT42811.1
gene	3120906	3121238	104706	105038	gene=IY08_16460	protein=hypothetical protein	protein_id=KGT42812.1
gene	3121546	3121800	105346	105600	gene=IY08_16465	protein=hypothetical protein	protein_id=KGT42813.1
gene	3121986	3122231	105786	106031	gene=IY08_16470	protein=hypothetical protein	protein_id=KGT42814.1
gene	3122427	3122861	106227	106661	gene=IY08_16475	protein=SMI1 / KNR4 family protein	protein_id=KGT42815.1
gene	3122976	3123155	106776	106955	gene=IY08_16480	protein=hypothetical protein	protein_id=KGT42816.1
gene	3123156	3123407	106956	107207	gene=IY08_16485	protein=hypothetical protein	protein_id=KGT42817.1
gene	3123531	3124055	107331	107855	gene=IY08_16490	protein=hypothetical protein	protein_id=KGT42818.1
gene	3124112	3124567	107912	108367	gene=IY08_16495	protein=hypothetical protein	protein_id=KGT42819.1
gene	3124596	3125063	108396	108863	gene=IY08_16500	protein=cytoplasmic protein	protein_id=KGT42820.1
gene	3125136	3125789	108936	109589	gene=IY08_16505	protein=SMI1/KNR4 family protein	protein_id=KGT42821.1
gene	3125903	3126052	109703	109852	gene=IY08_16510	protein=hypothetical protein	protein_id=KGT42822.1

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gene	3126759	3127415	110559	111215	gene=IY08_16520	protein=hypothetical protein	protein_id=KGT42823.1
gene	3127591	3128022	111391	111822	gene=IY08_16525	protein=SMI1/KNR4 family protein	protein_id=KGT42824.1
gene	3128041	3128532	111841	112332	gene=IY08_16530	protein=SMI1/KNR4 family protein	protein_id=KGT42825.1
gene	3129209	3129553	113009	113353	gene=IY08_16535	protein=hypothetical protein	protein_id=KGT42826.1
gene	3129910	3130380	113710	114180	gene=IY08_16540	protein=hypothetical protein	protein_id=KGT42827.1
gene	3130416	3130844	114216	114644	gene=IY08_16545	protein=hypothetical protein	protein_id=KGT42828.1
gene	3130849	3131151	114649	114951	gene=IY08_16550	protein=hypothetical protein	protein_id=KGT42829.1
gene	3131473	3131964	115273	115764	gene=IY08_16560	protein=GNAT family acetyltransferase	protein_id=KGT42830.1
gene	3132004	3132519	115804	116319	pseudo		
gene	3133052	3133561	116852	117361	gene=IY08_16570	protein=ankyrin	protein_id=KGT42831.1
gene	3133582	3135255	117382	119055	gene=IY08_16575	protein=membrane protein	protein_id=KGT42832.1
gene	3135289	3135615	119089	119415	gene=IY08_16580	protein=MFS transporter	protein_id=KGT42833.1
gene	3135615	3136334	119415	120134	gene=IY08_16585	protein=hypothetical protein	protein_id=KGT42834.1
gene	3136357	3136662	120157	120462	gene=IY08_16590	protein=hypothetical protein	protein_id=KGT42835.1
gene	3136689	3137111	120489	120911	gene=IY08_16595	protein=EsaC-like protein	protein_id=KGT42836.1
gene	3137757	3138476	121557	122276	gene=IY08_16600	protein=peptidase M15	protein_id=KGT42837.1
gene	3138537	3139772	122337	123572	gene=IY08_16605	protein=capsular biosynthesis protein	protein_id=KGT42838.1
gene	3140371	3140571	124171	124371	gene=IY08_16610	protein=hypothetical protein	protein_id=KGT42839.1
gene	3140555	3141751	124355	125551	gene=IY08_16615	protein=MFS transporter	protein_id=KGT42840.1
gene	3141869	3142102	125669	125902	gene=IY08_16620	protein=hypothetical protein	protein_id=KGT42841.1
gene	3142163	3143065	125963	126865	gene=IY08_16625	protein=3-oxoadipate enol-lactonase	protein_id=KGT42842.1
gene	3143255	3143671	127055	127471	gene=IY08_16630	protein=MarR family transcriptional regulator	protein_id=KGT42843.1
gene	3143687	3144886	127487	128686	gene=IY08_16635	protein=multidrug MFS transporter	protein_id=KGT42844.1
gene	3144987	3146246	128787	130046	gene=IY08_16640	protein=6-aminohexanoate hydrolase	protein_id=KGT42845.1
gene	3146420	3146902	130220	130702	gene=IY08_16645	protein=hypothetical protein	protein_id=KGT42846.1
gene	3147140	3148486	130940	132286	gene=IY08_16650	protein=short-chain fatty acid transporter	protein_id=KGT42847.1
gene	3148527	3148880	132327	132680	gene=IY08_16655	protein=group-specific protein	protein_id=KGT42848.1
gene	3148877	3149452	132677	133252	gene=IY08_16660	protein=NADPH dehydrogenase	protein_id=KGT42849.1
gene	3149476	3149865	133276	133665	gene=IY08_16665	protein=zinc finger SWIM domain-containing protein	protein_id=KGT42850.1
gene	3150127	3150384	133927	134184	gene=IY08_16670	protein=hypothetical protein	protein_id=KGT42851.1

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gene	3150937	3151659	134737	135459	gene=IY08_16680	protein=membrane protein	protein_id=KGT42853.1
gene	3151842	3152543	135642	136343	gene=IY08_16685	protein=membrane protein	protein_id=KGT42854.1
gene	3152516	3154171	136316	137971	gene=IY08_16690	protein=cobalt ABC transporter ATP-binding protein	protein_id=KGT42855.1
gene	3154150	3155028	137950	138828	gene=IY08_16695	protein=ABC transporter permease	protein_id=KGT42856.1
gene	3155051	3155890	138851	139690	gene=IY08_16700	protein=hypothetical protein	protein_id=KGT42857.1
gene	3155948	3157786	139748	141586	gene=IY08_16705	protein=cell wall anchor protein	protein_id=KGT42858.1
gene	3158126	3158605	141926	142405	gene=IY08_16710	protein=ribonuclease	protein_id=KGT42859.1
gene	3158805	3160235	142605	144035	gene=IY08_16715	protein=membrane protein	protein_id=KGT42860.1
gene	3160393	3161220	144193	145020	gene=IY08_16720	protein=ribonuclease	protein_id=KGT42861.1
gene	3161720	3162076	145520	145876	gene=IY08_16725	protein=ATPase	protein_id=KGT42862.1
gene	3162525	3163379	146325	147179	gene=IY08_16730	protein=acetyltransferase	protein_id=KGT42863.1
gene	3163851	3164228	147651	148028	gene=IY08_16735	protein=hypothetical protein	protein_id=KGT42864.1
gene	3165061	3165537	148861	149337	gene=IY08_16740	protein=regulatory protein	protein_id=KGT42865.1
gene	3165883	3167160	149683	150960	gene=IY08_16745	protein=histidine--tRNA ligase	protein_id=KGT42866.1
gene	3167321	3167632	151121	151432	gene=IY08_16750	protein=membrane protein	protein_id=KGT42867.1
gene	3167854	3168453	151654	152253	gene=IY08_16755	protein=hypothetical protein	protein_id=KGT42868.1
gene	3168545	3168925	152345	152725	gene=IY08_16760	protein=MarR family transcriptional regulator	protein_id=KGT42869.1
gene	3169055	3169738	152855	153538	gene=IY08_16765	protein=NAD(P)H nitroreductase YfkO	protein_id=KGT42870.1
gene	3169898	3170173	153698	153973	gene=IY08_16770	protein=cyclopropane-fatty-acyl-phospholipid synthase	protein_id=KGT42871.1
gene	3170224	3171282	154024	155082	gene=IY08_16775	protein=pyruvate kinase	protein_id=KGT42872.1
gene	3171565	3172041	155365	155841	gene=IY08_16780	protein=XoxI protein	protein_id=KGT42873.1
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gene	3173114	3173830	156914	157630	gene=IY08_16790	protein=lipoprotein	protein_id=KGT42875.1
gene	3174170	3174928	157970	158728	gene=IY08_16795	protein=3-ketoacyl-ACP reductase	protein_id=KGT42876.1
gene	3174986	3176644	158786	160444	gene=IY08_16800	protein=ABC transporter permease	protein_id=KGT42877.1
gene	3176637	3177362	160437	161162	gene=IY08_16805	protein=ABC transporter	protein_id=KGT42878.1
gene	3177451	3177645	161251	161445	gene=IY08_16810	protein=hypothetical protein	protein_id=KGT42879.1
gene	3177825	3178184	161625	161984	gene=IY08_16815	protein=hypothetical protein	protein_id=KGT42880.1
gene	3178172	3178372	161972	162172	gene=IY08_16820	protein=DNA-binding protein	protein_id=KGT42881.1
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gene	3180544	3181566	164344	165366	gene=IY08_16835	protein=protein tyrosine phosphatase	protein_id=KGT42884.1
gene	3181656	3182495	165456	166295	gene=IY08_16840	protein=hypothetical protein	protein_id=KGT42885.1
gene	3182547	3183269	166347	167069	gene=IY08_16845	protein=acetyltransferase	protein_id=KGT42886.1
gene	3183393	3184232	167193	168032	gene=IY08_16850	protein=hypothetical protein	protein_id=KGT42887.1
gene	3184250	3184696	168050	168496	gene=IY08_16855	protein=DNA mismatch repair protein MutT	protein_id=KGT42888.1
gene	3184705	3185703	168505	169503	gene=IY08_16860	protein=tryptophan--tRNA ligase	protein_id=KGT42889.1
gene	3186093	3186290	169893	170090	gene=IY08_16865	protein=hypothetical protein	protein_id=KGT42890.1
gene	3186342	3187463	170142	171263	gene=IY08_16870	protein=membrane protein	protein_id=KGT42891.1
gene	3187527	3187775	171327	171575	gene=IY08_16875	protein=membrane protein	protein_id=KGT42892.1
gene	3187985	3188446	171785	172246	gene=IY08_16880	protein=acetyltransferase	protein_id=KGT42893.1
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gene	3193659	3194573	177459	178373	gene=IY08_16900	protein=TPR repeat-containing protein	protein_id=KGT42897.1
gene	3194872	3195249	178672	179049	gene=IY08_16905	protein=lipoprotein	protein_id=KGT42898.1
gene	3195326	3195565	179126	179365	gene=IY08_16910	protein=membrane protein	protein_id=KGT42899.1
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gene	3196435	3196848	180235	180648	gene=IY08_16920	protein=ATP synthase subunit I	protein_id=KGT42901.1
gene	3196901	3198229	180701	182029	gene=IY08_16925	protein=membrane protein	protein_id=KGT42902.1
gene	3198349	3198729	182149	182529	gene=IY08_16930	protein=MerR family transcriptional regulator	protein_id=KGT42903.1
gene	3199018	3199791	182818	183591	gene=IY08_16935	protein=hypothetical protein	protein_id=KGT42904.1
gene	3199907	3200674	183707	184474	gene=IY08_16940	protein=glucose-1-phosphate cytidylyltransferase	protein_id=KGT42905.1
gene	3200676	3201731	184476	185531	gene=IY08_16945	protein=CDP-glucose 4,6-dehydratase	protein_id=KGT42906.1
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gene	3207577	3208644	191377	192444	gene=IY08_16990	protein=6-phosphogluconolactonase	protein_id=KGT42914.1
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gene	3210416	3211741	194216	195541	gene=IY08_17000	protein=gluconate permease	protein_id=KGT42916.1
gene	3212132	3212800	195932	196600	gene=IY08_17005	protein=transaldolase	protein_id=KGT42917.1
gene	3212910	3213803	196710	197603	gene=IY08_17010	protein=6-phosphogluconate dehydrogenase	protein_id=KGT42918.1
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gene	3215950	3217434	199750	201234	gene=IY08_17020	protein=glucose-6-phosphate dehydrogenase	protein_id=KGT42920.1
gene	3218033	3218212	201833	202012	pseudo		
gene	3218323	3219318	202123	203118	gene=IY08_17030	protein=quinone oxidoreductase	protein_id=KGT42921.1
gene	3219607	3221304	203407	205104	gene=IY08_17035	protein=bacillolysin	protein_id=KGT42922.1
gene	3221471	3223699	205271	207499	gene=IY08_17040	protein=enhancin	protein_id=KGT42923.1
gene	3224066	3225790	207866	209590	gene=IY08_17045	protein=chemotaxis protein	protein_id=KGT42924.1
gene	3226249	3226818	210049	210618	gene=IY08_17055	protein=nucleotidase	protein_id=KGT42925.1
gene	3226878	3227981	210678	211781	gene=IY08_17060	protein=5-amino-6-(5-phosphoribosylamino)uracil	protein_id=KGT42926.1
gene	3227974	3228711	211774	212511	gene=IY08_17065	protein=GTP cyclohydrolase	protein_id=KGT42927.1
gene	3229014	3229331	212814	213131	gene=IY08_17070	protein=HxIR family transcriptional regulator	protein_id=KGT42928.1
gene	3229665	3230264	213465	214064	gene=IY08_17075	protein=nitroreductase	protein_id=KGT42929.1
gene	3230749	3231225	214549	215025	gene=IY08_17080	protein=hypothetical protein	protein_id=KGT42930.1
gene	3231766	3232137	215566	215937	gene=IY08_17085	protein=membrane protein	protein_id=KGT42931.1
gene	3232205	3232392	216005	216192	pseudo		
gene	3233101	3233442	216901	217242	gene=IY08_17095	protein=alkylphosphonate utilization protein	protein_id=KGT42932.1
gene	3233722	3235485	217522	219285	gene=IY08_17100	protein=sulfate transporter	protein_id=KGT42933.1
gene	3235586	3236026	219386	219826	gene=IY08_17105	protein=DNA mismatch repair protein	protein_id=KGT42934.1
gene	3236028	3236381	219828	220181	gene=IY08_17110	protein=ArsR family transcriptional regulator	protein_id=KGT42935.1
gene	3236806	3238125	220606	221925	gene=IY08_17115	protein=septum formation initiator	protein_id=KGT42936.1
gene	3239228	3239563	223028	223363	gene=IY08_17120	protein=group-specific protein	protein_id=KGT42937.1
gene	3239687	3240100	223487	223900	gene=IY08_17125	protein=Rrf2 family transcriptional regulator	protein_id=KGT42938.1
gene	3240286	3240420	224086	224220	gene=IY08_17130	protein=molecular chaperone	protein_id=KGT42939.1
gene	3240467	3240862	224267	224662	gene=IY08_17135	protein=ArsR family transcriptional regulator	protein_id=KGT42940.1
gene	3241138	3241875	224938	225675	gene=IY08_17140	protein=GntR family transcriptional regulator	protein_id=KGT42941.1
gene	3241908	3242969	225708	226769	gene=IY08_17145	protein=oxidoreductase	protein_id=KGT42942.1

gene	3243202	3243618	227002	227418	gene=IY08_17150	protein=XoxI	protein_id=KGT42943.1
gene	3243779	3245155	227579	228955	gene=IY08_17155	protein=collagenase	protein_id=KGT42944.1
gene	3245523	3246089	229323	229889	gene=IY08_17160	protein=esterase	protein_id=KGT42945.1
gene	3246105	3246929	229905	230729	gene=IY08_17165	protein=hypothetical protein	protein_id=KGT42946.1
gene	3247116	3247964	230916	231764	gene=IY08_17170	protein=aminoglycoside phosphotransferase	protein_id=KGT42947.1
gene	3248152	3248901	231952	232701	gene=IY08_17175	protein=SMS protein	protein_id=KGT42948.1
gene	3248986	3249195	232786	232995	gene=IY08_17180	protein=hypothetical protein	protein_id=KGT42949.1
gene	3249277	3250176	233077	233976	gene=IY08_17185	protein=isomerase	protein_id=KGT42950.1
gene	3250188	3250964	233988	234764	pseudo		
gene	3250961	3251665	234761	235465	gene=IY08_17195	protein=short-chain dehydrogenase	protein_id=KGT42951.1
gene	3251662	3252225	235462	236025	gene=IY08_17200	protein=GNAT family acetyltransferase	protein_id=KGT42952.1
gene	3252408	3252956	236208	236756	gene=IY08_17205	protein=acetyltransferase	protein_id=KGT42953.1
gene	3253120	3254622	236920	238422	gene=IY08_17210	protein=acyl--CoA ligase	protein_id=KGT42954.1
gene	3254757	3255290	238557	239090	gene=IY08_17215	protein=NAD(P)H oxidoreductase	protein_id=KGT42955.1
gene	3255415	3255738	239215	239538	gene=IY08_17220	protein=MarR family transcriptional regulator	protein_id=KGT42956.1
gene	3255932	3256087	239732	239887	gene=IY08_17225	protein=hypothetical protein	protein_id=KGT42957.1
gene	3256181	3256456	239981	240256	gene=IY08_17230	protein=ArsR family transcriptional regulator	protein_id=KGT42958.1
gene	3256707	3260047	240507	243847	pseudo		
gene	3260220	3261557	244020	245357	gene=IY08_17240	protein=membrane protein	protein_id=KGT42959.1
gene	3261547	3262269	245347	246069	gene=IY08_17245	protein=RNA polymerase sigma factor SigI	protein_id=KGT42960.1
gene	3262845	3263606	246645	247406	gene=IY08_17250	protein=glycosyl transferase family 2	protein_id=KGT42961.1
gene	3264020	3265312	247820	249112	gene=IY08_17255	protein=glycosyl hydrolase	protein_id=KGT42962.1
gene	3265775	3266022	249575	249822	pseudo		
gene	3266044	3266676	249844	250476	gene=IY08_17265	protein=lysine transporter LysE	protein_id=KGT42963.1
gene	3266828	3267085	250628	250885	gene=IY08_17270	protein=hypothetical protein	protein_id=KGT42964.1
gene	3267232	3267711	251032	251511	gene=IY08_17275	protein=transcriptional regulator	protein_id=KGT42965.1
gene	3267821	3268783	251621	252583	gene=IY08_17280	protein=decaprenyl diphosphate synthase	protein_id=KGT42966.1
gene	3268947	3269696	252747	253496	gene=IY08_17285	protein=ABC transporter permease	protein_id=KGT42967.1
gene	3269697	3270458	253497	254258	gene=IY08_17290	protein=glycosyl transferase family 8	protein_id=KGT42968.1
gene	3270629	3270970	254429	254770	gene=IY08_17295	protein=cytoplasmic protein	protein_id=KGT42969.1
gene	3271046	3271366	254846	255166	gene=IY08_17300	protein=PadR family transcriptional regulator	protein_id=KGT42970.1

gene	3271830	3273146	255630	256946	gene=IY08_17305	protein=condensation protein	protein_id=KGT42971.1
gene	3274011	3275297	257811	259097	gene=IY08_17310	protein=hydroxylamine reductase	protein_id=KGT42972.1
gene	3276036	3276809	259836	260609	gene=IY08_17320	protein=beta-lactamase	protein_id=KGT42973.1
gene	3276965	3277246	260765	261046	gene=IY08_17325	protein=hypothetical protein	protein_id=KGT42974.1
gene	3277380	3277574	261180	261374	gene=IY08_17330	protein=hypothetical protein	protein_id=KGT42975.1
gene	3277620	3278657	261420	262457	gene=IY08_17335	protein=penicillin-binding protein	protein_id=KGT42976.1
gene	3278694	3278942	262494	262742	gene=IY08_17340	protein=hypothetical protein	protein_id=KGT42977.1
gene	3279222	3280265	263022	264065	gene=IY08_17345	protein=oxidoreductase	protein_id=KGT42978.1
gene	3280403	3281134	264203	264934	gene=IY08_17350	protein=phosphoesterase	protein_id=KGT42979.1
gene	3281156	3281848	264956	265648	gene=IY08_17355	protein=catabolite gene activator protein	protein_id=KGT42980.1
gene	3281957	3282403	265757	266203	gene=IY08_17360	protein=membrane protein	protein_id=KGT42981.1
gene	3282417	3282881	266217	266681	gene=IY08_17365	protein=membrane protein	protein_id=KGT42982.1
gene	3282971	3283465	266771	267265	gene=IY08_17370	protein=hypothetical protein	protein_id=KGT42983.1
gene	3283506	3284258	267306	268058	gene=IY08_17375	protein=N-acyl homoserine lactonase	protein_id=KGT42984.1
gene	3284686	3286077	268486	269877	gene=IY08_17380	protein=D-alanine/D-serine/glycine permease	protein_id=KGT42985.1
gene	3286657	3287856	270457	271656	gene=IY08_17385	protein=multidrug transporter CflA	protein_id=KGT42986.1
gene	3288219	3288785	272019	272585	gene=IY08_17390	protein=hypothetical protein	protein_id=KGT42987.1
gene	3288852	3289076	272652	272876	gene=IY08_17395	protein=hypothetical protein	protein_id=KGT42988.1
gene	3289395	3289673	273195	273473	gene=IY08_17405	protein=hypothetical protein	protein_id=KGT42989.1
gene	3290416	3291159	274216	274959	gene=IY08_17410	protein=short-chain dehydrogenase	protein_id=KGT42990.1
gene	3291270	3291932	275070	275732	gene=IY08_17415	protein=deacetylase	protein_id=KGT42991.1
gene	3291948	3292298	275748	276098	gene=IY08_17420	protein=hypothetical protein	protein_id=KGT42992.1
gene	3292561	3293886	276361	277686	gene=IY08_17425	protein=membrane protein	protein_id=KGT42993.1
gene	3293960	3294187	277760	277987	gene=IY08_17430	protein=hypothetical protein	protein_id=KGT42994.1
gene	3294287	3294838	278087	278638	pseudo		
gene	3295002	3295910	278802	279710	gene=IY08_17440	protein=iron-hydroxamate ABC transporter substrate-binding protein	protein_id=KGT42995.1
gene	3295932	3296948	279732	280748	gene=IY08_17445	protein=iron ABC transporter permease	protein_id=KGT42996.1
gene	3296949	3297983	280749	281783	gene=IY08_17450	protein=ferrichrome ABC transporter permease	protein_id=KGT42997.1
gene	3298259	3299023	282059	282823	gene=IY08_17455	protein=hypothetical protein	protein_id=KGT42998.1
gene	3299107	3300093	282907	283893	gene=IY08_17460	protein=hypothetical protein	protein_id=KGT42999.1

gene	3300303	3300758	284103	284558	gene=IY08_17465	protein=formate dehydrogenase	protein_id=KGT43000.1
gene	3300951	3301439	284751	285239	gene=IY08_17470	protein=damage-inducible protein DinB	protein_id=KGT43001.1
gene	3301553	3302029	285353	285829	gene=IY08_17475	protein=hypothetical protein	protein_id=KGT43002.1
gene	3302046	3302558	285846	286358	gene=IY08_17480	protein=hypothetical protein	protein_id=KGT43003.1
gene	3302861	3303754	286661	287554	gene=IY08_17485	protein=LysR family transcriptional regulator	protein_id=KGT43004.1
gene	3303878	3304843	287678	288643	gene=IY08_17490	protein=alcohol dehydrogenase	protein_id=KGT43005.1
gene	3305116	3305631	288916	289431	gene=IY08_17495	protein=hypothetical protein	protein_id=KGT43006.1
gene	3305835	3306092	289635	289892	gene=IY08_17500	protein=hypothetical protein	protein_id=KGT43007.1
gene	3306561	3307271	290361	291071	gene=IY08_17505	protein=phosphoglycerate mutase	protein_id=KGT43008.1
gene	3307432	3307956	291232	291756	gene=IY08_17510	protein=GCN5 family acetyltransferase	protein_id=KGT43009.1
gene	3307963	3309864	291763	293664	gene=IY08_17515	protein=mannonate oxidoreductase	protein_id=KGT43010.1
gene	3310314	3311027	294114	294827	gene=IY08_17520	protein=hypothetical protein	protein_id=KGT43011.1
gene	3311499	3313040	295299	296840	gene=IY08_17525	protein=alpha-amylase	protein_id=KGT43012.1
gene	3313244	3314035	297044	297835	gene=IY08_17530	protein=N-hydroxyarylamine O-acetyltransferase	protein_id=KGT43013.1
gene	3314153	3315940	297953	299740	gene=IY08_17535	protein=oligoendopeptidase F	protein_id=KGT43014.1
gene	3315987	3317033	299787	300833	gene=IY08_17540	protein=agmatine deiminase	protein_id=KGT43015.1
gene	3317221	3318042	301021	301842	gene=IY08_17545	protein=MerR family transcriptional regulator	protein_id=KGT43016.1
gene	3318085	3319062	301885	302862	gene=IY08_17550	protein=peptidyl-arginine deiminase	protein_id=KGT43017.1
gene	3319630	3320787	303430	304587	gene=IY08_17560	protein=agmatine deiminase	protein_id=KGT43018.1
gene	3321179	3322306	304979	306106	gene=IY08_17565	protein=penicillin-binding protein	protein_id=KGT43019.1
gene	3322564	3322794	306364	306594	gene=IY08_17570	protein=hypothetical protein	protein_id=KGT43020.1
gene	3322905	3324127	306705	307927	pseudo		
gene	3324214	3325065	308014	308865	gene=IY08_17580	protein=LysR family transcriptional regulator	protein_id=KGT43021.1
gene	3325058	3325567	308858	309367	gene=IY08_17585	protein=group-specific protein	protein_id=KGT43022.1
gene	3325606	3326550	309406	310350	gene=IY08_17590	protein=glycerophosphodiester phosphodiesterase	protein_id=KGT43023.1
gene	3326942	3328561	310742	312361	gene=IY08_17595	protein=FAD-binding monooxygenase	protein_id=KGT43024.1
gene	3328849	3328980	312649	312780	gene=IY08_17600	protein=transcriptional regulator	protein_id=KGT43025.1
gene	3329072	3329416	312872	313216	gene=IY08_17605	protein=ArsR family transcriptional regulator	protein_id=KGT43026.1
gene	3329435	3330436	313235	314236	gene=IY08_17610	protein=NADPH:quinone reductase	protein_id=KGT43027.1
gene	3330613	3332079	314413	315879	gene=IY08_17615	protein=hypothetical protein	protein_id=KGT43028.1
gene	3332334	3333428	316134	317228	gene=IY08_17620	protein=histidine kinase	protein_id=KGT43029.1

gene	3333425	3333637	317225	317437	gene=IY08_17625	protein=hypothetical protein	protein_id=KGT43030.1
gene	3333711	3334310	317511	318110	gene=IY08_17630	protein=transcriptional regulator	protein_id=KGT43031.1
gene	3334452	3334979	318252	318779	gene=IY08_17635	protein=hypothetical protein	protein_id=KGT43032.1
gene	3335003	3335350	318803	319150	gene=IY08_17640	protein=hypothetical protein	protein_id=KGT43033.1
gene	3335541	3336932	319341	320732	gene=IY08_17650	protein=2-hydroxy-acid oxidase	protein_id=KGT43034.1
gene	3337059	3337457	320859	321257	gene=IY08_17655	protein=membrane protein	protein_id=KGT43035.1
gene	3337711	3338214	321511	322014	gene=IY08_17660	protein=alanine acetyltransferase	protein_id=KGT43036.1
gene	3338418	3338600	322218	322400	gene=IY08_17665	protein=hypothetical protein	protein_id=KGT43037.1
gene	3338805	3338987	322605	322787	gene=IY08_17670	protein=hypothetical protein	protein_id=KGT43038.1
gene	3339489	3339980	323289	323780	gene=IY08_17675	protein=CDP-diacylglycerol--serine O-	protein_id=KGT43039.1
gene	3340363	3340548	324163	324348	gene=IY08_17685	protein=hypothetical protein	protein_id=KGT43040.1
gene	3340598	3342034	324398	325834	gene=IY08_17690	protein=Zn-dependent hydrolase	protein_id=KGT43041.1
gene	3342101	3343300	325901	327100	gene=IY08_17695	protein=pyridine nucleotide-disulfide oxidoreductase	protein_id=KGT43042.1
gene	3343838	3344512	327638	328312	gene=IY08_17700	protein=hypothetical protein	protein_id=KGT43043.1
gene	3345181	3345930	328981	329730	gene=IY08_17705	protein=glucose-1-phosphate cytidylyltransferase	protein_id=KGT43044.1
gene	3345951	3348020	329751	331820	gene=IY08_17710	protein=glycosyl transferase	protein_id=KGT43045.1
gene	3348103	3349062	331903	332862	gene=IY08_17715	protein=CDP-abequose synthase	protein_id=KGT43046.1
gene	3349091	3350179	332891	333979	gene=IY08_17720	protein=CDP-glucose 4,6-dehydratase	protein_id=KGT43047.1
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gene	3351001	3351576	1	576	gene=IY08_17725	protein=transposase	protein_id=KGT42708.1
gene	3352256	3353371	1256	2371	gene=IY08_17730	protein=histidine kinase	protein_id=KGT42709.1
gene	3353371	3353532	2371	2532	gene=IY08_17735	protein=histidine kinase	protein_id=KGT42710.1
gene	3353694	3355676	2694	4676	gene=IY08_17740	protein=chemotaxis protein	protein_id=KGT42711.1
gene	3356485	3356763	5485	5763	gene=IY08_17745	protein=hypothetical protein	protein_id=KGT42712.1
gene	3357311	3357685	6311	6685	gene=IY08_17750	protein=hypothetical protein	protein_id=KGT42713.1
gene	3357946	3358281	6946	7281	gene=IY08_17755	protein=hypothetical protein	protein_id=KGT42714.1
gene	3360439	3361707	9439	10707	gene=IY08_17770	protein=glycosyl hydrolase family 5	protein_id=KGT42715.1
gene	3362220	3362693	11220	11693	gene=IY08_17775	protein=aspartate phosphatase	protein_id=KGT42716.1
gene	3362845	3365574	11845	14574	gene=IY08_17780	protein=diguanylate cyclase	protein_id=KGT42717.1
gene	3365986	3366198	14986	15198	pseudo		
gene	3366592	3368070	15592	17070	gene=IY08_17790	protein=glycosyl transferase family 1	protein_id=KGT42718.1

gene	3368223	3368504	17223	17504	gene=IY08_17795	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT42719.1
gene	3368765	3369019	17765	18019	gene=IY08_17800	protein=hypothetical protein	protein_id=KGT42720.1
gene	3369098	3372379	18098	21379	gene=IY08_17805	protein=collagen-binding protein	protein_id=KGT42721.1
gene	3372951	3373304	21951	22304	gene=IY08_17810	protein=DNA mismatch repair protein MutT	protein_id=KGT42722.1
gene	3373677	3374117	22677	23117	gene=IY08_17815	protein=hypothetical protein	protein_id=KGT42723.1
gene	3374751	3376004	23751	25004	gene=IY08_17820	protein=sporulation kinase	protein_id=KGT42724.1
gene	3376487	3379259	25487	28259	gene=IY08_17825	protein=collagenase	protein_id=KGT42587.1
gene	3379512	3380189	28512	29189	gene=IY08_17830	protein=methyltransferase	protein_id=KGT42588.1
gene	3380480	3380998	29480	29998	gene=IY08_17835	protein=GCN5 family acetyltransferase	protein_id=KGT42589.1
gene	3381046	3381954	30046	30954	gene=IY08_17840	protein=glyoxalase	protein_id=KGT42590.1
gene	3382129	3383040	31129	32040	gene=IY08_17845	protein=vancomycin B-type resistance protein VanW	protein_id=KGT42591.1
gene	3383473	3383802	32473	32802	gene=IY08_17850	protein=hypothetical protein	protein_id=KGT42592.1
gene	3383918	3385009	32918	34009	gene=IY08_17855	protein=hypothetical protein	protein_id=KGT42593.1
gene	3385346	3385693	34346	34693	gene=IY08_17860	protein=hypothetical protein	protein_id=KGT42594.1
gene	3385724	3385882	34724	34882	pseudo		
gene	3386058	3386903	35058	35903	gene=IY08_17870	protein=exonuclease	protein_id=KGT42595.1
gene	3387092	3387292	36092	36292	gene=IY08_17875	protein=cold-shock protein	protein_id=KGT42596.1
gene	3387508	3388407	36508	37407	gene=IY08_17880	protein=BNR repeat-containing protein	protein_id=KGT42597.1
gene	3388424	3388867	37424	37867	gene=IY08_17885	protein=flavodoxin	protein_id=KGT42598.1
gene	3389092	3389712	38092	38712	gene=IY08_17890	protein=membrane protein	protein_id=KGT42599.1
gene	3389799	3390194	38799	39194	gene=IY08_17895	protein=DNA mismatch repair protein MutT	protein_id=KGT42600.1
gene	3390191	3390532	39191	39532	gene=IY08_17900	protein=cytoplasmic protein	protein_id=KGT42601.1
gene	3390643	3391200	39643	40200	gene=IY08_17905	protein=acetyltransferase	protein_id=KGT42602.1
gene	3391246	3398718	40246	47718	gene=IY08_17910	protein=reticulocyte-binding protein	protein_id=KGT42603.1
gene	3398835	3399584	47835	48584	gene=IY08_17915	protein=short-chain dehydrogenase	protein_id=KGT42604.1
gene	3399620	3400453	48620	49453	gene=IY08_17920	protein=acetyltransferase	protein_id=KGT42605.1
gene	3400520	3402028	49520	51028	gene=IY08_17925	protein=argininosuccinate lyase	protein_id=KGT42606.1
gene	3402130	3403239	51130	52239	gene=IY08_17930	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT42607.1
gene	3403355	3404287	52355	53287	gene=IY08_17935	protein=nucleoside hydrolase	protein_id=KGT42608.1
gene	3404411	3405844	53411	54844	gene=panF	protein=sodium/panthothenate symporter	protein_id=KGT42609.1
gene	3405848	3406126	54848	55126	gene=IY08_17945	protein=sodium:pantothenate symporter	protein_id=KGT42610.1

gene	3406400	3407884	55400	56884	gene=IY08_17950	protein=betaine-aldehyde dehydrogenase	protein_id=KGT42611.1
gene	3407935	3408675	56935	57675	gene=IY08_17955	protein=3-ketoacyl-ACP reductase	protein_id=KGT42612.1
gene	3408961	3409110	57961	58110	gene=IY08_17960	protein=cytochrome C biosynthesis protein	protein_id=KGT42613.1
gene	3409184	3411037	58184	60037	gene=IY08_17965	protein=squalene-hopene cyclase	protein_id=KGT42614.1
gene	3411137	3411562	60137	60562	gene=IY08_17970	protein=membrane protein	protein_id=KGT42615.1
gene	3411642	3412583	60642	61583	gene=IY08_17975	protein=transporter	protein_id=KGT42616.1
gene	3412676	3412924	61676	61924	gene=IY08_17980	protein=membrane protein	protein_id=KGT42617.1
gene	3413108	3413506	62108	62506	gene=IY08_17985	protein=hypothetical protein	protein_id=KGT42618.1
gene	3413549	3413773	62549	62773	gene=IY08_17990	protein=group-specific protein	protein_id=KGT42619.1
gene	3413789	3414838	62789	63838	gene=IY08_17995	protein=ATP-binding protein	protein_id=KGT42620.1
gene	3414911	3415147	63911	64147	gene=IY08_18000	protein=molybdenum cofactor biosynthesis protein MoaD	protein_id=KGT42621.1
gene	3415152	3415616	64152	64616	gene=IY08_18005	protein=molybdopterin (MPT) converting factor, subunit 2	protein_id=KGT42622.1
gene	3415597	3416904	64597	65904	gene=IY08_18010	protein=molybdopterin molybdenumtransferase	protein_id=KGT42623.1
gene	3416922	3417938	65922	66938	gene=IY08_18015	protein=thiamine biosynthesis protein MoeB	protein_id=KGT42624.1
gene	3417963	3418742	66963	67742	gene=IY08_18020	protein=formate/nitrite transporter	protein_id=KGT42625.1
gene	3418935	3419951	67935	68951	gene=IY08_18025	protein=molybdenum cofactor biosynthesis protein A	protein_id=KGT42626.1
gene	3419968	3420765	68968	69765	gene=IY08_18030	protein=formate dehydrogenase	protein_id=KGT42627.1
gene	3420782	3421126	69782	70126	gene=IY08_18035	protein=hypothetical protein	protein_id=KGT42628.1
gene	3421242	3421724	70242	70724	gene=IY08_18040	protein=hypothetical protein	protein_id=KGT42629.1
gene	3421737	3424676	70737	73676	gene=IY08_18045	protein=oxidoreductase	protein_id=KGT42630.1
gene	3424669	3424835	73669	73835	pseudo		
gene	3424973	3426511	73973	75511	gene=IY08_18055	protein=spore germination protein	protein_id=KGT42631.1
gene	3426508	3427605	75508	76605	gene=IY08_18060	protein=spore germination protein	protein_id=KGT42632.1
gene	3427606	3428742	76606	77742	gene=IY08_18065	protein=spore germination protein	protein_id=KGT42633.1
gene	3428817	3430199	77817	79199	gene=IY08_18070	protein=amino acid permease	protein_id=KGT42634.1
gene	3430699	3430839	79699	79839	gene=IY08_18075	protein=phosphonate ABC transporter permease	protein_id=KGT42635.1
gene	3430897	3434259	79897	83259	gene=IY08_18080	protein=phosphonate ABC transporter permease	protein_id=KGT42636.1
gene	3434339	3436435	83339	85435	gene=IY08_18085	protein=membrane protein	protein_id=KGT42637.1
gene	3436693	3437031	85693	86031	gene=IY08_18090	protein=glyoxalase	protein_id=KGT42638.1
gene	3437256	3437591	86256	86591	gene=IY08_18095	protein=hypothetical protein	protein_id=KGT42639.1
gene	3437726	3438100	86726	87100	gene=IY08_18100	protein=keratin	protein_id=KGT42640.1

gene	3438141	3438860	87141	87860	gene=IY08_18105	protein=methyltransferase	protein_id=KGT42641.1
gene	3438943	3440637	87943	89637	gene=IY08_18110	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT42642.1
gene	3441075	3442790	90075	91790	gene=IY08_18115	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT42643.1
gene	3443101	3444804	92101	93804	gene=IY08_18120	protein=peptide ABC transporter substrate-binding protein	protein_id=KGT42644.1
gene	3445151	3446188	94151	95188	gene=IY08_18125	protein=LytR family transcriptional regulator	protein_id=KGT42645.1
gene	3446206	3447204	95206	96204	gene=IY08_18130	protein=ECF-type sigma factor negative effector	protein_id=KGT42646.1
gene	3447217	3447750	96217	96750	gene=IY08_18135	protein=RNA polymerase subunit sigma-24	protein_id=KGT42647.1
gene	3447951	3448757	96951	97757	gene=IY08_18140	protein=ABC transporter permease	protein_id=KGT42648.1
gene	3448750	3449643	97750	98643	gene=IY08_18145	protein=ABC transporter ATP-binding protein	protein_id=KGT42649.1
gene	3449808	3450401	98808	99401	gene=IY08_18150	protein=TetR family transcriptional regulator	protein_id=KGT42650.1
gene	3450426	3451457	99426	100457	gene=IY08_18155	protein=oxidoreductase	protein_id=KGT42651.1
gene	3451728	3454151	100728	103151	gene=IY08_18160	protein=DNA gyrase subunit A	protein_id=KGT42652.1
gene	3454153	3456117	103153	105117	gene=gyrB	protein=DNA gyrase subunit B	protein_id=KGT42653.1
gene	3456240	3456455	105240	105455	gene=IY08_18170	protein=hypothetical protein	protein_id=KGT42654.1
gene	3456493	3456906	105493	105906	gene=IY08_18175	protein=CoA-binding protein	protein_id=KGT42655.1
gene	3456986	3458227	105986	107227	gene=IY08_18180	protein=serine protease	protein_id=KGT42656.1
gene	3458431	3459108	107431	108108	gene=IY08_18185	protein=PhoB family transcriptional regulator	protein_id=KGT42657.1
gene	3459127	3459579	108127	108579	gene=IY08_18190	protein=ribonucleoside-triphosphate reductase activating	protein_id=KGT42658.1
gene	3459576	3461435	108576	110435	gene=IY08_18195	protein=ribonucleoside-triphosphate reductase	protein_id=KGT42659.1
gene	3461661	3462257	110661	111257	gene=IY08_18200	protein=glycerol-3-phosphate acyltransferase	protein_id=KGT42660.1
gene	3462366	3462656	111366	111656	gene=IY08_18205	protein=hypothetical protein	protein_id=KGT42661.1
gene	3462683	3463102	111683	112102	gene=IY08_18210	protein=hypothetical protein	protein_id=KGT42662.1
gene	3463214	3464506	112214	113506	gene=IY08_18215	protein=glycosyl hydrolase	protein_id=KGT42663.1
gene	3464535	3464732	113535	113732	gene=IY08_18220	protein=small acid-soluble spore protein Tlp	protein_id=KGT42664.1
gene	3464832	3464966	113832	113966	gene=sspN	protein=acid-soluble spore protein N	protein_id=KGT42665.1
gene	3465010	3465153	114010	114153	gene=IY08_18230	protein=hypothetical protein	protein_id=KGT42666.1
gene	3465293	3466240	114293	115240	gene=IY08_18235	protein=DNA polymerase III subunit epsilon	protein_id=KGT42667.1
gene	3466356	3466931	115356	115931	gene=IY08_18240	protein=thiol:disulfide interchange protein tlpA	protein_id=KGT42668.1
gene	3467172	3467429	116172	116429	gene=IY08_18245	protein=hypothetical protein	protein_id=KGT42669.1
gene	3467453	3469101	116453	118101	pseudo		
gene	3469219	3471942	118219	120942	gene=IY08_18255	protein=aconitate hydratase	protein_id=KGT42670.1

gene	3472235	3472384	121235	121384	gene=sspO	protein=acid-soluble spore protein O	protein_id=KGT42671.1
gene	3472426	3473067	121426	122067	gene=IY08_18265	protein=chitooligosaccharide deacetylase	protein_id=KGT42672.1
gene	3473197	3473460	122197	122460	gene=IY08_18270	protein=hypothetical protein	protein_id=KGT42673.1
gene	3473582	3473704	122582	122704	gene=IY08_18275	protein=spore protein P	protein_id=KGT42674.1
gene	3473829	3474209	122829	123209	gene=IY08_18280	protein=spore coat protein	protein_id=KGT42675.1
gene	3474259	3475497	123259	124497	gene=IY08_18285	protein=MFS transporter	protein_id=KGT42676.1
gene	3475566	3475973	124566	124973	gene=IY08_18290	protein=hypothetical protein	protein_id=KGT42677.1
gene	3476075	3477310	125075	126310	gene=IY08_18295	protein=alanyl-tRNA synthetase	protein_id=KGT42678.1
gene	3477355	3477798	126355	126798	gene=IY08_18300	protein=DNA mismatch repair protein MutT	protein_id=KGT42679.1
gene	3477903	3478484	126903	127484	gene=IY08_18305	protein=cytoplasmic protein	protein_id=KGT42680.1
gene	3478495	3478719	127495	127719	gene=IY08_18310	protein=hypothetical protein	protein_id=KGT42681.1
gene	3478841	3479185	127841	128185	gene=IY08_18315	protein=hypothetical protein	protein_id=KGT42682.1
gene	3479298	3480389	128298	129389	gene=IY08_18320	protein=acetyl-CoA acetyltransferase	protein_id=KGT42683.1
gene	3480382	3481845	129382	130845	gene=IY08_18325	protein=acyl-CoA synthetase	protein_id=KGT42684.1
gene	3481912	3482487	130912	131487	gene=IY08_18330	protein=biotin biosynthesis protein BioY	protein_id=KGT42685.1
gene	3482611	3484224	131611	133224	gene=IY08_18335	protein=fatty-acid--CoA ligase	protein_id=KGT42686.1
gene	3484393	3485181	133393	134181	gene=IY08_18340	protein=XRE family transcriptional regulator	protein_id=KGT42687.1
gene	3485204	3485413	134204	134413	gene=IY08_18345	protein=hypothetical protein	protein_id=KGT42688.1
gene	3485410	3485970	134410	134970	gene=IY08_18350	protein=alanine acetyltransferase	protein_id=KGT42689.1
gene	3485967	3486170	134967	135170	gene=IY08_18355	protein=hypothetical protein	protein_id=KGT42690.1
gene	3486323	3487138	135323	136138	gene=IY08_18360	protein=acetyltransferase	protein_id=KGT42691.1
gene	3487310	3487522	136310	136522	gene=IY08_18365	protein=hypothetical protein	protein_id=KGT42692.1
gene	3487546	3487794	136546	136794	gene=IY08_18370	protein=hypothetical protein	protein_id=KGT42693.1
gene	3487814	3488266	136814	137266	gene=IY08_18375	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT42694.1
gene	3488282	3489103	137282	138103	gene=IY08_18380	protein=serine/threonine protein phosphatase	protein_id=KGT42695.1
gene	3489230	3490039	138230	139039	gene=IY08_18385	protein=hypothetical protein	protein_id=KGT42696.1
gene	3490059	3490430	139059	139430	gene=IY08_18390	protein=glyoxalase	protein_id=KGT42697.1
gene	3490668	3492200	139668	141200	gene=IY08_18395	protein=histidine kinase	protein_id=KGT42698.1
gene	3492244	3492852	141244	141852	gene=IY08_18400	protein=carboxylesterase	protein_id=KGT42699.1
gene	3492877	3493815	141877	142815	gene=IY08_18405	protein=ring-cleaving dioxygenase	protein_id=KGT42700.1
gene	3494167	3495645	143167	144645	gene=IY08_18410	protein=proline:sodium symporter PutP	protein_id=KGT42701.1

gene	3495944	3496432	144944	145432	gene=IY08_18415	protein=cobalamin biosynthesis protein CbiX	protein_id=KGT42702.1
gene	3496544	3498118	145544	147118	gene=IY08_18420	protein=glutamate synthase	protein_id=KGT42703.1
gene	3498186	3499313	147186	148313	gene=IY08_18425	protein=oxidoreductase	protein_id=KGT42704.1
gene	3499875	3500351	148875	149351	gene=IY08_18430	protein=transcription factor YdeB	protein_id=KGT42705.1
gene	3500593	3501564	149593	150564	gene=IY08_18435	protein=formimidoylglutamase	protein_id=KGT42706.1
gene	3501543	3502605	150543	151605	gene=IY08_18440	protein=imidazolonepropionase	protein_id=KGT42707.1]
gene	3502838	3504496	151838	153496	gene=IY08_18450	protein=uroporphobilinogen hydratase	protein_id=KGT42536.1
gene	3504520	3506037	153520	155037	gene=IY08_18455	protein=histidine ammonia-lyase	protein_id=KGT42537.1
gene	3506141	3506581	155141	155581	gene=hutP	protein=anti-terminator HutP	protein_id=KGT42538.1
gene	3506778	3507725	155778	156725	gene=IY08_18465	protein=methyltransferase	protein_id=KGT42539.1
gene	3507739	3508311	156739	157311	gene=IY08_18470	protein=4-methyl-5(B-hydroxyethyl)-thiazole monophosphate biosynthesis protein	protein_id=KGT42540.1
gene	3508308	3508895	157308	157895	gene=IY08_18475	protein=ATP-binding protein	protein_id=KGT42541.1
gene	3508849	3509043	157849	158043	pseudo		
gene	3509141	3509437	158141	158437	gene=IY08_18485	protein=hypothetical protein	protein_id=KGT42542.1
gene	3509541	3509972	158541	158972	gene=IY08_18490	protein=hypothetical protein	protein_id=KGT42543.1
gene	3510043	3510549	159043	159549	gene=IY08_18495	protein=membrane protein	protein_id=KGT42544.1
gene	3510640	3511347	159640	160347	gene=IY08_18500	protein=cytochrome C biogenesis protein	protein_id=KGT42545.1
gene	3511836	3512744	160836	161744	gene=IY08_18510	protein=multidrug transporter	protein_id=KGT42546.1
gene	3512877	3514022	161877	163022	gene=IY08_18515	protein=hydrolase	protein_id=KGT42547.1
gene	3514070	3515014	163070	164014	gene=IY08_18520	protein=bacitracin ABC transporter permease	protein_id=KGT42548.1
gene	3515007	3515918	164007	164918	gene=IY08_18525	protein=ABC transporter ATP-binding protein	protein_id=KGT42549.1
gene	3516009	3516584	165009	165584	gene=IY08_18530	protein=ABC transporter permease	protein_id=KGT42550.1
gene	3516754	3517353	165754	166353	gene=IY08_18535	protein=histidine kinase	protein_id=KGT42551.1
gene	3517444	3518346	166444	167346	gene=IY08_18540	protein=LysR family transcriptional regulator	protein_id=KGT42552.1
gene	3518500	3518865	167500	167865	gene=IY08_18545	protein=holin	protein_id=KGT42553.1
gene	3518862	3519539	167862	168539	gene=IY08_18550	protein=murein hydrolase export regulator	protein_id=KGT42554.1
gene	3519552	3519965	168552	168965	gene=IY08_18555	protein=DNA mismatch repair protein MutT	protein_id=KGT42555.1
gene	3520107	3520307	169107	169307	gene=IY08_18560	protein=hypothetical protein	protein_id=KGT42556.1
gene	3520675	3521430	169675	170430	gene=IY08_18565	protein=membrane protein	protein_id=KGT42557.1
gene	3521529	3521675	170529	170675	gene=IY08_18570	protein=phage protein	protein_id=KGT42558.1

gene	3521915	3522463	170915	171463	gene=IY08_18575	protein=hypothetical protein	protein_id=KGT42559.1
gene	3522487	3523506	171487	172506	gene=IY08_18580	protein=chromosome segregation protein	protein_id=KGT42560.1
gene	3523797	3524843	172797	173843	gene=IY08_18585	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT42561.1
gene	3524976	3526739	173976	175739	gene=IY08_18590	protein=multidrug ABC transporter ATP-binding protein	protein_id=KGT42562.1
gene	3526739	3528490	175739	177490	gene=IY08_18595	protein=ABC transporter ATP-binding protein	protein_id=KGT42563.1
gene	3528613	3528834	177613	177834	gene=IY08_18600	protein=hypothetical protein	protein_id=KGT42564.1
gene	3528913	3529353	177913	178353	gene=IY08_18605	protein=1-phosphatidylinositol phosphodiesterase	protein_id=KGT42565.1
gene	3529510	3531510	178510	180510	gene=IY08_18610	protein=transketolase	protein_id=KGT42566.1
gene	3531795	3532598	180795	181598	gene=IY08_18615	protein=phosphate ABC transporter permease	protein_id=KGT42567.1
gene	3532598	3533392	181598	182392	gene=IY08_18620	protein=phosphate ABC transporter permease	protein_id=KGT42568.1
gene	3533389	3534162	182389	183162	gene=IY08_18625	protein=phosphonate ABC transporter ATP-binding protein	protein_id=KGT42569.1
gene	3534246	3535184	183246	184184	gene=IY08_18630	protein=phosphonate-binding protein	protein_id=KGT42570.1
gene	3535371	3536954	184371	185954	gene=IY08_18635	protein=2', 3'-cyclic nucleotide 2'-phosphodiesterase	protein_id=KGT42571.1
gene	3536994	3537233	185994	186233	gene=IY08_18640	protein=hypothetical protein	protein_id=KGT42572.1
gene	3537279	3537935	186279	186935	gene=IY08_18645	protein=resolvase	protein_id=KGT42573.1
gene	3538077	3538697	187077	187697	gene=IY08_18650	protein=LexA family transcriptional regulator	protein_id=KGT42574.1
gene	3538790	3539593	187790	188593	gene=IY08_18655	protein=GNAT family acetyltransferase	protein_id=KGT42575.1
gene	3539594	3540136	188594	189136	gene=IY08_18660	protein=hypothetical protein	protein_id=KGT42576.1
gene	3540129	3540452	189129	189452	gene=IY08_18665	protein=PadR family transcriptional regulator	protein_id=KGT42577.1
gene	3541071	3542405	190071	191405	gene=IY08_18670	protein=glutamine synthetase	protein_id=KGT42578.1
gene	3542454	3542843	191454	191843	gene=IY08_18675	protein=transcriptional regulator	protein_id=KGT42579.1
gene	3543017	3544288	192017	193288	gene=IY08_18680	protein=hypothetical protein	protein_id=KGT42580.1
gene	3544281	3545555	193281	194555	gene=IY08_18685	protein=GTPase	protein_id=KGT42581.1
gene	3545648	3546271	194648	195271	gene=IY08_18690	protein=membrane protein	protein_id=KGT42582.1
gene	3546371	3546508	195371	195508	gene=IY08_18695	protein=hypothetical protein	protein_id=KGT42583.1
gene	3546540	3547496	195540	196496	gene=IY08_18700	protein=stage V sporulation protein K	protein_id=KGT42584.1
gene	3547761	3548726	196761	197726	gene=IY08_18705	protein=integrase	protein_id=KGT42585.1
gene	3548840	3549830	197840	198830	gene=IY08_18710	protein=hypothetical protein	protein_id=KGT42586.1
scaffold17							
gene	3549841	3550561	1	721	gene=IY08_18715	protein=hypothetical protein	protein_id=KGT42385.1]
gene	3550642	3550866	802	1026	gene=IY08_18720	protein=RNA-binding protein Hfq	protein_id=KGT42386.1

gene	3550888	3551841	1048	2001	gene=IY08_18725	protein=tRNA delta(2)-isopentenylpyrophosphate	protein_id=KGT42387.1
gene	3552022	3552267	2182	2427	gene=IY08_18730	protein=hypothetical protein	protein_id=KGT42388.1
gene	3552330	3553280	2490	3440	gene=IY08_18735	protein=enterotoxin	protein_id=KGT42389.1
gene	3553630	3555486	3790	5646	gene=IY08_18740	protein=PTS fructose transporter subunit IIC	protein_id=KGT42390.1
gene	3555500	3556411	5660	6571	gene=IY08_18745	protein=phosphofructokinase	protein_id=KGT42391.1
gene	3556408	3557160	6568	7320	gene=IY08_18750	protein=DeoR family transcriptional regulator	protein_id=KGT42392.1
gene	3557318	3558481	7478	8641	gene=IY08_18755	protein=butanol dehydrogenase	protein_id=KGT42393.1
gene	3558598	3559140	8758	9300	gene=IY08_18760	protein=membrane protein	protein_id=KGT42394.1
gene	3559317	3559433	9477	9593	gene=IY08_18765	protein=hypothetical protein	protein_id=KGT42395.1
gene	3559458	3559769	9618	9929	gene=IY08_18770	protein=hypothetical protein	protein_id=KGT42396.1
gene	3559940	3561334	10100	11494	gene=IY08_18775	protein=GABA permease	protein_id=KGT42397.1
gene	3561606	3562688	11766	12848	gene=IY08_18780	protein=chitinase	protein_id=KGT42398.1
gene	3562888	3563781	13048	13941	gene=IY08_18790	protein=metallophosphoesterase	protein_id=KGT42399.1
gene	3563975	3564790	14135	14950	gene=IY08_18795	protein=formate/nitrite transporter	protein_id=KGT42400.1
gene	3564930	3565202	15090	15362	gene=IY08_18800	protein=DNA-binding protein	protein_id=KGT42401.1
gene	3565222	3565701	15382	15861	gene=IY08_18805	protein=acetyltransferase	protein_id=KGT42402.1
gene	3565858	3568278	16018	18438	gene=IY08_18810	protein=ATPase P	protein_id=KGT42403.1
gene	3568374	3568580	18534	18740	gene=IY08_18815	protein=copper resistance protein CopZ	protein_id=KGT42404.1
gene	3568785	3569087	18945	19247	gene=IY08_18820	protein=transcriptional regulator	protein_id=KGT42405.1
gene	3569485	3570291	19645	20451	gene=IY08_18830	protein=methionine ABC transporter substrate-binding	protein_id=KGT42406.1
gene	3570844	3571071	21004	21231	gene=IY08_18835	protein=hypothetical protein	protein_id=KGT42407.1
gene	3571320	3572138	21480	22298	gene=IY08_18840	protein=IroE protein	protein_id=KGT42408.1
gene	3572154	3572975	22314	23135	gene=IY08_18845	protein=ABC transporter ATP-binding protein	protein_id=KGT42409.1
gene	3572990	3574012	23150	24172	gene=IY08_18850	protein=iron ABC transporter permease	protein_id=KGT42410.1
gene	3574005	3575012	24165	25172	gene=IY08_18855	protein=ferrichrome ABC transporter permease	protein_id=KGT42411.1
gene	3575040	3576005	25200	26165	gene=IY08_18860	protein=iron-uptake system-binding protein	protein_id=KGT42412.1
gene	3576307	3577065	26467	27225	gene=IY08_18865	protein=exodeoxyribonuclease III	protein_id=KGT42413.1
gene	3577220	3577816	27380	27976	gene=IY08_18870	protein=AraC family transcriptional regulator	protein_id=KGT42414.1
gene	3577797	3578327	27957	28487	gene=IY08_18875	protein=cysteine methyltransferase	protein_id=KGT42415.1
gene	3578324	3579235	28484	29395	gene=IY08_18880	protein=DNA-3-methyladenine glycosylase	protein_id=KGT42416.1
gene	3579274	3580506	29434	30666	gene=IY08_18885	protein=peptidase T	protein_id=KGT42417.1

gene	3580703	3581341	30863	31501	gene=IY08_18890	protein=membrane protein	protein_id=KGT42418.1
gene	3581434	3581751	31594	31911	gene=IY08_18895	protein=hypothetical protein	protein_id=KGT42419.1
gene	3582073	3582648	32233	32808	gene=IY08_18900	protein=phosphoglycerate mutase	protein_id=KGT42420.1
gene	3582789	3583604	32949	33764	gene=IY08_18905	protein=2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate	protein_id=KGT42421.1
gene	3584013	3586733	34173	36893	gene=IY08_18910	protein=diguanylate cyclase	protein_id=KGT42422.1
gene	3586829	3587893	36989	38053	gene=IY08_18915	protein=UDP-diphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	protein_id=KGT42423.1
gene	3587942	3588262	38102	38422	gene=IY08_18920	protein=hypothetical protein	protein_id=KGT42424.1
gene	3588289	3589200	38449	39360	gene=IY08_18925	protein=UDP-2-acetamido-2,6-dideoxy-hexulose 4-	protein_id=KGT42425.1
gene	3589197	3590183	39357	40343	gene=IY08_18930	protein=UDP-N-acetylglucosamine 4,6-dehydratase	protein_id=KGT42426.1
gene	3590485	3591663	40645	41823	gene=IY08_18935	protein=hypothetical protein	protein_id=KGT42427.1
gene	3591638	3592039	41798	42199	gene=IY08_18940	protein=hypothetical protein	protein_id=KGT42428.1
gene	3592062	3592487	42222	42647	gene=IY08_18945	protein=hypothetical protein	protein_id=KGT42429.1
gene	3592508	3593179	42668	43339	gene=IY08_18950	protein=hypothetical protein	protein_id=KGT42430.1
gene	3593203	3593559	43363	43719	gene=IY08_18955	protein=holin	protein_id=KGT42431.1
gene	3593593	3595026	43753	45186	gene=IY08_18960	protein=GntR family transcriptional regulator	protein_id=KGT42432.1
gene	3595213	3595404	45373	45564	gene=IY08_18965	protein=hypothetical protein	protein_id=KGT42433.1
gene	3595624	3596331	45784	46491	gene=IY08_18975	protein=GntR family transcriptional regulator	protein_id=KGT42434.1
gene	3596362	3597771	46522	47931	gene=IY08_18980	protein=aryl-phospho-beta-D-glucosidase	protein_id=KGT42435.1
gene	3597963	3598952	48123	49112	gene=IY08_18985	protein=1-phosphatidylinositol phosphodiesterase	protein_id=KGT42436.1
gene	3599132	3600973	49292	51133	gene=IY08_18990	protein=collagenase	protein_id=KGT42437.1
gene	3601265	3602062	51425	52222	gene=IY08_18995	protein=peptidoglycan-binding protein LysM	protein_id=KGT42438.1
gene	3602328	3603665	52488	53825	gene=IY08_19000	protein=NAD(FAD)-utilizing dehydrogenase	protein_id=KGT42439.1
gene	3604169	3606088	54329	56248	gene=IY08_19005	protein=hypothetical protein	protein_id=KGT42440.1
gene	3606135	3608918	56295	59078	gene=IY08_19010	protein=GTP-binding protein	protein_id=KGT42441.1
gene	3609423	3609608	59583	59768	gene=IY08_19015	protein=hypothetical protein	protein_id=KGT42442.1
gene	3609872	3611815	60032	61975	gene=IY08_19020	protein=DNA mismatch repair protein MutL	protein_id=KGT42443.1
gene	3611824	3614496	61984	64656	gene=IY08_19025	protein=DNA mismatch repair protein MutS	protein_id=KGT42444.1
gene	3614677	3615219	64837	65379	gene=IY08_19030	protein=spore coat protein	protein_id=KGT42445.1
gene	3615345	3615776	65505	65936	gene=IY08_19035	protein=master regulator for biofilm formation	protein_id=KGT42446.1
gene	3615780	3617309	65940	67469	gene=IY08_19040	protein=dimethylallyladenosine tRNA	protein_id=KGT42447.1

gene	3617739	3618605	67899	68765	gene=IY08_19045	protein=2-oxoacid ferredoxin oxidoreductase	protein_id=KGT42448.1
gene	3618592	3620349	68752	70509	gene=IY08_19050	protein=2-oxoglutarate ferredoxin oxidoreductase subunit	protein_id=KGT42449.1
gene	3620574	3621497	70734	71657	gene=IY08_19055	protein=diguanylate cyclase	protein_id=KGT42450.1
gene	3621556	3621816	71716	71976	gene=IY08_19060	protein=stage V sporulation protein S	protein_id=KGT42451.1
gene	3621966	3622760	72126	72920	gene=IY08_19065	protein=metallophosphoesterase	protein_id=KGT42452.1
gene	3622923	3624488	73083	74648	gene=IY08_19070	protein=ribonuclease	protein_id=KGT42453.1
gene	3624969	3625475	75129	75635	pseudo		
gene	3625660	3626283	75820	76443	gene=IY08_19080	protein=topoisomerase I	protein_id=KGT42454.1
gene	3627134	3628372	77294	78532	gene=IY08_19090	protein=damage-inducible protein CinA	protein_id=KGT42455.1
gene	3628393	3628971	78553	79131	gene=IY08_19095	protein=CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	protein_id=KGT42456.1
gene	3629036	3629947	79196	80107	gene=IY08_19100	protein=transcriptional regulator	protein_id=KGT42457.1
gene	3629969	3630754	80129	80914	gene=IY08_19105	protein=hypothetical protein	protein_id=KGT42458.1
gene	3630893	3631141	81053	81301	gene=IY08_19110	protein=hypothetical protein	protein_id=KGT42459.1
gene	3631217	3631930	81377	82090	gene=IY08_19115	protein=3-ketoacyl-ACP reductase	protein_id=KGT42460.1
gene	3632031	3633317	82191	83477	gene=IY08_19120	protein=zinc protease	protein_id=KGT42461.1
gene	3633318	3634592	83478	84752	gene=IY08_19125	protein=zinc protease	protein_id=KGT42462.1
gene	3634802	3635761	84962	85921	gene=IY08_19130	protein=sugar ABC transporter permease	protein_id=KGT42463.1
gene	3635762	3636820	85922	86980	gene=IY08_19135	protein=sugar ABC transporter permease	protein_id=KGT42464.1
gene	3636813	3638345	86973	88505	gene=IY08_19140	protein=heme ABC transporter ATP-binding protein	protein_id=KGT42465.1
gene	3638463	3639548	88623	89708	gene=IY08_19145	protein=CD4+ T-cell-stimulating antigen	protein_id=KGT42466.1
gene	3639641	3640366	89801	90526	gene=IY08_19150	protein=GntR family transcriptional regulator	protein_id=KGT42467.1
gene	3640904	3643285	91064	93445	gene=IY08_19155	protein=cell division protein FtsK	protein_id=KGT42468.1
gene	3643498	3643701	93658	93861	gene=IY08_19160	protein=ribonuclease	protein_id=KGT42469.1
gene	3643698	3644447	93858	94607	gene=IY08_19165	protein=translocation-enhancing protein TepA	protein_id=KGT42470.1
gene	3644549	3646219	94709	96379	gene=IY08_19170	protein=Zn-dependent hydrolase	protein_id=KGT42471.1
gene	3646724	3646928	96884	97088	pseudo		
gene	3646956	3647834	97116	97994	gene=IY08_19180	protein=dihydrodipicolinate synthase	protein_id=KGT42472.1
gene	3647846	3649078	98006	99238	gene=IY08_19185	protein=aspartate kinase	protein_id=KGT42473.1
gene	3649102	3650148	99262	100308	gene=IY08_19190	protein=aspartate-semialdehyde dehydrogenase	protein_id=KGT42474.1
gene	3650299	3650898	100459	101058	gene=spoVFB	protein=dipicolinate synthase subunit B	protein_id=KGT42475.1

gene	3650895	3651797	101055	101957	gene=IY08_19200	protein=dipicolinate synthase subunit A	protein_id=KGT42476.1
gene	3651968	3652219	102128	102379	gene=IY08_19205	protein=hypothetical protein	protein_id=KGT42477.1
gene	3652354	3653595	102514	103755	gene=IY08_19210	protein=zinc protease	protein_id=KGT42478.1
gene	3653682	3654581	103842	104741	gene=IY08_19215	protein=hypothetical protein	protein_id=KGT42479.1
gene	3654736	3656874	104896	107034	gene=IY08_19220	protein=polynucleotide phosphorylase	protein_id=KGT42480.1
gene	3657035	3657304	107195	107464	gene=IY08_19225	protein=30S ribosomal protein S15	protein_id=KGT42481.1
gene	3657405	3658376	107565	108536	gene=IY08_19230	protein=riboflavin biosynthesis protein RibF	protein_id=KGT42482.1
gene	3658420	3659343	108580	109503	gene=truB	protein=tRNA pseudouridine synthase B	protein_id=KGT42483.1
gene	3659430	3659786	109590	109946	gene=IY08_19240	protein=ribosome-binding factor A	protein_id=KGT42484.1
gene	3659802	3660083	109962	110243	gene=IY08_19245	protein=hypothetical protein	protein_id=KGT42485.1
gene	3660080	3662140	110240	112300	gene=IY08_19250	protein=translation initiation factor IF-2	protein_id=KGT42486.1
gene	3662145	3662456	112305	112616	gene=IY08_19255	protein=50S ribosomal protein L7	protein_id=KGT42487.1
gene	3662457	3662729	112617	112889	gene=IY08_19260	protein=RNA-binding protein	protein_id=KGT42488.1
gene	3662741	3663847	112901	114007	gene=nusA	protein=transcription elongation factor NusA	protein_id=KGT42489.1
gene	3663865	3664335	114025	114495	gene=IY08_19270	protein=ribosome maturation protein RimP	protein_id=KGT42490.1
gene	3664672	3668973	114832	119133	gene=polC	protein=DNA polymerase III PolC	protein_id=KGT42491.1
gene	3669098	3670798	119258	120958	gene=IY08_19280	protein=prolyl-tRNA synthetase	protein_id=KGT42492.1
gene	3670908	3672164	121068	122324	gene=IY08_19285	protein=zinc metalloprotease	protein_id=KGT42493.1
gene	3672182	3673324	122342	123484	gene=IY08_19290	protein=l-deoxy-D-xylulose 5-phosphate reductoisomerase	protein_id=KGT42494.1
gene	3673348	3674139	123508	124299	gene=IY08_19295	protein=phosphatidate cytidyltransferase	protein_id=KGT42495.1
gene	3674157	3674933	124317	125093	gene=IY08_19300	protein=UDP pyrophosphate synthase	protein_id=KGT42496.1
gene	3675019	3675576	125179	125736	gene=IY08_19305	protein=ribosome recycling factor	protein_id=KGT42497.1
gene	3675579	3676301	125739	126461	gene=pyrH	protein=uridylate kinase	protein_id=KGT42498.1
gene	3676368	3677255	126528	127415	gene=IY08_19315	protein=elongation factor Ts	protein_id=KGT42499.1
gene	3677359	3678060	127519	128220	gene=IY08_19320	protein=30S ribosomal protein S2	protein_id=KGT42500.1
gene	3678409	3679188	128569	129348	gene=IY08_19325	protein=transcriptional repressor CodY	protein_id=KGT42501.1
gene	3679266	3680657	129426	130817	gene=IY08_19330	protein=Clp protease ATPase	protein_id=KGT42502.1
gene	3680680	3681222	130840	131382	gene=IY08_19335	protein=ATP-dependent protease subunit HslV	protein_id=KGT42503.1
gene	3681265	3682164	131425	132324	gene=IY08_19340	protein=recombinase XerC	protein_id=KGT42504.1
gene	3682230	3683534	132390	133694	gene=gid	protein=tRNA (uracil-5-)-methyltransferase	protein_id=KGT42505.1
gene	3683588	3685666	133748	135826	gene=IY08_19350	protein=DNA topoisomerase I	protein_id=KGT42506.1

gene	3685811	3686680	135971	136840	gene=IY08_19355	protein=DNA-binding protein	protein_id=KGT42507.1
gene	3686769	3687671	136929	137831	gene=IY08_19360	protein=succinyl-CoA synthetase subunit alpha	protein_id=KGT42508.1
gene	3687691	3688851	137851	139011	gene=sucC	protein=succinyl-CoA synthetase subunit beta	protein_id=KGT42509.1
gene	3689046	3689819	139206	139979	gene=IY08_19370	protein=ribonuclease H	protein_id=KGT42510.1
gene	3689876	3690766	140036	140926	gene=IY08_19375	protein=GTPase	protein_id=KGT42511.1
gene	3690787	3691338	140947	141498	gene=IY08_19380	protein=signal peptidase I	protein_id=KGT42512.1
gene	3691440	3691784	141600	141944	gene=IY08_19385	protein=50S ribosomal protein L19	protein_id=KGT42513.1
gene	3691931	3692665	142091	142825	gene=IY08_19390	protein=tRNA (guanine-N1)-methyltransferase	protein_id=KGT42514.1
gene	3692665	3693180	142825	143340	gene=IY08_19395	protein=16S rRNA processing protein RimM	protein_id=KGT42515.1
gene	3693301	3693528	143461	143688	gene=IY08_19400	protein=RNA-binding protein	protein_id=KGT42516.1
gene	3693543	3693815	143703	143975	gene=rpsP	protein=30S ribosomal protein S16	protein_id=KGT42517.1
gene	3693917	3695266	144077	145426	gene=IY08_19410	protein=signal recognition particle	protein_id=KGT42518.1
gene	3695279	3695611	145439	145771	gene=IY08_19415	protein=hypothetical protein	protein_id=KGT42519.1
gene	3695745	3696734	145905	146894	gene=IY08_19420	protein=cell division protein FtsY	protein_id=KGT42520.1
gene	3696750	3700319	146910	150479	gene=IY08_19425	protein=chromosome segregation protein SMC	protein_id=KGT42521.1
gene	3700466	3701203	150626	151363	gene=IY08_19430	protein=ribonuclease III	protein_id=KGT42522.1
gene	3701262	3701495	151422	151655	gene=IY08_19435	protein=acyl carrier protein	protein_id=KGT42523.1
gene	3701565	3702305	151725	152465	gene=IY08_19440	protein=3-oxoacyl-ACP reductase	protein_id=KGT42524.1
gene	3702305	3703249	152465	153409	gene=IY08_19445	protein=malonyl CoA-ACP transacylase	protein_id=KGT42525.1
gene	3703264	3704256	153424	154416	gene=IY08_19450	protein=phosphate acyltransferase	protein_id=KGT42526.1
gene	3704253	3704846	154413	155006	gene=IY08_19455	protein=fatty acid biosynthesis transcriptional regulator	protein_id=KGT42527.1
gene	3704935	3706983	155095	157143	gene=IY08_19460	protein=ATP-dependent DNA helicase	protein_id=KGT42528.1
gene	3707274	3708950	157434	159110	gene=IY08_19465	protein=hypothetical protein	protein_id=KGT42529.1
gene	3708973	3709335	159133	159495	gene=IY08_19470	protein=hypothetical protein	protein_id=KGT42530.1
gene	3709712	3709900	159872	160060	gene=IY08_19475	protein=50S ribosomal protein L28	protein_id=KGT42531.1
gene	3709974	3710054	160134	160214	gene=IY08_19480	protein=stage V sporulation protein M	protein_id=KGT42532.1
gene	3710121	3710801	160281	160961	gene=IY08_19485	protein=thiamine pyrophosphokinase	protein_id=KGT42533.1
gene	3710871	3711515	161031	161675	gene=IY08_19490	protein=ribulose-phosphate 3-epimerase	protein_id=KGT42534.1
gene	3711518	3712399	161678	162559	gene=IY08_19495	protein=GTPase RsgA	protein_id=KGT42535.1
gene	3712705	3714678	162865	164838	gene=IY08_19500	protein=serine/threonine protein kinase	protein_id=KGT41388.1
gene	3714687	3715439	164847	165599	gene=IY08_19505	protein=protein phosphatase	protein_id=KGT41389.1

gene	3715444	3716532	165604	166692	gene=IY08_19510	protein=ribosomal RNA large subunit methyltransferase N	protein_id=KGT41390.1
gene	3716537	3717871	166697	168031	gene=IY08_19515	protein=16S rRNA methyltransferase	protein_id=KGT41391.1
gene	3717868	3718812	168028	168972	gene=IY08_19520	protein=methionyl-tRNA formyltransferase	protein_id=KGT41392.1
gene	3718836	3719306	168996	169466	gene=IY08_19525	protein=peptide deformylase	protein_id=KGT41393.1
gene	3719318	3721723	169478	171883	gene=IY08_19530	protein=primosomal protein N'	protein_id=KGT41394.1
gene	3721720	3722925	171880	173085	gene=IY08_19535	protein=phosphopantothenoylecysteine decarboxylase	protein_id=KGT41395.1
gene	3723098	3723310	173258	173470	gene=IY08_19540	protein=DNA-directed RNA polymerase subunit omega	protein_id=KGT41396.1
gene	3723313	3723930	173473	174090	gene=IY08_19545	protein=guanylate kinase	protein_id=KGT41397.1
gene	3723944	3724207	174104	174367	gene=IY08_19550	protein=hypothetical protein	protein_id=KGT41398.1
gene	3724275	3725150	174435	175310	gene=IY08_19555	protein=hypothetical protein	protein_id=KGT41399.1
gene	3725250	3727973	175410	178133	gene=IY08_19560	protein=ATPase	protein_id=KGT41400.1
gene	3728079	3729788	178239	179948	gene=IY08_19565	protein=hypothetical protein	protein_id=KGT41401.1
gene	3730133	3731203	180293	181363	gene=IY08_19570	protein=aminopeptidase	protein_id=KGT41402.1
gene	3731286	3731810	181446	181970	gene=IY08_19575	protein=integrase	protein_id=KGT41403.1
gene	3731993	3733378	182153	183538	gene=IY08_19580	protein=membrane protein	protein_id=KGT41404.1
gene	3733546	3733800	183706	183960	gene=IY08_19585	protein=membrane protein	protein_id=KGT41405.1
gene	3733817	3734494	183977	184654	gene=IY08_19590	protein=HAD family hydrolase	protein_id=KGT41406.1
gene	3734534	3735166	184694	185326	gene=IY08_19595	protein=orotate phosphoribosyltransferase	protein_id=KGT41407.1
gene	3735163	3735879	185323	186039	gene=IY08_19600	protein=orotidine 5'-phosphate decarboxylase	protein_id=KGT41408.1
gene	3735864	3736793	186024	186953	gene=IY08_19605	protein=dihydroorotate dehydrogenase	protein_id=KGT41409.1
gene	3736790	3737569	186950	187729	gene=IY08_19610	protein=dihydroorotate dehydrogenase	protein_id=KGT41410.1
gene	3737566	3740784	187726	190944	gene=IY08_19615	protein=carbamoyl phosphate synthase large subunit	protein_id=KGT41411.1
gene	3740769	3741866	190929	192026	gene=IY08_19620	protein=carbamoyl phosphate synthase small subunit	protein_id=KGT41412.1
gene	3741863	3743149	192023	193309	gene=IY08_19625	protein=dihydroorotase	protein_id=KGT41413.1
gene	3743133	3744047	193293	194207	gene=IY08_19630	protein=aspartate carbamoyltransferase catalytic subunit	protein_id=KGT41414.1
gene	3744196	3745479	194356	195639	gene=IY08_19635	protein=uracil permease	protein_id=KGT41415.1
gene	3745626	3746168	195786	196328	gene=IY08_19640	protein=bifunctional pyrimidine regulatory protein PyrR uracil phosphoribosyltransferase	protein_id=KGT41416.1
gene	3746372	3747280	196532	197440	gene=IY08_19645	protein=pseudouridine synthase	protein_id=KGT41417.1
gene	3747285	3747743	197445	197903	gene=IY08_19650	protein=peptidase A8	protein_id=KGT41418.1
gene	3747868	3748197	198028	198357	gene=IY08_19655	protein=molecular chaperone DnaK	protein_id=KGT41419.1

gene	3748355	3751120	198515	201280	gene=ileS	protein=isoleucine--tRNA ligase	protein_id=KGT41420.1
gene	3751467	3751973	201627	202133	gene=IY08_19665	protein=septum formation initiator	protein_id=KGT41421.1
gene	3752063	3752830	202223	202990	gene=IY08_19670	protein=RNA-binding protein S4	protein_id=KGT41422.1
gene	3752846	3753109	203006	203269	gene=IY08_19675	protein=membrane protein	protein_id=KGT41423.1
gene	3753116	3753586	203276	203746	gene=IY08_19680	protein=cell division protein SepF	protein_id=KGT41424.1
gene	3753606	3754280	203766	204440	gene=IY08_19685	protein=hypothetical protein	protein_id=KGT41425.1
gene	3754277	3755095	204437	205255	gene=IY08_19690	protein=laccase	protein_id=KGT41426.1
gene	3755216	3755497	205376	205657	gene=IY08_19695	protein=hypothetical protein	protein_id=KGT41427.1
gene	3755661	3756440	205821	206600	gene=IY08_19700	protein=sporulation sigma factor SigG	protein_id=KGT41428.1
gene	3756598	3757317	206758	207477	gene=IY08_19705	protein=sporulation sigma factor SigE	protein_id=KGT41429.1
gene	3757337	3758254	207497	208414	gene=IY08_19710	protein=peptidase	protein_id=KGT41430.1
gene	3758506	3759660	208666	209820	gene=IY08_19715	protein=cell division protein FtsZ	protein_id=KGT41431.1
gene	3759700	3761007	209860	211167	gene=IY08_19720	protein=cell division protein FtsA	protein_id=KGT41432.1
gene	3761407	3762177	211567	212337	gene=IY08_19730	protein=cell division protein FtsQ	protein_id=KGT41433.1
gene	3762276	3763181	212436	213341	gene=IY08_19735	protein=UDP-N-acetylenolpyruvoylglucosamine reductase	protein_id=KGT41434.1
gene	3763394	3764488	213554	214648	gene=IY08_19740	protein=UDP-diphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	protein_id=KGT41435.1
gene	3764592	3765683	214752	215843	gene=IY08_19745	protein=stage V sporulation protein E	protein_id=KGT41436.1
gene	3765774	3767126	215934	217286	gene=murD	protein=UDP-N-acetylmuramoyl-L-alanyl-D-glutamate synthetase	protein_id=KGT41437.1
gene	3767127	3768101	217287	218261	gene=IY08_19755	protein=phospho-N-acetylmuramoyl-pentapeptide-	protein_id=KGT41438.1
gene	3768124	3769599	218284	219759	gene=IY08_19760	protein=UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	protein_id=KGT41439.1
gene	3769784	3771700	219944	221860	gene=IY08_19765	protein=stage V sporulation protein D	protein_id=KGT41440.1
gene	3771782	3773881	221942	224041	gene=IY08_19770	protein=dihydropteridine reductase	protein_id=KGT41441.1
gene	3773954	3774316	224114	224476	gene=IY08_19775	protein=cell division protein FtsL	protein_id=KGT41442.1
gene	3774332	3775264	224492	225424	gene=IY08_19780	protein=16S rRNA methyltransferase	protein_id=KGT41443.1
gene	3775633	3777249	225793	227409	gene=IY08_19785	protein=hypothetical protein	protein_id=KGT41444.1
gene	3777329	3778213	227489	228373	gene=IY08_19790	protein=2-dehydropantoate 2-reductase	protein_id=KGT41445.1
gene	3778508	3778981	228668	229141	gene=IY08_19795	protein=hypothetical protein	protein_id=KGT41446.1
gene	3779015	3779521	229175	229681	gene=IY08_19800	protein=DNA-binding protein	protein_id=KGT41447.1

gene	3779651	3779824	229811	229984	gene=rpmF	protein=50S ribosomal protein L32	protein_id=KGT41448.1
gene	3779886	3780386	230046	230546	gene=IY08_19810	protein=hypothetical protein	protein_id=KGT41449.1
gene	3780600	3781781	230760	231941	gene=IY08_19815	protein=hypothetical protein	protein_id=KGT41450.1
gene	3781791	3782828	231951	232988	gene=IY08_19820	protein=hypothetical protein	protein_id=KGT41451.1
gene	3782821	3783612	232981	233772	gene=IY08_19825	protein=esterase	protein_id=KGT41452.1
gene	3783726	3784955	233886	235115	gene=IY08_19830	protein=sporulation protein	protein_id=KGT41453.1
gene	3784947	3785438	235107	235598	gene=IY08_19835	protein=phosphopantetheine adenylyltransferase	protein_id=KGT41454.1
gene	3785435	3786001	235595	236161	gene=IY08_19840	protein=DNA methyltransferase	protein_id=KGT41455.1
gene	3786500	3786889	236660	237049	gene=IY08_19845	protein=methylthioribose kinase	protein_id=KGT41456.1
gene	3786944	3787210	237104	237370	gene=IY08_19850	protein=hypothetical protein	protein_id=KGT41457.1
gene	3787337	3787789	237497	237949	gene=IY08_19855	protein=regulator	protein_id=KGT41458.1
gene	3787904	3788476	238064	238636	gene=IY08_19860	protein=phosphoglycerate mutase	protein_id=KGT41459.1
gene	3788553	3788798	238713	238958	gene=IY08_19865	protein=hypothetical protein	protein_id=KGT41460.1
gene	3788810	3789247	238970	239407	gene=IY08_19870	protein=cytoplasmic protein	protein_id=KGT41461.1
gene	3789434	3790468	239594	240628	gene=IY08_19875	protein=membrane protein	protein_id=KGT41462.1
gene	3790673	3791038	240833	241198	gene=IY08_19880	protein=hypothetical protein	protein_id=KGT41463.1
gene	3791085	3792083	241245	242243	gene=amiF	protein=formamidase	protein_id=KGT41464.1
gene	3792316	3793221	242476	243381	gene=IY08_19890	protein=cytochrome C oxidase assembly protein	protein_id=KGT41465.1
gene	3793302	3793634	243462	243794	gene=IY08_19895	protein=cytochrome B6	protein_id=KGT41466.1
gene	3793638	3794261	243798	244421	gene=IY08_19900	protein=cytochrome B oxidoreductase	protein_id=KGT41467.1
gene	3794261	3796123	244421	246283	gene=IY08_19905	protein=quinol oxidase subunit 1	protein_id=KGT41468.1
gene	3796157	3797206	246317	247366	gene=IY08_19910	protein=cytochrome B	protein_id=KGT41469.1
gene	3797300	3798223	247460	248383	gene=IY08_19915	protein=protoheme IX farnesyltransferase	protein_id=KGT41470.1
gene	3798721	3799656	248881	249816	gene=IY08_19920	protein=heme A synthase	protein_id=KGT41471.1
gene	3799740	3803186	249900	253346	gene=IY08_19925	protein=pyruvate carboxylase	protein_id=KGT41472.1
gene	3803519	3804697	253679	254857	gene=IY08_19930	protein=cell division protein FtsW	protein_id=KGT41473.1
gene	3804823	3805110	254983	255270	gene=IY08_19935	protein=hypothetical protein	protein_id=KGT41474.1
gene	3805266	3805763	255426	255923	gene=IY08_19940	protein=hypothetical protein	protein_id=KGT41475.1
gene	3805795	3807123	255955	257283	gene=IY08_19945	protein=hypothetical protein	protein_id=KGT41476.1
gene	3807370	3807825	257530	257985	gene=IY08_19950	protein=hypothetical protein	protein_id=KGT41477.1
gene	3807971	3808171	258131	258331	gene=IY08_19955	protein=hypothetical protein	protein_id=KGT41478.1

gene	3808207	3808482	258367	258642	gene=IY08_19960	protein=hypothetical protein	protein_id=KGT41479.1
gene	3808498	3808800	258658	258960	gene=IY08_19965	protein=membrane protein	protein_id=KGT41480.1
gene	3808958	3810802	259118	260962	gene=IY08_19970	protein=GTP-binding protein TypA	protein_id=KGT41481.1
gene	3810943	3811122	261103	261282	gene=IY08_19975	protein=methyltransferase	protein_id=KGT41482.1
gene	3811172	3811957	261332	262117	gene=IY08_19980	protein=inositol monophosphatase	protein_id=KGT41483.1
gene	3812046	3812234	262206	262394	gene=IY08_19985	protein=hypothetical protein	protein_id=KGT41484.1
gene	3812441	3813067	262601	263227	gene=IY08_19990	protein=hypothetical protein	protein_id=KGT41485.1
gene	3813149	3813418	263309	263578	gene=IY08_19995	protein=hypothetical protein	protein_id=KGT41486.1
gene	3813784	3815256	263944	265416	gene=IY08_20000	protein=arginine decarboxylase	protein_id=KGT41487.1
gene	3815332	3816162	265492	266322	gene=tgl	protein=transglutaminase	protein_id=KGT41488.1
gene	3816199	3816327	266359	266487	gene=IY08_20010	protein=phosphoesterase	protein_id=KGT41489.1
gene	3816372	3816500	266532	266660	gene=IY08_20015	protein=phosphoesterase	protein_id=KGT41490.1
gene	3816560	3816688	266720	266848	gene=IY08_20020	protein=phosphoesterase	protein_id=KGT41491.1
gene	3816883	3817179	267043	267339	gene=IY08_20025	protein=hypothetical protein	protein_id=KGT41492.1
gene	3817310	3817702	267470	267862	gene=IY08_20030	protein=protein TPR repeat	protein_id=KGT41493.1
gene	3817704	3817931	267864	268091	gene=IY08_20035	protein=hypothetical protein	protein_id=KGT41494.1
gene	3818166	3819578	268326	269738	gene=IY08_20040	protein=dihydrolipoamide dehydrogenase	protein_id=KGT41495.1
gene	3819584	3820873	269744	271033	gene=IY08_20045	protein=branched-chain alpha-keto acid dehydrogenase subunit E2	protein_id=KGT41496.1
gene	3820967	3821944	271127	272104	gene=IY08_20050	protein=2-oxoisovalerate dehydrogenase	protein_id=KGT41497.1
gene	3821948	3823063	272108	273223	gene=IY08_20055	protein=pyruvate dehydrogenase	protein_id=KGT41498.1
gene	3823578	3823724	273738	273884	gene=IY08_20060	protein=ABC transporter substrate-binding protein	protein_id=KGT41499.1
gene	3823893	3824447	274053	274607	gene=def	protein=peptide deformylase	protein_id=KGT41500.1
gene	3824508	3825281	274668	275441	gene=IY08_20070	protein=phosphatase	protein_id=KGT41501.1
gene	3825829	3826041	275989	276201	gene=IY08_20075	protein=hypothetical protein	protein_id=KGT41502.1
gene	3826046	3827713	276206	277873	gene=IY08_20080	protein=ribonuclease J	protein_id=KGT41503.1
gene	3827752	3828417	277912	278577	gene=IY08_20085	protein=potassium transporter Trk	protein_id=KGT41504.1
gene	3828500	3829366	278660	279526	gene=IY08_20090	protein=cytochrome C oxidase assembly protein	protein_id=KGT41505.1
gene	3829613	3830743	279773	280903	gene=IY08_20095	protein=N-acetyldiaminopimelate deacetylase	protein_id=KGT41506.1
gene	3830807	3831529	280967	281689	gene=IY08_20100	protein=2,3,4,5-tetrahydropyridine-2,6-carboxylate N-succinyltransferase	protein_id=KGT41507.1

gene	3831601	3832458	281761	282618	gene=IY08_20105	protein=LysR family transcriptional regulator	protein_id=KGT41508.1
gene	3832665	3833108	282825	283268	gene=IY08_20110	protein=CBS domain-containing protein YkuL	protein_id=KGT41509.1
gene	3833277	3833468	283437	283628	gene=IY08_20115	protein=recombinase XerD	protein_id=KGT41510.1
gene	3833589	3834107	283749	284267	gene=IY08_20120	protein=hypothetical protein	protein_id=KGT41511.1
gene	3834182	3834331	284342	284491	gene=IY08_20125	protein=hypothetical protein	protein_id=KGT41512.1
gene	3834573	3834809	284733	284969	gene=IY08_20130	protein=hypothetical protein	protein_id=KGT41513.1
gene	3835043	3835279	285203	285439	gene=IY08_20135	protein=glutaredoxin	protein_id=KGT41514.1
gene	3835408	3835896	285568	286056	gene=IY08_20140	protein=hypothetical protein	protein_id=KGT41515.1
gene	3836079	3837296	286239	287456	gene=IY08_20145	protein=diguanylate phosphodiesterase	protein_id=KGT41516.1
gene	3837552	3838316	287712	288476	gene=IY08_20150	protein=short-chain dehydrogenase	protein_id=KGT41517.1
gene	3838547	3839404	288707	289564	gene=IY08_20155	protein=metallophosphoesterase	protein_id=KGT41518.1
gene	3839502	3839738	289662	289898	gene=IY08_20160	protein=hypothetical protein	protein_id=KGT41519.1
gene	3839899	3842007	290059	292167	gene=IY08_20165	protein=polyphosphate kinase	protein_id=KGT41520.1
gene	3842116	3843654	292276	293814	gene=IY08_20170	protein=exopolyphosphatase	protein_id=KGT41521.1
gene	3843832	3844290	293992	294450	gene=IY08_20175	protein=cytoplasmic protein	protein_id=KGT41522.1
gene	3844322	3844984	294482	295144	gene=IY08_20180	protein=lipoprotein	protein_id=KGT41523.1
gene	3845599	3846252	295759	296412	gene=IY08_20185	protein=diguanylate cyclase	protein_id=KGT41524.1
gene	3846416	3846649	296576	296809	gene=IY08_20190	protein=hypothetical protein	protein_id=KGT41525.1
gene	3846681	3847181	296841	297341	gene=IY08_20195	protein=hypothetical protein	protein_id=KGT41526.1
gene	3847594	3849135	297754	299295	gene=IY08_20200	protein=major facilitator transporter	protein_id=KGT41527.1
gene	3849374	3849931	299534	300091	gene=IY08_20205	protein=PadR family transcriptional regulator	protein_id=KGT41528.1
gene	3850443	3852731	300603	302891	gene=IY08_20215	protein=5-methyltetrahydropteroyltryglutamate-- homocysteine methyltransferase	protein_id=KGT41529.1
gene	3852770	3853159	302930	303319	gene=IY08_20220	protein=competence protein	protein_id=KGT41530.1
gene	3853196	3853630	303356	303790	gene=IY08_20225	protein=DNA-entry nuclease	protein_id=KGT41531.1
gene	3853857	3854606	304017	304766	gene=IY08_20230	protein=cytoplasmic protein	protein_id=KGT41532.1
gene	3854645	3855919	304805	306079	gene=IY08_20235	protein=sporulation kinase	protein_id=KGT41533.1
gene	3856230	3856430	306390	306590	gene=IY08_20240	protein=hypothetical protein	protein_id=KGT41534.1
gene	3856553	3857716	306713	307876	gene=IY08_20245	protein=aromatic amino acid aminotransferase	protein_id=KGT41535.1
gene	3857730	3858752	307890	308912	gene=IY08_20250	protein=LacI family transcriptional regulator	protein_id=KGT41536.1
gene	3859022	3859864	309182	310024	gene=IY08_20255	protein=arabinogalactan ABC transporter permease	protein_id=KGT41537.1

gene	3859865	3861166	310025	311326	gene=IY08_20260	protein=arabinogalactan ABC transporter permease	protein_id=KGT41538.1
gene	3861243	3862502	311403	312662	gene=IY08_20265	protein=cyclodextrin-binding protein	protein_id=KGT41539.1
gene	3862826	3864586	312986	314746	gene=IY08_20270	protein=cyclomaltodextrinase	protein_id=KGT41540.1
gene	3864633	3866309	314793	316469	gene=IY08_20275	protein=oligo-1,6-glucosidase	protein_id=KGT41541.1
gene	3866572	3867672	316732	317832	gene=IY08_20280	protein=sugar ABC transporter ATP-binding protein	protein_id=KGT41542.1
gene	3867738	3868247	317898	318407	gene=IY08_20285	protein=hypothetical protein	protein_id=KGT41543.1
gene	3868319	3868408	318479	318568	gene=IY08_20290	protein=flagellar motor protein	protein_id=KGT41544.1
gene	3868620	3869075	318780	319235	gene=IY08_20295	protein=hypothetical protein	protein_id=KGT41545.1
gene	3869207	3869638	319367	319798	gene=IY08_20300	protein=lipoprotein	protein_id=KGT41546.1
gene	3869668	3870429	319828	320589	gene=IY08_20305	protein=lipoprotein	protein_id=KGT41547.1
gene	3870467	3871195	320627	321355	gene=IY08_20310	protein=membrane protein	protein_id=KGT41548.1
gene	3871412	3872137	321572	322297	gene=IY08_20315	protein=ATPase AAA	protein_id=KGT41549.1
gene	3872167	3873342	322327	323502	gene=IY08_20320	protein=acetyl-CoA acetyltransferase	protein_id=KGT41550.1
gene	3873482	3873931	323642	324091	gene=IY08_20325	protein=DNA mismatch repair protein MutT	protein_id=KGT41551.1
gene	3874039	3874332	324199	324492	gene=IY08_20330	protein=hypothetical protein	protein_id=KGT41552.1
gene	3874508	3875125	324668	325285	gene=IY08_20335	protein=hypothetical protein	protein_id=KGT41553.1
gene	3875141	3875278	325301	325438	gene=IY08_20340	protein=DNA-binding protein	protein_id=KGT42382.1
gene	3875297	3876058	325457	326218	gene=IY08_20345	protein=hypothetical protein	protein_id=KGT41554.1
gene	3876072	3876839	326232	326999	gene=IY08_20350	protein=NADH dehydrogenase	protein_id=KGT41555.1
gene	3876839	3877171	326999	327331	gene=IY08_20355	protein=PadR family transcriptional regulator	protein_id=KGT41556.1
gene	3877368	3878144	327528	328304	gene=IY08_20360	protein=3-hydroxybutyrate dehydrogenase	protein_id=KGT41557.1
gene	3878174	3878335	328334	328495	gene=IY08_20365	protein=ribonuclease Z	protein_id=KGT41558.1
gene	3878403	3879464	328563	329624	gene=mtnA	protein=methylthioribose-1-phosphate isomerase	protein_id=KGT41559.1
gene	3879461	3880642	329621	330802	gene=mtnK	protein=methylthioribose kinase	protein_id=KGT41560.1
gene	3880946	3881725	331106	331885	gene=IY08_20380	protein=hydrolase	protein_id=KGT41561.1
gene	3881824	3883002	331984	333162	gene=IY08_20385	protein=aminotransferase	protein_id=KGT41562.1
gene	3883237	3884481	333397	334641	gene=mtnW	protein=2,3-diketo-5-methylthiopentyl-1-phosphate enolase	protein_id=KGT41563.1
gene	3884478	3885137	334638	335297	gene=mtnX	protein=2-hydroxy-3-keto-5-methylthiopentenyl-1-phosphate phosphatase	protein_id=KGT41564.1
gene	3885134	3885772	335294	335932	gene=mtnB	protein=methylthioribulose-1-phosphate dehydratase	protein_id=KGT41565.1
gene	3885750	3886262	335910	336422	gene=IY08_20405	protein=acireductone dioxygenase	protein_id=KGT41566.1

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gene	3886866	3887198	337026	337358	gene=IY08_20415	protein=hypothetical protein	protein_id=KGT41568.1
gene	3887204	3888082	337364	338242	gene=IY08_20420	protein=oxidoreductase	protein_id=KGT41569.1
gene	3888087	3889223	338247	339383	gene=IY08_20425	protein=penicillin-binding protein	protein_id=KGT41570.1
gene	3889315	3890607	339475	340767	gene=IY08_20430	protein=diguanylate cyclase	protein_id=KGT41571.1
gene	3890935	3891552	341095	341712	gene=IY08_20435	protein=NAD(P)H nitroreductase	protein_id=KGT41572.1
gene	3891787	3892005	341947	342165	gene=IY08_20440	protein=hypothetical protein	protein_id=KGT41573.1
gene	3892202	3892570	342362	342730	gene=IY08_20445	protein=hypothetical protein	protein_id=KGT41574.1
gene	3892668	3894380	342828	344540	gene=IY08_20450	protein=phosphoenolpyruvate-protein phosphotransferase	protein_id=KGT41575.1
gene	3894380	3894643	344540	344803	gene=IY08_20455	protein=phosphocarrier protein HPr	protein_id=KGT41576.1
gene	3894779	3896842	344939	347002	gene=IY08_20460	protein=PTS system glucose-specific transporter subunit	protein_id=KGT41577.1
gene	3897182	3898030	347342	348190	gene=IY08_20465	protein=PtsGHI operon antiterminator	protein_id=KGT41578.1
gene	3898196	3899002	348356	349162	gene=IY08_20470	protein=HAD family hydrolase	protein_id=KGT41579.1
gene	3899076	3899753	349236	349913	gene=IY08_20475	protein=GntR family transcriptional regulator	protein_id=KGT41580.1
gene	3899737	3900525	349897	350685	gene=IY08_20480	protein=glucosamine-6-phosphate deaminase	protein_id=KGT41581.1
gene	3900530	3901672	350690	351832	gene=IY08_20485	protein=N-acetylglucosamine-6-phosphate deacetylase	protein_id=KGT41582.1
gene	3901884	3902786	352044	352946	gene=IY08_20490	protein=competence protein ComE	protein_id=KGT41583.1
gene	3902865	3903437	353025	353597	gene=IY08_20495	protein=segregation and condensation protein B	protein_id=KGT41584.1
gene	3903356	3903544	353516	353704	pseudo		
gene	3903596	3904339	353756	354499	gene=IY08_20505	protein=segregation and condensation protein A	protein_id=KGT41585.1
gene	3904509	3904604	354669	354764	gene=IY08_20510	protein=hypothetical protein	protein_id=KGT41586.1
gene	3904704	3905222	354864	355382	gene=IY08_20515	protein=hypothetical protein	protein_id=KGT41587.1
gene	3905243	3905611	355403	355771	gene=IY08_20520	protein=protein RibT	protein_id=KGT41588.1
gene	3906071	3906508	356231	356668	gene=IY08_20530	protein=peptidylprolyl isomerase	protein_id=KGT41589.1
gene	3906696	3907562	356856	357722	gene=IY08_20535	protein=hypothetical protein	protein_id=KGT41590.1
gene	3907594	3908397	357754	358557	gene=IY08_20540	protein=HAD family hydrolase	protein_id=KGT41591.1
gene	3908495	3909967	358655	360127	gene=IY08_20545	protein=stage V sporulation protein AF	protein_id=KGT41592.1
gene	3909954	3910523	360114	360683	gene=IY08_20550	protein=stage V sporulation protein AE	protein_id=KGT41593.1
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gene	3910883	3911899	361043	362059	gene=IY08_20560	protein=stage V sporulation protein AD	protein_id=KGT41595.1
gene	3911913	3912371	362073	362531	gene=IY08_20565	protein=stage V sporulation protein AC	protein_id=KGT41596.1

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gene	3913629	3915155	363789	365315	gene=IY08_20585	protein=transporter	protein_id=KGT41600.1
gene	3915291	3916049	365451	366209	gene=IY08_20590	protein=sporulation sigma factor SigF	protein_id=KGT41601.1
gene	3916062	3916502	366222	366662	gene=IY08_20595	protein=anti-sigma F factor	protein_id=KGT41602.1
gene	3916503	3916853	366663	367013	gene=IY08_20600	protein=anti-sigma F factor antagonist	protein_id=KGT41603.1
gene	3917023	3918213	367183	368373	gene=IY08_20605	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT41604.1
gene	3918380	3918799	368540	368959	gene=IY08_20610	protein=GntR family transcriptional regulator	protein_id=KGT41605.1
gene	3918765	3919646	368925	369806	gene=IY08_20615	protein=ABC transporter ATP-binding protein	protein_id=KGT41606.1
gene	3919636	3920724	369796	370884	gene=IY08_20620	protein=acetoin ABC transporter permease	protein_id=KGT41607.1
gene	3920920	3921465	371080	371625	gene=IY08_20625	protein=hypothetical protein	protein_id=KGT41608.1
gene	3921565	3921984	371725	372144	gene=IY08_20630	protein=MarR family transcriptional regulator	protein_id=KGT41609.1
gene	3922144	3922815	372304	372975	gene=IY08_20635	protein=membrane protein	protein_id=KGT41610.1
gene	3922950	3924239	373110	374399	gene=IY08_20640	protein=permease	protein_id=KGT41611.1
gene	3924270	3925232	374430	375392	gene=IY08_20645	protein=metal transporter	protein_id=KGT41612.1
gene	3925292	3926596	375452	376756	gene=deoA	protein=thymidine phosphorylase	protein_id=KGT41613.1
gene	3926604	3927425	376764	377585	gene=IY08_20655	protein=purine nucleoside phosphorylase	protein_id=KGT41614.1
gene	3927438	3928622	377598	378782	gene=IY08_20660	protein=phosphopentomutase	protein_id=KGT41615.1
gene	3928977	3929717	379137	379877	gene=IY08_20665	protein=hypothetical protein	protein_id=KGT41616.1
gene	3929865	3930755	380025	380915	gene=IY08_20670	protein=recombinase XerD	protein_id=KGT41617.1
gene	3930762	3930992	380922	381152	gene=IY08_20675	protein=membrane protein	protein_id=KGT41618.1
gene	3931096	3931551	381256	381711	gene=IY08_20680	protein=Fur family transcriptional regulator	protein_id=KGT41619.1
gene	3931659	3932306	381819	382466	gene=IY08_20685	protein=stage II sporulation protein M	protein_id=KGT41620.1
gene	3932432	3932983	382592	383143	gene=IY08_20690	protein=acetyltransferase	protein_id=KGT41621.1
gene	3933008	3933547	383168	383707	gene=IY08_20695	protein=ADP-ribose pyrophosphatase	protein_id=KGT41622.1
gene	3933622	3933756	383782	383916	gene=IY08_20700	protein=PadR family transcriptional regulator	protein_id=KGT41623.1
gene	3933849	3934763	384009	384923	gene=IY08_20705	protein=oxidoreductase	protein_id=KGT41624.1
gene	3934821	3935648	384981	385808	gene=IY08_20710	protein=glyoxal reductase	protein_id=KGT41625.1
gene	3935784	3936308	385944	386468	gene=IY08_20715	protein=glutamate-rich protein GrpB	protein_id=KGT41626.1
gene	3936375	3936638	386535	386798	gene=IY08_20720	protein=sulfurtransferase	protein_id=KGT41627.1

gene	3936840	3938429	387000	388589	gene=IY08_20725	protein=5'-nucleotidase	protein_id=KGT41628.1
gene	3938555	3939031	388715	389191	gene=IY08_20730	protein=CopG family transcriptional regulator	protein_id=KGT41629.1
gene	3939153	3940151	389313	390311	gene=IY08_20735	protein=alpha/beta hydrolase	protein_id=KGT41630.1
gene	3940283	3941602	390443	391762	gene=IY08_20740	protein=sodium:proton antiporter	protein_id=KGT41631.1
gene	3941627	3942490	391787	392650	gene=IY08_20745	protein=LacI family transcriptional regulator	protein_id=KGT41632.1
gene	3942590	3943072	392750	393232	gene=IY08_20750	protein=acetyltransferase	protein_id=KGT41633.1
gene	3943154	3944080	393314	394240	gene=IY08_20755	protein=alpha/beta hydrolase	protein_id=KGT41634.1
gene	3944090	3944335	394250	394495	gene=IY08_20760	protein=hypothetical protein	protein_id=KGT41635.1
gene	3944624	3944830	394784	394990	gene=IY08_20765	protein=zinc finger domain-containing protein	protein_id=KGT41636.1
gene	3945470	3946582	395630	396742	gene=IY08_20770	protein=5-amino-6-(5-phosphoribosylamino)uracil	protein_id=KGT41637.1
gene	3946564	3947208	396724	397368	gene=IY08_20775	protein=riboflavin synthase subunit alpha	protein_id=KGT41638.1
gene	3947221	3948414	397381	398574	gene=IY08_20780	protein=3,4-dihydroxy-2-butanone 4-phosphate synthase	protein_id=KGT41639.1
gene	3948433	3948894	398593	399054	gene=ribH	protein=6,7-dimethyl-8-ribityllumazine synthase	protein_id=KGT41640.1
gene	3948918	3949238	399078	399398	gene=IY08_20790	protein=hypothetical protein	protein_id=KGT41641.1
gene	3949421	3950419	399581	400579	gene=IY08_20795	protein=biotin synthase	protein_id=KGT41642.1
gene	3950421	3951230	400581	401390	gene=IY08_20800	protein=malonyl-CoA O-methyltransferase	protein_id=KGT41643.1
gene	3951196	3951936	401356	402096	gene=IY08_20805	protein=transporter	protein_id=KGT41644.1
gene	3951933	3953120	402093	403280	gene=IY08_20810	protein=8-amino-7-oxononanoate synthase	protein_id=KGT41645.1
gene	3953086	3953814	403246	403974	gene=IY08_20815	protein=dethiobiotin synthetase	protein_id=KGT41646.1
gene	3953814	3955202	403974	405362	gene=IY08_20820	protein=adenosylmethionine-8-amino-7-oxononanoate aminotransferase	protein_id=KGT41647.1
gene	3955325	3955681	405485	405841	gene=IY08_20825	protein=hypothetical protein	protein_id=KGT41648.1
gene	3956324	3957697	406484	407857	gene=IY08_20830	protein=sodium:proton antiporter	protein_id=KGT41649.1
gene	3957746	3960067	407906	410227	gene=cpdB	protein=2', 3'-cyclic nucleotide 2'-phosphodiesterase	protein_id=KGT41650.1
gene	3960433	3961212	410593	411372	gene=IY08_20840	protein=lipase	protein_id=KGT41651.1
gene	3961285	3961731	411445	411891	gene=IY08_20845	protein=MarR family transcriptional regulator	protein_id=KGT41652.1
gene	3961756	3961971	411916	412131	gene=IY08_20850	protein=hypothetical protein	protein_id=KGT41653.1
gene	3962029	3962589	412189	412749	gene=IY08_20855	protein=group-specific protein	protein_id=KGT41654.1
gene	3962728	3963678	412888	413838	gene=IY08_20860	protein=ornithine carbamoyltransferase	protein_id=KGT41655.1
gene	3963691	3964851	413851	415011	gene=IY08_20865	protein=acetylornithine aminotransferase	protein_id=KGT41656.1
gene	3964848	3965615	415008	415775	gene=IY08_20870	protein=acetylglutamate kinase	protein_id=KGT41657.1

gene	3965627	3966850	415787	417010	gene=IY08_20875	protein=N-acetylglutamate synthase	protein_id=KGT41658.1
gene	3966861	3967898	417021	418058	gene=IY08_20880	protein=N-acetyl-gamma-glutamyl-phosphate reductase	protein_id=KGT41659.1
gene	3968123	3968311	418283	418471	gene=IY08_20885	protein=hypothetical protein	protein_id=KGT41660.1
gene	3968340	3969134	418500	419294	gene=IY08_20890	protein=oxidoreductase	protein_id=KGT41661.1
gene	3969144	3970097	419304	420257	gene=IY08_20895	protein=hydrolase	protein_id=KGT41662.1
gene	3970263	3971102	420423	421262	gene=IY08_20900	protein=pyrroline-5-carboxylate reductase	protein_id=KGT41663.1
gene	3971149	3972027	421309	422187	gene=IY08_20905	protein=serine dehydratase	protein_id=KGT41664.1
gene	3972046	3972705	422206	422865	gene=IY08_20910	protein=serine dehydratase	protein_id=KGT41665.1
gene	3972745	3973083	422905	423243	gene=IY08_20915	protein=hypothetical protein	protein_id=KGT41666.1
gene	3973586	3974509	423746	424669	gene=IY08_20920	protein=ribonuclease Z	protein_id=KGT41667.1
gene	3974699	3974950	424859	425110	gene=IY08_20925	protein=hypothetical protein	protein_id=KGT41668.1
gene	3974986	3975525	425146	425685	gene=IY08_20930	protein=hypothetical protein	protein_id=KGT41669.1
gene	3976192	3978897	426352	429057	gene=IY08_20935	protein=magnesium ABC transporter ATPase	protein_id=KGT41670.1
gene	3979146	3980384	429306	430544	gene=polYA	protein=DNA polymerase IV	protein_id=KGT41671.1
gene	3980636	3980824	430796	430984	pseudo		
gene	3980869	3981987	431029	432147	gene=IY08_20955	protein=hypothetical protein	protein_id=KGT41672.1
gene	3982115	3982660	432275	432820	gene=IY08_20960	protein=alanine acetyltransferase	protein_id=KGT41673.1
gene	3982850	3982942	433010	433102	gene=IY08_20965	protein=hypothetical protein	protein_id=KGT41674.1
gene	3983015	3983254	433175	433414	gene=IY08_20970	protein=hypothetical protein	protein_id=KGT41675.1
gene	3983321	3983881	433481	434041	gene=IY08_20975	protein=L,D-transpeptidase	protein_id=KGT41676.1
gene	3983898	3984866	434058	435026	gene=IY08_20980	protein=hypothetical protein	protein_id=KGT41677.1
gene	3984967	3985689	435127	435849	gene=IY08_20985	protein=peptide ABC transporter ATP-binding protein	protein_id=KGT41678.1
gene	3985682	3986341	435842	436501	gene=IY08_20990	protein=arginine ABC transporter permease	protein_id=KGT41679.1
gene	3986378	3987157	436538	437317	gene=IY08_20995	protein=ABC transporter substrate-binding protein	protein_id=KGT41680.1
gene	3987169	3987375	437329	437535	pseudo		
gene	3987410	3987823	437570	437983	gene=IY08_21005	protein=hypothetical protein	protein_id=KGT41681.1
gene	3987968	3988375	438128	438535	gene=IY08_21010	protein=5-formyltetrahydrofolate cyclo-ligase	protein_id=KGT41682.1
gene	3988497	3988961	438657	439121	gene=IY08_21015	protein=DNA mismatch repair protein MutT	protein_id=KGT41683.1
gene	3989032	3989736	439192	439896	gene=IY08_21020	protein=membrane protein	protein_id=KGT41684.1
gene	3989843	3991021	440003	441181	gene=IY08_21025	protein=cell division protein FtsW	protein_id=KGT41685.1
gene	3991085	3991258	441245	441418	gene=IY08_21030	protein=hypothetical protein	protein_id=KGT41686.1

gene	3991364	3992683	441524	442843	gene=IY08_21035	protein=branched-chain alpha-keto acid dehydrogenase subunit E2	protein_id=KGT41687.1
gene	3992699	3993682	442859	443842	gene=IY08_21040	protein=2-oxoisovalerate dehydrogenase	protein_id=KGT41688.1
gene	3993696	3994697	443856	444857	gene=IY08_21045	protein=2-oxoisovalerate dehydrogenase	protein_id=KGT41689.1
gene	3994725	3996146	444885	446306	gene=IY08_21050	protein=dihydrolipoamide dehydrogenase	protein_id=KGT41690.1
gene	3996151	3997254	446311	447414	gene=IY08_21055	protein=butyrate kinase	protein_id=KGT41691.1
gene	3997342	3998442	447502	448602	gene=IY08_21060	protein=leucine dehydrogenase	protein_id=KGT41692.1
gene	3998477	3999376	448637	449536	gene=IY08_21065	protein=phosphate butyryltransferase	protein_id=KGT41693.1
gene	3999373	3999594	449533	449754	gene=IY08_21070	protein=hypothetical protein	protein_id=KGT41694.1
gene	3999572	4001644	449732	451804	gene=IY08_21075	protein=ATPase AAA	protein_id=KGT41695.1
gene	4001782	4002015	451942	452175	gene=IY08_21080	protein=hypothetical protein	protein_id=KGT41696.1
gene	4002065	4002793	452225	452953	gene=IY08_21085	protein=hypothetical protein	protein_id=KGT41697.1
gene	4002844	4002990	453004	453150	gene=IY08_21090	protein=hypothetical protein	protein_id=KGT41698.1
gene	4003232	4003795	453392	453955	pseudo		
gene	4004048	4004842	454208	455002	gene=IY08_21100	protein=chemotaxis protein CheY	protein_id=KGT41699.1
gene	4005133	4006431	455293	456591	gene=IY08_21110	protein=peptidase S55	protein_id=KGT41700.1
gene	4006550	4008289	456710	458449	gene=IY08_21115	protein=DNA recombination protein RecN	protein_id=KGT41701.1
gene	4008554	4009003	458714	459163	gene=IY08_21120	protein=arginine repressor	protein_id=KGT41702.1
gene	4009146	4009985	459306	460145	gene=IY08_21125	protein=rRNA methyltransferase	protein_id=KGT41703.1
gene	4009989	4011881	460149	462041	gene=IY08_21130	protein=1-deoxy-D-xylulose-5-phosphate synthase	protein_id=KGT41704.1
gene	4012183	4013073	462343	463233	gene=IY08_21135	protein=farnesyl-diphosphate synthase	protein_id=KGT41705.1
gene	4013073	4013303	463233	463463	gene=IY08_21140	protein=exodeoxyribonuclease VII small subunit	protein_id=KGT41706.1
gene	4013293	4014651	463453	464811	gene=IY08_21145	protein=exodeoxyribonuclease VII large subunit	protein_id=KGT41707.1
gene	4014678	4015538	464838	465698	gene=IY08_21150	protein=5,10-methylene-tetrahydrofolate cyclohydrolase	protein_id=KGT41708.1
gene	4015562	4015954	465722	466114	gene=IY08_21155	protein=antitermination protein NusB	protein_id=KGT41709.1
gene	4016301	4016693	466461	466853	gene=IY08_21160	protein=hypothetical protein	protein_id=KGT41710.1
gene	4016716	4018068	466876	468228	gene=IY08_21165	protein=acetyl-CoA carboxylase	protein_id=KGT41711.1
gene	4018085	4018573	468245	468733	gene=IY08_21170	protein=acetyl-CoA carboxylase	protein_id=KGT41712.1
gene	4019036	4019230	469196	469390	gene=IY08_21175	protein=DNA recombination protein RecO	protein_id=KGT41713.1
gene	4019344	4019988	469504	470148	gene=IY08_21180	protein=stage III sporulation protein AH	protein_id=KGT41714.1
gene	4020004	4020666	470164	470826	gene=IY08_21185	protein=stage III sporulation protein AG	protein_id=KGT41715.1

gene	4020656	4021288	470816	471448	gene=IY08_21190	protein=stage III sporulation protein AF	protein_id=KGT41716.1
gene	4021301	4022473	471461	472633	gene=IY08_21195	protein=stage III sporulation protein AE	protein_id=KGT41717.1
gene	4022484	4022762	472644	472922	gene=IY08_21200	protein=stage III sporulation protein AD	protein_id=KGT41718.1
gene	4022891	4023094	473051	473254	gene=IY08_21205	protein=stage III sporulation protein AC	protein_id=KGT41719.1
gene	4023109	4023624	473269	473784	gene=IY08_21210	protein=stage III sporulation protein AB	protein_id=KGT41720.1
gene	4023618	4024544	473778	474704	gene=IY08_21215	protein=stage III sporulation protein AA	protein_id=KGT41721.1
gene	4024572	4024853	474732	475013	gene=IY08_21220	protein=hypothetical protein	protein_id=KGT41722.1
gene	4025045	4025623	475205	475783	gene=IY08_21225	protein=GNAT family acetyltransferase	protein_id=KGT41723.1
gene	4025604	4025924	475764	476084	gene=IY08_21230	protein=hypothetical protein	protein_id=KGT41724.1
gene	4025961	4026518	476121	476678	gene=IY08_21235	protein=elongation factor P	protein_id=KGT41725.1
gene	4026540	4027601	476700	477761	gene=IY08_21240	protein=Xaa-Pro dipeptidase	protein_id=KGT41726.1
gene	4027606	4028046	477766	478206	gene=IY08_21245	protein=3-dehydroquinate dehydratase	protein_id=KGT41727.1
gene	4028126	4028587	478286	478747	gene=IY08_21250	protein=hypothetical protein	protein_id=KGT41728.1
gene	4028832	4029752	478992	479912	gene=IY08_21255	protein=membrane protein	protein_id=KGT41729.1
gene	4029832	4030233	479992	480393	gene=IY08_21260	protein=membrane protein	protein_id=KGT41730.1
gene	4030230	4030892	480390	481052	gene=IY08_21265	protein=HAD family hydrolase	protein_id=KGT41731.1
gene	4030947	4031375	481107	481535	gene=IY08_21270	protein=manganese transport transcriptional regulator	protein_id=KGT41732.1
gene	4031956	4032273	482116	482433	gene=IY08_21275	protein=PadR family transcriptional regulator	protein_id=KGT41733.1
gene	4032279	4032950	482439	483110	gene=IY08_21280	protein=hypothetical protein	protein_id=KGT41734.1
gene	4033152	4033994	483312	484154	gene=IY08_21285	protein=hypothetical protein	protein_id=KGT41735.1
gene	4034023	4034859	484183	485019	gene=IY08_21290	protein=octanoyltransferase	protein_id=KGT41736.1
gene	4035030	4035413	485190	485573	gene=IY08_21295	protein=hypothetical protein	protein_id=KGT41737.1
gene	4035454	4035930	485614	486090	gene=IY08_21300	protein=DNA polymerase III subunit delta	protein_id=KGT41738.1
gene	4036245	4037222	486405	487382	gene=IY08_21305	protein=LacI family transcriptional regulator	protein_id=KGT41739.1
gene	4037319	4037900	487479	488060	gene=IY08_21310	protein=TetR family transcriptional regulator	protein_id=KGT41740.1
gene	4037971	4038303	488131	488463	gene=IY08_21315	protein=multidrug resistance protein SMR	protein_id=KGT41741.1
gene	4038305	4038619	488465	488779	gene=IY08_21320	protein=transporter	protein_id=KGT41742.1
gene	4038635	4038892	488795	489052	gene=IY08_21325	protein=hypothetical protein	protein_id=KGT41743.1
gene	4038909	4039097	489069	489257	gene=IY08_21330	protein=hypothetical protein	protein_id=KGT41744.1
gene	4039167	4039316	489327	489476	gene=IY08_21335	protein=hypothetical protein	protein_id=KGT41745.1
gene	4039343	4039939	489503	490099	gene=IY08_21340	protein=ABC transporter permease	protein_id=KGT41746.1

gene	4039972	4040604	490132	490764	gene=IY08_21345	protein=ABC transporter substrate-binding protein	protein_id=KGT41747.1
gene	4040619	4041287	490779	491447	gene=IY08_21350	protein=ABC transporter permease	protein_id=KGT41748.1
gene	4041268	4042140	491428	492300	gene=IY08_21355	protein=sodium ABC transporter ATP-binding protein	protein_id=KGT41749.1
gene	4042146	4042520	492306	492680	gene=IY08_21360	protein=GntR family transcriptional regulator	protein_id=KGT41750.1
gene	4042639	4042830	492799	492990	gene=IY08_21365	protein=glycosyltransferase	protein_id=KGT41751.1
gene	4042901	4043125	493061	493285	gene=IY08_21370	protein=hypothetical protein	protein_id=KGT41752.1
gene	4043527	4045002	493687	495162	gene=IY08_21375	protein=glycine dehydrogenase	protein_id=KGT41753.1
gene	4044999	4046342	495159	496502	gene=IY08_21380	protein=glycine dehydrogenase	protein_id=KGT41754.1
gene	4046363	4047463	496523	497623	gene=IY08_21385	protein=glycine cleavage system protein T	protein_id=KGT41755.1
gene	4047854	4049536	498014	499696	gene=IY08_21390	protein=ATP-dependent helicase	protein_id=KGT41756.1
gene	4049523	4050320	499683	500480	gene=IY08_21395	protein=hypothetical protein	protein_id=KGT41757.1
gene	4050356	4050487	500516	500647	gene=IY08_21400	protein=hypothetical protein	protein_id=KGT41758.1
gene	4050585	4050812	500745	500972	gene=IY08_21405	protein=hypothetical protein	protein_id=KGT41759.1
gene	4051144	4051776	501304	501936	gene=IY08_21410	protein=membrane protein	protein_id=KGT41760.1
gene	4051842	4052042	502002	502202	gene=IY08_21415	protein=hypothetical protein	protein_id=KGT41761.1
gene	4052081	4052578	502241	502738	gene=IY08_21420	protein=shikimate kinase	protein_id=KGT41762.1
gene	4052694	4053344	502854	503504	gene=IY08_21425	protein=2OG-Fe(II) oxygenase	protein_id=KGT41763.1
gene	4053521	4053892	503681	504052	gene=IY08_21430	protein=competence protein ComG	protein_id=KGT41764.1
gene	4053889	4054359	504049	504519	gene=IY08_21435	protein=competence protein ComG	protein_id=KGT41765.1
gene	4054329	4054631	504489	504791	gene=IY08_21440	protein=competence protein ComG	protein_id=KGT41766.1
gene	4054624	4055079	504784	505239	gene=IY08_21445	protein=competence protein ComG	protein_id=KGT41767.1
gene	4055076	4055375	505236	505535	gene=IY08_21450	protein=competence protein ComG	protein_id=KGT41768.1
gene	4055387	4056418	505547	506578	gene=IY08_21455	protein=competence protein ComG	protein_id=KGT41769.1
gene	4056411	4057454	506571	507614	gene=IY08_21460	protein=competence protein ComG	protein_id=KGT41770.1
gene	4057660	4058355	507820	508515	gene=IY08_21465	protein=transcriptional regulator	protein_id=KGT41771.1
gene	4058481	4058723	508641	508883	gene=IY08_21470	protein=membrane protein	protein_id=KGT41772.1
gene	4058830	4060224	508990	510384	gene=IY08_21475	protein=sodium:dicarboxylate symporter	protein_id=KGT41773.1
gene	4060304	4060696	510464	510856	gene=IY08_21480	protein=DoxX	protein_id=KGT41774.1
gene	4060784	4060999	510944	511159	gene=IY08_21485	protein=hypothetical protein	protein_id=KGT41775.1
gene	4061252	4061563	511412	511723	gene=IY08_21490	protein=hypothetical protein	protein_id=KGT41776.1
gene	4061598	4062086	511758	512246	gene=IY08_21495	protein=hypothetical protein	protein_id=KGT41777.1

gene	4062166	4062540	512326	512700	gene=IY08_21500	protein=group-specific protein	protein_id=KGT41778.1
gene	4062636	4062896	512796	513056	gene=IY08_21505	protein=hypothetical protein	protein_id=KGT41779.1
gene	4063091	4064149	513251	514309	gene=IY08_21510	protein=UDP-diphospho-muramoylpentapeptide beta-N-acetylglucosaminyltransferase	protein_id=KGT41780.1
gene	4064168	4067566	514328	517726	gene=IY08_21515	protein=5-methyltetrahydrofolate--homocysteine methyltransferase	protein_id=KGT41781.1
gene	4067566	4069398	517726	519558	gene=IY08_21520	protein=homocysteine methyltransferase	protein_id=KGT41782.1
gene	4069460	4069714	519620	519874	gene=IY08_21525	protein=hypothetical protein	protein_id=KGT41783.1
gene	4069987	4071099	520147	521259	gene=IY08_21530	protein=cystathionine gamma-synthase	protein_id=KGT41784.1
gene	4071096	4072259	521256	522419	gene=IY08_21535	protein=cystathionine gamma-synthase	protein_id=KGT41785.1
gene	4072428	4072939	522588	523099	pseudo		
gene	4073373	4073663	523533	523823	gene=IY08_21545	protein=ArsR family transcriptional regulator	protein_id=KGT41786.1
gene	4073806	4074918	523966	525078	gene=IY08_21550	protein=cytoplasmic protein	protein_id=KGT41787.1
gene	4074928	4075557	525088	525717	gene=IY08_21555	protein=hypothetical protein	protein_id=KGT41788.1
gene	4075728	4075901	525888	526061	gene=IY08_21560	protein=membrane protein	protein_id=KGT41789.1
gene	4075982	4076965	526142	527125	gene=IY08_21565	protein=glucokinase	protein_id=KGT41790.1
gene	4076985	4077185	527145	527345	gene=IY08_21570	protein=cytoplasmic protein	protein_id=KGT41791.1
gene	4077289	4077867	527449	528027	gene=IY08_21575	protein=hypothetical protein	protein_id=KGT41792.1
gene	4077973	4078122	528133	528282	gene=IY08_21580	protein=50S ribosomal protein L33	protein_id=KGT41793.1
gene	4078192	4080546	528352	530706	gene=IY08_21585	protein=nucleotidyltransferase	protein_id=KGT41794.1
gene	4080886	4081542	531046	531702	gene=IY08_21590	protein=PhoU family transcriptional regulator	protein_id=KGT41795.1
gene	4081730	4082545	531890	532705	gene=IY08_21595	protein=phosphate ABC transporter ATP-binding protein	protein_id=KGT41796.1
gene	4082574	4083440	532734	533600	gene=IY08_21600	protein=phosphate ABC transporter permease	protein_id=KGT41797.1
gene	4083442	4084392	533602	534552	gene=IY08_21605	protein=phosphate ABC transporter permease	protein_id=KGT41798.1
gene	4084420	4085337	534580	535497	gene=IY08_21610	protein=phosphate ABC transporter substrate-binding	protein_id=KGT41799.1
gene	4085669	4087795	535829	537955	gene=IY08_21615	protein=penicillin-binding protein	protein_id=KGT41800.1
gene	4087905	4089182	538065	539342	gene=IY08_21620	protein=hypothetical protein	protein_id=KGT41801.1
gene	4089299	4089910	539459	540070	gene=IY08_21625	protein=superoxide dismutase	protein_id=KGT41802.1
gene	4090132	4090205	540292	540365	tRNA		
gene	4090447	4091205	540607	541365	gene=IY08_21640	protein=hypothetical protein	protein_id=KGT41803.1
gene	4091278	4091643	541438	541803	gene=IY08_21645	protein=hypothetical protein	protein_id=KGT41804.1

gene	4091799	4092911	541959	543071	gene=IY08_21650	protein=4-hydroxy-3-methylbut-2-en-1-yl diphosphate	protein_id=KGT41805.1
gene	4092988	4093401	543148	543561	gene=IY08_21655	protein=Fur family transcriptional regulator	protein_id=KGT41806.1
gene	4093415	4094248	543575	544408	gene=IY08_21660	protein=metal ABC transporter permease	protein_id=KGT41807.1
gene	4094248	4095018	544408	545178	gene=IY08_21665	protein=zinc ABC transporter ATP-binding protein	protein_id=KGT41808.1
gene	4095199	4096077	545359	546237	gene=IY08_21670	protein=membrane protein	protein_id=KGT41809.1
gene	4096227	4096481	546387	546641	gene=IY08_21675	protein=tRNA methyltransferase	protein_id=KGT41810.1
gene	4096501	4097397	546661	547557	gene=IY08_21680	protein=endonuclease IV	protein_id=KGT41811.1
gene	4097630	4098940	547790	549100	gene=IY08_21685	protein=DEAD/DEAH box helicase	protein_id=KGT41812.1
gene	4099122	4099859	549282	550019	gene=IY08_21690	protein=VrrA protein	protein_id=KGT41813.1
gene	4099949	4100899	550109	551059	gene=IY08_21695	protein=4-hydroxy-3-methylbut-2-enyl diphosphate	protein_id=KGT41814.1
gene	4100941	4102062	551101	552222	gene=IY08_21700	protein=hypothetical protein	protein_id=KGT41815.1
gene	4102059	4102766	552219	552926	gene=IY08_21705	protein=SAM-dependent methyltransferase	protein_id=KGT41816.1
gene	4102932	4103288	553092	553448	gene=IY08_21710	protein=cytochrome C	protein_id=KGT41817.1
gene	4103675	4104802	553835	554962	gene=IY08_21715	protein=RNA polymerase sigma factor RpoD	protein_id=KGT41818.1
gene	4104862	4106658	555022	556818	gene=IY08_21720	protein=DNA primase	protein_id=KGT41819.1
gene	4107020	4107151	557180	557311	gene=IY08_21730	protein=hypothetical protein	protein_id=KGT41820.1
gene	4107519	4108331	557679	558491	gene=IY08_21740	protein=phosphotransferase	protein_id=KGT41821.1
gene	4108361	4108996	558521	559156	gene=IY08_21745	protein=transcriptional repressor CcpN	protein_id=KGT41822.1
gene	4109101	4109847	559261	560007	gene=IY08_21750	protein=DNA recombination protein RecO	protein_id=KGT41823.1
gene	4109881	4110024	560041	560184	gene=IY08_21755	protein=hypothetical protein	protein_id=KGT41824.1
gene	4110201	4111106	560361	561266	gene=era	protein=GTPase Era	protein_id=KGT41825.1
gene	4111099	4111497	561259	561657	gene=IY08_21765	protein=cytidine deaminase	protein_id=KGT41826.1
gene	4111597	4111950	561757	562110	gene=IY08_21770	protein=diacylglycerol kinase	protein_id=KGT41827.1
gene	4111947	4112417	562107	562577	gene=IY08_21775	protein=rRNA maturation factor	protein_id=KGT41828.1
gene	4112414	4114558	562574	564718	gene=IY08_21780	protein=membrane protein	protein_id=KGT41829.1
gene	4114753	4115712	564913	565872	gene=IY08_21785	protein=phosphate starvation protein PhoH	protein_id=KGT41830.1
gene	4115716	4116915	565876	567075	gene=IY08_21790	protein=stage IV sporulation protein	protein_id=KGT41831.1
gene	4116905	4117015	567065	567175	gene=IY08_21795	protein=hypothetical protein	protein_id=KGT42383.1
gene	4117077	4117370	567237	567530	gene=IY08_21800	protein=sporulation protein YqfC	protein_id=KGT41832.1
gene	4117934	4118185	568094	568345	gene=IY08_21805	protein=hypothetical protein	protein_id=KGT42384.1
gene	4118289	4118732	568449	568892	gene=IY08_21810	protein=hypothetical protein	protein_id=KGT41833.1

gene	4118748	4118921	568908	569081	gene=IY08_21815	protein=30S ribosomal protein S21	protein_id=KGT41834.1
gene	4119242	4120594	569402	570754	gene=IY08_21820	protein=30S ribosomal protein S12 methylthiotransferase	protein_id=KGT41835.1
gene	4120601	4121350	570761	571510	gene=IY08_21825	protein=16S rRNA methyltransferase	protein_id=KGT41836.1
gene	4121495	4122433	571655	572593	gene=IY08_21830	protein=ribosomal protein L11 methyltransferase	protein_id=KGT41837.1
gene	4122462	4123577	572622	573737	gene=IY08_21835	protein=molecular chaperone DnaJ	protein_id=KGT41838.1
gene	4123782	4125617	573942	575777	gene=dnaK	protein=molecular chaperone DnaK	protein_id=KGT41839.1
gene	4125644	4126210	575804	576370	gene=IY08_21845	protein=heat shock protein GrpE	protein_id=KGT41840.1
gene	4126325	4127341	576485	577501	gene=IY08_21850	protein=HrcA family transcriptional regulator	protein_id=KGT41841.1
gene	4127475	4128614	577635	578774	gene=IY08_21855	protein=coproporphyrinogen III oxidase	protein_id=KGT41842.1
gene	4128666	4129040	578826	579200	gene=IY08_21860	protein=HxlR family transcriptional regulator	protein_id=KGT41843.1
gene	4129171	4130994	579331	581154	gene=IY08_21865	protein=elongation factor 4	protein_id=KGT41844.1
gene	4131205	4131570	581365	581730	gene=IY08_21870	protein=transcriptional regulator	protein_id=KGT41845.1
gene	4131567	4132670	581727	582830	gene=IY08_21875	protein=peptidase	protein_id=KGT41846.1
gene	4132851	4133108	583011	583268	gene=IY08_21880	protein=30S ribosomal protein S20	protein_id=KGT41847.1
gene	4133192	4134202	583352	584362	gene=IY08_21885	protein=DNA polymerase III subunit delta	protein_id=KGT41848.1
gene	4134549	4134683	584709	584843	gene=IY08_21890	protein=membrane protein	protein_id=KGT41849.1
gene	4134715	4137036	584875	587196	gene=IY08_21895	protein=competence protein ComEC	protein_id=KGT41850.1
gene	4137051	4137608	587211	587768	gene=IY08_21900	protein=competence protein ComE	protein_id=KGT41851.1
gene	4137672	4138271	587832	588431	gene=IY08_21905	protein=competence protein ComE	protein_id=KGT41852.1
gene	4138349	4139176	588509	589336	gene=IY08_21910	protein=competence protein	protein_id=KGT41853.1
gene	4139348	4140097	589508	590257	gene=IY08_21915	protein=methyltransferase	protein_id=KGT41854.1
gene	4140094	4140450	590254	590610	gene=IY08_21920	protein=ribosomal silencing factor RsfS	protein_id=KGT41855.1
gene	4140447	4141016	590607	591176	gene=IY08_21925	protein=phosphohydrolase	protein_id=KGT41856.1
gene	4141006	4141575	591166	591735	gene=IY08_21930	protein=nicotinate-nucleotide adenylyltransferase	protein_id=KGT41857.1
gene	4141713	4142006	591873	592166	gene=IY08_21935	protein=RNA-binding protein	protein_id=KGT41858.1
gene	4142012	4142845	592172	593005	gene=IY08_21940	protein=shikimate dehydrogenase	protein_id=KGT41859.1
gene	4142861	4143967	593021	594127	gene=IY08_21945	protein=GTPase	protein_id=KGT41860.1
gene	4143971	4144483	594131	594643	gene=IY08_21950	protein=hypothetical protein	protein_id=KGT41861.1
gene	4144730	4144885	594890	595045	gene=IY08_21955	protein=Sporulation inhibitor sda	protein_id=KGT41862.1
gene	4145071	4145859	595231	596019	gene=IY08_21960	protein=phosphatidylserine decarboxylase	protein_id=KGT41863.1
gene	4146149	4146862	596309	597022	gene=IY08_21965	protein=sporulation sigma factor SigK	protein_id=KGT41864.1

gene	4147045	4147935	597205	598095	gene=IY08_21970	protein=hypothetical protein	protein_id=KGT41865.1
gene	4147979	4149472	598139	599632	gene=IY08_21975	protein=cytoplasmic protein	protein_id=KGT41866.1
gene	4149561	4149710	599721	599870	gene=IY08_21980	protein=50S ribosomal protein L33	protein_id=KGT41867.1
gene	4149907	4150533	600067	600693	gene=IY08_21985	protein=NAD(P)H nitroreductase	protein_id=KGT41868.1
gene	4150883	4151533	601043	601693	gene=IY08_21990	protein=GTP pyrophosphokinase	protein_id=KGT41869.1
gene	4151611	4152078	601771	602238	gene=IY08_21995	protein=lipoprotein	protein_id=KGT41870.1
gene	4152133	4153518	602293	603678	gene=IY08_22000	protein=alkaline phosphatase	protein_id=KGT41871.1
gene	4153780	4154613	603940	604773	gene=IY08_22005	protein=acetyltransferase	protein_id=KGT41872.1
gene	4154629	4155513	604789	605673	gene=IY08_22010	protein=alpha/beta hydrolase	protein_id=KGT41873.1
gene	4155555	4156055	605715	606215	gene=IY08_22015	protein=DoxX family protein	protein_id=KGT41874.1
gene	4156320	4156856	606480	607016	gene=IY08_22020	protein=delta-aminolevulinic acid dehydratase	protein_id=KGT41875.1
gene	4156875	4157477	607035	607637	gene=IY08_22025	protein=phosphoglycerate mutase	protein_id=KGT41876.1
gene	4157646	4157984	607806	608144	gene=IY08_22030	protein=phosphoglycerate mutase	protein_id=KGT41877.1
gene	4158054	4158176	608214	608336	gene=IY08_22035	protein=HemX protein	protein_id=KGT41878.1
gene	4158368	4158898	608528	609058	gene=IY08_22040	protein=hypothetical protein	protein_id=KGT41879.1
gene	4159770	4161524	609930	611684	gene=IY08_22050	protein=phenylalanine 4-monooxygenase	protein_id=KGT41880.1
gene	4161505	4161819	611665	611979	gene=IY08_22055	protein=pterin-4-alpha-carbinolamine dehydratase	protein_id=KGT41881.1
gene	4161835	4162692	611995	612852	gene=IY08_22060	protein=glyoxalase	protein_id=KGT41882.1
gene	4162714	4163118	612874	613278	gene=IY08_22065	protein=DoxX	protein_id=KGT41883.1
gene	4163275	4163820	613435	613980	gene=IY08_22070	protein=DNA-binding protein	protein_id=KGT41884.1
gene	4163857	4164234	614017	614394	gene=IY08_22075	protein=enoyl-CoA hydratase	protein_id=KGT41885.1
gene	4164353	4164811	614513	614971	gene=IY08_22080	protein=acetyltransferase	protein_id=KGT41886.1
gene	4164868	4165374	615028	615534	gene=IY08_22085	protein=acetyltransferase	protein_id=KGT41887.1
gene	4165682	4166077	615842	616237	gene=IY08_22090	protein=ankyrin	protein_id=KGT41888.1
gene	4166044	4166862	616204	617022	gene=IY08_22095	protein=iron ABC transporter ATP-binding protein	protein_id=KGT41889.1
gene	4166849	4167877	617009	618037	gene=IY08_22100	protein=iron ABC transporter permease	protein_id=KGT41890.1
gene	4167882	4168829	618042	618989	gene=IY08_22105	protein=iron-hydroxamate ABC transporter substrate-binding protein	protein_id=KGT41891.1
gene	4168987	4169214	619147	619374	gene=IY08_22110	protein=membrane protein	protein_id=KGT41892.1
gene	4169342	4171945	619502	622105	gene=IY08_22115	protein=acetaldehyde dehydrogenase	protein_id=KGT41893.1
gene	4172210	4173343	622370	623503	gene=IY08_22120	protein=cystathionine gamma-synthase	protein_id=KGT41894.1

gene	4173347	4174270	623507	624430	gene=IY08_22125	protein=cysteine synthase	protein_id=KGT41895.1
gene	4174353	4175048	624513	625208	gene=IY08_22130	protein=5'-methylthioadenosine nucleosidase	protein_id=KGT41896.1
gene	4175063	4175701	625223	625861	gene=IY08_22135	protein=SAM-dependent methyltransferase	protein_id=KGT41897.1
gene	4175838	4176053	625998	626213	gene=IY08_22140	protein=hypothetical protein	protein_id=KGT41898.1
gene	4176088	4176750	626248	626910	gene=IY08_22145	protein=FMN-dependent NADH-azoreductase	protein_id=KGT41899.1
gene	4176867	4178621	627027	628781	gene=IY08_22150	protein=penicillin-binding protein	protein_id=KGT41900.1
gene	4178709	4179389	628869	629549	gene=IY08_22155	protein=hypothetical protein	protein_id=KGT41901.1
gene	4179670	4180146	629830	630306	gene=IY08_22160	protein=transcription elongation factor GreA	protein_id=KGT41902.1
gene	4180426	4181064	630586	631224	gene=IY08_22165	protein=uridine kinase	protein_id=KGT41903.1
gene	4181082	4182362	631242	632522	gene=IY08_22170	protein=protease	protein_id=KGT41904.1
gene	4182381	4183310	632541	633470	gene=IY08_22175	protein=peptidase U32	protein_id=KGT41905.1
gene	4183318	4183959	633478	634119	gene=IY08_22180	protein=SAM-dependent methyltransferase	protein_id=KGT41906.1
gene	4184166	4185233	634326	635393	gene=IY08_22185	protein=hypothetical protein	protein_id=KGT41907.1
gene	4185457	4185735	635617	635895	gene=IY08_22190	protein=hypothetical protein	protein_id=KGT41908.1
gene	4185748	4186161	635908	636321	gene=IY08_22195	protein=Holliday junction resolvase	protein_id=KGT41909.1
gene	4186165	4186431	636325	636591	gene=IY08_22200	protein=hypothetical protein	protein_id=KGT41910.1
gene	4186508	4189150	636668	639310	gene=alaS	protein=alanine--tRNA ligase	protein_id=KGT41911.1
gene	4189651	4189995	639811	640155	gene=IY08_22210	protein=hypothetical protein	protein_id=KGT41912.1
gene	4190040	4191107	640200	641267	gene=IY08_22215	protein=membrane protein	protein_id=KGT41913.1
gene	4191284	4191496	641444	641656	gene=IY08_22220	protein=hypothetical protein	protein_id=KGT41914.1
gene	4191543	4191671	641703	641831	gene=IY08_22225	protein=succinate dehydrogenase	protein_id=KGT41915.1
gene	4191690	4191878	641850	642038	gene=IY08_22230	protein=hypothetical protein	protein_id=KGT41916.1
gene	4192008	4194344	642168	644504	gene=IY08_22235	protein=hypothetical protein	protein_id=KGT41917.1
gene	4194440	4195099	644600	645259	gene=IY08_22240	protein=TPR repeat-containing protein YrrB	protein_id=KGT41918.1
gene	4195209	4196324	645369	646484	gene=IY08_22245	protein=thiouridylase	protein_id=KGT41919.1
gene	4196341	4197486	646501	647646	gene=IY08_22250	protein=cysteine desulfurase	protein_id=KGT41920.1
gene	4197522	4197938	647682	648098	gene=IY08_22255	protein=Rrf2 family transcriptional regulator	protein_id=KGT41921.1
gene	4198232	4199518	648392	649678	gene=IY08_22260	protein=recombinase RarA	protein_id=KGT41922.1
gene	4199556	4200197	649716	650357	gene=IY08_22265	protein=transcriptional regulator	protein_id=KGT41923.1
gene	4200446	4200628	650606	650788	gene=IY08_22270	protein=hypothetical protein	protein_id=KGT41924.1
gene	4200674	4201441	650834	651601	gene=IY08_22275	protein=hypothetical protein	protein_id=KGT41925.1

gene	4201783	4203558	651943	653718	gene=aspS	protein=aspartate--tRNA ligase	protein_id=KGT41926.1
gene	4203571	4204842	653731	655002	gene=IY08_22285	protein=histidyl-tRNA synthetase	protein_id=KGT41927.1
gene	4205197	4205373	655357	655533	gene=IY08_22290	protein=RNA polymerase subunit sigma-70	protein_id=KGT41928.1
gene	4205539	4205979	655699	656139	gene=IY08_22295	protein=D-tyrosyl-tRNA(Tyr) deacylase	protein_id=KGT41929.1
gene	4205996	4208179	656156	658339	gene=IY08_22300	protein=(p)ppGpp synthetase	protein_id=KGT41930.1
gene	4208390	4208902	658550	659062	gene=IY08_22305	protein=adenine phosphoribosyltransferase	protein_id=KGT41931.1
gene	4208950	4211289	659110	661449	gene=IY08_22310	protein=recombinase RecJ	protein_id=KGT41932.1
gene	4211391	4212284	661551	662444	gene=IY08_22315	protein=cation transporter	protein_id=KGT41933.1
gene	4212441	4214705	662601	664865	gene=IY08_22320	protein=preprotein translocase subunit SecD	protein_id=KGT41934.1
gene	4214975	4215259	665135	665419	gene=IY08_22325	protein=histidine kinase	protein_id=KGT41935.1
gene	4215444	4217003	665604	667163	gene=IY08_22330	protein=stage V sporulation protein B	protein_id=KGT41936.1
gene	4217084	4217731	667244	667891	gene=IY08_22335	protein=membrane protein	protein_id=KGT41937.1
gene	4217835	4218218	667995	668378	gene=IY08_22340	protein=TIGR04097 family integral membrane protein	protein_id=KGT41938.1
gene	4218255	4218515	668415	668675	gene=IY08_22345	protein=preprotein translocase subunit YajC	protein_id=KGT41939.1
gene	4218543	4219682	668703	669842	gene=IY08_22350	protein=queuine tRNA-ribosyltransferase	protein_id=KGT41940.1
gene	4219695	4220747	669855	670907	gene=IY08_22355	protein=S-adenosylmethionine tRNA ribosyltransferase	protein_id=KGT41941.1
gene	4220767	4220967	670927	671127	gene=IY08_22360	protein=hypothetical protein	protein_id=KGT41942.1
gene	4220964	4221965	671124	672125	gene=IY08_22365	protein=ATP-dependent DNA helicase RuvB	protein_id=KGT41943.1
gene	4221971	4222588	672131	672748	gene=IY08_22370	protein=ATP-dependent DNA helicase RuvA	protein_id=KGT41944.1
gene	4222777	4223721	672937	673881	gene=IY08_22375	protein=ferrichrome ABC transporter substrate-binding	protein_id=KGT41945.1
gene	4223735	4224265	673895	674425	gene=IY08_22380	protein=BofC protein	protein_id=KGT41946.1
gene	4224697	4225131	674857	675291	gene=IY08_22385	protein=branched-chain amino acid ABC transporter substrate-binding protein	protein_id=KGT41947.1
gene	4225165	4225806	675325	675966	gene=IY08_22390	protein=spore cortex protein	protein_id=KGT41948.1
gene	4225985	4227808	676145	677968	gene=IY08_22395	protein=peptigoglycan-binding protein LysM	protein_id=KGT41949.1
gene	4228034	4229140	678194	679300	gene=IY08_22400	protein=quinolinate synthetase	protein_id=KGT41950.1
gene	4229171	4230004	679331	680164	gene=IY08_22405	protein=nicotinate-nucleotide pyrophosphorylase	protein_id=KGT41951.1
gene	4230024	4231553	680184	681713	gene=IY08_22410	protein=L-aspartate oxidase	protein_id=KGT41952.1
gene	4231706	4232848	681866	683008	gene=IY08_22415	protein=cysteine desulfurase	protein_id=KGT41953.1
gene	4232848	4233390	683008	683550	gene=IY08_22420	protein=transcriptional regulator	protein_id=KGT41954.1
gene	4233470	4234117	683630	684277	gene=IY08_22425	protein=sulfurase	protein_id=KGT41955.1

gene	4234267	4234737	684427	684897	gene=IY08_22430	protein=hypothetical protein	protein_id=KGT41956.1
gene	4234913	4235764	685073	685924	gene=IY08_22435	protein=prephenate dehydratase	protein_id=KGT41957.1
gene	4235862	4237775	686022	687935	gene=IY08_22440	protein=ABC transporter permease	protein_id=KGT41958.1
gene	4237825	4239747	687985	689907	gene=IY08_22445	protein=ABC transporter permease	protein_id=KGT41959.1
gene	4239722	4240498	689882	690658	gene=IY08_22450	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT41960.1
gene	4240592	4241674	690752	691834	gene=IY08_22455	protein=ATPase	protein_id=KGT41961.1
gene	4241664	4242371	691824	692531	gene=IY08_22460	protein=transcriptional regulator	protein_id=KGT41962.1
gene	4242512	4243798	692672	693958	gene=IY08_22465	protein=GTPase ObgE	protein_id=KGT41963.1
gene	4243798	4244346	693958	694506	gene=IY08_22470	protein=sporulation protein	protein_id=KGT41964.1
gene	4244410	4244700	694570	694860	gene=IY08_22475	protein=50S ribosomal protein L27	protein_id=KGT41965.1
gene	4244704	4245048	694864	695208	gene=IY08_22480	protein=hypothetical protein	protein_id=KGT41966.1
gene	4245060	4245368	695220	695528	gene=IY08_22485	protein=50S ribosomal protein L21	protein_id=KGT41967.1
gene	4245538	4246926	695698	697086	gene=IY08_22490	protein=ribonuclease E	protein_id=KGT41968.1
gene	4246994	4247854	697154	698014	gene=IY08_22495	protein=stage IV sporulation protein FB	protein_id=KGT41969.1
gene	4247847	4248593	698007	698753	gene=IY08_22500	protein=peptidase M23	protein_id=KGT41970.1
gene	4248727	4249524	698887	699684	gene=IY08_22505	protein=cell division inhibitor MinD	protein_id=KGT41971.1
gene	4249527	4250213	699687	700373	gene=minC	protein=septum formation inhibitor	protein_id=KGT41972.1
gene	4250249	4250794	700409	700954	gene=IY08_22515	protein=rod shape-determining protein MreD	protein_id=KGT41973.1
gene	4250809	4251660	700969	701820	gene=IY08_22520	protein=rod shape-determining protein MreC	protein_id=KGT41974.1
gene	4251702	4252721	701862	702881	gene=IY08_22525	protein=rod shape-determining protein MreB	protein_id=KGT41975.1
gene	4253298	4254266	703458	704426	gene=IY08_22535	protein=signal transduction protein	protein_id=KGT41976.1
gene	4254282	4256681	704442	706841	gene=IY08_22540	protein=hypothetical protein	protein_id=KGT41977.1
gene	4257124	4260621	707284	710781	gene=IY08_22545	protein=hypothetical protein	protein_id=KGT41978.1
gene	4261074	4261760	711234	711920	gene=IY08_22550	protein=hypothetical protein	protein_id=KGT41979.1
gene	4261992	4262357	712152	712517	gene=IY08_22555	protein=transposase	protein_id=KGT41980.1
gene	4262359	4264272	712519	714432	gene=IY08_22560	protein=transposase	protein_id=KGT41981.1
gene	4264275	4265360	714435	715520	gene=IY08_22565	protein=transposase	protein_id=KGT41982.1
gene	4265474	4266034	715634	716194	gene=IY08_22570	protein=hypothetical protein	protein_id=KGT41983.1
gene	4266081	4266656	716241	716816	gene=IY08_22575	protein=septum formation protein Maf	protein_id=KGT41984.1
gene	4266889	4267839	717049	717999	gene=IY08_22580	protein=stage II sporulation protein B	protein_id=KGT41985.1
gene	4268005	4269306	718165	719466	gene=IY08_22585	protein=folylpolyglutamate synthase	protein_id=KGT41986.1

gene	4269400	4272045	719560	722205	gene=valS	protein=valine--tRNA ligase	protein_id=KGT41987.1
gene	4272568	4273593	722728	723753	gene=IY08_22595	protein=spore coat protein CotS	protein_id=KGT41988.1
gene	4273660	4274640	723820	724800	gene=IY08_22600	protein=stage VI sporulation protein D	protein_id=KGT41989.1
gene	4274750	4276039	724910	726199	gene=IY08_22605	protein=glutamate-1-semialdehyde aminotransferase	protein_id=KGT41990.1
gene	4276039	4277028	726199	727188	gene=IY08_22610	protein=delta-aminolevulinic acid dehydratase	protein_id=KGT41991.1
gene	4277049	4277801	727209	727961	gene=IY08_22615	protein=uroporphyrinogen-III synthase	protein_id=KGT41992.1
gene	4277804	4278733	727964	728893	gene=IY08_22620	protein=porphobilinogen deaminase	protein_id=KGT41993.1
gene	4278749	4279582	728909	729742	gene=IY08_22625	protein=cytochrome C assembly protein	protein_id=KGT41994.1
gene	4279600	4280934	729760	731094	gene=IY08_22630	protein=glutamyl-tRNA reductase	protein_id=KGT41995.1
gene	4281351	4281803	731511	731963	gene=IY08_22635	protein=MarR family transcriptional regulator	protein_id=KGT41996.1
gene	4281806	4282222	731966	732382	gene=IY08_22640	protein=Ohr subfamily peroxiredoxin	protein_id=KGT41997.1
gene	4282256	4282852	732416	733012	gene=engB	protein=GTP-binding protein	protein_id=KGT41998.1
gene	4282849	4285179	733009	735339	gene=IY08_22650	protein=peptidase	protein_id=KGT41999.1
gene	4285361	4287031	735521	737191	gene=IY08_22655	protein=Lon protease	protein_id=KGT42000.1
gene	4287138	4288397	737298	738557	gene=IY08_22660	protein=ATP-dependent protease	protein_id=KGT42001.1
gene	4288662	4289939	738822	740099	gene=tig	protein=trigger factor	protein_id=KGT42002.1
gene	4290249	4291247	740409	741407	gene=IY08_22670	protein=TPR repeat-containing protein	protein_id=KGT42003.1
gene	4291445	4291693	741605	741853	gene=IY08_22675	protein=hypothetical protein	protein_id=KGT42004.1
gene	4291989	4292146	742149	742306	pseudo		
gene	4292212	4292826	742372	742986	gene=IY08_22690	protein=hypothetical protein	protein_id=KGT42005.1
gene	4292921	4293121	743081	743281	gene=IY08_22695	protein=cytoplasmic protein	protein_id=KGT42006.1
gene	4293545	4293621	743705	743781	tRNA		
gene	4293623	4293696	743783	743856	tRNA		
gene	4293805	4294308	743965	744468	gene=IY08_22710	protein=metallophosphatase	protein_id=KGT42007.1
gene	4294322	4294930	744482	745090	gene=IY08_22715	protein=nucleoside-triphosphate diphosphatase	protein_id=KGT42008.1
gene	4294942	4295679	745102	745839	gene=IY08_22720	protein=ribonuclease PH	protein_id=KGT42009.1
gene	4295808	4296857	745968	747017	gene=IY08_22725	protein=sporulation protein	protein_id=KGT42010.1
gene	4297039	4297848	747199	748008	gene=IY08_22730	protein=glutamate racemase	protein_id=KGT42011.1
gene	4298124	4298795	748284	748955	gene=IY08_22735	protein=thiamine biosynthesis protein ThiJ	protein_id=KGT42012.1
gene	4298901	4299125	749061	749285	gene=IY08_22740	protein=LuxR family transcriptional regulator	protein_id=KGT42013.1
gene	4299291	4300586	749451	750746	gene=IY08_22745	protein=xanthine permease	protein_id=KGT42014.1

gene	4300684	4301925	750844	752085	gene=IY08_22755	protein=deaminase	protein_id=KGT42015.1
gene	4302109	4302294	752269	752454	gene=IY08_22760	protein=phage shock protein	protein_id=KGT42016.1
gene	4302356	4302928	752516	753088	gene=IY08_22765	protein=DNA-binding protein	protein_id=KGT42017.1
gene	4303029	4303994	753189	754154	gene=IY08_22770	protein=membrane protein	protein_id=KGT42018.1
gene	4304138	4304803	754298	754963	gene=IY08_22775	protein=porin	protein_id=KGT42019.1
gene	4304864	4305295	755024	755455	gene=IY08_22780	protein=Rrf2 family transcriptional regulator	protein_id=KGT42020.1
gene	4305414	4306640	755574	756800	gene=IY08_22785	protein=sodium export permease	protein_id=KGT42021.1
gene	4306643	4307527	756803	757687	gene=IY08_22790	protein=ABC transporter ATP-binding protein	protein_id=KGT42022.1
gene	4307870	4308697	758030	758857	gene=IY08_22795	protein=5'-nucleotidase	protein_id=KGT42023.1
gene	4308724	4309512	758884	759672	gene=motB	protein=flagellar motor protein MotB	protein_id=KGT42024.1
gene	4309502	4310296	759662	760456	gene=IY08_22805	protein=flagellar motor protein MotA	protein_id=KGT42025.1
gene	4310563	4311342	760723	761502	gene=IY08_22810	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT42026.1
gene	4311379	4311825	761539	761985	gene=IY08_22815	protein=hypothetical protein	protein_id=KGT42027.1
gene	4311918	4312679	762078	762839	gene=sdhB	protein=succinate dehydrogenase	protein_id=KGT42028.1
gene	4312672	4314465	762832	764625	gene=sdhA	protein=succinate dehydrogenase	protein_id=KGT42029.1
gene	4314479	4315105	764639	765265	gene=IY08_22830	protein=succinate dehydrogenase	protein_id=KGT42030.1
gene	4315406	4315855	765566	766015	gene=IY08_22835	protein=hypothetical protein	protein_id=KGT42031.1
gene	4315971	4317755	766131	767915	gene=IY08_22840	protein=excinuclease ABC subunit C	protein_id=KGT42032.1
gene	4317904	4318218	768064	768378	gene=IY08_22845	protein=thioredoxin	protein_id=KGT42033.1
gene	4318430	4319407	768590	769567	gene=IY08_22850	protein=electron transfer flavoprotein subunit alpha	protein_id=KGT42034.1
gene	4319444	4320217	769604	770377	gene=IY08_22855	protein=electron transfer flavoprotein subunit beta	protein_id=KGT42035.1
gene	4320296	4321072	770456	771232	gene=IY08_22860	protein=enoyl-CoA hydratase	protein_id=KGT42036.1
gene	4321084	4321716	771244	771876	gene=IY08_22865	protein=TetR family transcriptional regulator	protein_id=KGT42037.1
gene	4321778	4323463	771938	773623	gene=IY08_22870	protein=long-chain fatty acid--CoA ligase	protein_id=KGT42038.1
gene	4323652	4324815	773812	774975	gene=IY08_22875	protein=hypothetical protein	protein_id=KGT42039.1
gene	4325267	4326241	775427	776401	gene=IY08_22880	protein=ferrichrome ABC transporter substrate-binding	protein_id=KGT42040.1
gene	4326249	4328285	776409	778445	gene=IY08_22885	protein=iron-hydroxamate transporter permease	protein_id=KGT42041.1
gene	4328484	4329383	778644	779543	gene=IY08_22890	protein=hypothetical protein	protein_id=KGT42042.1
gene	4329538	4330041	779698	780201	gene=IY08_22895	protein=hypothetical protein	protein_id=KGT42043.1
gene	4330203	4330535	780363	780695	gene=IY08_22900	protein=Spore coat protein C	protein_id=KGT42044.1
gene	4330597	4331292	780757	781452	gene=IY08_22905	protein=hypothetical protein	protein_id=KGT42045.1

gene	4331317	4332189	781477	782349	gene=IY08_22910	protein=hypothetical protein	protein_id=KGT42046.1
gene	4332224	4332928	782384	783088	gene=IY08_22915	protein=bacitracin ABC transporter permease	protein_id=KGT42047.1
gene	4332963	4333124	783123	783284	gene=IY08_22920	protein=hypothetical protein	protein_id=KGT42048.1
gene	4333117	4334040	783277	784200	gene=IY08_22925	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT42049.1
gene	4334166	4335101	784326	785261	gene=IY08_22930	protein=histidine kinase	protein_id=KGT42050.1
gene	4335103	4335795	785263	785955	gene=IY08_22935	protein=PhoP family transcriptional regulator	protein_id=KGT42051.1
gene	4335964	4336137	786124	786297	gene=IY08_22940	protein=hypothetical protein	protein_id=KGT42052.1
gene	4336138	4336332	786298	786492	gene=IY08_22945	protein=hypothetical protein	protein_id=KGT42053.1
gene	4336371	4337570	786531	787730	gene=IY08_22950	protein=50S rRNA methyltransferase	protein_id=KGT42054.1
gene	4337866	4338189	788026	788349	gene=IY08_22955	protein=heme-degrading monooxygenase IsdG	protein_id=KGT42055.1
gene	4338262	4339026	788422	789186	gene=IY08_22960	protein=sortase	protein_id=KGT42056.1
gene	4339059	4339829	789219	789989	gene=IY08_22965	protein=iron ABC transporter ATP-binding protein	protein_id=KGT42057.1
gene	4339819	4340802	789979	790962	gene=IY08_22970	protein=ABC transporter permease	protein_id=KGT42058.1
gene	4340830	4341711	790990	791871	gene=IY08_22975	protein=heme ABC transporter substrate-binding protein	protein_id=KGT42059.1
gene	4344296	4344754	794456	794914	gene=IY08_22990	protein=cell surface protein	protein_id=KGT42060.1
gene	4344778	4345491	794938	795651	gene=IY08_22995	protein=cell surface protein	protein_id=KGT42061.1
gene	4345982	4347307	796142	797467	gene=IY08_23000	protein=branched-chain amino acid transporter	protein_id=KGT42062.1
gene	4347788	4348477	797948	798637	gene=IY08_23005	protein=pseudouridine synthase	protein_id=KGT42063.1
gene	4348550	4348642	798710	798802	gene=IY08_23010	protein=hypothetical protein	protein_id=KGT42064.1
gene	4348673	4351033	798833	801193	gene=IY08_23015	protein=recombination and DNA strand exchange inhibitor protein	protein_id=KGT42065.1
gene	4351053	4352771	801213	802931	gene=IY08_23020	protein=hypothetical protein	protein_id=KGT42066.1
gene	4352827	4353366	802987	803526	gene=IY08_23025	protein=membrane protein	protein_id=KGT42067.1
gene	4353368	4353637	803528	803797	gene=IY08_23030	protein=cell division protein ZapA	protein_id=KGT42068.1
gene	4353762	4354697	803922	804857	gene=IY08_23035	protein=ribonuclease HIII	protein_id=KGT42069.1
gene	4354814	4355083	804974	805243	gene=IY08_23040	protein=hypothetical protein	protein_id=KGT42070.1
gene	4355080	4355331	805240	805491	gene=IY08_23045	protein=hypothetical protein	protein_id=KGT42071.1
gene	4355373	4355507	805533	805667	gene=IY08_23050	protein=hypothetical protein	protein_id=KGT42072.1
gene	4355608	4356999	805768	807159	gene=IY08_23055	protein=asparaginyl-tRNA synthetase	protein_id=KGT42073.1
gene	4357458	4359878	807618	810038	gene=IY08_23060	protein=phenylalanyl-tRNA synthase subunit beta	protein_id=KGT42074.1
gene	4359897	4360931	810057	811091	gene=pheS	protein=phenylalanine--tRNA ligase	protein_id=KGT42075.1

gene	4361253	4362050	811413	812210	gene=IY08_23070	protein=23S rRNA methyltransferase	protein_id=KGT42076.1
gene	4362133	4362342	812293	812502	gene=IY08_23075	protein=small acid-soluble spore protein SspI	protein_id=KGT42077.1
gene	4362519	4363076	812679	813236	gene=IY08_23080	protein=phosphohydrolase	protein_id=KGT42078.1
gene	4363216	4363929	813376	814089	gene=IY08_23085	protein=CAAX protease	protein_id=KGT42079.1
gene	4364072	4364431	814232	814591	gene=IY08_23090	protein=DNA-binding protein	protein_id=KGT42080.1
gene	4364481	4364837	814641	814997	gene=IY08_23095	protein=ammonia permease	protein_id=KGT42081.1
gene	4364860	4366659	815020	816819	gene=IY08_23100	protein=MFS transporter	protein_id=KGT42082.1
gene	4366672	4367325	816832	817485	gene=IY08_23105	protein=multidrug efflux protein	protein_id=KGT42083.1
gene	4367622	4368239	817782	818399	gene=IY08_23110	protein=TetR family transcriptional regulator	protein_id=KGT42084.1
gene	4368280	4369365	818440	819525	gene=IY08_23115	protein=peptidase M28	protein_id=KGT42085.1
gene	4369436	4369927	819596	820087	gene=IY08_23120	protein=dUTPase	protein_id=KGT42086.1
gene	4370370	4370726	820530	820886	gene=IY08_23125	protein=50S ribosomal protein L20	protein_id=KGT42087.1
gene	4370764	4370964	820924	821124	gene=rpml	protein=50S ribosomal protein L35	protein_id=KGT42088.1
gene	4370986	4371486	821146	821646	gene=IY08_23135	protein=translation initiation factor IF-3	protein_id=KGT42089.1
gene	4371884	4373821	822044	823981	gene=IY08_23140	protein=threonyl-tRNA synthase	protein_id=KGT42090.1
gene	4374129	4375010	824289	825170	gene=IY08_23145	protein=hypothetical protein	protein_id=KGT42091.1
gene	4375245	4375442	825405	825602	gene=IY08_23150	protein=hypothetical protein	protein_id=KGT42092.1
gene	4375474	4376412	825634	826572	gene=IY08_23155	protein=primosomal protein DnaI	protein_id=KGT42093.1
gene	4376446	4377855	826606	828015	gene=IY08_23160	protein=Replication initiation and membrane attachment	protein_id=KGT42094.1
gene	4378008	4378469	828168	828629	gene=nrdR	protein=transcriptional regulator NrdR	protein_id=KGT42095.1
gene	4378753	4379145	828913	829305	gene=IY08_23170	protein=S-adenosylmethionine decarboxylase	protein_id=KGT42096.1
gene	4379522	4380550	829682	830710	gene=IY08_23175	protein=glyceraldehyde-3-phosphate dehydrogenase	protein_id=KGT42097.1
gene	4380660	4381262	830820	831422	gene=IY08_23180	protein=dephospho-CoA kinase	protein_id=KGT42098.1
gene	4381314	4381946	831474	832106	gene=IY08_23185	protein=membrane protein	protein_id=KGT42099.1
gene	4382019	4382849	832179	833009	gene=IY08_23190	protein=5-hydroxymethyluracil DNA glycosylase	protein_id=KGT42100.1
gene	4382862	4385495	833022	835655	gene=IY08_23195	protein=DNA polymerase I	protein_id=KGT42101.1
gene	4385781	4387544	835941	837704	gene=IY08_23200	protein=alkaline phosphatase	protein_id=KGT42102.1
gene	4387537	4388256	837697	838416	gene=IY08_23205	protein=chemotaxis protein CheY	protein_id=KGT42103.1
gene	4388928	4389401	839088	839561	gene=IY08_23220	protein=enoyl-CoA hydratase	protein_id=KGT42104.1
gene	4389617	4390555	839777	840715	gene=IY08_23225	protein=malate dehydrogenase	protein_id=KGT42105.1
gene	4390575	4391867	840735	842027	gene=IY08_23230	protein=isocitrate dehydrogenase	protein_id=KGT42106.1

gene	4392028	4393143	842188	843303	gene=IY08_23235	protein=citrate synthase	protein_id=KGT42107.1
gene	4393256	4393474	843416	843634	gene=IY08_23240	protein=hypothetical protein	protein_id=KGT42108.1
gene	4393564	4394025	843724	844185	gene=IY08_23245	protein=membrane protein	protein_id=KGT42109.1
gene	4394590	4395708	844750	845868	gene=IY08_23250	protein=membrane protein	protein_id=KGT42110.1
gene	4396337	4396726	846497	846886	gene=IY08_23255	protein=exclusion suppressor FxsA	protein_id=KGT42111.1
gene	4396922	4398679	847082	848839	gene=IY08_23260	protein=pyruvate kinase	protein_id=KGT42112.1
gene	4398733	4399692	848893	849852	gene=IY08_23265	protein=6-phosphofructokinase	protein_id=KGT42113.1
gene	4399821	4400795	849981	850955	gene=IY08_23270	protein=acetyl-CoA carboxylase subunit alpha	protein_id=KGT42114.1
gene	4400783	4401652	850943	851812	gene=IY08_23275	protein=acetyl-CoA carboxyl transferase	protein_id=KGT42115.1
gene	4401838	4402482	851998	852642	gene=IY08_23280	protein=GntR family transcriptional regulator	protein_id=KGT42116.1
gene	4402497	4403735	852657	853895	gene=IY08_23285	protein=malate dehydrogenase	protein_id=KGT42117.1
gene	4403839	4407165	853999	857325	gene=dnaE	protein=DNA polymerase III DnaE	protein_id=KGT42118.1
gene	4407283	4407621	857443	857781	gene=IY08_23295	protein=sporulation protein	protein_id=KGT42119.1
gene	4407618	4408121	857778	858281	gene=IY08_23300	protein=molybdenum cofactor biosynthesis protein MoaA	protein_id=KGT42120.1
gene	4408173	4409105	858333	859265	gene=IY08_23305	protein=oligoribonuclease	protein_id=KGT42121.1
gene	4409265	4409570	859425	859730	gene=IY08_23310	protein=membrane protein	protein_id=KGT42122.1
gene	4409578	4409841	859738	860001	gene=IY08_23315	protein=hypothetical protein	protein_id=KGT42123.1
gene	4410057	4411370	860217	861530	gene=IY08_23320	protein=hypothetical protein	protein_id=KGT42124.1
gene	4411615	4411776	861775	861936	gene=IY08_23325	protein=hypothetical protein	protein_id=KGT42125.1
gene	4411818	4412501	861978	862661	gene=IY08_23330	protein=metal-dependent hydrolase	protein_id=KGT42126.1
gene	4412651	4413748	862811	863908	gene=IY08_23335	protein=metallopeptidase	protein_id=KGT42127.1
gene	4413789	4414163	863949	864323	gene=IY08_23340	protein=lipoprotein	protein_id=KGT42128.1
gene	4414238	4414444	864398	864604	gene=IY08_23345	protein=hypothetical protein	protein_id=KGT42129.1
gene	4414983	4415438	865143	865598	gene=IY08_23350	protein=acetyltransferase	protein_id=KGT42130.1
gene	4415512	4415856	865672	866016	gene=IY08_23355	protein=hypothetical protein	protein_id=KGT42131.1
gene	4415859	4416647	866019	866807	gene=IY08_23360	protein=acetyltransferase	protein_id=KGT42132.1
gene	4416644	4416976	866804	867136	gene=IY08_23365	protein=hypothetical protein	protein_id=KGT42133.1
gene	4417021	4417443	867181	867603	gene=IY08_23370	protein=hypothetical protein	protein_id=KGT42134.1
gene	4417583	4418716	867743	868876	gene=IY08_23375	protein=alanine dehydrogenase	protein_id=KGT42135.1
gene	4418931	4419722	869091	869882	gene=fabG	protein=3-ketoacyl-ACP reductase	protein_id=KGT42136.1
gene	4419870	4420328	870030	870488	gene=IY08_23385	protein=universal stress protein UspA	protein_id=KGT42137.1

gene	4420370	4421065	870530	871225	gene=IY08_23390	protein=membrane protein	protein_id=KGT42138.1
gene	4421161	4421340	871321	871500	gene=IY08_23395	protein=ProA domain protein	protein_id=KGT42139.1
gene	4421413	4422801	871573	872961	gene=IY08_23400	protein=argininosuccinate lyase	protein_id=KGT42140.1
gene	4422798	4424003	872958	874163	gene=IY08_23405	protein=argininosuccinate synthase	protein_id=KGT42141.1
gene	4424170	4424487	874330	874647	gene=IY08_23410	protein=radical SAM protein	protein_id=KGT42142.1
gene	4424502	4424711	874662	874871	gene=IY08_23415	protein=hypothetical protein	protein_id=KGT42143.1
gene	4425565	4426227	875725	876387	gene=IY08_23425	protein=membrane protein	protein_id=KGT42144.1
gene	4426259	4427092	876419	877252	gene=IY08_23430	protein=ABC transporter substrate-binding protein	protein_id=KGT42145.1
gene	4427230	4427865	877390	878025	gene=IY08_23435	protein=amino acid permease	protein_id=KGT42146.1
gene	4427935	4428369	878095	878529	gene=IY08_23440	protein=DNA mismatch repair protein MutT	protein_id=KGT42147.1
gene	4428393	4429586	878553	879746	gene=IY08_23445	protein=acetate kinase	protein_id=KGT42148.1
gene	4429886	4430872	880046	881032	gene=IY08_23450	protein=DNA methylase	protein_id=KGT42149.1
gene	4431072	4431572	881232	881732	gene=IY08_23455	protein=peroxidase	protein_id=KGT42150.1
gene	4431707	4432102	881867	882262	gene=IY08_23460	protein=spore protein	protein_id=KGT42151.1
gene	4432115	4432753	882275	882913	gene=IY08_23465	protein=Yvgn And cofactor Nadph	protein_id=KGT42152.1
gene	4432959	4433762	883119	883922	gene=ppnK	protein=inorganic polyphosphate kinase	protein_id=KGT42153.1
gene	4433915	4435483	884075	885643	gene=IY08_23475	protein=amidohydrolase	protein_id=KGT42154.1
gene	4435555	4435986	885715	886146	gene=IY08_23480	protein=3-demethylubiquinone-9 3-methyltransferase	protein_id=KGT42155.1
gene	4436089	4437675	886249	887835	gene=IY08_23485	protein=acyl--CoA ligase	protein_id=KGT42156.1
gene	4437867	4438064	888027	888224	gene=IY08_23490	protein=spore protein	protein_id=KGT42157.1
gene	4438144	4439358	888304	889518	gene=IY08_23495	protein=thiamine biosynthesis protein ThiI	protein_id=KGT42158.1
gene	4439366	4440508	889526	890668	gene=IY08_23500	protein=cysteine desulfurase	protein_id=KGT42159.1
gene	4440677	4442389	890837	892549	gene=IY08_23505	protein=septation ring formation regulator EzrA	protein_id=KGT42160.1
gene	4442600	4443439	892760	893599	gene=IY08_23510	protein=LysR family transcriptional regulator	protein_id=KGT42161.1
gene	4443564	4444508	893724	894668	gene=IY08_23515	protein=transporter	protein_id=KGT42162.1
gene	4444520	4445158	894680	895318	gene=IY08_23520	protein=transcriptional regulator	protein_id=KGT42163.1
gene	4445306	4445785	895466	895945	gene=IY08_23525	protein=GAF domain-containing protein	protein_id=KGT42164.1
gene	4445847	4447022	896007	897182	gene=IY08_23530	protein=methionine gamma-lyase	protein_id=KGT42165.1
gene	4447422	4448024	897582	898184	gene=IY08_23535	protein=30S ribosomal protein S4	protein_id=KGT42166.1
gene	4448322	4448741	898482	898901	gene=IY08_23540	protein=hypothetical protein	protein_id=KGT42167.1
gene	4448980	4449225	899140	899385	gene=IY08_23550	protein=hypothetical protein	protein_id=KGT42168.1

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gene	4449760	4451262	899920	901422	gene=IY08_23560	protein=cytoplasmic protein	protein_id=KGT42170.1
gene	4451268	4451690	901428	901850	gene=IY08_23565	protein=hypothetical protein	protein_id=KGT42171.1
gene	4451781	4452947	901941	903107	gene=IY08_23570	protein=hypothetical protein	protein_id=KGT42172.1
gene	4453008	4453688	903168	903848	gene=IY08_23575	protein=hypothetical protein	protein_id=KGT42173.1
gene	4453853	4454316	904013	904476	pseudo		
gene	4454382	4454510	904542	904670	gene=IY08_23585	protein=transporter	protein_id=KGT42174.1
gene	4454638	4455894	904798	906054	gene=IY08_23590	protein=tyrosine--tRNA ligase	protein_id=KGT42175.1
gene	4456271	4456516	906431	906676	gene=IY08_23595	protein=hypothetical protein	protein_id=KGT42176.1
gene	4456497	4457042	906657	907202	gene=IY08_23600	protein=RNA polymerase sigma70 factor	protein_id=KGT42177.1
gene	4457023	4457478	907183	907638	gene=IY08_23605	protein=hypothetical protein	protein_id=KGT42178.1
gene	4457545	4458102	907705	908262	gene=IY08_23610	protein=acetyltransferase	protein_id=KGT42179.1
gene	4458190	4459908	908350	910068	gene=IY08_23615	protein=acetyl-CoA synthetase	protein_id=KGT42180.1
gene	4460085	4460717	910245	910877	gene=IY08_23620	protein=acetoin dehydrogenase	protein_id=KGT42181.1
gene	4460735	4461379	910895	911539	gene=IY08_23625	protein=acetoin utilization protein AcuB	protein_id=KGT42182.1
gene	4461349	4462542	911509	912702	gene=IY08_23630	protein=histone deacetylase	protein_id=KGT42183.1
gene	4462779	4463645	912939	913805	gene=IY08_23635	protein=proline iminopeptidase	protein_id=KGT42184.1
gene	4463684	4463971	913844	914131	gene=IY08_23640	protein=hypothetical protein	protein_id=KGT42185.1
gene	4464097	4464786	914257	914946	gene=IY08_23645	protein=transcriptional regulator	protein_id=KGT42186.1
gene	4464788	4466242	914948	916402	gene=IY08_23650	protein=histidine kinase	protein_id=KGT42187.1
gene	4466392	4467072	916552	917232	gene=IY08_23655	protein=ankyrin	protein_id=KGT42188.1
gene	4467152	4468078	917312	918238	gene=IY08_23660	protein=virulence factor MviM	protein_id=KGT42189.1
gene	4468207	4468608	918367	918768	gene=IY08_23665	protein=mechanosensitive ion channel protein MscL	protein_id=KGT42190.1
gene	4468657	4468929	918817	919089	gene=IY08_23670	protein=transcriptional regulator	protein_id=KGT42191.1
gene	4469372	4470370	919532	920530	gene=IY08_23680	protein=catabolite control protein A	protein_id=KGT42192.1
gene	4470418	4470594	920578	920754	gene=IY08_23685	protein=hypothetical protein	protein_id=KGT42193.1
gene	4470863	4471936	921023	922096	gene=IY08_23690	protein=chorismate mutase	protein_id=KGT42194.1
gene	4472103	4473125	922263	923285	gene=IY08_23695	protein=sex pheromone	protein_id=KGT42195.1
gene	4473243	4473569	923403	923729	gene=IY08_23700	protein=hypothetical protein	protein_id=KGT42196.1
gene	4473569	4474126	923729	924286	gene=IY08_23705	protein=general stress protein	protein_id=KGT42197.1
gene	4474269	4475384	924429	925544	gene=IY08_23710	protein=aminopeptidase	protein_id=KGT42198.1

gene	4475419	4475823	925579	925983	gene=IY08_23715	protein=hypothetical protein	protein_id=KGT42199.1
gene	4475900	4476391	926060	926551	gene=IY08_23720	protein=GNAT family acetyltransferase	protein_id=KGT42200.1
gene	4476388	4476936	926548	927096	gene=IY08_23725	protein=alanine acetyltransferase	protein_id=KGT42201.1
gene	4477119	4478429	927279	928589	gene=IY08_23730	protein=UDP-N-acetylmuramate--alanine ligase	protein_id=KGT42202.1
gene	4478681	4479799	928841	929959	gene=IY08_23735	protein=nicotinate phosphoribosyltransferase	protein_id=KGT42203.1
gene	4479861	4483738	930021	933898	pseudo		
gene	4483894	4484847	934054	935007	gene=IY08_23745	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT42204.1
gene	4484888	4485232	935048	935392	gene=IY08_23750	protein=thiamine transporter	protein_id=KGT42205.1
gene	4485458	4486072	935618	936232	gene=IY08_23755	protein=tRNA-binding protein	protein_id=KGT42206.1
gene	4486069	4486881	936229	937041	gene=IY08_23760	protein=hypothetical protein	protein_id=KGT42207.1
gene	4486961	4487275	937121	937435	gene=IY08_23765	protein=thioredoxin	protein_id=KGT42208.1
gene	4487358	4487867	937518	938027	gene=yjjX	protein=NTPase	protein_id=KGT42209.1
gene	4488149	4489222	938309	939382	gene=IY08_23775	protein=peptidase M28	protein_id=KGT42210.1
gene	4489371	4489682	939531	939842	gene=IY08_23780	protein=peptidase M4	protein_id=KGT42211.1
gene	4489981	4490835	940141	940995	gene=IY08_23785	protein=hypothetical protein	protein_id=KGT42212.1
gene	4490904	4491557	941064	941717	gene=IY08_23790	protein=tRNA (guanine-N7)-methyltransferase	protein_id=KGT42213.1
gene	4491787	4492065	941947	942225	gene=IY08_23795	protein=hypothetical protein	protein_id=KGT42214.1
gene	4492069	4492866	942229	943026	gene=IY08_23800	protein=phosphotransferase	protein_id=KGT42215.1
gene	4493094	4495235	943254	945395	gene=IY08_23805	protein=pullulanase	protein_id=KGT42216.1
gene	4495350	4495440	945510	945600	pseudo		
gene	4495447	4495992	945607	946152	gene=IY08_23815	protein=2'-5' RNA ligase	protein_id=KGT42217.1
gene	4496096	4497502	946256	947662	gene=IY08_23820	protein=dipeptidase PepV	protein_id=KGT42218.1
gene	4497860	4498081	948020	948241	gene=IY08_23825	protein=hypothetical protein	protein_id=KGT42219.1
gene	4498161	4498889	948321	949049	gene=IY08_23830	protein=pseudouridine synthase	protein_id=KGT42220.1
gene	4498931	4500583	949091	950743	gene=IY08_23835	protein=cell division protein	protein_id=KGT42221.1
gene	4500878	4502149	951038	952309	gene=IY08_23840	protein=hypothetical protein	protein_id=KGT42222.1
gene	4502434	4503873	952594	954033	gene=IY08_23845	protein=DSBA oxidoreductase	protein_id=KGT42223.1
gene	4503903	4504226	954063	954386	gene=IY08_23850	protein=ArsR family transcriptional regulator	protein_id=KGT42224.1
gene	4504227	4504658	954387	954818	gene=IY08_23855	protein=hypothetical protein	protein_id=KGT42225.1
gene	4505082	4505309	955242	955469	gene=IY08_23860	protein=hypothetical protein	protein_id=KGT42226.1
gene	4505344	4505526	955504	955686	gene=IY08_23865	protein=Sporulation protein cse60	protein_id=KGT42227.1

gene	4505528	4505764	955688	955924	gene=IY08_23870	protein=hypothetical protein	protein_id=KGT42228.1
gene	4506109	4506603	956269	956763	gene=IY08_23875	protein=transcription factor YdeB	protein_id=KGT42229.1
gene	4506675	4507460	956835	957620	gene=IY08_23880	protein=sugar dehydrogenase	protein_id=KGT42230.1
gene	4507474	4508331	957634	958491	gene=IY08_23885	protein=glucose transporter GlcU	protein_id=KGT42231.1
gene	4508368	4508787	958528	958947	gene=IY08_23890	protein=hypothetical protein	protein_id=KGT42232.1
gene	4508881	4509114	959041	959274	gene=IY08_23895	protein=molybdenum cofactor biosynthesis protein MoaD	protein_id=KGT42233.1
gene	4509117	4509581	959277	959741	gene=IY08_23900	protein=molybdopterin (MPT) converting factor, subunit 2	protein_id=KGT42234.1
gene	4509578	4510093	959738	960253	gene=IY08_23905	protein=molybdopterin-guanine dinucleotide biosynthesis protein B	protein_id=KGT42235.1
gene	4510063	4511352	960223	961512	gene=IY08_23910	protein=molybdopterin molybdenumtransferase	protein_id=KGT42236.1
gene	4511436	4511921	961596	962081	gene=IY08_23915	protein=molybdenum cofactor biosynthesis protein C	protein_id=KGT42237.1
gene	4511959	4512972	962119	963132	gene=IY08_23920	protein=thiamine biosynthesis protein MoeB	protein_id=KGT42238.1
gene	4512989	4514002	963149	964162	gene=IY08_23925	protein=molybdenum cofactor biosynthesis protein A	protein_id=KGT42239.1
gene	4514203	4518132	964363	968292	gene=IY08_23930	protein=BclA	protein_id=KGT42240.1
gene	4518249	4518572	968409	968732	gene=IY08_23935	protein=hypothetical protein	protein_id=KGT42241.1
gene	4518593	4518817	968753	968977	gene=IY08_23940	protein=hypothetical protein	protein_id=KGT42242.1
gene	4518896	4519201	969056	969361	gene=IY08_23945	protein=sulfurtransferase	protein_id=KGT42243.1
gene	4519399	4519581	969559	969741	gene=IY08_23950	protein=4-hydroxy-2-ketovalerate aldolase	protein_id=KGT42244.1
gene	4519631	4520755	969791	970915	gene=IY08_23955	protein=homoserine acetyltransferase	protein_id=KGT42245.1
gene	4521571	4522938	971731	973098	gene=IY08_23960	protein=spore germination protein GerA	protein_id=KGT42246.1
gene	4522955	4524049	973115	974209	gene=IY08_23965	protein=spore germination protein GerH	protein_id=KGT42247.1
gene	4524025	4525104	974185	975264	gene=IY08_23970	protein=spore germination protein GerH	protein_id=KGT42248.1
gene	4525195	4525380	975355	975540	gene=IY08_23975	protein=hypothetical protein	protein_id=KGT42249.1
gene	4525478	4525900	975638	976060	gene=IY08_23980	protein=Cof	protein_id=KGT42250.1
gene	4525945	4526889	976105	977049	gene=IY08_23985	protein=VrrB	protein_id=KGT42251.1
gene	4527040	4527468	977200	977628	gene=IY08_23990	protein=acetyltransferase	protein_id=KGT42252.1
gene	4527496	4529904	977656	980064	gene=IY08_23995	protein=leucyl-tRNA synthetase	protein_id=KGT42253.1
gene	4530377	4531570	980537	981730	gene=IY08_24000	protein=multidrug MFS transporter	protein_id=KGT42254.1
gene	4531870	4533093	982030	983253	gene=IY08_24005	protein=potassium transporter	protein_id=KGT42255.1
gene	4533097	4533594	983257	983754	gene=IY08_24010	protein=potassium transporter	protein_id=KGT42256.1
gene	4533628	4534194	983788	984354	gene=IY08_24015	protein=integrase	protein_id=KGT42257.1

gene	4534542	4536401	984702	986561	gene=IY08_24020	protein=ABC transporter permease	protein_id=KGT42258.1
gene	4536418	4537179	986578	987339	gene=IY08_24025	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT42259.1
gene	4537535	4538557	987695	988717	gene=IY08_24030	protein=membrane protein	protein_id=KGT42260.1
gene	4538694	4538843	988854	989003	gene=IY08_24035	protein=glycogen biosynthesis protein GlgD	protein_id=KGT42261.1
gene	4538859	4539122	989019	989282	gene=IY08_24040	protein=hypothetical protein	protein_id=KGT42262.1
gene	4539234	4540193	989394	990353	gene=IY08_24045	protein=hypothetical protein	protein_id=KGT42263.1
gene	4540190	4540762	990350	990922	gene=IY08_24050	protein=rRNA methyltransferase	protein_id=KGT42264.1
gene	4541045	4541878	991205	992038	gene=IY08_24055	protein=ABC transporter ATP-binding protein	protein_id=KGT42265.1
gene	4541897	4542577	992057	992737	gene=IY08_24060	protein=ABC transporter permease	protein_id=KGT42266.1
gene	4542602	4543276	992762	993436	gene=IY08_24065	protein=amino acid racemase	protein_id=KGT42267.1
gene	4543432	4544733	993592	994893	gene=IY08_24070	protein=sulfite reductase subunit alpha	protein_id=KGT42268.1
gene	4544771	4545835	994931	995995	gene=IY08_24075	protein=tetraprenyl-beta-curcumene synthase	protein_id=KGT42269.1
gene	4545876	4546679	996036	996839	gene=IY08_24080	protein=phospholipase	protein_id=KGT42270.1
gene	4546754	4547266	996914	997426	gene=IY08_24085	protein=transferase	protein_id=KGT42271.1
gene	4547410	4547943	997570	998103	gene=IY08_24090	protein=phosphoesterase	protein_id=KGT42272.1
gene	4547956	4549098	998116	999258	gene=IY08_24095	protein=glycosyl transferase	protein_id=KGT42273.1
gene	4549380	4549982	999540	1000142	gene=IY08_24100	protein=molybdopterin-guanine dinucleotide biosynthesis protein A	protein_id=KGT42274.1
gene	4549979	4550488	1000139	1000648	gene=IY08_24105	protein=molybdenum cofactor biosynthesis protein B	protein_id=KGT42275.1
gene	4550725	4550904	1000885	1001064	gene=IY08_24110	protein=hypothetical protein	protein_id=KGT42276.1
gene	4550911	4551090	1001071	1001250	gene=IY08_24115	protein=hypothetical protein	protein_id=KGT42277.1
gene	4551111	4551635	1001271	1001795	gene=IY08_24120	protein=acetyltransferase	protein_id=KGT42278.1
gene	4551677	4552876	1001837	1003036	gene=IY08_24125	protein=S-adenosylmethionine synthetase	protein_id=KGT42279.1
gene	4553396	4554982	1003556	1005142	gene=IY08_24130	protein=phosphoenolpyruvate carboxykinase	protein_id=KGT42280.1
gene	4555317	4555700	1005477	1005860	gene=IY08_24135	protein=ATP synthase subunit I	protein_id=KGT42281.1
gene	4555980	4556201	1006140	1006361	gene=IY08_24140	protein=hypothetical protein	protein_id=KGT42282.1
gene	4556230	4557135	1006390	1007295	gene=IY08_24145	protein=membrane protein	protein_id=KGT42283.1
gene	4557433	4557756	1007593	1007916	gene=IY08_24150	protein=heme biosynthesis protein HemY	protein_id=KGT42284.1
gene	4557922	4558098	1008082	1008258	gene=IY08_24155	protein=hypothetical protein	protein_id=KGT42285.1
gene	4558131	4559051	1008291	1009211	gene=IY08_24160	protein=hypothetical protein	protein_id=KGT42286.1
gene	4559474	4560694	1009634	1010854	gene=IY08_24165	protein=histidine kinase	protein_id=KGT42287.1

gene	4560691	4561944	1010851	1012104	gene=IY08_24170	protein=histidine kinase	protein_id=KGT42288.1
gene	4562195	4563004	1012355	1013164	gene=IY08_24175	protein=alpha/beta hydrolase	protein_id=KGT42289.1
gene	4563213	4565282	1013373	1015442	gene=IY08_24180	protein=phosphoglycerol transferase	protein_id=KGT42290.1
gene	4565663	4565893	1015823	1016053	gene=IY08_24185	protein=Heme/copper-type cytochrome/quinol oxidase	protein_id=KGT42291.1
gene	4565904	4566200	1016064	1016360	gene=IY08_24190	protein=hypothetical protein	protein_id=KGT42292.1
gene	4566321	4567328	1016481	1017488	gene=IY08_24195	protein=hypothetical protein	protein_id=KGT42293.1
gene	4567340	4568104	1017500	1018264	gene=IY08_24200	protein=spermidine/putrescine ABC transporter ATP-binding protein	protein_id=KGT42294.1
gene	4568097	4568903	1018257	1019063	gene=IY08_24205	protein=ABC transporter permease	protein_id=KGT42295.1
gene	4568938	4569165	1019098	1019325	gene=IY08_24210	protein=hypothetical protein	protein_id=KGT42296.1
gene	4569393	4570505	1019553	1020665	gene=IY08_24215	protein=hypothetical protein	protein_id=KGT42297.1
gene	4570598	4571269	1020758	1021429	gene=IY08_24220	protein=HAD family hydrolase	protein_id=KGT42298.1
gene	4571475	4572011	1021635	1022171	gene=IY08_24225	protein=diaminopimelate epimerase	protein_id=KGT42299.1
gene	4572124	4572603	1022284	1022763	gene=IY08_24230	protein=7,8-dihydro-8-oxoguanine-triphosphatase	protein_id=KGT42300.1
gene	4572688	4573005	1022848	1023165	gene=IY08_24235	protein=hydrolase	protein_id=KGT42301.1
gene	4573089	4573238	1023249	1023398	gene=IY08_24240	protein=ABC transporter ATP-binding protein	protein_id=KGT42302.1
gene	4573404	4573631	1023564	1023791	gene=IY08_24250	protein=hypothetical protein	protein_id=KGT42303.1
gene	4573657	4573908	1023817	1024068	gene=IY08_24255	protein=hypothetical protein	protein_id=KGT42304.1
gene	4573984	4574226	1024144	1024386	gene=IY08_24260	protein=hypothetical protein	protein_id=KGT42305.1
gene	4574259	4574732	1024419	1024892	gene=IY08_24265	protein=S-ribosylhomocysteinase	protein_id=KGT42306.1
gene	4574861	4575097	1025021	1025257	gene=IY08_24270	protein=hypothetical protein	protein_id=KGT42307.1
gene	4575094	4575657	1025254	1025817	gene=IY08_24275	protein=carbonic anhydrase	protein_id=KGT42308.1
gene	4575882	4577231	1026042	1027391	gene=IY08_24280	protein=cytochrome D ubiquinol oxidase subunit I	protein_id=KGT42309.1
gene	4577221	4578249	1027381	1028409	gene=IY08_24285	protein=cytochrome C oxidase assembly protein	protein_id=KGT42310.1
gene	4578416	4578649	1028576	1028809	gene=IY08_24290	protein=spore germination protein GerPF	protein_id=KGT42311.1
gene	4579324	4580358	1029484	1030518	gene=IY08_24295	protein=membrane protein	protein_id=KGT42312.1
gene	4580546	4581418	1030706	1031578	gene=IY08_24300	protein=membrane protein	protein_id=KGT42313.1
gene	4581635	4582453	1031795	1032613	gene=IY08_24305	protein=lipoprotein	protein_id=KGT42314.1
gene	4582466	4582972	1032626	1033132	gene=IY08_24310	protein=hypothetical protein	protein_id=KGT42315.1
gene	4582994	4583398	1033154	1033558	gene=IY08_24315	protein=cell surface protein	protein_id=KGT42316.1
gene	4583478	4584143	1033638	1034303	gene=IY08_24320	protein=phage-shock protein	protein_id=KGT42317.1

gene	4584547	4585125	1034707	1035285	gene=IY08_24325	protein=hypothetical protein	protein_id=KGT42318.1
gene	4585162	4585332	1035322	1035492	gene=IY08_24330	protein=hydrolase	protein_id=KGT42319.1
gene	4585346	4587334	1035506	1037494	gene=IY08_24335	protein=ferrous iron transporter B	protein_id=KGT42320.1
gene	4587331	4587558	1037491	1037718	gene=IY08_24340	protein=iron transporter FeoA	protein_id=KGT42321.1
gene	4587941	4588612	1038101	1038772	gene=IY08_24345	protein=proton-coupled thiamine transporter YuaJ	protein_id=KGT42322.1
gene	4588821	4590671	1038981	1040831	gene=IY08_24350	protein=histidine kinase	protein_id=KGT42323.1
gene	4590668	4591357	1040828	1041517	gene=IY08_24355	protein=PhoB family transcriptional regulator	protein_id=KGT42324.1
gene	4591397	4592017	1041557	1042177	gene=IY08_24360	protein=peptidase	protein_id=KGT42325.1
gene	4592107	4592598	1042267	1042758	gene=IY08_24365	protein=cell surface protein	protein_id=KGT42326.1
gene	4592778	4593110	1042938	1043270	gene=IY08_24370	protein=hypothetical protein	protein_id=KGT42327.1
gene	4593294	4593509	1043454	1043669	gene=IY08_24375	protein=membrane protein	protein_id=KGT42328.1
gene	4593671	4594198	1043831	1044358	gene=IY08_24380	protein=hypoxanthine phosphoribosyltransferase	protein_id=KGT42329.1
gene	4594374	4595276	1044534	1045436	gene=IY08_24385	protein=bis(5'-nucleosyl)-tetrphosphatase	protein_id=KGT42330.1
gene	4595317	4595826	1045477	1045986	gene=IY08_24390	protein=hypothetical protein	protein_id=KGT42331.1
gene	4595851	4596522	1046011	1046682	gene=IY08_24395	protein=hypothetical protein	protein_id=KGT42332.1
gene	4596712	4597683	1046872	1047843	gene=IY08_24400	protein=ATPase	protein_id=KGT42333.1
gene	4597724	4598482	1047884	1048642	gene=IY08_24405	protein=lipoyl synthase	protein_id=KGT42334.1
gene	4598467	4598736	1048627	1048896	gene=IY08_24410	protein=hypothetical protein	protein_id=KGT42335.1
gene	4599031	4599210	1049191	1049370	gene=IY08_24415	protein=hypothetical protein	protein_id=KGT42336.1
gene	4599320	4599919	1049480	1050079	gene=IY08_24420	protein=alkaline phosphatase	protein_id=KGT42337.1
gene	4599919	4600497	1050079	1050657	gene=IY08_24425	protein=SAM-dependent methyltransferase	protein_id=KGT42338.1
gene	4600640	4602589	1050800	1052749	gene=IY08_24430	protein=ABC transporter permease	protein_id=KGT42339.1
gene	4602576	4603346	1052736	1053506	gene=IY08_24435	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT42340.1
gene	4603653	4604525	1053813	1054685	gene=IY08_24440	protein=AraC family transcriptional regulator	protein_id=KGT42341.1
gene	4604576	4605214	1054736	1055374	gene=IY08_24445	protein=hypothetical protein	protein_id=KGT42342.1
gene	4605238	4605873	1055398	1056033	gene=IY08_24450	protein=membrane protein SdpI	protein_id=KGT42343.1
gene	4605870	4606142	1056030	1056302	gene=IY08_24455	protein=ArsR family transcriptional regulator	protein_id=KGT42344.1
gene	4606352	4607047	1056512	1057207	gene=IY08_24460	protein=transcriptional regulator	protein_id=KGT42345.1
gene	4607050	4608072	1057210	1058232	gene=IY08_24465	protein=membrane protein	protein_id=KGT42346.1
gene	4608167	4610146	1058327	1060306	gene=IY08_24470	protein=ABC transporter permease	protein_id=KGT42347.1
gene	4610215	4612170	1060375	1062330	gene=IY08_24475	protein=ABC transporter permease	protein_id=KGT42348.1

gene	4612191	4612943	1062351	1063103	gene=IY08_24480	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT42349.1
gene	4612940	4614913	1063100	1065073	gene=IY08_24485	protein=ABC transporter permease	protein_id=KGT42350.1
gene	4614967	4615158	1065127	1065318	gene=IY08_24490	protein=hypothetical protein	protein_id=KGT42351.1
gene	4615327	4616652	1065487	1066812	gene=IY08_24495	protein=hypothetical protein	protein_id=KGT42352.1
gene	4616768	4617493	1066928	1067653	gene=IY08_24500	protein=GntR family transcriptional regulator	protein_id=KGT42353.1
gene	4617493	4618509	1067653	1068669	gene=IY08_24505	protein=2-dehydro-3-deoxygluconokinase	protein_id=KGT42354.1
gene	4618502	4619257	1068662	1069417	gene=IY08_24510	protein=2-dehydro-3-deoxyphosphooctonate aldolase	protein_id=KGT42355.1
gene	4619259	4620362	1069419	1070522	gene=IY08_24515	protein=L-seryl-tRNA selenium transferase	protein_id=KGT42356.1
gene	4620340	4621440	1070500	1071600	gene=IY08_24520	protein=amidohydrolase	protein_id=KGT42357.1
gene	4621798	4622658	1071958	1072818	gene=IY08_24525	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT42358.1
gene	4622741	4623847	1072901	1074007	gene=IY08_24530	protein=histidine kinase	protein_id=KGT42359.1
gene	4623840	4624538	1074000	1074698	gene=IY08_24535	protein=DeoR family transcriptional regulator	protein_id=KGT42360.1
gene	4624794	4625900	1074954	1076060	gene=IY08_24540	protein=N-acylamino acid racemase	protein_id=KGT42361.1
gene	4626056	4627212	1076216	1077372	pseudo		
gene	4627209	4627661	1077369	1077821	gene=IY08_24550	protein=DNA-binding protein	protein_id=KGT42362.1
gene	4627821	4629305	1077981	1079465	gene=IY08_24560	protein=O-succinylbenzoic acid--CoA ligase	protein_id=KGT42363.1
gene	4629623	4630441	1079783	1080601	gene=IY08_24565	protein=dihydroxynaphthoic acid synthetase	protein_id=KGT42364.1
gene	4630511	4631323	1080671	1081483	gene=IY08_24570	protein=esterase	protein_id=KGT42365.1
gene	4631320	4633074	1081480	1083234	gene=IY08_24575	protein=2-succinyl-5-enolpyruvyl-6-hydroxy-3-cyclohexene-1-carboxylate synthase	protein_id=KGT42366.1
gene	4633071	4634465	1083231	1084625	gene=IY08_24580	protein=isochorismate synthase	protein_id=KGT42367.1
gene	4634660	4635613	1084820	1085773	gene=IY08_24590	protein=1,4-dihydroxy-2-naphthoate octaprenyltransferase	protein_id=KGT42368.1
gene	4635723	4636454	1085883	1086614	gene=IY08_24595	protein=hypothetical protein	protein_id=KGT42369.1
gene	4636499	4636699	1086659	1086859	gene=IY08_24600	protein=cold-shock protein	protein_id=KGT42370.1
gene	4637091	4637873	1087251	1088033	gene=IY08_24605	protein=hypothetical protein	protein_id=KGT42371.1
gene	4638088	4638237	1088248	1088397	gene=IY08_24610	protein=alcohol dehydrogenase	protein_id=KGT42372.1
gene	4638576	4639298	1088736	1089458	gene=IY08_24615	protein=lipase	protein_id=KGT42373.1
gene	4639375	4639509	1089535	1089669	gene=IY08_24620	protein=hypothetical protein	protein_id=KGT42374.1
gene	4639613	4642021	1089773	1092181	gene=IY08_24625	protein=maltodextrin phosphorylase	protein_id=KGT42375.1
gene	4642040	4643470	1092200	1093630	gene=IY08_24630	protein=glycogen synthase	protein_id=KGT42376.1
gene	4643583	4644617	1093743	1094777	gene=IY08_24635	protein=glycogen biosynthesis protein glgD	protein_id=KGT42377.1

gene	4644636	4645766	1094796	1095926	gene=glgC	protein=glucose-1-phosphate adenylyltransferase	protein_id=KGT42378.1
gene	4645714	4647651	1095874	1097811	gene=IY08_24645	protein=glycogen branching protein	protein_id=KGT42379.1
gene	4648240	4648857	1098400	1099017	gene=IY08_24650	protein=hypothetical protein	protein_id=KGT42380.1
gene	4649079	4650023	1099239	1100183	gene=IY08_24655	protein=lactate dehydrogenase	protein_id=KGT42381.1
gene	4650699	4650770	1100859	1100930	tRNA		
gene	4650776	4650866	1100936	1101026	tRNA		
gene	4650874	4650948	1101034	1101108	tRNA		
scaffold18							
gene	4651396	4652076	436	1116	gene=IY08_24680	protein=methyltransferase	protein_id=KGT41359
gene	4652169	4653164	1209	2204	gene=IY08_24685	protein=potassium channel protein	protein_id=KGT41360
gene	4653151	4653564	2191	2604	gene=IY08_24690	protein=hypothetical protein	protein_id=KGT41361
gene	4653672	4655024	2712	4064	gene=IY08_24695	protein=glucose-6-phosphate isomerase	protein_id=KGT41362
gene	4654993	4655199	4033	4239	gene=IY08_24700	protein=hypothetical protein	protein_id=KGT41363
gene	4655299	4655532	4339	4572	gene=IY08_24705	protein=membrane protein	protein_id=KGT41364
gene	4655642	4655986	4682	5026	gene=IY08_24710	protein=general stress protein	protein_id=KGT41365
gene	4656240	4657430	5280	6470	gene=IY08_24715	protein=aromatic amino acid aminotransferase	protein_id=KGT41366
gene	4657427	4657924	6467	6964	gene=IY08_24720	protein=AsnC family transcriptional regulator	protein_id=KGT41367
gene	4658043	4659035	7083	8075	gene=IY08_24725	protein=bifunctional glyoxylate/hydroxypyruvate reductase	protein_id=KGT41368
gene	4659145	4659984	8185	9024	gene=IY08_24730	protein=hydrolase	protein_id=KGT41369
gene	4660105	4660356	9145	9396	gene=IY08_24735	protein=hypothetical protein	protein_id=KGT41370
gene	4660474	4661625	9514	10665	gene=IY08_24740	protein=cystathionine beta-lyase	protein_id=KGT41371
gene	4661803	4662342	10843	11382	gene=IY08_24745	protein=superoxide dismutase	protein_id=KGT41372
gene	4662411	4662587	11451	11627	gene=IY08_24750	protein=hypothetical protein	protein_id=KGT41373
gene	4662752	4663135	11792	12175	gene=IY08_24755	protein=kinase	protein_id=KGT41374
gene	4663176	4663799	12216	12839	gene=IY08_24760	protein=sporulation inhibitor KapD	protein_id=KGT41375
gene	4664090	4665415	13130	14455	gene=IY08_24765	protein=membrane protein	protein_id=KGT41376
gene	4665484	4665951	14524	14991	gene=IY08_24770	protein=hypothetical protein	protein_id=KGT41377
gene	4666069	4666782	15109	15822	gene=IY08_24775	protein=DNA alkylation repair protein	protein_id=KGT41378
gene	4667129	4668505	16169	17545	gene=IY08_24780	protein=glycyl-tRNA ligase	protein_id=KGT41379
gene	4668545	4668928	17585	17968	gene=IY08_24785	protein=esterase	protein_id=KGT41380
gene	4669024	4669767	18064	18807	gene=IY08_24790	protein=ferritin	protein_id=KGT41381

gene	4669818	4670411	18858	19451	gene=IY08_24795	protein=biotin biosynthesis protein BioC	protein_id=KGT41382
gene	4670456	4671343	19496	20383	gene=IY08_24800	protein=UTP--glucose-1-phosphate uridylyltransferase	protein_id=KGT41383
gene	4671451	4673175	20491	22215	gene=IY08_24805	protein=phosphoglucomutase	protein_id=KGT41384
gene	4673319	4673924	22359	22964	gene=IY08_24810	protein=hypothetical protein	protein_id=KGT41385
gene	4674337	4675578	23377	24618	gene=IY08_24815	protein=leucyl aminopeptidase	protein_id=KGT41386
gene	4676130	4676474	25170	25514	gene=IY08_24825	protein=transporter	protein_id=KGT41387
scaffold19							
gene	4676701	4676921	1	221	gene=IY08_24830	protein=phosphoribose diphosphate:decaprenyl-phosphate phosphoribosyltransferase	protein_id=KGT41285.1
gene	4677117	4677737	417	1037	gene=IY08_24835	protein=hypothetical protein	protein_id=KGT41286.1
gene	4677824	4678141	1124	1441	gene=IY08_24840	protein=membrane protein	protein_id=KGT41287.1
gene	4678138	4678644	1438	1944	gene=IY08_24845	protein=NUDIX hydrolase	protein_id=KGT41288.1
gene	4678768	4679976	2068	3276	gene=IY08_24850	protein=NADH dehydrogenase	protein_id=KGT41289.1
gene	4680438	4681427	3738	4727	gene=IY08_24855	protein=ferredoxin-NADP reductase	protein_id=KGT41290.1
gene	4681539	4690445	4839	13745	gene=IY08_24860	protein=cell surface protein	protein_id=KGT41291.1
gene	4690916	4691395	14216	14695	gene=IY08_24865	protein=DNA-binding protein	protein_id=KGT41292.1
gene	4691561	4692808	14861	16108	gene=IY08_24870	protein=macrolide transporter	protein_id=KGT41293.1
gene	4692826	4693707	16126	17007	gene=IY08_24875	protein=decarboxylase	protein_id=KGT41294.1
gene	4693787	4694248	17087	17548	gene=IY08_24880	protein=hypothetical protein	protein_id=KGT41295.1
gene	4694278	4694631	17578	17931	gene=IY08_24885	protein=membrane protein	protein_id=KGT41296.1
gene	4695518	4695871	18818	19171	gene=IY08_24895	protein=hypothetical protein	protein_id=KGT41297.1
gene	4695913	4696779	19213	20079	gene=IY08_24900	protein=diaminopimelate epimerase	protein_id=KGT41298.1
gene	4697048	4697287	20348	20587	gene=IY08_24905	protein=hypothetical protein	protein_id=KGT41299.1
gene	4697634	4698704	20934	22004	gene=IY08_24910	protein=NADH dehydrogenase	protein_id=KGT41300.1
gene	4698938	4699111	22238	22411	gene=IY08_24915	protein=stage II sporulation protein E	protein_id=KGT41301.1
gene	4699167	4699826	22467	23126	gene=IY08_24920	protein=ABC transporter ATP-binding protein	protein_id=KGT41302.1
gene	4699810	4700607	23110	23907	gene=IY08_24925	protein=membrane protein	protein_id=KGT41303.1
gene	4700807	4701148	24107	24448	gene=IY08_24930	protein=alkylphosphonate utilization protein	protein_id=KGT41304.1
gene	4701308	4701589	24608	24889	gene=IY08_24935	protein=hypothetical protein	protein_id=KGT41305.1
gene	4701659	4702447	24959	25747	gene=IY08_24940	protein=hypothetical protein	protein_id=KGT41306.1
gene	4702824	4703156	26124	26456	gene=IY08_24945	protein=hypothetical protein	protein_id=KGT41307.1

gene	4703207	4703875	26507	27175	gene=IY08_24950	protein=hypothetical protein	protein_id=KGT41308.1
gene	4703999	4704793	27299	28093	gene=IY08_24955	protein=nucleotidyltransferase	protein_id=KGT41309.1
gene	4704846	4705154	28146	28454	gene=IY08_24960	protein=disulfide oxidoreductase	protein_id=KGT41310.1
gene	4705350	4705586	28650	28886	gene=IY08_24965	protein=nitrogen fixation protein NifU	protein_id=KGT41311.1
gene	4706017	4706232	29317	29532	gene=IY08_24970	protein=carbonic anhydrase	protein_id=KGT41312.1
gene	4706292	4707293	29592	30593	gene=IY08_24975	protein=spore coat protein CotS	protein_id=KGT41313.1
gene	4707414	4707905	30714	31205	gene=IY08_24980	protein=hypothetical protein	protein_id=KGT41314.1
gene	4707929	4708408	31229	31708	gene=IY08_24985	protein=acetyltransferase	protein_id=KGT41315.1
gene	4708571	4709674	31871	32974	gene=IY08_24990	protein=citrate lyase subunit beta	protein_id=KGT41316.1
gene	4709619	4710965	32919	34265	gene=IY08_24995	protein=adenine/guanine phosphoribosyltransferase	protein_id=KGT41317.1
gene	4710971	4712083	34271	35383	gene=IY08_25000	protein=hypothetical protein	protein_id=KGT41318.1
gene	4712080	4712895	35380	36195	gene=IY08_25005	protein=haloacid dehalogenase	protein_id=KGT41319.1
gene	4713450	4714031	36750	37331	gene=IY08_25015	protein=NAD(P)H dehydrogenase	protein_id=KGT41320.1
gene	4714257	4715021	37557	38321	gene=IY08_25020	protein=HAD family hydrolase	protein_id=KGT41321.1
gene	4715131	4715763	38431	39063	gene=IY08_25025	protein=decarboxylase	protein_id=KGT41322.1
gene	4715844	4716284	39144	39584	gene=IY08_25030	protein=hypothetical protein	protein_id=KGT41323.1
gene	4716432	4717403	39732	40703	gene=glpX	protein=fructose 1,6-bisphosphatase	protein_id=KGT41324.1
gene	4717420	4717686	40720	40986	gene=IY08_25040	protein=cytoplasmic protein	protein_id=KGT41325.1
gene	4717716	4717928	41016	41228	pseudo		
gene	4718057	4718554	41357	41854	gene=IY08_25050	protein=cytoplasmic protein	protein_id=KGT41326.1
gene	4718591	4718893	41891	42193	gene=IY08_25055	protein=hypothetical protein	protein_id=KGT41327.1
gene	4719012	4719590	42312	42890	gene=IY08_25060	protein=lipoprotein	protein_id=KGT41328.1
gene	4719625	4720359	42925	43659	gene=IY08_25065	protein=MerR family transcriptional regulator	protein_id=KGT41329.1
gene	4720460	4721275	43760	44575	gene=IY08_25070	protein=membrane protein	protein_id=KGT41330.1
gene	4721306	4721739	44606	45039	pseudo		
gene	4721874	4722428	45174	45728	gene=IY08_25080	protein=phosphoglycerate mutase	protein_id=KGT41331.1
gene	4722503	4722982	45803	46282	gene=IY08_25085	protein=DNA-binding protein	protein_id=KGT41332.1
gene	4723003	4723899	46303	47199	gene=IY08_25090	protein=lipoyl synthase	protein_id=KGT41333.1
gene	4724089	4725072	47389	48372	gene=IY08_25095	protein=peptidase M23	protein_id=KGT41334.1
gene	4725146	4725877	48446	49177	gene=IY08_25100	protein=sporulation protein	protein_id=KGT41335.1
gene	4725932	4726234	49232	49534	gene=IY08_25105	protein=hypothetical protein	protein_id=KGT41336.1

gene	4726300	4727580	49600	50880	gene=IY08_25110	protein=5'-nucleotidase	protein_id=KGT41337.1
gene	4728382	4729779	51682	53079	gene=IY08_25115	protein=Fe-S cluster assembly protein SufB	protein_id=KGT41338.1
gene	4729828	4730259	53128	53559	gene=IY08_25120	protein=nitrogen fixation protein NifU	protein_id=KGT41339.1
gene	4730249	4731469	53549	54769	gene=IY08_25125	protein=cysteine desulfurase	protein_id=KGT41340.1
gene	4731469	4732761	54769	56061	gene=IY08_25130	protein=Fe-S cluster assembly protein SufD	protein_id=KGT41341.1
gene	4732777	4733562	56077	56862	gene=IY08_25135	protein=iron ABC transporter ATP-binding protein	protein_id=KGT41342.1
gene	4733801	4734613	57101	57913	gene=IY08_25140	protein=methionine ABC transporter substrate-binding	protein_id=KGT41343.1
gene	4734636	4735301	57936	58601	gene=IY08_25145	protein=methionine ABC transporter permease	protein_id=KGT41344.1
gene	4735294	4736319	58594	59619	gene=IY08_25150	protein=methionine ABC transporter ATP-binding protein	protein_id=KGT41345.1
gene	4736336	4736458	59636	59758	pseudo		
gene	4736861	4737205	60161	60505	gene=IY08_25160	protein=hypothetical protein	protein_id=KGT41346.1
gene	4737358	4737657	60658	60957	gene=IY08_25170	protein=thioredoxin	protein_id=KGT41347.1
gene	4737670	4738014	60970	61314	gene=IY08_25175	protein=TOPRIM domain-containing protein	protein_id=KGT41348.1
gene	4738634	4739017	61934	62317	gene=IY08_25180	protein=glycine cleavage system protein H	protein_id=KGT41349.1
gene	4739059	4739424	62359	62724	gene=IY08_25185	protein=hypothetical protein	protein_id=KGT41350.1
gene	4739836	4740363	63136	63663	gene=IY08_25190	protein=lipoprotein	protein_id=KGT41351.1
gene	4740507	4741154	63807	64454	gene=IY08_25195	protein=phosphoesterase	protein_id=KGT41352.1
gene	4741220	4742233	64520	65533	gene=IY08_25200	protein=membrane protein	protein_id=KGT41353.1
gene	4742256	4743206	65556	66506	gene=ldh	protein=lactate dehydrogenase	protein_id=KGT41354.1
gene	4743454	4743702	66754	67002	gene=IY08_25210	protein=coat protein F	protein_id=KGT41355.1
gene	4743716	4743901	67016	67201	gene=IY08_25215	protein=hypothetical protein	protein_id=KGT41356.1
gene	4744714	4745262	68014	68562	gene=IY08_25230	protein=TetR family transcriptional regulator	protein_id=KGT41357.1
gene	4745266	4745988	68566	69288	gene=IY08_25235	protein=metallo-beta-lactamase	protein_id=KGT41358.1
gene	4746168	4747952	69468	71252	gene=IY08_25245	protein=acyl-CoA dehydrogenase	protein_id=KGT40826.1
gene	4748051	4748167	71351	71467	gene=IY08_25250	protein=MerR family transcriptional regulator	protein_id=KGT40827.1
gene	4748294	4749466	71594	72766	gene=IY08_25260	protein=acetyl-CoA acetyltransferase	protein_id=KGT40828.1
gene	4749488	4751869	72788	75169	gene=IY08_25265	protein=3-hydroxyacyl-CoA dehydrogenase	protein_id=KGT40829.1
gene	4752105	4752251	75405	75551	gene=IY08_25270	protein=hypothetical protein	protein_id=KGT40830.1
gene	4752339	4753178	75639	76478	gene=IY08_25275	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT40831.1
gene	4753201	4754118	76501	77418	gene=IY08_25280	protein=proline dehydrogenase	protein_id=KGT40832.1
gene	4754429	4754674	77729	77974	gene=IY08_25285	protein=hypothetical protein	protein_id=KGT40833.1

gene	4754723	4755025	78023	78325	gene=IY08_25290	protein=hypothetical protein	protein_id=KGT40834.1
gene	4755103	4757103	78403	80403	gene=IY08_25295	protein=chemotaxis protein	protein_id=KGT40835.1
gene	4757290	4758048	80590	81348	gene=IY08_25300	protein=TrmB family transcriptional regulator	protein_id=KGT40836.1
gene	4758076	4758258	81376	81558	gene=IY08_25305	protein=hypothetical protein	protein_id=KGT40837.1
gene	4758335	4759507	81635	82807	gene=IY08_25310	protein=major facilitator transporter	protein_id=KGT40838.1
gene	4759627	4760937	82927	84237	gene=IY08_25315	protein=serine/threonine protein kinase	protein_id=KGT40839.1
gene	4761405	4761632	84705	84932	gene=IY08_25320	protein=accessory gene regulator AgrC	protein_id=KGT40840.1
gene	4761710	4762525	85010	85825	gene=IY08_25325	protein=hypothetical protein	protein_id=KGT40841.1
gene	4762655	4763437	85955	86737	gene=IY08_25330	protein=hypothetical protein	protein_id=KGT40842.1
gene	4763466	4763750	86766	87050	gene=IY08_25335	protein=hypothetical protein	protein_id=KGT40843.1
gene	4764028	4764921	87328	88221	gene=IY08_25340	protein=hypothetical protein	protein_id=KGT40844.1
gene	4765027	4765548	88327	88848	gene=IY08_25345	protein=acetyltransferase	protein_id=KGT40845.1
gene	4766008	4766394	89308	89694	gene=IY08_25350	protein=hypothetical protein	protein_id=KGT40846.1
gene	4766642	4766782	89942	90082	gene=IY08_25355	protein=hypothetical protein	protein_id=KGT40847.1
gene	4766879	4767931	90179	91231	gene=IY08_25360	protein=cytochrome C oxidase subunit II	protein_id=KGT40848.1
gene	4767974	4768681	91274	91981	gene=IY08_25365	protein=hypothetical protein	protein_id=KGT40849.1
gene	4768671	4768892	91971	92192	gene=IY08_25370	protein=XRE family transcriptional regulator	protein_id=KGT40850.1
gene	4769123	4769737	92423	93037	gene=IY08_25375	protein=alkaline phosphatase	protein_id=KGT40851.1
gene	4770139	4770579	93439	93879	gene=IY08_25380	protein=hypothetical protein	protein_id=KGT40852.1
gene	4770610	4771071	93910	94371	gene=IY08_25385	protein=ErfK/YbiS/YcfS/YnhG family protein	protein_id=KGT40853.1
gene	4771436	4772101	94736	95401	gene=IY08_25390	protein=transcriptional regulator	protein_id=KGT40854.1
gene	4772079	4773521	95379	96821	gene=IY08_25395	protein=histidine kinase	protein_id=KGT40855.1
gene	4773663	4774565	96963	97865	gene=IY08_25400	protein=multidrug transporter	protein_id=KGT40856.1
gene	4774633	4774887	97933	98187	gene=IY08_25405	protein=hypothetical protein	protein_id=KGT40857.1
gene	4774929	4776563	98229	99863	gene=IY08_25410	protein=methionyl-tRNA synthetase	protein_id=KGT40858.1
gene	4776999	4777817	100299	101117	gene=IY08_25415	protein=methyltransferase	protein_id=KGT40859.1
gene	4778231	4779925	101531	103225	gene=IY08_25420	protein=chemotaxis protein	protein_id=KGT40860.1
gene	4780139	4781830	103439	105130	gene=IY08_25425	protein=chemotaxis protein	protein_id=KGT40861.1
gene	4781950	4782267	105250	105567	gene=IY08_25430	protein=DNA methyltransferase	protein_id=KGT40862.1
gene	4782345	4783994	105645	107294	gene=IY08_25435	protein=peptidase M4	protein_id=KGT40863.1
gene	4784151	4784849	107451	108149	gene=IY08_25440	protein=pirin	protein_id=KGT40864.1

gene	4784901	4785311	108201	108611	gene=IY08_25445	protein=MarR family transcriptional regulator	protein_id=KGT40865.1
gene	4785423	4785857	108723	109157	gene=IY08_25450	protein=hypothetical protein	protein_id=KGT40866.1
gene	4786023	4787222	109323	110522	gene=IY08_25455	protein=potassium transporter	protein_id=KGT40867.1
gene	4787227	4787721	110527	111021	gene=IY08_25460	protein=potassium transporter	protein_id=KGT40868.1
gene	4787776	4787949	111076	111249	gene=IY08_25465	protein=hypothetical protein	protein_id=KGT40869.1
gene	4788131	4789564	111431	112864	gene=IY08_25470	protein=sodium:alanine symporter	protein_id=KGT40870.1
gene	4789734	4790174	113034	113474	gene=IY08_25475	protein=general stress protein	protein_id=KGT40871.1
gene	4790824	4791021	114124	114321	gene=IY08_25485	protein=hypothetical protein	protein_id=KGT40872.1
gene	4791038	4791319	114338	114619	pseudo		
gene	4791424	4792002	114724	115302	gene=IY08_25495	protein=lysine decarboxylase	protein_id=KGT40873.1
gene	4792076	4792399	115376	115699	gene=IY08_25500	protein=hypothetical protein	protein_id=KGT40874.1
gene	4792453	4792959	115753	116259	gene=IY08_25505	protein=ferritin	protein_id=KGT40875.1
gene	4793110	4794279	116410	117579	gene=IY08_25510	protein=hypothetical protein	protein_id=KGT40876.1
gene	4794323	4795504	117623	118804	gene=IY08_25515	protein=pyrimidine nucleoside transporter NupC	protein_id=KGT40877.1
gene	4795855	4797036	119155	120336	gene=IY08_25520	protein=pyrimidine nucleoside transporter NupC	protein_id=KGT40878.1
gene	4797332	4798774	120632	122074	gene=IY08_25525	protein=sodium:alanine symporter	protein_id=KGT40879.1
gene	4799106	4800536	122406	123836	gene=IY08_25530	protein=sodium:alanine symporter	protein_id=KGT40880.1
gene	4800841	4801479	124141	124779	gene=IY08_25535	protein=hypothetical protein	protein_id=KGT40881.1
gene	4801526	4804729	124826	128029	gene=IY08_25540	protein=peptidase M60	protein_id=KGT40882.1
gene	4805301	4806221	128601	129521	gene=IY08_25545	protein=adhesin	protein_id=KGT40883.1
gene	4806330	4807169	129630	130469	gene=IY08_25550	protein=glyoxal reductase	protein_id=KGT40884.1
gene	4807186	4808400	130486	131700	gene=IY08_25555	protein=MFS sugar transporter	protein_id=KGT40885.1
gene	4808743	4809087	132043	132387	gene=IY08_25560	protein=MarR family transcriptional regulator	protein_id=KGT40886.1
gene	4809523	4809963	132823	133263	gene=IY08_25565	protein=hypothetical protein	protein_id=KGT40887.1
gene	4810008	4811186	133308	134486	gene=IY08_25570	protein=pyridine nucleotide-disulfide oxidoreductase	protein_id=KGT40888.1
gene	4811495	4812754	134795	136054	gene=IY08_25575	protein=tyrosine--tRNA ligase	protein_id=KGT40889.1
gene	4813124	4814041	136424	137341	gene=murB	protein=UDP-N-acetylenolpyruvoylglucosamine reductase	protein_id=KGT40890.1
gene	4814424	4814819	137724	138119	gene=IY08_25585	protein=lysine methyltransferase	protein_id=KGT40891.1
gene	4815028	4816530	138328	139830	gene=IY08_25590	protein=chemotaxis protein	protein_id=KGT40892.1
gene	4816563	4817621	139863	140921	gene=IY08_25595	protein=endonuclease	protein_id=KGT40893.1
gene	4817968	4818372	141268	141672	gene=IY08_25600	protein=camphor resistance protein CrcB	protein_id=KGT40894.1

gene	4818369	4818725	141669	142025	gene=IY08_25605	protein=camphor resistance protein CrcB	protein_id=KGT40895.1
gene	4818755	4818994	142055	142294	gene=IY08_25610	protein=competence protein ComK	protein_id=KGT40896.1
gene	4819061	4819273	142361	142573	gene=IY08_25615	protein=hypothetical protein	protein_id=KGT40897.1
gene	4819415	4820608	142715	143908	gene=IY08_25620	protein=MFS transporter	protein_id=KGT40898.1
gene	4820614	4822161	143914	145461	gene=IY08_25625	protein=ABC transporter ATP-binding protein	protein_id=KGT40899.1
gene	4822599	4823114	145899	146414	gene=IY08_25630	protein=spermidine acetyltransferase	protein_id=KGT40900.1
gene	4823388	4823864	146688	147164	gene=IY08_25635	protein=hypothetical protein	protein_id=KGT40901.1
gene	4823913	4824317	147213	147617	gene=IY08_25640	protein=protein PsiE-like protein	protein_id=KGT40902.1
gene	4824367	4825329	147667	148629	pseudo		
gene	4825791	4826756	149091	150056	gene=IY08_25650	protein=lipoprotein	protein_id=KGT40903.1
gene	4826963	4828501	150263	151801	gene=IY08_25655	protein=alveolysin	protein_id=KGT40904.1
gene	4828561	4828747	151861	152047	pseudo		
gene	4828951	4829703	152251	153003	gene=IY08_25665	protein=iron ABC transporter ATP-binding protein	protein_id=KGT40905.1
gene	4829700	4830764	153000	154064	gene=IY08_25670	protein=iron ABC transporter permease	protein_id=KGT40906.1
gene	4830761	4831777	154061	155077	gene=IY08_25675	protein=iron ABC transporter permease	protein_id=KGT40907.1
gene	4831797	4832813	155097	156113	gene=IY08_25680	protein=iron ABC transporter substrate-binding protein	protein_id=KGT40908.1
gene	4833141	4833818	156441	157118	gene=IY08_25685	protein=transcriptional regulator	protein_id=KGT40909.1
gene	4834699	4835166	157999	158466	gene=IY08_25690	protein=single-stranded DNA-binding protein	protein_id=KGT40910.1
gene	4835415	4837859	158715	161159	gene=IY08_25695	protein=ribonuclease R	protein_id=KGT40911.1
gene	4838002	4838745	161302	162045	gene=IY08_25700	protein=carboxylesterase	protein_id=KGT40912.1
gene	4838904	4839137	162204	162437	gene=IY08_25705	protein=preprotein translocase subunit SecG	protein_id=KGT40913.1
gene	4839232	4839924	162532	163224	gene=IY08_25710	protein=hypothetical protein	protein_id=KGT40914.1
gene	4839921	4840289	163221	163589	gene=IY08_25715	protein=holin-like protein	protein_id=KGT40915.1
gene	4840642	4841592	163942	164892	gene=IY08_25720	protein=nucleoside hydrolase	protein_id=KGT40916.1
gene	4841644	4842939	164944	166239	gene=eno	protein=enolase	protein_id=KGT40917.1
gene	4842970	4844499	166270	167799	gene=IY08_25730	protein=phosphoglyceromutase	protein_id=KGT40918.1
gene	4844496	4845251	167796	168551	gene=tpiA	protein=triosephosphate isomerase	protein_id=KGT40919.1
gene	4845284	4846468	168584	169768	gene=pgk	protein=phosphoglycerate kinase	protein_id=KGT40920.1
gene	4846608	4847612	169908	170912	gene=IY08_25745	protein=glyceraldehyde-3-phosphate dehydrogenase	protein_id=KGT40921.1
gene	4847639	4848667	170939	171967	gene=IY08_25750	protein=central glycolytic genes regulator	protein_id=KGT40922.1
gene	4848803	4849048	172103	172348	gene=IY08_25755	protein=glutaredoxin	protein_id=KGT40923.1

gene	4849058	4850365	172358	173665	gene=IY08_25760	protein=RNA polymerase sigma54 factor	protein_id=KGT40924.1
gene	4852087	4852449	175387	175749	gene=IY08_25775	protein=hypothetical protein	protein_id=KGT40925.1
gene	4852465	4853070	175765	176370	gene=IY08_25780	protein=hypothetical protein	protein_id=KGT40926.1
gene	4853079	4853471	176379	176771	gene=IY08_25785	protein=hypothetical protein	protein_id=KGT40927.1
gene	4853471	4853737	176771	177037	gene=IY08_25790	protein=hypothetical protein	protein_id=KGT40928.1
gene	4854755	4854988	178055	178288	gene=IY08_25795	protein=hypothetical protein	protein_id=KGT40929.1
gene	4855393	4855656	178693	178956	gene=IY08_25800	protein=hypothetical protein	protein_id=KGT40930.1
gene	4856408	4856617	179708	179917	gene=IY08_25805	protein=hypothetical protein	protein_id=KGT40931.1
gene	4856729	4857001	180029	180301	gene=IY08_25810	protein=hypothetical protein	protein_id=KGT40932.1
gene	4857783	4858763	181083	182063	gene=IY08_25815	protein=DNA integration/recombination/inversion protein	protein_id=KGT40933.1
gene	4858993	4859068	182293	182368	tRNA		
gene	4859273	4859479	182573	182779	gene=IY08_25825	protein=hypothetical protein	protein_id=KGT40934.1
gene	4859573	4860061	182873	183361	gene=IY08_25830	protein=lipoprotein	protein_id=KGT40935.1
gene	4860091	4860567	183391	183867	gene=IY08_25835	protein=stage V sporulation protein AC	protein_id=KGT40936.1
gene	4860568	4861584	183868	184884	gene=IY08_25840	protein=SpoVAD	protein_id=KGT40937.1
gene	4861581	4861931	184881	185231	gene=IY08_25845	protein=stage V sporulation protein AEB	protein_id=KGT40938.1
gene	4861943	4862149	185243	185449	gene=IY08_25850	protein=NADH dehydrogenase	protein_id=KGT40939.1
gene	4862170	4863039	185470	186339	gene=IY08_25855	protein=membrane protein	protein_id=KGT40940.1
gene	4863280	4863861	186580	187161	gene=IY08_25860	protein=Clp protease	protein_id=KGT40941.1
gene	4863984	4864164	187284	187464	pseudo		
gene	4864381	4864629	187681	187929	gene=IY08_25870	protein=phosphocarrier protein Chr	protein_id=KGT40942.1
gene	4864653	4865603	187953	188903	gene=IY08_25875	protein=sporulation regulator WhiA	protein_id=KGT40943.1
gene	4865692	4866645	188992	189945	gene=IY08_25880	protein=hypothetical protein	protein_id=KGT40944.1
gene	4866649	4867530	189949	190830	gene=IY08_25885	protein=glmZ(sRNA)-inactivating NTPase	protein_id=KGT40945.1
gene	4867551	4868009	190851	191309	gene=IY08_25890	protein=NUDIX hydrolase	protein_id=KGT40946.1
gene	4868239	4869045	191539	192345	gene=IY08_25895	protein=membrane protein	protein_id=KGT40947.1
gene	4869211	4870167	192511	193467	gene=IY08_25900	protein=thioredoxin reductase	protein_id=KGT40948.1
gene	4870253	4871764	193553	195064	gene=IY08_25905	protein=TPR repeat-containing protein	protein_id=KGT40949.1
gene	4871904	4872416	195204	195716	gene=IY08_25910	protein=acetyltransferase	protein_id=KGT40950.1
gene	4872450	4873100	195750	196400	gene=IY08_25915	protein=pyrophosphatase	protein_id=KGT40951.1
gene	4873168	4873980	196468	197280	gene=IY08_25920	protein=diacylglycerol transferase	protein_id=KGT40952.1

gene	4874007	4874936	197307	198236	gene=IY08_25925	protein=serine kinase	protein_id=KGT40953.1
gene	4875093	4875473	198393	198773	gene=IY08_25930	protein=membrane protein	protein_id=KGT40954.1
gene	4875589	4876038	198889	199338	gene=IY08_25935	protein=ATP synthase F1 subunit delta	protein_id=KGT40955.1
gene	4876098	4878974	199398	202274	gene=IY08_25940	protein=excinuclease ABC subunit A	protein_id=KGT40956.1
gene	4878980	4880956	202280	204256	gene=IY08_25945	protein=excinuclease ABC subunit B	protein_id=KGT40957.1
gene	4881107	4881538	204407	204838	gene=IY08_25950	protein=lipoprotein	protein_id=KGT40958.1
gene	4881584	4882204	204884	205504	gene=IY08_25955	protein=membrane protein	protein_id=KGT40959.1
gene	4882201	4882962	205501	206262	gene=IY08_25960	protein=MerR family transcriptional regulator	protein_id=KGT40960.1
gene	4883063	4883290	206363	206590	gene=IY08_25965	protein=membrane protein	protein_id=KGT40961.1
gene	4883438	4883635	206738	206935	gene=IY08_25970	protein=Cro/C1 family transcriptional regulator	protein_id=KGT40962.1
gene	4883953	4884975	207253	208275	gene=IY08_25975	protein=membrane protein	protein_id=KGT40963.1
gene	4885127	4886020	208427	209320	gene=IY08_25980	protein=LysR family transcriptional regulator	protein_id=KGT40964.1
gene	4886072	4886440	209372	209740	gene=IY08_25985	protein=MerR family transcriptional regulator	protein_id=KGT40965.1
gene	4886445	4886984	209745	210284	gene=IY08_25990	protein=NAD(P)H-dependent oxidoreductase	protein_id=KGT40966.1
gene	4887256	4888890	210556	212190	gene=IY08_25995	protein=ABC transporter ATP-binding protein	protein_id=KGT40967.1
gene	4888991	4889302	212291	212602	gene=IY08_26000	protein=hypothetical protein	protein_id=KGT40968.1
gene	4889368	4891083	212668	214383	gene=IY08_26005	protein=multidrug ABC transporter ATP-binding protein	protein_id=KGT40969.1
gene	4891396	4892580	214696	215880	gene=IY08_26010	protein=membrane protein	protein_id=KGT40970.1
gene	4892690	4894174	215990	217474	gene=IY08_26015	protein=peptidase S41	protein_id=KGT40971.1
gene	4894245	4895138	217545	218438	gene=IY08_26020	protein=cell division protein FtsX	protein_id=KGT40972.1
gene	4895128	4895772	218428	219072	gene=IY08_26025	protein=cell division protein FtsE	protein_id=KGT40973.1
gene	4896099	4896422	219399	219722	gene=IY08_26030	protein=cytochrome C'	protein_id=KGT40974.1
gene	4896678	4896836	219978	220136	gene=IY08_26035	protein=hypothetical protein	protein_id=KGT40975.1
gene	4896863	4897843	220163	221143	gene=IY08_26040	protein=peptide chain release factor 2	protein_id=KGT40976.1
gene	4898106	4900613	221406	223913	gene=IY08_26050	protein=preprotein translocase subunit SecA	protein_id=KGT40977.1
gene	4901117	4901644	224417	224944	gene=IY08_26055	protein=hypothetical protein	protein_id=KGT40978.1
gene	4901686	4902324	224986	225624	gene=IY08_26060	protein=multidrug ABC transporter ATP-binding protein	protein_id=KGT40979.1
gene	4902328	4903092	225628	226392	gene=IY08_26065	protein=hypothetical protein	protein_id=KGT40980.1
gene	4903164	4903859	226464	227159	gene=IY08_26070	protein=hypothetical protein	protein_id=KGT40981.1
gene	4903846	4904634	227146	227934	gene=IY08_26075	protein=hypothetical protein	protein_id=KGT40982.1
gene	4904662	4905231	227962	228531	gene=IY08_26080	protein=hypothetical protein	protein_id=KGT40983.1

gene	4905336	4905809	228636	229109	gene=IY08_26085	protein=hypothetical protein	protein_id=KGT40984.1
gene	4906214	4906756	229514	230056	gene=IY08_26090	protein=sigma-54 modulation protein	protein_id=KGT40985.1
gene	4907079	4907276	230379	230576	gene=IY08_26095	protein=cold-shock protein	protein_id=KGT40986.1
gene	4907403	4907975	230703	231275	gene=IY08_26100	protein=competence protein ComF	protein_id=KGT40987.1
gene	4908110	4909459	231410	232759	gene=IY08_26105	protein=competence protein ComF	protein_id=KGT40988.1
gene	4909587	4911014	232887	234314	gene=IY08_26110	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT40989.1
gene	4911163	4911477	234463	234777	gene=IY08_26115	protein=HxIR family transcriptional regulator	protein_id=KGT40990.1
gene	4911548	4911668	234848	234968	pseudo		
gene	4911649	4912491	234949	235791	gene=IY08_26125	protein=DegV domain-containing protein	protein_id=KGT40991.1
gene	4913550	4914668	236850	237968	gene=IY08_26135	protein=LytR family transcriptional regulator	protein_id=KGT40992.1
gene	4914706	4915821	238006	239121	gene=IY08_26140	protein=UDP-N-acetylglucosamine 2-epimerase	protein_id=KGT40993.1
gene	4915896	4917221	239196	240521	gene=IY08_26145	protein=UDP-glucose 6-dehydrogenase	protein_id=KGT40994.1
gene	4917753	4918826	241053	242126	gene=IY08_26150	protein=glycosyl transferase	protein_id=KGT40995.1
gene	4919026	4919763	242326	243063	gene=IY08_26155	protein=peptidoglycan N-acetylglucosamine deacetylase	protein_id=KGT40996.1
gene	4919868	4922543	243168	245843	gene=IY08_26160	protein=transcription antiterminator BglG	protein_id=KGT40997.1
gene	4923128	4923541	246428	246841	gene=IY08_26180	protein=hypothetical protein	protein_id=KGT40998.1
gene	4923730	4924911	247030	248211	gene=IY08_26185	protein=ChrA protein	protein_id=KGT40999.1
gene	4924950	4925654	248250	248954	gene=IY08_26190	protein=hypothetical protein	protein_id=KGT41000.1
gene	4925704	4927029	249004	250329	gene=IY08_26195	protein=diacetylchitobiose-6-phosphate hydrolase	protein_id=KGT41001.1
gene	4927033	4927356	250333	250656	gene=IY08_26200	protein=PTS cellobiose transporter subunit IIA	protein_id=KGT41002.1
gene	4927538	4928845	250838	252145	gene=IY08_26205	protein=PTS lactose transporter subunit IIC	protein_id=KGT41003.1
gene	4928862	4929164	252162	252464	gene=IY08_26210	protein=PTS chitobiose transporter subunit IIB	protein_id=KGT41004.1
gene	4929511	4929828	252811	253128	gene=IY08_26215	protein=PTS cellobiose transporter subunit IIA	protein_id=KGT41005.1
gene	4929838	4931139	253138	254439	gene=IY08_26220	protein=PTS cellobiose transporter subunit IIC	protein_id=KGT41006.1
gene	4931154	4931456	254454	254756	gene=IY08_26225	protein=PTS chitobiose transporter subunit IIB	protein_id=KGT41007.1
gene	4931680	4932897	254980	256197	gene=IY08_26230	protein=sodium:proton antiporter	protein_id=KGT41008.1
gene	4933046	4934203	256346	257503	gene=IY08_26235	protein=membrane protein	protein_id=KGT41009.1
gene	4934243	4934623	257543	257923	gene=IY08_26240	protein=glyoxalase	protein_id=KGT41010.1
gene	4934664	4936664	257964	259964	gene=IY08_26245	protein=phage infection protein	protein_id=KGT41011.1
gene	4936799	4937683	260099	260983	gene=IY08_26250	protein=LysR family transcriptional regulator	protein_id=KGT41012.1
gene	4937731	4938816	261031	262116	gene=IY08_26255	protein=transcriptional regulator	protein_id=KGT41013.1

gene	4938908	4939057	262208	262357	gene=IY08_26260	protein=hypothetical protein	protein_id=KGT41014.1
gene	4939312	4940667	262612	263967	gene=IY08_26265	protein=cytochrome D ubiquinol oxidase subunit I	protein_id=KGT41015.1
gene	4940660	4941685	263960	264985	gene=IY08_26270	protein=membrane protein	protein_id=KGT41016.1
gene	4942156	4943514	265456	266814	gene=IY08_26275	protein=arsenic transporter	protein_id=KGT41017.1
gene	4943616	4945376	266916	268676	gene=IY08_26280	protein=thiamine biosynthesis protein ThiC	protein_id=KGT41018.1
gene	4945676	4947337	268976	270637	gene=IY08_26285	protein=L-lactate permease	protein_id=KGT41019.1
gene	4947633	4947950	270933	271250	gene=IY08_26290	protein=hypothetical protein	protein_id=KGT41020.1
gene	4948022	4948513	271322	271813	gene=IY08_26295	protein=peptidase	protein_id=KGT41021.1
gene	4948564	4948929	271864	272229	gene=IY08_26300	protein=hypothetical protein	protein_id=KGT41022.1
gene	4949476	4951404	272776	274704	gene=IY08_26305	protein=hypothetical protein	protein_id=KGT41023.1
gene	4952046	4952918	275346	276218	gene=IY08_26315	protein=D-amino acid aminotransferase	protein_id=KGT41024.1
gene	4953129	4954865	276429	278165	gene=IY08_26325	protein=peptidase M24	protein_id=KGT41025.1
gene	4955233	4956444	278533	279744	gene=IY08_26335	protein=Na ⁺ dependent nucleoside transporter	protein_id=KGT41026.1
gene	4956706	4957461	280006	280761	gene=IY08_26340	protein=dGTP triphosphohydrolase	protein_id=KGT41027.1
gene	4957458	4958759	280758	282059	gene=IY08_26345	protein=N-acetylglucosaminyltransferase	protein_id=KGT41028.1
gene	4958906	4959040	282206	282340	gene=IY08_26350	protein=hypothetical protein	protein_id=KGT41029.1
gene	4959437	4960951	282737	284251	gene=IY08_26355	protein=glycine/betaine ABC transporter permease	protein_id=KGT41030.1
gene	4961616	4962494	284916	285794	gene=IY08_26360	protein=enterotoxin	protein_id=KGT41031.1
gene	4962576	4962878	285876	286178	gene=IY08_26365	protein=hypothetical protein	protein_id=KGT41032.1
gene	4963009	4964373	286309	287673	gene=IY08_26370	protein=membrane protein	protein_id=KGT41033.1
gene	4964386	4965936	287686	289236	gene=IY08_26375	protein=membrane protein	protein_id=KGT41034.1
gene	4965942	4966433	289242	289733	gene=IY08_26380	protein=hypothetical protein	protein_id=KGT41035.1
gene	4966592	4968211	289892	291511	gene=IY08_26385	protein=hypothetical protein	protein_id=KGT41036.1
gene	4968195	4970951	291495	294251	gene=IY08_26390	protein=ATP-dependent helicase	protein_id=KGT41037.1
gene	4971024	4971509	294324	294809	gene=IY08_26395	protein=hypothetical protein	protein_id=KGT41038.1
gene	4971621	4971845	294921	295145	gene=IY08_26400	protein=hypothetical protein	protein_id=KGT41039.1
gene	4971962	4972177	295262	295477	gene=IY08_26405	protein=potassium channel protein	protein_id=KGT41040.1
gene	4972199	4972597	295499	295897	gene=IY08_26410	protein=hypothetical protein	protein_id=KGT41041.1
gene	4972788	4973264	296088	296564	gene=IY08_26415	protein=competence protein	protein_id=KGT41042.1
gene	4973319	4973789	296619	297089	gene=IY08_26420	protein=RNA polymerase factor sigma-70	protein_id=KGT41043.1
gene	4974010	4974690	297310	297990	gene=IY08_26425	protein=membrane protein	protein_id=KGT41044.1

gene	4974804	4976006	298104	299306	gene=IY08_26430	protein=macrolide ABC transporter permease	protein_id=KGT41045.1
gene	4976003	4976683	299303	299983	gene=IY08_26435	protein=macrolide ABC transporter ATP-binding protein	protein_id=KGT41046.1
gene	4976680	4977873	299980	301173	gene=IY08_26440	protein=RND transporter MFP subunit	protein_id=KGT41047.1
gene	4978112	4979446	301412	302746	gene=IY08_26445	protein=MFS transporter	protein_id=KGT41048.1
gene	4979466	4980500	302766	303800	gene=IY08_26450	protein=ABC transporter substrate-binding protein	protein_id=KGT41049.1
gene	4980497	4981279	303797	304579	gene=IY08_26455	protein=homoserine dehydrogenase	protein_id=KGT41050.1
gene	4981346	4982776	304646	306076	gene=IY08_26460	protein=histidine kinase	protein_id=KGT41051.1
gene	4982788	4983459	306088	306759	gene=IY08_26465	protein=XRE family transcriptional regulator	protein_id=KGT41052.1
gene	4983580	4984572	306880	307872	gene=IY08_26470	protein=UDP-glucose 4-epimerase	protein_id=KGT41053.1
gene	4984656	4985486	307956	308786	gene=IY08_26475	protein=EPSX protein	protein_id=KGT41054.1
gene	4985585	4986493	308885	309793	gene=IY08_26480	protein=membrane-bound transcriptional regulator LytR	protein_id=KGT41055.1
gene	4986621	4987646	309921	310946	gene=IY08_26485	protein=NAD-dependent epimerase	protein_id=KGT41056.1
gene	4987624	4988994	310924	312294	gene=IY08_26490	protein=UDP-glucose 6-dehydrogenase	protein_id=KGT41057.1
gene	4989212	4990672	312512	313972	gene=IY08_26495	protein=polysaccharide biosynthesis protein	protein_id=KGT41058.1
gene	4990685	4991818	313985	315118	gene=IY08_26500	protein=poly-gamma-glutamate biosynthesis protein	protein_id=KGT41059.1
gene	4991849	4992772	315149	316072	gene=IY08_26505	protein=glycosyl transferase	protein_id=KGT41060.1
gene	4992819	4994075	316119	317375	gene=IY08_26510	protein=hypothetical protein	protein_id=KGT41061.1
gene	4994284	4995375	317584	318675	gene=IY08_26515	protein=hypothetical protein	protein_id=KGT41062.1
gene	4995494	4996552	318794	319852	gene=IY08_26520	protein=hypothetical protein	protein_id=KGT41063.1
gene	4996566	4997036	319866	320336	gene=IY08_26525	protein=hypothetical protein	protein_id=KGT41064.1
gene	4997087	4997911	320387	321211	gene=IY08_26530	protein=glycosyl transferase	protein_id=KGT41065.1
gene	4998027	4998731	321327	322031	gene=IY08_26535	protein=glycosyl transferase	protein_id=KGT41066.1
gene	4998757	4999980	322057	323280	gene=IY08_26540	protein=capsular biosynthesis protein	protein_id=KGT41067.1
gene	5000077	5001888	323377	325188	gene=IY08_26545	protein=polysaccharide biosynthesis protein EpsC	protein_id=KGT41068.1
gene	5001949	5002830	325249	326130	gene=IY08_26550	protein=UTP--glucose-1-phosphate uridylyltransferase	protein_id=KGT41069.1
gene	5003077	5003844	326377	327144	gene=IY08_26555	protein=tyrosine protein phosphatase	protein_id=KGT41070.1
gene	5003956	5004657	327256	327957	gene=IY08_26560	protein=tyrosine protein kinase	protein_id=KGT41071.1
gene	5004647	5005393	327947	328693	gene=IY08_26565	protein=capsular biosynthesis protein	protein_id=KGT41072.1
gene	5005654	5006331	328954	329631	gene=IY08_26570	protein=tyrosine protein kinase	protein_id=KGT41073.1
gene	5006677	5007111	329977	330411	gene=IY08_26575	protein=3-hydroxyacyl-ACP dehydratase	protein_id=KGT41074.1
gene	5007539	5008540	330839	331840	gene=IY08_26580	protein=rod shape-determining protein MreB	protein_id=KGT41075.1

gene	5008701	5008973	332001	332273	gene=IY08_26585	protein=stage III sporulation protein D	protein_id=KGT41076.1
gene	5009282	5009416	332582	332716	gene=IY08_26590	protein=ABC transporter ATP-binding protein	protein_id=KGT41077.1
gene	5009558	5010463	332858	333763	gene=IY08_26595	protein=peptidase M23	protein_id=KGT41078.1
gene	5010625	5011329	333925	334629	gene=IY08_26600	protein=ABC transporter permease	protein_id=KGT41079.1
gene	5011329	5012171	334629	335471	gene=IY08_26605	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT41080.1
gene	5012352	5013359	335652	336659	gene=IY08_26610	protein=transcriptional regulator	protein_id=KGT41081.1
gene	5013460	5014479	336760	337779	gene=IY08_26615	protein=stage II sporulation protein D	protein_id=KGT41082.1
gene	5014686	5015990	337986	339290	gene=IY08_26620	protein=UDP-N-acetylglucosamine 1-	protein_id=KGT41083.1
gene	5016030	5016740	339330	340040	gene=IY08_26625	protein=membrane protein	protein_id=KGT41084.1
gene	5016786	5017022	340086	340322	gene=IY08_26630	protein=membrane protein	protein_id=KGT41085.1
gene	5017225	5018739	340525	342039	gene=IY08_26635	protein=NADH:ubiquinone oxidoreductase subunit N	protein_id=KGT41086.1
gene	5018747	5020249	342047	343549	gene=IY08_26640	protein=NADH:ubiquinone oxidoreductase subunit M	protein_id=KGT41087.1
gene	5020246	5022108	343546	345408	gene=IY08_26645	protein=NADH:ubiquinone oxidoreductase subunit L	protein_id=KGT41088.1
gene	5022139	5022453	345439	345753	gene=IY08_26650	protein=NADH dehydrogenase	protein_id=KGT41089.1
gene	5022446	5022970	345746	346270	gene=IY08_26655	protein=NADH:ubiquinone oxidoreductase subunit J	protein_id=KGT41090.1
gene	5022967	5023386	346267	346686	gene=IY08_26660	protein=NADH dehydrogenase	protein_id=KGT41091.1
gene	5023412	5024413	346712	347713	gene=IY08_26665	protein=NADH:ubiquinone oxidoreductase subunit H	protein_id=KGT41092.1
gene	5024413	5025513	347713	348813	gene=IY08_26670	protein=NADH dehydrogenase	protein_id=KGT41093.1
gene	5025516	5026754	348816	350054	gene=IY08_26675	protein=NADH dehydrogenase	protein_id=KGT41094.1
gene	5026751	5027269	350051	350569	gene=IY08_26680	protein=NADH dehydrogenase	protein_id=KGT41095.1
gene	5027260	5027628	350560	350928	gene=IY08_26685	protein=NADH:ubiquinone oxidoreductase subunit A	protein_id=KGT41096.1
gene	5027883	5030612	351183	353912	gene=IY08_26690	protein=diguanylate cyclase	protein_id=KGT41097.1
gene	5030636	5031280	353936	354580	gene=IY08_26695	protein=membrane protein	protein_id=KGT41098.1
gene	5031330	5032115	354630	355415	gene=IY08_26700	protein=membrane protein	protein_id=KGT41099.1
gene	5032253	5032654	355553	355954	gene=IY08_26705	protein=ATP synthase F0F1 subunit epsilon	protein_id=KGT41100.1
gene	5032675	5034081	355975	357381	gene=IY08_26710	protein=ATP F0F1 synthase subunit beta	protein_id=KGT41101.1
gene	5034201	5035061	357501	358361	gene=IY08_26715	protein=ATP synthase F0F1 subunit gamma	protein_id=KGT41102.1
gene	5035398	5036906	358698	360206	gene=IY08_26720	protein=ATP F0F1 synthase subunit alpha	protein_id=KGT41103.1
gene	5036918	5037460	360218	360760	gene=IY08_26725	protein=ATP synthase F0F1 subunit delta	protein_id=KGT41104.1
gene	5037457	5037963	360757	361263	gene=IY08_26730	protein=ATP F0F1 synthase subunit B	protein_id=KGT41105.1
gene	5038093	5038311	361393	361611	gene=IY08_26735	protein=ATP synthase F0F1 subunit C	protein_id=KGT41106.1

gene	5038368	5039087	361668	362387	gene=IY08_26740	protein=ATP synthase subunit A	protein_id=KGT41107.1
gene	5039095	5039487	362395	362787	gene=IY08_26745	protein=ATP synthase subunit I	protein_id=KGT41108.1
gene	5039487	5039711	362787	363011	gene=IY08_26750	protein=membrane protein	protein_id=KGT41109.1
gene	5039738	5039851	363038	363151	gene=IY08_26755	protein=histidine kinase	protein_id=KGT41110.1
gene	5040231	5040860	363531	364160	gene=upp	protein=uracil phosphoribosyltransferase	protein_id=KGT41111.1
gene	5041133	5042374	364433	365674	gene=IY08_26765	protein=serine hydroxymethyltransferase	protein_id=KGT41112.1
gene	5042628	5043200	365928	366500	gene=IY08_26770	protein=hypothetical protein	protein_id=KGT41113.1
gene	5043267	5043710	366567	367010	gene=IY08_26775	protein=ribose 5-phosphate isomerase	protein_id=KGT41114.1
gene	5043808	5044248	367108	367548	gene=IY08_26780	protein=protein tyrosine phosphatase	protein_id=KGT41115.1
gene	5044490	5044987	367790	368287	gene=IY08_26785	protein=PTS glucose transporter subunit IIA	protein_id=KGT41116.1
gene	5045375	5045761	368675	369061	gene=IY08_26790	protein=oxidoreductase	protein_id=KGT41117.1
gene	5045921	5046532	369221	369832	gene=IY08_26795	protein=hypothetical protein	protein_id=KGT41118.1
gene	5046652	5046851	369952	370151	pseudo		
gene	5046848	5047126	370148	370426	gene=IY08_26805	protein=hypothetical protein	protein_id=KGT41119.1
gene	5047357	5047905	370657	371205	gene=IY08_26815	protein=membrane protein	protein_id=KGT41120.1
gene	5047983	5049023	371283	372323	gene=IY08_26820	protein=tRNA threonylcarbamoyladenosine biosynthesis	protein_id=KGT41121.1
gene	5049132	5049590	372432	372890	gene=IY08_26825	protein=mechanosensitive ion channel protein	protein_id=KGT41122.1
gene	5049640	5050503	372940	373803	gene=IY08_26830	protein=stage II sporulation protein R	protein_id=KGT41123.1
gene	5050616	5051467	373916	374767	gene=IY08_26835	protein=SAM-dependent methyltransferase	protein_id=KGT41124.1
gene	5051467	5052534	374767	375834	gene=IY08_26840	protein=peptide chain release factor 1	protein_id=KGT41125.1
gene	5052926	5053513	376226	376813	gene=IY08_26845	protein=thymidine kinase	protein_id=KGT41126.1
gene	5053622	5053867	376922	377167	gene=rpmE2	protein=50S ribosomal protein L31 type B	protein_id=KGT41127.1
gene	5054393	5055664	377693	378964	gene=IY08_26855	protein=transcription termination factor Rho	protein_id=KGT41128.1
gene	5056059	5057024	379359	380324	gene=glpX	protein=fructose 1,6-bisphosphatase	protein_id=KGT41129.1
gene	5057141	5058430	380441	381730	gene=IY08_26875	protein=UDP-N-acetylglucosamine 1-	protein_id=KGT41130.1
gene	5058762	5059619	382062	382919	gene=IY08_26880	protein=fructose-bisphosphate aldolase	protein_id=KGT41131.1
gene	5059830	5060198	383130	383498	gene=IY08_26885	protein=chemotaxis protein CheY	protein_id=KGT41132.1
gene	5060400	5060924	383700	384224	gene=IY08_26890	protein=hypothetical protein	protein_id=KGT41133.1
gene	5060956	5062563	384256	385863	gene=IY08_26895	protein=CTP synthetase	protein_id=KGT41134.1
gene	5062821	5063351	386121	386651	gene=IY08_26900	protein=DNA-directed RNA polymerase subunit delta	protein_id=KGT41135.1
gene	5063507	5064136	386807	387436	gene=IY08_26905	protein=TetR family transcriptional regulator	protein_id=KGT41136.1

gene	5064203	5065342	387503	388642	gene=IY08_26910	protein=acyl-CoA dehydrogenase	protein_id=KGT41137.1
gene	5065364	5066494	388664	389794	gene=IY08_26915	protein=acyl-CoA dehydrogenase	protein_id=KGT41138.1
gene	5066568	5067419	389868	390719	gene=IY08_26920	protein=3-hydroxybutyryl-CoA dehydrogenase	protein_id=KGT41139.1
gene	5067469	5068650	390769	391950	gene=IY08_26925	protein=acetyl-CoA acetyltransferase	protein_id=KGT41140.1
gene	5068762	5070873	392062	394173	gene=IY08_26930	protein=hypothetical protein	protein_id=KGT41141.1
gene	5071319	5072512	394619	395812	gene=IY08_26935	protein=cardiolipin synthetase	protein_id=KGT41142.1
gene	5072545	5073498	395845	396798	gene=uvrE	protein=UV damage repair endonuclease UvrE	protein_id=KGT41143.1
gene	5073625	5076303	396925	399603	gene=IY08_26945	protein=diguanylate cyclase	protein_id=KGT41144.1
gene	5076320	5076466	399620	399766	gene=IY08_26950	protein=PapR	protein_id=KGT41145.1
gene	5076556	5077413	399856	400713	gene=IY08_26955	protein=transcriptional regulator	protein_id=KGT41146.1
gene	5077582	5079333	400882	402633	gene=IY08_26960	protein=bacillolysin	protein_id=KGT41147.1
gene	5079373	5079975	402673	403275	gene=IY08_26965	protein=transcriptional regulator	protein_id=KGT41148.1
gene	5079972	5081102	403272	404402	gene=IY08_26970	protein=histidine kinase	protein_id=KGT41149.1
gene	5081103	5081837	404403	405137	gene=IY08_26975	protein=ABC transporter permease	protein_id=KGT41150.1
gene	5081834	5082736	405134	406036	gene=IY08_26980	protein=ABC transporter ATP-binding protein	protein_id=KGT41151.1
gene	5082942	5083688	406242	406988	gene=IY08_26985	protein=methionine aminopeptidase	protein_id=KGT41152.1
gene	5084449	5093103	407749	416403	gene=IY08_26990	protein=collagen-binding protein	protein_id=KGT41153.1
gene	5093596	5094996	416896	418296	gene=IY08_26995	protein=aminopeptidase	protein_id=KGT41154.1
gene	5095143	5095517	418443	418817	gene=IY08_27000	protein=hypothetical protein	protein_id=KGT41155.1
gene	5095544	5096215	418844	419515	gene=IY08_27005	protein=ECF-type sigma factor negative effector	protein_id=KGT41156.1
gene	5096199	5096513	419499	419813	gene=IY08_27010	protein=ECF-type sigma factor negative effector	protein_id=KGT41157.1
gene	5096500	5097026	419800	420326	pseudo		
gene	5097417	5099087	420717	422387	gene=argS	protein=arginine--tRNA ligase	protein_id=KGT41158.1
gene	5099087	5099524	422387	422824	gene=IY08_27025	protein=hypothetical protein	protein_id=KGT41159.1
gene	5099727	5100713	423027	424013	gene=IY08_27030	protein=peptidase S66	protein_id=KGT41160.1
gene	5100738	5101100	424038	424400	gene=IY08_27035	protein=hypothetical protein	protein_id=KGT41161.1
gene	5101333	5102370	424633	425670	gene=IY08_27040	protein=transcriptional regulator	protein_id=KGT41162.1
gene	5102757	5103629	426057	426929	gene=IY08_27045	protein=agmatinase	protein_id=KGT41163.1
gene	5103848	5104675	427148	427975	gene=IY08_27050	protein=spermidine synthase	protein_id=KGT41164.1
gene	5104840	5106003	428140	429303	gene=IY08_27055	protein=major facilitator transporter	protein_id=KGT41165.1
gene	5106009	5106416	429309	429716	gene=IY08_27060	protein=MerR family transcriptional regulator	protein_id=KGT41166.1

gene	5106569	5107294	429869	430594	gene=IY08_27070	protein=hypothetical protein	protein_id=KGT41167.1
gene	5107396	5109447	430696	432747	gene=IY08_27075	protein=penicillin-binding protein	protein_id=KGT41168.1
gene	5109482	5109991	432782	433291	gene=IY08_27080	protein=hypothetical protein	protein_id=KGT41169.1
gene	5110017	5110691	433317	433991	gene=IY08_27085	protein=zinc metalloprotease	protein_id=KGT41170.1
gene	5110804	5110989	434104	434289	gene=IY08_27090	protein=4-oxalocrotonate tautomerase	protein_id=KGT41171.1
gene	5111029	5112333	434329	435633	gene=IY08_27095	protein=hypothetical protein	protein_id=KGT41172.1
gene	5112479	5113417	435779	436717	gene=IY08_27100	protein=ferrichrome ABC transporter substrate-binding	protein_id=KGT41173.1
gene	5113608	5114420	436908	437720	gene=IY08_27105	protein=iron ABC transporter ATP-binding protein	protein_id=KGT41174.1
gene	5114436	5115452	437736	438752	gene=IY08_27110	protein=iron ABC transporter permease	protein_id=KGT41175.1
gene	5115449	5116504	438749	439804	gene=IY08_27115	protein=ferrichrome ABC transporter permease	protein_id=KGT41176.1
gene	5116816	5117040	440116	440340	gene=IY08_27120	protein=hypothetical protein	protein_id=KGT41177.1
gene	5117326	5118018	440626	441318	gene=IY08_27125	protein=transcriptional regulator	protein_id=KGT41178.1
gene	5118147	5118992	441447	442292	gene=IY08_27130	protein=octanoyltransferase	protein_id=KGT41179.1
gene	5119041	5120012	442341	443312	gene=eutD	protein=phosphotransacetylase	protein_id=KGT41180.1
gene	5120268	5121011	443568	444311	gene=IY08_27140	protein=heme peroxidase	protein_id=KGT41181.1
gene	5121211	5122482	444511	445782	gene=IY08_27145	protein=D-alanyl-D-alanine carboxypeptidase	protein_id=KGT41182.1
gene	5122656	5123078	445956	446378	gene=IY08_27150	protein=cell wall hydrolase	protein_id=KGT41183.1
gene	5123106	5123534	446406	446834	gene=IY08_27155	protein=spore germination protein GerQ	protein_id=KGT41184.1
gene	5123566	5123934	446866	447234	gene=IY08_27160	protein=membrane protein	protein_id=KGT41185.1
gene	5123999	5124286	447299	447586	gene=IY08_27165	protein=hypothetical protein	protein_id=KGT41186.1
gene	5124293	5125285	447593	448585	gene=IY08_27170	protein=potassium channel protein	protein_id=KGT41187.1
gene	5125381	5126664	448681	449964	gene=IY08_27175	protein=purine permease	protein_id=KGT41188.1
gene	5126893	5127714	450193	451014	gene=IY08_27180	protein=haloacid dehalogenase	protein_id=KGT41189.1
gene	5127924	5128217	451224	451517	gene=IY08_27185	protein=membrane protein	protein_id=KGT41190.1
gene	5128259	5128936	451559	452236	gene=IY08_27190	protein=uracil-DNA glycosylase	protein_id=KGT41191.1
gene	5128956	5129948	452256	453248	gene=IY08_27195	protein=ABC transporter permease	protein_id=KGT41192.1
gene	5129941	5130858	453241	454158	gene=IY08_27200	protein=ABC transporter ATP-binding protein	protein_id=KGT41193.1
gene	5130855	5131664	454155	454964	gene=IY08_27205	protein=lipase	protein_id=KGT41194.1
gene	5131747	5132724	455047	456024	gene=IY08_27210	protein=LacI family transcriptional regulator	protein_id=KGT41195.1
gene	5132822	5133448	456122	456748	gene=IY08_27215	protein=membrane protein	protein_id=KGT41196.1
gene	5133478	5134773	456778	458073	gene=IY08_27220	protein=homoserine dehydrogenase	protein_id=KGT41197.1

gene	5134915	5135820	458215	459120	gene=IY08_27225	protein=homoserine O-succinyltransferase	protein_id=KGT41198.1
gene	5135804	5137102	459104	460402	gene=IY08_27230	protein=O-acetylhomoserine	protein_id=KGT41199.1
gene	5137620	5138849	460920	462149	gene=IY08_27235	protein=chloride channel protein	protein_id=KGT41200.1
gene	5138895	5139590	462195	462890	gene=IY08_27240	protein=HAD family hydrolase	protein_id=KGT41201.1
gene	5139698	5140369	462998	463669	gene=IY08_27245	protein=XRE family transcriptional regulator	protein_id=KGT41202.1
gene	5140430	5141056	463730	464356	gene=IY08_27250	protein=FMN-dependent NADH-azoreductase	protein_id=KGT41203.1
gene	5141248	5141895	464548	465195	gene=IY08_27255	protein=LuxR family transcriptional regulator	protein_id=KGT41204.1
gene	5141916	5143487	465216	466787	gene=IY08_27260	protein=histidine kinase	protein_id=KGT41205.1
gene	5143622	5144446	466922	467746	gene=IY08_27265	protein=pyridoxal kinase	protein_id=KGT41206.1
gene	5144533	5145591	467833	468891	gene=IY08_27270	protein=diguanylate cyclase	protein_id=KGT41207.1
gene	5145737	5145940	469037	469240	gene=IY08_27275	protein=cytosolic protein	protein_id=KGT41208.1
gene	5145933	5148008	469233	471308	gene=IY08_27280	protein=carbon starvation protein A	protein_id=KGT41209.1
gene	5148131	5148847	471431	472147	gene=IY08_27285	protein=chemotaxis protein CheY	protein_id=KGT41210.1
gene	5149066	5150265	472366	473565	gene=IY08_27290	protein=major facilitator transporter	protein_id=KGT41211.1
gene	5150480	5151220	473780	474520	gene=IY08_27295	protein=acetylglucosaminyl diphospho-UDP acetyl-beta-D-mannosaminyltransferase	protein_id=KGT41212.1
gene	5151242	5152351	474542	475651	gene=IY08_27300	protein=glycosyl transferase	protein_id=KGT41213.1
gene	5152447	5153919	475747	477219	gene=IY08_27305	protein=hypothetical protein	protein_id=KGT41214.1
gene	5154384	5155016	477684	478316	gene=IY08_27310	protein=membrane protein	protein_id=KGT41215.1
gene	5155151	5156452	478451	479752	gene=IY08_27315	protein=chemotaxis protein	protein_id=KGT41216.1
gene	5156543	5157856	479843	481156	gene=IY08_27320	protein=membrane protein	protein_id=KGT41217.1
gene	5158155	5158667	481455	481967	gene=IY08_27325	protein=acyl-CoA thioester hydrolase	protein_id=KGT41218.1
gene	5158863	5159306	482163	482606	gene=IY08_27330	protein=hypothetical protein	protein_id=KGT41219.1
gene	5159532	5160512	482832	483812	gene=IY08_27335	protein=beta-1,3-N-acetylglucosaminyltransferase	protein_id=KGT41220.1
gene	5160610	5162025	483910	485325	gene=IY08_27340	protein=sugar translocase	protein_id=KGT41221.1
gene	5162374	5165052	485674	488352	gene=IY08_27345	protein=multidrug transporter	protein_id=KGT41222.1
gene	5165136	5166074	488436	489374	gene=IY08_27350	protein=glycosyltransferase	protein_id=KGT41223.1
gene	5166231	5167784	489531	491084	gene=IY08_27355	protein=heme ABC transporter ATP-binding protein	protein_id=KGT41224.1
gene	5167977	5169371	491277	492671	gene=IY08_27360	protein=acyltransferase	protein_id=KGT41225.1
gene	5169384	5170601	492684	493901	gene=IY08_27365	protein=hypothetical protein	protein_id=KGT41226.1
gene	5170653	5171522	493953	494822	gene=IY08_27370	protein=TetR family transcriptional regulator	protein_id=KGT41227.1

gene	5171663	5174779	494963	498079	gene=IY08_27375	protein=Swarming motility protein SwrC	protein_id=KGT41228.1
gene	5174807	5175772	498107	499072	gene=IY08_27380	protein=methionine sulfoxide reductase	protein_id=KGT41229.1
gene	5175863	5176906	499163	500206	gene=IY08_27385	protein=membrane protein	protein_id=KGT41230.1
gene	5177231	5177923	500531	501223	gene=IY08_27390	protein=antiholin LrgB	protein_id=KGT41231.1
gene	5177959	5178390	501259	501690	gene=IY08_27395	protein=murein hydrolase transporter LrgA	protein_id=KGT41232.1
gene	5178523	5179263	501823	502563	gene=IY08_27400	protein=two-component response regulator	protein_id=KGT41233.1
gene	5179241	5181010	502541	504310	gene=IY08_27405	protein=histidine kinase	protein_id=KGT41234.1
gene	5181335	5182633	504635	505933	gene=IY08_27410	protein=MFS transporter	protein_id=KGT41235.1
gene	5182686	5184254	505986	507554	gene=IY08_27415	protein=BCCT transporter	protein_id=KGT41236.1
gene	5184615	5185685	507915	508985	gene=IY08_27420	protein=nitric oxide synthase	protein_id=KGT41237.1
gene	5185903	5186529	509203	509829	gene=IY08_27425	protein=superoxide dismutase	protein_id=KGT41238.1
gene	5186618	5187496	509918	510796	gene=IY08_27430	protein=epimerase	protein_id=KGT41239.1
gene	5187605	5188195	510905	511495	gene=IY08_27435	protein=acetamide transporter	protein_id=KGT41240.1
gene	5188654	5189670	511954	512970	gene=IY08_27440	protein=UDP-galactose-4-epimerase	protein_id=KGT41241.1
gene	5189855	5190502	513155	513802	gene=IY08_27445	protein=hemolysin	protein_id=KGT41242.1
gene	5190667	5191227	513967	514527	gene=IY08_27450	protein=cytoplasmic protein	protein_id=KGT41243.1
gene	5191268	5192713	514568	516013	gene=IY08_27455	protein=RNA helicase	protein_id=KGT41244.1
gene	5193191	5194174	516491	517474	gene=IY08_27460	protein=guanosine 5'-monophosphate oxidoreductase	protein_id=KGT41245.1
gene	5194310	5194414	517610	517714	gene=IY08_27465	protein=oligoendopeptidase F	protein_id=KGT41246.1
gene	5194452	5195330	517752	518630	gene=IY08_27470	protein=Fe-S oxidoreductase	protein_id=KGT41247.1
gene	5195550	5197568	518850	520868	gene=IY08_27475	protein=ATPase	protein_id=KGT41248.1
gene	5197637	5198116	520937	521416	gene=IY08_27480	protein=50S rRNA methyltransferase	protein_id=KGT41249.1
gene	5198176	5198361	521476	521661	gene=IY08_27485	protein=50S ribosomal protein L31	protein_id=KGT41250.1
gene	5198415	5199590	521715	522890	gene=IY08_27490	protein=2-alkenal reductase	protein_id=KGT41251.1
gene	5199654	5200448	522954	523748	gene=IY08_27495	protein=metallo-beta-lactamase	protein_id=KGT41252.1
gene	5200432	5201274	523732	524574	gene=IY08_27500	protein=hypothetical protein	protein_id=KGT41253.1
gene	5201255	5202571	524555	525871	gene=IY08_27505	protein=hypothetical protein	protein_id=KGT41254.1
gene	5202568	5204409	525868	527709	gene=IY08_27510	protein=histidine kinase	protein_id=KGT41255.1
gene	5204413	5205117	527713	528417	gene=IY08_27515	protein=PhoP family transcriptional regulator	protein_id=KGT41256.1
gene	5205402	5205474	528702	528774	tRNA		
gene	5205516	5205591	528816	528891	tRNA		

gene	5205613	5205684	528913	528984	tRNA		
gene	5205690	5205765	528990	529065	tRNA		
gene	5205907	5207196	529207	530496	gene=IY08_27540	protein=adenylosuccinate synthetase	protein_id=KGT41257.1
gene	5207413	5208774	530713	532074	gene=IY08_27545	protein=DNA helicase	protein_id=KGT41258.1
gene	5208802	5209248	532102	532548	gene=IY08_27550	protein=50S ribosomal protein L9	protein_id=KGT41259.1
gene	5209245	5211218	532545	534518	gene=IY08_27555	protein=hypothetical protein	protein_id=KGT41260.1
gene	5211297	5212232	534597	535532	gene=IY08_27560	protein=membrane protein	protein_id=KGT41261.1
gene	5212313	5212546	535613	535846	gene=IY08_27565	protein=30S ribosomal protein S18	protein_id=KGT41262.1
gene	5212592	5213104	535892	536404	gene=IY08_27570	protein=single-stranded DNA-binding protein	protein_id=KGT41263.1
gene	5213131	5213421	536431	536721	gene=IY08_27575	protein=30S ribosomal protein S6	protein_id=KGT41264.1
gene	5213613	5214713	536913	538013	gene=IY08_27580	protein=GTP-binding protein	protein_id=KGT41265.1
gene	5214829	5215026	538129	538326	gene=IY08_27585	protein=hypothetical protein	protein_id=KGT41266.1
gene	5215047	5215928	538347	539228	gene=IY08_27590	protein=mechanosensitive ion channel protein MscS	protein_id=KGT41267.1
gene	5216188	5216784	539488	540084	gene=IY08_27595	protein=sporulation protein	protein_id=KGT41268.1
gene	5216805	5217662	540105	540962	gene=IY08_27600	protein=plasmid partitioning protein ParB	protein_id=KGT41269.1
gene	5217649	5218410	540949	541710	gene=IY08_27605	protein=sporulation initiation inhibitor Soj	protein_id=KGT41270.1
gene	5218601	5219473	541901	542773	gene=IY08_27610	protein=chromosome partitioning protein ParB	protein_id=KGT41271.1
gene	5219579	5220298	542879	543598	gene=IY08_27615	protein=16S rRNA methyltransferase	protein_id=KGT41272.1
gene	5220320	5222209	543620	545509	gene=IY08_27620	protein=tRNA uridine 5-carboxymethylaminomethyl modification protein	protein_id=KGT41273.1
gene	5222256	5223632	545556	546932	gene=IY08_27625	protein=tRNA modification GTPase	protein_id=KGT41274.1
gene	5223859	5224476	547159	547776	gene=IY08_27630	protein=Jag protein	protein_id=KGT41275.1
gene	5224473	5225240	547773	548540	gene=IY08_27635	protein=OxaA-like protein precursor	protein_id=KGT41276.1
gene	5225293	5225640	548593	548940	gene=IY08_27640	protein=ribonuclease P	protein_id=KGT41277.1
gene	5225717	5225851	549017	549151	gene=IY08_27645	protein=50S ribosomal protein L34	protein_id=KGT41278.1
gene	5226416	5227756	549716	551056	gene=IY08_27650	protein=chromosomal replication initiation protein	protein_id=KGT41279.1
gene	5227935	5229080	551235	552380	gene=IY08_27655	protein=DNA polymerase III subunit beta	protein_id=KGT41280.1
gene	5229208	5229420	552508	552720	gene=IY08_27660	protein=hypothetical protein	protein_id=KGT41281.1
gene	5229433	5230560	552733	553860	gene=IY08_27665	protein=recombinase RecF	protein_id=KGT41282.1
gene	5230599	5232521	553899	555821	gene=gyrB	protein=DNA gyrase subunit B	protein_id=KGT41283.1
gene	5232610	5235081	555910	558381	gene=IY08_27675	protein=DNA gyrase subunit A	protein_id=KGT41284.1

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gene	5235439	5235945	19	525	gene=IY08_27680	protein=hypothetical protein	protein_id=KGT40676.1
gene	5236982	5237359	1562	1939	gene=IY08_27685	protein=GntR family transcriptional regulator	protein_id=KGT40677.1
gene	5237359	5238057	1939	2637	gene=IY08_27690	protein=ABC transporter	protein_id=KGT40678.1
gene	5238054	5238884	2634	3464	gene=IY08_27695	protein=ABC transporter permease	protein_id=KGT40679.1
gene	5238924	5239658	3504	4238	gene=IY08_27700	protein=membrane protein	protein_id=KGT40680.1
gene	5239969	5240244	4549	4824	gene=IY08_27705	protein=hypothetical protein	protein_id=KGT40681.1
gene	5240297	5240530	4877	5110	gene=IY08_27710	protein=hypothetical protein	protein_id=KGT40682.1
gene	5240771	5241004	5351	5584	gene=IY08_27715	protein=hypothetical protein	protein_id=KGT40683.1
gene	5241259	5241423	5839	6003	gene=IY08_27720	protein=phage protein	protein_id=KGT40684.1
gene	5241978	5242454	6558	7034	gene=IY08_27725	protein=transcription factor YdeB	protein_id=KGT40685.1
gene	5242666	5243565	7246	8145	gene=IY08_27730	protein=fatty acid desaturase	protein_id=KGT40686.1
gene	5244111	5244410	8691	8990	gene=IY08_27735	protein=hypothetical protein	protein_id=KGT40687.1
gene	5244949	5245152	9529	9732	gene=IY08_27740	protein=cold-shock protein	protein_id=KGT40688.1
gene	5245558	5246103	10138	10683	gene=IY08_27745	protein=hypothetical protein	protein_id=KGT40689.1
gene	5246229	5246468	10809	11048	gene=IY08_27750	protein=phosphatidylserine synthase	protein_id=KGT40690.1
gene	5246465	5247370	11045	11950	gene=IY08_27755	protein=ABC transporter ATP-binding protein	protein_id=KGT40691.1
gene	5247367	5248155	11947	12735	gene=IY08_27760	protein=membrane protein	protein_id=KGT40692.1
gene	5248631	5249032	13211	13612	gene=IY08_27765	protein=hypothetical protein	protein_id=KGT40693.1
gene	5250818	5251084	15398	15664	gene=IY08_27770	protein=hypothetical protein	protein_id=KGT40694.1
gene	5251978	5252184	16558	16764	gene=IY08_27780	protein=hypothetical protein	protein_id=KGT40695.1
gene	5253391	5253884	17971	18464	pseudo		
gene	5254518	5255996	19098	20576	gene=IY08_27795	protein=GntR family transcriptional regulator	protein_id=KGT40696.1
gene	5256363	5256782	20943	21362	gene=IY08_27800	protein=thioesterase	protein_id=KGT40697.1
gene	5256839	5257615	21419	22195	gene=IY08_27805	protein=phenazine biosynthesis protein	protein_id=KGT40698.1
gene	5257634	5258098	22214	22678	gene=IY08_27810	protein=endoribonuclease L-PSP	protein_id=KGT40699.1
gene	5258836	5259309	23416	23889	gene=IY08_27825	protein=EBSC protein	protein_id=KGT40700.1
gene	5259395	5259757	23975	24337	gene=IY08_27830	protein=hypothetical protein	protein_id=KGT40701.1
gene	5260423	5261424	25003	26004	gene=IY08_27835	protein=excisionase	protein_id=KGT40702.1
gene	5261828	5263000	26408	27580	gene=IY08_27840	protein=integrase	protein_id=KGT40703.1
gene	5263312	5264607	27892	29187	gene=IY08_27845	protein=amino acid permease	protein_id=KGT40704.1

gene	5264758	5265198	29338	29778	gene=IY08_27850	protein=AsnC family transcriptional regulator	protein_id=KGT40705.1
gene	5265368	5265556	29948	30136	gene=IY08_27855	protein=hypothetical protein	protein_id=KGT40706.1
gene	5265537	5266145	30117	30725	gene=IY08_27860	protein=cell division protein Fic	protein_id=KGT40707.1
gene	5266419	5266610	30999	31190	gene=IY08_27865	protein=hypothetical protein	protein_id=KGT40708.1
gene	5266806	5267252	31386	31832	gene=IY08_27870	protein=spermidine acetyltransferase	protein_id=KGT40709.1
gene	5267620	5268570	32200	33150	pseudo		
gene	5269761	5270747	34341	35327	gene=IY08_27880	protein=choloylglycine hydrolase	protein_id=KGT40710.1
gene	5270921	5271148	35501	35728	pseudo		
gene	5271426	5271620	36006	36200	gene=IY08_27890	protein=hypothetical protein	protein_id=KGT40711.1
gene	5271688	5271963	36268	36543	gene=IY08_27895	protein=hypothetical protein	protein_id=KGT40712.1
gene	5272260	5273228	36840	37808	gene=IY08_27900	protein=membrane protein	protein_id=KGT40713.1
gene	5273239	5273898	37819	38478	gene=IY08_27905	protein=GntR family transcriptional regulator	protein_id=KGT40714.1
gene	5274260	5274595	38840	39175	gene=IY08_27910	protein=transposase	protein_id=KGT40715.1
gene	5274618	5274806	39198	39386	gene=IY08_27915	protein=homocysteine methyltransferase	protein_id=KGT40716.1
gene	5276169	5277647	40749	42227	gene=IY08_27920	protein=FAD-binding monooxygenase	protein_id=KGT40717.1
gene	5277893	5278930	42473	43510	gene=IY08_27925	protein=peptidase M15	protein_id=KGT40718.1
gene	5279178	5280011	43758	44591	gene=IY08_27930	protein=peptidase M15	protein_id=KGT40719.1
gene	5280753	5282528	45333	47108	gene=IY08_27935	protein=peptidoglycan-binding protein	protein_id=KGT40720.1
gene	5282596	5283642	47176	48222	gene=IY08_27940	protein=peptidoglycan-binding protein	protein_id=KGT40721.1
gene	5283882	5284823	48462	49403	gene=IY08_27945	protein=endonuclease I	protein_id=KGT40722.1
gene	5285300	5285947	49880	50527	gene=IY08_27950	protein=hypothetical protein	protein_id=KGT40723.1
gene	5287089	5288150	51669	52730	gene=IY08_27960	protein=protease	protein_id=KGT40724.1
gene	5288183	5288500	52763	53080	gene=IY08_27965	protein=hypothetical protein	protein_id=KGT40725.1
gene	5288902	5289978	53482	54558	gene=IY08_27970	protein=recombinase XerS	protein_id=KGT40726.1
gene	5291026	5291502	55606	56082	pseudo		
gene	5292968	5293442	57548	58022	pseudo		
gene	5293956	5295338	58536	59918	gene=IY08_28000	protein=hydrolase	protein_id=KGT40727.1
gene	5295994	5297487	60574	62067	gene=IY08_28005	protein=peptide transporter	protein_id=KGT40728.1
gene	5297726	5298718	62306	63298	gene=IY08_28010	protein=hypothetical protein	protein_id=KGT40729.1
gene	5298832	5298999	63412	63579	gene=IY08_28015	protein=membrane protein	protein_id=KGT40730.1
gene	5299453	5299644	64033	64224	gene=IY08_28020	protein=hypothetical protein	protein_id=KGT40731.1

gene	5301463	5301783	66043	66363	gene=IY08_28025	protein=membrane protein	protein_id=KGT40732.1
gene	5302370	5304838	66950	69418	gene=IY08_28030	protein=ABC transporter permease	protein_id=KGT40733.1
gene	5304835	5305548	69415	70128	gene=IY08_28035	protein=peptide ABC transporter ATP-binding protein	protein_id=KGT40734.1
gene	5305570	5306370	70150	70950	gene=IY08_28040	protein=hypothetical protein	protein_id=KGT40735.1
gene	5307049	5307741	71629	72321	gene=IY08_28045	protein=transcriptional regulator	protein_id=KGT40736.1
gene	5307746	5308978	72326	73558	gene=IY08_28050	protein=histidine kinase	protein_id=KGT40737.1
gene	5309496	5310518	74076	75098	gene=IY08_28055	protein=histidine kinase	protein_id=KGT40738.1
gene	5310515	5311186	75095	75766	gene=IY08_28060	protein=XRE family transcriptional regulator	protein_id=KGT40739.1
gene	5311268	5313256	75848	77836	gene=IY08_28065	protein=ABC transporter	protein_id=KGT40740.1
gene	5313246	5314013	77826	78593	gene=IY08_28070	protein=multidrug ABC transporter ATP-binding protein	protein_id=KGT40741.1
gene	5314281	5314514	78861	79094	gene=IY08_28075	protein=transposase	protein_id=KGT40742.1
gene	5314551	5314840	79131	79420	pseudo		
gene	5315522	5317480	80102	82060	gene=IY08_28090	protein=ABC transporter permease	protein_id=KGT40743.1
gene	5318470	5319471	83050	84051	gene=IY08_28095	protein=teicoplanin resistance protein VanZ	protein_id=KGT40744.1
gene	5320954	5321163	85534	85743	gene=IY08_28100	protein=DNA mismatch repair protein MutT	protein_id=KGT40745.1
gene	5321443	5323272	86023	87852	gene=IY08_28105	protein=ABC transporter permease	protein_id=KGT40746.1
gene	5323289	5324050	87869	88630	gene=IY08_28110	protein=bacitracin ABC transporter ATP-binding protein	protein_id=KGT40747.1
gene	5324300	5325376	88880	89956	gene=IY08_28115	protein=histidine kinase	protein_id=KGT40748.1
gene	5325373	5326059	89953	90639	gene=IY08_28120	protein=DeoR family transcriptional regulator	protein_id=KGT40749.1
gene	5327905	5328288	92485	92868	gene=IY08_28130	protein=alpha-ketoglutarate permease	protein_id=KGT40750.1
gene	5329020	5329490	93600	94070	gene=IY08_28135	protein=NTP pyrophosphohydrolase	protein_id=KGT40751.1
gene	5330142	5331086	94722	95666	gene=IY08_28140	protein=acetyl-CoA carboxylase subunit alpha	protein_id=KGT40752.1
gene	5331119	5331565	95699	96145	gene=IY08_28145	protein=MarR family transcriptional regulator	protein_id=KGT40753.1
gene	5331933	5332238	96513	96818	gene=IY08_28150	protein=transposase	protein_id=KGT40754.1
gene	5332205	5333089	96785	97669	gene=IY08_28155	protein=transposase	protein_id=KGT40755.1
gene	5333688	5334257	98268	98837	gene=IY08_28160	protein=methyltransferase	protein_id=KGT40756.1
gene	5334671	5336086	99251	100666	gene=IY08_28165	protein=phosphatidylinositol phosphodiesterase	protein_id=KGT40757.1
gene	5336651	5338027	101231	102607	gene=IY08_28170	protein=chitin-binding protein	protein_id=KGT40758.1
gene	5339418	5340461	103998	105041	gene=IY08_28175	protein=cell filamentation protein Fic	protein_id=KGT40759.1
gene	5341319	5342827	105899	107407	gene=IY08_28180	protein=spore germination protein	protein_id=KGT40760.1
gene	5342814	5343917	107394	108497	gene=IY08_28185	protein=spore germination protein XA	protein_id=KGT40761.1

gene	5343914	5345041	108494	109621	gene=IY08_28190	protein=spore germination protein XA	protein_id=KGT40762.1
gene	5346892	5347440	111472	112020	gene=IY08_28205	protein=hypothetical protein	protein_id=KGT40763.1
gene	5347731	5350454	112311	115034	gene=IY08_28210	protein=fibronectin	protein_id=KGT40764.1
gene	5350559	5352925	115139	117505	gene=IY08_28215	protein=fibronectin	protein_id=KGT40765.1
gene	5353453	5355693	118033	120273	gene=IY08_28220	protein=hypothetical protein	protein_id=KGT40766.1
gene	5356139	5356333	120719	120913	gene=IY08_28225	protein=hypothetical protein	protein_id=KGT40767.1
gene	5356445	5356738	121025	121318	gene=IY08_28230	protein=ArsR family transcriptional regulator	protein_id=KGT40768.1
gene	5357522	5358616	122102	123196	gene=IY08_28235	protein=histidine kinase	protein_id=KGT40769.1
gene	5359370	5359783	123950	124363	gene=IY08_28245	protein=hypothetical protein	protein_id=KGT40770.1
gene	5360327	5360620	124907	125200	gene=IY08_28250	protein=ArsR family transcriptional regulator	protein_id=KGT40771.1
gene	5360681	5361133	125261	125713	gene=IY08_28255	protein=2-oxoglutarate dehydrogenase	protein_id=KGT40772.1
gene	5361176	5361463	125756	126043	pseudo		
gene	5361536	5361739	126116	126319	gene=IY08_28265	protein=hypothetical protein	protein_id=KGT40773.1
gene	5361791	5362386	126371	126966	pseudo		
gene	5362479	5362689	127059	127269	pseudo		
gene	5362864	5362980	127444	127560	gene=IY08_28280	protein=DNA topoisomerase I	protein_id=KGT40774.1
gene	5363185	5364042	127765	128622	gene=IY08_28285	protein=glucose transporter GlcU	protein_id=KGT40775.1
gene	5364059	5364844	128639	129424	gene=IY08_28290	protein=sugar dehydrogenase	protein_id=KGT40776.1
gene	5365170	5365595	129750	130175	gene=IY08_28295	protein=hypothetical protein	protein_id=KGT40777.1
gene	5366238	5366972	130818	131552	gene=IY08_28305	protein=DNA integration/recombination/inversion protein	protein_id=KGT40778.1
gene	5367273	5367908	131853	132488	gene=IY08_28315	protein=hypothetical protein	protein_id=KGT40779.1
gene	5367925	5368308	132505	132888	gene=IY08_28320	protein=hypothetical protein	protein_id=KGT40780.1
gene	5368605	5369240	133185	133820	gene=IY08_28325	protein=hypothetical protein	protein_id=KGT40781.1
gene	5369237	5369869	133817	134449	gene=IY08_28330	protein=hypothetical protein	protein_id=KGT40782.1
gene	5371505	5372431	136085	137011	gene=IY08_28335	protein=hypothetical protein	protein_id=KGT40783.1
gene	5373582	5375195	138162	139775	gene=IY08_28340	protein=N-acetylmuramoyl-L-alanine amidase	protein_id=KGT40784.1
gene	5376408	5376704	140988	141284	gene=IY08_28345	protein=hypothetical protein	protein_id=KGT40785.1
gene	5377134	5377301	141714	141881	gene=IY08_28355	protein=transposase	protein_id=KGT40786.1
gene	5377774	5378448	142354	143028	gene=IY08_28365	protein=hypothetical protein	protein_id=KGT40787.1
gene	5378704	5378955	143284	143535	gene=IY08_28370	protein=hypothetical protein	protein_id=KGT40788.1
gene	5379095	5379868	143675	144448	gene=IY08_28375	protein=hypothetical protein	protein_id=KGT40789.1

gene	5380001	5380969	144581	145549	gene=IY08_28380	protein=ornithine cyclodeaminase	protein_id=KGT40790.1
gene	5380997	5381974	145577	146554	gene=IY08_28385	protein=pyridoxal-5'-phosphate-dependent protein subunit	protein_id=KGT40791.1
gene	5382095	5383027	146675	147607	gene=IY08_28390	protein=ornithine carbamoyltransferase	protein_id=KGT40792.1
gene	5383816	5384514	148396	149094	gene=IY08_28400	protein=4-phosphopantetheinyl transferase	protein_id=KGT40793.1
gene	5384763	5391299	149343	155879	gene=IY08_28405	protein=peptide synthetase	protein_id=KGT40794.1
gene	5391541	5392239	156121	156819	gene=IY08_28410	protein=surfactin synthetase	protein_id=KGT40795.1
gene	5392316	5396812	156896	161392	gene=IY08_28415	protein=peptide synthetase	protein_id=KGT40796.1
gene	5396794	5397873	161374	162453	gene=IY08_28420	protein=FkbH	protein_id=KGT40797.1
gene	5397870	5400953	162450	165533	gene=IY08_28425	protein=peptide ABC transporter	protein_id=KGT40798.1
gene	5400969	5402045	165549	166625	gene=IY08_28430	protein=alkanesulfonate monooxygenase	protein_id=KGT40799.1
gene	5402064	5409752	166644	174332	gene=IY08_28435	protein=gramicidin synthetase	protein_id=KGT40800.1
gene	5409727	5411304	174307	175884	gene=IY08_28440	protein=peptide synthetase	protein_id=KGT40801.1
gene	5411301	5412494	175881	177074	gene=IY08_28445	protein=acyl-CoA dehydrogenase	protein_id=KGT40802.1
gene	5412494	5412739	177074	177319	gene=IY08_28450	protein=acyl carrier protein	protein_id=KGT40803.1
gene	5412770	5413618	177350	178198	gene=IY08_28455	protein=3-hydroxybutyryl-CoA dehydrogenase	protein_id=KGT40804.1
gene	5413659	5414876	178239	179456	gene=IY08_28460	protein=malonyl CoA-acyl carrier protein	protein_id=KGT40805.1
gene	5414896	5416023	179476	180603	gene=IY08_28465	protein=antibiotic resistance protein	protein_id=KGT40806.1
gene	5416020	5417168	180600	181748	gene=IY08_28470	protein=acyl-CoA dehydrogenase	protein_id=KGT40807.1
gene	5417165	5417428	181745	182008	gene=IY08_28475	protein=acyl carrier protein	protein_id=KGT40808.1
gene	5417461	5420112	182041	184692	gene=IY08_28480	protein=bacitracin synthetase	protein_id=KGT40809.1
gene	5420431	5426154	185011	190734	gene=IY08_28485	protein=lichenysin synthetase	protein_id=KGT40810.1
gene	5426181	5436191	190761	200771	gene=IY08_28490	protein=beta-ketoacyl synthase	protein_id=KGT40811.1
gene	5438103	5438759	202683	203339	gene=IY08_28500	protein=hypothetical protein	protein_id=KGT40812.1
gene	5438929	5440344	203509	204924	gene=IY08_28505	protein=2-isopropylmalate synthase	protein_id=KGT40813.1
gene	5440341	5441405	204921	205985	gene=IY08_28510	protein=hydrolase	protein_id=KGT40814.1
gene	5441420	5441857	206000	206437	gene=IY08_28515	protein=hypothetical protein	protein_id=KGT40815.1
gene	5441872	5442738	206452	207318	gene=IY08_28520	protein=molybdopterin biosynthesis protein MoeB	protein_id=KGT40816.1
gene	5442752	5443600	207332	208180	gene=IY08_28525	protein=molybdopterin biosynthesis protein MoeB	protein_id=KGT40817.1
gene	5445461	5445850	210041	210430	gene=IY08_28540	protein=hypothetical protein	protein_id=KGT40818.1
gene	5445874	5446383	210454	210963	gene=IY08_28545	protein=hypothetical protein	protein_id=KGT40819.1
gene	5446478	5446930	211058	211510	gene=IY08_28550	protein=histidine kinase	protein_id=KGT40820.1

gene	5447280	5448680	211860	213260	gene=IY08_28565	protein=multidrug transporter MatE	protein_id=KGT40821.1
gene	5449610	5450476	214190	215056	gene=IY08_28570	protein=alpha/beta hydrolase	protein_id=KGT40822.1
gene	5450544	5451746	215124	216326	gene=IY08_28575	protein=glycosyl transferase	protein_id=KGT40823.1
gene	5452040	5452570	216620	217150	gene=IY08_28580	protein=GNAT family acetyltransferase	protein_id=KGT40824.1
gene	5452980	5453951	217560	218531	gene=IY08_28585	protein=esterase	protein_id=KGT40825.1

prot_acc	prot_desc	prot_score	prot_mass	pep_query	pep_exp_mz	pep_exp_mr	pep_score	pep_expect	pep_res_before	pep_seq	pep_res_after
KGT40398.1	bacteriocin ABC transporter ATPase, partial [Bacillus cereus]	30	32920	72	487.28	972.545	30.1	0.0062	K	EINRTALR	N
KGT40399.1	GntR family transcriptional regulator, partial [Bacillus cereus]	14	32148	551	695.86	1389.71	14	0.049	R	VALSSTNSLEEL	I
KGT40407.1	carbonic anhydrase [Bacillus cereus]	21	21397	337	679.356	678.348	21.2	0.036	K	TLNGMK	H
KGT40418.1	fibronectin [Bacillus cereus]	82	82074	1745	732.862	1463.71	82.3	2.60E-08	K	ISSGTWENNSN	N
KGT40418.1	fibronectin [Bacillus cereus]	82	82074	816	372.894	1115.66	10.8	0.15	K	KK	N
KGT40418.1	fibronectin [Bacillus cereus]	82	82074	816	372.894	1115.66	10.8	0.15	K	KIYPNKPTR	L
KGT40418.1	fibronectin [Bacillus cereus]	82	82074	2887	774.058	2319.15	8.17	0.17	K	YIVNQDPVPPLL	A
KGT40445.1	PhoP family transcriptional regulator [Bacillus cereus]	22	27678	951	587.322	1172.63	21.8	0.046	K	NKYDEMIR	D
KGT40513.1	hypothetical protein IY08_29645 [Bacillus cereus]	26	27214	176	604.318	1206.62	26.3	0.007	K	KNILIVDDDK	N
KGT40513.1	hypothetical protein IY08_29645 [Bacillus cereus]	26	27214	149	575.81	1149.61	8.05	1	K	EKELMEGSIR	W
KGT40528.1	aspartate phosphatase [Bacillus cereus]	21	41847	670	777.401	1552.79	21	0.036	K	RLTSNAFEGR	T
KGT40610.1	hypothetical protein IY08_28935 [Bacillus cereus]	23	7379	240	616.404	615.396	23.3	0.033	K	ANEVFSISPGYE	Q
KGT40688.1	cold-shock protein [Bacillus cereus]	23	7406	159	590.308	1178.6	22.5	0.037	K	KDLLK	G
KGT40714.1	GntR family transcriptional regulator [Bacillus cereus]	23	24995	240	616.404	615.396	23.3	0.033	K	GNVKWVFNGEK	S
KGT40760.1	spore gernimation protein [Bacillus cereus]	23	56084	144	421.759	841.504	1.92	1.5	K	KDIK	Y
KGT40760.1	spore gernimation protein [Bacillus cereus]	23	56084	462	652.812	1303.61	23.3	0.019	K	NIGLIRR	N
KGT40764.1	fibronectin [Bacillus cereus]	0	1E+05	275	635.336	634.329	4.67	1.6	K	GSHDGFIENTV	S
KGT40765.1	fibronectin [Bacillus cereus]	26	88818	240	616.404	615.396	25.7	0.019	K	K	N
KGT40826.1	acyl-CoA dehydrogenase [Bacillus cereus]	73	65683	606	552.811	1103.61	40.8	0.00017	K	KVQIK	L

KGT40826.1	acyl-CoA dehydrogenase [Bacillus	73	65683	750	596.802	1191.59	49.8	6.10E-05	R	IFEGTNEINR	L
KGT40826.1	acyl-CoA dehydrogenase [Bacillus	77	65683	489	508.32	1014.63	7.63	0.22	R	LIVPGTFLR	K
KGT40826.1	acyl-CoA dehydrogenase [Bacillus	77	65683	676	573.774	1145.53	15.5	0.11	K	TYAAESSVYR	T
KGT40826.1	acyl-CoA dehydrogenase [Bacillus cereus]	77	65683	1441	896.461	1790.91	19.6	0.015	K	LAAYALTEPGS	
										GSDALGAK	T
KGT40863.1	peptidase M4 [Bacillus cereus]	38	60513	1540	697.346	1392.68	38.1	0.00027	R	QAALQSAEDLY	
										GK	N
										YTGTADNGGV	
KGT40863.1	peptidase M4 [Bacillus cereus]	39	60513	2551	654.978	1961.91	14.6	0.043	R	HINSSINNK	A
KGT40863.1	peptidase M4 [Bacillus cereus]	385	60513	227	529.762	1057.51	40.1	0.00031	K	YLTANSDFK	M
KGT40863.1	peptidase M4 [Bacillus cereus]	385	60513	286	563.782	1125.55	57.6	7.90E-06	K	TGQFNLFDGK	R
KGT40863.1	peptidase M4 [Bacillus cereus]	385	60513	314	583.786	1165.56	46.9	0.00011	R	QSFEIAQDTK	T
KGT40863.1	peptidase M4 [Bacillus cereus]	385	60513	431	641.83	1281.65	67.6	9.90E-07	K	TGQFNLFDGKR	G
KGT40863.1	peptidase M4 [Bacillus cereus]	385	60513	676	522.592	1564.75	69.8	6.10E-07	K	AAYLVSEGGDH	
										YGVK	V
										QAALQSAEDLY	
KGT40863.1	peptidase M4 [Bacillus cereus]	385	60513	786	574.962	1721.86	25.7	0.0039	R	GKNSK	A
										SWDLGADIYTP	
KGT40863.1	peptidase M4 [Bacillus cereus]	385	60513	1087	697.346	2089.02	74.9	9.50E-08	K	DKPGDALR	S
										NESGALNESLS	
KGT40863.1	peptidase M4 [Bacillus cereus]	390	60513	1169	751.036	2250.09	22.3	0.018	K	DIMGVMVEKK	S
KGT40883.1	adhesin [Bacillus cereus]	47	34294	397	624.817	1247.62	46.7	6.10E-05	K	QIDINDLDFR	N
KGT40883.1	adhesin [Bacillus cereus]	49	34294	208	520.269	1038.52	18	0.021	K	QTPAGGFSFK	V
										SPQELGVSDW	
KGT40883.1	adhesin [Bacillus cereus]	49	34294	424	637.801	1273.59	1.31	2.4	K	R	E
										GTPTIQNAVVL	
KGT40883.1	adhesin [Bacillus cereus]	182	34294	115	756.427	1510.84	53.2	1.60E-05	K	LER	S
										EAHYATQLAV	
KGT40883.1	adhesin [Bacillus cereus]	182	34294	151	572.304	1713.89	28.3	0.0039	R	WNALK	Q
										NDFFETGLYTV	
KGT40883.1	adhesin [Bacillus cereus]	182	34294	178	924.94	1847.87	5.73	0.29	K	ETNAK	S

									ASASEELQEIT	
									MSVTPTEEQEA	
KGT40883.1	adhesin [Bacillus cereus]	182	34294	360	907.466	2719.38	1.93	2.9 K	VLK	N
KGT40917.1	enolase [Bacillus cereus]	72	46417	1004	678.888	1355.76	43.9	0.00011 R	EALEVIIIEAIEK	A
									GLNTAVGDEG	
KGT40917.1	enolase [Bacillus cereus]	72	46417	1571	973.469	1944.92	30.4	0.0014 K	GFAPNLGSNR	E
									LGANAILGVSM	
									AVAHAAADFV	
KGT40917.1	enolase [Bacillus cereus]	72	46417	1922	905.17	2712.49	27.4	0.0025 K	GLPLYR	Y
KGT40917.1	enolase [Bacillus cereus]	80	46417	517	519.284	1036.55	23.3	0.018 M	STIIDVYAR	E
KGT40917.1	enolase [Bacillus cereus]	80	46417	763	602.801	1203.59	18.4	0.03 R	AMIELDGTPNK	G
									ESIRMGAEVFH	
KGT40917.1	enolase [Bacillus cereus]	80	46417	1283	802.43	1602.84	1.45	3.9 K	ALK	A
									IEDELGEIAVYD	
KGT40917.1	enolase [Bacillus cereus]	80	46417	1345	832.424	1662.83	13.2	0.058 R	GIK	S
									VQLVGDDLFT	
KGT40917.1	enolase [Bacillus cereus]	80	46417	1363	838.949	1675.88	15.1	0.15 K	NTQK	L
									IGDKVQLVGDD	
KGT40917.1	enolase [Bacillus cereus]	42	46417	526	697.378	2089.11	25.9	0.0088 R	LFVTNTQK	L
KGT40918.1	phosphoglyceromutase [Bacillus	65	56403	429	483.277	964.539	26.8	0.008 R	VVYQSLTR	V
	phosphoglyceromutase [Bacillus								ETGVGQFATIS	
KGT40918.1	cereus]	65	56403	957	661.837	1321.66	55.9	9.10E-06 K	GR	Y
KGT40918.1	phosphoglyceromutase [Bacillus	65	56403	551	532.242	1062.47	14.3	0.1 R	EAEFPGEER	I
									EGGILGDIAPT	
	phosphoglyceromutase [Bacillus								MLTLLNVEQPK	
KGT40918.1	cereus]	65	56403	1972	963.163	2886.47	5.5	1.3 R	EMTGK	T
	phosphoglycerate kinase [Bacillus								IVGIDSIPSNWE	
KGT40920.1	cereus]	43	42485	1586	998.525	1995.04	29.2	0.0057 K	GVDIGPK	T
									AVGQALADAE	
	phosphoglycerate kinase [Bacillus								DTYSVIGGGDS	
KGT40920.1	cereus]	43	42485	1869	855.752	2564.24	33.4	0.0024 K	AAAVEK	F

KGT40920.1	phosphoglycerate kinase [Bacillus cereus]	43	42485	1261	528.926	1583.76	3.89	0.49	R	FYAGEEEKNDALAK	E
KGT40920.1	phosphoglycerate kinase [Bacillus cereus]	43	42485	1403	581.328	1740.96	7.95	0.34	K	ALSNPERPFTAIIGGAK	V
KGT40920.1	phosphoglycerate kinase [Bacillus cereus]	43	42485	1982	747.148	2984.56	8.96	0.33	R	AHASTAGIADYLPAVSGLLMEK	A
KGT40920.1	phosphoglycerate kinase [Bacillus cereus]	17	42485	964	657.384	1969.13	16.7	0.025	K	ELDVLGKALSNPERPFTAI	D
KGT40920.1	phosphoglycerate kinase [Bacillus cereus]	34	42485	260	679.007	2034	2.62	0.62	K	IGGAKVKEFAALADIFVN	A
KGT40974.1	cytochrome C~ [Bacillus cereus]	27	11357	1576	703.331	1404.65	27	0.0075	R	DAFGAAHRGSMSPGLIQGE	K
KGT40974.1	cytochrome C~ [Bacillus cereus]	27	11357	1071	613.829	1225.64	9.68	0.37	K	DAK	-
KGT41074.1	3-hydroxyacyl-ACP dehydratase [Bacillus cereus]	71	16047	613	497.782	993.55	27.3	0.0048	R	KVSEWLAEHK	I
KGT41074.1	3-hydroxyacyl-ACP dehydratase [Bacillus cereus]	71	16047	713	529.794	1057.57	62.6	3.20E-06	K	YPFLLVDK	A
KGT41074.1	3-hydroxyacyl-ACP dehydratase [Bacillus cereus]	71	16047	1007	599.844	1197.67	5.69	0.66	K	ILEVDEGKR	L
KGT41081.1	transcriptional regulator [Bacillus cereus]	17	38652	1973	773.404	1544.79	16.6	0.055	K	KQVRPGDQLRANQLPEMELKV	G
KGT41101.1	ATP FOF1 synthase subunit beta [Bacillus cereus]	180	50936	2389	899.952	1797.89	104	1.70E-10	R	EK	Q
KGT41101.1	ATP FOF1 synthase subunit beta [Bacillus cereus]	195	50936	1052	610.814	1219.61	23	0.011	R	ALSPEIVGEEHY	V
KGT41101.1	ATP FOF1 synthase subunit beta [Bacillus cereus]	195	50936	1268	651.84	1301.67	3.35	1.5	R	QAPAFEELSTK	F
KGT41101.1	ATP FOF1 synthase subunit beta [Bacillus cereus]	195	50936	1904	757.91	1513.81	2.03	2.7	K	VTQIMGPVVDVK	F
KGT41101.1	ATP FOF1 synthase subunit beta [Bacillus cereus]	195	50936	2488	637.308	1908.9	17.3	0.024	K	GRVTQIMGPVVDVK	L

KGT41101.1	ATP FOF1 synthase subunit beta [Bacillus cereus]	59	50936	834	626.816	1251.62	24.8	0.0048	R	TVAMSSTDGLV R	G
KGT41101.1	ATP FOF1 synthase subunit beta [Bacillus cereus]	59	50936	1111	718.383	1434.75	38.2	0.00026	R	FTQAGSEVSAL LGR	M
KGT41101.1	ATP FOF1 synthase subunit beta [Bacillus cereus]	59	50936	850	630.865	1259.72	3.98	1.2	K	LPEIYNALTVK	Q
KGT41101.1	ATP FOF1 synthase subunit beta [Bacillus cereus]	57	50936	296	685.88	1369.75	43.8	0.00014	R	LVGGIEEVIENA K	K
KGT41101.1	ATP FOF1 synthase subunit beta [Bacillus cereus]	57	50936	557	742.727	2225.16	30.9	0.0032	R	GTEVEDTGKPIS VPVGDVTLGR	V
KGT41101.1	ATP FOF1 synthase subunit beta [Bacillus cereus]	61	50936	73	488.285	974.555	4.46	1.1	K	IGLFGGAGVGK	T
KGT41102.1	ATP synthase FOF1 subunit gamma [Bacillus cereus]	65	31586	1349	665.375	1328.73	64.6	1.10E-06	K	IQEVVASIAQGS K	G
KGT41102.1	ATP synthase FOF1 subunit gamma [Bacillus cereus]	51	31586	366	610.82	1219.62	51.3	1.50E-05	R	GLAGGYNSNVL R	T
KGT41103.1	ATP FOF1 synthase subunit alpha [Bacillus cereus]	59	54656	653	512.811	1023.61	58.7	1.40E-06	K	AIDALVPIGR	G
KGT41103.1	ATP FOF1 synthase subunit alpha [Bacillus cereus]	59	54656	557	469.756	937.497	4.12	1.7	K	FAAAINGFK	K
KGT41103.1	ATP FOF1 synthase subunit alpha [Bacillus cereus]	35	54656	747	595.372	1188.73	34.6	0.00035	K	QVIILYALTR	G
KGT41112.1	serine hydroxymethyltransferase [Bacillus cereus]	71	45282	516	438.251	874.488	71	4.30E-07	R	IGTAAVTSR	G
KGT41112.1	serine hydroxymethyltransferase [Bacillus cereus]	71	45282	1541	697.352	1392.69	5.17	0.33	K	TYAQNIINNAN R	L
KGT41112.1	serine hydroxymethyltransferase [Bacillus cereus]	23	45282	282	559.327	1116.64	23.4	0.017	K	LIVAGASAYPR AVAFGEALQD	V
KGT41112.1	serine hydroxymethyltransferase [Bacillus cereus]	23	45282	1319	928.464	2782.37	13	0.26	K	DFKTYAQNIIN NANR	L

	tRNA threonylcarbamoyladenosine										
KGT41121.1	biosynthesis protein [Bacillus	15	37430	45	544.296	1086.58	15.3		0.037	K	VTAGLNTVGVR M
	3-hydroxybutyryl-CoA										VPVEVNDPFGF
KGT41139.1	dehydrogenase [Bacillus cereus]	53	31475	145	838.423	1674.83	53.2		1.00E-05	K	VSNR I
	3-hydroxybutyryl-CoA										ILLPMINEAIYTL
KGT41139.1	dehydrogenase [Bacillus cereus]	57	31475	295	756.744	2267.21	21		0.029	R	YEGVATK E
											ANVAASDVEEV
	acetyl-CoA acetyltransferase										IFGTVIQGGQG
KGT41140.1	[Bacillus cereus]	33	41248	1931	914.815	2741.42	33.4		0.0017	R	QIPSR Q
KGT41154.1	aminopeptidase [Bacillus cereus]	19	50758	509	864.404	863.397	19.5		0.047	K	SEEWASR Y
	spermidine synthase [Bacillus										QYLPSIAGALD
KGT41164.1	cereus]	36	31123	994	668.023	2001.05	35.7		0.0012	K	NERVEVK V
	ferrichrome ABC transporter										DMILDEVAEFV
KGT41173.1	substrate-binding protein [Bacillus	38	35208	129	797.911	1593.81	23.2		0.0067	K	LGK -
	ferrichrome ABC transporter										IYGDYGYGSVIF
KGT41173.1	substrate-binding protein [Bacillus	38	35208	302	778.083	2331.23	31.1		0.0027	R	NDLKLPAVK G
	phosphotransacetylase [Bacillus										LAKEELVKPILV
KGT41180.1	cereus]	21	34825	2227	560.345	1678.01	21.2		0.0076	R	GNR E
	phosphotransacetylase [Bacillus										SPETEKVVEAT
KGT41180.1	cereus]	19	34825	508	673.347	1344.68	10.7		0.099	K	R I
	phosphotransacetylase [Bacillus										GDANVFVFPSL
KGT41180.1	cereus]	19	34825	985	999.506	1997	19.2		0.016	K	EAGNIGYK I
	phosphotransacetylase [Bacillus										GISIVLPEGTDE
KGT41180.1	cereus]	19	34825	1090	699.386	2095.14	15.1		0.069	K	RILGAAER L
											LGNFEAVGPIL
	phosphotransacetylase [Bacillus										QGLNMPVNDL
KGT41180.1	cereus]	19	34825	1236	619.052	2472.18	2.33		0.6	R	SR G
											YGEFGTFFVGN
KGT41181.1	heme peroxidase [Bacillus cereus]	30	28759	1775	763.719	2288.13	30		0.0015	R	ILPDEKVEK F
	spore germination protein GerQ										
KGT41184.1	[Bacillus cereus]	91	16090	1002	599.299	1196.58	57		1.00E-05	K	QATVVMTYER G
	hypothetical protein IY08_27505										
KGT41254.1	[Bacillus cereus]	23	49969	240	616.404	615.396	23.3		0.033	K	KQVIK D

KGT41291.1	cell surface protein [Bacillus cereus]	23	3E+05	240	616.404	615.396	23.3	0.033	M	KQVLK	C
KGT41291.1	cell surface protein [Bacillus cereus]	23	3E+05	491	421.231	840.448	2	1.6	K	TVNNPAPK	L
KGT41291.1	cell surface protein [Bacillus cereus]	23	3E+05	506	430.242	858.469	4.76	1.5	K	IASNKTPK	L
										VMAKYPEITDT	
KGT41291.1	cell surface protein [Bacillus cereus]	23	3E+05	2228	841.392	1680.77	0.51	3.8	K	EER	S
										QNNDNGIEFLS	
KGT41291.1	cell surface protein [Bacillus cereus]	23	3E+05	2819	1113.5	2224.99	1.48	1.9	K	QSVKVNGEK	L
	methionine ABC transporter									IKDGVDPVSAT	
KGT41343.1	substrate-binding protein [Bacillus	62	29878	1337	663.869	1325.72	62.1	1.90E-06	K	PK	D
	glucose-6-phosphate isomerase									ALSFIGEHEITYL	
KGT41362.1	[Bacillus cereus]	162	50391	2177	824.942	1647.87	81.5	3.30E-08	K	R	D
	glucose-6-phosphate isomerase									TLADNEGYETF	
KGT41362.1	[Bacillus cereus]	51	50391	1704	1084.52	2167.02	26.2	0.0095	K	VIPDDVGGR	F
										GIFPSSANFSTD	
	glucose-6-phosphate isomerase									LHSLGQYVQEG	
KGT41362.1	[Bacillus cereus]	51	50391	1895	870.755	2609.24	8.4	0.77	K	R	R
										TGAGNDFLGW	
	glucose-6-phosphate isomerase									VDLPLQYDKEE	
KGT41362.1	[Bacillus cereus]	51	50391	1929	914.45	2740.33	5.41	1.4	K	FAR	I
	glucose-6-phosphate isomerase										
KGT41362.1	[Bacillus cereus]	30	50391	210	625.823	1249.63	23.6	0.026	K	SGTTTEPALAFR	I
										GAAAGRDDFG	
	glucose-6-phosphate isomerase									TSELEENPAYQ	
KGT41362.1	[Bacillus cereus]	30	50391	598	929.434	2785.28	24.5	0.015	K	YAVVR	N
	sporulation inhibitor KapD [Bacillus										
KGT41375.1	cereus]	19	23980	452	495.28	988.544	19	0.048	K	GISFPELVK	K
KGT41384.1	phosphoglucomutase [Bacillus	204	64271	440	488.279	974.543	31.4	0.0041	K	TIVTSEIGR	T
	phosphoglucomutase [Bacillus										
KGT41384.1	cereus]	204	64271	1101	713.878	1425.74	57.4	7.40E-06	K	TLYDGLLEVFEK	Y
	phosphoglucomutase [Bacillus									AYGLDVTDTLT	
KGT41384.1	cereus]	204	64271	1187	750.885	1499.75	68.4	6.90E-07	K	GFK	F
	phosphoglucomutase [Bacillus									GITTYVFESLRP	
KGT41384.1	cereus]	204	64271	1808	785.104	2352.29	101	1.20E-10	R	TPVLSFAVR	H

KGT41384.1	phosphoglucomutase [Bacillus cereus]	211	64271	1214	764.385	1526.76	17.4	0.097	K	VGADVLIATDP DADR	L
KGT41384.1	phosphoglucomutase [Bacillus cereus]	211	64271	1376	563.305	1686.89	21.4	0.034	K	YGFFREDLVSLT LK	G
KGT41384.1	phosphoglucomutase [Bacillus cereus]	211	64271	1400	577.611	1729.81	3.06	2.4	K	SPNPEEHAAFE YAIR	D
KGT41384.1	phosphoglucomutase [Bacillus cereus]	211	64271	1761	753.677	2258.01	11	0.28	K	YQLEDGSWFCL RPSGTEPK	I
KGT41384.1	phosphoglucomutase [Bacillus cereus]	211	64271	1979	980.183	2937.53	23.7	0.018	K	TDGLLHIIGQEV DDAYAAELNN VIINK	E
KGT41441.1	dihydropteridine reductase [Bacillus cereus]	16	76068	261	628.347	627.34	7.64	0.17	K	QKHSK	K
KGT41441.1	dihydropteridine reductase [Bacillus cereus]	16	76068	1420	675.84	1349.67	15.5	0.053	R	SSNVAFAILGD QK	L
KGT41442.1	cell division protein FtsL [Bacillus cereus]	24	13653	290	645.397	644.39	23.6	0.027	M	TNLAVK	Y
KGT41495.1	dihydrolipoamide dehydrogenase [Bacillus cereus]	240	49593	188	611.286	1220.56	58.3	4.50E-06	R	GIIEIDEQCR	T
KGT41495.1	dihydrolipoamide dehydrogenase [Bacillus cereus]	240	49593	290	678.335	1354.66	41.3	0.00013	R	GEAYFVDANTL R	V
KGT41495.1	dihydrolipoamide dehydrogenase [Bacillus cereus]	240	49593	355	752.853	1503.69	60.1	4.20E-06	R	VMTEDAAQTY TFK	N
KGT41495.1	dihydrolipoamide dehydrogenase [Bacillus cereus]	240	49593	414	818.891	1635.77	26.7	0.01	K	ANLGGVCLNV GCIPSK	A
KGT41495.1	dihydrolipoamide dehydrogenase [Bacillus cereus]	240	49593	442	867.973	1733.93	67.1	7.30E-07	R	ALSLNSTDGFL QLVTR	K
KGT41495.1	dihydrolipoamide dehydrogenase [Bacillus cereus]	246	49593	76	493.802	985.59	22.9	0.016	K	LTGGVEGLLK	G
KGT41495.1	dihydrolipoamide dehydrogenase [Bacillus cereus]	246	49593	377	769.944	1537.87	9.86	0.21	R	VINSTGALSLEI PK	K
KGT41495.1	dihydrolipoamide dehydrogenase [Bacillus cereus]	246	49593	422	556.639	1666.89	12.8	0.22	R	RPNTQEIGLEQ VGVK	M

KGT41495.1	dihydrolipoamide dehydrogenase [Bacillus cereus]	246	49593	434	857.978	1713.94	16.7	0.07	K	NAVLATGSTPIE IPGFK	Y
KGT41495.1	dihydrolipoamide dehydrogenase [Bacillus cereus]	246	49593	549	729.411	2185.21	13	0.068	R	TNVPNIYAIGDI VPGPPLAHK	A
KGT41496.1	branched-chain alpha-keto acid dehydrogenase subunit E2 [Bacillus cereus]	36	45930	1103	714.861	1427.71	35.7	0.00045	K	AQPIPAGEYPE TR	E
KGT41496.1	branched-chain alpha-keto acid dehydrogenase subunit E2 [Bacillus cereus]	36	45930	1599	670.371	2008.09	7.74	0.46	K	NGEIVAAPVLA LSLSFDHR	L
KGT41529.1	5- methyltetrahydropteroyltriglutamat e--homocysteine methyltransferase	34	87398	668	570.326	1138.64	34.2	0.00069	R	VIQVDEPALR	E
KGT41550.1	acetyl-CoA acetyltransferase [Bacillus cereus]	33	42042	905	576.853	1151.69	32.9	0.00051	R	ITVSLIHELK	R
KGT41550.1	acetyl-CoA acetyltransferase [Bacillus cereus]	33	42042	587	484.248	966.481	1.34	4.3	K	QHRWGQR	L
KGT41550.1	acetyl-CoA acetyltransferase [Bacillus cereus]	74	42042	618	556.318	1110.62	51.3	1.60E-05	K	IMGIGPAPAIR IVGYSVAGVDP	K
KGT41550.1	acetyl-CoA acetyltransferase [Bacillus cereus]	74	42042	767	602.833	1203.65	39.5	0.0003	R	K	I
KGT41550.1	acetyl-CoA acetyltransferase [Bacillus cereus]	74	42042	802	409.558	1225.65	2.55	1.8	-	MHNVVITAAV R	S
KGT41550.1	acetyl-CoA acetyltransferase [Bacillus cereus]	74	42042	1536	955.005	1907.99	4.17	0.41	K	AIESGYFDDQIV PITIK	E
KGT41550.1	acetyl-CoA acetyltransferase [Bacillus cereus]	74	42042	1575	977.009	1952	12.7	0.065	R	TAALAAGFPDT VTGYTIQR	Q
KGT41550.1	acetyl-CoA acetyltransferase [Bacillus cereus]	108	42042	218	903.524	1805.03	35.2	0.00031	K	NVTPVELAVPV LQEAVK	R
KGT41550.1	acetyl-CoA acetyltransferase [Bacillus cereus]	108	42042	247	654.72	1961.14	51.6	6.90E-06	K	NVTPVELAVPV LQEAVKR	G
KGT41568.1	hypothetical protein IY08_20415 [Bacillus cereus]	34	13334	1703	726.313	1450.61	33.7	0.00047	K	YDFEPEFEYGR	D

KGT41568.1	hypothetical protein IY08_20415 [Bacillus cereus]	34	13334	2902	783.338	2346.99	0.79	1.4 K	FDEMIDTVQRA TCMQINER	Q
KGT41575.1	phosphoenolpyruvate-protein phosphotransferase [Bacillus cereus]	38	62819	893	642.296	1282.58	37.6	0.00065 R	LCLDEQDVFR	T
KGT41575.1	phosphoenolpyruvate-protein phosphotransferase [Bacillus cereus]	39	62819	671	571.769	1141.52	10.2	0.35 K	EMNPFLGYR	A
KGT41575.1	phosphoenolpyruvate-protein phosphotransferase [Bacillus cereus]	39	62819	722	587.807	1173.6	16.5	0.079 K	SITNEAAEIAR	L
KGT41575.1	phosphoenolpyruvate-protein phosphotransferase [Bacillus cereus]	39	62819	927	652.347	1302.68	2.41	3.8 K	KSITNEAAEIAR TLNIQGIAASSG	L
KGT41575.1	phosphoenolpyruvate-protein phosphotransferase [Bacillus cereus]	39	62819	1311	814.475	1626.94	17.4	0.018 M	IAIAK NVKQAEENA	A
KGT41610.1	membrane protein [Bacillus cereus]	16	24593	2032	788.398	1574.78	10.4	0.21 K	VQSK AGEVYDIAVSN	Q
KGT41610.1	membrane protein [Bacillus cereus] hypothetical protein IY08_20665	16	24593	2226	839.926	1677.84	16.2	0.032 K	GANVAK	G
KGT41616.1	[Bacillus cereus] zinc finger domain-containing	18	27648	491	421.231	840.448	17.6	0.045 K	HEFIPAK	E
KGT41636.1	protein [Bacillus cereus] zinc finger domain-containing	30	7509	539	461.261	920.506	30.4	0.0033 K	GKFESVVR VQIKVNDNGSF	A
KGT41636.1	protein [Bacillus cereus] 6,7-dimethyl-8-ribityllumazine	30	7509	1498	689.361	1376.71	1.47	0.73 K	R MVFEGLVGT	V
KGT41640.1	synthase [Bacillus cereus] 6,7-dimethyl-8-ribityllumazine	24	16284	1528	694.373	1386.73	24.1	0.0055 -	GLK	V
KGT41640.1	synthase [Bacillus cereus] 2~, 3~-cyclic nucleotide 2~-	32	16284	1323	660.882	1319.75	15.2	0.058 K	YDAVITLGTVIR YDVISLGNHEF	G
KGT41650.1	phosphodiesterase [Bacillus cereus] 2~, 3~-cyclic nucleotide 2~-	39	85058	2916	792.049	2373.13	39	0.00022 K	NYGLDYLNK	V
KGT41650.1	phosphodiesterase [Bacillus cereus] 2~, 3~-cyclic nucleotide 2~-	42	85058	902	576.332	1150.65	1.21	1.8 R	QIIVKYMQK APINSYFSLVQD	I
KGT41650.1	phosphodiesterase [Bacillus cereus]	42	85058	3019	878.789	2633.35	19.7	0.044 K	DPSVQIVTNAQ K	W

KGT41650.1	2~, 3~-cyclic nucleotide 2~-phosphodiesterase [Bacillus cereus]	42	85058	3057	923.156	2766.45	2.32	1.8	K	KTEEQPLVNIGY PTYNFDILDGLK	Y
KGT41687.1	branched-chain alpha-keto acid dehydrogenase subunit E2 [Bacillus cereus]	23	47463	240	616.404	615.396	23.3	0.033	R	KDILK	L
KGT41687.1	branched-chain alpha-keto acid dehydrogenase subunit E2 [Bacillus cereus]	57	47463	1001	677.872	1353.73	41	0.00027	K	LVESGNIPQAG AAK	K
KGT41687.1	branched-chain alpha-keto acid dehydrogenase subunit E2 [Bacillus cereus]	57	47463	1846	826.783	2477.33	34.2	0.0013	K	VEAAKPVSVPT MPGDIEIPVTG	K
KGT41688.1	2-oxoisovalerate dehydrogenase [Bacillus cereus]	27	35876	1127	726.323	1450.63	26.6	0.0031	R	VR SNNDWTCPTVI	A
KGT41688.1	2-oxoisovalerate dehydrogenase [Bacillus cereus]	33	35876	1216	765.896	1529.78	20.4	0.012	K	R GEVPEDDYVLPI	A
KGT41688.1	2-oxoisovalerate dehydrogenase [Bacillus cereus]	33	35876	1464	910.434	1818.85	4.22	1.5	R	GK LAGPDVPAMP	F
KGT41688.1	2-oxoisovalerate dehydrogenase [Bacillus cereus]	121	35876	647	507.954	1520.84	42.5	0.00012	K	YAPTMEK LAQDGISAHILD	T
KGT41688.1	2-oxoisovalerate dehydrogenase [Bacillus cereus]	121	35876	807	583.325	1746.95	83.8	1.20E-08	R	LR TVYPLDKEAIE	T
KGT41688.1	2-oxoisovalerate dehydrogenase [Bacillus cereus]	129	35876	640	754.841	1507.67	13.3	0.15	K	AASK ATHGLYDQFGE	A
KGT41688.1	2-oxoisovalerate dehydrogenase [Bacillus cereus]	129	35876	903	629.017	1884.03	17.4	0.055	R	DR LIKGEVPEDDYV	A
KGT41688.1	2-oxoisovalerate dehydrogenase [Bacillus cereus]	129	35876	1329	718.354	2869.39	19.9	0.014	R	LPIGK APFGGGVHGA	I
KGT41690.1	dihydrolipoamide dehydrogenase [Bacillus cereus]	85	50880	2570	993.509	1985	76.1	1.00E-07	R	LYHSQSVEAMF ANQPGLK	G
KGT41690.1	dihydrolipoamide dehydrogenase [Bacillus cereus]	85	50880	1517	692.844	1383.67	2.45	1.2	K	QANTQNIGLEN TDIVVEK	C

	dihydrolipoamide dehydrogenase								ALVYGESDGFV	
KGT41690.1	[Bacillus cereus]	78	50880	234	642.827	1283.64	39.1	0.00057 K	K	L
	dihydrolipoamide dehydrogenase								GYIQTNEFYQT	
KGT41690.1	[Bacillus cereus]	78	50880	349	746.36	1490.71	58	6.40E-06 K	K	E
	dihydrolipoamide dehydrogenase									
KGT41690.1	[Bacillus cereus]	84	50880	81	503.273	1004.53	24.3	0.021 K	IDVFEGIGR	I
	dihydrolipoamide dehydrogenase									
KGT41690.1	[Bacillus cereus]	84	50880	292	679.364	1356.71	3.92	2.1 K	TILPLEDQDVSK	E
	dihydrolipoamide dehydrogenase								TALVEKENLGG	
KGT41690.1	[Bacillus cereus]	84	50880	447	586.966	1757.87	8.81	0.78 K	TCLHK	G
	dihydrolipoamide dehydrogenase								TILPLEDQDVSK	
KGT41690.1	[Bacillus cereus]	84	50880	486	634.664	1900.97	16.1	0.14 K	EMQR	L
	leucine dehydrogenase [Bacillus								NAAAGLNLGG	
KGT41692.1	cereus]	213	40025	545	528.796	1055.58	66.2	8.00E-07 K	AK	T
KGT41692.1	leucine dehydrogenase [Bacillus	213	40025	688	576.286	1150.56	55.9	1.20E-05 R	DGIATYVAADR	L
KGT41692.1	leucine dehydrogenase [Bacillus	213	40025	733	590.78	1179.55	54.9	1.30E-05 K	EAFGTDNLEGK	V
	leucine dehydrogenase [Bacillus								AIIAIHDTTLGP	
KGT41692.1	cereus]	213	40025	1424	593.005	1775.99	32	0.00092 K	ALGGTR	M
	leucine dehydrogenase [Bacillus								MWTYDSEEAAL	
KGT41692.1	cereus]	213	40025	1532	950.424	1898.83	25.4	0.0073 R	EDALR	L
									HGDIIHEMGIV	
									YAPDYVINAGG	
	leucine dehydrogenase [Bacillus								VINVADELYGY	
KGT41692.1	cereus]	213	40025	2082	966.731	3862.9	52.4	2.30E-05 R	NR	E
KGT41692.1	leucine dehydrogenase [Bacillus	222	40025	354	435.756	869.497	12.7	0.1 K	TVIIGDPR	K
KGT41692.1	leucine dehydrogenase [Bacillus	222	40025	386	458.276	914.537	20.2	0.063 K	LIVTDINK	E
KGT41692.1	leucine dehydrogenase [Bacillus	222	40025	636	557.814	1113.61	19.9	0.042 K	VIAGSANNQLK	E
KGT41692.1	leucine dehydrogenase [Bacillus	222	40025	665	569.804	1137.59	9.06	0.58 R	VESIYDTIAK	V
KGT41692.1	leucine dehydrogenase [Bacillus	222	40025	895	642.839	1283.66	18.7	0.061 M	TLEIFEYLEK	Y
KGT41692.1	leucine dehydrogenase [Bacillus	222	40025	914	647.856	1293.7	23.4	0.02 K	RVESIYDTIAK	V
	leucine dehydrogenase [Bacillus								VIAVQGVGNV	
KGT41692.1	cereus]	222	40025	1392	572.973	1715.9	6.01	0.27 K	AYHLCK	H

KGT41693.1	phosphate butyryltransferase [Bacillus cereus]	21	31628	1473	915.023	1828.03	20.8	0.0083	K	ADILLVPTIEAG NVLYK	S
KGT41693.1	phosphate butyryltransferase [Bacillus cereus]	35	31628	1070	688.732	2063.17	35.4	0.00029	K	AAIIQNTVEVA QAIGIDLPK	V
KGT41693.1	phosphate butyryltransferase [Bacillus cereus]	35	31628	209	520.814	1039.61	2.7	0.72	K	GNIPTANILK	A
KGT41693.1	phosphate butyryltransferase [Bacillus cereus]	35	31628	1189	775.713	2324.12	9.92	0.12	K	DCIVDGPLALD NAVSQIAAEHK	G
KGT41693.1	phosphate butyryltransferase [Bacillus cereus]	35	31628	1298	885.84	2654.5	11.3	0.073	K	GIVSDVAGKAD ILLVPTIEAGNV LYK	S
KGT41693.1	phosphate butyryltransferase [Bacillus cereus]	35	31628	1340	975.839	2924.49	13	0.22	K	VAPIAAVEVVN PAMQATIDAA MLTQMNR	R
KGT41712.1	acetyl-CoA carboxylase [Bacillus cereus]	73	17874	3047	916.446	2746.32	59.1	7.00E-06	K	ITSPMVGTFFYSS SSPDTPPYVSV GDR	V
KGT41712.1	acetyl-CoA carboxylase [Bacillus cereus]	73	17874	1142	627.853	1253.69	7.69	0.43	R	GNEVVAVQAP AAK	Q
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	40	54946	2056	529.605	1585.79	28.8	0.002	R	FAGFANIHPLQ DEK	T
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	47	54946	586	481.25	960.485	25.1	0.023	R	HYTALSNR	N
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	47	54946	719	531.764	1061.51	1.08	1	K	RLDETMAAR	K
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	47	54946	2456	625.605	1873.79	2.37	0.61	R	NHGVDSGFYPL GSCTMK	Y
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	146	54946	909	431.864	1292.57	37.8	0.00043	R	AYHEANGDFN R	T
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	146	54946	999	677.346	1352.68	35.1	0.0011	R	LAPFYDLPFDR	H
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	146	54946	1281	534.938	1601.79	23.8	0.0058	K	SNENGLVDLED LKR	V
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	146	54946	1288	805.485	1608.95	21.9	0.0064	K	ADLIPYLPKPILE K	T

KGT41753.1	glycine dehydrogenase [Bacillus cereus]	146	54946	1696	716.7	2147.08	32.3	0.00094	K	EVEENPEVVQE APHTTVIK	R
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	146	54946	1883	861.454	2581.34	45.1	0.00013	K	VIVPDSAHTN PASATVAGFETI	S
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	158	54946	412	472.75	943.486	12.7	0.26	K	TVK HEFVLSGR	R
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	158	54946	1060	696.359	1390.7	21.9	0.02	K	NQDQALIFEVS K	E
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	158	54946	1196	504.282	1509.82	21.2	0.025	R	VKPFYGNFGIN VR	A
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	158	54946	1352	556.29	1665.85	2.77	3.1	-	MKNQDQALIFE VSK	E
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	158	54946	1549	959.978	1917.94	1.59	0.71	R	AVTEYAVLNAN YMMRR	L
KGT41753.1	glycine dehydrogenase [Bacillus cereus]	158	54946	1618	510.493	2037.94	9.53	0.48	K	TENGYHFNYDR PEAIGR	V
KGT41754.1	glycine dehydrogenase [Bacillus cereus]	73	49625	1199	637.841	1273.67	61.8	1.60E-06	R	LVGQTVDSGD KR	G
KGT41754.1	glycine dehydrogenase [Bacillus cereus]	101	49625	568	539.285	1076.56	26.5	0.0056	K	NIIGGYDLGR	D
KGT41754.1	glycine dehydrogenase [Bacillus cereus]	101	49625	915	432.242	1293.7	26.7	0.0089	K	ILVSSAVHPESR	A
KGT41754.1	glycine dehydrogenase [Bacillus cereus]	101	49625	1587	999.57	1997.13	38.3	0.00024	K	SLFIVSSNPLSLG ALTPPGK	F
KGT41754.1	glycine dehydrogenase [Bacillus cereus]	101	49625	1934	695.355	2777.39	32.8	0.00083	K	EYASFLGAGVY DHYAPVIVDHV	S
KGT41802.1	superoxide dismutase [Bacillus cereus]	22	22650	1213	508.25	1521.73	12.5	0.067	K	ISR FGSFDAFKEEF	A
KGT41802.1	superoxide dismutase [Bacillus cereus]	22	22650	1518	941.501	1880.99	22.2	0.031	K	AK SVEELVANLNE	T
KGT41817.1	cytochrome C [Bacillus cereus]	41	12613	740	537.806	1073.6	41.3	0.00044	K	VPEAIR DEIKEILSK	G
KGT41839.1	molecular chaperone DnaK [Bacillus cereus]	16	65786	1268	651.84	1301.67	0.68	2.8	K	VDAAEVAKATE AK	E

KGT41839.1	molecular chaperone DnaK [Bacillus cereus]	16	65786	1380	670.341	1338.67	16	0.031	K	ASAEAYLGETV TK	A
KGT41839.1	molecular chaperone DnaK [Bacillus cereus]	16	65786	2027	525.281	1572.82	1.83	1.1	R	QAITNPNTIMS VKR	H
KGT41839.1	molecular chaperone DnaK [Bacillus cereus]	44	65786	1614	678.031	2031.07	44.2	0.00012	K	DAGFAPSELDK VILVGGSTR	I
KGT41839.1	molecular chaperone DnaK [Bacillus cereus]	44	65786	602	551.795	1101.58	20	0.078	K	NELEEIRAK	K
KGT41839.1	molecular chaperone DnaK [Bacillus cereus]	44	65786	839	627.846	1253.68	12.7	0.15	R	FQLTDLPPAPR KDALQEIVQQL	G
KGT41839.1	molecular chaperone DnaK [Bacillus cereus]	44	65786	1296	807.449	1612.88	5.19	1.1	K	TVK	L
KGT41871.1	alkaline phosphatase [Bacillus phenylalanine 4-monooxygenase [Bacillus cereus]	20	50477	498	423.717	845.418	19.8	0.028	R	DQLLNDK LVSGLSEAEQIS	N
KGT41880.1	ferrichrome ABC transporter substrate-binding protein [Bacillus ferrichrome ABC transporter	38	64526	1058	694.873	1387.73	38.3	0.00065	K	R	L
KGT41945.1	substrate-binding protein [Bacillus ferrichrome ABC transporter	17	35558	201	513.787	1025.56	3.69	0.98	K	GEATIPVNP	R
KGT41945.1	substrate-binding protein [Bacillus ferrichrome ABC transporter	17	35558	941	964.522	1927.03	0.38	3.4	K	VAPTVVLETNL EDWRGK	F
KGT41945.1	substrate-binding protein [Bacillus ABC transporter permease [Bacillus cereus]	17	35558	1098	703.738	2108.19	16.7	0.022	K	VDLEAVTALKP DLIILNNR	Q
KGT41958.1	ABC transporter permease [Bacillus cereus]	20	74547	443	380.201	758.387	3.02	2	K	LNEDLR	K
KGT41958.1	ABC transporter permease [Bacillus cereus]	20	74547	885	573.27	1144.52	20	0.021	K	WFHNIASDR EIQLQVMNQP	K
KGT41958.1	hypothetical protein IY08_22540 [Bacillus cereus]	20	74547	2885	1158.55	2315.08	0.54	1	K	YQFVFNGQK	E
KGT41977.1	valine--tRNA ligase [Bacillus cereus]	23	93098	240	616.404	615.396	23.3	0.033	K	KIDIK	I
KGT41987.1	valine--tRNA ligase [Bacillus cereus]	27	1E+05	1619	709.874	1417.73	22.5	0.03	R	EIPIADEYVEK ITPAHDPNDFE	D
KGT41987.1	valine--tRNA ligase [Bacillus cereus]	27	1E+05	2229	561.267	1680.78	24.5	0.017	K	VGNR	H

										ELPELNDEFKAE	
										ADEAVATLDEL	
KGT42002.1	trigger factor [Bacillus cereus]	36	47316	1911	897.116	2688.33	36	0.0012	K	K	A
										FGIESLYQDALD	
KGT42002.1	trigger factor [Bacillus cereus]	36	47316	1563	968.034	1934.05	0.62	2.2	R	IILPK	A
										VKLTEQQLMA	
										DLWYQTAGET	
KGT42023.1	5~-nucleotidase [Bacillus cereus]	41	31110	2944	818.417	2452.23	41	0.00014	K	K	A
KGT42023.1	5~-nucleotidase [Bacillus cereus]	41	31110	771	546.794	1091.57	2.2	0.87	K	EHILLQDPK	E
KGT42029.1	succinate dehydrogenase [Bacillus cereus]	45	66127	745	540.272	1078.53	44.7	0.0002	R	TEEGLLDFR	R
KGT42029.1	succinate dehydrogenase [Bacillus cereus]	29	66127	418	477.275	952.534	10.4	0.17	R	HEVAGLVTK	Y
										AAEAGVNVLEF	
KGT42029.1	succinate dehydrogenase [Bacillus cereus]	29	66127	1531	633.7	1898.08	18.2	0.015	K	SLVPVKR	S
										FEGEGNAPAFH	
KGT42029.1	succinate dehydrogenase [Bacillus cereus]	29	66127	1893	651.823	2603.26	27.2	0.011	K	YEDVDISLIKPR	K
										VADYGIVGDLF	
KGT42034.1	electron transfer flavoprotein subunit alpha [Bacillus cereus]	43	34474	1882	861.138	2580.39	43	0.00011	K	EVVPLLTEEFKK	L
										SGDVSSITVDV	
KGT42034.1	electron transfer flavoprotein subunit alpha [Bacillus cereus]	43	34474	771	603.814	1205.61	9.83	0.28	R	K	D
										SEEGFKPLKELA	
										DVLGGAVGAS	
KGT42034.1	electron transfer flavoprotein subunit alpha [Bacillus cereus]	43	34474	1801	777.42	2329.24	11.8	0.24	K	R	G
KGT42036.1	enoyl-CoA hydratase [Bacillus cereus]	14	28049	91	516.306	515.299	13.6	0.043	K	QIAGK	S
										ILTDNSLALQVT	
KGT42040.1	substrate-binding protein [Bacillus cereus]	38	36034	1615	708.412	1414.81	37.7	0.00037	R	K	K
										DITGFVLGGHG	
KGT42105.1	malate dehydrogenase [Bacillus cereus]	102	33477	2578	666.677	1997.01	66.8	8.10E-07	K	DDMVPLVR	Y
										VIGQSGVLDTA	
KGT42105.1	malate dehydrogenase [Bacillus cereus]	47	33477	786	608.342	1214.67	47.2	0.00011	R	R	F
										IIELELLADEKEA	
KGT42105.1	malate dehydrogenase [Bacillus cereus]	47	33477	1506	624.018	1869.03	17.7	0.046	K	LDR	S

KGT42105.1	malate dehydrogenase [Bacillus cereus]	47	33477	1584	997.046	1992.08	18.2	0.044	K	ELADVVLVDIP	
KGT42105.1	malate dehydrogenase [Bacillus cereus]	44	33477	522	681.88	1361.75	13.3	0.17	R	QLENPTK	G
KGT42112.1	pyruvate kinase [Bacillus cereus]	41	62321	665	515.797	1029.58	40.8	0.00032	R	TFIAQELNLSVK	D
KGT42112.1	pyruvate kinase [Bacillus cereus]	44	62321	1130	729.388	1456.76	44.3	0.00018	K	KASDVLEIR	E
KGT42112.1	pyruvate kinase [Bacillus cereus]	44	62321	652	562.813	1123.61	17.5	0.048	K	SPIVAVTSDEQ	
KGT42113.1	6-phosphofructokinase [Bacillus cereus]	46	34411	783	858.444	1714.87	46	6.70E-05	R	VGR	R
KGT42135.1	alanine dehydrogenase [Bacillus cereus]	180	40086	500	512.335	1022.66	23.7	0.0043	K	VDFIAASFVR	K
KGT42135.1	alanine dehydrogenase [Bacillus cereus]	180	40086	881	638.832	1275.65	28.1	0.0024	R	IGVLTSGGDSP	
KGT42135.1	alanine dehydrogenase [Bacillus cereus]	180	40086	1008	679.376	1356.74	32.3	0.0028	K	GMNAAIR	A
KGT42135.1	alanine dehydrogenase [Bacillus cereus]	180	40086	1129	728.895	1455.78	47.9	7.20E-05	R	GILLAGVPGVK	R
KGT42135.1	alanine dehydrogenase [Bacillus cereus]	180	40086	1258	789.908	1577.8	54	1.20E-05	K	QLDDIFGNQVK	T
KGT42135.1	alanine dehydrogenase [Bacillus cereus]	180	40086	1714	728.741	2183.2	74.8	5.50E-08	R	VTIIGGGQAGT	
KGT42135.1	alanine dehydrogenase [Bacillus cereus]	192	40086	945	659.311	1316.61	18.9	0.041	K	NAAK	I
KGT42135.1	alanine dehydrogenase [Bacillus cereus]	192	40086	951	659.819	1317.62	20	0.044	R	SLPLLAPMSEV	
KGT42135.1	alanine dehydrogenase [Bacillus cereus]	192	40086	959	661.851	1321.69	26	0.012	R	AGR	M
KGT42135.1	alanine dehydrogenase [Bacillus cereus]	192	40086	1659	1052.59	2103.17	15.9	0.036	R	VASIAYETVQLD	
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	60	58099	968	590.317	1178.62	60.2	2.30E-06	K	NR	S
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	353	435.712	869.41	46.1	7.20E-05	R	EGLILFTYLHLA	
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	514	517.78	1033.55	30.2	0.0029	K	PEPELTK	A
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	514	517.78	1033.55	30.2	0.0029	K	EPVASEYGYFR	E
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	514	517.78	1033.55	30.2	0.0029	K	ITTHDNPTYEK	H
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	514	517.78	1033.55	30.2	0.0029	K	MAAQIGAQFL	
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	514	517.78	1033.55	30.2	0.0029	K	EK	N
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	514	517.78	1033.55	30.2	0.0029	K	TSTLALTNTVTP	
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	514	517.78	1033.55	30.2	0.0029	K	YAVQIANK	G
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	514	517.78	1033.55	30.2	0.0029	K	LTSTGAVSAST	
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	514	517.78	1033.55	30.2	0.0029	K	GK	Y
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	514	517.78	1033.55	30.2	0.0029	K	MNLGYTR	A
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	514	517.78	1033.55	30.2	0.0029	K	AIELANEFK	A

KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	603	551.801	1101.59	30.6	0.0023	K	TTLSADPNRK	L
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	716	390.214	1167.62	26.8	0.0085	K	EKEELFVFK	G
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	964	665.856	1329.7	40.4	0.0005	R	AMIQAALNGEL AK	T
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	1165	740.89	1479.77	23.9	0.0057	R	IVLIGGTEYAGE MK	K
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	1305	813.887	1625.76	87.1	8.70E-09	R	IADYNDTTLTE NTR	A
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	1422	887.966	1773.92	38.7	0.00023	K	KFDSVSEDIINL GGPIA	-
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	1430	892.456	1782.9	64.3	9.40E-07	K	VFLVNTGWTG GEYGVGK	R
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	2029	821.914	3283.63	29.7	0.0055	K	HDIFGLEVPLH VPGVPDEVLM PEQTWADK	A
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	555	58099	2077	919.718	3674.84	62.1	1.90E-06	K	CVNLSHEKEPQ IFDAITFGSVLE NVIINDQTR	I
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	560	58099	1302	542.294	1623.86	14.8	0.12	R	IVLIGGTEYAGE MKK	S
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	560	58099	1364	559.923	1676.75	2.73	2	K	EQAMYHFLSGY TSK	L
KGT42280.1	phosphoenolpyruvate carboxykinase [Bacillus cereus]	560	58099	1923	907.118	2718.33	5.24	0.39	K	EPQIFDAITFGS VLENIINDQTR	I
KGT42294.1	spermidine/putrescine ABC transporter ATP-binding protein	25	28968	68	456.235	910.455	25.2	0.011	-	MSFLQIR	N
KGT42371.1	hypothetical protein IY08_24605 [Bacillus cereus]	28	28019	1493	688.383	1374.75	27.9	0.0064	K	IIPVDLTEYQGK	V
KGT42381.1	lactate dehydrogenase [Bacillus cereus]	72	34691	724	588.815	1175.62	72.4	1.90E-07	R	VIGSGTTLDSAR	F

KGT42398.1	chitinase [Bacillus cereus]	82	39538	1276	653.279	1304.54	37.6	0.00017	K	NNFEFSNNYR	T
										GLMSWSINWD	
KGT42398.1	chitinase [Bacillus cereus]	82	39538	1636	712.335	1422.66	36.3	0.0012	R	AK	N
										VVLSIGGQNGV	
KGT42398.1	chitinase [Bacillus cereus]	82	39538	2568	991.554	1981.09	29.8	0.0019	K	VLLPDNASK	Q
										KVLSIGGQNG	
KGT42398.1	chitinase [Bacillus cereus]	82	39538	2681	703.737	2108.19	24.6	0.0042	K	VVLLPDNASK	Q
										WDVINVSFGET	
KGT42398.1	chitinase [Bacillus cereus]	67	39538	744	826.391	1650.77	67.1	9.40E-07	K	GGDR	S
KGT42398.1	chitinase [Bacillus cereus]	67	39538	322	586.292	1170.57	1.23	2.8	R	TYFDGLSLQK	-
KGT42398.1	chitinase [Bacillus cereus]	67	39538	390	620.31	1238.61	18	0.1	K	ISNQSGYPAFR	G
										NPTTPQIVNLIS	
KGT42398.1	chitinase [Bacillus cereus]	67	39538	733	818.977	1635.94	11.9	0.064	K	AIR	T
										LLVGYYWHNFD	
KGT42398.1	chitinase [Bacillus cereus]	67	39538	955	650.008	1947	5.59	1.8	K	NGTGIK	L
										STVEFSPVYGT	
KGT42398.1	chitinase [Bacillus cereus]	67	39538	1266	861.756	2582.25	15.1	0.039	R	DAEFKSDISYLK	S
										SDQVMIGLPAA	
										PAAAPSGGYIS	
KGT42398.1	chitinase [Bacillus cereus]	67	39538	1324	935.141	2802.4	9.29	0.64	R	PTEMKK	A
KGT42398.1	chitinase [Bacillus cereus]	411	39538	81	639.358	1276.7	48.8	6.00E-05	R	FINSIQSLIDK	Y
										STVEFSPVYGT	
KGT42398.1	chitinase [Bacillus cereus]	411	39538	213	888.926	1775.84	82.1	2.00E-08	R	DAEFK	S
	methionine ABC transporter									ELDANYFQGIP	
KGT42406.1	substrate-binding protein [Bacillus	22	29774	2368	892.453	1782.89	22	0.014	K	FLEK	E
	iron-uptake system-binding protein										
KGT42412.1	[Bacillus cereus]	47	35624	1258	648.33	1294.64	47.2	3.70E-05	K	IIKDYNSDAEK	A
	iron-uptake system-binding protein										
KGT42412.1	[Bacillus cereus]	56	35624	247	623.341	622.334	25.3	0.014	K	ISFEK	L
	iron-uptake system-binding protein										
KGT42412.1	[Bacillus cereus]	77	35624	329	590.318	1178.62	42.5	0.00034	K	YLEKELEGAK	S
	iron-uptake system-binding protein									LRANELFLYPEG	
KGT42412.1	[Bacillus cereus]	77	35624	1252	849.123	2544.35	53	1.40E-05	R	VYFNPVIYK	D

KGT42412.1	iron-uptake system-binding protein [Bacillus cereus]	84	35624	336	592.829	1183.64	18	0.048	K	DLGLTAPEQLK	T
KGT42412.1	iron-uptake system-binding protein [Bacillus cereus]	84	35624	937	961.481	1920.95	2.86	0.54	K	VFVNVDPM	T
KGT42412.1	iron-uptake system-binding protein [Bacillus cereus]	84	35624	1060	684.028	2049.06	4.88	0.36	K	QGGTAWSK	T
KGT42412.1	iron-uptake system-binding protein [Bacillus cereus]	84	35624	1127	714.361	2140.06	20.7	0.021	K	KVFVNVDPM	T
KGT42412.1	iron-uptake system-binding protein [Bacillus cereus]	84	35624	1277	866.116	2595.33	20.5	0.04	K	AQGGTAWSK	T
KGT42412.1	iron-uptake system-binding protein [Bacillus cereus]	84	35624	1355	759.938	3035.72	7.17	0.19	K	VAPTFPVSHVS	L
KGT42412.1	iron-uptake system-binding protein [Bacillus cereus]	193	35624	243	1030.02	2058.02	47.2	3.80E-05	K	TNWEDNLK	L
KGT42412.1	iron-uptake system-binding protein [Bacillus cereus]	193	35624	399	820.684	3278.71	27.9	0.0044	K	LAELNPDYIFLQ	V
KGT42412.1	iron-uptake system-binding protein [Bacillus cereus]	206	35624	296	1138.59	2275.17	14.7	0.042	R	YEASENKNPK	V
KGT42412.1	iron-uptake system-binding protein [Bacillus cereus]	206	35624	317	802.764	2405.27	5.81	0.97	K	IATASLESMED	Y
KGT42417.1	peptidase T [Bacillus cereus]	24	45885	194	613.369	612.362	2.61	0.55	K	AAVLGIKPVGAI	E
KGT42417.1	peptidase T [Bacillus cereus]	24	45885	385	458.27	914.526	24.4	0.025	M	TVGGKLPK	Y
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	44	64546	832	626.297	1250.58	44.1	0.00015	R	VLEEIESNPIWQ	E
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	457	497.231	992.447	19.2	0.039	R	SMNAAK	E
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	501	512.746	1023.48	0.8	3.7	K	MQPNFETLLQL	F
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	712	584.298	1166.58	23.6	0.024	R	KPDVITSSTKFP	F
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	712	584.298	1166.58	23.6	0.024	R	AETAEK	F
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	712	584.298	1166.58	23.6	0.024	R	ANELFLYPEGV	D
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	712	584.298	1166.58	23.6	0.024	R	YFNPVIYK	D
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	712	584.298	1166.58	23.6	0.024	R	MQPNFETLLQL	F
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	712	584.298	1166.58	23.6	0.024	R	KPDVITSSTK	F
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	712	584.298	1166.58	23.6	0.024	R	IEPVR	E
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	712	584.298	1166.58	23.6	0.024	R	KQELIER	F
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	712	584.298	1166.58	23.6	0.024	R	YEVTEDGVSPR	V
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	712	584.298	1166.58	23.6	0.024	R	GAIEEAMTR	L
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	712	584.298	1166.58	23.6	0.024	R	VNMMQLEK	A
KGT42449.1	2-oxoglutarate ferredoxin oxidoreductase subunit alpha	52	64546	712	584.298	1166.58	23.6	0.024	R	LGYYLYGYR	H

	2-oxoglutarate ferredoxin								LIHPFPTAEIDPL	
KGT42449.1	oxidoreductase subunit alpha	52	64546	1378	563.993	1688.96	17.2	0.019	R	VK K
	dihydrodipicolinate synthase									TALQMVGLDV
KGT42472.1	[Bacillus cereus]	44	31243	1686	723.394	1444.77	44.4	8.70E-05	K	GSVR L
	dihydrodipicolinate synthase									VTDSLFPASP
KGT42472.1	[Bacillus cereus]	92	31243	693	795.419	1588.82	42.8	0.00027	R	TPVK T
	dihydrodipicolinate synthase									
KGT42472.1	[Bacillus cereus]	106	31243	467	655.373	1308.73	16.9	0.036	R	LPLLPLTEER V
	dihydrodipicolinate synthase									AIAESTPLPVML
KGT42472.1	[Bacillus cereus]	106	31243	941	964.522	1927.03	25.2	0.011	K	YNVPGR S
	dihydrodipicolinate synthase									LPLLPLTEEERV
KGT42472.1	[Bacillus cereus]	106	31243	1297	883.829	2648.46	21.7	0.012	R	TLQSVMQSIPR -
KGT42478.1	zinc protease [Bacillus cereus]	33	47073	709	529.302	1056.59	32.6	0.0028	R	NGKNELLR K
KGT42478.1	zinc protease [Bacillus cereus]	33	47073	946	586.316	1170.62	1.57	2.9	R	IVMENIPTVR S
	polynucleotide phosphorylase									YGDТАVLSTAT
KGT42480.1	[Bacillus cereus]	30	78303	1055	692.853	1383.69	30	0.0015	R	ASK E
	polynucleotide phosphorylase									
KGT42480.1	[Bacillus cereus]	30	78303	608	553.304	1104.59	12	0.21	K	QVFSIDLAGR Q
	polynucleotide phosphorylase									VAGTAQGVTA
KGT42480.1	[Bacillus cereus]	30	78303	1284	802.438	1602.86	0.18	4.7	K	LQMDIK I
	polynucleotide phosphorylase									
KGT42480.1	[Bacillus cereus]	18	78303	127	686.876	1371.74	1.47	3.2	K	QINKIIEETGVK I
										IGVLTVLEGSTD
KGT42499.1	elongation factor Ts [Bacillus cereus]	73	32551	1356	837.461	1672.91	73.3	1.60E-07	R	EAAAK D
KGT42499.1	elongation factor Ts [Bacillus cereus]	73	32551	365	439.756	877.497	12.8	0.18	R	RFEIVSK T
	urocanate hydratase [Bacillus									IINEMVANGEL
KGT42536.1	cereus]	51	61042	2581	1007.04	2012.07	51.1	3.10E-05	R	SAPIVIGR D
KGT42536.1	urocanate hydratase [Bacillus	135	61042	670	571.759	1141.5	34.2	0.00084	R	ICWLGYGER A
	urocanate hydratase [Bacillus									VLTSDPGMGV
KGT42536.1	cereus]	135	61042	828	623.827	1245.64	57.5	1.20E-05	R	VR H
	urocanate hydratase [Bacillus									
KGT42536.1	cereus]	135	61042	906	645.333	1288.65	32.6	0.0041	R	QQVEFQGLPSR I

KGT42536.1	urocanate hydratase [Bacillus cereus]	135	61042	978	670.831	1339.65	37.2	0.0005	K	GAITFDYGNNI R	Q
KGT42536.1	urocanate hydratase [Bacillus cereus]	135	61042	1723	735.439	2203.29	32.4	0.00058	K	KEPISIGLLGNA AEILPELVK	R
KGT42536.1	urocanate hydratase [Bacillus cereus]	135	61042	1794	773.736	2318.19	25.8	0.0038	R	WVALSGDPEDI YKTDEVILR	E
KGT42536.1	urocanate hydratase [Bacillus cereus]	143	61042	522	522.26	1042.51	18.6	0.053	K	LREEDPER	Y
KGT42536.1	urocanate hydratase [Bacillus cereus]	143	61042	713	584.362	1166.71	9.17	0.12	R	VLLANSNLVPK NWESYQAIVDS	W
KGT42536.1	urocanate hydratase [Bacillus cereus]	143	61042	1238	776.889	1551.76	4.64	1.1	R	LK	T
KGT42536.1	urocanate hydratase [Bacillus cereus]	143	61042	1712	725.74	2174.2	5.31	0.43	K	TLESDETLLVQS GKPVAIFK	S
KGT42536.1	urocanate hydratase [Bacillus cereus]	143	61042	1957	935.802	2804.38	26.2	0.012	R	MLMNNLDPEV AEKPEELVVYG GIGR	A
KGT42566.1	transketolase [Bacillus cereus]	101	72415	873	637.318	1272.62	29	0.006	R	VEDGNDIEAIA K	A
KGT42566.1	transketolase [Bacillus cereus]	101	72415	1384	851.417	1700.82	27.2	0.0028	K	IMEEYGFTVEN VVR	K
KGT42566.1	transketolase [Bacillus cereus]	101	72415	1398	576.339	1726	43	5.00E-05	R	LALESTNKPTAL VLTR	Q
KGT42566.1	transketolase [Bacillus cereus]	101	72415	1664	704.034	2109.08	34.3	0.00061	K	TYGGTFFVFSD YLRPAIR	L
KGT42566.1	transketolase [Bacillus cereus]	101	72415	1716	1098.05	2194.09	33.2	0.003	R	YVGLEGDVLGI DTFGASAPGEK	I
KGT42566.1	transketolase [Bacillus cereus]	102	72415	497	511.274	1020.53	12.9	0.37	R	TTIGFGSPNK	S
KGT42566.1	transketolase [Bacillus cereus]	102	72415	991	673.819	1345.62	8.38	0.52	R	SFSESVEDRYK	A
KGT42566.1	transketolase [Bacillus cereus]	102	72415	1102	476.272	1425.79	10.7	0.26	K	ADEKRPTLIEVR EFAMGAAMN	T
KGT42566.1	transketolase [Bacillus cereus]	102	72415	1465	607.633	1819.88	14.2	0.046	R	GIALHGGLK	T

									EYAWTAEQD	
									FHVAEEVDNF	
KGT42566.1	transketolase [Bacillus cereus]	102	72415	1962	705.331	2817.3	6.57	0.84	K	RK T
	glutamine synthetase [Bacillus cereus]	135	50420	1771	738.343	1474.67	56	9.00E-06	K	MMFDGSSIEGF I
KGT42578.1	glutamine synthetase [Bacillus cereus]	43	50420	446	492.264	982.512	27.4	0.0061	K	LTPPDVDR N
KGT42578.1	glutamine synthetase [Bacillus cereus]	43	50420	829	623.877	1245.74	22.9	0.0065	R	LQFTDLLGVK N
	glutamine synthetase [Bacillus cereus]									SVDPAANPYLV
KGT42578.1	glutamine synthetase [Bacillus cereus]	43	50420	1828	800.771	2399.29	24.5	0.0089	R	MATLLAAGLD GIK N
	glutamine synthetase [Bacillus cereus]									HAPAFTAIANP
KGT42578.1	glutamine synthetase [Bacillus cereus]	43	50420	1451	601.32	1800.94	7.38	0.2	K	TVNSYK R
	glutamine synthetase [Bacillus cereus]									LICDIYNADGTP
KGT42578.1	glutamine synthetase [Bacillus cereus]	43	50420	1612	1014.45	2026.88	11.3	0.17	R	FDGDPR N
	glutamine synthetase [Bacillus cereus]									VLKEMEALGFS
KGT42578.1	glutamine synthetase [Bacillus cereus]	43	50420	1976	974.162	2919.46	5.62	0.99	R	DFNLGPEPEFFL FK V
KGT42611.1	betaine-aldehyde dehydrogenase [Bacillus cereus]	34	53823	569	539.303	1076.59	33.8	0.0018	K	IAFTGSTPVGK Q
	betaine-aldehyde dehydrogenase [Bacillus cereus]									SQLAVNLHEK V
KGT42611.1	betaine-aldehyde dehydrogenase [Bacillus cereus]	36	53823	666	569.819	1137.62	2.44	1.6	M	LMYKLADLMEE
	betaine-aldehyde dehydrogenase [Bacillus cereus]									HK E
KGT42611.1	betaine-aldehyde dehydrogenase [Bacillus cereus]	36	53823	1315	818.92	1635.82	2.97	1.3	R	IVGQTIPVSGDY
	betaine-aldehyde dehydrogenase [Bacillus cereus]									FNYTR H
KGT42611.1	betaine-aldehyde dehydrogenase [Bacillus cereus]	36	53823	1557	965.492	1928.97	13.1	0.074	K	GVINIVPGFGES
	betaine-aldehyde dehydrogenase [Bacillus cereus]									AGQALVNHPL
KGT42611.1	betaine-aldehyde dehydrogenase [Bacillus cereus]	36	53823	1857	844.463	2530.37	20.1	0.027	K	VDK I
	betaine-aldehyde dehydrogenase [Bacillus cereus]									KLNQGVGLNPE
KGT42611.1	betaine-aldehyde dehydrogenase [Bacillus cereus]	36	53823	1878	860.459	2578.36	5.99	0.76	K	TTIGPLVSEEQQ K R
KGT42626.1	molybdenum cofactor biosynthesis protein A [Bacillus cereus]	25	39174	766	545.817	1089.62	24.9	0.0076	K	IKINMVVQK G

KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	131	63436	561	473.26	944.505	48.5	6.10E-05	K	AELDTLGVK	A
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	131	63436	2098	802.437	1602.86	37.4	0.0009	K	MLLEDAAIAPL YQR	G
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	131	63436	2888	774.374	2320.1	57.6	4.30E-06	K	YGLESDDTTLYN GPFTLTDDWK	H
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	138	63436	532	456.733	911.451	24.6	0.014	K	DFVFAWK	R
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	202	63436	448	492.765	983.515	53.6	1.10E-05	K	TPSTYFLR	L
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	202	63436	749	595.827	1189.64	36.7	0.00036	K	LDEINFNVVK	D
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	202	63436	910	647.327	1292.64	55.1	1.80E-05	R	VNLYESGQIDR	S
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	202	63436	1507	624.333	1869.98	43.8	0.00019	K	NAQAINEGKAE LDTLGVK	A
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	202	63436	1671	707.7	2120.08	33.9	0.00077	K	ELGKDAITVELL NYDGDGAK	K
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	202	63436	583	544.772	1087.53	13.5	0.2	K	WSNGEPVTAK	D
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	202	63436	1648	1044.06	2086.1	2.11	2.2	K	GLTNVILNDGS TPADYLVPK	E
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	232	63436	103	534.829	1067.64	21.3	0.0089	K	NLPGLTVNLK	N
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	232	63436	299	687.354	1372.69	50.6	2.40E-05	R	SGLTSEFVDKYK	S
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	232	63436	370	510.259	1527.75	24.3	0.0052	K	GIVHHPVGGDY SYK	W
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	232	63436	584	854.786	2561.34	27.1	0.007	K	GLTNVILNDGS TPADYLVPKF AK	S
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	235	63436	72	487.28	972.545	15	0.2	K	RGGQDTVLLK	S

KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	235	63436	74	492.286	982.557	12.9	0.11	R	GDAIVQRPK	V
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	235	63436	86	513.252	1024.49	6.9	1	K	WAYITEDK	-
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	235	63436	364	506.954	1517.84	21.1	0.031	K	TVKLDEINFNV	D
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	235	63436	510	1003.49	2004.97	8.43	0.89	K	VK	
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	235	63436	537	714.363	2140.07	20.4	0.054	K	QVLNLTESQEIP	A
KGT42642.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	235	63436	537	714.363	2140.07	20.4	0.054	K	SMDSAK	
KGT42643.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	199	64325	654	513.258	1024.5	30.9	0.0036	K	ATDQVSFLALN	L
KGT42643.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	199	64325	738	537.308	1072.6	43.8	7.80E-05	R	NVMEGLYR	
KGT42643.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	199	64325	1614	708.315	1414.62	87.8	3.60E-09	K	HEQGWQLK	K
KGT42643.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	199	64325	1614	708.315	1414.62	87.8	3.60E-09	K	EAIALSVDKK	G
KGT42643.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	199	64325	1614	708.315	1414.62	87.8	3.60E-09	K	SPYNQMSYSN	
KGT42643.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	44	64325	798	611.301	1220.59	43.7	8.00E-05	K	PK	Y
KGT42643.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	44	64325	798	611.301	1220.59	43.7	8.00E-05	K	HNISPEYSFK	W
KGT42643.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	52	64325	527	703.044	2106.11	36.6	0.0009	R	LLDKNTAAEYA	
KGT42643.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	52	64325	543	719.667	2155.98	34.4	0.0017	K	FIAYYIK	N
KGT42643.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	52	64325	543	719.667	2155.98	34.4	0.0017	K	SNKEEYGEYAE	
KGT42643.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	52	64325	491	961.002	1919.99	6.22	1.4	K	SSTFFLR	L
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	52	64325	491	961.002	1919.99	6.22	1.4	K	LFLEEDAGLVPL	
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	52	64325	491	961.002	1919.99	6.22	1.4	K	YQTGR	S
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	85	63826	2474	949.022	1896.03	54.7	9.80E-06	K	NAEAINKGKPK	
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	85	63826	2474	949.022	1896.03	54.7	9.80E-06	K	VTELGVK	A
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	87	63826	2792	723.345	2167.01	4.45	0.38	R	NNKEEFGTYSQ	
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	87	63826	2792	723.345	2167.01	4.45	0.38	R	VSTFFLR	M
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	87	63826	2873	1153.06	2304.11	16.8	0.078	K	YGLESDDTVYN	
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	87	63826	2873	1153.06	2304.11	16.8	0.078	K	GPFVLTDWK	H
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	398	310.156	927.446	28.5	0.0041	K		
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	398	310.156	927.446	28.5	0.0041	K	YDDMIKK	A

KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	481	504.739	1007.46	35.7	0.001	K	AGTELMGDAK	K
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	732	590.319	1178.62	40.8	0.00045	K	LDEINYSVVK	E
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	934	654.347	1306.68	49.2	6.90E-05	K	VGEYVKDQIEK	N
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	1150	736.396	1470.78	77.9	5.30E-08	K	TTAEYAFIAFPIK	N
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	1192	503.286	1506.84	23.7	0.0095	K	TVKLDEINYSVV	
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	1390	570.951	1709.83	37.2	0.00033	K	K	E
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	1416	590.677	1769.01	46.6	2.80E-05	K	GLATGPDGKDF	
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	1665	1056.51	2111.01	31.9	0.001	K	QETFK	N
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	1684	709.387	2125.14	41	0.00027	K	LLLEQDVALVPL	
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	1738	741.054	2220.14	48.4	2.90E-05	K	YQR	G
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	613	63826	1884	864.121	2589.34	139	4.30E-14	R	NTDNLGSQILG	
KGT42644.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	624	63826	544	528.751	1055.49	20.1	0.03	K	NTMEGLYR	L
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	807	557.274	1112.53	71.8	1.80E-07	R	NLANVILNDGS	
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2299	867.498	1732.98	2.47	0.74	K	KPADFLVPK	G
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2677	1053.02	2104.03	2.05	1	K	ELGKDQVTIELL	
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2940	811.39	2431.15	0.93	1.3	K	NYDTGNAK	K
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2940	811.39	2431.15	0.93	1.3	K	VNLFDTGAIKF	
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2940	811.39	2431.15	0.93	1.3	K	ALLSGEFVDKY	
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2940	811.39	2431.15	0.93	1.3	K	R	N
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2940	811.39	2431.15	0.93	1.3	K	DFAYAWQR	L
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2940	811.39	2431.15	0.93	1.3	K	SGDSVYSLASK	Y
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2940	811.39	2431.15	0.93	1.3	K	TRLPSGYTLSTT	
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2940	811.39	2431.15	0.93	1.3	K	LVPK	T
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2940	811.39	2431.15	0.93	1.3	K	IMMGQNLYGF	
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2940	811.39	2431.15	0.93	1.3	K	DWKLPFK	Q
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2940	811.39	2431.15	0.93	1.3	K	SQMPPQKIMM	
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	72	48106	2940	811.39	2431.15	0.93	1.3	K	GQNLYGFDWK	L

KGT42663.1	glycosyl hydrolase [Bacillus cereus]	103	48106	55	589.345	1176.68	47.6	4.00E-05	R	LLVENFTITK	K
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	103	48106	82	639.361	1276.71	59.1	4.90E-06	K	FITNILQTAEK	Y
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	103	48106	357	867.482	2599.43	29.1	0.0017	R	AVESIAYLQPST	A
KGT42663.1	glycosyl hydrolase [Bacillus cereus]	103	48106	195	865.489	1728.96	5.87	0.65	R	IPIKESLVNATR	E
KGT42670.1	aconitate hydratase [Bacillus cereus]	20	99193	1325	823.454	1644.89	11.7	0.24	K	AVESIAYLQPST	V
KGT42670.1	aconitate hydratase [Bacillus cereus]	20	99193	1466	911.48	1820.95	20.3	0.044	K	IPIK	K
KGT42670.1	aconitate hydratase [Bacillus cereus]	20	99193	1483	923.493	1844.97	9.45	0.47	K	LTGTLPSGTTAT	V
KGT42670.1	aconitate hydratase [Bacillus cereus]	20	99193	1844	821.429	2461.27	18.7	0.054	K	DVALK	V
KGT42709.1	histidine kinase [Bacillus cereus]	34	44200	1531	695.361	1388.71	33.5	0.0026	K	EIEDVVQSVVT	G
KGT42709.1	histidine kinase [Bacillus cereus]	34	44200	296	650.364	649.357	21	0.051	-	SELFK	G
KGT42736.1	disulfide oxidoreductase [Bacillus cereus]	21	88560	658	566.29	1130.57	20.8	0.044	K	ALENAGVGNV	Y
KGT42783.1	hypothetical protein IY08_16305	13	41030	2617	1022.51	2043.01	13	0.06	R	SQLPYSVK	D
KGT42845.1	6-aminoheptanoate hydrolase	43	47377	102	660.325	1318.64	43.2	9.00E-05	K	AVVAPVGTQG	W
KGT42845.1	6-aminoheptanoate hydrolase	43	47377	358	871.087	2610.24	10.6	0.1	K	LGFNEQEFDKE	R
KGT42926.1	5-amino-6-(5-phosphoribosylamino)uracil	25	40144	68	456.235	910.455	25.2	0.011	R	VK	N
KGT42930.1	hypothetical protein IY08_17080	17	18051	762	545.295	1088.58	17.3	0.024	K	LGEQSTASQLID	M
KGT42980.1	catabolite gene activator protein	23	26839	335	734.888	1467.76	22.7	0.028	R	K	K

	hypothetical protein IY08_17475								VTVTRPAVYNN	
KGT43002.1	[Bacillus cereus]	48	17798	2359	592.97	1775.89	47.5	9.00E-05	K	EADAR I
										AEGYPSVFYGD
KGT43012.1	alpha-amylase [Bacillus cereus]	25	58268	468	908.916	1815.82	8.71	0.52	R	YYGTK G
										EGDSVHANSGL
										ATLISDGP GGA
KGT43012.1	alpha-amylase [Bacillus cereus]	25	58268	540	718.371	2152.09	25	0.019	R	K W
KGT43018.1	agmatine deiminase [Bacillus	14	43754	174	576.327	575.32	6.14	0.68	R	KNVSK Q
KGT43018.1	agmatine deiminase [Bacillus	14	43754	824	560.286	1118.56	6.99	0.71	K	NVSKQSGIER V
KGT43018.1	agmatine deiminase [Bacillus	14	43754	1021	604.306	1206.6	13.7	0.053	K	TPYKNDAQIR K
	glycerophosphodiester									
KGT43023.1	phosphodiesterase [Bacillus cereus]	62	35877	1015	602.335	1202.66	26.3	0.0034	K	VPTLEEIFQK Y
	glycerophosphodiester									DGQLIAMHDT
KGT43023.1	phosphodiesterase [Bacillus cereus]	62	35877	1964	771.377	1540.74	50.4	1.90E-05	K	AVDR T
										YNVMVFNLNQ
KGT43053.1	stress protein [Bacillus cereus]	66	19666	2496	959.94	1917.87	29.2	0.0042	R	NYEDR F
KGT43071.1	chitin-binding protein [Bacillus	56	73630	774	547.296	1092.58	55.8	1.10E-05	K	ITLTDIFDR T
KGT43071.1	chitin-binding protein [Bacillus	56	73630	174	576.327	575.32	7.77	0.47	R	KVSDK Q
	chitin-binding protein [Bacillus									TRATLTNLENG
KGT43071.1	cereus]	56	73630	1316	660.328	1318.64	17.7	0.097	K	K Q
	hemolysin BL lytic component L2									
KGT43102.1	[Bacillus cereus]	61	49291	737	537.295	1072.57	61.4	4.40E-06	R	QINELTDLK L
	hemolysin BL lytic component L2									AYLDDLEKQNNQ
KGT43102.1	[Bacillus cereus]	61	49291	1746	732.879	1463.74	0.44	0.91	R	K I
	hemolysin BL lytic component L2									LEVLQEMAMT
KGT43102.1	[Bacillus cereus]	61	49291	2610	1018.97	2035.92	13.4	0.18	R	NQENAGR Q
	hemolysin BL lytic component L2									LSTNVDTTNEQ
KGT43102.1	[Bacillus cereus]	28	49291	1622	684.007	2049	27.8	0.0025	K	SQKDTLR Q
										SMLLLTQNDLH
	hemolysin BL lytic component L2									TFANQVDVELD
KGT43102.1	[Bacillus cereus]	32	49291	1987	761.403	3041.58	5.52	0.88	K	LLKR Y
	hemolysin BL lytic component L2									
KGT43102.1	[Bacillus cereus]	369	49291	39	555.264	1108.51	33.3	0.0021	K	SFVDNKEDR E

KGT43102.1	hemolysin BL lytic component L2 [Bacillus cereus]	369	49291	178	816.419	1630.82	69.6	3.90E-07	K	NVISYLEEQVYK F	-
KGT43102.1	hemolysin BL lytic component L2 [Bacillus cereus]	369	49291	180	822.932	1643.85	73.2	1.40E-07	K	EIIEPAAQAGV AAYNK	G
KGT43102.1	hemolysin BL lytic component L2 [Bacillus cereus]	369	49291	309	751.718	2252.13	89.1	4.60E-09	K	LKDFD TDVATA QGILSTDGTGK	I
KGT43102.1	hemolysin BL lytic component L2 [Bacillus cereus]	369	49291	373	904.833	2711.48	95.8	5.20E-10	K	AIQN DLQQIALI PGALNEQGFAI FK	E
KGT43102.1	hemolysin BL lytic component L2 [Bacillus cereus]	369	49291	381	947.527	2839.56	38.4	0.00025	K	KAIQN DLQQIA LIPGALNEQGF AIFK	E
KGT43102.1	hemolysin BL lytic component L2 [Bacillus cereus]	373	49291	12	500.776	999.538	22.3	0.02	K	QGEIAAAAAAK	T
KGT43102.1	hemolysin BL lytic component L2 [Bacillus cereus]	373	49291	41	556.293	1110.57	12.4	0.2	K	TFGVFAEVNK	L
KGT43118.1	bromoperoxidase [Bacillus cereus]	39	30965	1642	713.369	1424.72	29.1	0.006	K	EFNEALLSFLKD MLDLGIPVGAG	-
KGT43122.1	amidohydrolase [Bacillus cereus]	32	68239	2063	794.902	1587.79	32.2	0.001	R	SDATR	V
KGT43122.1	amidohydrolase [Bacillus cereus]	38	68239	240	616.404	615.396	23.3	0.033	K	KIDLK IDNSDDENPVIS	R
KGT43131.1	hydrolase [Bacillus cereus]	74	57976	2771	1068.53	2135.05	74.3	1.10E-07	K	TTL SFIR NQIYILGHSQG	H
KGT43131.1	hydrolase [Bacillus cereus]	74	57976	2501	960.957	1919.9	8.75	0.78	K	GMMLPK	M
KGT43135.1	deoxyribodipyrimidine photolyase [Bacillus cereus]	26	55851	467	501.306	1000.6	25.6	0.0072	K	ELGSTLIIR	K
KGT43135.1	deoxyribodipyrimidine photolyase [Bacillus cereus]	26	55851	848	630.817	1259.62	3.03	2.3	K	EEELLSVWQK QVNSFIRQLIW	G
KGT43135.1	deoxyribodipyrimidine photolyase [Bacillus cereus]	26	55851	1242	781.43	1560.84	2.93	2.4	K	R	E
KGT43157.1	gamma-glutamyl kinase [Bacillus	19	39305	337	679.356	678.348	19.4	0.054	K	LGTGGMK	S
KGT43282.1	acetyltransferase [Bacillus cereus]	21	16308	774	547.296	1092.58	0.07	4.2	R	IEGEYIKNK	V

[illegible]

KGT43479.1	chitosanase [Bacillus cereus]	100	50707	2822	1118.47	2234.93	38.5	0.00014	K	DFLEESEYTNAY YYNASR	V
KGT43479.1	chitosanase [Bacillus cereus]	100	50707	3000	640.317	2557.24	41	0.00014	K	AQGHFDSATD GDLDIAYSLLLA HK	Q
KGT43479.1	chitosanase [Bacillus cereus]	100	50707	3031	672.348	2685.36	21.9	0.0088	K	KAQGHFDSAT DGDLDIAYSLLL AHK	Q
KGT43479.1	chitosanase [Bacillus cereus]	100	50707	502	428.232	854.45	8.86	0.33	K	IYDGLFK	T
KGT43479.1	chitosanase [Bacillus cereus]	35	50707	95	524.265	1046.52	34.6	0.0015	R	LNLGDWDSK NDLSSLPGGYY	S
KGT43479.1	chitosanase [Bacillus cereus]	35	50707	314	706.861	1411.71	4.43	2.1	K	VK YSPNTGLISDFV	G
KGT43479.1	chitosanase [Bacillus cereus]	26	50707	656	770.408	1538.8	1.84	2.4	K	VK	N
KGT43479.1	chitosanase [Bacillus cereus]	1113	50707	8	481.257	960.5	26	0.0089	K	VSSWIQNK	T
KGT43479.1	chitosanase [Bacillus cereus]	1113	50707	27	539.247	1076.48	35	0.00075	R	AFYEFTGDK WVNSGWDW	T
KGT43479.1	chitosanase [Bacillus cereus]	1113	50707	97	654.794	1307.57	49.6	3.30E-05	K	MK IVMDYAMYGE	N
KGT43479.1	chitosanase [Bacillus cereus]	1113	50707	101	660.301	1318.59	64.4	9.30E-07	R	K QWGSNGTVNY	R
KGT43479.1	chitosanase [Bacillus cereus]	1113	50707	125	683.842	1365.67	79.4	8.10E-08	K	LK SSQNPNLMG	E
KGT43479.1	chitosanase [Bacillus cereus]	1113	50707	196	866.921	1731.83	74.9	1.50E-07	K	WVVADSK SSQNPNLMG	K
KGT43479.1	chitosanase [Bacillus cereus]	1113	50707	224	620.984	1859.93	102	2.80E-10	K	WVVADSKK SSLDTRPSDW	A
KGT43479.1	chitosanase [Bacillus cereus]	1113	50707	235	640.304	1917.89	87.3	9.40E-09	K	MMSHLR EMKFPQQVN YAGVIKPNHVT	A
KGT43479.1	chitosanase [Bacillus cereus]	1113	50707	429	850.193	3396.74	133	1.40E-13	K	QESLNASVR	S

										GEITGDADGFK	
										PLGTSEGQGYG	
										MIITVLMAGYD	
KGT43479.1	chitosanase [Bacillus cereus]	1113	50707	444	977.714	3906.83	39.1	0.00045	K	SNAQK	I
	2-haloalkanoic acid dehalogenase										
KGT43521.1	[Bacillus cereus]	23	27094	1032	458.604	1372.79	23.2	0.012	K	AVDNLFLLVLEK	C
	hypothetical protein IY08_13565									INIHKSVSPEML	
KGT43543.1	[Bacillus cereus]	16	12897	969	990.561	1979.11	15.6	0.043	K	AWLNK	Q
	hypothetical protein IY08_13615										
KGT43553.1	[Bacillus cereus]	23	12876	247	623.341	622.334	23.2	0.023	K	LSFQK	T
KGT43685.1	lysyl-tRNA synthetase [Bacillus	23	61250	493	510.257	1018.5	22.7	0.036	K	ELSVLNTNK	M
	lysyl-tRNA synthetase [Bacillus										
KGT43685.1	cereus]	23	61250	1034	687.858	1373.7	5.61	1.2	K	LNWKIDWPMR	W
	hypothetical protein IY08_12550									MQIGSNIHTLS	
KGT43694.1	[Bacillus cereus]	21	13085	2186	828.902	1655.79	21	0.013	-	QPTK	I
KGT43748.1	carboxylase [Bacillus cereus]	28	57014	970	666.386	1330.76	27.7	0.0047	K	LFAQELITGLAR	I
KGT43748.1	carboxylase [Bacillus cereus]	35	57014	503	514.279	1026.54	24.4	0.011	K	IAALPEEER	A
KGT43748.1	carboxylase [Bacillus cereus]	35	57014	550	531.766	1061.52	12.5	0.33	K	VTLEEMGGAR	M
	aminoacyl-histidine dipeptidase										
KGT43789.1	[Bacillus cereus]	42	54726	467	501.306	1000.6	41.6	0.00018	R	ESVATILIR	T
	aminoacyl-histidine dipeptidase										
KGT43789.1	[Bacillus cereus]	42	54726	661	567.261	1132.51	0.07	3	R	TEDVGQVEEK	L
	aminoacyl-histidine dipeptidase									NLEVIQDEALN	
KGT43789.1	[Bacillus cereus]	42	54726	1479	613.694	1838.06	5.53	0.28	R	VIIKK	E
	aminoacyl-histidine dipeptidase									GLVESSTNLGVI	
KGT43789.1	[Bacillus cereus]	42	54726	1695	715.718	2144.13	4.05	1.4	K	ETLQDEIK	L
	2-methylcitrate dehydratase										
KGT43808.1	[Bacillus cereus]	33	53685	508	430.27	858.525	33.1	0.00067	K	VATTAVVAK	M
	2-methylcitrate dehydratase									EVLEM MIKAHE	
KGT43808.1	[Bacillus cereus]	33	53685	3049	919.119	2754.34	2.5	0.7	R	IQGVLAENSL	V
	2-methylcitrate dehydratase									VPGTSYVLDPV	
KGT43808.1	[Bacillus cereus]	46	53685	226	637.855	1273.7	46	0.00013	R	K	G

KGT43808.1	2-methylcitrate dehydratase [Bacillus cereus]	46	53685	394	795.473	1588.93	5.16	0.3	K	LLGPVVPGTIVP NGTR	V
KGT43812.1	methylmalonate-semialdehyde dehydrogenase [Bacillus cereus]	31	53088	471	400.235	798.456	31.3	0.0011	R	TPLLAER	L
KGT43812.1	methylmalonate-semialdehyde dehydrogenase [Bacillus cereus]	74	53088	748	595.807	1189.6	45.7	7.40E-05	K	TLTDATGEVQR	G
KGT43812.1	methylmalonate-semialdehyde dehydrogenase [Bacillus cereus]	74	53088	1083	706.878	1411.74	46.6	0.0001	R	LVELFYEAGFPK	G
KGT43828.1	diguanylate cyclase [Bacillus cereus]	21	3E+05	124	550.291	1098.57	5.14	1.2	R	GIAKNEELPK LEMGNQGSAL	S
KGT43828.1	diguanylate cyclase [Bacillus cereus]	21	3E+05	474	922.494	1842.97	5.37	1.2	R	DVLLPLR GVIVPMRGLSN	A
KGT43828.1	diguanylate cyclase [Bacillus cereus]	21	3E+05	540	718.371	2152.09	20.7	0.05	K	FLMAMQQK GSVIVAAAGNA	F
KGT43836.1	alkaline serine protease [Bacillus cereus]	52	42354	1351	665.851	1329.69	51.9	3.10E-05	K	GNTK SVGANVLSKDD	A
KGT43836.1	alkaline serine protease [Bacillus cereus]	52	42354	1087	616.824	1231.63	0.93	1.1	K	K IQAPQAWDSQ	L
KGT43836.1	alkaline serine protease [Bacillus cereus]	184	42354	246	650.329	1298.64	56.3	1.10E-05	K	R VAIIDTGVQGS	S
KGT43836.1	alkaline serine protease [Bacillus cereus]	184	42354	465	603.326	1806.96	94.2	2.00E-09	K	HPDLASK VLDNQSGSTLD	V
KGT43836.1	alkaline serine protease [Bacillus cereus]	184	42354	467	907.48	1812.95	62.5	2.20E-06	R	AVAQGIR	E
KGT43836.1	alkaline serine protease [Bacillus cereus]	1515	42354	194	506.759	1011.5	44	0.00013	K	ISGTGTYWK	N
KGT43836.1	alkaline serine protease [Bacillus cereus]	1515	42354	204	517.776	1033.54	28	0.0024	R	QIESTTDK QIESTTDKISGT	I
KGT43836.1	alkaline serine protease [Bacillus cereus]	1515	42354	1015	1014.52	2027.03	63.7	1.10E-06	R	GTYWK	N
KGT43836.1	alkaline serine protease [Bacillus cereus]	1515	42354	1226	816.734	2447.18	149	9.10E-15	K	ANYPAYYSEVIA VASTDQSDRK VISLSLGAPNG	S
KGT43836.1	alkaline serine protease [Bacillus cereus]	1515	42354	1270	862.795	2585.36	95.4	1.00E-09	K	GTALQQAVQY AWNK	G

KGT43836.1	alkaline serine protease [Bacillus cereus]	1515	42354	1272	863.074	2586.2	61.6	3.20E-06	K	SSFSTYGSWVD VAAPGSNIYSTY K	G
KGT43836.1	alkaline serine protease [Bacillus cereus]	1515	42354	1308	905.772	2714.29	64.7	1.00E-06	R	KSSFSTYGSWV DVAAPGSNIYS TYK	G
KGT43836.1	alkaline serine protease [Bacillus cereus]	1515	42354	1402	888.697	3550.76	60.8	3.50E-06	K	GSTYQSLSGTS MATPHVAGVA ALLANQGYSNT QIR	Q
KGT43836.1	alkaline serine protease [Bacillus cereus]	1515	42354	1185	1160.54	2319.06	3.35	1.9	K	ANYPAYYSEVIA VASTDQSDR	K
KGT43836.1	alkaline serine protease [Bacillus cereus]	1515	42354	1424	976.02	3900.05	13	0.11	K	VISLSLGAPNG GTALQQAVQY AWNKGSVIVA AAGNAGNTK	A
KGT43955.1	TPR repeat-containing protein [Bacillus cereus]	19	2E+05	97	527.782	1053.55	18.6	0.039	K	ETNTLSYVK	N
KGT43959.1	peptidase M36 [Bacillus cereus]	44	54664	577	478.263	954.511	44.5	9.00E-05	R	YIQLGFK	N
KGT43959.1	peptidase M36 [Bacillus cereus]	53	54664	2539	973.936	1945.86	22	0.017	K	VNVNGTTDDN SFYSPSTK	A
KGT43959.1	peptidase M36 [Bacillus cereus]	53	54664	2940	811.39	2431.15	18.4	0.023	K	VVVHSNNPFG AWETFIDAENG K	L
KGT43959.1	peptidase M36 [Bacillus cereus]	22	54664	277	665.873	1329.73	22.2	0.026	K	VFLPNPVVSSG SK	V
KGT43959.1	peptidase M36 [Bacillus cereus]	61	54664	77	622.307	1242.6	61	3.70E-06	K	STNLQFNYTR	A
KGT43981.1	penicillin-binding protein [Bacillus cereus]	27	54633	1535	636.672	1906.99	26.9	0.003	M	SKIETPVMTSL QTTVEK	M
KGT43981.1	penicillin-binding protein [Bacillus cereus]	27	54633	825	622.823	1243.63	10.8	0.11	K	EATESLPEQIK	G
KGT43981.1	penicillin-binding protein [Bacillus cereus]	27	54633	917	647.889	1293.76	2.28	0.59	K	DLNVPGVAVA VIK	D

KGT43981.1	penicillin-binding protein [Bacillus cereus]	27	54633	1368	839.935	1677.86	0.8	1	K	EAVTPNTRFAI GSSTK	A
KGT43981.1	penicillin-binding protein [Bacillus cereus]	27	54633	1803	778.044	2331.11	6.71	0.23	K	LEDYTGTFEHP AYGTLQVYK	R
KGT43998.1	sporulation protein [Bacillus cereus]	49	35417	242	538.288	1074.56	34.9	0.0011	R	SGPSTTSVIR	Q
KGT43998.1	sporulation protein [Bacillus cereus]	49	35417	271	552.79	1103.57	33.6	0.003	R	NGPSTSSSVIR	Q
KGT43998.1	sporulation protein [Bacillus cereus]	49	35417	1124	710.36	2128.06	1.17	0.78	K	LVIDAGHGGYD SGAVGNGLVEK	N
KGT44000.1	D-amino acid aminotransferase [Bacillus cereus]	38	33955	121	767.886	1533.76	37.6	0.00044	R	GFQFGDGIYEV FR	L
KGT44011.1	ethanol-active dehydrogenase/acetaldehyde-active reductase [Bacillus cereus]	94	37364	681	574.807	1147.6	72	2.50E-07	K	VAFNSAVDAVR	A
KGT44011.1	ethanol-active dehydrogenase/acetaldehyde-active reductase [Bacillus cereus]	94	37364	1408	585.684	1754.03	37.4	0.00018	R	LVLDGIEVVGSL VGTRK	D
KGT44011.1	ethanol-active dehydrogenase/acetaldehyde-active reductase [Bacillus cereus]	94	37364	426	481.261	960.508	0.54	0.89	K	IADDVTSLK	I
KGT44011.1	ethanol-active dehydrogenase/acetaldehyde-active reductase [Bacillus cereus]	94	37364	1306	813.975	1625.94	11.3	0.074	R	LVLDGIEVVGSL VGTR	K
KGT44041.1	lysine 2,3-aminomutase [Bacillus cereus]	23	54698	2197	830.95	1659.88	23.3	0.0066	K	IALQPNYLISQS ADK	V
KGT44041.1	lysine 2,3-aminomutase [Bacillus cereus]	23	54698	3027	666.58	2662.29	6.12	0.27	K	TKYDLEDPLHE DEDSPVPGLTH R	Y
KGT44095.1	formate--tetrahydrofolate ligase [Bacillus cereus]	47	60599	2008	783.449	1564.88	46.8	2.80E-05	K	VVLVTAINPTP AGEGK	S
KGT44095.1	formate--tetrahydrofolate ligase [Bacillus cereus]	422	60599	454	331.206	990.595	31.2	0.0014	K	LSLDIFKR	L

	formate--tetrahydrofolate ligase								STVTVGLGQAF	
KGT44095.1	[Bacillus cereus]	422	60599	956	661.357	1320.7	49.2	2.40E-05	K	NK I
	formate--tetrahydrofolate ligase									SDIEIAQEASM
KGT44095.1	[Bacillus cereus]	422	60599	975	669.317	1336.62	39	0.00058	K	K
	formate--tetrahydrofolate ligase									
KGT44095.1	[Bacillus cereus]	422	60599	1032	458.604	1372.79	38	0.00041	K	LGRPSDFIVTIR E
	formate--tetrahydrofolate ligase									NVVIGLGGPVQ
KGT44095.1	[Bacillus cereus]	422	60599	1137	731.433	1460.85	43.6	4.40E-05	R	GVPR E
	formate--tetrahydrofolate ligase									AAGIKPEAVVIV
KGT44095.1	[Bacillus cereus]	422	60599	1287	536.672	1607	37.5	0.00018	R	ATIR A
	formate--tetrahydrofolate ligase									IVVAYNFANQP
KGT44095.1	[Bacillus cereus]	422	60599	1344	831.968	1661.92	53.7	1.10E-05	R	VTVK D
	formate--tetrahydrofolate ligase									TVIALREPSLGP
KGT44095.1	[Bacillus cereus]	422	60599	1447	600.344	1798.01	34	0.0006	K	TMGLK G
	formate--tetrahydrofolate ligase									HVETIQSFGVP
KGT44095.1	[Bacillus cereus]	422	60599	1590	667.038	1998.09	50.4	2.30E-05	K	FVIAINK F
	formate--tetrahydrofolate ligase									FITDTDAEVTYL
KGT44095.1	[Bacillus cereus]	422	60599	1819	793.682	2378.02	43.8	8.70E-05	K	QEWCNER G
	formate--tetrahydrofolate ligase									EIEKGENNYAPL
KGT44095.1	[Bacillus cereus]	422	60599	1898	874.106	2619.29	46.4	7.10E-05	K	YELELPLEEK I
	formate--tetrahydrofolate ligase									ELKPSIGAGFIV
KGT44095.1	[Bacillus cereus]	422	60599	1908	892.162	2673.46	39.1	0.00025	R	ALTGTMLTMP
	formate--tetrahydrofolate ligase									GLPK Q
KGT44095.1	[Bacillus cereus]	445	60599	804	614.789	1227.56	10.9	0.25	K	TQYSLSDDATK L
	formate--tetrahydrofolate ligase									SDIEIAQEASM
KGT44095.1	[Bacillus cereus]	445	60599	1144	733.365	1464.72	4.59	0.37	K	KK I
	formate--tetrahydrofolate ligase									QPAALQMDVN
KGT44095.1	[Bacillus cereus]	445	60599	1217	766.361	1530.71	8.38	0.55	K	EDGK A
	formate--tetrahydrofolate ligase									KQLAQYEGEG
KGT44095.1	[Bacillus cereus]	445	60599	1788	772.028	2313.06	4.7	1.3	R	WSNLPVCMAT T
	formate--tetrahydrofolate ligase									IQEIAADLNILE
KGT44095.1	[Bacillus cereus]	445	60599	1871	858.759	2573.26	4.98	1.6	K	DELEPYGHHYK G

	Protein	Length	Score	Decomposition	Mass	pI	MW	K _d	Charge	Peptide	Modifications
KGT44189.1	general stress protein [Bacillus cereus]	88	16669	1363	667.366	1332.72	48.7	6.70E-05	K	KVANWNVLYV	L
KGT44189.1	general stress protein [Bacillus cereus]	28	16669	1131	729.854	1457.69	27.8	0.0077	K	EYLATSSVSEGT	E
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	31	63050	1264	650.336	1298.66	30.7	0.0037	R	VFVNAMEGLY	L
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	31	63050	2028	787.419	1572.82	0.4	2.4	K	DTVKLDEINVS	E
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	31	63050	2659	1045.5	2088.99	20.1	0.049	K	ELGQDTITVELL	K
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	251	63050	150	575.825	1149.63	37.5	0.00062	R	NDDNGSR	Y
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	251	63050	231	642.315	1282.62	75.7	7.90E-08	R	VILTSEFVDK	T
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	251	63050	333	489.945	1466.81	47	6.20E-05	K	AQDFVYAWQR	A
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	251	63050	451	885.899	1769.78	42.1	0.0002	K	VNKGELPADQL	V
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	251	63050	606	961.186	2880.53	58	3.30E-06	K	GVK	F
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	256	63050	88	516.26	1030.51	8.61	0.66	R	ETSTGVNLYDS	I
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	256	63050	141	565.329	1128.64	6.38	0.81	K	DQADR	E
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	256	63050	255	653.849	1305.68	19.6	0.074	K	ILIGQDAAISPT	N
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	256	63050	358	757.354	1512.69	17.6	0.074	K	YGQSTAYLEKP	W
KGT44206.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	256	63050	559	1116.11	2230.2	3.83	1.5	K	FVK	F
KGT44207.1	fosfomicin resistance protein FosB [Bacillus cereus]	23	16647	1370	669.323	1336.63	22.7	0.026	K	VGDFIKEELEK	L

KGT44285.1	Xaa-Pro aminopeptidase [Bacillus cereus]	59	48653	1684	722.878	1443.74	59.2	2.80E-06	K	AIGLIQEDEELS	
KGT44285.1	Xaa-Pro aminopeptidase [Bacillus cereus]	59	48653	1783	738.872	1475.73	2.73	0.93	K	WVGKTVSNEE	Y
KGT44292.1	FMN-dependent NADH-azoreductase [Bacillus cereus]	18	25530	577	478.263	954.511	18.2	0.038	M	AEK	I
KGT44292.1	FMN-dependent NADH-azoreductase [Bacillus cereus]	18	25530	790	551.784	1101.55	0.5	1	-	GLFSSLFGK	K
KGT44393.1	MFS transporter [Bacillus cereus]	18	65005	464	394.244	786.473	10.1	0.47	K	MGLFSSLFGK	K
KGT44393.1	MFS transporter [Bacillus cereus]	18	65005	999	598.333	1194.65	17.6	0.053	R	KEELIR	D
KGT44441.1	hypothetical protein IY08_08475 [Bacillus cereus]	20	33589	478	504.24	1006.47	20.3	0.043	R	KIHNPMVNLK	L
KGT44446.1	fumarate hydratase [Bacillus cereus]	14	50380	352	688.373	687.365	13.6	0.053	K	GMNQSVMQAR	S
KGT44446.1	fumarate hydratase [Bacillus cereus]	14	50380	565	474.745	947.475	6.7	0.68	K	MIAPKE	-
KGT44465.1	RNA polymerase sigma factor SigW [Bacillus cereus]	14	13520	166	595.802	1189.59	14.2	0.23	K	KSAALSNQK	L
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	722	532.262	1062.51	64.8	8.40E-07	R	LRELPENYR	D
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	1440	678.841	1355.67	78.3	6.50E-08	K	INTNINSMR	T
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	1791	738.878	1475.74	85.2	2.10E-08	K	ANDAGAQAAA	
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2024	787.391	1572.77	130	5.50E-13	R	QALGK	E
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2068	796.41	1590.8	77.1	6.50E-08	R	TIAVQTLDNAD	
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2535	648.981	1943.92	42.7	9.90E-05	K	TSK	Q
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2684	707.341	2119	31.5	0.0011	K	INNASDDAAGL	
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2912	787.733	2360.18	51.3	2.90E-05	K	AIATR	M
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2912	787.733	2360.18	51.3	2.90E-05	K	TADSAMNSVS	
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2912	787.733	2360.18	51.3	2.90E-05	K	NILLR	M
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2912	787.733	2360.18	51.3	2.90E-05	K	EQIDYISTNTEF	
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2912	787.733	2360.18	51.3	2.90E-05	K	NDKK	L
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2912	787.733	2360.18	51.3	2.90E-05	K	LEDYNKANDA	
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2912	787.733	2360.18	51.3	2.90E-05	K	GAQAAAQALG	
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2912	787.733	2360.18	51.3	2.90E-05	K	K	E
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2912	787.733	2360.18	51.3	2.90E-05	K	ILNEAGISMLSQ	
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2912	787.733	2360.18	51.3	2.90E-05	K	ANQTPQMVSQ	L

									MRDLANQSAN	
									GTNTNENQAA	
KGT44484.1	flagellin [Bacillus cereus]	1476	39119	2955	825.725	2474.15	59.8	4.60E-06	R	LNK E
KGT44484.1	flagellin [Bacillus cereus]	1490	39119	63	491.243	490.235	4.8	0.35	K	TGADK A
										RINNASDDAAG
KGT44484.1	flagellin [Bacillus cereus]	1490	39119	2284	577.312	1728.91	13	0.071	K	LAIATR M
										DLANQSANGT
										NTNENQAALN
KGT44484.1	flagellin [Bacillus cereus]	1490	39119	3081	964.789	2891.35	19.6	0.039	R	KEFDALK E
KGT44484.1	flagellin [Bacillus cereus]	91	39119	966	665.869	1329.72	5.9	1.2	K	QININLSNVSTK E
										ANASGAIASIDT
KGT44484.1	flagellin [Bacillus cereus]	91	39119	1068	701.881	1401.75	4.44	1.1	K	ALK N
										QNQAKMSNA
KGT44484.1	flagellin [Bacillus cereus]	91	39119	1097	713.33	1424.65	4.46	1.3	R	MDR L
										ESGLGVAANNT
KGT44484.1	flagellin [Bacillus cereus]	226	39119	488	958.001	1913.99	24.9	0.0046	R	QDGISLIR T
										ARESGLGVAAN
KGT44484.1	flagellin [Bacillus cereus]	226	39119	538	714.716	2141.13	31.2	0.0031	R	NTQDGISLIR T
KGT44484.1	flagellin [Bacillus cereus]	240	39119	44	588.297	587.29	8.67	0.3	R	QNQAK M
										ELGLDTLSIGTD
KGT44484.1	flagellin [Bacillus cereus]	240	39119	435	573.313	1716.92	9.94	0.37	K	KVEK T
										ATLGATLNRLD
KGT44484.1	flagellin [Bacillus cereus]	240	39119	501	658.697	1973.07	23.8	0.012	R	FNVNNLK S
										LETTDLKANAS
KGT44484.1	flagellin [Bacillus cereus]	240	39119	552	735.068	2202.18	10.9	0.18	K	GAIASIDTALK N
										ANASGAIASIDT
KGT44484.1	flagellin [Bacillus cereus]	194	39119	1063	687.036	2058.09	7	0.77	K	ALKNIASNR A
KGT44484.1	flagellin [Bacillus cereus]	1518	39119	7	458.763	915.511	27.2	0.005	R	ATLGATLNR L
KGT44484.1	flagellin [Bacillus cereus]	1518	39119	26	538.782	1075.55	41	0.00057	R	LDFNVNNLK S
										AAFDADVTA
KGT44484.1	flagellin [Bacillus cereus]	1518	39119	64	605.793	1209.57	24.6	0.005	K	MK E
KGT44484.1	flagellin [Bacillus cereus]	1518	39119	79	626.816	1251.62	54.3	2.00E-05	K	IETKLEDYNK A

KGT44484.1	flagellin [Bacillus cereus]	1518	39119	124	681.363	1360.71	47.7	4.60E-05	K	ELGLDTLSIGTD K	V
KGT44484.1	flagellin [Bacillus cereus]	1518	39119	194	577.276	1728.81	72	2.20E-07	K	AAFDADVTAA MKEFDK	V
KGT44484.1	flagellin [Bacillus cereus]	1518	39119	258	1015.94	2029.86	45.7	3.50E-05	K	SQSSSMASAAS QIEDADMAK	E
KGT44484.1	flagellin [Bacillus cereus]	1518	39119	286	716.374	2146.1	115	1.70E-11	K	ANDAGAQAAA QALGKEFATLT K	L
KGT44484.1	flagellin [Bacillus cereus]	1518	39119	295	1094.51	2187.01	60.7	4.20E-06	R	DLANQSANGT NTNENQAALN K	E
KGT44496.1	aminotransferase [Bacillus cereus]	45	50550	2807	735.702	2204.08	31.3	0.0012	K	QLQTLSYFPMS QSHEPAIK	L
KGT44496.1	aminotransferase [Bacillus cereus]	39	50550	383	712.878	2847.48	38.8	0.00043	R	SAQMGSLLLEQ LKDEIGEHLVG DIR	G
KGT44639.1	glutamate dehydrogenase [Bacillus cereus]	63	47646	601	490.276	978.537	63.1	2.30E-06	R		K
KGT44639.1	glutamate dehydrogenase [Bacillus cereus]	69	47646	318	661.323	660.315	25.5	0.016	K	TQQQR	E
KGT44639.1	glutamate dehydrogenase [Bacillus cereus]	53	47646	1179	747.405	1492.8	30.9	0.003	R	VVVQGFGNAG SFLAK	F
KGT44639.1	glutamate dehydrogenase [Bacillus cereus]	53	47646	1561	645.021	1932.04	39.9	0.00027	K	LGYPNEVYELLK EPIR	M
KGT44639.1	glutamate dehydrogenase [Bacillus cereus]	53	47646	1827	600.323	2397.26	8.93	0.4	R	IDEFNSPGFITG KPLVLGGSHGR	E
KGT44691.1	ATP-dependent DNA helicase [Bacillus cereus]	20	1E+05	1032	458.604	1372.79	20.3	0.024	K	MAESLQLLVLE K	N
KGT44694.1	aspartate aminotransferase [Bacillus cereus]	21	43365	465	603.326	1806.96	21	0.042	K	AVIINSPSNPTG MIYSK	E
KGT44711.1	peptidase M32 [Bacillus cereus]	49	59123	1450	601.312	1800.91	38.1	0.00044	R	IEADELTYPHVV MVR	Y

										QLNYDFEAGRL	
										DETVHPFEITLN	
KGT44711.1	peptidase M32 [Bacillus cereus]	49	59123	1969	720.112	2876.42	26.2	0.0035	K	R	G
										YELEKELFDGTL	
KGT44711.1	peptidase M32 [Bacillus cereus]	53	59123	1461	604.655	1810.94	4.42	0.38	R	QVK	D
KGT44822.1	signal peptide protein [Bacillus	15	17105	457	390.235	778.456	15	0.05	R	YKVEIK	G
										VAFSDDAEGTP	
KGT44832.1	peptidase M6 [Bacillus cereus]	192	86674	1816	739.359	1476.7	75.5	8.40E-08	K	QLK	L
										WTVGPKPFPIE	
KGT44832.1	peptidase M6 [Bacillus cereus]	192	86674	2325	585.988	1754.94	67.8	7.30E-07	R	GTQAK	V
										NQPDGLIDHL	
										MIIHAGVGQEA	
KGT44832.1	peptidase M6 [Bacillus cereus]	192	86674	2988	636.571	2542.25	31.3	0.0032	K	GGGK	L
KGT44832.1	peptidase M6 [Bacillus cereus]	201	86674	474	400.734	799.453	14	0.14	K	WLTVP GK	A
										FEVVGQADDN	
KGT44832.1	peptidase M6 [Bacillus cereus]	201	86674	2157	817.893	1633.77	15.3	0.038	K	SAGAVR	L
										GIGLATYLDQS	
KGT44832.1	peptidase M6 [Bacillus cereus]	80	86674	147	733.398	1464.78	40.5	0.00038	K	VTK	S
										MLFGNEPFTLD	
KGT44832.1	peptidase M6 [Bacillus cereus]	80	86674	316	763.708	2288.1	58.1	5.00E-06	K	DGSKIETFK	Q
KGT44832.1	peptidase M6 [Bacillus cereus]	80	86674	18	524.26	1046.5	0.2	3.9	K	EAANGDQLTK	D
	oligoendopeptidase F [Bacillus									ALINSPFREELE	
KGT44885.1	cereus]	67	66437	1592	667.346	1999.02	50.2	4.70E-05	K	AYYGK	Q
										APFIFSNFNGTS	
	oligoendopeptidase F [Bacillus									GDIDVLTHEAG	
KGT44885.1	cereus]	67	66437	2070	882.428	3525.68	35.6	0.00094	K	HAFQVYESR	K
KGT44885.1	oligoendopeptidase F [Bacillus	67	66437	561	534.782	1067.55	9.25	0.45	K	NFVELGYAR	M
KGT44885.1	oligoendopeptidase F [Bacillus	67	66437	919	648.818	1295.62	12	0.33	K	QLFALAECDLK	T
	oligoendopeptidase F [Bacillus									TLSQLIPFMQG	
KGT44885.1	cereus]	67	66437	1019	681.878	1361.74	5.39	1.2	R	K	E
	oligoendopeptidase F [Bacillus									TDYNAEMVAN	
KGT44885.1	cereus]	67	66437	1121	723.818	1445.62	16.1	0.048	R	YR	Q

KGT44885.1	oligoendopeptidase F [Bacillus cereus]	67	66437	1534	634.696	1901.07	3.42	0.91	R	QQVLDYIVPVT TELRK	R
KGT44885.1	oligoendopeptidase F [Bacillus cereus]	67	66437	2068	879.914	3515.63	13.3	0.18	R	HSVDTTDTFYK EEQDFDEFSP VVQGYGTK	Y
KGT44889.1	7-cyano-7-deazaguanine synthase [Bacillus cereus]	16	24892	117	531.295	530.288	16.1	0.036	K	QVGAR DGAMQVNQN	H
KGT45013.1	catalase [Bacillus cereus]	112	56040	2721	1060.99	2119.97	73	2.00E-07	R	PSTINYPEPSR	H
KGT45013.1	catalase [Bacillus cereus]	115	56040	571	475.745	949.475	18.2	0.02	R	DLFDAIEK LTTNQGAPVG	G
KGT45013.1	catalase [Bacillus cereus]	112	56040	424	836.403	1670.79	26.7	0.0098	R	DNQNSR AAFLQNEGTT	T
KGT45013.1	catalase [Bacillus cereus]	112	56040	455	889.963	1777.91	90.9	4.70E-09	K	PVFVR LGANYLQIPVN CPYAAVQNQQ	F
KGT45013.1	catalase [Bacillus cereus]	112	56040	577	836.086	2505.24	32.7	0.0025	R	R	D
KGT45013.1	catalase [Bacillus cereus]	124	56040	136	563.784	1125.55	24.6	0.016	R	LFSYPDTQR	Y
KGT45013.1	catalase [Bacillus cereus]	124	56040	140	564.791	1127.57	13.9	0.17	K	LLAVCNFFR RGPVLLEDYHL	A
KGT45013.1	catalase [Bacillus cereus]	124	56040	423	556.641	1666.9	25.6	0.011	R	VEK FSTVIHGQGSP	L
KGT45013.1	catalase [Bacillus cereus]	124	56040	497	652.332	1953.97	8.79	0.83	R	ETARDPR FYTEEGNYDIV	G
KGT45013.1	catalase [Bacillus cereus]	124	56040	583	844.086	2529.24	12.1	0.37	K	GNHLPVFFIR KGETLAIVGESG	D
KGT45041.1	peptide ABC transporter ATP-binding protein [Bacillus cereus]	47	38083	1656	716.884	1431.75	47	4.00E-05	K	SGK QRVVIAMALAC	S
KGT45041.1	peptide ABC transporter ATP-binding protein [Bacillus cereus]	47	38083	2035	788.89	1575.76	2.44	0.59	R	NPK MTVGDIIAEGI	L
KGT45042.1	peptide ABC transporter ATP-binding protein [Bacillus cereus]	36	35328	892	623.669	1867.99	36.1	0.001	R	DIHGLAK SLLSAIPLDPD	S
KGT45042.1	peptide ABC transporter ATP-binding protein [Bacillus cereus]	36	35328	765	843.455	1684.9	18.1	0.073	K	YER	N

KGT45042.1	peptide ABC transporter ATP-binding protein [Bacillus cereus]	36	35328	1084	694.313	2079.92	16.8	0.065	R	IVYDPSQHNYG	E
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	498	62003	1142	627.853	1253.69	49.6	2.80E-05	R	SEAPTMR	E
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	498	62003	1969	772.376	1542.74	93.7	2.10E-09	R	AVNGDIVKPNV	E
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	498	62003	2412	912.436	1822.86	30.5	0.0044	K	K	E
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	501	62003	586	481.25	960.485	7.05	1.5	K	VMTNTMEGLY	D
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	495	510.796	1019.58	29	0.0046	R	SLGK	D
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	575	542.764	1083.51	38	0.00054	K	DTSTPINLYETN	A
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	778	404.566	1210.68	58.1	3.90E-06	R	AIDR	A
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	861	633.833	1265.65	24.9	0.0061	K	KDGSDVNAR	W
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1065	699.388	1396.76	49.6	4.60E-05	R	KAISLAFDR	K
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1283	802.43	1602.84	27.9	0.0089	K	DFVYAWQR	A
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1581	662.674	1985	44.6	0.00013	K	LNQKDPALANK	N
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1831	806.427	2416.26	28.8	0.0063	K	TGEYLKGELEK	N
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1954	933.475	2797.4	26.9	0.0092	K	ASLLAEFIDKYK	G
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	359	62003	580	363.216	1086.63	3.33	2	K	MLLDDAAIVPV	G
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	359	62003	609	553.809	1105.6	13.8	0.23	R	YQR	G
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1954	933.475	2797.4	26.9	0.0092	K	GKPDFQTVEDT	L
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1954	933.475	2797.4	26.9	0.0092	K	SVFFLR	L
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1954	933.475	2797.4	26.9	0.0092	K	NLLEAEKMLLD	G
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1954	933.475	2797.4	26.9	0.0092	K	DAAIVPVYQR	G
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1954	933.475	2797.4	26.9	0.0092	K	QVINLIETQEIP	V
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1954	933.475	2797.4	26.9	0.0092	K	TMDPALSADA	V
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1954	933.475	2797.4	26.9	0.0092	K	VSSR	V
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1954	933.475	2797.4	26.9	0.0092	K	IKQQPFAQK	L
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	355	62003	1954	933.475	2797.4	26.9	0.0092	K	ASLLAEFIDK	Y

KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	359	62003	644	560.272	1118.53	21.5	0.036	K	EMSPDQLGVK	A
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	359	62003	645	560.275	1118.54	13.2	0.23	K	SAYIMYDIK	N
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	359	62003	1789	772.076	2313.21	18.1	0.051	K	ELGKNEIELELL NEDVELSK KPFVDTLNNG SKPATGLIPDNF	K
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	359	62003	1919	675.873	2699.46	17.2	0.041	R	IK	G
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	801	62003	173	602.839	1203.66	31.9	0.0038	K	IEEVNFNIVK	D
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	801	62003	362	506.253	1515.74	27.4	0.0091	K	YSNPKYDEIIMK	A
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	815	62003	66	443.721	885.428	21.8	0.02	K	YGGDLSFK	W
KGT45044.1	peptide ABC transporter substrate-binding protein [Bacillus cereus]	815	62003	541	718.685	2153.03	7.63	1.1	K	WSNGEPVTAK DFVYAWQR	A
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	114	70202	1051	691.832	1381.65	42.8	0.00025	R	YIQFLESDDPR	V
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	114	70202	1125	724.387	1446.76	41.6	0.00013	K	LNELEALLFEEL	-
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	114	70202	1224	513.278	1536.81	35.7	0.0013	R	LYLLNHYLEGFR	G
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	114	70202	1357	558.948	1673.82	25.3	0.0043	R	DLSVYEHALEEI	
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	129	70202	457	497.231	992.447	1.44	2.3	R	TR	Q
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	129	70202	787	608.804	1215.59	8.6	0.64	K	NNFNARVR	K
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	129	70202	1024	684.859	1367.7	16.5	0.095	K	AGVDMASPEP	
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	129	70202	1071	469.59	1405.75	23.2	0.01	K	VK	E
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	129	70202	1257	789.426	1576.84	22.7	0.027	K	QILEEGQPAVE	
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	129	70202	1257	789.426	1576.84	22.7	0.027	K	R	Y
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	129	70202	1257	789.426	1576.84	22.7	0.027	K	AGSSDYPIEVLK	
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	129	70202	1257	789.426	1576.84	22.7	0.027	K	K	A
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	129	70202	1257	789.426	1576.84	22.7	0.027	K	SLNVLGDEYVDI	
KGT45052.1	oligopeptidase PepB [Bacillus cereus]	129	70202	1257	789.426	1576.84	22.7	0.027	K	LK	E

	oligopeptidase PepB [Bacillus								LEDIFQTDAEW	
KGT45052.1	cereus]	129	70202	1807	780.72	2339.14	19.4	0.015	R	EKEFQAIK E
KGT45075.1	ATPase [Bacillus cereus]	19	34257	296	369.675	737.335	19.1	0.036	R	QAYEAR E
KGT45075.1	ATPase [Bacillus cereus]	19	34257	618	556.318	1110.62	1.15	1.7	K	IQLIRGMHK N
KGT45076.1	helicase [Bacillus cereus]	23	89741	827	623.805	1245.6	23.1	0.021	K	ASTQFFEMIR A
KGT45090.1	membrane protein [Bacillus cereus]	25	55598	385	458.27	914.526	24.9	0.022	R	ISQGLLER K
	antifungal polypeptide [Bacillus									ITGTWVTGEYV
KGT45109.1	cereus]	173	12745	2737	709.676	2126.01	57	4.50E-06	K	QGHYSNSK Q
	hypothetical protein IY08_04860									
KGT45111.1	[Bacillus cereus]	14	14597	146	575.288	1148.56	14.2	0.25	-	MAHKSTGVFR V
	hypothetical protein IY08_04695									NGGSGSFYAAA
KGT45154.1	[Bacillus cereus]	21	14727	695	579.776	1157.54	21.2	0.03	R	R T
	hypothetical protein IY08_04695									TQILKDDFSLIN
KGT45154.1	[Bacillus cereus]	21	14727	1406	583.65	1747.93	8.88	0.54	R	GER E
	hypothetical protein IY08_04725									QLEKEMQQSLL
KGT45159.1	[Bacillus cereus]	13	14393	1157	738.402	1474.79	13.2	0.22	K	K T
KGT45224.1	glucosaminidase [Bacillus cereus]	128	70021	75	621.314	1240.61	39.5	0.0005	K	YENEFLWIK D
										VISDNPTVTEAY
KGT45224.1	glucosaminidase [Bacillus cereus]	128	70021	176	810.929	1619.84	47.7	3.40E-05	K	IAK E
										TFGDETFYQYF
KGT45224.1	glucosaminidase [Bacillus cereus]	128	70021	290	1082.51	2163	60.5	3.60E-06	K	NYLSLR S
										YNVNALFLYSLA
										IHESYYGTSALA
KGT45224.1	glucosaminidase [Bacillus cereus]	128	70021	380	936.816	2807.43	34.5	0.0017	K	K D
										SIKPDSPLIGLG
KGT45224.1	glucosaminidase [Bacillus cereus]	128	70021	108	662.896	1323.78	0.18	0.96	K	K K
KGT45283.1	DNA helicase [Bacillus cereus]	14	48670	592	485.293	968.572	13.9	0.041	K	RPLLSDLR E
	hypothetical protein IY08_04625									
KGT45289.1	[Bacillus cereus]	23	6010	448	492.765	983.515	22.8	0.013	R	EVSAYFLR K
	hypothetical protein IY08_04625									
KGT45289.1	[Bacillus cereus]	22	6010	70	598.359	597.352	6.99	0.2	K	KPTPR R
	transcriptional regulator TenI									
KGT45306.1	[Bacillus cereus]	19	22883	255	627.392	626.385	19	0.013	K	KGVPAR G

KGT45326.1	peptide ABC transporter ATP-binding protein [Bacillus cereus]	21	24249	450	494.282	986.549	21.4	0.05	-	MIQLANVAK	G
										NAQFMIETGEV	
										HALMGENGAG	
KGT45425.1	sugar ABC transporter ATP-binding protein [Bacillus cereus]	23	54370	1188	774.374	2320.1	23.2	0.0087	K	K	S
KGT45452.1	DNA-binding protein [Bacillus cereus]	55	56202	669	519.262	1036.51	55.2	6.60E-06	R	YNALGDVSAK	T
KGT45452.1	DNA-binding protein [Bacillus cereus]	55	56202	2330	879.429	1756.84	2.48	1.3	R	QNTTTKYNETV	
										TINK	K
KGT45452.1	DNA-binding protein [Bacillus cereus]	55	56202	2423	915.954	1829.89	1.75	0.68	K	VNVVQIDSNTI	
KGT45452.1	DNA-binding protein [Bacillus cereus]	122	56202	180	605.326	1208.64	28.7	0.0061	K	GQATLR	L
KGT45452.1	DNA-binding protein [Bacillus cereus]	122	56202	185	608.831	1215.65	28.5	0.0041	K	YNETVTINKK	-
KGT45452.1	DNA-binding protein [Bacillus cereus]	122	56202	259	656.318	1310.62	47.2	7.10E-05	K	GLVYLPENPSK	W
										SEQDAMLQYV	
KGT45452.1	DNA-binding protein [Bacillus cereus]	122	56202	403	802.896	1603.78	21.9	0.0094	K	K	N
KGT45452.1	DNA-binding protein [Bacillus cereus]	122	56202	478	619.66	1855.96	65.1	1.40E-06	K	AAFIGDSSPVE	
KGT45452.1	DNA-binding protein [Bacillus cereus]	122	56202	478	619.66	1855.96	65.1	1.40E-06	K	DATPK	Y
KGT45452.1	DNA-binding protein [Bacillus cereus]	122	56202	478	619.66	1855.96	65.1	1.40E-06	K	GVSSVAMHAG	
KGT45452.1	DNA-binding protein [Bacillus cereus]	133	56202	312	703.883	1405.75	13	0.26	K	STLAITNPK	L
KGT45452.1	DNA-binding protein [Bacillus cereus]	133	56202	460	599.944	1796.81	10.1	0.27	K	TIVSPEQSFGIT	
										K	G
										NGGSIFFIADHY	
KGT45483.1	peptidoglycan transglycosylase [Bacillus cereus]	20	29499	1120	481.275	1440.8	20.5	0.028	K	NADR	N
										STPITYEDLKDY	
KGT45452.1	DNA-binding protein [Bacillus cereus]	133	56202	608	977.167	2928.48	24.4	0.019	K	NVFIVPEANIPY	
										K	K
KGT45483.1	peptidoglycan transglycosylase [Bacillus cereus]	20	29499	1120	481.275	1440.8	20.5	0.028	K	VALNPMTKLFY	
										K	A
										ASVENIKAGGV	
KGT45483.1	peptidoglycan transglycosylase [Bacillus cereus]	20	29499	1816	792.091	2373.25	3.31	1.8	R	VQGGSTITQQL	
										SK	N
KGT45497.1	flotillin [Bacillus cereus]	86	57562	417	476.765	951.516	35	0.00084	K	EVLEGLHR	A
KGT45497.1	flotillin [Bacillus cereus]	86	57562	656	565.794	1129.57	28.8	0.0074	K	AQGTAEADVIR	L

KGT45497.1	flotillin [Bacillus cereus]	86	57562	1077	705.92	1409.83	24.5	0.0036	K	QGVPTVNGV SIK	V
KGT45497.1	flotillin [Bacillus cereus]	86	57562	1128	726.353	1450.69	40.5	0.00052	R	ADADLSYELQQ AK	A
KGT45497.1	flotillin [Bacillus cereus]	86	57562	1520	942.495	1882.98	28.4	0.0063	R	TVGPDEALIVT GNWLGGGK	N
KGT45497.1	flotillin [Bacillus cereus]	90	57562	367	444.743	887.471	9.13	0.82	K	QIELEEK GGGTFVVPIM	E
KGT45497.1	flotillin [Bacillus cereus]	90	57562	884	639.337	1276.66	4.99	0.34	R	QR	A
KGT45510.1	glycerol-3-phosphate ABC transporter substrate-binding alanine dehydrogenase [Bacillus	21	50384	91	516.306	515.299	20.8	0.0083	K	AGALGK GAGLGSGFTDA	Y
KGT45533.1	cereus]	95	40315	1446	899.935	1797.86	21.1	0.045	K	QYVEAGAK YTGSSDNGGV	I
KGT45540.1	bacillolysin [Bacillus cereus]	732	60882	2498	640.967	1919.88	122	2.90E-12	R	HTNSGIINK SLNTTSLGSSYY	Q
KGT45540.1	bacillolysin [Bacillus cereus]	732	60882	2592	1010.49	2018.96	30	0.0021	K	LQDNTR AGAVQAAADL YGANSAEVA	G
KGT45540.1	bacillolysin [Bacillus cereus]	732	60882	2622	683.021	2046.04	41.7	0.00012	R	AV K	Q
KGT45540.1	bacillolysin [Bacillus cereus]	732	60882	2648	693.01	2076.01	40.5	0.00054	K	RYTGSSDNGGV HTNSGIINK	Q
KGT45540.1	bacillolysin [Bacillus cereus]	732	60882	2708	707.379	2119.11	29.3	0.0048	K	QAYLLANGGTH YGVTVTGIGK	D
KGT45540.1	bacillolysin [Bacillus cereus]	759	60882	781	550.278	1098.54	12.3	0.24	R	NSINDAGAPLK GVLGDTKSLNT TLSGSSYYLQD	S
KGT45540.1	bacillolysin [Bacillus cereus]	759	60882	3032	897.448	2689.32	23.9	0.014	K	NTR	G
KGT45540.1	bacillolysin [Bacillus cereus]	49	60882	477	925.941	1849.87	21.5	0.034	R	ANTQYFTQSTT FSQAR	A
KGT45540.1	bacillolysin [Bacillus cereus]	1786	60882	147	428.239	854.463	46	5.00E-05	K	LGAIYYR	A
KGT45540.1	bacillolysin [Bacillus cereus]	1786	60882	247	361.16	1080.46	48.9	2.50E-05	K	YGDPDHYSK	R
KGT45540.1	bacillolysin [Bacillus cereus]	1786	60882	252	543.778	1085.54	46.9	7.10E-05	R	GATIFTYDAK	N

KGT45540.1	bacillolysin [Bacillus cereus]	1786	60882	261	549.802	1097.59	34.9	0.00081	K	DKLGAIYYR	A
KGT45540.1	bacillolysin [Bacillus cereus]	1786	60882	386	619.287	1236.56	52.8	1.90E-05	K	YGDPDHYSKR ATFNRSINDA	Y
KGT45540.1	bacillolysin [Bacillus cereus]	1786	60882	768	563.958	1688.85	63.1	1.20E-06	K	GAPLK NPDWEIGEDIY	S
KGT45540.1	bacillolysin [Bacillus cereus]	1786	60882	798	867.406	1732.8	62.8	1.90E-06	R	TPGK SMSDPTKYGDP	A
KGT45540.1	bacillolysin [Bacillus cereus]	1786	60882	861	609.936	1826.79	22	0.0098	R	DHYSK QAYLLANGGTH YGVTVTGIGKD	R
KGT45540.1	bacillolysin [Bacillus cereus]	1786	60882	1204	591.812	2363.22	71.8	2.50E-07	K	K	L
KGT45540.1	bacillolysin [Bacillus cereus]	1786	60882	1344	979.498	2935.47	66.9	5.30E-07	R	AGAVQAAADL YGANSAEVAHV KQSFSAVGVN STLPGLTWADA DNVFNAAYDA AAVDAHYYAG	-
KGT45540.1	bacillolysin [Bacillus cereus]	1786	60882	1380	840.399	3357.57	29.4	0.0054	R	K	T
KGT45540.1	bacillolysin [Bacillus cereus]	1812	60882	146	426.693	851.371	9.78	0.24	K	TYDYKK	A
KGT45540.1	bacillolysin [Bacillus cereus]	1812	60882	276	557.338	1112.66	18.5	0.028	K	AVVKPVTGTNK VGTKGKVLD	V
KGT45540.1	bacillolysin [Bacillus cereus]	1812	60882	289	566.322	1130.63	5.91	1.3	K	TK	S
KGT45551.1	ArsR family transcriptional regulator [Bacillus cereus]	79	11242	1096	618.305	1234.6	79.2	6.30E-08	R	ISEEDVQMLR	A
KGT45559.1	2-amino-3-ketobutyrate CoA ligase [Bacillus cereus]	44	43174	743	539.279	1076.54	43.9	0.00026	K	EMLDEAILK	Y
KGT45570.1	trehalose-6-phosphate hydrolase [Bacillus cereus]	42	65393	1923	508.282	1521.82	42.2	0.00019	K	LNLRPYESIVYR	Y
KGT45574.1	adenylosuccinate lyase [Bacillus adenylosuccinate lyase [Bacillus cereus]	22	50095	412	472.75	943.486	1.47	3.4	R	HADVAFTR AVSETPALGEE	A
KGT45574.1	cereus]	22	50095	845	629.816	1257.62	16.7	0.09	R	R	K

KGT45574.1	adenylosuccinate lyase [Bacillus cereus]	22	50095	1037	688.336	1374.66	20.9	0.041	R	NPIGSENMTGL AR	V
KGT45574.1	adenylosuccinate lyase [Bacillus cereus]	22	50095	1180	498.931	1493.77	6.09	0.36	R	THGVHAEPTTF GLK	L
KGT45574.1	adenylosuccinate lyase [Bacillus cereus]	22	50095	1613	676.971	2027.89	3.24	1.2	R	GYMMTAYENV PLWHER	D
KGT45574.1	adenylosuccinate lyase [Bacillus cereus]	22	50095	1767	758.092	2271.25	1.56	1	K	QANEIILKDLEN FVSILANK	A
KGT45582.1	phosphoribosylaminoimidazolecarb oxamide formyltransferase [Bacillus cereus]	109	55624	1502	932.485	1862.96	55.4	6.40E-06	R	AYEADPVSIFG GIIAANR	E
KGT45582.1	phosphoribosylaminoimidazolecarb oxamide formyltransferase [Bacillus cereus]	109	55624	1956	935.144	2802.41	71	2.60E-07	K	ETIAKPDVTFAD AIENIDIGGPT	S
KGT45582.1	phosphoribosylaminoimidazolecarb oxamide formyltransferase [Bacillus cereus]	114	55624	407	465.77	929.525	21.7	0.037	K	MIR	A
KGT45582.1	phosphoribosylaminoimidazolecarb oxamide formyltransferase [Bacillus cereus]	114	55624	746	595.329	1188.64	2.84	0.64	K	IAITQAGEK	H
KGT45582.1	phosphoribosylaminoimidazolecarb oxamide formyltransferase [Bacillus cereus]	114	55624	1000	677.393	1352.77	17	0.043	K	EFTEPAVVAVK AGITAIQPGGS	D
KGT45582.1	phosphoribosylaminoimidazolecarb oxamide formyltransferase [Bacillus cereus]	114	55624	1182	748.828	1495.64	16	0.039	K	IR	V
KGT45582.1	phosphoribosylaminoimidazolecarb oxamide formyltransferase [Bacillus cereus]	114	55624	1619	681.035	2040.08	14.2	0.14	K	DDMTIGVGAG QMNR	V
KGT45583.1	phosphoribosylamine--glycine ligase [Bacillus cereus]	19	46094	1009	679.849	1357.68	18.8	0.018	R	AGITAIQPGGS IRDEDSIK	V
KGT45592.1	1-pyrroline-5-carboxylate dehydrogenase [Bacillus cereus]	59	56402	244	649.843	1297.67	58.7	6.40E-06	K	FGDPETEVVLP R	L
KGT45608.1	4-aminobutyrate aminotransferase [Bacillus cereus]	56	50045	617	498.279	994.544	55.8	9.60E-06	K	SIVASAFGFSG QK	C
KGT45608.1	4-aminobutyrate aminotransferase [Bacillus cereus]	110	50045	119	545.306	1088.6	27.9	0.0024	K	INEQIPGPK	A
KGT45608.1	4-aminobutyrate aminotransferase [Bacillus cereus]	110	50045	230	641.877	1281.74	42.5	7.90E-05	K	LAALAPGSFDK SLGAGVPISGVI	Q
KGT45608.1	4-aminobutyrate aminotransferase [Bacillus cereus]	110	50045	230	641.877	1281.74	42.5	7.90E-05	K	GR	K

KGT45608.1	4-aminobutyrate aminotransferase [Bacillus cereus]	110	50045	293	679.843	1357.67	28.6	0.0021	K	FGFGPFAPEVY	A
KGT45608.1	4-aminobutyrate aminotransferase [Bacillus cereus]	110	50045	384	773.953	1545.89	52.8	6.80E-06	R	GLLLLSAGTYG	V
KGT45608.1	4-aminobutyrate aminotransferase [Bacillus cereus]	110	50045	78	494.803	987.591	14.1	0.08	K	RPGIIAFSK	G
KGT45608.1	4-aminobutyrate aminotransferase [Bacillus cereus]	110	50045	92	521.754	1041.49	14.2	0.12	K	APFPYEYR	R
KGT45608.1	4-aminobutyrate aminotransferase [Bacillus cereus]	110	50045	458	894.984	1787.95	5.26	1.8	K	QVLFLNSGAEA VENAVK	I
KGT45613.1	peptidase M29 [Bacillus cereus]	27	45341	1719	729.864	1457.71	27	0.0029	K	VFPDVAPEEQE	L
KGT45613.1	peptidase M29 [Bacillus cereus]	30	45341	469	399.716	797.418	17.7	0.028	R	AK HEPIFR	K
KGT45613.1	peptidase M29 [Bacillus cereus]	23	45341	1523	942.963	1883.91	3.6	1.2	K	EGAAFMSIYAE	G
KGT45613.1	peptidase M29 [Bacillus cereus]	23	45341	1679	709.032	2124.08	23.5	0.011	R	NPDLLK	A
KGT45625.1	amidohydrolase [Bacillus cereus]	32	41566	679	574.303	1146.59	31.9	0.0046	-	LKFDLAPEEAFA	L
KGT45628.1	alkyl hydroperoxide reductase [Bacillus cereus]	105	20831	506	430.242	858.469	29.4	0.0052	R	EFPSWK	I
KGT45628.1	alkyl hydroperoxide reductase [Bacillus cereus]	105	20831	2611	679.657	2035.95	29.3	0.004	K	MKTLELQER	G
KGT45628.1	alkyl hydroperoxide reductase [Bacillus cereus]	105	20831	1537	464.603	1390.79	10.8	0.21	-	DASILVNK	A
KGT45647.1	hypothetical protein IY08_01845 [Bacillus cereus]	24	41688	385	458.27	914.526	24.4	0.025	K	ANAYHNGEFIQ	F
KGT45653.1	ABC transporter substrate-binding protein [Bacillus cereus]	28	29524	61	602.296	1202.58	28.3	0.0067	K	VTDESLK	S
KGT45677.1	chitinase [Bacillus cereus]	300	74536	1402	673.873	1345.73	66.8	9.40E-07	K	MLLIGTEVKPFK	N
KGT45677.1	chitinase [Bacillus cereus]	300	74536	1473	684.386	1366.76	57.8	4.30E-06	R	QKLEIER	A
KGT45677.1	chitinase [Bacillus cereus]	300	74536	1581	704.381	1406.75	67.2	1.10E-06	K	KVFAESTVAFLR	Y

									VPYLYNATTGT	
KGT45677.1	chitinase [Bacillus cereus]	300	74536	2992	849.057	2544.15	48.8	5.20E-05	K	FISYDDNESMK Y
KGT45677.1	chitinase [Bacillus cereus]	300	74536	561	473.26	944.505	0.73		3.7 K	SQPTALTVK T
										SYPGSGTTWED
KGT45677.1	chitinase [Bacillus cereus]	300	74536	2066	796.302	1590.59	6.69		0.21 K	CDK Y
KGT45677.1	chitinase [Bacillus cereus]	70	74536	647	560.832	1119.65	23		0.0086 K	LVLGVPFYGR G
KGT45677.1	chitinase [Bacillus cereus]	70	74536	817	620.343	1238.67	63.9		1.50E-06 K	VFAESTVAFLR A
KGT45677.1	chitinase [Bacillus cereus]	72	74536	800	612.298	1222.58	16.9		0.026 R	NYQVADIDASK L
KGT45677.1	chitinase [Bacillus cereus]	72	74536	833	626.332	1250.65	9.13		0.17 K	WSTTTNSITIK N
										AGAEDGKQYLL
KGT45677.1	chitinase [Bacillus cereus]	42	74536	517	679.354	2035.04	42.1		0.00019 K	TIASGASQR Y
										TIISVGGWTWS
KGT45677.1	chitinase [Bacillus cereus]	55	74536	342	738.886	1475.76	21.9		0.045 K	NR F
										IVGYFPSWGVY
KGT45677.1	chitinase [Bacillus cereus]	55	74536	354	750.884	1499.75	6.98		0.95 K	GR N
	chemical-damaging agent resistance									SQNFGQVGNA
KGT45693.1	protein C [Bacillus cereus]	25	20954	1092	712.357	1422.7	17.8		0.1 R	FVR L
	chemical-damaging agent resistance									FNAVGSQFQG
KGT45693.1	protein C [Bacillus cereus]	25	20954	1332	825.449	1648.88	25.1		0.011 K	GLGALVR A
										ETDFIFYNNLQS
	chemical-damaging agent resistance									PCGSVLHTGDN
KGT45693.1	protein C [Bacillus cereus]	25	20954	1933	925.081	2772.22	6.23		0.58 K	R T
KGT45732.1	penicillin-binding protein [Bacillus	14	46832	1021	604.306	1206.6	14.1		0.048 K	VNNDIYSILR N
	penicillin-binding protein [Bacillus									YIPNFPQGNSI
KGT45732.1	cereus]	14	46832	2134	810.405	1618.8	2.86		1.1 K	QLK H
	penicillin-binding protein [Bacillus									AFVATAIMQLK
KGT45732.1	cereus]	14	46832	2240	847.924	1693.83	3.18		1.1 K	DQNK L
	penicillin-binding protein [Bacillus									NGSVYVVLLSNI
KGT45732.1	cereus]	14	46832	2460	939.476	1876.94	1.31		0.75 K	QNNIK S
	formate acetyltransferase [Bacillus									SGVITGLPDAY
KGT45740.1	cereus]	30	84810	933	653.336	1304.66	22.7		0.014 K	GR G
	formate acetyltransferase [Bacillus									
KGT45740.1	cereus]	30	84810	1006	679.355	1356.7	22.4		0.029 R	TSTFLDIYIER D

KGT45740.1	formate acetyltransferase [Bacillus cereus]	30	84810	1061	696.391	1390.77	0.87	3.6	K	ALLYAINGGKD EK	S
KGT45740.1	formate acetyltransferase [Bacillus cereus]	30	84810	1120	481.275	1440.8	20.5	0.028	R	VALYGIDHLIEA K	K
KGT45740.1	formate acetyltransferase [Bacillus cereus]	30	84810	1845	821.443	2461.31	7.6	0.68	R	FLHTLDNLGPA PEPNLTVLWSK	Q
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	333	407.228	812.441	34.1	0.00099	R	ALEEPVR	Q
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	334	408.745	815.475	30.8	0.0045	K	LVAEVASK	T
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	385	458.27	914.526	28.8	0.0089	K	GRNVVLEK	K
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	389	460.244	918.473	44.8	0.00021	K	SATVESLGR	A
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	435	486.791	971.567	29.7	0.0042	K	TISKPIEGK	S
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	450	494.282	986.549	45.1	0.00021	R	GVDTLANAVK	V
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	490	509.76	1017.51	80.1	5.60E-08	R	IEDALNSTR	A
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	491	509.775	1017.54	29.9	0.0059	K	VGAATETELK	E
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	526	522.801	1043.59	47	0.0001	K	AVTAAIEELK	T
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	761	600.816	1199.62	40.1	0.00032	K	NVTAGANPMG LR	K
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	927	652.347	1302.68	118	9.60E-12	K	VGAATETELKE R	K
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1013	680.85	1359.68	39.3	0.0002	R	VGNDGVITLEE SK	G
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1097	713.33	1424.65	80.8	3.10E-08	R	AQLEETTSEFD R	E

KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1219	766.922	1531.83	70.4	3.70E-07	K	FGSPLITNDGVT IAK	E
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1272	798.366	1594.72	56.2	8.60E-06	K	EIELEDAFENM GAK	L
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1337	827.963	1653.91	58.1	3.00E-06	R	QIAINAGLEGSV VVER	L
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1343	554.316	1659.93	50.9	1.90E-05	K	KFGSPLITNDG VTIAK	E
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1371	841.899	1681.78	84	1.80E-08	R	AQLEETTSEFD REK	L
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1496	930.431	1858.85	61.9	2.30E-06	K	GFTTELDVVEG MQFDR	G
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1515	627.006	1878	94.2	1.60E-09	K	MEAVLDNPYILI TDKK	I
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1545	959.971	1917.93	53.7	9.20E-06	K	ENTTVVEGVGS TEQIEAR	I
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1552	964.028	1926.04	61.6	2.40E-06	K	VASIVAEGDEA TGINIVLR	A
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1632	1034.03	2066.05	28.8	0.002	R	AAVEEGIVAGG GTSLMNVYTK	V
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1662	1053.53	2105.05	47.3	0.0001	K	TNDVAGDGTT TATVLAQAMIR	E
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1753	749.393	2245.16	80.2	4.40E-08	K	AMLEDIAILTG GEVITEELGR	D
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1816	792.091	2373.25	76.1	9.40E-08	R	KAMLEDIAILTG GEVITEELGR	D
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1837	817.44	2449.3	31.1	0.0027	R	ALEEPVRQIAIN AGLEGSVVVER	L
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1865	854.431	2560.27	117	1.10E-11	K	VGVGFNAAATG EWWNMLESIGI VDPK	V

KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2059	57370	1904	887.123	2658.35	105	1.40E-10	K	SSIAQVAAISAA DEEVGQLIAEA MER	V
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2090	57370	195	307.697	613.379	12.5	0.15	K	VTLGPK	G
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2090	57370	277	351.215	700.415	6.31	0.86	R	NVVLEK	K
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2090	57370	285	360.176	718.337	16.4	0.095	K	APGFGDR	R
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2090	57370	296	369.675	737.335	19.1	0.036	K	FSEEAR	R
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2090	57370	339	414.27	826.525	17.3	0.019	K	LAGGVAVIK	V
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2090	57370	411	467.77	933.526	22.6	0.016	R	GTFNVVAVK GYASPYMITDS	A
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2090	57370	1140	732.327	1462.64	12.4	0.15	R	DK	M
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2090	57370	1322	548.626	1642.86	13.4	0.18	R	EGLKNVTAGA NPMGLR	K
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2090	57370	1401	867.96	1733.9	6.17	1.2	K	MEAVLDNPYILI TDK	K
KGT45780.1	molecular chaperone GroEL [Bacillus cereus]	2090	57370	2020	1067.85	3200.52	18.6	0.053	R	VGNDGVITLEE SKGFTTELDVV EGMQFDR	G
KGT45781.1	GMP synthase [Bacillus cereus]	31	57913	2231	841.965	1681.92	30.6	0.0022	R	VLGSELGIPDEI VWR	Q
KGT45781.1	GMP synthase [Bacillus cereus]	31	57913	151	560.284	559.277	1	0.79	K	AMNPK	G
KGT45781.1	GMP synthase [Bacillus cereus]	31	57913	2415	912.448	1822.88	1.34	1.2	K	TFSEGFMNVI KVDK	E
KGT45781.1	GMP synthase [Bacillus cereus]	36	57913	667	569.823	1137.63	26.8	0.0051	R	QPFPGPGLGIR AGLDREIWQYF	V
KGT45781.1	GMP synthase [Bacillus cereus]	36	57913	1694	714.029	2139.07	27.5	0.0093	K	TALPGMR	S
KGT45781.1	GMP synthase [Bacillus cereus]	36	57913	461	500.283	998.551	11.7	0.16	R	IPWDVLEK	I

									TATTAVALMGS	
KGT45803.1	arginase [Bacillus cereus]	27	32382	705	798.919	1595.82	27.2	0.0028 R	LFGEK	L
	glucosamine--fructose-6-phosphate									APFTAELDASDI
KGT45808.1	aminotransferase [Bacillus cereus]	128	66027	1883	753.878	1505.74	76.2	7.10E-08 R	EK	G
	glucosamine--fructose-6-phosphate									FTLVHNGVIEN
KGT45808.1	aminotransferase [Bacillus cereus]	128	66027	2457	625.674	1874	69.1	4.70E-07 R	YELVK	K
	glucosamine--fructose-6-phosphate									GYDSAGIAVQA
KGT45808.1	aminotransferase [Bacillus cereus]	128	66027	2531	971.466	1940.92	12.9	0.28 R	ENGVVVYK	E
	glucosamine--fructose-6-phosphate									
KGT45808.1	aminotransferase [Bacillus cereus]	298	66027	775	606.333	1210.65	64.8	1.20E-06 K	EIDEQPLVIR	N
	glucosamine--fructose-6-phosphate									ALTITNVPGSTL
KGT45808.1	aminotransferase [Bacillus cereus]	298	66027	1106	715.403	1428.79	49.6	4.30E-05 K	SR	E
	glucosamine--fructose-6-phosphate									YQDENGIEILN
KGT45808.1	aminotransferase [Bacillus cereus]	298	66027	1477	918.425	1834.83	53.1	1.60E-05 K	QDIR	N
	glucosamine--fructose-6-phosphate									CGIVGFIGEQLD
KGT45808.1	aminotransferase [Bacillus cereus]	298	66027	1579	660.35	1978.03	21.4	0.0099 M	AKEILLK	G
										NTLSLLHGSYAI
	glucosamine--fructose-6-phosphate									GLLDAENPNMI
KGT45808.1	aminotransferase [Bacillus cereus]	298	66027	1975	973.173	2916.5	35.5	0.0013 R	YVAK	N
	glucosamine--fructose-6-phosphate									
KGT45808.1	aminotransferase [Bacillus cereus]	301	66027	341	418.731	835.447	5.43	1.4 K	QFLATTR	N
	glucosamine--fructose-6-phosphate									AVLVQTNEMG
KGT45808.1	aminotransferase [Bacillus cereus]	301	66027	982	671.846	1341.68	16.6	0.11 R	HK	A
	glucosamine--fructose-6-phosphate									CGIVGFIGEQLD
KGT45808.1	aminotransferase [Bacillus cereus]	301	66027	1050	691.826	1381.64	6.17	0.89 M	AK	E
	glucosamine--fructose-6-phosphate									AYTAQLAVLSIL
KGT45808.1	aminotransferase [Bacillus cereus]	301	66027	1476	611.359	1831.06	8.19	0.15 K	AADIAK	A
	glucosamine--fructose-6-phosphate									EADYTLPLYAG
KGT45808.1	aminotransferase [Bacillus cereus]	301	66027	1663	1055.05	2108.08	2.17	0.62 R	PEIAVASTK	A
	peptide ABC transporter substrate-									
KGT45828.1	binding protein [Bacillus cereus]	63	61233	173	602.839	1203.66	8.11	0.92 K	LEEINFNVVK	D
	pyrroline-5-carboxylate reductase									
KGT45831.1	[Bacillus cereus]	19	29183	239	327.701	653.388	19.2	0.012 M	LTKHR	I

KGT45862.1	HAD family hydrolase [Bacillus 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus]	21	32292	200	588.335	587.327	10.2	0.11	K	VINSR IVAYSGLETGN	C
KGT45866.1	dioxygenase [Bacillus cereus] 4-hydroxyphenylpyruvate dioxygenase [Bacillus cereus]	26	42066	889	640.334	1278.65	26.1	0.0053	K	R	E
KGT45866.1	homogentisate 1,2-dioxygenase [Bacillus cereus]	26	42066	583	544.772	1087.53	0.19	4.2	K	FPINPADGK FLVVEANSQITT	R
KGT45868.1	[Bacillus cereus]	39	45213	2029	787.921	1573.83	38.8	0.00023	K	PR AGITEPILVLGP	R
KGT45878.1	alanine racemase [Bacillus cereus]	17	43792	2127	808.977	1615.94	17.4	0.02	R	SPPR	D
KGT45888.1	Clp protease ClpX [Bacillus cereus]	22	90572	76	621.851	1241.69	22.4	0.021	K	VQKEVEALIGR	G
KGT45894.1	glutamyl-tRNA synthetase [Bacillus cereus]	93	55642	785	608.331	1214.65	51.8	1.40E-05	R	TALFNLYFAR ELTEEQVKEFEA	H
KGT45894.1	glutamyl-tRNA synthetase [Bacillus cereus]	93	55642	1442	598.623	1792.85	28.3	0.0043	R	EGR VATTGQTHGPE	I
KGT45894.1	glutamyl-tRNA synthetase [Bacillus cereus]	93	55642	1651	696.722	2087.14	45.5	6.30E-05	R	LPNAIALLGK	E
KGT45894.1	glutamyl-tRNA synthetase [Bacillus cereus]	93	55642	542	525.776	1049.54	11.1	0.14	K	LYEDLLER	G
KGT45894.1	glutamyl-tRNA synthetase [Bacillus cereus]	93	55642	657	566.288	1130.56	9.54	0.52	R	NVAGGEESQLK AFAGQIEALEA	Y
KGT45894.1	glutamyl-tRNA synthetase [Bacillus cereus]	93	55642	1511	625.99	1874.95	4.11	0.49	R	MEPAAIK TEFDVELTSAG	A
KGT45907.1	50S ribosomal protein L7/L12 [Bacillus cereus]	25	12510	1856	748.366	1494.72	25.5	0.0041	K	AQK	I
KGT45910.1	DNA-directed RNA polymerase subunit beta~ [Bacillus cereus]	29	1E+05	533	458.778	915.542	29.4	0.0034	R	KGLADTALK	T
KGT45910.1	DNA-directed RNA polymerase subunit beta~ [Bacillus cereus]	36	1E+05	318	661.323	660.315	25.5	0.016	K	TAQGQR QEVVVQGEVE	R
KGT45910.1	DNA-directed RNA polymerase subunit beta~ [Bacillus cereus]	36	1E+05	1384	671.867	1341.72	2.04	3	R	AR	T
KGT45913.1	30S ribosomal protein S7 [Bacillus elongation factor Tu [Bacillus cereus]	18	17899	255	627.392	626.385	18.4	0.014	K	GPVAKR TTLTAAITTVLA	D
KGT45915.1	[Bacillus cereus]	60	43004	930	652.396	1302.78	33.5	0.00045	K	K	A

KGT45915.1	elongation factor Tu [Bacillus cereus]	60	43004	1158	738.436	1474.86	24.8	0.0033	R	QVGVPYIVVFL NK	C
KGT45915.1	elongation factor Tu [Bacillus cereus]	60	43004	1353	834.46	1666.91	31.4	0.0026	K	LLDQAQAGDNI GALLR	G
KGT45915.1	elongation factor Tu [Bacillus cereus]	64	43004	1713	727.708	2180.1	17.8	0.025	R	ETDKPFLMPVE DVFSITGR	G
KGT45915.1	elongation factor Tu [Bacillus cereus]	103	43004	228	939.485	1876.96	23.8	0.0059	R	DLLSEYGFPGD DIPVIK	G
KGT45915.1	elongation factor Tu [Bacillus cereus]	109	43004	374	912.798	2735.37	20.4	0.012	K	VGDVVEIIGLAE ENASTTVTGVE MFR	K
KGT45932.1	50S ribosomal protein L6 [Bacillus cereus]	18	19504	2201	832.429	1662.84	17.5	0.023	R	ALIGNMVEGVT EGFAR	G
KGT45944.1	DNA-directed RNA polymerase subunit alpha [Bacillus cereus]	17	34960	92	648.341	1294.67	16.8	0.027	R	GYGTTLGNSLR R	I
KGT45969.1	methionine--tRNA ligase [Bacillus cereus]	20	75333	2848	762.752	2285.23	20.3	0.028	K	KAEELNITPQAY VDNIVAGIK	E
KGT45969.1	methionine--tRNA ligase [Bacillus cereus]	58	75333	1385	851.452	1700.89	41.1	0.00019	R	INFDLANDLGN LLNR	T
KGT45969.1	methionine--tRNA ligase [Bacillus cereus]	58	75333	1425	593.611	1777.81	34.8	0.0014	K	FYEDNPHFIQP ESR	K
KGT45969.1	methionine--tRNA ligase [Bacillus cereus]	63	75333	876	637.794	1273.57	18	0.042	K	MDISYDDFIR SFYITTPIIYPSG	T
KGT45969.1	methionine--tRNA ligase [Bacillus cereus]	63	75333	1315	818.92	1635.82	20.5	0.024	K	K QTGIMLMPFLT	L
KGT45969.1	methionine--tRNA ligase [Bacillus cereus]	63	75333	1411	883.474	1764.93	17.2	0.099	R	VAPSK	M
KGT45984.1	transcription-repair coupling factor [Bacillus cereus]	14	1E+05	146	575.288	1148.56	14.2	0.25	K	IMMYKQFR VNEMLYIDENQ	G
KGT45989.1	spore coat protein [Bacillus cereus]	41	11627	2228	841.392	1680.77	41.5	0.0003	K	GEK	T
KGT45995.1	hypoxanthine phosphoribosyltransferase [Bacillus cereus]	37	20225	1300	658.358	1314.7	37.2	0.0011	K	VLISEEQIQEK	V
KGT45999.1	cysteine synthase [Bacillus cereus]	35	32898	278	557.765	1113.51	35.4	0.00084	K	TEQAFEYAR	R

	inosine-5-monophosphate									
KGT46010.1	dehydrogenase [Bacillus cereus]	55	52618	1019	603.804	1205.59	55.5	6.30E-06	K	VGIGPGSICTTR V
	inosine-5-monophosphate									EGLTFDDVLLV
KGT46010.1	dehydrogenase [Bacillus cereus]	89	52618	1233	772.923	1543.83	75.3	1.30E-07	K	PAR S
	inosine-5-monophosphate									
KGT46010.1	dehydrogenase [Bacillus cereus]	93	52618	488	507.335	1012.65	0.35	0.92	R	KLVGIITNR D
	inosine-5-monophosphate									AGMGYCGAQ
KGT46010.1	dehydrogenase [Bacillus cereus]	93	52618	1380	846.866	1691.72	20.7	0.018	R	DLEFLR E
	inosine-5-monophosphate									VVAGVGVPQL
KGT46010.1	dehydrogenase [Bacillus cereus]	93	52618	1702	1083.04	2164.06	2.27	0.94	R	TAVYDCATEAR K
	inosine-5-monophosphate									
KGT46010.1	dehydrogenase [Bacillus cereus]	27	52618	253	652.866	1303.72	19.2	0.056	K	LVGIITNRDMR F
	pyridoxal biosynthesis protein									GGVIMDVVNA
KGT46012.1	[Bacillus cereus]	18	31937	1687	723.868	1445.72	17.8	0.03	K	EQAK I