

Bold indicates differences in gene content; grey indicates blocks of genes absent in a genome
Column B is the best hit from the Propionibacterium acnes SK137 genome (e-value threshold was set to 1e-10).

Isolate: SK137	Gene ID	raft genome of Isolate P. humerusii (454	Gene ID	Start	Stop	Carroll genome	
			Prop003	/length=31777	%G+C=62.1	/description=[Propionibacterium]	
transporter, major facilitator family protein	HMPREF0675_4152	putative ribonuclease	328907359	Prop003_1	1309	2553 + B 1084 putative tRNA-processing ribonuclease; K07058 (db=KEGG)	
putative ribonuclease	HMPREF0675_4151	transcriptional regulator	328907358	Prop003_2	2639	3226 + B 4150 hypothetical protein (db=KEGG)	
hypothetical protein	HMPREF0675_4150	hypothetical protein	328907357	Prop003_3	3410	3889 + C hypothetical protein; K08999 hypothetical protein (db=KEGG evaluate=2.0	
hypothetical protein	HMPREF0675_4149	regulatory protein	328907356	Prop003_4	3969	4679 + B 4148 transcriptional regulator, MerR family (db=KEGG)	
transcriptional regulator, MerR family	HMPREF0675_4148	FHA domain protein	328907355	Prop003_5	4679	5260 + B 1084 putative signal transduction protein GarA (db=KEGG)	
FHA domain protein	HMPREF0675_4147	putative glycine cleavage system H protein	328907354	Prop003_6	5269	5649 + C putative glycine cleavage system H protein; K02437 glycine cleavage sys	
glycine cleavage H-protein	HMPREF0675_4146	hypothetical protein	328907353	Prop003_7	5726	6478 + B 1082 hypothetical protein (db=KEGG)	
hypothetical protein	HMPREF0675_4145	small basic protein	328907352	Prop003_8	6471	6803 + C small basic protein (db=KEGG evaluate=3.0e-45 bit_score=183.0 identity=	
small basic protein	HMPREF0675_4144	membrane associated protein	328907351	Prop003_9	6846	7592 + B 4143 hypothetical protein (db=KEGG)	
hypothetical protein	HMPREF0675_4143	putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosph	328907350	Prop003_10	7613	8266 + B 4142 putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltr	
putative CDP-diacylglycerol--glycerol-3-phosphate 3-phosph	HMPREF0675_4142	CDP-diacylglycerol--glycerol-3-phosphate 3-ph	328907349	Prop003_11	8312	8935 + B 4141 CDP-alcohol phosphatidyltransferase; K00995 CDP-diacylglycerol--	
CDP-alcohol phosphatidyltransferase(EC:2.7.8.5)	HMPREF0675_4141	putative HIT family protein	328907348	Prop003_12	8928	9488 + B 1077 putative HIT family protein (db=KEGG)	
HIT family protein	HMPREF0675_4140	threonine--tRNA ligase(EC:6.1.1.3)	328907347	Prop003_13	9481	11535 + B 4139 thrS; threonine--tRNA ligase (EC:6.1.1.3); K01868 threonyl-tRNA s	
threonine--tRNA ligase(EC:6.1.1.3)	HMPREF0675_4139	response regulator receiver domain protein	328907346	Prop003_14	11624	12256 + B 4138 putative hemoglobin-dependent two component system response re	
putative Hemoglobin-dependent two component system res	HMPREF0675_4138	putative two-component system sensor kinase	328907345	Prop003_15	12253	12990 + B 4137 histidine kinase (db=KEGG)	
histidine kinase	HMPREF0675_4137	hypothetical protein	328907343				
		tryptophanase	328907342				
		hypothetical protein	328907341				
		YheO-like protein	328907340				
		hypothetical protein	328907339				
		hypothetical protein	328907338				
		hypothetical protein	328907337				
hypothetical protein	HMPREF0675_4136		Prop003_16	13704	14765 + C	hypothetical protein; K02004 (db=KEGG evaluate=8.0e-32 bit_score	
			Prop003_17	14799	15587 + C	ABC transporter-like protein; K02003 (db=KEGG evaluate=9.0e-63)	
ABC transporter, ATP-binding protein	HMPREF0675_3054		328907334	Prop003_18	15544	16608 + B	4135 oxidoreductase, zinc-binding dehydrogenase family protein;
oxidoreductase, zinc-binding dehydrogenase family protein	HMPREF0675_4135	hypothetical protein	328907333	Prop003_19	17838	18596 + B	1066 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_4134						
(tRNA)	HMPREF0675_4133						
(tRNA)	HMPREF0675_4132						
(tRNA)	HMPREF0675_4131						
polyphosphate:nucleotide phosphotransferase, PK2 family	HMPREF0675_4130	polyphosphate:nucleotide phosphotransferase,	328907335	Prop003_20	18653	19507 + B	4130 polyphosphate:nucleotide phosphotransferase, PK2 family (EC:2.7
amino acid permease	HMPREF0675_4129						
tryptophan 2,3-dioxygenase(EC:4.1.99.1)	HMPREF0675_4128						
YheO-like protein	HMPREF0675_4127						
hypothetical protein	HMPREF0675_4126	peptide methionine sulfoxide reductase MsrB	328907334	Prop003_21	19642	20088 + C	msrB; methionine-R-sulfoxide reductase (EC:1.8.4.-); K07305 peptide-m
methionine-R-sulfoxide reductase(EC:1.8.4.12)	HMPREF0675_4125	enoyl-CoA hydratase/carnitine racemase	328907333	Prop003_22	20211	20780 + B	1064 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_4124	3'-5' exonuclease	328907332	Prop003_23	20777	22015 + B	1063 ribonuclease D (EC:3.1.26.3); K03684 ribonuclease D [EC:3.1.13.5
3'-5' exonuclease(EC:3.1.13.5)	HMPREF0675_4123	1-deoxy-D-xylulose-5-phosphate synthase	328907331	Prop003_24	22052	23920 + C	1122 des; 1-deoxy-D-xylulose-5-phosphate synthase (EC:2.2.1.7); K016
1-deoxy-D-xylulose-5-phosphate synthase(EC:2.2.1.7)	HMPREF0675_4122		Prop003_25	24126	25262 + C	putative esterase (db=KEGG evaluate=3.0e-40 bit_score=169.0 id	
			Prop003_26	25473	28142 + B	1061 aconitate hydratase (EC:4.2.1.3); K01681 aconitate hydratase 1 [E	
aconitate hydratase 1(EC:4.2.1.3)	HMPREF0675_4121	hypothetical protein	328907329	Prop003_27	28515	28748 + E	GENE: 7268S..72918 - (rbs_motif=None rbs_spacer=None)
			Prop003_28	28768	30570 + C	site-specific recombinase; K06400 site-specific DNA recombinase	
			Prop003_29	30658	31494 + C	hypothetical protein (db=KEGG evaluate=3.0e-73 bit_score=278.0 id	
			Prop003_30	31514	31735 + C	hypothetical protein (db=KEGG evaluate=1.0e-24 bit_score=115.0 id	
paired read link			Prop002	/length=1194	%G+C=68.17	/description=[Propionibacterium]	
			Prop002_1	1	66 + E	GENE: 6714..6779 - (rbs_motif=None rbs_spacer=None)	
			Prop005	/length=354481	%G+C=63.6	/description=[Propionibacterium]	
			Prop005_1	715	1920 + B	putative RNA methyltransferase (partial) (db=KEGG evaluate=8.0e	
putative 23S rRNA (uracil-5)-methyltransferase Ruma	HMPREF0675_4120	deoxyribonuclease/rho motif-related TRAM	328907328	Prop005_2	2165	4189 + B	1050 SAM-dependent methyltransferase related to tRNA; K00599 [EC:2.1
transporter, major facilitator family protein	HMPREF0675_4119	putative membrane protein	328907327	Prop005_3	4300	5019 + B	4119 membrane family protein (db=KEGG)
TrkA-N domain protein	HMPREF0675_4118	TrkA-C domain protein	328907326	Prop005_4	5062	5721 + B	1058 trk system potassium uptake protein TrkA; K03499 trk system pota
TrkA-C domain protein	HMPREF0675_4117	nucleic acid-binding domain protein	328907325	Prop005_5	6727	7461 + B	4117 TrkA-C domain protein; K03499 trk system potassium uptake prote
nucleic acid-binding domain protein	HMPREF0675_4116	hypothetical protein	328907324	Prop005_6	7505	7978 + C	hypothetical protein (db=KEGG evaluate=1.0e-43 bit_score=178.0 identity
hypothetical protein	HMPREF0675_4115	dUTP diphosphatase	328907323	Prop005_7	7956	8516 + C	hypothetical protein (db=KEGG evaluate=3.0e-53 bit_score=211.0 identity
Deoxyuridine 5'-triphosphate nucleotidohydrolase(EC:3.6.1	HMPREF0675_4114	hypothetical protein	328907322	Prop005_8	8534	8854 + C	hypothetical protein (db=KEGG evaluate=1.0e-43 bit_score=189.0 identity
hypothetical protein	HMPREF0675_4113	thymidine kinase	328907321	Prop005_9	9429	10499 + B	4110 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_4112	type I phosphodiesterase/nucleotide pyrophosph	328907320	Prop005_10	11219	12361 + B	1049 thymidine kinase (EC:2.7.1.21); K00857 thymidine kinase [EC:2.7
hypothetical protein	HMPREF0675_4111	type I phosphodiesterase/nucleotide pyrophosph	328907319	Prop005_11	12358	13020 + B	1048 type I phosphodiesterase/ nucleotide pyrophosphatase (db=KEGG)
thymidine kinase(EC:2.7.1.21)	HMPREF0675_4110	ABC transporter ATPase	328907318	Prop005_12	13226	14098 + B	4106 hypothetical protein (db=KEGG)
type I phosphodiesterase/nucleotide pyrophosphatase	HMPREF0675_4109	DNA gyrase/topoisomerase IV, A subunit	328907317	Prop005_13	14164	16815 + B	1045 DNA topoisomerase IV subunit A [EC:5.99.1.3]; K02469 DNA gyras
hypothetical protein	HMPREF0675_4108	hypothetical protein	328907316				
hypothetical protein	HMPREF0675_4107		Prop005_18	16832	17314 + C	can; carbonic anhydrase (EC:4.2.1.1); K01673 carbonic anhydrase	
DNA gyrase/topoisomerase IV, A subunit(EC:5.99.1.3)	HMPREF0675_4106	major facilitator superfamily permease	328907315	Prop005_19	17384	18715 + B	1044 major facilitator superfamily permease; K03086 RNA polymerase primary sig
hypothetical protein	HMPREF0675_4104	anaerobic C4-dicarboxylate transporter	328907314	Prop005_20	20178	20888 + B	1043 anaerobic C4-dicarboxylate transporter; K03302 anaerobic C4-dicar
transporter, major facilitator family protein	HMPREF0675_4103	DNA topoisomerase IV subunit B	328907313	Prop005_21	20400	21278 + B	4101 DNA gyrase, B subunit, C-terminal domain protein; K02470 DNA g
transporter, anaerobic C4-dicarboxylate uptake (Dcu) family	HMPREF0675_4102	DNA topoisomerase IV subunit B	328907312	Prop005_22	21557	22207 + C	hypothetical protein (db=KEGG evaluate=1.0e-19 bit_score=99.4 id
DNA gyrase, B subunit, C-terminal domain protein(EC:5.99	HMPREF0675_4101	DNA topoisomerase IV subunit B	328907311	Prop005_23	22244	22573 + C	hypothetical protein (db=KEGG evaluate=1.0e-11 bit_score=72.4 id
DNA gyrase, B subunit, C-terminal domain protein(EC:5.99	HMPREF0675_4100	acetyltransferase, GNAT family	328907310	Prop005_24	22770	22976 + C	hypothetical protein (db=KEGG evaluate=1.0e-30 bit_score=134.0 identity
hypothetical protein	HMPREF0675_4099	putative lipase	328907309				
			Prop005_25	22969	23709 + C	S51 family peptidase (db=KEGG evaluate=1.0e-64 bit_score=249.0 id	
peptidase family S51	HMPREF0675_4756	acetyltransferase, GNAT family	328906067	Prop005_26	23794	25209 + B	car; can; 0341 yhc; cryptic C4-dicarboxylate transporter DcuD; K03326
hypothetical protein	HMPREF0675_4098	hypothetical protein	328907307	Prop005_27	25213	25794 + B	1040 hypothetical protein (db=KEGG)
acetyltransferase, GNAT family	HMPREF0675_4097						
hypothetical protein	HMPREF0675_4096						
hypothetical protein	HMPREF0675_4095						
hypothetical protein	HMPREF0675_4094						
hypothetical protein	HMPREF0675_4093	putative lipase	328907305	Prop005_28	25924	27168 + B	1035 putative lipase (EC:3.1.1.3); K01046 triacylglycerol lipase [EC:3.1.
hypothetical protein(EC:3.1.1.3)	HMPREF0675_4092		Prop005_29	27109	27720 + B	1034 transcriptional regulator (db=KEGG)	
			Prop005_30	27827	30397 + B	4092 glycoside hydrolase, family 2; K01192 beta-mannosidase [EC:3.2.1	
glycoside hydrolase, family 2(EC:3.2.1.25)	HMPREF0675_4092	beta-mannosidase	328907304				
			Prop005_31	30467	32005 + B	1032 RNA polymerase sigma factor; K03086 RNA polymerase primary sig	
RNA polymerase sigma factor RpoD	HMPREF0675_4091	sigma-70 region 2	328907302	Prop005_32	32350	33288 + B	1031 RNA polymerase principal sigma factor HrdD (db=KEGG)
RNA polymerase principal sigma factor HrdD	HMPREF0675_4090	transposase family protein	328908011	Prop005_33	33796	34272 + C	tnpA; transposase (db=KEGG evaluate=6.0e-47 bit_score=188.0 id
		transposase	328908013	Prop005_34	34415	34732 + C	tnpA; transposase (db=KEGG evaluate=6.0e-47 bit_score=155.0 id
hypothetical protein	HMPREF0675_3932	putative acyl-CoA thioesterase II(EC:3.1.2.-)	328907301	Prop005_35	35540	35824 + D	IPRSCAN: seg (db=Seg db_id=seg from:38 to=50)
putative acyl-CoA thioesterase II(EC:3.1.2.-)	HMPREF0675_4089	lacto-N-biose phosphorylase 2	328907300	Prop005_36	37152	39326 + B	0083 hypothetical protein (db=KEGG); possibly glycosyl hydrolase
1,3-bis-(6-phospho)-N-acetylglucosamine phosphorylase	HMPREF0675_3088	ATP-dependent helicase HrpA(EC:3.6.1.-)	328907289	Prop005_38	39429	42578 + B	4088 hrpA; ATP-dependent helicase HrpA; K03578 ATP-dependent helica
ATP-dependent helicase HrpA(EC:3.6.1.-)	HMPREF0675_4088	ATP-dependent helicase HrpA	328907288	Prop005_39	43086	43502 + E	GENE: 120270..120686 + (rbs_motif=GGAG/GAGG rbs_spacer=5-10bp)
ATP-dependent helicase HrpA(EC:3.6.1.-)	HMPREF0675_4087	putative universal stress protein UsaP	328907287	Prop005_40	43580	43804 + C	IPRSCAN: seg (db=Seg db_id=seg from:38 to=56)
universal stress family protein	HMPREF0675_4086	hypothetical protein	328907286	Prop005_41	43842	44696 + B	1028 putative universal stress protein UsaP (db=KEGG)
hypothetical protein	HMPREF0675_4085	ribonucleoside-diphosphate reductase, adenosylcobalamin-c	328907285	Prop005_42	44786	45712 + B	1027 hypothetical protein (db=KEGG)
ribonucleoside-diphosphate reductase, adenosylcobalamin-c	HMPREF0675_4084	transcriptional regulator NrdR	328907284	Prop005_43	45908	48757 + B	1026 vitamin B12-dependent ribonucleotide reductase (EC:1.17.4.1); K01
putative transcriptional regulator NrdR	HMPREF0675_4083	hypothetical protein	328907283	Prop005_44	48839	49345 + C	ndrR; transcriptional regulator NrdR; K07738 transcriptional repressor N
hypothetical protein	HMPREF0675_4082	lexA DNA binding domain protein	328907282	Prop005_45	49571	49921 + C	lexA; LexA DNA binding domain protein (EC:3.4.21.88); K01356 repres
LexA DNA binding domain protein(EC:3.4.21.88)	HMPREF0675_4081	putative ATP-dependent helicase	328907281	Prop005_46	50205	50888 + C	4081 putative ATP-dependent helicase; K03722 ATP-dependent DNA helic
putative ATP-dependent helicase(EC:3.6.1.-)	HMPREF0675_4080	GTP-binding protein HflX	328907280	Prop005_47	52936	54411 + B	4080 hflX; GTP-binding protein HflX; K03665 GTP-binding protein HflX (d
GTP-binding protein HflX	HMPREF0675_4079	diaminopimelate epimerase	328907279	Prop005_48	54510	55334 + B	4079 dppA; diaminopimelate epimerase (EC:5.1.1.7); K01778 diaminopim
diaminopimelate epimerase(EC:5.1.1.7)	HMPREF0675_4078	RNA isopentenyltransferase	328907278	Prop005_49	56416	56616 + C	1019 miaA; tRNA delta(2)-isopentenylpyrophosphate transferase (EC:2.5
RNA isopentenyltransferase(EC:2.5.1.75)	HMPREF0675_4077	RNA modification enzyme, MiaB family	328907277	Prop005_50	56769	58253 + B	1017 MiaB family protein (db=KEGG)
hypothetical protein	HMPREF0675_4076	C4-dicarboxylate anaerobic carrier	328907276	Prop005_51	58303	58422 + C	C4-dicarboxylate anaerobic carrier (db=KEGG evaluate=2.0e-13 bit_score=
RNA-(16)A37 thiotransferase enzyme MiaB	HMPREF0675_4075	aldose 1-epimerase	328907275	Prop005_52	60026	60925 + B	4074 aldose 1-epimerase (db=KEGG)
C4-dicarboxylate anaerobic carrier	HMPREF0675_4074	RNA binding metal dependent phosphohydrola	328907274	Prop005_53	60691	62378 + B	4073 conserved hypothetical protein YmdA/YtgF; K06950 (db=KEGG)
aldose 1-epimerase(EC:5.1.3.3)	HMPREF0675_4073	regulatory protein RecX	328907273	Prop005_54	62704	63219 + C	recX; regulatory protein RecX; K03565 regulatory protein (db=KEGG eva
conserved hypothetical protein YmdA/YtgF	HMPREF0675_4072	ReaC protein	328907272	Prop005_55	63249	64295 + C	4071 recA; protein ReaC; K03553 recombination protein ReaC (db=KEGG
regulatory protein RecX	HMPREF0675_4071	hypothetical protein	328907271	Prop005_56	64603	64809 + C	hypothetical protein (db=KEGG evaluate=8.0e-27 bit_score=122.0 identity
protein RecA	HMPREF0675_4070	transcriptional regulator, DeoR family	328907270	Prop005_57	64896	65705 + C	1010 putative transcriptional regulator protein; K02081 DeoR family tra
transcriptional regulator, DeoR family	HMPREF0675_4069	DNA-binding protein	328907269	Prop005_58	65971	66066 + B	CNA-binding protein (db=KEGG evaluate=2.0e-40 bit_score=167.0 identity
DNA-binding protein	HMPREF0675_4068	competence/damage-inducible protein CnaC C-terminal dom	328907268	Prop005_59	66649	67269 + B	1007 phosphatidylglycerophosphate synthase; K00995 CDP-diacylglycer
competence/damage-inducible protein CnaC C-terminal dom	HMPREF0675_4067	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltr	328907267	Prop005_60	67390	68814 + B	1006 radical SAM superfamily protein (db=KEGG)
CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltr	HMPREF0675_4066	putative fructosamine kinase	328907266	Prop005_61	68850	69656 + B	1005 putative fructosamine kinase (db=KEGG)
ribosomal protein S12 methylthiotransferase RimO	HMPREF0675_4065	AAA family ATPase	328907265				
fructosamine kinase	HMPREF0675_4064	hypothetical protein	328907264				
			Prop005_62	69782	70432 + B	4063 ypgY; orotate phosphoribosyltransferase (EC:2.4.2.10); K00762 or	
orotate phosphoribosyltransferase(EC:2.4.2.10)	HMPREF0675_4063	orotidine 5'-phosphate decarboxylase	328907263	Prop005_63	70461	71171 + B	1003 orotidine 5'-phosphate decarboxylase (EC:4.1.1.23); K01591 orot
orotidine 5'-phosphate decarboxylase(EC:4.1.1.23)	HMPREF0675_4062</						

Dihydroorotate dehydrogenase, catalytic subunit(EC:1.3.3.3. HMPREF0675_4061	dihydroorotate dehydrogenase 18	328907261	Prop005_67	71198	72121	+	B	1002 dihydroorotate dehydrogenase B, catalytic subunit (EC:1.3.3.1); K0
oxidoreductase, FAD-binding protein	dihydroorotate dehydrogenase electron transfr	328907260	Prop005_68	72118	72912	+	B	1001 dihydroorotate dehydrogenase electron transfer subunit; K02823 d
carbamoyl-phosphate synthase, large subunit(EC:6.3.5.5)	carbamoyl-phosphate synthase, large subunit	328907259	Prop005_69	72312	76118	+	B	1000 carb; carbamoyl phosphate synthase large subunit (EC:6.3.5.5); K
carbamoyl-phosphate synthase, small subunit(EC:6.3.5.5)	carbamoyl-phosphate synthase, small subunit	328907258	Prop005_70	76118	77206	+	B	4058 carbA; carbamoyl-phosphate synthase, small subunit (EC:6.3.5.5);
Dihydroorotase(EC:3.5.2.3)	dihydroorotase	328907257	Prop005_71	77203	78507	+	B	0998 dihydroorotase (EC:3.5.2.3); K01465 dihydroorotase (EC:3.5.2.3) (
aspartate carbamoyltransferase(EC:2.3.1.3.2)	aspartate carbamoyltransferase	328907256	Prop005_72	78537	79481	+	B	0997 pyrB; aspartate carbamoyltransferase catalytic subunit (EC:2.1.3.2;
uracil phosphoribosyltransferase/pyrimidine operon regulat	pyrimidine operon regulatory protein/uracil ph	328907255	Prop005_73	79478	80053	+	B	0995 bifunctional pyrimidine regulatory protein PyrR uracil phosphoribos
oxidoreductase, aldo/keto reductase family protein	oxidoreductase, aldo/keto reductase family prt	328907254	Prop005_74	80211	81224	+	B	0994 putative oxidoreductase protein (db=KEGG)
		Prop005_75	81269	81577	+	D	IPRSCAN: seg (db=Seg db_id=seg from=53 to=62)	
hypothetical protein	hypothetical protein	328907253						
hypothetical protein	hypothetical protein	328907252						
hypothetical protein	hypothetical protein	328907250	Prop005_76	81574	83820	+	B	kfl1:kflA_3310 glycoside hydrolase family 3 domain protein; K05349 beta-
hypothetical protein	hypothetical protein	328907249	Prop005_77	83921	84325	+	C	hypothetical protein (db=KEGG evalua=9.0e-62 bit_score=238.0 identity
	endo-beta-N-acetylglucosaminidase H	328907248						
glycosyl hydrolase, family 18(EC:3.2.1.96)								
pyruvate dehydrogenase (acetyl-transferring), homodimeric	pyruvate dehydrogenase subunit E1	328907247	Prop005_78	84442	87195	+	B	4049 aceE; pyruvate dehydrogenase (acetyl-transferring), homodimeric t
hypothetical protein	putative transcriptional regulator, PucR family	328907246	Prop005_79	87560	88663	+	B	0988 hypothetical protein (db=KEGG)
MFS transporter, sugar porter (SP) family protein	galactose-proton symporter	328907245	Prop005_80	88683	90032	+	B	0987 galactose-proton symporter (db=KEGG)
hypothetical protein	hypothetical protein	328907244	Prop005_81	90286	90648	+	C	hypothetical protein (db=KEGG evalua=2.0e-54 bit_score=213.0 identity
2-dehydropanoate 2-reductase(EC:1.1.1.169)	2-dehydropanoate 2-reductase	328907243	Prop005_82	90648	91562	+	B	0985 2-dehydropanoate 2-reductase (EC:1.1.1.169); K00077 2-dehydro
[acyl-carrier-protein] S-malonyltransferase family protein(HMPREF0675_4044	hypothetical protein	328907242	Prop005_83	91690	92622	+	B	0984 acyl-carrier-protein S-malonyltransferase (EC:2.3.1.39); K00645 [a
3-oxoacyl-[acyl-carrier-protein] synthase 3(EC:2.3.1.180)	putative beta-ketoacyl-acyl carrier protein syn	328907241	Prop005_84	92619	93617	+	B	4043 fabH; 3-oxoacyl-[acyl-carrier-protein] synthase 3 (EC:2.3.1.41); K
hypothetical protein	acyl carrier protein	328907240	Prop005_85	93699	93944	+	B	acpP; acyl carrier protein; K02078 acyl carrier protein (db=KEGG evalua
putative beta-ketoacyl-acyl-carrier-protein synthase II(EC: HMPREF0675_4042	putative beta-ketoacyl-acyl-carrier-protein syn	328907239	Prop005_86	94017	95291	+	B	0980 3-oxoacyl-[acyl-carrier-protein] synthase I (EC:2.3.1.41); K09458
hypothetical protein	hypothetical protein	328907238						
pyridoxal phosphate enzyme, YggS family	pyridoxal phosphate enzyme, YggS family	328907237	Prop005_87	95351	95854	+	C	hypothetical protein (db=KEGG evalua=6.0e-66 bit_score=252.0 identity
von Willebrand factor type A domain protein	von Willebrand factor type A domain protein	328907236	Prop005_88	95928	96647	+	B	4039 pyridoxal phosphate enzyme, YggS family (db=KEGG)
hypothetical protein	aerotolerance protein BatA	328907235	Prop005_89	96702	97655	+	B	4038 von Willebrand factor type A domain protein; K07114 (db=KEGG)
ATPase family associated with various cellular activities (AA	hypothetical protein	328907234	Prop005_90	97655	98629	+	B	0976 aerotolerance protein BatA; K07114 (db=KEGG)
hypothetical protein	hypothetical protein	328907233	Prop005_91	98626	99669	+	B	0975 putative MoxR (db=KEGG)
hypothetical protein	hypothetical protein	328907232	Prop005_92	99679	100803	+	B	0974 MoxR-like ATPase; K03924 MoxR-like ATPase (EC:3.6.3.-) (db=KEG
hypothetical protein	hypothetical protein	328907231	Prop005_93	100955	101875	+	B	2378 hypothetical protein (db=KEGG)
Cof-like hydrolase	Cof-like hydrolase	328907230	Prop005_94	101875	102672	+	B	4032 Cof-like hydrolase; K07024 (db=KEGG)
hypothetical protein	hypothetical protein	328907229						
	triacylglycerol lipase	328907228	Prop005_95	102808	103842	+	B	4856 triacylglycerol lipase (EC:3.1.1.3) (db=KEGG)
triacylglycerol lipase(EC:3.1.1.3)								
hypothetical protein	hypothetical protein	328907227						
(rRNA)		328907226						
		328907225						
		328907224						
hypothetical protein	hypothetical protein	328907223	Prop005_96	104661	105704	+	C	arsB; membrane efflux protein (db=KEGG evalua=4.0e-34 bit_score=145
amino acid permease	putative amino acid permease	328907222	Prop005_97	105690	107060	+	B	0969 putative amino acid permease (db=KEGG)
dethiobiotin synthetase	dethiobiotin synthetase	328907221	Prop005_98	107057	107761	+	B	0968 dethiobiotin synthetase (EC:6.3.3.3); K01935 dethiobiotin synthet
adenosylmethionine-8-amino-7-oxononanoate transaminasi	adenosylmethionine-8-amino-7-oxononanoate	328907220	Prop005_99	107758	109014	+	B	0967 adenosylmethionine-8-amino-7-oxononanoate aminotransferase (E
hypothetical protein	hypothetical protein	328907219	Prop005_100	109131	109823	+	B	0966 glutamine amidotransferase subunit PdxT; K06861 glutamine amid
pyridoxal 5'-phosphate synthase, glutamine subunit Pdx2	pyridoxal 5'-phosphate synthase, glutamine	328907218	Prop005_101	109774	110679	+	B	0965 pyridoxal biosynthesis lase PdxS; K06215 pyridoxine biosynthesis
pyridoxine biosynthesis protein	transcriptional regulator	328907217	Prop005_102	110745	112160	+	B	0964 transcriptional regulator; K00375 GntR family transcriptional regula
cysteine synthase A(EC:2.3.1.47)	cysteine synthase A	328907216	Prop005_103	112213	113488	+	B	0963 cysteine synthase (EC:2.5.1.47); K01738 cysteine synthase A [EC;
hypothetical protein	hypothetical protein	328907215	Prop005_104	113487	114517	+	B	0962 redox protein, regulate of disulfide formation (db=KEGG)
YeeE/YeeF family protein	YeeE/YeeF family protein	328907214	Prop005_105	113447	114517	+	B	UniRef50_UPI000050F819 hypothetical protein Bin8_01687 n=1 Tax=Br
hypothetical protein	hypothetical protein	328907213						
trehalose-phosphatase(EC:3.1.3.12)	trehalose-phosphatase	328907212	Prop005_106	114957	115832	+	B	4020 otsB; trehalose-phosphatase (EC:3.1.3.12); K01087 trehalose-phos
putative alpha,alpha-trehalose-phosphatase synthase (UDP-f	alpha,alpha-trehalose-phosphatase synthase	328907211	Prop005_107	115975	117378	+	B	4019 putative alpha,alpha-trehalose-phosphatase synthase (UDP-forming)
luciferase family oxidoreductase, group 1	putative luciferase-like monooxygenase	328907210						
(rRNA)								
hypothetical protein	hypothetical protein	328907209	Prop005_108	117679	118185	+	C	hypothetical protein (db=KEGG evalua=1.0e-68 bit_score=261.0 identity
sigma-70, region 4	sigma-70, region 4	328907208	Prop005_109	118199	119011	+	B	0958 RNA polymerase sigma factor (db=KEGG)
DNA primase	DNA primase	328907207	Prop005_110	119098	120942	+	B	4014 dnaG; DNA primase (EC:2.7.7.-); K02316 DNA primase [EC:2.7.7.-;
conserved hypothetical protein TIGR00245	putative membrane protein	328907206	Prop005_111	120985	121779	+	B	4013 conserved hypothetical protein TIGR00245; K02069 putative ABC
putative dGTPase(EC:3.1.5.1)	deoxyguanosinetriphosphate triphosphohydroly	328907205	Prop005_112	121809	122927	+	B	0955 deoxyguanosinetriphosphate triphosphohydrolyase; K01129 dGTPase
TIM-barrel protein, nifR3 family	phosphoribosyltransferase	328907204	Prop005_113	122976	124070	+	B	4011 TIM-barrel protein, nifR3 family (db=KEGG)
cob(II)lynnic acid a,c-diamide reductase(EC:2.4.2.21)	phosphoribosyltransferase	328907203	Prop005_114	124037	125053	+	D	IPRSCAN: seg (db=Seg db_id=seg from=158 to=174)
cob(II)lynnic acid a,c-diamide reductase(EC:2.4.2.21)	phosphoribosyltransferase	328907202	Prop005_115	125054	125263	+	E	GENE: 202416.202625 - (rbs_motif=None rbs_spacer=None)
cob(II)lynnic acid a,c-diamide reductase(EC:2.4.2.21)	phosphoribosyltransferase	328907201	Prop005_116	125384	126025	+	B	0954 phosphoribosyltransferase (db=KEGG evalua=2.0e-64 bit_score=248.0 k
hypothetical protein	hydrolase, NUDIX family	328907200	Prop005_117	126086	126838	+	B	NUDIX hydrolase (db=KEGG evalua=3.0e-50 bit_score=201.0 ide
	quinolinate synthetase complex, A subuni	328907201	Prop005_118	126938	127945	+	B	pfr:PFREUD_09220 nadB1; L-aspartate oxidase (LASPO) (quinol
	hypothetical protein	328907200						
Succinate dehydrogenase flavoprotein subunit(EC:1.3.99.1	L-aspartate oxidase	328907199	Prop005_119	127938	129518	+	B	pfr:PFREUD_09210 nadB1; L-aspartate oxidase (LASPO) (quinol
succinate dehydrogenase and fumarate reductase iron-sulfu	nicotinate-nucleotide pyrophosphorylase	328907198	Prop005_120	129513	130405	+	B	pfr:PFREUD_09200 nadC; nicotinate-nucleotide pyrophosphorylase
succinate dehydrogenase or fumarate reductase, flavoprotein	succinate dehydrogenase/fumarate reductase i	328907197	Prop005_121	130489	131247	+	B	4009 succinate dehydrogenase and fumarate reductase iron-sulfur prote
succinate dehydrogenase (or fumarate reductase) cytochorr	succinate dehydrogenase or fumarate reductase, flavoprotein	328907196	Prop005_122	131244	133376	+	B	4008 sdhA; succinate dehydrogenase or fumarate reductase, flavoprotein
hypothetical protein	putative succinate dehydrogenase subunit C	328907195	Prop005_123	133373	134143	+	B	0950 putative succinate dehydrogenase subunit C; K00241 succinate deh
	glycyl-tRNA synthetase	328907194						
	ABC transporter, ATP-binding protein	328907193						
	efflux ABC transporter, permease protein	328907192						
	hypothetical protein	328907191						
	putative oligopeptidase B	328907190						
glycine--tRNA ligase(EC:6.1.1.14)	glycyl-tRNA synthetase	328907189	Prop005_124	134273	135691	+	B	0949 glycyl-tRNA synthetase (EC:6.1.1.14); K01880 glycyl-tRNA synthet
transcriptional regulator, Fur family	transcriptional regulator, Fur family	328907188	Prop005_125	135904	136314	+	C	transcriptional regulator, Fur family; K03711 Fur family transcriptional reg
transcriptional regulator, Fur family	two-component system response regulator	328907187	Prop005_126	136315	136989	+	B	0947 two-component system response regulator (db=KEGG)
hypothetical protein	hypothetical protein	328907186						
histidine kinase	hypothetical protein	328907185	Prop005_127	137036	137569	+	D	IPRSCAN: seg (db=Seg db_id=seg from=23 to=37)
DNA repair protein RecQ	histidine kinase	328907184	Prop005_128	137601	138612	+	B	0945 putative histidine kinase (db=KEGG)
hypothetical protein	DNA repair protein RecQ	328907183	Prop005_129	139026	139766	+	B	0944 recQ; DNA repair protein RecQ; K03584 DNA repair protein RecQ (r
di-trans,poly-cis-decaprenylcyclotransferase(EC:2.5.1.31)	hypothetical protein	328907182	Prop005_130	139910	140575	+	B	0943 hypothetical protein (db=KEGG)
2-isopropylmalate synthase(EC:2.3.3.13)	undecaprenyl pyrophosphate synthetase	328907181	Prop005_131	140801	141496	+	B	0942 undecaprenyl pyrophosphate synthetase (EC:2.5.1.31); K00806 un
amidohydrolase family protein	2-isopropylmalate synthase	328907180	Prop005_132	141525	143429	+	B	3997 leuA; 2-isopropylmalate synthase (EC:2.3.3.13); K01649 2-isoprop
	putative metal-dependent hydrolase	328907179	Prop005_133	143431	144957	+	B	3996 amidohydrolase family protein; K07047 (db=KEGG)
	amidohydrolase family protein	328907178						
GTP-binding protein Era	GTP-binding protein Era	328907177	Prop005_134	144972	145994	+	B	3995 era; GTP-binding protein Era; K03595 GTP-binding protein Era (db=
CBS domain protein	CBS domain protein	328907176	Prop005_135	145987	147285	+	B	0938 putative hemolysin (db=KEGG)
metalloprotein, YbeY family	metalloprotein, YbeY family	328907175	Prop005_136	147282	147479	+	C	putative metalloprotease; K07042 (db=KEGG evalua=6.0e-71 bit_score=
Phosphate starvation-inducible protein PhoH, predicted ATP	PhoH family protein	328907174	Prop005_137	147476	149017	+	B	3992 phoH; phosphate starvation-inducible protein PhoH, predicted ATPa
hypothetical protein	hypothetical protein	328907173	Prop005_138	149336	149593	+	E	GENE: 226762.227019 - (rbs_motif=None rbs_spacer=None)
hypothetical protein	hypothetical protein	328907172	Prop005_139	150018	151022	+	B	3989 ppi; prolyl aminopeptidase (EC:3.4.11.5); K01259 proline iminopep
prolyl aminopeptidase(EC:3.4.11.5)	hypothetical protein	328907171						
hypothetical protein	putative membrane protein	328907170	Prop005_140	151183	151812	+	B	0931 hypothetical protein; K09125 hypothetical protein (db=KEGG)
hypothetical protein	putative ABC transporter permease	328907169	Prop005_141	152002	153213	+	B	3987 hypothetical protein; K01992 ABC-2 type transport system permeas
ABC transporter, ATP-binding protein	ABC transporter, ATP-binding protein	328907168	Prop005_142	153210	154142	+	B	3986 ABC transporter, ATP-binding protein; K01990 ABC-2 type transport
transcriptional regulator, LuxR family	response regulator receiver domain protein	328907167	Prop005_143	154227	154883	+	B	0926 putative two-component response regulator (db=KEGG)
	histidine kinase	328907166						
histidine kinase	histidine kinase	328907165						
tRNA-guanine transglycosylase(EC:2.4.2.29)	tRNA-guanine transglycosylase	328907164	Prop005_144	154883	156184	+	B	0925 putative two-component system sensor kinase (db=KEGG)
hypothetical protein	putative membrane protein	328907163	Prop005_145	156280	157521	+	B	0924 queuine/archaeosine tRNA-ribosyltransferase (EC:2.4.2.29); K0077
hypothetical protein(EC:2.7.7.23)	UDP-N-acetylglucosamine pyrophosphorylase	328907162	Prop005_146	157647	158036	+	D	IPRSCAN: seg (db=Seg db_id=seg from=35 to=47)
ATP-dependent DNA helicase, RecQ family(EC:3.6.1.-)	ATP-dependent DNA helicase, RecQ family	328907161	Prop005_147	158418	158888	+	B	IPRSCAN: seg (db=Seg db_id=seg from=138 to=152)
DoxX protein	DoxX protein	328907160	Prop005_148	158746	159842	+	B	0923 hypothetical protein (db=KEGG)
PTS system, mannitol-specific IIC component	PTS system, mannitol-specific IIC component	328907159	Prop005_149	159885	161102	+	B	3981 hypothetical protein; K00972 UDP-N-acetylglucosamine pyrophosph
phosphoenolpyruvate-dependent sugar phosphotrans	PTS system, mannitol-specific IIC component	328907158	Prop005_150	161186	163336	+	B	3980 ATP-dependent DNA helicase, RecQ family (EC:3.6.1.-); K03654 AT
oxidoreductase, zinc-binding dehydrogenase family p	PTS system, mannitol-specific IIC component	328907157	Prop005_151	163503	163913	+	C	DoxX protein (db=KEGG evalua=2.0e-45 bit_score=184.0 identity=80.34
RNA methyltransferase, RsmE family(EC:2.1.1.-)	RNA methyltransferase, RsmE family	328907156	Prop005_152	164029	164763	+	B	0917 hypothetical protein; K09761 ribosomal RNA small subunit methyltr
putative chaperone protein DnaJ	chaperone protein DnaJ2	328907155						

naphthase, S54 (rhomboid) family protein	HMMPREF0675_3965	peptidase, S54 family	328907141	Prop005_164	176118	176735 +	B	0908 hypothetical protein (db=KEGG)
naphthoate synthase (EC:4.1.3.36)	HMMPREF0675_3964	naphthoate synthase	328907140	Prop005_165	176615	177106 +	E	GENE: 254041..254532 - (rbs_motif=None rbs_spacer=None)
naphthoate synthase (EC:4.1.3.36)	HMMPREF0675_3964	naphthoate synthase	328907140	Prop005_166	177591	177758 +	C	naphthoate synthase (EC:4.1.3.36); K01661 naphthoate synthase [EC:4.1.3.36]
hypothetical protein (EC:6.2.1.26)	HMMPREF0675_3963	0-succinylbenzoic acid-CoA ligase	328907139	Prop005_167	177798	178964 +	B	3963 hypothetical protein; K01911 0-succinylbenzoic acid-CoA ligase [EC:6.2.1.26]
hypothetical protein	HMMPREF0675_3962							
isochorismate synthase (EC:5.4.4.2; EC:5.4.4.2)	HMMPREF0675_3961	isochorismate synthase	328907138	Prop005_168	179158	180228 +	B	3961 isochorismate synthase (EC:5.4.4.2); K02552 menaquinone-specific isochorismate synthase
		naphthoate synthase	328907137					
		0-succinylbenzoic acid-CoA ligase	328907136					
		hypothetical protein	328907135					
		hypothetical protein	328907134					
			328907133	Prop005_169	180255	181430 +	C	putative lysophospholipase (db=KEGG eval=9.0e-111 bit_score)
			328907132	Prop005_170	181579	183192 +	B	0903 menaquinone biosynthesis protein; K02551 2-succinyl-5-enolpyruvylputative 0-succinylbenzoic acid (OSB) synthetase (EC:4.2.1.11)
			328907131	Prop005_171	183189	184199 +	B	0902 0-succinylbenzoate synthase (EC:4.2.1.1); K02549 0-succinylbenzoate synthase
			328907130	Prop005_172	184196	186031 +	B	0901 GTP-binding protein LepA; K03596 GTP-binding protein LepA (db=KEGG)
			328907129	Prop005_173	186212	188085 +	B	3957 alpha amyrase, catalytic domain protein; K05341 amylosucrase [EC:3.2.1.21]
			328907128	Prop005_174	188231	188497 +	C	rps7; ribosomal protein S20; K02968 small subunit ribosomal protein S20
			328907127	Prop005_175	188685	189650 +	B	0897 DNA polymerase III, delta subunit; K02340 DNA polymerase III subunit III
			328907126	Prop005_176	189716	191431 +	B	0945 type III restriction enzyme, res subunit (db=KEGG)
			328907125					
			328907124	Prop005_177	191578	193914 +	B	0895 putative ComE operon protein 3; K02238 competence protein ComE
			328907123	Prop005_178	193901	194719 +	C	ComE operon protein 1; K02237 competence protein ComEA (db=KEGG)
			328907122	Prop005_179	194908	197879 +	B	3951 leucine; leucine--tRNA ligase (EC:6.1.1.4); K01869 leucyl-tRNA synthetase
			328907121	Prop005_180	197532	198359 +	B	0892 membrane associated protein, DUF125 (db=KEGG)
			328907120	Prop005_181	198379	199383 +	B	0891 hypothetical protein (db=KEGG)
			328907119					
			328907118	Prop005_182	199523	200080 +	C	putative glucoamylase S1/S2 precursor (db=KEGG eval=4.0e-50 bit_score)
			328907117	Prop005_183	200190	201896 +	B	0888 malate dehydrogenase (EC:1.1.1.38); K00027 malate dehydrogenase
			328907116	Prop005_184	201939	202907 +	B	0945 L-lactate dehydrogenase (EC:1.1.1.27); K00016 L-lactate dehydrogenase
			328907115	Prop005_185	203006	203566 +	C	0880 uld; 3-keto-L-gulonate-6-phosphate decarboxylase (EC:2.5.1.3); K00788 thiamine
			328907114	Prop005_186	203553	204386 +	B	0885 hydroxyethylthiazole kinase (EC:2.7.1.50); K00878 hydroxyethylthiazole kinase
			328907113					
			328907112					
			328907111	Prop005_187	204917	205927 +	C	putative S12 family peptidase (db=KEGG eval=2.0e-29 bit_score)
			328907110					
			328907109	Prop005_188	205932	207290 +	B	3941 transporter, major facilitator family protein; K03699 MFS transporter
			328907108	Prop005_189	207325	208275 +	B	3940 putative 2-keto-3-deoxygluconate kinase (EC:2.7.1.45); K00874 2-keto-3-deoxygluconate kinase
			328907107	Prop005_190	208272	208940 +	B	3939 putative L-ribulose-5-phosphate 4-epimerase; K01786 L-ribulose-5-phosphate 4-epimerase
			328907106	Prop005_191	209032	209919 +	B	3938 putative hexulose-6-phosphate isomerase (db=KEGG)
			328907105	Prop005_192	209916	210569 +	B	0880 uld; 3-keto-L-gulonate-6-phosphate decarboxylase (EC:2.5.1.3); K00788 thiamine
			328907104	Prop005_193	210575	211567 +	B	0879 putative phosphotriesterase; K07048 (db=KEGG)
			328907103	Prop005_194</				

hypothetical protein	HMPREF0675_3867	hypothetical protein	328907046					
hypothetical protein	HMPREF0675_3866	peptide ABC transporter ATPase	328907045					
hypothetical protein	HMPREF0675_3865	ABC transporter, ATP-binding protein	328907044					
periplasmic binding protein	HMPREF0675_3864	periplasmic binding protein	328907043					
iron chelate uptake ABC transporter, FeCt family, per	HMPREF0675_3863	iron chelate uptake ABC transporter, FeCt fam	328907042					
ABC transporter, ATP-binding protein (EC:3.6.3.34)	HMPREF0675_3862	putative ferrichrome transport ATP-binding pro	328907041					
CobN/magnesium chelataase domain protein (EC:6.6.1.1)	HMPREF0675_3861	CobN/magnesium chelataase domain prot	328907040					
		CobN/magnesium chelataase domain prot	328907039					
		CobN/magnesium chelataase domain prot	328907038					
hypothetical protein	HMPREF0675_3860	hypothetical protein	328907037					
ATPase family associated with various cellular activiti	HMPREF0675_3859	von Willebrand factor type A domain prot	328907036					
		von Willebrand factor type A domain prot	328907035					
magnesium chelataase, subunit ChiI (EC:6.6.1.1)	HMPREF0675_3858	magnesium chelataase, subunit ChiI	328907034					
		hypothetical protein	328907033					
htaa	HMPREF0675_3857	HtaA domain protein	328907032					
		HtaA domain protein	328907031					
dephospho-CoA kinase(EC:2.7.1.24)	HMPREF0675_3856	dephospho-CoA kinase	Prop005_235	255926	256936 +	C	hypothetical protein (db=KEGG eval=1.0e-19 bit_score=100.0	
			328907030				coA); dephospho-CoA kinase (EC:2.7.1.24); K00859 dephospho-CoA kin	
			Prop005_236	256971	257615 +	C		
			Prop005_237	257615	258088 +	D	PRSCAN: PROKAR_LIPOPROTEIN (db=ProteinScan db_id=PPS1257 from	
ABC transporter, ATP-binding protein	HMPREF0675_3855	ABC transporter, ATP-binding protein	Prop005_238	258127	259800 +	B	0784 ABC-type transport system, fused ATPase and permease; K06147 A	
ABC transporter, ATP-binding protein	HMPREF0675_3854	ABC transporter, ATP-binding protein	328907028	259797	261482 +	B	0783 ABC transporter ATP-binding protein; K06147 ATP-binding cassette,	
hypothetical protein	HMPREF0675_3853							
Heme ABC transporter, ATPase component HmuV(EC:3.6.3	HMPREF0675_3852	ABC transporter, ATP-binding protein	328907027	Prop005_240	261482	262288 +	B	3852 heme ABC transporter, ATPase component HmuV; K02013 iron com
Heme ABC transporter, permease protein HmuU	HMPREF0675_3851	ABC-type transporter, permease component	328907026	Prop005_241	262288	263346 +	B	3851 hmuU; heme ABC transporter, permease protein HmuU; K02015 iro
Heme ABC transporter, cell surface heme and hemoprotein	HMPREF0675_3850	HmuT-like heme-binding lipoprotein	328907025	Prop005_242	263343	264446 +	B	0780 hmuU receptor precursor; K02016 iron complex transport system s
hypothetical protein	HMPREF0675_3849							
HtaA	HMPREF0675_3848	putative Fe transporter	328907024	Prop005_243	264519	265931 +	B	0779 putative for Fe-transport (db=KEGG)
30S ribosomal protein S1	HMPREF0675_3847	30S ribosomal protein S1	328907023	Prop005_244	266371		B	3947 rpsA; 30S ribosomal protein S1; K02945 small subunit ribosomal pr
sortase family protein	HMPREF0675_3846	sortase family protein	328907020	Prop005_245	268019	268957 +	C	sortase family protein (db=KEGG eval=3.0e-68 bit_score=262.0 identi
putative Predicted D-lactate dehydrogenase, Fe-S protein	HMPREF0675_3845	putative D-lactate dehydrogenase, Fe-S protein	328907019	Prop005_246	269037	271880 +	B	0775 oxidoreductase, putative D-lactate dehydrogenase (db=KEGG)
cysteine-rich domain protein	HMPREF0675_3844							
		oxidoreductase, putative D-lactate dehydri	328907018					
		hypothetical protein	328907017	Prop005_247	272411	272761 +	E	GENE: 350093..350443 + (rbs_motif=None rbs_spacer=None)
		hypothetical protein	328907016					
		hypothetical protein	328907015					
DNA-directed DNA polymerase(EC:2.7.7.7)	HMPREF0675_3843	DNA polymerase I	328907014	Prop005_248	278228	275506 +	B	UniRef90_D4HCU8 DNA-directed DNA polymerase n=5 Tax=Propionibacte
hypothetical protein	HMPREF0675_3842	hypothetical protein	328907013	Prop005_249	275578	275991 +	C	hypothetical protein (db=KEGG eval=9.0e-69 bit_score=261.0 identity
response regulator receiver domain protein	HMPREF0675_3841	response regulator receiver domain protein	328907012	Prop005_250	276011	276658 +	B	3841 response regulator receiver domain protein; K07183 response regu
(rRNA)	HMPREF0675_3840							
putative CrcB protein	HMPREF0675_3839	putative CrcB protein	Prop005_251	276925	277296 +	C	putative CrcB protein; K06199 CrcB protein (db=KEGG eval=1.1	
putative CrcB protein	HMPREF0675_3838		328907011	Prop005_252	277729	277724 +	C	CrcB-like protein; K06199 CrcB protein (db=KEGG eval=1.0e-40 bit_sc
hypothetical protein	HMPREF0675_3837	USpA domain protein	328907010	Prop005_253	277713	278290 +	C	USpA domain protein (db=KEGG eval=3.0e-34 bit_score=147.0
pyruvate kinase(EC:2.7.1.40)	HMPREF0675_3836	pyruvate kinase	328907009	Prop005_254	278577		B	3836 pyruvate kinase (EC:2.7.1.40); K00873 pyruvate kinase [EC:2.7.1.4
Ribosomal large subunit pseudouridine synthase D(EC:5.4	HMPREF0675_3835	pseudouridine synthase, RluA family	328907008	Prop005_255	280129	281049 +	B	3836 ribosomal large subunit pseudouridine synthase D (EC:4.2.1.70); K
		hypothetical protein	328907007					
signal peptidase II(EC:3.4.23.36)	HMPREF0675_3835	lipoprotein signal peptidase	328907006	Prop005_256	281046	281552 +	C	lspA; signal peptidase II (EC:3.4.23.36); K03101 signal peptidase II [EC:
C4-type zinc finger protein, DksA/TrfA family	HMPREF0675_3834	C4-type zinc finger protein, DksA/TrfA family	328907005	Prop005_257	281612	282091 +	C	putative DNA-binding protein (db=KEGG eval=1.0e-73 bit_score=277.1
DvIVA domain protein	HMPREF0675_3833	S-adenosyl-N-acetylmuramoyl-pentapeptide- tra	328907004	Prop005_258	282251	283342 +	C	0765 putative immunogenic protein antigen 84 (db=KEGG)
YGGT family protein	HMPREF0675_3832	YGGT family protein	328907003	Prop005_259	283494	283784 +	C	hypothetical protein (db=KEGG eval=3.0e-25 bit_score=117.0 identity
putative cell division protein	HMPREF0675_3831	putative cell division protein	328907002	Prop005_260	283796	284359 +	C	putative cell division protein; K09772 cell division inhibitor SepF (db=KEC
uncharacterized protein, YliH family	HMPREF0675_3830	membrane protein YliH	328907001	Prop005_261	284439	285224 +	C	0762 hypothetical protein; K05810 conserved hypothetical protein (db=K
cell division protein FtsZ	HMPREF0675_3829	cell division protein FtsZ	328907000	Prop005_262	285226	286479 +	B	3829 ftsZ; cell division protein FtsZ; K03531 cell division protein FtsZ (dt
POTRA domain protein, FtsQ-type	HMPREF0675_3828	hypothetical protein, FtsQ-type	328906999	Prop005_263	286602	287315 +	B	0760 cell division protein FtsQ; K03589 cell division protein FtsQ (db=KE
UDP-N-acetylmuramate--L-alanine ligase(EC:6.3.2.8)	HMPREF0675_3827	UDP-N-acetylmuramate--L-alanine ligase	328906998	Prop005_264	287315	288730 +	B	3827 murC; UDP-N-acetylmuramate--L-alanine ligase (EC:6.3.2.8); K019
UDP-N-acetylglucosamine--N-acetylmuramyl- (pentapeptide)	HMPREF0675_3826	putative undecaprenyldiphospho-muramoyler	328906997	Prop005_265	288762	289865 +	B	3826 UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyroph
cell division protein FtsW	HMPREF0675_3825	cell division protein FtsW	328906996	Prop005_266	289902	291200 +	B	3825 ftsW; cell division protein FtsW; K03588 cell division protein FtsW (i
UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase(EC:3	HMPREF0675_3824	UDP-N-acetylmuramoyl-L-alanine--D-glutamat	328906995	Prop005_267	291193	292689 +	B	3824 murD; UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase (EC:6
phospho-N-acetylmuramoyl-pentapeptide- transferase(EC:3	HMPREF0675_3823	phospho-N-acetylmuramoyl-pentapeptide- tra	328906994	Prop005_268	292689	294741 +	C	0766 putative immunogenic protein antigen 84 (db=KEGG)
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine lig	HMPREF0675_3822	UDP-N-acetylmuramyl pentapeptide synthase	328906993	Prop005_269	293738	295195 +	B	0754 UDP-N-acetylmuramyl pentapeptide synthase (EC:6.3.2.10); K0192
UDP-N-acetylmuramoylalanyl-D-glutamate--2, 6-diaminopir	HMPREF0675_3821	UDP-N-acetylmuramoylalanyl-D-glutamate--2	328906992	Prop005_270	295192	296781 +	B	3821 UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate li
penicillin-binding protein, transpeptidase domain protein	HMPREF0675_3820	penicillin-binding protein, transpeptidase domi	328906991	Prop005_271	296778	298532 +	B	3820 penicillin-binding protein, transpeptidase domain protein; K03587 c
putative cell division protein FtsL	HMPREF0675_3819	putative cell division protein FtsL	328906990	Prop005_272	298703	299167 +	C	hypothetical protein (db=KEGG eval=6.0e-51 bit_score=202.0 identity
S-adenosyl-methyltransferase MraW(EC:2.1.1.-)	HMPREF0675_3818	S-adenosyl-methyltransferase MraW	328906989	Prop005_273	310758	319283 +	B	0750 S-adenosyl-methyltransferase MraW (EC:2.1.1.-); K03438 S-adenos
protein MraZ	HMPREF0675_3817	protein MraZ	328906988	Prop005_274	300320	300748 +	B	mraZ; protein MraZ; K03925 MraZ protein (db=KEGG eval=1.0e-74 bit
ATPase family associated with various cellular activities (AA	HMPREF0675_3816	magnesium chelataase, subunit ChiI	328906987	Prop005_275	301028	302071 +	B	3816 ATPase family associated with various cellular activities (AAA); K03
hypothetical protein	HMPREF0675_3815	hypothetical protein	328906986	Prop005_276	302068	303294 +	B	3815 hypothetical protein (db=KEGG)
transglutaminase-like protein	HMPREF0675_3814	transglutaminase-like protein	328906985	Prop005_277	303291	305510 +	B	3814 transglutaminase-like protein (db=KEGG)
hypothetical protein	HMPREF0675_3813	hypothetical protein	328906984	Prop005_278	305527	309668 +	B	hypothetical protein (db=KEGG eval=1.0e-16 bit_score=88.6 identity=
aminomethyltransferase(EC:2.1.2.10)	HMPREF0675_3812	aminomethyltransferase	328906983	Prop005_279	306094	307029 +	B	3812 gcvT; aminomethyltransferase (EC:2.1.2.10); K00605 aminomethyl
glycine cleavage system H protein	HMPREF0675_3811	glycine cleavage system H protein	328906982	Prop005_280	307254	307625 +	C	gcvH; glycine cleavage system H protein; K02437 glycine cleavage syste
glycine dehydrogenase(EC:1.4.4.2)	HMPREF0675_3810	glycine dehydrogenase	328906981	Prop005_281	307625	310615 +	B	0742 glycine dehydrogenase (EC:1.4.4.2); K00281 glycine dehydrogenas
transcriptional regulator, GntR family	HMPREF0675_3809	transcriptional regulator, GntR family	328906980	Prop005_282	310726	311418 +	B	3809 transcriptional regulator, GntR family (db=KEGG)
		hypothetical protein	328906979					
transcriptional regulator, GntR family	HMPREF0675_3809	GntR family transcriptional regulator	328906977	Prop005_283	311604	312341 +	B	0740 GntR family transcriptional regulator (db=KEGG)
		shikimate kinase	328906976	Prop005_284	312452	312976 +	C	gluconokinase (EC:2.7.1.12); K00851 gluconokinase (EC:2.7.1.12)
hypothetical protein	HMPREF0675_3808							
GntP family permease	HMPREF0675_3807	gluconate permease	328906975	Prop005_285	313006	314376 +	B	0738 gluconate permease; K03299 gluconate; + symporter, GntP family
		gluconate permease	328906974					
Hsp20/alpha crystallin family protein	HMPREF0675_3806	Hsp20/alpha crystallin family protein	328906973	Prop005_286	314450	314908 +	C	HSP20/alpha crystallin family protein; K13993 HSP20 family protein (db=
hypothetical protein	HMPREF0675_3804	putative hydrolase	328906972	Prop005_287	315029	315757 +	B	3804 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_3805	hypothetical protein	328906971	Prop005_288	315808	316974 +	B	0734 putative carotenoid dehydrogenase (db=KEGG)
hypothetical protein	HMPREF0675_3803	DNA or RNA helicase, Superfamily I family pro	328906970	Prop005_289	317058	319283 +	B	0733 putative helicase protein (db=KEGG)
hypothetical protein	HMPREF0675_3802		Prop005_290	319180	320118 +		C	metF; 5,10-methylenetetrahydrofolate reductase (EC:1.5.1.20); K
polyphrenyl synthetase(EC:2.5.1.1)	HMPREF0675_3801	geranylgeranyl pyrophosphate synthase	328906969	Prop005_291	320210	321307 +	B	0732 geranylgeranyl pyrophosphate synthase (EC:2.5.1.1); K13787 ger
hypothetical protein	HMPREF0675_3800	hypothetical protein	328906968	Prop005_292	321318	321716 +	C	hypothetical protein (db=KEGG eval=7.0e-50 bit_score=198.0 identity
ribonuclease(EC:3.1.27.3)	HMPREF0675_3799	ribonuclease	328906967					
		hypothetical protein	328906966					
kinase domain protein(EC:2.7.11.1)	HMPREF0675_3798	kinase domain protein	328906965	Prop005_293	322282	323700 +	B	3798 kinase domain protein; K08884 serine/threonine protein kinase, ba
hypothetical protein	HMPREF0675_3797	putative membrane protein	328906964	Prop005_294	323798	324709 +	B	0728 membrane spanning protein DUF6 (db=KEGG)
3-deoxy-7-phosphoheptulonate synthase(EC:2.5.1.54)	HMPREF0675_3796	putative Zn-dependent hydrolase	328906963	Prop005_295	324914	325429 +	E	GENE: 402658..403173 + (rbs_motif=None rbs_spacer=None)
		3-deoxy-7-phosphoheptulonate synthase	328906962	Prop005_296	325448	326875 +	B	0726 phospho-2-dehydro-3-deoxyheptulonate aldolase (EC:2.5.1.54); K01
		hypothetical protein	328906961					
hypothetical protein	HMPREF0675_3794	putative acyltransferase	Prop005_297	326939	327130 +		D	IPRSCAN: coiled-coil (db=Coil db_id=coil from=16 to=45 eval=NA)
hypothetical protein	HMPREF0675_3794	putative acyltransferase	328906960	Prop005_298	327182	327538 +	E	GENE: 404926..405282 + (rbs_motif=None rbs_spacer=None)
acyltransferase(EC:2.3.1.51)	HMPREF0675_3793	acyltransferase	328906959	Prop005_299	327663	328418 +	B	0724 putative acyltransferase; K00655 1-acyl-sn-glycerol-3-phosphate ac
hypothetical protein	HMPREF0675_3792	hypothetical protein	328906958	Prop005_300	328479	328886 +	C	hypothetical protein (db=KEGG eval=2.0e-30 bit_score=134.0 identity
Putative sugar kinase(EC:2.7.1.2)	HMPREF0675_3791	glucokinase	328906957	Prop005_301	328891	329961 +	B	0722 glucokinase (EC:2.7.1.2); K00845 glucokinase [EC:2.7.1.2] (db=K
NlpC/P60 family protein	HMPREF0675_3790	NlpC/P60 family protein	328906956	Prop005_302	329968	330288 +	C	NlpC/P60 family protein (db=KEGG eval=1.0e-51 bit_score=204.0 ider
NlpC/P60 family protein	HMPREF0675_3790	NlpC/P60 family protein	328906955	Prop005_303	330520	331128 +	D	IPRSCAN: seg (db=Seg db_id=seg from=2 to=30)
exonuclease, DNA polymerase III, epsilon subunit family pr	HMPREF0675_3789	GIY-YIG catalytic domain protein	328906954	Prop005_304	331227	333152 +	B	0720 hypothetical protein; K02342 DNA polymerase III subunit epsilon I
		hypothetical protein	328906953	Prop005_305	333072	333716 +	C	hypothetical protein (db=KEGG eval=2.0e-64 bit_score=248.0 i
peptidyl-prolyl cis-trans isomerase, cyclophilin-type(EC:5.2	HMPREF0675_3788	peptidyl-prolyl cis-trans isomerase, cyclophilin	328906952	Prop005_306	333849	334361 +	B	3788 peptidyl-prolyl cis-trans isomerase, cyclophilin-type; K03967 peptid
hypothetical protein	HMPREF0675_3787	putative regulatory protein	328906953	Prop005_307	334545	335690 +	B	3787 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_3786	hypothetical protein	328906952	Prop005_308	336162	336434 +	C	hypothetical protein (db=KEGG eval=8.0e-17 bit_score=89.6 identity=
hypothetical protein(EC:3.4.23.43; EC:2.1.1.-)	HMPREF0675_3785	hypothetical protein	328906951	Prop005_309	336444	337154 +	C	hypothetical protein; K02654 leader peptidase (prelin peptidase) / N-m
hypothetical protein	HMPREF0675_3784	Anthrhanilate phosphoribosyltransferase	328906950	Prop005_310	337141	338193 +	B	pfr:PFREUD_15830 trpD; anthranilate phosphoribosyltransferase (EC:2.4
		hypothetical protein	328906949					
hypothetical protein	HMPREF0675_3783	putative response regulator	328906948	Prop005_311	338208	338651 +	C	putative response regulator (db=KEGG eval=4.0e-64 bit_score=246.0
cytochrome c oxidase, subunit III(EC:1.9.3.1)	HMPREF0675_3782	cytochrome c oxidase, subunit III	328906947	Prop005_312	3390			

2-oxoglutarate dehydrogenase, E2 component, dihydrolipo	HMPREF0675_3762	2-oxoglutarate dehydrogenase, E2 component	328906925	Prop024_1	415	1110	+	B	0693 dihydrolipoamide acyltransferase (EC:2.3.1.61); K00658 2-oxogluta
lipoyl(octanoyl) transferase(EC:2.3.1.181)	HMPREF0675_3761	lipoyl(octanoyl) transferase	328906924	Prop024_2	1121	2035	+	B	3761 lipB; lipoyl(octanoyl) transferase (EC:2.3.1.181); K03801 lipoyl(oct
cytochrome c oxidase Caa3 assembly factor	HMPREF0675_3760	cytochrome c oxidase Caa3 assembly factor	328906923	Prop024_3	2085	4028	+	B	0691 putative permease; K02351 putative membrane protein; K0745 p
copper-exporting ATPase(EC:3.6.3.4)	HMPREF0675_3759	cation-transporting P-type ATPase A	328906922	Prop024_4	4025	6268	+	B	0690 cation-transporting P-type ATPase A (EC:3.6.3.-); K01552 [EC:3.6.3
lipoyl synthase(EC:2.8.1.8)	HMPREF0675_3758	lipoyl synthase	328906921	Prop024_5	6255	7271	+	B	0689 lipoyl synthase; K03644 lipoyl acid synthetase [EC:2.8.1.8] (db=KE
hypothetical protein		hypothetical protein	328906920						
CAMP factor (Cfa)	HMPREF0675_3757	hypothetical protein	328906919						
	HMPREF0675_3756	hypothetical protein	328906918						
		cAMP factor	328906917						
		hypothetical protein	328906916						
transporter, major facilitator family protein	HMPREF0675_3755	transporter, major facilitator family protein	328906915						
BNR/Asp-box repeat protein(EC:3.2.1.18)	HMPREF0675_3754	BNR/Asp-box repeat protein	328906914						
BNR/Asp-box repeat protein(EC:3.2.1.18)	HMPREF0675_3753	BNR/Asp-box repeat protein	328906912						
hypothetical protein	HMPREF0675_3752	integral membrane protein	328906911	Prop024_6	7417	8187	+	B	0683 hypothetical protein (db=KEGG)
ABC transporter, ATP-binding protein	HMPREF0675_3751	ABC transporter, ATP-binding protein	328906910	Prop024_7	8195	9997	+	B	3751 ABC transporter, ATP-binding protein (db=KEGG)
hypothetical protein(EC:2.4.1.-)	HMPREF0675_5433	putative membrane protein	328906909	Prop024_8	10048	11226	+	B	5433 hypothetical protein; K13671 alpha-1,2-mannosyltransferase [EC:2
		hypothetical protein	328906908						
		putative hemin import ATP-binding protel	328906907						
		hypothetical protein	328906906						
		F5/8 type C domain protein	328906905						
		F5/8 type C domain protein	328906904						
hypothetical protein	HMPREF0675_3750								
putative PTS system, N-acetylglucosamine-specific IIA com	HMPREF0675_3749	glucose-specific phosphotransferase enzyme II	328906903	Prop024_9	11205	11657	+	C	putative PTS system, N-acetylglucosamine-specific IIA component; K027
phosphotransferase system, EIIB(EC:2.7.1.69)	HMPREF0675_3748	phosphotransferase system, EIIB	328906902	Prop024_10	11657	11887	+	C	phosphotransferase system, EIIB; K02803 PTS system, N-acetylglucosa
phosphotransferase system, EIIB(EC:2.7.1.69)	HMPREF0675_3747	PTS system, glucose-specific IIB component	328906901	Prop024_11	12034	12282	+	C	phosphotransferase system, EIIB (db=KEGG eval=7.0e-28 bit_score=1
putative histidine utilization repressor	HMPREF0675_3746	putative histidine utilization repressor	328906900	Prop024_12	12279	13004	+	B	0676 GntR family transcriptional regulator; K03710 GntR family transcrip
		hypothetical protein	328906899						
hypothetical protein	HMPREF0675_3745								
phosphotransferase system, EIIC	HMPREF0675_3744	phosphotransferase system, EIIC	328906898	Prop024_13	13218	14606	+	B	0675 PTS system, glucose-specific IIB component (EC:2.7.1.69); K028
hypothetical protein	HMPREF0675_3743	DedA family membrane protein	328906897	Prop024_14	14677	15285	+	C	hypothetical protein (db=KEGG eval=6.0e-81 bit_score=30.03 identity
glycosyltransferase, group 1 family protein	HMPREF0675_3742	glycosyltransferase, group 1 family protein	328906896	Prop024_15	15309	16421	+	B	3742 glycosyltransferase, group 1 family protein (EC:2.4.-); (db=KEGG)
RDD family protein	HMPREF0675_3741	RDD family protein	328906895	Prop024_16	16427	16732	+	C	RDD family protein (db=KEGG eval=2.0e-36 bit_score=154.0 identity=
glutamine synthetase, type I(EC:6.3.1.2)	HMPREF0675_3740	glutamine synthetase, type I	328906894	Prop024_17	16962	18383	+	B	0671 glutamine synthetase (EC:6.3.1.2); K01915 glutamine synthetase [
		hypothetical protein	328906893						
hypothetical protein	HMPREF0675_3739			Prop024_18	18494	19369	+	C	hypothetical protein (db=KEGG eval=9.0e-58 bit_score=227.0 identity
hypothetical protein	HMPREF0675_3738								
hypothetical protein	HMPREF0675_3737								
dinuclear metal center protein, YbgI family	HMPREF0675_3736	dinuclear metal center protein, YbgI family	328906892	Prop024_19	19418	21085	+	B	0668 NIF3 (NGG1P interacting factor 3) (db=KEGG)
hypothetical protein	HMPREF0675_3735	putative membrane protein	328906891	Prop024_20	21110	22411	+	B	0667 hypothetical protein (db=KEGG)
[glutamate--ammonia--ligase] adenyllyltransferase(EC:2.7.7	HMPREF0675_3734	putative glutamate-ammonia--ligase adenyllyl	328906890	Prop024_21	22412	24076	+	B	0666 bifunctional glutamine-synthetase adenyllyltransferase/deadenyltran
[glutamate--ammonia--ligase] adenyllyltransferase(EC:2.7.7	HMPREF0675_3734	putative glutamate-ammonia--ligase adenyllyl	328906890	Prop024_22	24732	25397	+	D	IPRSCAN: seg (db=Seg db_id=seg from=36 to=47)
hypothetical protein	HMPREF0675_3733	hypothetical protein	328906889	Prop024_23	25557	26360	+	B	3733 hypothetical protein (db=KEGG)
Glutamine synthetase type I(EC:6.3.1.2)	HMPREF0675_3732	glutamine synthetase, beta-grasp domain prot	328906888	Prop024_24	26483	27784	+	B	0664 glutamine synthetase (EC:6.3.1.2); K01915 glutamine synthetase [
hypothetical protein	HMPREF0675_3731	hypothetical protein	328906887	Prop024_25	27889	28758	+	B	3732 hypothetical protein (db=KEGG)
		ABC transporter inner membrane protein	328906886	Prop024_26	28763	28957	+	C	hypothetical protein (db=KEGG eval=2.0e-10 bit_score=68.2 id
		ABC transporter ATP-binding protein	328906885	Prop024_27	29042	30430	+	B	cpu:cpfr. 01474 hypothetical protein; K02004 (db=KEGG)
ABC transporter, ATP-binding protein	HMPREF0675_3729	hypothetical protein	328906884						
methionine aminopeptidase, type I(EC:3.4.11.18)	HMPREF0675_3730	ABC transporter ATP-binding protein	328906883	Prop024_28	30430	31140	+	B	cpu:cpfr. 01473 hypothetical protein; K02003 (db=KEGG)
		methionine aminopeptidase, type I	328906882	Prop024_29	31217	32071	+	B	0661 methionine aminopeptidase (EC:3.4.11.18); K01265 methionyl ami
		ABC transporter related protein	328906881						
ABC transporter, ATP-binding protein	HMPREF0675_5221		328908025	Prop024_30	32078	33784	+	B	ske:Sked_24230 ABC transporter ATPase (db=KEGG)
			328906880	Prop024_31	33898	34608	+	C	ABC-type dipeptide transport system, periplasmic component; K0
			328907577	Prop024_32	34933	35577	+	C	dipeptide ABC transporter periplasmic protein; K02035 peptide/n
ABC transporter, permease protein	HMPREF0675_4341		328906879	Prop024_33	35662	36303	+	C	dipeptide/oligopeptide/nickel ABC transporter permease; K02033 peptide
ABC transporter, permease protein	HMPREF0675_5219		328906544	Prop024_34	36644	36958	+	C	dipeptide/oligopeptide/nickel ABC transporter permease; K02034 peptide
			328906544	Prop024_35	37146	37664	+	C	dipeptide/oligopeptide/nickel ABC transporter permease; K02034
hypothetical protein	HMPREF0675_3729								
Carbon starvation protein A	HMPREF0675_3728	carbon starvation protein A	328906880	Prop024_36	38099	40372	+	B	0660 carbon starvation protein A; K06200 carbon starvation protein (db=
hypothetical protein	HMPREF0675_3727								
		carbon starvation protein	328906879						
		hypothetical protein	328906878						
		putative proline-histidine transporter	328906877						
		hypothetical protein	328906876						
		UbiE/COQ5 methyltransferase	328906875						
		hypothetical protein	328906874						
hypothetical protein	HMPREF0675_3726	ferredoxin	328906873	Prop024_37	40607	41239	+	C	putative NADH:ubiquinone oxidoreductase (db=KEGG eval=8.0e-69 bit
ABC transporter, ATP-binding protein(EC:3.6.3.34)	HMPREF0675_3725	ABC transporter, ATP-binding protein	328906872	Prop024_38	41236	42608	+	B	3725 ABC transporter, ATP-binding protein; K02013 iron complex transp
iron chelate uptake ABC transporter, FeCT family, permease	HMPREF0675_3724	iron transport system, permease protein	328906871	Prop024_39	42027	43019	+	B	0657 iron transport system, permease protein; K02015 iron complex tra
periplasmic binding protein	HMPREF0675_3723	iron transport system substrate-binding protei	328906870	Prop024_40	43058	44071	+	B	0656 iron transport system substrate-binding protein; K02016 iron compl
		hypothetical protein	328906869						
hypothetical protein	HMPREF0675_3721								
hypothetical protein	HMPREF0675_3720								
(ncRNA)	HMPREF0675_3719	Zn-ribbon protein possibly nucleic acid-binding	328906868	Prop024_41	44442	45182	+	D	IPRSCAN: seg (db=Seg db_id=seg from=2 to=15)
hypothetical protein	HMPREF0675_3718	Zn-ribbon protein possibly nucleic acid-binding	328906868	Prop024_42	44992	45729	+	B	0651 hypothetical protein; K07164 (db=KEGG)
peptidase, M24 family(EC:3.4.11.9)	HMPREF0675_3717	peptidase, M24 family	328906867	Prop024_43	45952	47448	+	B	0650 Xaa-Pro aminopeptidase I (EC:3.4.11.9); K01262 Xaa-Pro aminope
hypothetical protein	HMPREF0675_3716	putative membrane protein	328906866	Prop024_44	47501	48106	+	B	0649 putative cytochrome oxidase assembly protein; K02259 cytochrome
		putative membrane protein	328906865						
hypothetical protein	HMPREF0675_3715	hypothetical protein	328906864	Prop024_45	48483	49899	+	C	hypothetical protein (db=KEGG eval=6.0e-65 bit_score=249.0 identity
CBS domain protein	HMPREF0675_3714	CBS domain protein	328906863	Prop024_46	48998	50098	+	D	IPRSCAN: seg (db=Seg db_id=seg from=33 to=57)
hypothetical protein	HMPREF0675_3713	integral membrane protein	328906862	Prop024_47	50355	50879	+	C	hypothetical protein (db=KEGG eval=6.0e-76 bit_score=285.0 identity
cellulase (glycosyl hydrolase family 5)	HMPREF0675_3712	ATP-binding protein	328906861	Prop024_48	50942	52096	+	B	0645 ATP-binding protein; K03593 ATP-binding protein involved in chrom
putative twin arginine-targeting protein translocase TatB	HMPREF0675_3711								
dihydrodipicolinate synthase(EC:4.2.1.52)	HMPREF0675_3710	MtaA/family protein	328906860	Prop024_49	52174	52587	+	C	putative twin arginine-targeting protein translocase TatB; K03117 sec-ind
O-methyltransferase	HMPREF0675_3709	dihydrodipicolinate synthase	328906859	Prop024_50	52638	53519	+	B	0642 dihydrodipicolinate synthase (EC:4.2.1.52); K01714 dihydrodipicoli
glucose-1-phosphate adenyllyltransferase(EC:2.7.7.27)	HMPREF0675_3708	methyltransferase	328906858	Prop024_51	53589	54242	+	B	3708 O-methyltransferase (db=KEGG)
glycogen synthase	HMPREF0675_3707	glucose-1-phosphate adenyllyltransferase	328906857	Prop024_52	54457	55650	+	D	IPRSCAN: seg (db=Seg db_id=seg from=8 to=19)
hypothetical protein	HMPREF0675_3705	glycogen synthase, Corynebacterium family	328906856	Prop024_53	55685	56872	+	B	3706 glycogen synthase (EC:2.4.1.21) (db=KEGG)
DivIVA domain protein	HMPREF0675_3704	hypothetical protein	328906855	Prop024_54	56956	57123	+	C	hypothetical protein (db=KEGG eval=1.0e-20 bit_score=101.0 identity
succinyl-diaminopimelate desuccinylase(EC:3.5.1.18)	HMPREF0675_3703	DivIVA domain protein	328906854	Prop024_55	57164	57469	+	C	hypothetical protein (db=KEGG eval=3.0e-21 bit_score=103.0 identity
		dipeptide	328906853	Prop024_56	57469	58566	+	B	0636 succinyl-diaminopimelate desuccinylase; K01439 succinyl-diaminop
		ABC superfamily ATP binding cassette tra	328906852						
		peptide ABC transporter ATP-binding prot	328906851						
		hypothetical protein	328906850						
transcriptional regulator, TetR family	HMPREF0675_3702								
putative ATP synthase F0, A subunit	HMPREF0675_3701								
hypothetical protein	HMPREF0675_3700								
amidinotransferase(EC:2.1.4.1)	HMPREF0675_3699								
hypothetical protein	HMPREF0675_3698								
2,3,4,5-tetrahydrodipyrindine-2,6-dicarboxylate N-succinyltran	HMPREF0675_3697	2,3,4,5-tetrahydrodipyrindine-2,6-dicarboxylate N	328906849	Prop024_57	58758	58985	+	E	GENE: 491287..491514 + (rbs_motif=None rbs_spacer=None)
hypothetical protein	HMPREF0675_3696	conserved protein, putative lipoprotein	328906848	Prop024_58	58982	59944	+	B	3697 dapD; 2,3,4,5-tetrahydrodipyrindine-2,6-dicarboxylate N-succinyltrans
succinyl-diaminopimelate transaminase	HMPREF0675_3695	conserved protein, putative lipoprotein	328906847	Prop024_59	59946	60893	+	B	0629 putative lipoprotein (db=KEGG)
ferredoxin family protein	HMPREF0675_3694	succinyl-diaminopimelate transaminase	328906846	Prop024_60	60897	62006	+	B	0628 N-succinyl-diaminopimelate aminotransferase (EC:2.6.1.17) (db=KE
NAD(P) transhydrogenase subunit beta(EC:1.6.1.2)	HMPREF0675_3693	putative ferredoxin	328906845	Prop024_61	62003	62425	+	C	ferredoxin family protein (db=KEGG eval=2.0e-53 bit_score=210.0 ide
NAD(P)(+) transhydrogenase (AB-specific), alpha subunit(	HMPREF0675_3692	pyridine nucleotide transhydrogenase	328906844	Prop024_62	62472	63893	+	B	3693 NAD(P) transhydrogenase subunit beta (EC:1.6.1.2); K00325 NAD(P
NAD(P)(+) transhydrogenase (AB-specific), alpha subunit(	HMPREF0675_3692	transhydrogenase	328906844	Prop024_63	63897	64364	+	C	pntA; NAD(P)(+) transhydrogenase (AB-specific), alpha subunit (EC:1.6.
		transhydrogenase	328906844	Prop024_64	64803	65366	+	D	IPRSCAN: seg (db=Seg db_id=seg from=5 to=17)
		hypothetical protein	328906843						
		hypothetical protein	328906842						
hypothetical protein	HMPREF0675_3691								
acetyltransferase, GNAT family(EC:2.3.1.183)	HMPREF0675_3690	N-acetyltransferase	328906841	Prop024_65	65744	66241	+	C	acetyltransferase, GNAT family; K03823 phosphinothricin acetyltransfera
phosphoribosyl transferase domain protein	HMPREF0675_3689	phosphoribosyl transferase domain protein	328906840	Prop024_66	66380	66883	+	B	0623 putative purine phosphoribosyltransferase (db=KEGG)
DAK1 domain protein(EC:2.7.1.29)	HMPREF0675_3688	DAK1 domain protein	328906839	Prop024_67	66885	68582	+	B	3688 DAK1 domain protein; K00863 dihydroxyacetone kinase [EC:2.7.1.2
		DAK1 domain protein	328906838						
oxidoreductase, zinc-binding dehydrogenase family protein(	HMPREF0675_3687	zinc-binding dehydrogenase	328906837	Prop024_68	68709	69758	+	B	3687 oxidoreductase, zinc-binding dehydrogenase family protein (db=KE
proline dehydrogenase/aldehyde dehydrogenase (NA	HMPREF0675_3686</								

hypothetical protein	HMPREF0675_3179	bacterial extracellular solute-binding prot	328906826	Prop024_73	74713	75639 +	B	UniRef90_D1YBK6 Bacterial extracellular solute-binding protein, f
hypothetical protein	HMPREF0675_3666	ABC-type transport system, permease protein	328906825	Prop024_74	75666	76610 +	B	ckp-ckrop. 1364 ABC transporter permease; K02029 polar amino acid tra
putative histidine transport ATP-binding protein hisP(EC:3.1.1.1)	HMPREF0675_3665	ABC transporter, ATP-binding protein	328906824	Prop024_75	76646	77407 +	B	3665 putative histidine transport ATP-binding protein HisP (db=KEGG
S4 domain protein	HMPREF0675_3664	S4 domain protein	328906823	Prop024_76	77453	77668 +	C	hypothetical protein (db=KEGG evalua=4.0e-29 bit_score=129.0 identity
peptidase families S8 and S53	HMPREF0675_3663	peptidase families S8 and S53	328906822	Prop024_77	77743	79224 +	B	3663 peptidase families S8 and S53 (EC:3.4.21.-) (db=KEGG)
LAO/AO transport system ATPase(EC:2.7.-)	HMPREF0675_3662	LAO/AO transport system ATPase	328906821	Prop024_78	79438	80526 +	B	0597 arginine/ornithine transport system ATPase; K07588 LAO/AO transp
Methylmalonyl-CoA mutase(EC:5.4.99.2)	HMPREF0675_3661	methylmalonyl-CoA mutase	328906820	Prop024_79	80633	82822 +	B	0596 methylmalonyl-CoA mutase (EC:5.4.99.2); K01847 methylmalonyl-
methylmalonyl-CoA mutase, small subunit(EC:5.4.99.2)	HMPREF0675_3660	methylmalonyl-CoA mutase small subunit	328906819	Prop024_80	82819	84729 +	B	0595 methylmalonyl-CoA mutase small subunit (EC:5.4.99.2); K01847 m
hypothetical protein	HMPREF0675_3659	hypothetical protein						
hypothetical protein	HMPREF0675_3656	hypothetical protein						
hypothetical protein	HMPREF0675_3657	hypothetical protein						
hypothetical protein	HMPREF0675_3655	hypothetical protein						
		Lysophospholipase L2	328906817	Prop024_81	85132	86094 +	C	alpha/beta hydrolase fold (db=KEGG evalua=1.0e-60 bit_score=2
				Prop024_82	86326	86808 +	C	undecaprenyl-phosphate galactose phosphotransferase (EC:2.7.8.
				Prop024_83	86923	87225 +	C	transposase for IS2404 (db=KEGG evalua=2.0e-17 bit_score=91.8
				Prop024_84	87253	87573 +	C	transposase, IS4 (db=KEGG evalua=3.0e-18 bit_score=94.0 ident
				Prop024_85	87894	89174 +	C	capsular exopolysaccharide biosynthesis protein (db=KEGG evalua
UDP-glucose dehydrogenase(EC:1.1.1.22)	HMPREF0675_3654	nucleotide sugar dehydrogenase	328906816	Prop024_86	89241	90407 +	B	3654 UDP-glucose dehydrogenase (EC:1.1.1.22); K00012 UDPglucose 6-
alpha amylase, catalytic domain protein(EC:3.2.1.1)	HMPREF0675_3653	alpha amylase, catalytic domain protein	328906815	Prop024_87	90411	91646 +	B	3653 alpha amylase, catalytic domain protein (db=KEGG)
putative lysine-specific permease	HMPREF0675_3652	lysine-specific permease	328906814	Prop024_88	91700	93139 +	B	3652 putative lysine-specific permease; K11733 lysine-specific permease
Thiol peroxidase, Tpx-type(EC:1.11.1.15)	HMPREF0675_3651	thiol peroxidase	328906813	Prop024_89	93296	93799 +	B	0590 thiol peroxidase (EC:1.11.1.-); K11065 thiol peroxidase, atypical 2-
oxidoreductase, aldo/keto reductase family protein(EC:1.1.1.1)	HMPREF0675_3650	oxidoreductase, putative aldo/keto reductase	328906812	Prop024_90	93851	94816 +	B	0589 oxidoreductase, putative aldo/keto reductase (db=KEGG)
ACT domain protein	HMPREF0675_3649	ACT domain protein	328906811	Prop024_91	94841	95359 +	C	hypothetical protein (db=KEGG evalua=1.0e-67 bit_score=258.0 identity
hypothetical protein	HMPREF0675_3648	hypothetical protein	328906810	Prop024_92	95383	96114 +	B	3648 hypothetical protein (db=KEGG)
arginine repressor, C-terminal domain protein	HMPREF0675_4459	arginine repressor	328906807	Prop024_93	96746	97372 +	C	arginine repressor; K03402 transcriptional regulator of arginine r
hypothetical protein	HMPREF0675_3647	hypothetical protein						
carbamate kinase(EC:2.7.2.2)	HMPREF0675_3646	carbamate kinase	328906806					
ornithine carbamoyltransferase(EC:2.1.3.3)	HMPREF0675_3645	ornithine carbamoyltransferase	328906805	Prop008_1	/length=1931	%G+C=60.64	/description=[Propionibacterium]	
ornithine carbamoyltransferase(EC:2.1.3.3)	HMPREF0675_3644	ornithine carbamoyltransferase	328906804	Prop008_1	927	1931 +	B	0584 ornithine carbamoyltransferase, catabolic (EC:2.1.3.3); K00611 orn
ornithine carbamoyltransferase(EC:2.1.3.3)	HMPREF0675_3645	ornithine carbamoyltransferase	328906805	Prop018_7	/length=5206	%G+C=57.74	/description=[Propionibacterium]	
arginine deiminase(EC:3.5.3.6)	HMPREF0675_3644	arginine deiminase	328906804	Prop018_7	5113	5205 +	E	GENE: 3374..3466 + (rbs_motif=AGGAG rbs_spacer=5-10bp)
Arginine/ornithine antiporter ArcD	HMPREF0675_3643	arginine/ornithine antiporter	328906803	Prop018_6	3802	5046 +	B	3644 arcD; arginine deiminase (EC:3.5.3.6); K01478 arginine deiminase
		hypothetical protein	328906802	Prop018_5	2169	3650 +	B	0582 arginine/ornithine antiporter; K03758 arginine:ornithine antiporter
		hypothetical protein	328906801	Prop018_4	1740	1853 +	E	GENE: 1..114 - (rbs_motif=GGA/GAG/AGG rbs_spacer=5-10bp)
		hypothetical protein	328906800	Prop018_3	1524	1673 +	D	IPRSCAN: HAD-like (db=superfamily db_id=SSF56784 from=1 to=
		hypothetical protein	328906799	Prop018_2	1558	1673 +	D	ThiD/PfpI domain protein (db=KEGG evalua=1.0e-50 bit_score=2
		hypothetical protein	328906798	Prop018_1	140	781 +	C	short chain dehydrogenase (db=KEGG evalua=2.0e-42 bit_score=
		hypothetical protein	328906797	Prop016	/length=38000	%G+C=61.47	/description=[Propionibacterium]	
		ribosomal protein L28	328907999					
		hypothetical protein	328908000					
		hypothetical protein	328908001					
		transposase, mutator family protein	328908002					
		mutator family transposase	328908003					
		hypothetical protein	328908004					
		hypothetical protein	328908005					
		hypothetical protein	328908006					
		hypothetical protein	328908007					
		5-methyltetrahydropteroylitr glutamate--	328908008					
		hypothetical protein	328908009					
		hypothetical protein	328908010					
		transposase family protein	328908011					
		hypothetical protein	328908012					
		transposase	328908013					
		hypothetical protein	328908014					
		putative plasmid maintenance system ant	328907890					
		hypothetical protein	328907891					
		hypothetical protein	328907892					
		hypothetical protein	328907893	Prop016_36	36819	37127 +	C	predicted membrane protein (db=KEGG evalua=4.0e-15 bit_score
		hypothetical protein	328907894	Prop016_35	35440	36573 +	B	cdi:DIP0348 hypothetical protein (db=KEGG)
		hypothetical protein	328907895	Prop016_34	34890	35159 +	D	IPRSCAN: S-adenosyl-L-methionine-dependent methyltransferase
		hypothetical protein	328907896	Prop016_33	34660	35159 +	D	ThiD/PfpI domain protein (db=KEGG evalua=1.0e-50 bit_score=2
		hypothetical protein	328907897	Prop016_32	33971	34174 +	B	GENE: 33971..34174 - (rbs_motif=None rbs_spacer=None)
		hypothetical protein	328907898	Prop016_31	32538	33815 +	B	fre:Franae1_614 hypothetical protein; K07133 (db=KEGG)
		hypothetical protein	328907899	Prop016_30	30815	31888 +	B	3635 ychF; GTP-binding protein YchF; K06942 (db=KEGG)
		hypothetical protein	328907900	Prop016_29	29489	30760 +	B	0574 putative aminopeptidase 2; K01269 aminopeptidase (EC:3.4.11.-) (
		hypothetical protein	328907901	Prop016_28	28181	29401 +	B	3633 putative flagellar protein Flis; K09760 DNA recombination protein R
		hypothetical protein	328907902	Prop016_27	27204	28175 +	B	3632 ispH; 4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC:1.1
		hypothetical protein	328907903	Prop016_26	24245	27055 +	B	3630 phosphoesterase family protein (db=KEGG)
		hypothetical protein	328907904	Prop016_25	24006 +	27055 +	B	0560 xseA; exodeoxyribonuclease VII, large subunit (EC:3.1.11.6); K0364
		hypothetical protein	328907905	Prop016_24	22511	22762 +	C	xseB; exodeoxyribonuclease VII, small subunit (EC:3.1.11.6); K03602 id
		hypothetical protein	328907906	Prop016_23	21989	22504 +	C	hypothetical protein (db=KEGG evalua=6.0e-68 bit_score=259.0 identity
		hypothetical protein	328907907	Prop016_22	20543	21910 +	B	3626 PhoH family protein; K07175 PhoH-like ATPase (db=KEGG)
		hypothetical protein	328907908	Prop016_21	19746	20414 +	B	0565 putative hemolysin; K11068 hemolysin III (db=KEGG)
		hypothetical protein	328907909	Prop016_20	18775	19596 +	B	0564 undecaprenyl pyrophosphate synthase (EC:2.5.1.31); K12503 short
		hypothetical protein	328907910	Prop016_19	16741	18756 +	B	3623 hypothetical protein; K06888 (db=KEGG)
		hypothetical protein	328907911	Prop016_18	16474	16683 +	C	Putative uncharacterized protein n=1 Tax=Propionibacterium acn
		hypothetical protein	328907912	Prop016_17	16010	16447 +	C	hypothetical protein (db=KEGG evalua=1.0e-54 bit_score=214.0 identity
		hypothetical protein	328907913	Prop016_16	15425	15718 +	C	greA; transcription elongation factor GreA; K03624 transcription elongati
		hypothetical protein	328907914	Prop016_15	14369	15355 +	B	0560 hypothetical protein (db=KEGG)
		hypothetical protein	328907915	Prop016_14	13109	14341 +	B	0559 membrane spanning protein (db=KEGG)
		hypothetical protein	328907916	Prop016_13	12324	13007 +	B	3617 putative uracil-DNA glycosylase; K03648 uracil-DNA glycosylase [EC
		hypothetical protein	328907917	Prop016_12	10991	12184 +	B	UniRef90_D3ML42 Putative uncharacterized protein n=1 Tax=Pro
		hypothetical protein	328907918	Prop016_11	10128	11009 +	C	viral replication-associated protein (db=KEGG evalua=1.0e-18 bit
		hypothetical protein	328907919	Prop016_10	8444	9883 +	C	UniRef90_D3ML43 Putative uncharacterized protein n=1 Tax=Pro
		hypothetical protein	328907920	Prop016_9	7993	8367 +	E	GENE: 7993..8367 + (rbs_motif=AGGA rbs_spacer=5-10bp)
		hypothetical protein	328907921	Prop016_8	7566	7670 +	D	IPRSCAN: transmembrane_regions (db=TMHMM db_id=tmhmm fr
		hypothetical protein	328907922	Prop016_7	5950	7569 +	B	0557 sodium and chloride-dependent transporter; K03308 neurotransmit
		hypothetical protein	328907923	Prop016_6	5170	5802 +	B	0556 peptide methionine sulfoxide reductase; K07304 peptide-methionin
		hypothetical protein	328907924	Prop016_5	4272	5135 +	B	0555 aldo/keto reductase (db=KEGG)
		hypothetical protein	328907925	Prop016_4	3325	4215 +	C	hypothetical protein (db=KEGG evalua=1.0e-55 bit_score=218.0 identity
		hypothetical protein	328907926	Prop016_3	1274	3262 +	B	0554 OPT family oligopeptide transporter (db=KEGG)
		hypothetical protein	328907927	Prop016_2	768	1199 +	C	GtrA family membrane protein (db=KEGG evalua=5.0e-64 bit_score=246
		hypothetical protein	328907928	Prop016_1	129	590 +	C	hypothetical protein (db=KEGG evalua=2.0e-53 bit_score=211.0
		hypothetical protein	328907929	Prop016_0				
		hypothetical protein	328907930	Prop016_0				
		hypothetical protein	328907931	Prop016_0				
		hypothetical protein	328907932	Prop016_0				
		hypothetical protein	328907933	Prop016_0				
		hypothetical protein	328907934	Prop016_0				
		hypothetical protein	328907935	Prop016_0				
		hypothetical protein	328907936	Prop016_0				
		hypothetical protein	328907937	Prop016_0				
		hypothetical protein	328907938	Prop016_0				
		hypothetical protein	328907939	Prop016_0				
		hypothetical protein	328907940	Prop016_0				
		hypothetical protein	328907941	Prop016_0				
		hypothetical protein	328907942	Prop016_0				
		hypothetical protein	328907943	Prop016_0				
		hypothetical protein	328907944	Prop016_0				
		hypothetical protein	328907945	Prop016_0				
		hypothetical protein	328907946	Prop016_0				
		hypothetical protein	328907947	Prop016_0				
		hypothetical protein	328907948	Prop016_0				
		hypothetical protein	328907949	Prop016_0				
		hypothetical protein	328907950	Prop016_0				
		hypothetical protein	328907951	Prop016_0				
		hypothetical protein	328907952	Prop016_0				
		hypothetical protein	328907953	Prop016_0				
		hypothetical protein	328907954	Prop016_0				
		hypothetical protein	328907955	Prop016_0				
		hypothetical protein	328907956	Prop016_0				
		hypothetical protein	328907957	Prop016_0				
		hypothetical protein	328907958	Prop016_0				
		hypothetical protein	328907959	Prop016_0				
		hypothetical protein	328907960	Prop016_0				
		hypothetical protein	328907961	Prop016_0				
		hypothetical protein	328907962	Prop016_0				
		hypothetical protein	328907963	Prop016_0				
		hypothetical protein	328907964	Prop016_0				
		hypothetical protein	328907965	Prop016_0				
		hypothetical protein	328907966	Prop016_0				
		hypothetical protein	328907967	Prop016_0				
		hypothetical protein	328907968	Prop016_0				
		hypothetical protein	328907969	Prop016_0				
		hypothetical protein	328907970	Prop016_0				
		hypothetical protein	328907971	Prop016_0				
		hypothetical protein	328907972	Prop016_0				
		hypothetical protein	328907973	Prop016_0				
		hypothetical protein	328907974	Prop016_0				
		hypothetical protein	328907975	Prop016_0				
		hypothetical protein	328907976	Prop016_0				
		hypothetical protein	328907977	Prop016_0				
		hypothetical protein	328907978	Prop016_0				
		hypothetical protein						

hypothetical protein	HMPREF0675_3592	putative lipoprotein	32890369	Prop013_17	18373	19512 +	B	0540 hypothetical protein (db=KEGG)
		alcohol dehydrogenase	32890369					
		putative D-lactate dehydrogenase	32890368					
		D-isomer specific 2-hydroxyacid dehydrogenase	32890367					
		aminoacyl-tRNA hydrolase	32890366					
oxidoreductase, zinc-binding dehydrogenase family protein	HMPREF0675_3591							
hypothetical protein	HMPREF0675_3590							
hypothetical protein	HMPREF0675_3589							
hypothetical protein	HMPREF0675_3588							
aminoacyl-tRNA hydrolase(EC:3.1.1.29)	HMPREF0675_3587		32890365	Prop013_18	19516	20043 +	C	pth; aminoacyl-tRNA hydrolase (EC:3.1.1.29); K01056 peptidyl-tRNA hyc
ribosomal protein L25, Ctc-form	HMPREF0675_3586	ribosomal L25P family protein	32890364	Prop013_19	20178	20795 +	B	0535 ribosomal L25P family protein; K02897 large subunit ribosomal prot
hypothetical protein	HMPREF0675_3585	putative secreted protein	32890363					
hypothetical protein	HMPREF0675_3584	putative secreted protein	32890362					
hypothetical protein	HMPREF0675_3583	putative secreted protein	32890361					
Ribose-phosphate pyrophosphokinase(EC:2.7.6.1)	HMPREF0675_3582	ribose-phosphate pyrophosphokinase	32890360	Prop013_20	20980	21948 +	B	0531 ribose-phosphate pyrophosphokinase (EC:2.7.6.1); K00948 ribose-
UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-ph	HMPREF0675_3581	N-acetylglucosamine-1-phosphate uridylyltransf	32890359	Prop013_21	21945	23270 +	B	3581 glmU; UDP-N-acetylglucosamine diphosphorylase/glucosamine-1-ph
transcriptional regulator, TetR family	HMPREF0675_3579	TetR family transcriptional regulator	32890358	Prop013_22	23546	24178 +	B	3579 transcriptional regulator, TetR family (db=KEGG)
transcriptional regulator, MarR family	HMPREF0675_3578	MarR family regulator	32890357	Prop013_23	24160	24641 +	C	transcriptional regulator, MarR family (db=KEGG evalua=1.0e-73 bit_scor
4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase(	HMPREF0675_3577	4-diphosphocytidyl-2-C-methyl-D-erythritol kir	32890356	Prop013_24	24678	25466 +	B	3577 isP; 4-(cytidine 5'-diphospho)-2-C-methyl-D-erythritol kinase (EC:
dimethyladenosine transferase(EC:2.1.1.1)	HMPREF0675_3576	dimethyladenosine transferase	32890355	Prop013_25	25670	26566 +	B	3576 ksgA; dimethyladenosine transferase (EC:2.1.1.1.); K02528 16S rRN
hydrolase, TaqD family(EC:3.1.21.-)	HMPREF0675_3575	hydrolase, TaqD family	32890354	Prop013_26	26563	27471 +	B	0525 Dnaase; K03424 TaqD Dnaase family protein (EC:3.1.21.-) (db=KEGG
S-adenosylmethionine-dependent methyltransferase, YraJ	HMPREF0675_3574	S-adenosylmethionine-dependent methyltransf	32890353	Prop013_27	27468	28379 +	B	0524 putative tetraaryle (corrin/porphyrin) methylase; K07056 (db=KE
dolichyl-phosphate-mannose-protein mannosyltransferase	HMPREF0675_3573	putative dolichyl-phosphate-mannose-protein	32890352	Prop013_28	28440	29969 +	B	0523 putative dolichyl-phosphate-mannose-protein mannosyltransferase
uracil-xanthine permease	HMPREF0675_3572	uracil-xanthine permease	32890351	Prop013_29	30054	31538 +	B	3572 uracil-xanthine permease (db=KEGG)
hypothetical protein	HMPREF0675_3571	putative magnesium and cobalt transport prot	32890350	Prop013_30	31571	32659 +	B	UnikRef01_D10644 Putative magnesium and cobalt transport protein Cov
oxidoreductase, aldo/keto reductase family protein	HMPREF0675_4054	oxidoreductase, putative aldo/keto reductase	328906812	Prop013_32	33303	33863 +	C	aldo/keto reductase (db=KEGG evalua=2.0e-46 bit_score=188.0
				Prop013_33	33844	34323 +	C	aldo/keto reductase (db=KEGG evalua=2.0e-33 bit_score=144.0
glycine oxidase ThiO(EC:1.4.3.19)	HMPREF0675_3569	FAD dependent oxidoreductase	328903349					
thiamine biosynthesis protein ThiS	HMPREF0675_3568	thiamine biosynthesis protein ThiS	328903348					
thiazole biosynthesis protein ThiG	HMPREF0675_3567	thiazole biosynthesis protein ThiG	328903347					
molybdopterin biosynthesis-like protein MoeZ family	HMPREF0675_3566	MoeZ-like protein	328903346					
hypothetical protein	HMPREF0675_3565							
		anaerobic dimethyl sulfoxide reductase, A	328903345					
		anaerobic dimethyl sulfoxide reductase, A	328903344					
		anaerobic dimethyl sulfoxide reductase, A	328903343					
		anaerobic dimethyl sulfoxide reductase, A	328903342					
		dimethylsulfoxide reductase, chain B	328903341					
		anaerobic dimethyl sulfoxide reductase, chain B	328903340					
		anaerobic dimethyl sulfoxide reductase, chain B	328903339					
		hypothetical protein	328903338					
hypothetical protein	HMPREF0675_3562	molybdopterin-guanine dinucleotide bios	328903337					
hypothetical protein	HMPREF0675_3561	hypothetical protein	328903336					
molybdenum cofactor synthesis domain protein	HMPREF0675_3560	molybdopterin biosynthesis protein	328903335					
hypothetical protein	HMPREF0675_3559	hypothetical protein	328903334					
transporter, major facilitator family protein	HMPREF0675_3558	nitrate/nitrite transporter	328903333					
nitrate reductase, alpha subunit(EC:1.7.99.4)	HMPREF0675_3557	nitrate reductase, alpha subunit	328903332					
nitrate reductase, beta subunit(EC:1.7.99.4)	HMPREF0675_3556	nitrate reductase beta chain	328903331					
nitrate reductase molybdenum cofactor assembly cha	HMPREF0675_3555	nitrate reductase molybdenum cofactor a	328903330					
respiratory nitrate reductase, gamma subunit(EC:1.7.99.5)	HMPREF0675_3554	nitrate reductase gamma subunit	328903329					
NiC-like protein(EC:3.6.3.29)	HMPREF0675_3553							
molybdate ABC transporter, periplasmic molybdate-b	HMPREF0675_3552	ABC transporter, putative molybdenum transp	328903328					
Molybdate-binding domain of MoDE	HMPREF0675_3551	molybdate ABC transporter, periplasmic n	328903327					
hypothetical protein	HMPREF0675_3549	TOBE domain protein	328903326					
molybdenum cofactor biosynthesis protein A	HMPREF0675_3548	molybdenum cofactor biosynthesis protei	328903325					
This family protein	HMPREF0675_3547	This family protein	328903324					
molybdopterin converting factor, subunit 2	HMPREF0675_3546	molybdopterin synthase MoaE	328903323					
molybdenum cofactor synthesis domain protein	HMPREF0675_3546	molybdenum cofactor biosynthesis protei	328903322					
molybdenum cofactor biosynthesis protein C	HMPREF0675_3545	molybdenum cofactor biosynthesis protei	328903321					
cytoplasmic chaperone TorD	HMPREF0675_3544	cytoplasmic chaperone TorD	328903320					
(tRNA)	HMPREF0675_3543							
		hypothetical protein	328903319					
		hypothetical protein	328903318					
		hypothetical protein	328903317					
		hypothetical protein	328903316					
		hypothetical protein	328903315					
		hypothetical protein	328903314					
		hypothetical protein	328903313					
		putative polyketide synthase	328903312					
		putative polyketide synthase	328903311					
		hypothetical protein	328903310					
		hypothetical protein	328903309					
		hypothetical protein	328903308					
		hypothetical protein	328903307					
		hypothetical protein	328903307					
ABC transporter, ATP-binding protein	HMPREF0675_3127	ABC transporter, ATP-binding protein	328906454	Prop007_1	374	2113 +	B	aa1:AAR_03750 putative drug resistance ATP-binding protein (db=KEGG;
hypothetical protein	HMPREF0675_3542	hypothetical protein	328903306	Prop007_2	2714	3745 +	C	hypothetical protein (db=KEGG evalua=4.0e-16 bit_score=89.4 id
acylttransferase, GNAT family(EC:2.3.1.128)	HMPREF0675_3541	acylttransferase, GNAT family	328903305	Prop007_3	3781	4446 +	C	3542 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_3540	molybdopterin biosynthesis enzyme	328903304	Prop007_4	4660	5154 +	C	acylttransferase, GNAT family; K03790 ribosomal-protein-alanine N-acet
5-formyltetrahydrofolate cyclo-lyase(EC:6.3.3.2)	HMPREF0675_3539	5-formyltetrahydrofolate cyclo-lyase	328903303	Prop007_6	6751	7371 +	B	3539 5-formyltetrahydrofolate cyclo-lyase (EC:6.3.3.2); K01934 5-form
regulatory protein, FmdB family	HMPREF0675_3538	hypothetical protein	328903302	Prop007_7	7455	7751 +	C	hypothetical protein (db=KEGG evalua=5.0e-28 bit_score=126.0
SAF domain protein	HMPREF0675_3537	SAF domain protein	328903302	Prop007_8	7987	8511 +	C	hypothetical protein (db=KEGG evalua=6.0e-60 bit_score=232.0 identity
large conductance mechanosensitive channel protein	HMPREF0675_3536	large conductance mechanosensitive channel	328903301	Prop007_9	8625	8993 +	C	large conductance mechanosensitive channel; K03282 large conductance
hypothetical protein	HMPREF0675_3535	hypothetical protein	328903300					
UTP--glucose-1-phosphate uridylyltransferase(EC:2.7.7.9)	HMPREF0675_3534	UTP--glucose-1-phosphate uridylyltransferase	328902899	Prop007_10	9368	10762 +	B	0489 UTP--glucose-1-phosphate uridylyltransferase (EC:2.7.7.9); K0096;
hypothetical protein	HMPREF0675_3533	hypothetical protein	328902898	Prop007_11	10807	12609 +	B	UniRef90_A37GA5 Putative uncharacterized protein n=1 Tax=Jan
(tRNA)	HMPREF0675_3532	hypothetical protein	328902897	Prop007_12	12750	13397 +	C	hypothetical protein (db=KEGG evalua=2.0e-51 bit_score=205.0
MFS transporter, sugar porter (SP) family protein	HMPREF0675_3531	sugar transporter family protein	328902897	Prop007_13	13639	15255 +	B	3531 MFS transporter, sugar porter (SP) family protein (db=KEGG)
thioredoxin	HMPREF0675_3530	thiol-disulfide isomerase	328902896	Prop007_14	15431	15796 +	C	trxA_1; thioredoxin (db=KEGG evalua=1.0e-61 bit_score=238.0 identity
hypothetical protein	HMPREF0675_3529	hypothetical protein	328902895	Prop007_15	15956	17035 +	B	0486 hypothetical protein (db=KEGG)
iron dependent repressor, N-terminal DNA binding domain	HMPREF0675_3528	repressor	328902894	Prop007_16	17056	17754 +	B	0485 repressor; K03709 DtxR family transcriptional regulator, Mn-depend
putative N-acetylglucosamine-6-phosphate deacetylase(EC	HMPREF0675_3527	putative N-acetylglucosamine-6-phosphate de	328902893	Prop007_17	17905	19077 +	C	3527 putative N-acetylglucosamine-6-phosphate deacetylase; K01443 N
putative phosphoserine aminotransferase(EC:2.6.1.52)	HMPREF0675_3526	putative phosphoserine aminotransferase	328902892	Prop007_18	19132	20250 +	B	3526 putative phosphoserine aminotransferase (EC:2.6.1.52); K00831 pl
hypothetical protein	HMPREF0675_3525	hypothetical protein	328902891	Prop007_19	20247	21248 +	C	0482 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_3524	hypothetical protein	328902890	Prop007_20	21390	22100 +	C	0484 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_3523	hypothetical protein	328902889					
hypothetical protein	HMPREF0675_3522	xanthine/uracil permease family protein	328902888	Prop007_21	22075	23478 +	B	3524 putative xanthine/uracil permease; K06901 putative MFS transport
hypothetical protein	HMPREF0675_3521	hypothetical protein	328902887	Prop007_22	23602	23880 +	C	hypothetical protein (db=KEGG evalua=2.0e-38 bit_score=160.0 identity
MoeA N-terminal region (domain 1 and II)	HMPREF0675_3520	hypothetical protein	328902886	Prop007_23	23903	24703 +	B	0478 hypothetical protein (db=KEGG)
cold-shock DNA-binding domain protein	HMPREF0675_3519	cold-shock DNA-binding domain protein	328902885	Prop007_24	24703	25086 +	C	cold-shock DNA-binding domain protein; K03704 cold shock protein (beta
glucosamine-6-phosphate deaminase(EC:3.5.99.6)	HMPREF0675_3518	glucosamine-6-phosphate deaminase	328902884	Prop007_25	25228	26013 +	B	0476 nagB; glucosamine-6-phosphate deaminase (EC:3.5.99.6); K02564
hypothetical protein	HMPREF0675_3518							
hypothetical protein	HMPREF0675_3517	DeaD/DeaH box family protein	328902882	Prop007_26	26937	29066 +	B	3517 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_3516							
		hypothetical protein	328902881					
		hypothetical protein	328902880					
		hypothetical protein	328902879					
DEAD/DEAH box helicase(EC:3.6.1.-)	HMPREF0675_3514	DEAD/DEAH box helicase	328902878	Prop007_27	29129	30787 +	B	3515 DEAD/DEAH box helicase; K10843 DNA excision repair protein ERC
hypothetical protein	HMPREF0675_3513	secreted protein	328902877	Prop007_28	30876	31823 +	B	0472 hypothetical protein (db=KEGG)
CutC family protein	HMPREF0675_3513	CutC family protein	328902876	Prop007_29	31851	32337 +	B	3513 CutC family protein; K06201 copper homeostasis protein (db=KEGG
CAAX amino terminal protease family protein	HMPREF0675_3512	CAAX amino terminal protease family protein	328902875	Prop007_30	32541	33332 +	C	0470 hypothetical protein; K07052 (db=KEGG)
		oxidoreductase, NAD-binding domain prot	328902874					
		putative myo-inositol catabolism protein	328902873					
		hypothetical protein	328902872					
		hypothetical protein	328902871					
		hypothetical protein	328902870					
		putative sugar transporter YfiG	328902869					
		putative myo-inositol 2-dehydrogenase 1	328902868					
dihydrodipicolinate reductase(EC:1.1.1.18)	HMPREF0675_3511							
AP endonuclease, family 2(EC:4.2.1.44)	HMPREF0675_3510							
hypothetical protein	HMPREF0675_3509							
hypothetical protein	HMPREF0675_3508							
hypothetical protein	HMPREF0675_3507							
MFS transporter, sugar porter (SP) family protein	HMPREF0675_3506							
oxidoreductase, NAD-binding domain protein	HMPREF0675_3505							
putative Glyceralddehyde-3-phosphate ketol-isomeras	HMPREF0675_3504							
AP endonuclease, family 2	HMPREF0675_3503							
AP endonuclease, family 2	HMPREF0675_3502							
oxidoreductase, NAD-binding domain protein	HMPREF0675_3501							
periplasmic binding protein and sugar binding domain	HMPREF0675_3500							

[illegible]

oxidoreductase, short chain dehydrogenase/reductase family HMPREF0675_3392	oxidoreductase, short chain dehydrogenase/re	328908144	Prop007_110	110165	110932 +	B	0350 short chain dehydrogenase (db=KEGG)
exopolysaccharide biosynthesis polyphenyl glycosylphosphotransferase family HMPREF0675_3391	exopolysaccharide biosynthesis polyphenyl gly	328908143	Prop007_111	110964	112349 +	B	0349 putative glycosyltransferase (db=KEGG)
folate-binding protein YgfZ HMPREF0675_3390	putative glycosyl cleavage T-protein	328908142	Prop007_112	112390	113334 +	B	0390 ygfZ, folate-binding protein YgfZ; K06980 (db=KEGG)
hypothetical protein HMPREF0675_3389	hypothetical protein	328908141	Prop007_113	113336	113836 +	B	0347 hypothetical protein (db=KEGG)
D-tyrosyl-tRNA(Tyr) deacylase [EC:3.1.-]	D-tyrosyl-tRNA deacylase	328908139	Prop007_114	114030	114467 +	C	dttd; D-tyrosyl-tRNA(Tyr) deacylase [EC:3.1.-]; K07560 D-tyrosyl-tRNA(
hypothetical protein HMPREF0675_3388	hypothetical protein	328908138	Prop007_115	114477	115361 +	B	0345 hypothetical protein (db=KEGG)
transcriptional regulatory protein, C-terminal domain protein HMPREF0675_3386	transcriptional regulatory protein	328908137	Prop007_116	115472	116116 +	B	0344 transcriptional regulatory protein (db=KEGG)
polyphosphate kinase I [EC:2.7.4.1]	polyphosphate kinase	328908136	Prop007_117	116259	118364 +	B	0343 polyphosphate kinase [EC:2.7.4.1]; K00937 polyphosphate kinase I
hydrolase, NUDIX family HMPREF0675_3384	hydrolase, NUDIX family	328908135	Prop007_118	118371	119312 +	B	0342 hypothetical protein (db=KEGG)
phosphate ABC transporter, phosphate-binding protein PstS HMPREF0675_3383	phosphate ABC transporter, phosphate-binding	328908134	Prop007_119	119490	120641 +	B	0383 pstS; phosphate ABC transporter, phosphate-binding protein PstS; I
phosphate ABC transporter, permease protein PstC HMPREF0675_3382	putative phosphate transport system permeas	328908133	Prop007_120	120749	121753 +	B	0340 putative phosphate transport system permease protein PstC; K020
phosphate ABC transporter, permease protein PstA HMPREF0675_3381	putative phosphate ABC transporter, permease protein	328908132	Prop007_121	121750	122602 +	B	0339 phosphate transport system permease protein PstA; K02038 phospho
phosphate ABC transporter, ATP-binding protein [EC:3.6.3.2] HMPREF0675_3380	putative phosphate transport ATP-binding prot	328908131	Prop007_122	122701	123477 +	B	0338 phosphate transport ATP-binding protein PstB; K02036 phosphate t
siderophore-interacting FAD-binding domain protein HMPREF0675_3379	hypothetical protein	328908130					
iron chelate uptake ABC transporter, FeCT family, permease HMPREF0675_3377	iron chelate uptake ABC transporter, FeCT fam	328908129	Prop007_123	123974	124951 +	B	0336 putative permease, FeCtd transport family protein; K02015 iron co
ABC transporter, ATP-binding protein [EC:3.6.3.34] HMPREF0675_3376	ABC transporter, ATPase component	328908128	Prop007_124	124948	125706 +	B	0376 ABC transporter, ATP-binding protein; K02013 iron complex transpo
periplasmic binding protein HMPREF0675_3375	putative ABC-type transporter, periplasmic con	328908127	Prop007_125	125868	126737 +	B	0334 putative ABC-type transporter, periplasmic component; K02016 iron
		Prop007_126	126734	127504 +	C		hypothetical protein (db=KEGG eval=5.0e-63 bit_score=244.0
		Prop007_127	127450	127620 +	E		GENE: 600802.600972 - (rbs_motif=None rbs_spacer=None)
		Prop007_128	127795	128748 +	B		UniRef90_UP1000185C06C Mrr restriction system protein n=1 Ta
mycothione reductase [EC:1.8.1.7] HMPREF0675_3374	mycothione reductase	328908126	Prop007_129	128861	130261 +	B	0333 mycothione reductase [EC:1.8.1.7]; K03083 glutathione reductase
hypothetical protein HMPREF0675_3373	putative membrane protein	328908125	Prop007_130	130537	131283 +	B	0373 hypothetical protein (db=KEGG)
pyruvate:ferredoxin (flavodoxin) oxidoreductase [EC:1.2.7.-] HMPREF0675_3372	dihydroxy-acid dehydratase threonine dehydratase biosynthetic	328908124	Prop007_131	131475	133352 +	B	eca:EC4226 iIVd; dihydroxy-acid dehydratase [EC:4.2.1.9]; K016
		328908123	Prop007_132	133364	134887 +	B	ddd:Dda3937_00252 iIVa, ile; threonine dehydratase biosynthetic
oxidoreductase, short chain dehydrogenase/reductase family HMPREF0675_3371	oxidoreductase, short chain dehydrogenase	328908122	Prop007_133	134911	135705 +	B	0371 oxidoreductase, short chain dehydrogenase/reductase family prot
RNA polymerase sigma factor, sigma-70 family HMPREF0675_3370	RNA polymerase sigma factor, sigma-70 family	328908121	Prop007_134	135709	137079 +	B	0329 putative sigma subunit (db=KEGG)
cytochrome c-type biogenesis protein CcsB HMPREF0675_3369	Cytochrome c-type biogenesis protein CcsB	328908120	Prop007_135	137159	138052 +	B	0369 ccsB; cytochrome c-type biogenesis protein CcsB (db=KEGG)
ResB-like protein HMPREF0675_3368	ResB-like protein	328908119	Prop007_136	138049	139650 +	B	0368 ResB-like protein; K07399 cytochrome c biogenesis protein (db=KE
cytochrome C biogenesis protein transmembrane region HMPREF0675_3367	cytochrome C biogenesis protein transmembra	328908118	Prop007_137	139650	140411 +	B	0367 cytochrome c biogenesis protein transmembrane region; K06196
thioredoxin HMPREF0675_3366	thioredoxin	328908117	Prop007_138	140408	140935 +	B	0307 glutathyl-HRNA reductase, HemA [EC:1.2.1.7]; K02492 glutathyl-HR
phosphoglycerate mutase family protein HMPREF0675_3365	phosphoglycerate mutase family protein	328908116	Prop007_139	140974	141531 +	B	0365 phosphoglycerate mutase family protein (db=KEGG)
uroporphyrinogen-III synthase [EC:4.2.1.75,EC:2.1.1.107] HMPREF0675_3364	uroporphyrinogen-III synthase, HemD	328908115	Prop007_140	141720	143435 +	B	0364 hemD_2; uroporphyrinogen-III synthase [EC:4.2.1.75]; K13542 un
glutaredoxin-like protein HMPREF0675_3363	glutaredoxin-like protein	328908114	Prop007_141	143559	143759 +	C	glutaredoxin-like protein (db=KEGG eval=4.0e-24 bit_score=113.0 ide
hypothetical protein	hypothetical protein	328908113					
pyrroline-5-carboxylate reductase [EC:1.5.1.2] HMPREF0675_3362	pyrroline-5-carboxylate reductase	328908112	Prop007_142	144159	144950 +	B	0361 proC; pyrroline-5-carboxylate reductase [EC:1.5.1.2]; K00286 pyrri
aspartate-semialdehyde dehydrogenase [EC:1.2.1.11] HMPREF0675_3361	aspartate-semialdehyde dehydrogenase	328908111	Prop007_143	144947	145978 +	B	0360 asd; aspartate-semialdehyde dehydrogenase [EC:1.2.1.11]; K0013
CAAX amino terminal protease family protein HMPREF0675_3359	CAAX amino terminal protease family protein	328908110	Prop007_144	146023	146856 +	B	0317 putative protease; K07052 (db=KEGG)
proline dehydrogenase [EC:1.5.99.8] HMPREF0675_3358	proline dehydrogenase	328908109	Prop007_145	146859	147818 +	B	0358 proline dehydrogenase [EC:1.5.99.8]; K00318 proline dehydrogena
AP endonuclease, family 2 HMPREF0675_3357	AP endonuclease, family 2	328908108	Prop007_146	147815	148660 +	B	0357 AP endonuclease, family 2 (db=KEGG)
hypothetical protein HMPREF0675_3356	glycosyltransferase	328908107	Prop007_147	148861	149499 +	B	0314 hypothetical protein (db=KEGG)
NAD-dependent malic enzyme	NAD-dependent malic enzyme	328908106					
hypothetical protein	hypothetical protein	328908105					
NAD-dependent malic enzyme [EC:1.1.1.38]	hypothetical protein	328908104	Prop007_148	149563	151209 +	B	0313 malate dehydrogenase [EC:1.1.1.38]; K00027 malate dehyd
DNA repair protein RadA; K04845 DNA repair protein RadA/Kms (dt HMPREF0675_3354	DNA repair protein RadA	328908103	Prop007_149	151263	152663 +	B	0312 DNA repair protein RadA; K04845 DNA repair protein RadA/Kms (dt
putative DNA integrity scanning protein HMPREF0675_3353	putative DNA integrity scanning protein	328908102	Prop007_150	152713	153816 +	B	0353 putative DNA integrity scanning protein; K07067 (db=KEGG)
		Prop007_151	153775	153864 +	E		GENE: 627190.627279 - (rbs_motif=None rbs_spacer=None)
hypothetical protein HMPREF0675_3352	hypothetical protein	328908101	Prop007_152	153894	154610 +	C	hypothetical protein (db=KEGG eval=7.0e-66 bit_score=253.0 identity
ferrochelatase [EC:4.99.1.1] HMPREF0675_3351	ferrochelatase	328908100	Prop007_153	154610	156715 +	B	0308 ferrochelatase, HemH [EC:4.99.1.1]; K01772 ferrochelatase [EC:4
glutamyl-tRNA(Glu) reductase, N-terminal domain protein [EC:1.1.1.13] HMPREF0675_3350	glutamyl-tRNA reductase, N-terminal domain protein	328908099	Prop007_154	156712	158040 +	B	0307 glutamyl-tRNA reductase, HemA [EC:1.2.1.7]; K02492 glutamyl-tR
uroporphyrinogen decarboxylase [EC:4.1.1.37] HMPREF0675_3349	uroporphyrinogen decarboxylase, HemE	328908098	Prop007_155	158176	159237 +	B	0306 uroporphyrinogen decarboxylase, HemE; K01599 uroporphyrinogen
protoporphyrinogen oxidase [EC:1.3.3.4] HMPREF0675_3348	protoporphyrinogen oxidase	328908097	Prop007_156	159261	160691 +	B	0305 putative protoporphyrinogen oxidase, HemY [EC:1.3.3.4]; K00231
hydroxymethylbilane synthase [EC:2.5.1.61] HMPREF0675_3347	hydroxymethylbilane synthase	328908096	Prop007_157	160727	161740 +	B	0304 hemC; porphobilinogen deaminase [EC:2.5.1.61]; K01749 hydroxyl
uroporphyrinogen-III synthase [EC:4.2.1.75] HMPREF0675_3346	uroporphyrinogen-III synthase	328908095	Prop007_158	161737	162462 +	B	0303 uroporphyrinogen-III synthase, HemD; K01719 uroporphyrinogen-I
porphobilinogen synthase [EC:4.2.1.24] HMPREF0675_3345	porphobilinogen synthase	328908094	Prop007_159	162493	163539 +	B	0345 hemB; porphobilinogen synthase [EC:4.2.1.24]; K01698 porphobil
glutamate-1-semialdehyde-2,1-aminomutase [EC:5.4.3.8] HMPREF0675_3344	glutamate-1-semialdehyde-2,1-aminomutase	328908093	Prop007_160	163587	164894 +	B	0344 hemI; glutamate-1-semialdehyde-2,1-aminomutase [EC:5.4.3.8]; I
putative A/G-specific adenine glycosylase [EC:3.2.2.-] HMPREF0675_3343	A/G-specific adenine glycosylase	328908092	Prop007_161	164908	165783 +	B	0343 putative A/G-specific adenine glycosylase; K03575 A/G-specific ade
	hypothetical protein	328908091					
	transcriptional regulator, DeoR family	328908090					
	hypothetical protein	328908089					
	4-hydroxythreonine-4-phosphate dehydr	328908088					
	putative sugar transporter	328908087					
	hypothetical protein	328908086					
hypothetical protein	para-aminobenzoate synthase	328908085					
putative N-acetylglucosamine-6-phosphate 2-epimerase HMPREF0675_3342	putative N-acetylglucosamine-6-phosphate 2	328908084	Prop007_162	165780	166316 +	C	hypothetical protein (db=KEGG eval=7.0e-45 bit_score=182.0
hypothetical protein HMPREF0675_3341	putative N-acetylmannosamine-6-phosphate 2	328908083	Prop007_163	166465	167181 +	C	nanE; putative N-acetylmannosamine-6-phosphate 2-epimerase [EC:2.7.1.69]
hypothetical protein [EC:5.1.3.9] HMPREF0675_3340	PTS system, glucose-like IIB component	328908082	Prop007_164	167183	168721 +	B	0340 PTS system, glucose-like IIB component [EC:2.7.1.69] K0013
PTS system, glucose-like IIB component HMPREF0675_3339	PTS system, glucose/sucrose specific IIA subu	328908081	Prop007_165	168733	169206 +	C	PTS system, glucose/sucrose specific IIA subunit; K02777 PTS system, gl
putative PTS system, glucose-specific IIA component [EC:2 HMPREF0675_3338	PRD domain protein	328908080	Prop007_166	169211	170104 +	B	0292 hypothetical protein; K03488 beta-glucoside operon transcriptional
PRD domain protein HMPREF0675_3337	hypothetical protein	328908079					
histidine kinase HMPREF0675_3336	putative two-component sensor kinase	328908078					
transcriptional regulator, LuxR family HMPREF0675_3335	putative two component response regulat	328908077					
hypothetical protein HMPREF0675_3334	para-aminobenzoate synthase	328908076	Prop007_167	170147	171049 +	B	0287 membrane spanning protein (db=KEGG)
peptidase, S54 (rhomoid) family protein HMPREF0675_3333	area amidolyase related protein	328908075	Prop007_168	171046	171945 +	B	0332 conserved hypothetical protein TIGR01777; K07071 (db=KEGG)
conserved hypothetical protein TIGR01777 HMPREF0675_3332	putative sugar transporter	328908074	Prop007_169	172013	173500 +	B	0285 putative sugar transporter (db=KEGG)
drug resistance MFS transporter, drug:H+ antiporter-2 (14) HMPREF0675_3331	putative sugar transporter	328908073					
allophanate hydrolase subunit 2 HMPREF0675_3330	allophanate hydrolase subunit 2	328908072	Prop007_170	173572	174444 +	B	0284 allophanate hydrolase subunit 2 (db=KEGG)
conserved hypothetical protein TIGR00370 HMPREF0675_3329	conserved hypothetical protein	328908071	Prop007_171	174451	175061 +	B	0283 allophanate hydrolase subunit 1 (db=KEGG)
Lactam utilization protein LAMB HMPREF0675_3328	Lamb/Ycsf family protein	328908070	Prop007_172	175058	175828 +	B	0282 Lamb/Ycsf family protein; K07160 (db=KEGG)
hypothetical protein HMPREF0675_3327	Permease	328908069	Prop007_173	176380	176721 +	C	membrane spanning protein (db=KEGG eval=2.0e-58 bit_score=227.0
hypothetical protein HMPREF0675_3326	putative membrane protein	328908068	Prop007_174	176718	177704 +	B	0326 hypothetical protein (db=KEGG)
hypothetical protein HMPREF0675_3325	hypothetical protein	328908067	Prop007_175	177875	178729 +	B	0325 hypothetical protein (db=KEGG)
negative regulator of genetic competence CtpC/MecB HMPREF0675_3324	negative regulator of genetic competence CtpC	328908066	Prop007_176	178794	181325 +	B	0324 ctpC; negative regulator of genetic competence CtpC/MecB; K03696
hypothetical protein HMPREF0675_3323	LSR2-like protein	328908065	Prop007_177	181586	181903 +	C	hypothetical protein (db=KEGG eval=6.0e-27 bit_score=122.0 identity
respiratory-chain NADH dehydrogenase, 49 Kd subunit [EC: HMPREF0675_3322	respiratory-chain NADH dehydrogenase, 49 Kd	328908064	Prop007_178	182106	183221 +	B	0322 respiratory-chain NADH dehydrogenase, 49 Kd subunit; K00333 NA
putative cell division topological specificity factor MinE HMPREF0675_3321	putative cell division topological specificity fact	328908063	Prop007_179	183315	183992 +	C	0275 hypothetical protein (db=KEGG)
hypothetical protein HMPREF0675_3320	hypothetical protein	328908062	Prop007_180	184077	184616 +	C	hypothetical protein (db=KEGG eval=2.0e-75 bit_score=284.0 identity
2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosph HMPREF0675_3319	putative hydroxymethylidihydropteridine diphosp	328908061	Prop007_181	184613	185171 +	C	0307 2-amino-4-hydroxy-6-hydroxymethylidihydropteridine diphosphok
dihydroneopterin aldolase [EC:4.1.2.25] HMPREF0675_3318	dihydroneopterin aldolase	328908060	Prop007_182	185167	185529 +	C	folB; dihydroneopterin aldolase; K01633 dihydroneopterin aldolase [EC:4
hydroxyterate synthase [EC:2.5.1.15] HMPREF0675_3317	dihydroterate synthase	328908059	Prop007_183	185594	186442 +	B	0271 dihydroneopterin aldolase; K00796 dihydroterate synthase [EC:2
hypothetical protein HMPREF0675_3316	hypothetical protein	328908058					
hypothetical protein HMPREF0675_3315	hypothetical protein	328908057					
hypothetical protein HMPREF0675_3314	hypothetical protein	328908056					
hypothetical protein HMPREF0675_3313	hypothetical protein	328908055	Prop007_184	186931	187479 +	C	hypothetical protein (db=KEGG eval=4.0e-33 bit_score=144.0 identity
hypothetical protein HMPREF0675_3309	hypothetical protein	328908054	Prop007_185	187490	188095 +	D	IPRSCAN: Peptidase_A24 (db=HMPfam db_id=PF01478 from=7
hypothetical protein HMPREF0675_3312	hypothetical protein	328908053	Prop007_186	188132	188761 +	C	hypothetical protein (db=KEGG eval=1.0e-21 bit_score=106.0 identity
putative outer membrane protein A	putative outer membrane protein A	328908052					
OmpA family protein HMPREF0675_3311	hypothetical protein	328908051	Prop007_187	188764	189858 +	B	0263 putative outer membrane protein A (db=KEGG)
	hypothetical protein	328908050					
	LuxR response regulator receiver	328908049					
	internal membrane sensor signal transdu	328908048					
	Type II secretion system F domain protein	328908047					
	Type II secretion system protein E	328908046					
	Type II secretion system protein E	328908045					
	septom site-determining protein	328908044					
	hypothetical protein	328908043					
	response regulator receiver protein	328908042					
	Flp pilus assembly protein CpaB	328908041					
	hypothetical protein	328908040					
	hypothetical protein	328908039					
GTP cyclohydrolase I [EC:3.5.4.16] HMPREF0675_3308	GTP cyclohydrolase I	3289					

hypothetical protein	HMPREF0675_3298	hypothetical protein	328908027						
		beta-lactamase related protein	328908026						
		putative ABC transporter ATP-binding protein	328908025						
		ABC-type dipeptide/oligopeptide/nickel t	328908024						
		ABC-type dipeptide/oligopeptide/nickel t	328908023						
		putative peptide transport system secret	328908022						
		membrane protein	328908021						
		membrane dipeptidase	328908020						
		amino transferase	328908019						
FAD dependent oxidoreductase(EC:1.4.3.4)	HMPREF0675_3297	putative flavin-containing amine oxidase	328908018	Prop007_202	202619	203965 +	B	0250 putative flavin-containing amine oxidase (EC:1.4.3.-); K00280 [EC:	
		membrane protein	328908017						
		hypothetical protein	328908016	Prop007_203	204471	204887 +	C	YdhG; YdhG; K05937 hypothetical protein (db=KEGG eval=1.0e	
				Prop015_39	40278	41843 +	B	ahc:Arch_1578 resolvase domain protein (db=KEGG)	
recombinase	HMPREF0675_3129		328906796	Prop015_38	39022	40281 +	B	3130 recombinase (db=KEGG)	
recombinase	HMPREF0675_3130		328906795	Prop015_37	37345	38166 +	B	ncu:HMPREF0573_11206 N-acetylmuramoyl-L-alanine amidase (	
N-acetylmuramoyl-L-alanine amidase	HMPREF0675_3133		328906794	Prop015_36	36872	37348 +	C	holin protein (db=KEGG eval=7.0e-38 bit_score=159.0 identity	
			328906793	Prop015_35	36344	36820 +	E	GENE: 36530..37006 - (rbs_motif=GGAG/GAGG rbs_spacer=5-10)	
		hypothetical protein	328906798						
		decarboxylase family protein	328906797						
		hypothetical protein	328906796						
		chaperone dnaJ 3	328906795						
		putative ATP/GTP-binding protein	328906794						
		hypothetical protein	328906793						
		hypothetical protein	328906792						
		Peptidoglycan-binding LysM	328906791						
		hypothetical protein	328906790						
		putative membrane protein, TadE related	328906789						
		hypothetical protein	328906788						
		hypothetical protein	328906787						
		type II secretion system F domain protein	328906786						
		type II secretion system F domain protein	328906785						
		hypothetical protein	328906784						
		hypothetical protein	328906783						
		SAF domain protein	328906782						
		ribbon-helix-helix protein, CopG family	328906781						
		hypothetical protein	328906780						
(tRNA)	HMPREF0675_3296			Prop015_34	34526	36208 +	B	0249 hypothetical protein (db=KEGG)	
hypothetical protein	HMPREF0675_3295	hypothetical protein	328906778	Prop015_33	34131	34463 +	C	hypothetical protein (db=KEGG eval=1.0e-39 bit_score=164.0 identity	
hypothetical protein	HMPREF0675_3294	hypothetical protein	328906777	Prop015_32	32299	33996 +	B	3293 hydrolase, alpha/beta domain protein (db=KEGG)	
hydrolase, alpha/beta domain protein	HMPREF0675_3293	hydrolase, alpha/beta domain protein	328906776	Prop015_31	31610	32302 +	C	hypothetical protein (db=KEGG eval=4.0e-83 bit_score=310.0 identity	
hypothetical protein	HMPREF0675_3292	DoxX protein	328906775	Prop015_30	30666	31472 +	B	0245 hypothetical protein (db=KEGG)	
DoxX protein	HMPREF0675_3291	DNA polymerase III subunit delta' (EC:2.7.7.7)	328906774	Prop015_29	29305	30561 +	B	3290 holB; DNA polymerase III, delta' subunit (EC:2.7.7.7); K02341 DNM	
DNA polymerase III, delta' subunit(EC:2.7.7.7)	HMPREF0675_3290	dTMP kinase	328906772	Prop015_28	28624	29271 +	C	putative thymidylate kinase (EC:2.7.4.9); K00943 dTMP kinase (EC:2.7.4	
dTMP kinase(EC:2.7.4.9)	HMPREF0675_3289	hypothetical protein	328906771	Prop015_27	27144	28631 +	B	0242 hypothetical protein (db=KEGG)	
hypothetical protein	HMPREF0675_3288	DNA topoisomerase	328906770	Prop015_26	24356	27142 +	B	0241 DNA topoisomerase I (EC:5.99.1.2); K03168 DNA topoisomerase I	
DNA topoisomerase(EC:5.99.1.2)	HMPREF0675_3287	hypothetical protein	328906769						
		hemerythrin HHE cation binding domain-conta	328906768	Prop015_25	23827	24117 +	C	hypothetical protein (db=KEGG eval=1.0e-43 bit_score=178.0 identity	
hypothetical protein	HMPREF0675_3286	methyltransferase small domain protein	328906767	Prop015_24	22506	23726 +	B	0238 putative transferase (db=KEGG)	
methyltransferase, HemK family	HMPREF0675_3285	putative DEAH-box helicase	328906766	Prop015_23	19912	22179 +	B	0237 putative helicase; K06877 (db=KEGG)	
putative DEAH-box helicase		ATPase-like protein	328906765						
		hypothetical protein	328906764						
		TadE-like protein	328906763						
hypothetical protein	HMPREF0675_3283	hypothetical protein	328906762	Prop015_22	19174	19689 +	D	IPRSCAN: seg (db=Seg db_id=seg from=65 to=76)	
TadE-like protein	HMPREF0675_3282	hypothetical protein	328906761	Prop015_21	18893	19210 +	C	hypothetical protein (db=KEGG eval=6.0e-45 bit_score=182.0 identity	
hypothetical protein	HMPREF0675_3281	hypothetical protein	328906760						
		type II secretion system F domain protein	328906759	Prop015_20	18654	18803 +	C	type II secretion system F domain protein (db=KEGG eval=2.0e-76 bit	
hypothetical protein	HMPREF0675_3280	type II secretion system F domain protein	328906758	Prop015_19	17569	18318 +	D	IPRSCAN: seg (db=Seg db_id=seg from=7 to=24)	
type II secretion system F domain protein	HMPREF0675_3279	type II secretion system F domain protein	328906757	Prop015_18	16802	17572 +	B	3278 hypothetical protein (db=KEGG)	
hypothetical protein	HMPREF0675_3278	putative secretory protein	328906756	Prop015_17	15639	16805 +	B	0230 putative secretory protein; K02283 pilus assembly protein CpaF (db	
helicase/secretion neighborhood ATPase	HMPREF0675_3277	CpaE-like protein	328906755						
		CpaE-like protein	328906754	Prop015_16	14584	15642 +	B	0229 hypothetical protein (db=KEGG)	
CpaE-like protein	HMPREF0675_3275	hypothetical protein	328906753						
		putative methyltransferase	328906752	Prop015_15	13698	14456 +	B	0228 putative methyltransferase (EC:2.1.1.-); K00599 [EC:2.1.1.-] (db=	
methyltransferase domain protein	HMPREF0675_3276	Na+/H+ antiporter NhaA	328906751	Prop015_14	12262	13497 +	B	3274 nhaA; Na+/H+ antiporter NhaA; K03313 Na+/H+ antiporter, NhaA	
Na+/H+ antiporter NhaA	HMPREF0675_3274	hypothetical protein	328906750	Prop015_13	11699	12307 +	D	IPRSCAN: seg (db=Seg db_id=seg from=6 to=19)	
hypothetical protein	HMPREF0675_3273	putative NTP pyrophosphohydrolase	328906749	Prop015_12	10885	11541 +	B	3272 hydrolase, NUDIX family (db=KEGG)	
hydrolase, NUDIX family	HMPREF0675_3272	antioxidant, AhpC/TSA family	328906748	Prop015_11	10301	10888 +	B	0224 hypothetical protein (db=KEGG)	
hypothetical protein	HMPREF0675_3271	hypothetical protein	328906747						
		putative endonuclease III	328906746	Prop015_10	9591	10304 +	B	0223 putative endonuclease III (EC:4.2.99.18); K10773 endonuclease III	
endonuclease III(EC:4.2.99.18)	HMPREF0675_3270	cyclic nucleotide-binding domain protein	328906745	Prop015_9	8752	9483 +	B	3269 transcriptional regulator, Crp/Fnr family (db=KEGG)	
transcriptional regulator, Crp/Fnr family	HMPREF0675_3269	endoribonuclease L-PSP	328906744	Prop015_8	8195	8650 +	C	endoribonuclease L-PSP (db=KEGG eval=4.0e-49 bit_score=196.0 ideo	
endoribonuclease L-PSP	HMPREF0675_3268	hypothetical protein	328906743	Prop015_7	8025	8198 +	C	hypothetical protein (db=KEGG eval=4.0e-25 bit_score=116.0 identity	
hypothetical protein	HMPREF0675_3267	putative regulatory protein	328906742	Prop015_6	7758	8324 +	B	0207 transcriptional regulator (db=KEGG)	
hypothetical protein	HMPREF0675_3266	oxidoreductase, NAD-binding domain protein	328906741	Prop015_5	6594	7616 +	B	3265 oxidoreductase, NAD-binding domain protein (db=KEGG)	
oxidoreductase, NAD-binding domain protein	HMPREF0675_3265	oxidoreductase, NAD-binding domain prot	328906740						
		two-component system response regulat	328906739						
		anticodon-binding domain protein	328906738						
hypothetical protein	HMPREF0675_3264			Prop010_12	13922	14884 +	B	3232 phosphotransferase enzyme family protein (db=KEGG)	
serine transporter	HMPREF0675_3263								
hypothetical protein	HMPREF0675_3262								
isoleucine-tRNA ligase(EC:6.1.1.5)	HMPREF0675_3261	isoleucine-tRNA ligase	328906737	Prop015_4	3248	6514 +	B	0216 lleS; isoleucyl-tRNA synthetase (EC:6.1.1.5); K01870 isoleucyl-tRN	
isoleucine-tRNA ligase(EC:6.1.1.5)	HMPREF0675_3260	putative membrane protein	328906736	Prop015_3	2607 +		E	GENE: 2128..2607 - (rbs_motif=None rbs_spacer=None)	
hypothetical protein	HMPREF0675_3259	ABC transporter, ATP-binding protein	328906735	Prop015_2	960	2165 +	B	0214 hypothetical protein (db=KEGG)	
ABC transporter, ATP-binding protein	HMPREF0675_3258	ABC transporter, ATP-binding protein	328906734	Prop015_1	229	963 +	B	0213 putative ABC transporter (db=KEGG)	
hypothetical protein	HMPREF0675_3257			Prop010_10	15166	15657 +	D	hypothetical, IPRSCAN: seg (db=Seg db_id=seg from=22 to=26)	
hypothetical protein	HMPREF0675_3256	putative hydrolase	328906735	Prop010_11	1518 +		B	0212 putative hydrolase; K07024 (db=KEGG)	
Cof-like hydrolase	HMPREF0675_3255	HAD hydrolase, family IIB	328906734	Prop010_2	1528	2214 +	B	3255 HAD hydrolase, family IIB; K07024 (db=KEGG)	
HAD hydrolase, family IIB	HMPREF0675_3254	putative membrane protein	328906733	Prop010_3	2449	4269 +	B	3254 hypothetical protein (db=KEGG)	
hypothetical protein	HMPREF0675_3253	efflux ABC transporter, permease protein	328906732	Prop010_4	4292	6970 +	B	3253 efflux ABC transporter, permease protein (db=KEGG)	
efflux ABC transporter, permease protein	HMPREF0675_3252	ABC transporter, ATP-binding protein	328906731	Prop010_5	6970	7752 +	B	3252 ABC transporter, ATP-binding protein; K02003 (db=KEGG)	
ABC transporter, ATP-binding protein	HMPREF0675_3251	transcriptional regulator	328906730	Prop010_6	7758	8324 +	B	0207 transcriptional regulator (db=KEGG)	
transcriptional regulator, PadR family	HMPREF0675_3250	putative recombination protein RecR	328906729	Prop010_7	8431	9036 +	B	0206 putative recombination protein RecR; K06187 recombination protein	
recombination protein RecR	HMPREF0675_3249	DNA-binding protein, YbaB/EbfC family	328906728	Prop010_8	9067	9390 +	C	DNA-binding protein, YbaB/EbfC family; K09747 hypothetical protein (db	
DNA-binding protein, YbaB/EbfC family	HMPREF0675_3248	DNA polymerase III, subunit gamma and tau(EC:2.7.7.7)	328906727	Prop010_9	9506	12373 +	C	3248 dnaX; DNA polymerase III, subunit gamma and tau (EC:2.7.7.7); K	
DNA polymerase III, subunit gamma and tau(EC:2.7.7.7)	HMPREF0675_3247	hypothetical protein	328906726	Prop010_10	12468	12824 +	C	hypothetical protein (db=KEGG eval=1.0e-57 bit_score=224.0 identity	
hypothetical protein	HMPREF0675_3246								
(ncRNA)	HMPREF0675_3245	putative heat shock protein	328906725	Prop010_11	13184	13549 +	C	S4 domain protein; K04762 ribosome-associated heat shock protein Hsp1	
S4 domain protein	HMPREF0675_3244								
(tRNA)	HMPREF0675_3243	putative lipoprotein	328906724						
hypothetical protein	HMPREF0675_3242	RHS repeat-associated core domain protein	328906723						
YD repeat protein	HMPREF0675_3241	RHS repeat-associated core domain protein	328906722						
RHS repeat-associated core domain protein	HMPREF0675_3240	hypothetical protein	328906721						
hypothetical protein	HMPREF0675_3239	hypothetical protein	328906720						
hypothetical protein	HMPREF0675_3238	hypothetical protein	328906719						
hypothetical protein	HMPREF0675_3237	hypothetical protein	328906718						
YD repeat protein	HMPREF0675_3236	hypothetical protein	328906717						
YD repeat protein	HMPREF0675_3235	DNA segregation ATPase FtsK /SpoIIIE	328906716						
YD repeat protein	HMPREF0675_3234	YD repeat protein	328906715						
hypothetical protein	HMPREF0675_3233	hypothetical protein	328906714						
phosphotransferase enzyme family protein	HMPREF0675_3232	phosphotransferase enzyme family protein	328906713						
		hypothetical protein	328906712						
		hypothetical protein	328906711						
		phosphotransferase enzyme family protein	328906710	Prop010_12	13922	14884 +	B	3232 phosphotransferase enzyme family protein (db=KEGG)	
		hypothetical protein	328906709						
		hypothetical protein	328906708						
				Prop010_13	15166	15657 +	D	hypothetical, IPRSCAN: seg (db=Seg db_id=seg from=22 to=26)	
				Prop010_14	16898	17491 +	C	maltoiligosyl trehalose synthase (EC:5.4.99.15); K06044 (1->4)-	
				Prop010_15	17491	19242 +	D	bfa:Bfae_13810 maltoiligosyl trehalose hydrolase (EC:3.2.1.141)	
				Prop010_16	19452	20198 +	D	IPRSCAN: TAT_signal_seg: Tat (twin-arginine tra (db=HMMTrig d	
				Prop010_17	20680	22170 +	D	bfa:Bfae_02670 exopolysaccharide biosynthesis polyprenyl glyco	
				Prop010_18	22170	22667 +	D	hypothetical, IPRSCAN: seg (db=Seg db_id=seg from=67 to=82)	
				Prop010_19	23089	23466 +	C	CMP-N-acetylneuraminic acid synthetase; K00983 N-acetylneurami	
				Prop010_20	23508	25772 +	C	rdn:HMPREF0733_11425 N-acetylneuraminic acid synthetase	
				Prop010_21	25772	26815 +	C	glycosyltransferase (db=KEGG eval=3.0e-58 bit_score=229.0 i	
				Prop010_22	26812	28980 +	C	flaG; group A glycosyl transferase (EC:2.4.1.-) (db=KEGG eval=	
				Prop010_23	29250	30128 +	C	ExoV domain-containing protein (db=KEGG eval=3.0e-18 bit_s	
1,4-alpha-glucan branching enzyme(EC:2.4.1.18)	HMPREF0675_4173	1,4-alpha-glucan branching enzyme	328907384						
exopolysaccharide biosynthesis polyprenyl glycosylphosphol	HMPREF0675_3391	exopolysaccharide biosynthesis polyprenyl gly	328908143						
ABC transporter, ATP-binding protein	HMPREF0675_5002	glycosyltransferase, group 1 family protein	328905940						
ABC transporter, ATP-binding protein	HMPREF0675_5002								

[illegible]

pyridine nucleotide-disulfide oxidoreductase	HMPPREF0675_3152	reductase, ferredoxin	328905932	Prop010_93	111974	113134 +	B	0139 reductase, ferredoxin (db=KEGG)
amino acid/peptide transporter (Peptide:H+ symporter)	HMPPREF0675_3151	dipeptide/tripeptide permease	328905931	Prop010_94	113449	115050 +	B	3151 amino acid/peptide transporter (peptide:H+ symporter); K03305 pr
hypothetical protein	HMPPREF0675_3150	putative membrane protein	328905930	Prop010_95	115288	116655 +	B	3150 hypothetical protein (db=KEGG)
oxidoreductase, NAD-binding domain protein	HMPPREF0675_3149	NAD-dependent dehydrogenase	328905929	Prop010_96	116763	117755 +	B	0136 NAD-dependent dehydrogenase (EC:1.1.1.18) (db=KEGG)
DegT/Dnr/ErpC1/StrS aminotransferase family protein	HMPPREF0675_3148	aspartate aminotransferase	328905928	Prop010_97	117755	118867 +	B	0135 aspartate aminotransferase (db=KEGG)
bacterial transferase hexapeptide repeat protein	HMPPREF0675_3147	bacterial transferase hexapeptide repeat prote	328905927	Prop010_98	118959	119576 +	B	3147 bacterial transferase hexapeptide repeat protein (db=KEGG)
hypothetical protein	HMPPREF0675_3146	hypothetical protein	328905926					
O-antigen polymerase	HMPPREF0675_3145	O-antigen polymerase	328905925					
hypothetical protein	HMPPREF0675_3144	glycosyltransferase, group 1 family protein	328905924					
glycosyltransferase, group 1 family protein	HMPPREF0675_3143	O-antigen polymerase	328905933	Prop010_99	119703	121040 +	D	IPRSCAN: seg (db=Seg db_id=seg from=45 to=66)
glycosyltransferase, group 1 family protein	HMPPREF0675_3143	putative glycosyl transferase	328905923	Prop010_100	121037	122410 +	C	glycosyl transferase, group 1 (db=KEGG evalue=3.0e-49 bit_score=199.1
hypothetical protein	HMPPREF0675_3142	putative membrane protein	328905922	Prop010_101	122492	123745 +	C	putative tyrosine-protein kinase (db=KEGG evalue=7.0e-15 bit_si
hypothetical protein	HMPPREF0675_3141	putative membrane protein	328905921	Prop010_102	123881	125269 +	C	hypothetical protein (db=KEGG evalue=2.0e-28 bit_score=130.0 identity
hypothetical protein	HMPPREF0675_3140	putative membrane protein	328905920	Prop010_103	125227	126414 +	B	3141 hypothetical protein (db=KEGG)
transglycosylase	HMPPREF0675_3139	transglycosylase	328905919	Prop010_104	126411	127952 +	B	0127 membrane spanning protein (db=KEGG)
hypothetical protein	HMPPREF0675_3138	transglycosylase	328905918		127962	130286 +	B	3139 transglycosylase (db=KEGG)
hypothetical protein	HMPPREF0675_3137	hypothetical protein	328905917	Prop010_106	130279	130698 +	C	hypothetical protein (db=KEGG evalue=1.0e-68 bit_score=261.0 identity
hypothetical protein	HMPPREF0675_3136	hypothetical protein	328905915					
peptidase, M16 (pitriylisin) family	HMPPREF0675_3135	peptidase M16 inactive domain protein	328905914	Prop010_107	130902	132176 +	B	3136 peptidase, M16 (pitriylisin) family (EC:3.4.24.-) (db=KEGG)
peptidase, M16 (pitriylisin) family	HMPPREF0675_3135	M16 family peptidase	328905913	Prop010_108	132176	133534 +	B	0122 M16 family peptidase (db=KEGG)
(tRNA)	HMPPREF0675_3134							
N-acetylmutamoyl-L-alanine amidase	HMPPREF0675_3133							
hypothetical protein	HMPPREF0675_3132							
hypothetical protein	HMPPREF0675_3131							
recombinase	HMPPREF0675_3130							
hypothetical protein	HMPPREF0675_3129							
hypothetical protein	HMPPREF0675_3128							
ABC transporter, ATP-binding protein	HMPPREF0675_3127							
hypothetical protein	HMPPREF0675_3126							
hypothetical protein	HMPPREF0675_3125							
		hypothetical protein	328905912	Prop010_109	133944	134429 +	E	GENE: 134331..134816 + (rbs_motif=None rbs_spacer=None)
DNA-binding response regulator KdpE	HMPPREF0675_3124	two-component response regulator, KdpE	328905911	Prop010_110	134546	135235 +	B	0119 two-component response regulator, KdpE; K07667 two-component
Osmosensitive K+ channel histidine kinase KdpD (EC:2.7.1.1)	HMPPREF0675_3123	Osmosensitive K+ channel histidine kinase KdpD	328905910	Prop010_111	135232	135984 +	B	0118 two-component sensor, KdpD; K07646 two-component system, Om
Osmosensitive K+ channel histidine kinase KdpD (EC:2.7.1.1)	HMPPREF0675_3123	Osmosensitive K+ channel histidine kinase KdpD	328905910	Prop010_112	136390	137796 +	D	IPRSCAN: seg (db=Seg db_id=seg from=4 to=18)
K+-transporting ATPase, C subunit(EC:3.6.3.12)	HMPPREF0675_3122	potassium-transporting ATPase C chain	328905909	Prop010_113	137806	139411 +	C	kdpC; K+-transporting ATPase, C subunit (EC:3.6.3.12); K01548 K+-tran
K+-transporting ATPase, B subunit(EC:3.6.3.12)	HMPPREF0675_3121	K+-transporting ATPase, B subunit	328905908	Prop010_114	138424	140538 +	B	3121 kdpC; K+-transporting ATPase, B subunit (EC:3.6.3.12); K01547 K-
K+-transporting ATPase, A subunit(EC:3.6.3.12)	HMPPREF0675_3120	K+-transporting ATPase, A subunit	328905907	Prop010_115	140541	142214 +	B	3120 kdpC; K+-transporting ATPase, A subunit (EC:3.6.3.12); K01546 K-
putative K+-transporting ATPase, F subunit	HMPPREF0675_3119	putative K+-transporting ATPase, F subunit	328905906					
hypothetical protein	HMPPREF0675_3118	hypothetical protein	328905905					
hypothetical protein	HMPPREF0675_3117	hypothetical protein	328905904					
putative thiamine-phosphate pyrophosphorylase(EC:2.5.1.1)	HMPPREF0675_3116	thiamine-phosphate pyrophosphorylase	328905903	Prop010_116	142585	143238 +	C	putative thiamine-phosphate pyrophosphorylase; K00788 thiamine-phos
hypothetical protein	HMPPREF0675_3115							
hypothetical protein	HMPPREF0675_3114							
hydroxyethylthiazole kinase (EC:2.7.1.50)	HMPPREF0675_3113	hydroxyethylthiazole kinase, sugar kinase	328905902	Prop010_117	143235	144005 +	C	hydroxyethylthiazole kinase, sugar kinase family: K00878 hydrox
putative ATP synthase F0 A subunit	HMPPREF0675_3112	Major Facilitator Superfamily transporter	328905901	Prop010_118	144002	145357 +	B	hfaA; hfaA_27350 major facilitator superfamily transporter (db=KEGG)
phosphomethylpyrimidine kinase(EC:2.7.4.7)	HMPPREF0675_3113	phosphomethylpyrimidine kinase	328905900	Prop010_119	145415	146131 +	C	thdD; phosphomethylpyrimidine kinase (EC:2.7.4.7); K00941 hydroymet
phosphomethylpyrimidine kinase(EC:2.7.4.7)	HMPPREF0675_3113	phosphomethylpyrimidine kinase	328905900	Prop010_120	146420	146950 +	D	IPRSCAN: seg (db=Seg db_id=seg from=2 to=17)
hypothetical protein	HMPPREF0675_3112	myosin-crossreactive antigen	328905899					
hypothetical protein	HMPPREF0675_3111	hypothetical protein	328905898	Prop010_121	147729	149039 +	B	3112 hypothetical protein; K10254 myosin-crossreactive antigen (db=KE
hypothetical protein	HMPPREF0675_3110	hypothetical protein	328905897					
periplasmic binding protein	HMPPREF0675_3109	periplasmic binding protein	328905896	Prop010_122	149101	149880 +	B	3111 hypothetical protein (db=KEGG)
hypothetical protein	HMPPREF0675_3109	periplasmic binding protein	328905895					
iron chelate uptake ABC transporter, FeCT family, per	HMPPREF0675_3108	periplasmic binding protein	328905894	Prop010_123	150394	151518 +	B	0106 periplasmic-binding protein of ABC transporter; K02016 iron comple
ABC transporter, ATP-binding protein(EC:3.6.3.34)	HMPPREF0675_3107	iron chelate uptake ABC transporter, FeCT fam	328905892					
putative bacteriochlorophyll 4-vinyl reductase	HMPPREF0675_3106	hypothetical protein	328905891					
CobN component of cobalt chelatase involved in B12 biosyn	HMPPREF0675_3105	hypothetical protein	328905890					
cobaltochelatase subunit(EC:6.6.1.1)	HMPPREF0675_3104	hypothetical protein	328905889					
cobaltochelatase subunit(EC:6.6.1.1)	HMPPREF0675_3104	hypothetical protein	328905888					
cobaltochelatase subunit(EC:6.6.1.1)	HMPPREF0675_3104	hypothetical protein	328905887					
magnesium chelatase, subunit ChlI(EC:6.6.1.1)	HMPPREF0675_3103	hypothetical protein	328905886					
ABC transporter, ATP-binding protein	HMPPREF0675_3102	hypothetical protein	328905885					
ABC transporter, ATP-binding protein	HMPPREF0675_3101	hypothetical protein	328905884					
catalase(EC:1.11.1.6)	HMPPREF0675_3100	hypothetical protein	328905883					
hypothetical protein	HMPPREF0675_3099	hypothetical protein	328905882					
transporter, anaerobic C4-dicarboxylate uptake (Dcu) family	HMPPREF0675_3098	hypothetical protein	328905881					
aspartate ammonia-lyase(EC:4.3.1.1)	HMPPREF0675_3097	hypothetical protein	328905880					
hypothetical protein	HMPPREF0675_3096	hypothetical protein	328905879					
putative nitrite reductase, copper-dependent	HMPPREF0675_3095	hypothetical protein	328905878					
putative nitrite reductase, copper-dependent	HMPPREF0675_3095	hypothetical protein	328905877					
transcriptional regulator, ArsR family	HMPPREF0675_3094	hypothetical protein	328905876					
phosphofructokinase(EC:2.7.1.11)	HMPPREF0675_3093	hypothetical protein	328905875					
hypothetical protein	HMPPREF0675_3092	hypothetical protein	328905874					
transcriptional regulator, LacI family	HMPPREF0675_3091	hypothetical protein	328905873					
ABC transporter, permease protein	HMPPREF0675_3089	hypothetical protein	328905872					
ABC transporter, permease protein	HMPPREF0675_3088	hypothetical protein	328905871					
carbohydrate ABC transporter, carbohydrate-binding	HMPPREF0675_3087	hypothetical protein	328905870					
hypothetical protein	HMPPREF0675_3086	hypothetical protein	328905869					
ROK family protein	HMPPREF0675_3085	hypothetical protein	328905868					
1,3-beta-galactosyl-N-acetylhexosamine phosphoryla	HMPPREF0675_3084	hypothetical protein	328905867					
hypothetical protein	HMPPREF0675_3083	hypothetical protein	328905866					
hypothetical protein	HMPPREF0675_3082	hypothetical protein	328905865					
glycogen/starch/alpha-glucan phosphorylase(EC:2.4.1.1)	HMPPREF0675_3081	hypothetical protein	328905864					
chloride transporter, ClC family	HMPPREF0675_3080	hypothetical protein	328905863					
succinate-semialdehyde dehydrogenase(EC:1.2.1.16)	HMPPREF0675_3079	hypothetical protein	328905862					
ABC transporter, ATP-binding protein(EC:3.6.3.34)	HMPPREF0675_3078	hypothetical protein	328905861					
iron chelate uptake ABC transporter, FeCT family, per	HMPPREF0675_3077	hypothetical protein	328905860					
periplasmic binding protein	HMPPREF0675_3076	hypothetical protein	328905859					
methyitransferase domain protein	HMPPREF0675_3075	hypothetical protein	328905858					
ABC transporter, ATP-binding protein	HMPPREF0675_3074	hypothetical protein	328905857					
efflux ABC transporter, permease protein	HMPPREF0675_3073	hypothetical protein	328905856					
YhgE/Pip N-terminal domain protein	HMPPREF0675_3072	hypothetical protein	328905855					
MMPL family protein	HMPPREF0675_3071	hypothetical protein	328905854					
transcriptional regulator, TetR family	HMPPREF0675_3070	hypothetical protein	328905853					
UDP-glucose 4-epimerase(EC:5.1.3.2)	HMPPREF0675_3069	hypothetical protein	328905852					
histidine kinase	HMPPREF0675_3068	hypothetical protein	328905851					
kinase, PfkB family	HMPPREF0675_3067	hypothetical protein	328905850					
glycosyl hydrolase family 20, catalytic domain protein(EC:3.2.1.22)	HMPPREF0675_3066	hypothetical protein	328905849					
hypothetical protein	HMPPREF0675_3065	hypothetical protein	328905848					
HAD hydrolase, family 1A, variant 3	HMPPREF0675_3064	hypothetical protein	328905847					
hypothetical protein	HMPPREF0675_3063	hypothetical protein	328905846					
glycosyl hydrolase family 38 N-terminal domain protein(EC:3.2.1.22)	HMPPREF0675_3062	hypothetical protein	328905845					
glycosyl hydrolase family 38 N-terminal domain protein(EC:3.2.1.22)	HMPPREF0675_3061	hypothetical protein	328905844					
transcriptional regulator, DeoR family	HMPPREF0675_3060	hypothetical protein	328905843					
bacterial extracellular solute-binding protein	HMPPREF0675_3059	hypothetical protein	328905842					
ABC transporter, permease protein	HMPPREF0675_3058	hypothetical protein	328905841					
ABC transporter, permease protein	HMPPREF0675_3057	hypothetical protein	328905840					
hypothetical protein	HMPPREF0675_3056	hypothetical protein	328905839					
hypothetical protein	HMPPREF0675_3055	hypothetical protein	328905838					
hypothetical protein	HMPPREF0675_3054	hypothetical protein	328905837					
hypothetical protein	HMPPREF0675_3053	hypothetical protein	328905836					
hypothetical protein	HMPPREF0675_3052	hypothetical protein	328905835					
hypothetical protein	HMPPREF0675_3051	hypothetical protein	328905834					
hypothetical protein	HMPPREF0675_3050	hypothetical protein	328905833					
		hypothetical protein	328905832					
		hypothetical protein	328905831					
		hypothetical protein	328905830					
		hypothetical protein	328905829					
		hypothetical protein	328905828					
		hypothetical protein	328905827					
		hypothetical protein	328905826					
		hypothetical protein	328905825					
		hypothetical protein	328905824					
		hypothetical protein	328905823					
		hypothetical protein	328905822					
		hypothetical protein	328905821					
		hypothetical protein	328905820					
		hypothetical protein	328905819					
		hypothetical protein	328905818					
		hypothetical protein	328905817					
		hypothetical protein	328905816					
		hypothetical protein	328905815					
		hypothetical protein	328905814					
		hypothetical protein	328905813					
		hypothetical protein	328905812					

ABC transporter, permease protein	HMPPREF0675_3058	ABC-type transporter, ATPase component	328908128	Prop010_174	210959	211564	+	C	extracellular solute-binding protein family 1 (db=KEGG evalua=1.0e-25
ABC transporter, permease protein	HMPPREF0675_3435	sugar ABC superfamily ATP binding cassette tr	328907296	Prop010_175	211570	212463	+	C	binding-protein-dependent transport systems inner membrane compo
ABC transporter, permease protein	HMPPREF0675_3435	sugar ABC superfamily ATP binding cassette tr	328907297	Prop010_176	212580	213317	+	C	binding-protein-dependent transport systems inner membrane compo
				Prop010_177	213336	214067	+	C	arylsulfatase (db=KEGG evalua=2.0e-78 bit_score=295.0 identity
				Prop010_178	214152	214811	+	C	arylsulfatase (db=KEGG evalua=3.0e-59 bit_score=231.0 identity
				Prop010_179	214886	216595	+	B	0040 formate--tetrahydrofolate ligase (EC:6.3.4.3); K01938 formate--tet
formate--tetrahydrofolate ligase(EC:6.3.4.3)	HMPPREF0675_3049	formate--tetrahydrofolate ligase	328905834						
		phosphoenolpyruvate-dependent sugar pl	328905833						
		PTS system, galactitol-specific IIC compo	328905832						
		PTS system, Lactose/Cellobiose specific I	328905831						
		oxidoreductase, zinc-binding dehydrogen	328905830						
		phosphoenolpyruvate-dependent sugar pl	328905829						
		putative L-ribulose-5-phosphate 4-epime	328905828						
			328905827	Prop010_180	216704	218140	+	B	kse:Ksed_22930 amino acid transporter (db=KEGG) (probably split with I
transporter, major facilitator family protein	HMPPREF0675_3048	transporter, major facilitator family protein	328905827	Prop010_181	218497	219840	+	B	0043 membrane associated protein (db=KEGG)
LysM domain protein	HMPPREF0675_3047	LysM domain protein	328905826	Prop010_182	219844	222240	+	B	3047 lysM; LysM domain protein (db=KEGG)
		LysM domain protein	328905825						
		LysM domain protein	328905824						
		putative membrane protein	328905823						
hypothetical protein	HMPPREF0675_3046	hypothetical protein	328905822						
hypothetical protein	HMPPREF0675_3044	hypothetical protein	328905821	Prop010_183	223420	223614	+	C	hypothetical protein (db=KEGG evalua=1.0e-17 bit_score=91.7 identity=
type II secretion system F domain protein	HMPPREF0675_3043	type II secretion system F domain protein	328905820	Prop010_184	227702	224604	+	B	0043 membrane associated protein (db=KEGG)
type II secretion system F domain protein	HMPPREF0675_3042	type II secretion system F domain protein	328905819	Prop010_185	224597	225472	+	C	type II secretion system F domain protein (db=KEGG evalua=6.0e-72 bi
type II/IV secretion system protein	HMPPREF0675_3041	secretion system protein	328905818	Prop010_186	225463	226947	+	B	0041 secretion system protein (db=KEGG)
hypothetical protein	HMPPREF0675_3040	hypothetical protein	328905817	Prop010_187	226944	227765	+	B	3040 hypothetical protein (db=KEGG)
SAF domain protein	HMPPREF0675_3039	SAF domain protein	328905816	Prop010_188	227762	228235	+	C	SAF domain protein (db=KEGG evalua=5.0e-59 bit_score=229.0 identity
hypothetical protein	HMPPREF0675_3038	putative lipoprotein	328905815	Prop010_189	228732	229391	+	C	0038 hypothetical protein (db=KEGG)
		acyltransferase, GNAT family	328905814						
acetyltransferase, GNAT family	HMPPREF0675_3036	phospholipase, patatin family	328905813	Prop010_190	229766	230044	+	E	GENE: 230787_231065 + (rbs_motif=None rbs_spacer=None)
phospholipase, patatin family	HMPPREF0675_3037	phospholipase, patatin family	328905813	Prop010_191	230041	230919	+	B	3037 phospholipase, patatin family (db=KEGG)
histidinol-phosphate transaminase(EC:2.6.1.9)		aminostransferase, class I/II	328905812	Prop010_192	230923	231981	+	B	3035 hisC_1; histidinol-phosphate transaminase (EC:2.6.1.9); K00817 hi
		hypothetical protein	328905811						
hypothetical protein	HMPPREF0675_3034	hypothetical protein	328905810						
transcriptional regulator, Deor family	HMPPREF0675_3033	transcriptional regulator, Deor family	328905809						
		hypothetical protein	328905808						
		putative phosphatase	328905807						
		hypothetical protein	328905806						
		putative hydrolase	328905805						
		hypothetical protein	328905804						
		hypothetical protein	328905803						
				Prop010_203	243086	244597	+	C	0015 ABC transporter protein; K10441 ribose transport system permease pr
hypothetical protein	HMPPREF0675_3032	hypothetical protein		Prop010_202	242031	242429	+	C	ribose ABC transporter; K10440 ribose transport system permease protei
hypothetical protein	HMPPREF0675_3031	hypothetical protein		Prop010_201	240098	241039	+	B	0014 putative transcriptional regulator; K02529 LacI family transcrip
hypothetical protein	HMPPREF0675_3030	hypothetical protein		Prop010_200	240098	241039	+		

hydrolyase, alpha/beta domain protein	HMPREF0675_5390	Prop010_253	302959	303891 +	B	2312 lipase/esterase (db=KEGG)
transporter, major facilitator family protein	HMPREF0675_5389	Prop010_254	303893	305140 +	B	2311 putative sucrose symporter (db=KEGG)
RNA pseudouridine synthase	HMPREF0675_5388	328905742	Prop010_255	305517 306392 +	B	2310 putative RNA pseudouridylylase (db=KEGG)
thioredoxin-disulfide reductase [EC:1.8.1.9]	HMPREF0675_5387	328905741	Prop010_256	306557 307609 +	B	2309 thioredoxin reductase [EC:1.8.1.9]; K00384 thioredoxin reductase
transcriptional regulator, LacI family	HMPREF0675_5386	328905740	Prop010_257	307687 308718 +	C	transcriptional regulator, LacI family (db=KEGG eval=3.0e-83)
hypothetical protein [EC:3.2.1.55]	HMPREF0675_5386	Prop010_258	308873	310207 +	C	sro:Sros_2485 alpha-N-arabinofuranosidase; K01209 alpha-N-arabinofuranosidase
trypsin [EC:3.4.21.-]	HMPREF0675_5385	328905739	Prop006_227	253292 255358 +	B	2307 trypsin-like serine protease; K06372 putative serine protease
hypothetical protein	HMPREF0675_5384	328905738	Prop006_226	252755 253873 +	B	3384 hypothetical protein (db=KEGG)
glycerol uptake facilitator protein	HMPREF0675_5383	328905737	Prop006_225	251987 252739 +	B	2305 glycerol uptake facilitator protein; K02440 glycerol uptake facilitator
glycerol kinase [EC:2.7.1.30]	HMPREF0675_5382	328905736	Prop006_224	250376 251899 +	B	2304 glycerol kinase 2 [EC:2.7.1.30]; K00864 glycerol kinase [EC:2.7.1.1]
Tat (twin-arginine translocation) pathway signal sequence	HMPREF0675_5381	328905735	Prop006_223	248144 249946 +	B	5380 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_5380	328905734	Prop006_222	245980 248070 +	B	5379 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_5379	328905733	Prop006_221	244379 245878 +	B	2301 putative RNA nucleotidyltransferase; K00970 poly(A) polymerase
RNA adenyllyltransferase [EC:2.7.7.19]	HMPREF0675_5377	328905732	Prop006_220	244001 244258 +	C	hypothetical protein (db=KEGG eval=8.0e-26 bit_score=119.0 identity)
hypothetical protein	HMPREF0675_5376	328905732	Prop006_219	242744 243763 +	B	2299 glycerate kinase [EC:2.7.1.31]; K00865 glycerate kinase [EC:2.7.1.1]
glycerate kinase [EC:2.7.1.31]	HMPREF0675_5375	328905731	Prop006_218	241147 242004 +	B	2298 putative mechanosensitive ion channel; K03442 small conductance
transporter, small conductance mechanosensitive ion channel	HMPREF0675_5374	328905730	Prop006_217	240329 241021 +	B	5374 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_5373	328905729	Prop006_216	239317 240324 +	B	2296 transcription regulator CsrR (db=KEGG)
transcriptional regulator, LacI family	HMPREF0675_5372	328905728	Prop006_215	237774 239114 +	B	2295 solute-binding lipoprotein (db=KEGG)
bacterial extracellular solute-binding protein	HMPREF0675_5371	328905727	Prop006_214	236628 237536 +	B	5371 predicted galacto-N-biose/-lacto-N-biose 1 ABC transporter, permease
Predicted galacto-N-biose/-lacto-N-biose 1 ABC transporter	HMPREF0675_5370	328905726	Prop006_213	235715 236626 +	B	5370 putative predicted galacto-N-biose/-lacto-N-biose 1 ABC transporter
putative Predicted galacto-N-biose/-lacto-N-biose 1 ABC transporter	HMPREF0675_5369	328905725	Prop006_212	234102 235508 +	B	2292 fumC; fumarate hydratase [EC:4.2.1.2]; K01679 fumarate hydratase
hypothetical protein	HMPREF0675_5368	328905724	Prop006_211	232870 233751 +	B	5367 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_5367	328905723	Prop006_210	231829 232698 +	C	hypothetical protein (db=KEGG eval=3.0e-35 bit_score=152.0 identity)
hypothetical protein	HMPREF0675_5366	328905722	Prop006_209	229618 230517 +	B	5366 hypothetical protein (db=KEGG eval=3.0e-35 bit_score=152.0 identity)
nucleotidyl transferase [EC:2.7.7.24]	HMPREF0675_5365	328905720	Prop006_208	228068 231704 +	B	2288 glucose-1-phosphate thymidyltransferase [EC:2.7.7.24]; K00973
GHMP kinase, N-terminal domain protein [EC:2.7.1.6]	HMPREF0675_5364	328905719	Prop006_207	226981 230871 +	B	5364 GHMP kinase, N-terminal domain protein; K00849 galactokinase
putative phosphoglucomutase, alpha-D-glucose phosphate-6-epimerase [EC:5.1.1.1]	HMPREF0675_5363	328905718	Prop006_206	226143 229567 +	B	2286 phosphoglucomutase/phosphomannomutase
D-serine/D-alanine/glycine transporter	HMPREF0675_5361	328905716	Prop006_205	225151 226530 +	B	5361 D-serine/D-alanine/glycine transporter (db=KEGG)
D-serine/D-alanine/glycine transporter	HMPREF0675_5360	328905715	Prop006_204	223902 224684 +	B	2283 D-serine/D-alanine/glycine transporter; K03293 amino acid transporter
alanine racemase	HMPREF0675_5359	328905713	Prop006_203	222014 223429 +	C	hypothetical protein (db=KEGG eval=1.0e-38 bit_score=161.0 identity)
putative reactivating factor for D-orithine aminomutase	HMPREF0675_5358	328905712	Prop006_202	221137 222121 +	D	IPRSCAN: Prokaryotic lipoproteins and lipoprotein localization factors
hypothetical protein	HMPREF0675_5357	328905711	Prop006_201	220184 220831 +	B	2259 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_5356	328905710	Prop006_200	219838 220184 +	B	2259 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_5355	328905709	Prop006_199	218824 219336 +	C	hypothetical protein (db=KEGG eval=6.0e-54 bit_score=213.0 identity)
hypothetical protein	HMPREF0675_5354	328905708	Prop006_198	218224 219336 +	C	hypothetical protein (db=KEGG eval=6.0e-54 bit_score=213.0 identity)
hypothetical protein	HMPREF0675_5353	328905707	Prop006_197	217132 218157 +	B	2272 citrate synthase 1 (EC:2.3.3.1); K01647 citrate synthase [EC:2.3.3.1]
hypothetical protein	HMPREF0675_5352	328905706	Prop006_196	215558 216844 +	B	5348 rlpA; lipoprotein A-like protein (db=KEGG)
hypothetical protein	HMPREF0675_5351	328905705	Prop006_195	214051 215253 +	B	5347 Erk/YbIs/Ycfs/YnhG (db=KEGG)
hypothetical protein	HMPREF0675_5350	328905704	Prop006_194	212555 213781 +	D	IPRSCAN: Prokaryotic lipoproteins and lipoprotein localization factors
hypothetical protein	HMPREF0675_5349	328905703	Prop006_193	212194 212319 +	D	IPRSCAN: Prokaryotic lipoproteins and lipoprotein localization factors
hypothetical protein	HMPREF0675_5348	328905702	Prop006_192	211310 212068 +	D	IPRSCAN: Prokaryotic lipoproteins and lipoprotein localization factors
hypothetical protein	HMPREF0675_5347	328905701	Prop006_191	210099 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5346	328905700	Prop006_190	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5345	328905699	Prop006_189	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5344	328905698	Prop006_188	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5343	328905697	Prop006_187	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5342	328905696	Prop006_186	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5341	328905695	Prop006_185	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5340	328905694	Prop006_184	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5339	328905693	Prop006_183	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5338	328905692	Prop006_182	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5337	328905691	Prop006_181	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5336	328905690	Prop006_180	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5335	328905689	Prop006_179	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5334	328905688	Prop006_178	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5333	328905687	Prop006_177	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5332	328905686	Prop006_176	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5331	328905685	Prop006_175	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5330	328905684	Prop006_174	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5329	328905683	Prop006_173	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5328	328905682	Prop006_172	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5327	328905681	Prop006_171	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5326	328905680	Prop006_170	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5325	328905679	Prop006_169	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5324	328905678	Prop006_168	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5323	328905677	Prop006_167	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5322	328905676	Prop006_166	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5321	328905675	Prop006_165	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5320	328905674	Prop006_164	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5319	328905673	Prop006_163	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5318	328905672	Prop006_162	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5317	328905671	Prop006_161	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5316	328905670	Prop006_160	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5315	328905669	Prop006_159	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5314	328905668	Prop006_158	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5313	328905667	Prop006_157	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5312	328905666	Prop006_156	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5311	328905665	Prop006_155	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5310	328905664	Prop006_154	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5309	328905663	Prop006_153	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5308	328905662	Prop006_152	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5307	328905661	Prop006_151	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5306	328905660	Prop006_150	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5305	328905659	Prop006_149	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5304	328905658	Prop006_148	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5303	328905657	Prop006_147	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5302	328905656	Prop006_146	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5301	328905655	Prop006_145	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5300	328905654	Prop006_144	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5299	328905653	Prop006_143	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5298	328905652	Prop006_142	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5297	328905651	Prop006_141	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5296	328905650	Prop006_140	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5295	328905649	Prop006_139	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5294	328905648	Prop006_138	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5293	328905647	Prop006_137	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5292	328905646	Prop006_136	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5291	328905645	Prop006_135	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5290	328905644	Prop006_134	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5289	328905643	Prop006_133	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5288	328905642	Prop006_132	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5287	328905641	Prop006_131	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5286	328905640	Prop006_130	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5285	328905639	Prop006_129	209665 210425 +	C	hypothetical protein (db=KEGG eval=2.0e-23 bit_score=111.0 identity)
hypothetical protein	HMPREF0675_5284	328905638	Prop006_128	209665 210425 +	C	hypothetical protein (db=KEGG eval=2

hypothetical protein	HMMPREF0675_5294	hypothetical protein	328907636	ProP006_137	150311	151261 +	B	UniRef90_COV075 Mm2+, Zn2+ ABC superfamily ATP binding cassette tra
serine/threonine-type ABC transporter, permease subunit	HMMPREF0675_5291	ABC transporter ATP-binding protein	328907636	ProP006_136	149368	149309 +	C	ABC-3 protein, K11708 manganese/zinc/rn transport system permease
anchored repeat-type ABC transporter, permease subunit	HMMPREF0675_4571	ABC transporter ATP-binding protein	328907635	ProP006_135	148622	150371 +	C	UniRef90_COV073 ABC superfamily ATP binding cassette transporter, ABC
anchored repeat-type ABC transporter, ATP-binding subunit	HMMPREF0675_4570	anchored repeat-type ABC transporter, ATP-bi	328907635	ProP006_134	147615	148565 +	B	cdi:DP169 hypothetical protein, K11707 manganese/zinc/rn transport
anchored repeat ABC transporter, substrate-binding protein	HMMPREF0675_4569	hypothetical protein	328906619	ProP006_133	146690	147456 +	B	5272 aa; leucyltransferase (EC:2.3.2.6); K0684 leucyl/phenylalanine-tr
leucyltransferase (EC:2.3.2.6)	HMMPREF0675_5293	leucyltransferase	328906618	ProP006_132	145718	146647 +	B	prf:PFREUD_01330 pheA; prephenate dehydratase (EC:4.2.1.51);
hypothetical protein	HMMPREF0675_5292	hypothetical protein	328906617					
serine-tRNA ligase (EC:6.1.1.11)	HMMPREF0675_5291	serine-tRNA ligase	328906616	ProP006_131	144750	145529 +	D	IPRSCAN: seg (db=Seg db_id=seg from 25 to 49)
hypothetical protein	HMMPREF0675_5290	hypothetical protein	328906615	ProP006_130	143194	144468 +	B	5291 serS; serine-tRNA ligase (EC:6.1.1.11); K01875 seryl-tRNA synthet
hypothetical protein	HMMPREF0675_5289	hypothetical protein	328906614					
transcriptional regulator, IclR family, C-terminal domain	HMMPREF0675_5288	IclR family transcriptional regulator	328906613	ProP006_129	141872	143197 +	B	2218 hypothetical protein (db=KEGG)
acyl-CoA dehydrogenase, C-terminal domain protein	HMMPREF0675_5287	acyl-CoA dehydrogenase	328906612					
CoA-transferase family III	HMMPREF0675_5286	putative L-carnitine dehydratase	328906611					
electron transfer flavoprotein domain protein	HMMPREF0675_5285	electron transfer flavoprotein domain pro	328906610					
electron transfer flavoprotein FAD-binding domain protein	HMMPREF0675_5284	electron transfer flavoprotein FAD-binding	328906607					
permease oxidoreductase (EC:1.5.5.-)	HMMPREF0675_5283	FAD cytosine oxidoreductase	328906605					
permease, cytosine/purine, uracil, thiamine, allantoin	HMMPREF0675_5282	purine cytosine permease-like protein	328906604					
hypothetical protein	HMMPREF0675_5281	hypothetical protein	328906603	ProP006_128	141046	141819 +	B	2205 HAD superfamily hydrolase (db=KEGG)
B3/4 domain protein	HMMPREF0675_5280	transcription factor WhiB	328906602	ProP006_127	140623	140899 +	C	whiB_3, transcription factor WhiB (db=KEGG eval=8.0e-75 bit_score=
cupin domain protein	HMMPREF0675_5279	transporter, CPA2 family	328906601	ProP006_126	137910	140057 +	C	5273 aa; leucyltransferase (EC:2.3.2.6); K0684 leucyl/phenylalanine-tr
ABC-2 type transporter	HMMPREF0675_5277	membrane protein, putative permease	328906600	ProP006_125	137381	138163 +	C	transporter, major facilitator family protein (db=KEGG eval=2.0e-45 bi
ABC transporter, ATP-binding protein	HMMPREF0675_5276	transporter, major facilitator family protein	328906599					
thiazolylpeptide-type bactericin	HMMPREF0675_5275	hypothetical protein	328906598					
HAD hydrolase, family IIB	HMMPREF0675_5274	HAD superfamily hydrolase	328906603	ProP006_128	141046	141819 +	B	2205 HAD superfamily hydrolase (db=KEGG)
transcription factor WhiB	HMMPREF0675_5273	transcription factor WhiB	328906602	ProP006_127	140623	140899 +	C	whiB_3, transcription factor WhiB (db=KEGG eval=8.0e-75 bit_score=
transporter, CPA2 family	HMMPREF0675_5272	transporter, CPA2 family	328906601	ProP006_126	137910	140057 +	C	5273 aa; leucyltransferase (EC:2.3.2.6); K0684 leucyl/phenylalanine-tr
transporter, major facilitator family protein	HMMPREF0675_5271	membrane protein, putative permease	328906600	ProP006_125	137381	138163 +	C	transporter, major facilitator family protein (db=KEGG eval=2.0e-45 bi
transcriptional regulator, IclR family, C-terminal domain	HMMPREF0675_5270	IclR family transcriptional regulator	328906612					
acyl-CoA dehydrogenase, C-terminal domain protein	HMMPREF0675_5269	acyl-CoA dehydrogenase	328906611					
CoA-transferase family III	HMMPREF0675_5268	putative L-carnitine dehydratase	328906610					
electron transfer flavoprotein domain protein	HMMPREF0675_5267	electron transfer flavoprotein domain pro	328906607					
electron transfer flavoprotein FAD-binding domain protein	HMMPREF0675_5266	electron transfer flavoprotein FAD-binding	328906605					
permease oxidoreductase (EC:1.5.5.-)	HMMPREF0675_5265	FAD cytosine oxidoreductase	328906604					
permease, cytosine/purine, uracil, thiamine, allantoin	HMMPREF0675_5264	purine cytosine permease-like protein	328906603	ProP006_128	141046	141819 +	B	2205 HAD superfamily hydrolase (db=KEGG)
hypothetical protein	HMMPREF0675_5263	transcription factor WhiB	328906602	ProP006_127	140623	140899 +	C	whiB_3, transcription factor WhiB (db=KEGG eval=8.0e-75 bit_score=
B3/4 domain protein	HMMPREF0675_5262	transporter, CPA2 family	328906601	ProP006_126	137910	140057 +	C	5273 aa; leucyltransferase (EC:2.3.2.6); K0684 leucyl/phenylalanine-tr
cupin domain protein	HMMPREF0675_5261	membrane protein, putative permease	328906600					

ABC transporter, ATP-binding protein	Prop006_45	49274	49906 +	C	ABC transporter, ATP-binding protein; K02003 (db=KEGG eval=8.0e-3)
	Prop006_44	48036	48983 +	C	integrate catalytic domain-containing protein (db=KEGG eval=)
	Prop006_43	47649	47801 +	D	IPRSCAN: seg (db=Seg db_id=seg from=5 to=17)
	Prop006_42	47342	47593 +	D	IPRSCAN: seg (db=Seg db_id=seg from=4 to=16)
	Prop006_41	46460	46774 +	E	GENE: 261925..262239 - (rbs_motif=AGxAG rbs_spacer=5-10bp)
	Prop006_40	44949	46340 +	B	pfr:PFREUD_24530 tnpA; transposase (db=KEGG)
	Prop006_39	43998	44732 +	E	GENE: 259463..260197 - (rbs_motif=GGAGG rbs_spacer=5-10bp)
	Prop006_38	43564	44019 +	E	GENE: 259029..259484 - (rbs_motif=None rbs_spacer=None)
	Prop006_37	42186	42500 +	E	GENE: 257604..257918 - (rbs_motif=GGAG/GAGG rbs_spacer=5-)
	Prop006_36	41544	42065 +	C	Zn peptidase (db=KEGG eval=3.0e-10 bit_score=67.8 identity=)
	Prop006_35	40923	41468 +	C	prophage ps3 protein 01 (db=KEGG eval=2.0e-22 bit_score=10)
	Prop006_34	40154	40699 +	D	IPRSCAN: seg (db=Seg db_id=seg from=86 to=99)
	Prop006_33	39326	39520 +	E	GENE: 254744..254938 - (rbs_motif=None rbs_spacer=None)
	Prop006_32	38727	39329 +	E	GENE: 254145..254747 - (rbs_motif=None rbs_spacer=None)
	Prop006_31	38351	38617 +	E	GENE: 253769..254035 + (rbs_motif=AGGA rbs_spacer=5-10bp)
	Prop006_30	36592	37782 +	C	hypothetical protein (db=KEGG eval=6.0e-42 bit_score=175.0)
	Prop006_29	36153	36422 +	E	GENE: 251571..251840 - (rbs_motif=None rbs_spacer=None)
DNA protecting protein DprA	Prop006_28	35713	36144 +	C	dprA; DNA protecting protein DprA; K04096 DNA processing prote
ABC transporter, ATP-binding protein	Prop006_27	34026	35648 +	C	clfCIIa_2755 carbohydrate kinase, FGGY-like protein (db=KEGG)
hypothetical protein(EC:3.2.1.55)	Prop006_26	32398	33936 +	B	aua:AAur_0688 abfA; alpha-L-arabinofuranosidase (EC:3.2.1.55);
hypothetical protein	Prop006_25	30738	32075 +	B	bfa:Bfae_29450 ABC-type sugar transport system, periplasmic compon
ABC transporter, permease protein	Prop006_24	29748	30713 +	B	bfa:Bfae_29440 permease component of ABC-type sugar transporter; K0
ABC transporter, permease protein	Prop006_23	28844	29668 +	C	bfa:Bfae_29430 ABC-type sugar transport system, permease compon
transcriptional regulator, LacI family	Prop006_22	27775	28830 +	C	aua:AAur_0684 LacI family transcriptional regulator (db=KEGG)
	Prop006_21	27365	27562 +	C	cebR; CebR cellobiose transport system transcriptional regulator;
MFS transporter, sugar porter (SP) family protein	Prop006_20	25862	27259 +	C	ire:Ireu_0479 sugar transporter (EC:1.3.1.74) (db=KEGG)
putative L-ribulose-5-phosphate 4-epimerase(EC:5.1.3.4)	Prop006_19	24804	25520 +	B	bfa:Bfae_29510 L-ribulose-5-phosphate 4-epimerase; K01786 L-r
ABC transporter, ATP-binding protein	Prop006_18	23233	24744 +	C	bfa:Bfae_29550 L-arabinose isomerase (EC:5.3.1.4); K01804 L-ar
transcriptional regulator, LacI family	Prop006_17	22094	23107 +	B	Uniref90_C0W683 LacI family transcription regulator n=1 Tax=
	Prop006_16	21675	22151 +	D	IPRSCAN: seg (db=Seg db_id=seg from=40 to=52)
	Prop006_15	20024	20932 +	B	nca:Noca_2154 integrase catalytic subunit (db=KEGG)
	Prop006_14	19677	20027 +	C	transposase IS3/IS911 family protein (db=KEGG eval=1.0e-25
(tRNA)	HMPREF0675_5203				
hypothetical protein	HMPREF0675_5202	hypothetical protein	328906530	Prop006_13	18459 19157 + C hypothetical protein (db=KEGG eval=2.0e-54 bit_score=215.0 identity
cutinase	HMPREF0675_5201	cutinase	328906529	Prop006_12	17390 18454 + B 5201 cutinase (db=KEGG)
Raf-like protein	HMPREF0675_5200	Raf-like protein	328906528	Prop006_11	16702 17163 + C Raf-like protein; K06910 (db=KEGG eval=4.0e-78 bit_score=292.0 ide
anaerobic ribonucleoside-triphosphate reductase(EC:1.17.4)	HMPREF0675_5198	anaerobic ribonucleoside-triphosphate reducta	328906527	Prop006_10	13905 16241 + B 5198 nrdD; anaerobic ribonucleoside-triphosphate reductase (EC:1.17.4.
anaerobic ribonucleoside-triphosphate reductase activating	HMPREF0675_5197	anaerobic ribonucleoside-triphosphate reducta	328906526	Prop006_9	13891 13909 + C anaerobic ribonucleoside-triphosphate reductase activating protein
DEAD/DEAH box helicase	HMPREF0675_5196	DEAD/DEAH box helicase	328906525	Prop006_8	10804 13395 + B 5196 DEAD/DEAH box helicase (db=KEGG)
	HMPREF0675_5195	hypothetical protein	328906524		
ferritin-like protein	HMPREF0675_5194	ferritin-like protein	328906523	Prop006_7	10016 10546 + B 5195 ferritin-like protein; K04047 starvation-inducible DNA-binding prote
hypothetical protein(EC:4.1.3.16; EC:4.1.2.14)	HMPREF0675_5193	putative aldolase	328906522	Prop006_6	9161 9838 + C putative aldolase; K01625 2-dehydro-3-deoxyphosphogluconate aldolase
hypothetical protein	HMPREF0675_5192	glucose-6-phosphate isomerase	328906520	Prop006_5	6262 7944 + B 5192 pgj; glucose-6-phosphate isomerase (EC:5.3.1.9); K01810 glucose-
glucose-6-phosphate isomerase(EC:5.3.1.9)	HMPREF0675_5191	hypothetical protein	328906519		
	HMPREF0675_5190	hypothetical protein	328906518		
hypothetical protein	HMPREF0675_5189	hypothetical protein	328906516	Prop006_4	4105 6015 + C von Willebrand factor type A; K07114 (db=KEGG eval=9.0e-51 bit_sco
hypothetical protein	HMPREF0675_5188	hypothetical protein	328906515	Prop006_3	3436 4089 + B 5190 hypothetical protein (db=KEGG)
oxidoreductase, aldo/keto reductase family protein(EC:1.1	HMPREF0675_5187	2,5-diketo-D-gluconic acid reductase A	328906515	Prop006_2	2522 3343 + B 5189 oxidoreductase, aldo/keto reductase family protein (db=KEGG)
arginine--tRNA ligase(EC:6.1.1.19)	HMPREF0675_5186	arginine--tRNA ligase	328906514	Prop006_1	680 2350 + B 5188 argS; arginine--tRNA ligase (EC:6.1.1.19); K01887 arginyl-tRNA sy
	HMPREF0675_5185	hypothetical protein	328906513	Prop012_1	/length=211779 /%G+C=63.58 /description=(Propionibacterium)
hypothetical protein	HMPREF0675_5184	hypothetical protein	328906512		
hypothetical protein	HMPREF0675_5183	hypothetical protein	328906511	Prop012_194	210538 211632 + C hypothetical protein (db=KEGG eval=3.0e-31 bit_score=139.0
hypothetical protein	HMPREF0675_5182	hypothetical protein	328906510	Prop012_193	210238 210361 + C ribosomal protein S6; K02919 large subunit ribosomal protein E
hypothetical protein	HMPREF0675_5181	hypothetical protein	328906509	Prop012_192	209749 210153 + C hypothetical protein (db=KEGG eval=6.0e-37 bit_score=155.0
hypothetical protein	HMPREF0675_5180	hypothetical protein	328906508	Prop012_191	209545 209739 + D IPRSCAN: seg (db=Seg db_id=seg from=6 to=26)
ROK family protein(EC:2.7.1.63)	HMPREF0675_5179	polyposphate glucokinase/transcriptional regi	328906511	Prop012_190	208535 209350 + B 2125 polyposphate glucokinase/transcriptional regulator; K00886 polypl
hypothetical protein	HMPREF0675_5178	membrane-flanked domain protein	328906510	Prop012_189	206604 208160 + C membrane-flanked domain protein; K08981 putative membrane protein (
hypothetical protein	HMPREF0675_5177	membrane-flanked domain protein	328906509	Prop012_188	206119 206607 + C membrane-flanked domain protein; K09167 hypothetical protein (db=KE
ribonucleoside-diphosphate reductase, beta subunit(EC:1.1	HMPREF0675_5176	ribonucleotide-diphosphate reductase subunit	328906508	Prop012_187	204973 205959 + B 5179 ribonucleoside-diphosphate reductase, beta subunit (EC:1.17.4.1);
ribonucleoside-diphosphate reductase, alpha subunit(EC:1	HMPREF0675_5175	ribonucleotide-diphosphate reductase subunit	328906507	Prop012_186	202372 204936 + B 2121 ribonucleotide-diphosphate reductase subunit alpha (EC:1.17.4.1);
	HMPREF0675_5174	hypothetical protein	328906506		
	HMPREF0675_5173	hypothetical protein	328906505		
	HMPREF0675_5172	hypothetical protein	328906504		
transporter, major facilitator family protein	HMPREF0675_5171	hypothetical protein	328906503	Prop012_185	200797 201897 + B 2118 NADH:flavin oxidoreductase (db=KEGG)
hypothetical protein	HMPREF0675_5170	hypothetical protein	328906502	Prop012_184	200481 200759 + C hypothetical protein; K09780 hypothetical protein (db=KEGG eval=1.0
oxidoreductase, FAD/FMN-binding protein	HMPREF0675_5169	oxidoreductase, FAD/FMN-binding	328906501	Prop012_183	198795 200276 + B 5172 cvpA; CvpA family protein (db=KEGG)
hypothetical protein	HMPREF0675_5168	hypothetical protein	328906500	Prop012_182	
CvpA family protein	HMPREF0675_5167	putative isopentenyl-diphosphate delta-isomer	328906499	Prop012_181	198336 198710 + C putative isopentenyl-diphosphate delta-isomerase; K01823 isopentenyl-d
hypothetical protein	HMPREF0675_5166	putative asparaginase	328906498	Prop012_180	197412 198332 + B 2114 putative asparaginase (EC:3.5.1.1); K13051 beta-aspartyl-peptidas
putative isopentenyl-diphosphate delta-isomerase(EC:5.3	HMPREF0675_5165	putative asparaginase	328906497	Prop012_179	196951 197157 + D IPRSCAN: seg (db=Seg db_id=seg from=11 to=28)
hypothetical protein(EC:3.4.19.5)	HMPREF0675_5164	putative asparaginase	328906496	Prop012_178	196039 196866 + C peptidase M23 (db=KEGG eval=5.0e-35 bit_score=151.0 identi
	HMPREF0675_5163	hypothetical protein	328906495	Prop012_177	
	HMPREF0675_5162	hypothetical protein	328906494	Prop012_176	
ATPase/histidine kinase/DNA gyrase B/HSP90 domain protei	HMPREF0675_5161	sensor histidine kinase/response regulator	328906493	Prop012_175	194969 196032 + B 5167 ATPase/histidine kinase/DNA gyrase B/HSP90 domain protein; K076
transcriptional regulatory protein, C-terminal domain protei	HMPREF0675_5160	response regulator receiver domain protein	328906492	Prop012_174	193910 194608 + B 5166 transcriptional regulatory protein, C-terminal domain protein; K076
hypothetical protein	HMPREF0675_5159	S51 family peptidase	328906491	Prop012_173	192837 193913 + B 5165 hypothetical protein (db=KEGG)
low molecular weight phosphotyrosine protein phosphatase	HMPREF0675_5158	low molecular weight phosphotyrosine phosphat	328906490	Prop012_172	192231 192773 + B 5164 low molecular weight phosphotyrosine protein phosphatase; K0110
hypothetical protein	HMPREF0675_5157	alpha/beta hydrolase fold protein	328906489	Prop012_171	191748 192041 + C hypothetical protein (db=KEGG eval=7.0e-40 bit_score=165.0 identity
CAMP factor (Cfa)	HMPREF0675_5156	cAMP factor 3	328906488	Prop012_170	190777 191592 + B 2108 cAMP factor; K11045 cAMP factor (db=KEGG)
	HMPREF0675_5155	hypothetical protein	328906487		
hypothetical protein	HMPREF0675_5154	hypothetical protein	328906486		
hypothetical protein	HMPREF0675_5153	hypothetical protein	328906485		
cellulase (glycosyl hydrolase family 5)	HMPREF0675_5152	hypothetical protein	328906484		
triacylglycerol lipase(EC:3.1.1.3)	HMPREF0675_5151	hypothetical protein	328906483		
	HMPREF0675_5150	hypothetical protein	328906482		
	HMPREF0675_5149	hypothetical protein	328906481		
hypothetical protein	HMPREF0675_5148	hypothetical protein	328906480		
hypothetical protein	HMPREF0675_5147	hypothetical protein	328906479		
HTH domain protein	HMPREF0675_5146	hypothetical protein	328906478		
hypothetical protein	HMPREF0675_5145	hypothetical protein	328906477		
hypothetical protein	HMPREF0675_5144	hypothetical protein	328906476		
hypothetical protein	HMPREF0675_5143	hypothetical protein	328906475		
hypothetical protein	HMPREF0675_5142	hypothetical protein	328906474		
hypothetical protein	HMPREF0675_5141	hypothetical protein	328906473		
hypothetical protein	HMPREF0675_5140	hypothetical protein	328906472		
hypothetical protein	HMPREF0675_5139	hypothetical protein	328906471		
hypothetical protein	HMPREF0675_5138	hypothetical protein	328906470		
hypothetical protein	HMPREF0675_5137	hypothetical protein	328906469		
hypothetical protein	HMPREF0675_5136	hypothetical protein	328906468		
	HMPREF0675_5135	hypothetical protein	328906467		
ABC transporter, ATP-binding protein	HMPREF0675_5134	ABC-type transport system, permease pr	328906466		
hypothetical protein	HMPREF0675_5133	ABC-type transport system, permease protein	328906465		
ABC transporter, ATP-binding protein	HMPREF0675_5132	ABC transport system, ATP-binding protein	328906464		
ABC transporter, ATP-binding protein	HMPREF0675_5131	ABC transporter, ATP-binding protein	328906463		
transcriptional regulator, TetR family	HMPREF0675_5130	transcriptional regulator, TetR family	328906462		
	HMPREF0675_5129	hypothetical protein	328906461		
	HMPREF0675_5128	hypothetical protein	328906460		
	HMPREF0675_5127	hypothetical protein	328906459		
	HMPREF0675_5126	hypothetical protein	328906458		
cupin domain protein	HMPREF0675_5125	hypothetical protein	328906457		
hypothetical protein	HMPREF0675_5124	hypothetical protein	328906456		
	HMPREF0675_5123	hypothetical protein	328906455		
	HMPREF0675_5122	hypothetical protein	328906454		
	HMPREF0675_5121	hypothetical protein	328906453		
	HMPREF0675_5120	hypothetical protein	328906452		
	HMPREF0675_5119	hypothetical protein	328906451		
	HMPREF0675_5118	hypothetical protein	328906450		
	HMPREF0675_5117	hypothetical protein	328906449		
	HMPREF0675_5116	hypothetical protein	328906448		
	HMPREF0675_5115	hypothetical protein	328906447		
	HMPREF0675_5114	hypothetical protein	328906446		
	HMPREF0675_5113	hypothetical protein	328906445		
	HMPREF0675_5112	hypothetical protein	328906444		
	HMPREF0675_5111	hypothetical protein	328906443		
	HMPREF0675_5110	hypothetical protein	328906442		
	HMPREF0675_5109	hypothetical protein	328906441		
	HMPREF0675_5108	hypothetical protein	328906440		
	HMPREF0675_5107	hypothetical protein	328906439		
	HMPREF0675_5106	hypothetical protein	328906438		
	HMPREF0675_5105	hypothetical protein	328906437		
	HMPREF0675_5104	hypothetical protein	328906436		
	HMPREF0675_5103	hypothetical protein	328906435		
	HMPREF0675_5102	hypothetical protein	328906434		
	HMPREF0675_5101	hypothetical protein	328906433		
	HMPREF0675_5100	hypothetical protein	328906432		
	HMPREF0675_5099	hypothetical protein	328906431		
	HMPREF0675_5098	hypothetical protein	328906430		
	HMPREF0675_5097	hypothetical protein	328906429		
	HMPREF0675_5096	hypothetical protein	328906428		
	HMPREF0675_5095	hypothetical protein	328906427		
	HMPREF0675_5094	hypothetical protein	328906426		
	HMPREF0675_5093	hypothetical protein	328906425		
	HMPREF0675_5092	hypothetical protein	328906424		
	HMPREF0675_5091	hypothetical protein	328906423		
	HMPREF0675_5090	hypothetical protein	328906422		
	HMPREF0675_5089	hypothetical protein	328906421		
	HMPREF0675_5088	hypothetical protein	328906420		
	HMPREF0675_5087	hypothetical protein	328906419		
	HMPREF0675_5086	hypothetical protein	328906418		
	HMPREF0675_5085	hypothetical protein	328906417		
	HMPREF0675_5084	hypothetical protein	328906416		
	HMPREF0675_5083	hypothetical protein	328906415		
	HMPREF0675_5082	hypothetical protein	328906414		
	HMPREF0675_5081	hypothetical protein	328906413		
	HMPREF0675_5080	hypothetical protein	328906412		
	HMPREF0675_5079	hypothetical protein	328906411		
	HMPREF0675_5078	hypothetical protein	328906410		
	HMPREF0675_5077	hypothetical protein	328906409		
	HMPREF0675_5076	hypothetical protein	328906408		
	HMPREF0675_5075	hypothetical protein	328906407		
	HMPREF0675_5074	hypothetical protein	32890640		

[illegible]

alkyl hydroperoxide reductase, F subunit peroxidoxin(EC:1.11.1.15)	HMPPREF0675_5055	alkyl hydroperoxide reductase subunit F	328906357	Prop012_78	82180	83754 +	B	1990 alkyl hydroperoxide reductase subunit F (EC:1.8.1.-); K03387 alkyl
phosphoribosylaminimidazole succinocarboxamide synthase I	HMPPREF0675_5054	alkyl hydroperoxide reductase C22 protein	328906356	Prop012_77	81459	82082 +	B	1989 alkyl hydroperoxide reductase C22 protein (EC:1.8.1.-); K03386 pe
phosphoribosylformylglycinamide synthase I	HMPPREF0675_5053	phosphoribosylaminimidazole succinocarboxamide synthase I	328906355	Prop012_76	80095	81384 +	B	5053 purC; phosphoribosylaminimidazole succinocarboxamide synthase I
phosphoribosylformylglycinamide synthase II	HMPPREF0675_5052	phosphoribosylformylglycinamide synthase I	328906354	Prop012_75	79418	80092 +	B	5052 purC; phosphoribosylformylglycinamide synthase I (EC:6.3.5.3);
BadF/BadG/BcrA/BcrD ATPase family protein	HMPPREF0675_5051	phosphoribosylformylglycinamide synthase I	328906353	Prop012_74	78353	79315 +	B	5051 BadF/BadG/BcrA/BcrD ATPase family protein (db=KEGG)
hypothetical protein	HMPPREF0675_3696	hypothetical protein	328906352	Prop012_73	78099	78356 +	E	GENE: 78448..78705 + (rbs_motif=AGGA rbs_spacer=5-10bp)
hypothetical protein	HMPPREF0675_5050	lipoprotein chitinase	328906351	Prop012_72	77970 +	77970 +	C	cell wall-associated hydrolase, invasion-associated protein (db=KEGG)
thrombospondin type 3 repeat protein	HMPPREF0675_5049	hypothetical protein	328906350	Prop012_71	76583	77296 +	C	hypothetical protein (db=KEGG eval=7.0e-45 bit_score=183.0)
hypothetical protein	HMPPREF0675_5048	acid phosphatase	328906349	Prop012_70	75025	76524 +	B	1982 acid phosphatase (db=KEGG)
PA2 family protein	HMPPREF0675_5047	pyridine nucleotide-disulfide oxidoreductase	328906348	Prop012_69	74407	74979 +	B	1981 pyridine nucleotide-disulphide oxidoreductase (db=KEGG)
pyridine nucleotide-disulfide oxidoreductase	HMPPREF0675_5046	YkuG protein	328906347	Prop012_67	72705	73370 +	C	protein of unknown function (DUF1906)/putative peptidoglycan b
		YkuG protein	328906346	Prop012_66	70988	72616 +	B	svi:Swlr_19400 protein of unknown function (DUF1906)/putative
		secreted protein	328906346	Prop012_66	70285	70974 +	B	hypothetical protein (db=KEGG eval=1.0e-18 bit_score=96.3 id
hypothetical protein	HMPPREF0675_5045	putative lipoprotein	328906345	Prop012_65	69851	70288 +	C	hypothetical protein (db=KEGG eval=5.0e-68 bit_score=259.0 identity
hypothetical protein	HMPPREF0675_5044	membrane alanyl aminopeptidase (EC:3.4.11.2)	328906344	Prop012_64	67153	69711 +	B	5043 pepN_2; membrane alanyl aminopeptidase (EC:3.4.11.2); K01256
membrane alanyl aminopeptidase (EC:3.4.11.2)	HMPPREF0675_5043	transporter, major facilitator family protein	328906343	Prop012_63	65821	67119 +	B	5042 transporter, major facilitator family protein (db=KEGG)
transporter, major facilitator family protein	HMPPREF0675_5042	phosphoribosylformylglycinamide synthase II	328906342	Prop012_62	65079	65492 +	C	hypothetical protein (db=KEGG eval=3.0e-13 bit_score=77.0 identity=
phosphoribosylformylglycinamide synthase II	HMPPREF0675_5041	phosphoribosylformylglycinamide synthase I	328906342	Prop012_61	64644	65072 +	C	Putative uncharacterized protein n=1 TaxoMikrobacterium phage Mm1 Re
phosphoribosylformylglycinamide synthase I	HMPPREF0675_5041	phosphoribosylformylglycinamide synthase I	328906342	Prop012_60	63423	64517 +	B	5041 purL; phosphoribosylformylglycinamide synthase II (EC:6.3.5.3);
hypothetical protein	HMPPREF0675_5040	hypothetical protein	328906341	Prop012_59	61226	63304 +	B	1976 para-aminobenzoate synthase (EC:4.1.3.-); K13950 para-aminoben
aminodeoxychorismate synthase, component I	HMPPREF0675_5039	putative membrane protein	328906339	Prop012_58	60577	61104 +	C	nitric-oxide reductase subunit B (EC:1.7.99.7); K04561 nitric-oxide reduc
hypothetical protein	HMPPREF0675_5038	hypothetical protein	328906338	Prop012_57	59814	60239 +	C	stomatin/prohibitin-like protein (db=KEGG eval=4.0e-31 bit_score=13
Putative stomatin/prohibitin-family membrane protease sub	HMPPREF0675_5037	stomatin/prohibitin-like protein	328906337	Prop012_56	58431	59774 +	B	1972 stomatin/prohibitin-like protein (db=KEGG)
peptidase dimerization domain protein	HMPPREF0675_5036	peptide dimerization domain protein	328906336	Prop012_55	56998	57252 +	C	hypothetical protein (db=KEGG eval=5.0e-23 bit_score=109.0 identity
hypothetical protein	HMPPREF0675_5035	putative membrane protein	328906335	Prop012_54	55429	56934 +	B	5034 purF; amidophosphoribosyltransferase (EC:2.4.2.14); K00764 amid
amidophosphoribosyltransferase(EC:2.4.2.14)	HMPPREF0675_5034	amidophosphoribosyltransferase	328906334	Prop012_53	54365	55432 +	B	5033 purM; phosphoribosylformylglycinamide cyclo-lyase (EC:6.3.3.1);
phosphoribosylformylglycinamide cyclo-lyase(EC:6.3.3.1)	HMPPREF0675_5033	phosphoribosylaminimidazole synthetase	328906333	Prop012_52	54026	54349 +	C	hypothetical protein (db=KEGG eval=4.0e-39 bit_score=162.0 identity
hypothetical protein	HMPPREF0675_5032	hydrolase, alpha/beta domain protein	328906332	Prop012_51	53876	54133 +	C	5004 ABC transporter, ATP-binding protein (db=KEGG)
hydrolase, alpha/beta domain protein	HMPPREF0675_5031	hydrolase, alpha/beta domain protein	328906329	Prop012_50	53054	53866 +	B	5031 hydrolase, alpha/beta domain protein (db=KEGG)
hypothetical protein	HMPPREF0675_5030	hypothetical protein	328906328	Prop012_49	51596	52906 +	B	5030 bacterial extracellular solute-binding protein; K02027 multi
bacterial extracellular solute-binding protein	HMPPREF0675_5029	ABC transporter, permease protein	328907986	Prop012_48	50525	51421 +	B	1965 binding-protein-dependent transport permease; K02025 multiple su
ABC transporter, permease protein	HMPPREF0675_5028	ABC transporter, permease protein	328907986	Prop012_48	50525	51421 +	B	5028 ABC transporter, permease protein; K02026 multiple sugar transpor
(tRNA)	HMPPREF0675_5027	hypothetical protein	328907976	Prop012_47	49593	50525 +	B	
(tRNA)	HMPPREF0675_5026	hypothetical protein	328907976	Prop012_47	49593	50525 +	B	
(tRNA)	HMPPREF0675_5025	hypothetical protein	328907976	Prop012_47	49593	50525 +	B	
hypothetical protein	HMPPREF0675_5024	hypothetical protein	328906328	Prop012_46	46894	48321 +	C	putative cell wall-associated hydrolase (db=KEGG eval=2.0e-71 bit_sc
NipC/P60 family protein	HMPPREF0675_5023	hypothetical protein	328906327	Prop012_46	46894	48321 +	C	putative cell wall-associated hydrolase (db=KEGG eval=2.0e-71 bit_sc
hypothetical protein	HMPPREF0675_5022	hypothetical protein	328906326	Prop012_45	45443	46222 +	B	5015 putative HAD hydrolase TIGR01457; K02566 NagD protein (db=KEE
(tRNA)	HMPPREF0675_5021	hypothetical protein	328906325	Prop012_45	45443	46222 +	B	5015 putative HAD hydrolase TIGR01457; K02566 NagD protein (db=KEE
bacterial extracellular solute-binding protein	HMPPREF0675_5020	sugar phosphatase/hydrolase	328906324	Prop012_45	45443	46222 +	B	5015 putative HAD hydrolase TIGR01457; K02566 NagD protein (db=KEE
ABC transporter, permease protein	HMPPREF0675_5019	patatin-like phospholipase	328906323	Prop012_44	43871	45373 +	B	1953 patatin-like phospholipase (db=KEGG)
Neuraminidase Nanp	HMPPREF0675_5018	phospholipase, patatin family	328906322	Prop012_44	43871	45373 +	B	1953 patatin-like phospholipase (db=KEGG)
ROK family protein	HMPPREF0675_5017	L-lactate dehydrogenase	328906321	Prop012_43	42855	43820 +	B	1952 L-lactate dehydrogenase (EC:1.1.1.27); K00016 L-lactate dehydrog
putative HAD hydrolase TIGR01457	HMPPREF0675_5016	L-lactate dehydrogenase	328906321	Prop012_43	42855	43820 +	B	1952 L-lactate dehydrogenase (EC:1.1.1.27); K00016 L-lactate dehydrog
phospholipase, patatin family	HMPPREF0675_5015	L-lactate dehydrogenase	328906321	Prop012_43	42855	43820 +	B	1952 L-lactate dehydrogenase (EC:1.1.1.27); K00016 L-lactate dehydrog
lactate/malate dehydrogenase, NAD binding domain protein	HMPPREF0675_5014	L-lactate dehydrogenase	328906321	Prop012_43	42855	43820 +	B	1952 L-lactate dehydrogenase (EC:1.1.1.27); K00016 L-lactate dehydrog
lactate/malate dehydrogenase, NAD binding domain protein	HMPPREF0675_5013	L-lactate dehydrogenase	328906321	Prop012_43	42855	43820 +	B	1952 L-lactate dehydrogenase (EC:1.1.1.27); K00016 L-lactate dehydrog
hypothetical protein	HMPPREF0675_5012	L-lactate dehydrogenase	328906321	Prop012_43	42855	43820 +	B	1952 L-lactate dehydrogenase (EC:1.1.1.27); K00016 L-lactate dehydrog
cation diffusion facilitator family transporter	HMPPREF0675_5011	cytidine and deoxycytidylate deaminase zinc-b	328906320	Prop012_42	40695	41534 +	B	5011 cation diffusion facilitator family transporter (db=KEGG)
cytidine and deoxycytidylate deaminase zinc-binding region	HMPPREF0675_5010	cytidine and deoxycytidylate deaminase zinc-b	328906319	Prop012_40	40140	40598 +	C	cytidine and deoxycytidylate deaminase zinc-binding region; K01493 dCM
dihydroxyacetone kinase, phosphotransfer subunit	HMPPREF0675_5009	PTS protein, putative dihydroxyacetone kinase	328906318	Prop012_39	39586	40017 +	C	PTS protein, putative dihydroxyacetone kinase phosphotransfer protein (c
dihydroxyacetone kinase, L subunit(EC:2.7.1.-)	HMPPREF0675_5008	dihydroxyacetone kinase, L subunit	328906317	Prop012_38	38936	39589 +	B	5008 dhac; dihydroxyacetone kinase, L subunit (EC:2.7.-.-); K05879 dihy
dihydroxyacetone kinase, DhaK subunit(EC:2.7.1.-)	HMPPREF0675_5007	dihydroxyacetone kinase, DhaK subunit	328906316	Prop012_37	37947	38948 +	B	1947 hypothetical protein; K05878 dihydroxyacetone kinase, N-terminal
transporter, major facilitator family protein	HMPPREF0675_5006	membrane protein, putative permease	328906315	Prop012_36	37458	37856 +	C	transporter, major facilitator family protein (db=KEGG eval=9.0e-67 bi
transporter, major facilitator family protein	HMPPREF0675_5005	membrane protein, putative permease	328906314	Prop012_35	36614	36913 +	E	GENE: 36719..37018 - (rbs_motif=None rbs_spacer=None)
1,4-dihydroxy-2-naphthoate octaprenyltransferase(EC:2.5.-	HMPPREF0675_5004	ABC transporter, ATP-binding protein	328906313	Prop012_34	35488	36375 +	B	5005 menA; 1,4-dihydroxy-2-naphthoate octaprenyltransferase (EC:2.5.-
hypothetical protein	HMPPREF0675_5003	ABC transporter, ATP-binding protein	328906312	Prop012_33	35269	35445 +	D	TPRSCAN: seg (db=Seg db_id=seg from 14 to=23)
ABC transporter, ATP-binding protein	HMPPREF0675_5002	ABC transporter, ATP-binding protein	328906161	Prop012_32	34360	35058 +	B	5004 ABC transporter, ATP-binding protein (db=KEGG)
hypothetical protein	HMPPREF0675_5001	ABC transporter, ATP-binding protein	328906159	Prop012_31	32073	34358 +	B	5003 hypothetical protein; K02004 (db=KEGG)
nuclease, RecB family	HMPPREF0675_5000	ABC transporter, ATP-binding protein	328906158	Prop012_30	30261	32048 +	B	5002 ABC transporter, ATP-binding protein (db=KEGG)
nuclease, RecB family	HMPPREF0675_4999	hypothetical protein	328906157	Prop012_29	29500	30117 +	B	5000 nuclease, RecB family (db=KEGG)
ubiquinone/menaquinone biosynthesis methyltransferase(E	HMPPREF0675_4998	nuclease, RecB family	328906156	Prop012_28	28849	28965 +	E	GENE: 28890..29006 - (rbs_motif=None rbs_spacer=None)
heme ABC exporter, ATP-binding protein CcmA	HMPPREF0675_4997	ubiquinone/menaquinone biosynthesis methylt	328906155	Prop012_27	27699	28367 +	B	4999 ubiE; ubiquinone/menaquinone biosynthesis methyltransferase (EC:
hypothetical protein	HMPPREF0675_4996	ABC transporter ATP-binding protein	328906309	Prop012_26	26945	27589 +	B	1942 ABC transporter ATP-binding protein (db=KEGG)
chorismate binding enzyme(EC:5.4.4.2)	HMPPREF0675_4995	putative membrane protein	328906308	Prop012_25	25215	26948 +	B	1941 ABC transporter permease (db=KEGG)
hypothetical protein	HMPPREF0675_4994	chorismate binding enzyme	328906307	Prop012_24	23925	25190 +	B	4996 chorismate binding enzyme; K02552 menaquinone-specific isochori
geranylgeranyl reductase family protein	HMPPREF0675_4993	hypothetical protein	328906306	Prop012_23	22463	23749 +	B	1938 putative electron transfer oxidoreductase (db=KEGG)
NADH-ubiquinone/plastoquinone oxidoreductase, chain 3(E	HMPPREF0675_4992	geranylgeranyl reductase family protein	328906304	Prop012_23	22463	23749 +	B	1938 putative electron transfer oxidoreductase (db=KEGG)
NADH-ubiquinone oxidoreductase chain B(EC:1.6.5.3)	HMPPREF0675_4991	NADH dehydrogenase subunit A	328906303	Prop012_22	21982	22389 +	C	NADH-ubiquinone/plastoquinone oxidoreductase, chain 3 (EC:1.6.9.53); i
NADH dehydrogenase, C subunit(EC:1.6.5.3)	HMPPREF0675_4990	NADH dehydrogenase subunit B	328906302	Prop012_21	21334	21891 +	B	1937 NADH dehydrogenase subunit B (EC:1.6.5.3); K00331 NADH dehyd
NADH dehydrogenase subunit D(EC:1.6.5.3)	HMPPREF0675_4989	NADH dehydrogenase subunit C	328906301	Prop012_20	20507	21337 +	B	1934 NADH dehydrogenase subunit C (EC:1.6.5.3); K00332 NADH dehyd
NADH-quinone oxidoreductase, E subunit(EC:1.6.5.3)	HMPPREF0675_4988	NADH dehydrogenase subunit D	328906300	Prop012_19	19206	20507 +	B	1933 NADH dehydrogenase subunit D (EC:1.6.5.3); K00333 NADH dehyd
NADH oxidoreductase (quinone), F subunit(EC:1.6.5.3)	HMPPREF0675_4987	NADH dehydrogenase subunit E	328906299	Prop012_18	18424	19209 +	B	4989 nuoE; NADH-quinone oxidoreductase, E subunit; K00334 NADH dehy
NADH dehydrogenase (quinone), G subunit(EC:1.6.5.3)	HMPPREF0675_4986	NADH dehydrogenase I chain F	328906298	Prop012_17	17093	18427 +	B	1931 NADH dehydrogenase I chain F (EC:1.6.5.3); K00335 NADH dehydr
NADH dehydrogenase(EC:1.6.5.3)	HMPPREF0675_4985	NADH dehydrogenase subunit G	328906297	Prop012_16	14658	17096 +	B	1930 NADH dehydrogenase subunit G (EC:1.6.5.3); K00336 NADH dehyd
NADH-ubiquinone oxidoreductase chain L(EC:1.6.5.3)	HMPPREF0675_4984	NADH dehydrogenase	328906296	Prop012_15	13339	14661 +	B	1929 NADH dehydrogenase subunit H (EC:1.6.5.3); K00337 NADH dehyd
proton-translocating NADH-quinone oxidoreductase, chain	HMPPREF0675_4983	NADH-ubiquinone oxidoreductase, chain I	328906295	Prop012_14	12764	13339 +	B	4985 NADH-quinone oxidoreductase, chain I; K00338 NADH dehydrogen
proton-translocating NADH-quinone oxidoreductase, chain	HMPPREF0675_4982	NADH-ubiquinone/plastoquinone oxidoreducta	328906294	Prop012_13	11907	12767 +	B	1926 NADH dehydrogenase subunit J (EC:1.6.5.3); K00339 NADH dehyd
proton-translocating NADH-quinone oxidoreductase, chain	HMPPREF0675_4981	NADH dehydrogenase subunit K	328906293	Prop012_12	11611	11910 +	C	NADH-ubiquinone oxidoreductase chain K (EC:1.6.5.3); K00340 NADH dehy
proton-translocating NADH-quinone oxidoreductase, chain	HMPPREF0675_4980	NADH dehydrogenase subunit L	328906292	Prop012_11	9714	11057 +	B	1924 NADH dehydrogenase subunit L (EC:1.6.5.3); K00341 NADH dehyd
polyprenyl synthetase(EC:2.5.1.30)	HMPPREF0675_4979	NADH dehydrogenase subunit M	328906291	Prop012_10	8203	9696 +	B	1923 NADH dehydrogenase subunit M (EC:1.6.5.3); K00342 NADH dehyd
precorrin-6A synthase (deacytylating)(EC:2.1.1.152)	HMPPREF0675_4978	proton-translocating NADH-quinone oxidoredu	328906290	Prop012_9	6590	8206 +	B	1922 NADH dehydrogenase subunit N (EC:1.6.5.3); K00343 NADH dehyd
HcpH/HpaI aldolase/citrate lyase family protein(EC:4.1.3.6	HMPPREF0675_4977	heptaprenyl diphosphate synthase component	328906289	Prop012_8	5424	6398 +	B	4978 polyprenyl synthetase; K00805 heptaprenyl diphosphate synthase [
hypothetical protein	HMPPREF0675_4976	precorrin-6A synthase	328906288	Prop012_7	4601	5385 +	B	1920 precorrin-6A synthase; K02228 precorrin-6A synthase (EC:2.1.1.15
hypothetical protein	HMPPREF0675_4975	citrate lyase beta chain	328906287	Prop012_6	3633	4466 +	B	1919 citrate lyase beta chain (EC:4.1.3.6); K01644 citrate lyase subunit I
hypothetical protein	HMPPREF0675_4974	hypothetical protein	328906286	Prop012_5	3061	3612 +	C	hypothetical protein (db=KEGG eval=1.0e-28 bit_score=129.0)
ABC transporter, ATP-binding protein	HMPPREF0675_4973	hypothetical protein	328906285	Prop012_4	2796	3101 +	C	hypothetical protein (db=KEGG eval=3.0e-27 bit_score=123.0)
hypothetical protein	HMPPREF0675_4972	ABC transporter, ATP-binding protein	328906185	Prop012_3	1405	2799 +	B	4973 hypothetical protein (db=KEGG)
hypothetical protein	HMPPREF0675_4971	ABC transporter, ATP-binding protein	328906185	Prop012_2	1465	1307 +	B	1915 ABC transporter, ATP-binding protein; K01990 ABC-2 type transpor
hypothetical protein	HMPPREF0675_4970	hypothetical protein	328906185	Prop012_1	223	465 +	C	hypothetical protein (db=KEGG eval=3.0e-34 bit_score=147.0)
hypothetical protein	HMPPREF0675_4969	hypothetical protein	328906185	Prop012_1	223	465 +	C	hypothetical protein (db=KEGG eval=3.0e-34 bit_score=147.0)
ABC transporter, ATP-binding protein(EC:3.6.3.-)	HMPPREF0675_4968	hypothetical protein	328906286	Prop021_7	5019	5459 +	C	hypothetical protein (db=KEGG eval=1.0e-45 bit_score=184.0)
efflux ABC transporter, permease protein	HMPPREF							

2-oxoglutarate oxidoreductase, beta subunit(EC:1.2.7.3)	HMPPREF0675_4962	2-oxoglutarate ferredoxin oxidoreductase subu	328906275	Prop0222_3	2622	3707 +	B	1905 2-oxoglutarate ferredoxin oxidoreductase subunit beta; K0175 2-o
2-oxoglutarate oxidoreductase, alpha subunit(EC:1.2.7.3)	HMPPREF0675_4961	2-oxoglutarate oxidoreductase, alpha subunit	328906274	Prop0222_4	3709	5805 +	B	1904 pyruvate:ferredoxin oxidoreductase (alpha subunit); K0174 2-oxo
hypothetical protein	HMPPREF0675_4960	hypothetical protein	328906272	Prop0222_5				
NADH ubiquinone oxidoreductase, 20 Kd subunit	HMPPREF0675_4959	NADH ubiquinone oxidoreductase, 20 Kd subu	328906271	Prop0222_6	5824	6222 +	C	NADH ubiquinone oxidoreductase, 20 Kd subunit (db=KEGG evalua=7.0e
respiratory-chain NADH dehydrogenase, 30 Kd subunit	HMPPREF0675_4958	NADH dehydrogenase subunit	328906270	Prop0222_7	6219	6833 +	C	respiratory-chain NADH dehydrogenase, 30 Kd subunit (db=KEGG evalua
4Fe-4S binding domain protein	HMPPREF0675_4957	NADH dehydrogenase subunit	328906269	Prop0222_8	6830	7138 +	C	4Fe-4S binding domain protein (db=KEGG evalua=4.0e-44 bit_score=17
hypothetical protein	HMPPREF0675_4956	putative membrane protein	328906268	Prop0222_9	7135	8724 +	B	2956 hypothetical protein (db=KEGG
iron dependent repressor, N-terminal DNA binding domain	HMPPREF0675_4955	ABC transporter ATP-binding protein	328906267	Prop0222_10	8741	9415 +	C	Mn-dependent transcriptional regulator; K03709 DtxR family tran
anchored repeat-type ABC transporter, permealase subunit	HMPPREF0675_4954	anchored repeat-type ABC transporter, ATP-bir	328906266	Prop0222_11	9322	10263 +	C	iron/manganese/zinc ABC transporter inner membrane subunit; K09819
anchored repeat-type ABC transporter, ATP-binding subunit	HMPPREF0675_4953	periplasmic solute binding protein	328906265	Prop0222_12	10260	11000 +	C	ABC transporter-like protein; K09820 manganese/iron transport syst
enoyl-CoA hydratase/isomerase family protein(EC:4.2.1.17	HMPPREF0675_4952	exodeoxyribonuclease III	328906264	Prop0222_13	10997	11917 +	B	nop:ROP_70570 mmiC; manganese ABC transporter manganese-binding f
exodeoxyribonuclease III(EC:3.1.11.2)	HMPPREF0675_4951	exodeoxyribonuclease III	328906263	Prop0222_14	12036	13049 +	B	4955 enoyl-CoA hydratase/isomerase family protein; K01692 enoyl CoA I
(tRNA)	HMPPREF0675_4950	exodeoxyribonuclease III	328906262	Prop0222_15	13051	13944 +	B	1898 exodeoxyribonuclease III(EC:3.1.11.2); K01142 exodeoxyribonuc
(tRNA)	HMPPREF0675_4949	exodeoxyribonuclease III	328906261	Prop0222_16	13997	14311 +	E	acetyltransferase (db=KEGG evalua=4.0e-15 bit_score=83.6 iden
ribosomal protein L33	HMPPREF0675_4948	exodeoxyribonuclease III	328906260	Prop0222_17	14339	14863 +	E	GENE: 44816.45340 - (rbs_motif=None rbs_spacer=None)
UDP-N-acetylenolpyruvoylglucosamine reductase, C-termin	HMPPREF0675_4947	exodeoxyribonuclease III	328906259	Prop0222_18				
aminotransferase, class I/II	HMPPREF0675_4946	exodeoxyribonuclease III	328906258	Prop0222_19				
(tRNA)	HMPPREF0675_4945	exodeoxyribonuclease III	328906257	Prop0222_20				
preprotein translocase, SecE subunit	HMPPREF0675_4944	exodeoxyribonuclease III	328906256	Prop0222_21				
transcription termination/antitermination factor NusG	HMPPREF0675_4943	exodeoxyribonuclease III	328906255	Prop0222_22				
ribosomal protein L11	HMPPREF0675_4942	exodeoxyribonuclease III	328906254	Prop0222_23				
ribosomal protein L1	HMPPREF0675_4941	exodeoxyribonuclease III	328906253	Prop0222_24				
hypothetical protein	HMPPREF0675_4940	hypothetical protein	328906252	Prop0222_25				
ribosomal protein L10	HMPPREF0675_4939	ribosomal protein L10	328906251	Prop0222_26				
ribosomal protein L7/L12	HMPPREF0675_4938	ribosomal protein L7/L12	328906250	Prop0222_27				
DNA-directed RNA polymerase, beta subunit(EC:2.7.7.6)	HMPPREF0675_4937	DNA-directed RNA polymerase, beta subunit	328906249	Prop0222_28				
DNA-directed RNA polymerase, beta' subunit(EC:2.7.7.6)	HMPPREF0675_4936	DNA-directed RNA polymerase, beta' subunit	328906248	Prop0222_29				
actinobacterial surface-anchored protein	HMPPREF0675_4935	actinobacterial surface-anchored protein	328906247	Prop0222_30				
hypothetical protein	HMPPREF0675_4934	hypothetical protein	328906246	Prop0222_31				
hypothetical protein	HMPPREF0675_4933	hypothetical protein	328906245	Prop0222_32				
ribosomal protein S12	HMPPREF0675_4932	ribosomal protein S12	328906244	Prop0222_33				
ribosomal protein S7	HMPPREF0675_4931	ribosomal protein S7	328906243	Prop0222_34				
translation elongation factor G(EC:3.6.5.3)	HMPPREF0675_4930	translation elongation factor G	328906242	Prop0222_35				
hypothetical protein	HMPPREF0675_4929	hypothetical protein	328906241	Prop0222_36				
hypothetical protein	HMPPREF0675_4928	hypothetical protein	328906240	Prop0222_37				
hypothetical protein	HMPPREF0675_4927	hypothetical protein	328906239	Prop0222_38				
translation elongation factor Tu(EC:3.6.5.3)	HMPPREF0675_4926	elongation factor Tu	328906238	Prop0222_39				
hypothetical protein	HMPPREF0675_4925	membrane-spanning protein	328906237	Prop0222_40				
Tat (twin-arginine translocation) pathway signal sequence(	HMPPREF0675_4924	2',3'-cyclic-nucleotide 2'-phosphodiesterase pr	328906236	Prop0222_41				
glutamine--tRNA ligase(EC:6.1.1.18)	HMPPREF0675_4923	glutamyl--tRNA synthetase	328906235	Prop0222_42				
glutamate--tRNA ligase(EC:6.1.1.17)	HMPPREF0675_4922	glutamate--tRNA ligase	328906234	Prop0222_43				
hypothetical protein	HMPPREF0675_4921	hypothetical protein	328906233	Prop0222_44				
hypothetical protein	HMPPREF0675_4920	hypothetical protein	328906232	Prop0222_45				
hypothetical protein	HMPPREF0675_4919	hypothetical protein	328906231	Prop0222_46				
6-carboxyhexanoate--CoA ligase(EC:2.3.1.147)	HMPPREF0675_4918	6-carboxyhexanoate--CoA ligase	328906230	Prop0222_47				
ribosomal protein S10	HMPPREF0675_4917	30S ribosomal protein S10	328906229	Prop0222_48				
50S ribosomal protein L3	HMPPREF0675_4916	50S ribosomal protein L3	328906228	Prop0222_49				
ribosomal protein L4/L1 family	HMPPREF0675_4915	ribosomal protein L4/L1 family	328906227	Prop0222_50				
ribosomal protein L23	HMPPREF0675_4914	50S ribosomal protein L23	328906226	Prop0222_51				
ribosomal protein L2	HMPPREF0675_4913	50S ribosomal protein L2	328906225	Prop0222_52				
ribosomal protein S19	HMPPREF0675_4912	30S ribosomal protein S19	328906224	Prop0222_53				
ribosomal protein L22	HMPPREF0675_4911	50S ribosomal protein L22	328906223	Prop0222_54				
ribosomal protein S3	HMPPREF0675_4910	30S ribosomal protein S3	328906222	Prop0222_55				
ribosomal protein L16	HMPPREF0675_4909	ribosomal protein L16	328906221	Prop0222_56				
ribosomal protein L29	HMPPREF0675_4908	50S ribosomal protein L29	328906220	Prop0222_57				
30S ribosomal protein S17	HMPPREF0675_4907	30S ribosomal protein S17	328906219	Prop0222_58				
hypothetical protein	HMPPREF0675_4906	hypothetical protein	328906218	Prop0222_59				
hypothetical protein	HMPPREF0675_4905	hypothetical protein	328906217	Prop0222_60				
ribosomal protein L14	HMPPREF0675_4904	50S ribosomal protein L14	328906216	Prop0222_61				
ribosomal protein L24	HMPPREF0675_4903	50S ribosomal protein L24	328906215	Prop0222_62				
ribosomal protein L5	HMPPREF0675_4902	50S ribosomal protein L5	328906214	Prop0222_63				
ribosomal protein S14p/S29e	HMPPREF0675_4901	50S ribosomal protein S14	328906213	Prop0222_64				
ribosomal protein S8	HMPPREF0675_4900	50S ribosomal protein S8	328906212	Prop0222_65				
ribosomal protein L6	HMPPREF0675_4900	50S ribosomal protein L6	328906211	Prop0222_66				
ribosomal protein L18	HMPPREF0675_4899	50S ribosomal protein L18	328906210	Prop0222_67				
ribosomal protein S5	HMPPREF0675_4898	30S ribosomal protein S5	328906209	Prop0222_68				
ribosomal protein L30	HMPPREF0675_4897	50S ribosomal protein L30	328906208	Prop0222_69				
ribosomal protein L15	HMPPREF0675_4896	50S ribosomal protein L15	328906207	Prop0222_70				
ABC transporter, permealase protein	HMPPREF0675_4895	ABC transporter, permealase protein	328906206	Prop0222_71				
ABC transporter, permealase protein	HMPPREF0675_4894	ABC transporter, permealase protein	328906205	Prop0222_72				
ABC transporter, ATP-binding protein	HMPPREF0675_4893	ABC transporter, ATP-binding protein	328906204	Prop0222_73				
bacterial extracellular solute-binding protein, family 5	HMPPREF0675_4892	bacterial extracellular solute-binding protein, f	328906203	Prop0222_74				
hypothetical protein	HMPPREF0675_4891	hypothetical protein	328906202	Prop0222_75				
hypothetical protein	HMPPREF0675_4890	hypothetical protein	328906201	Prop0222_76				
bacterial extracellular solute-binding protein, family 5	HMPPREF0675_4889	bacterial extracellular solute-binding protein, f	328906200	Prop0222_77				
glycerophosphodiester phosphodiesterase family prot	HMPPREF0675_4888	hypothetical protein	328906199	Prop0222_78				
transporter, major facilitator family protein	HMPPREF0675_4887	hypothetical protein	328906198	Prop0222_79				
hypothetical protein	HMPPREF0675_4886	hypothetical protein	328906197	Prop0222_80				
preprotein translocase, SecY' subunit	HMPPREF0675_4885	preprotein translocase subunit SecY'	328906196	Prop0222_81				
Adenylyl kinase(EC:2.7.4.3)	HMPPREF0675_4884	adenylate kinase	328906195	Prop0222_82				
methionine aminopeptidase, type I(EC:3.4.11.18)	HMPPREF0675_4883	methionine aminopeptidase, type I	328906194	Prop0222_83				
hypothetical protein	HMPPREF0675_4882	hypothetical protein	328906193	Prop0222_84				
hypothetical protein	HMPPREF0675_4881	hypothetical protein	328906192	Prop0222_85				
translation initiation factor IF-1	HMPPREF0675_4880	translation initiation factor IF-1	328906191	Prop0222_86				
ribosomal protein L36	HMPPREF0675_4879	hypothetical protein	328906190	Prop0222_87				
hypothetical protein	HMPPREF0675_4878	hypothetical protein	328906189	Prop0222_88				
30S ribosomal protein S13	HMPPREF0675_4877	30S ribosomal protein S13	328906188	Prop0222_89				
30S ribosomal protein S11	HMPPREF0675_4876	30S ribosomal protein S11	328906187	Prop0222_90				
ribosomal protein S4	HMPPREF0675_4875	30S ribosomal protein S4	328906186	Prop0222_91				
DNA-directed RNA polymerase, alpha subunit(EC:2.7.7.6)	HMPPREF0675_4874	DNA-directed RNA polymerase, alpha subunit	328906185	Prop0222_92				
ribosomal protein L17	HMPPREF0675_4873	ribosomal protein L17	328906184	Prop0222_93				
glycosyltransferase, group 1 family protein	HMPPREF0675_4872	glycosyltransferase, group 1 family protein	328906183	Prop0222_94				
hypothetical protein	HMPPREF0675_4871	hypothetical protein	328906182	Prop0222_95				
transporter, major facilitator family protein	HMPPREF0675_4870	transporter, major facilitator family protein	328906181	Prop0222_96				
hypothetical protein	HMPPREF0675_4869	hypothetical protein	328906180	Prop0222_97				
glycosyl hydrolase family 35(EC:3.2.1.23)	HMPPREF0675_4868	glycosyl hydrolase family 35	328906179	Prop0222_98				
superoxide dismutase(EC:1.15.1.1)	HMPPREF0675_4867	superoxide dismutase	328906178	Prop0222_99				
putative ABC-type multidrug transport system, ATPase com	HMPPREF0675_4866	ABC transporter, ATP-binding protein	328906177	Prop0222_100				
hypothetical protein	HMPPREF0675_4865	hypothetical protein	328906176	Prop0222_101				
oxidoreductase, short chain dehydrogenase/reductas	HMPPREF0675_4864	oxidoreductase, short chain dehydrogena	328906175	Prop0222_102				
hypothetical protein	HMPPREF0675_4863	hypothetical protein	328906174	Prop0222_103				
ABC transporter, ATP-binding protein	HMPPREF0675_4862	ABC transporter, ATP-binding protein	328906173	Prop0222_104				
putative Transmembrane component SCO2323 of energizin	HMPPREF0675_4861	cobalt transport protein	328906172	Prop0222_105				
methyltransferase small domain protein	HMPPREF0675_4860	methyltransferase small domain protein	328906171	Prop0222_106				
trRNA pseudouridine synthase A	HMPPREF0675_4859	trRNA pseudouridine synthase A	328906170	Prop0222_107				

RNA pseudouridine synthase A (EC:5.4.99.12) tRNA (guanine-N(7)-)-methyltransferase (EC:2.1.1.133)	HMPPREF0675_4866 HMPPREF0675_4867	methyltransferase hypothetical protein	328906178 328906177	Prop222_100 Prop222_101	97093 93717	+ B	1808 methyltransferase; K03439 tRNA (guanine-N7-)-methyltransferase
hypothetical protein	HMPPREF0675_4865			Prop222_101	98126	98482 +	E GENE: 198121.198477 + (rbs_motif=None rbs_spacer=None)
hypothetical protein	HMPPREF0675_4864	hypothetical protein	328906176	Prop222_102 Prop222_103	98583 99720	99478 + 100667 +	B C 4662 hypothetical protein (db=KEGG hypothetical protein (db=KEGG evalua=3.0e-104 bit_score=381.6
glycosyl hydrolase family 85 hypothetical protein	HMPPREF0675_4863 HMPPREF0675_4862	hypothetical protein	328906175				
ribosomal protein L13	HMPPREF0675_4861	S05 ribosomal protein L13	328906174	Prop222_104	101124	101609 +	C rplM; S05 ribosomal protein L13; K02871 large subunit ribosomal protein
ribosomal protein S9	HMPPREF0675_4860	ribosomal protein S9	328906173	Prop222_105	101632	102153 +	C rpsL; S03 ribosomal protein S9; K02996 small subunit ribosomal protein
phosphoglucomutase (EC:5.4.2.10)	HMPPREF0675_4859	phosphoglucomutase/phosphomannomutase	328906172	Prop222_106	102494	103810 +	B rps01; phosphoglucomutase/phosphomannomutase; K03431 phosphoglu
hypothetical protein	HMPPREF0675_4858	hypothetical protein	328906171	Prop222_107	103821	104588 +	C UniRef90_01YEZO Putative uncharacterized protein n=1 Tax=Propioniba
pantothenate kinase (EC:2.7.1.33)	HMPPREF0675_4857	pantothenate kinase	328906170	Prop222_108	104626	105636 +	B 1799 pantothenate kinase (EC:2.7.1.33); K00867 type 1 pantothenate ki
triacylglycerol lipase (EC:3.1.1.3) triacylglycerol lipase (EC:3.1.1.3) hypothetical protein	HMPPREF0675_4856 HMPPREF0675_4855 HMPPREF0675_4854	triacylglycerol lipase triacylglycerol lipase triacylglycerol lipase	328906168 328907228 328906167	Prop222_109 Prop222_109 Prop222_110	105739 106755 +		B 1796 triacylglycerol lipase precursor (EC:3.1.1.3); K01046 triacylglycerol
glutamine-fructose-6-phosphate transaminase (isomerizing)	HMPPREF0675_4853	D-fructose-6-phosphate amidotransferase	328906166	Prop222_110	106936	108783 +	B 4853 glmS; glutamine-fructose-6-phosphate transaminase (isomerizing)
putative histidine transport ATP-binding protein hspC (EC:3.1.HMPPREF0675_3665		ABC transporter, ATP-binding protein	328906165				
		ABC-type transport system, permease protein	328906164	Prop222_111 Prop222_112 Prop222_113 Prop222_114	108849 109619 110268 110951	109622 + 110284 + 110927 + 111880 +	B C C C 4ba3;LeuB_0353 ABC transporter related; K10041 putative glutamine trans amino acid permease protein SP0710; K10040 putative glutamine amino acid ABC transporter; permease protein; K02029 polar amino acid UniRef90_D0WRFX CjaA protein n=1 Tax=Actinomyces sp. oral ta
putative holo-[acyl-carrier-protein] synthase (EC:2.7.HMPPREF0675_4852 YjeF C-terminal domain family protein glycosyltransferase, group 1 family protein (EC:2.4.1.-)	HMPPREF0675_4852 HMPPREF0675_4851 HMPPREF0675_4850	hypothetical protein hypothetical protein hypothetical protein	328906164 328906163 328906162	Prop222_115 Prop222_116	112670 114186	114515 + 115325 +	B C C 1792 hypothetical protein (db=KEGG) 4850 glycosyltransferase, group 1 family protein (EC:2.4.-); K12583 ph
ABC transporter, ATP-binding protein hypothetical protein hypothetical protein hypothetical protein DEAD/DEAH box helicase DEAD/DEAH box helicase hypothetical protein ATPase, YjeF family universal bacterial protein YeaZ ribosomal-protein-alanine acetyltransferase (EC:2.3.1.128 putative glycoproteinase GCP (EC:3.4.24.57)	HMPPREF0675_4849 HMPPREF0675_4848 HMPPREF0675_4847 HMPPREF0675_4846 HMPPREF0675_4845 HMPPREF0675_4844 HMPPREF0675_4843 HMPPREF0675_4842 HMPPREF0675_4841 HMPPREF0675_4840 HMPPREF0675_4839	hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein hypothetical protein	328906161 328906160 328906159 328906158 328906158 328906158 328906157 328906156 328906155 328906154 328906153	Prop222_117 Prop222_118 Prop222_119 Prop222_120 Prop222_121 Prop222_122 Prop222_123 Prop222_124	115681 116872 117523 118006 118894 119784 121974 120449 120898 121394	116565 + 117183 + 117978 + 118719 + 119784 + 119784 + 120452 + 120898 + 121394 +	D E C C C C C C C C C IPRSCAN: seg (db=Seg db_id=seg from=16 to=40) GENE: 179420.179731 + (rbs_motif=None rbs_spacer=None) 4825 guaB; inosine-5'-monophosphate dehydrogenase (EC:1.1.2.05); K 4843 hypothetical protein (db=KEGG) 4842 ATPase, YjeF family; K06925 (db=KEGG) 4841 yeaZ; universal bacterial protein YeaZ (db=KEGG) rmlI; ribosomal-protein-alanine acetyltransferase; K03789 ribosomal-p 4839 putative glycoproteinase GCP; K01409 D-sialoglycoprotein endopepti
hydrolase, NUDIX family (EC:3.6.1.-)	HMPPREF0675_4838	hydrolase, NUDIX family	328906152 328906151 328906150 328906149 328906148 328906147	Prop222_125 Prop222_126	123608 124291	123402 + 124291 +	B C C C C C pPr:PFREUD_11360 pepC (Blmh); aminopeptidase C (bleomycin h 1781 putative 7,8-dihydro-8-oxoguanine-triphosphatase; K03574 7,8-di
periplasmic binding protein iron chelate uptake ABC transporter, FeCT family, per ABC transporter, ATP-binding protein (EC:3.6.3.34)	HMPPREF0675_4837 HMPPREF0675_4836 HMPPREF0675_4835 HMPPREF0675_4834	periplasmic binding protein periplasmic binding protein periplasmic binding protein periplasmic binding protein	328906147 328906146 328906145 328906144	Prop222_127 Prop222_128 Prop222_129 Prop222_130	124313 124738 + 124924 126201	124738 + 126153 + 127028 + 127137	C C C C hypothetical protein (db=KEGG evalua=2.0e-57 bit_score=224

arginine deiminase (EC:3.5.3.6)	HMPREF0675_4764	membrane family protein	328906078						
hypothetical protein	HMPREF0675_4764	arginine deiminase	3289060804	Prop022_190	200178	201389 +	B	sna:SnaS_6447 arginine deiminase (EC:3.5.3.6); K01478 arginine	
hypothetical protein	HMPREF0675_4763	putative adhesion protein	328906077	Prop022_191	201416	201835 +	C	hypothetical protein (db=KEGG evalua=1.0e-49 bit_score=197.0 identity	
hypothetical protein		putative adhesion protein	328906076						
hypothetical protein		putative adhesion protein	328906075						
hypothetical protein		thrombospondin type 3 repeat protein	328906074						
hypothetical protein		thrombospondin type 3 repeat protein	328906073						
septum formation protein Maf	HMPREF0675_4762	septum formation protein Maf	328906072	Prop022_192	201876	202469 +	B	1709 Maf-like protein; K06287 septum formation protein (db=KEGG)	
hypothetical protein	HMPREF0675_4760	Maf-like protein	328906071						
carboxyl transferase domain protein(EC:6.4.1.3)	HMPREF0675_4759	hypothetical protein	328906070	Prop022_193	202519	202737 +	C	hypothetical protein (db=KEGG evalua=1.0e-30 bit_score=134.0 identity	
hypothetical protein	HMPREF0675_4758	carboxyl transferase domain protein	328906069	Prop022_194	202749	204323 +	B	4759 carboxyl transferase domain protein; K01966 propionyl-CoA carbox	
hypothetical protein	HMPREF0675_4757	putative BirA bifunctional protein	328906068	Prop022_195	202573	205355 +	B	1705 putative BirA bifunctional protein; K03524 BirA family transcriptions	
peptidase family S51	HMPREF0675_4756	peptidase family S51	328906067	Prop022_196	205403	206119 +	B	4756 peptidase family S51 (db=KEGG)	
Tat (twin-arginine translocation) pathway signal sequence	HMPREF0675_4755	Tat pathway signal sequence domain protein	328906066	Prop022_197	206106	206645 +	C	hypothetical protein (db=KEGG evalua=8.0e-48 bit_score=192.0 identity	
phosphoribosylaminimidazole carboxylase, ATPase subunit	HMPREF0675_4754	phosphoribosylaminimidazole carboxylase, A1	328906065	Prop022_198	207081	208253 +	B	4754 purK; phosphoribosylaminimidazole carboxylase, ATPase subunit (	
phosphoribosylaminimidazole carboxylase, catalytic subunit	HMPREF0675_4753	phosphoribosylaminimidazole carboxylase, ca	328906064	Prop022_199	208246	208836 +	C	purE; phosphoribosylaminimidazole carboxylase, catalytic subunit; K015	
beta galactosidase small chain(EC:3.2.1.23)	HMPREF0675_4752	beta galactosidase small chain	328906062						
putative transcriptional regulator	HMPREF0675_4749	putative transcriptional regulator	328906061	Prop022_200	208909	211881 +	B	4752 beta galactosidase small chain (db=KEGG)	
hypothetical protein	HMPREF0675_4750	succinoglycan biosynthesis protein ExoA	328906060	Prop022_201	212154	213077 +	B	4749 putative transcriptional regulator (db=KEGG)	
conserved hypothetical protein TIGR03089	HMPREF0675_4748	hypothetical protein	328906059	Prop022_202	213555	214589 +	B	1698 succinoglycan biosynthesis protein ExoA (db=KEGG)	
hypothetical protein	HMPREF0675_4746	hypothetical protein	328906058	Prop022_203	214592	215314 +	C	hypothetical protein (db=KEGG evalua=2.0e-89 bit_score=331.0 identity	
putative mannose-1-phosphate guanylyltransferase/mannose-6-phosphate guanylyltransferase	HMPREF0675_4747	putative mannose-1-phosphate guanylyltransf	328906057	Prop022_204	215391	216467 +	B	4747 putative mannose-1-phosphate guanylyltransferase/mannose-6-ph	
hypothetical protein	HMPREF0675_4745	hypothetical protein	328906056	Prop022_205	216464	217198 +	C	hypothetical protein (db=KEGG evalua=6.0e-44 bit_score=180.0 identity	
transcription factor WhiB	HMPREF0675_4744	hypothetical protein	328906055	Prop022_206	217347	217604 +	C	whiB_2; transcription factor WhiB (db=KEGG evalua=2.0e-41 bit_score=	
hypothetical protein	HMPREF0675_4743	putative glycosyl transferase	328906054	Prop022_207	217687	221106 +	B	1693 putative glycosyl transferase (db=KEGG)	
hypothetical protein	HMPREF0675_4742	hypothetical protein	328906053	Prop022_208	221250	222641 +	B	4742 hypothetical protein (db=KEGG)	
hypothetical protein	HMPREF0675_4741	hypothetical protein	328906052	Prop022_209	222654	223073 +	C	hypothetical protein (db=KEGG evalua=1.0e-64 bit_score=248.0 identity	
hypothetical protein	HMPREF0675_4740	hypothetical protein	328906051	Prop022_210	223150	223623 +	C	hypothetical protein (db=KEGG evalua=9.0e-53 bit_score=208.0 identity	
hypothetical protein	HMPREF0675_4739	hypothetical protein	328906050	Prop022_211	223634	223912 +	C	hypothetical protein (db=KEGG evalua=4.0e-29 bit_score=129.0 identity	
hypothetical protein	HMPREF0675_4738	hypothetical protein	328906049	Prop022_212	223909	224928 +	B	1688 hypothetical protein (db=KEGG)	
cation diffusion facilitator family transporter	HMPREF0675_4737	cation transport protein	328906048	Prop022_213	224925	225953 +	B	1687 cation transport protein (db=KEGG)	
3-dehydroquinate dehydratase, type II(EC:4.2.1.10)	HMPREF0675_4736	3-dehydroquinate dehydratase	328906047	Prop022_214	225950	226381 +	C	3-dehydroquinate dehydratase (EC:4.2.1.10); K03786 3-dehydroquinate	
hypothetical protein	HMPREF0675_4735	hypothetical protein	328906046	Prop022_215	226437	226763 +	C	hypothetical protein (db=KEGG evalua=1.0e-37 bit_score=158.0 identity	
RDD family protein	HMPREF0675_4734	RDD family protein	328906045	Prop022_216	226812	227597 +	B	4734 RDD family protein (db=KEGG)	
4-alpha-glucanotransferase	HMPREF0675_4733	4-alpha-glucanotransferase	328906044						
4-alpha-glucanotransferase	HMPREF0675_4732	4-alpha-glucanotransferase	328906043						
DNA-binding protein HU	HMPREF0675_4731	DNA-binding protein HU	328906042						
putative nicotinate phosphoribosyltransferase(EC:2.4.2.11)	HMPREF0675_4730	putative nicotinate phosphoribosyltransferase	328906041	Prop022_217	227620	229791 +	B	1683 4-alpha-glucanotransferase (amylomaltase) (EC:2.4.1.25); K00705	
ATP-dependent Clp protease adaptor protein ClpS	HMPREF0675_4729	ATP-dependent Clp protease adaptor protein C	328906040	Prop022_218	229893	230168 +	C	hup; DNA-binding protein HU; K03530 DNA-binding protein HU-beta (db	
NiR-like protein	HMPREF0675_4728	hypothetical protein	328906039	Prop022_219	230365	231705 +	B	4731 putative nicotinate phosphoribosyltransferase (EC:2.4.2.11); K0076	
ferrous iron transport protein B	HMPREF0675_4727	ferrous iron transport protein B	328906038	Prop022_220	231780	232073 +	C	clpS; ATP-dependent Clp protease adaptor protein ClpS; K06891 ATP-dep	
FecA domain protein	HMPREF0675_4726	ferrous iron transport protein A	328906037	Prop022_221	232070	232630 +	C	hypothetical protein (db=KEGG evalua=1.0e-67 bit_score=258.0 identity	
glutamate racemase(EC:5.1.1.3)	HMPREF0675_4725	glutamate racemase	328906036	Prop022_222	232634	233152 +	C	hypothetical protein (db=KEGG evalua=2.0e-64 bit_score=247.0 identity	
tRNA nucleotidyltransferase(EC:2.7.7.56)	HMPREF0675_4724	tRNA nucleotidyltransferase	328906035	Prop022_223	233176	235140 +	B	1677 ferrous iron transport protein B; K04759 ferrous iron transport prot	
non-canonical purine NTP pyrophosphatase, RdgB/HAM1 family	HMPREF0675_4723	non-canonical purine NTP pyrophosphatase, R	328906034	Prop022_224	235193	235516 +	C	ferrous iron transport protein A (db=KEGG evalua=3.0e-38 bit_score=16	
thymidylate synthase(EC:2.1.1.45)	HMPREF0675_4722	thymidylate synthase	328906033	Prop022_225	235618	236541 +	B	1675 glutamate racemase (EC:5.1.1.3); K01776 glutamate racemase [EC	
dihydrofolate reductase(EC:1.5.1.3)	HMPREF0675_4721	dihydrofolate reductase	328906032	Prop022_226	236618	237352 +	B	4724 rph; tRNA nucleotidyltransferase (EC:2.7.7.56); K00989 ribonuclea	
ImpB/MucB/SamB family protein(EC:2.7.7.7)	HMPREF0675_4720	ImpB/MucB/SamB family protein	328906031	Prop022_227	237349	237963 +	B	4723 rdgB; non-canonical purine NTP pyrophosphatase, RdgB/HAM1 fami	
hypothetical protein		hypothetical protein	328906030	Prop022_228	237905	238777 +	B	4722 thya; thymidylate synthase (EC:2.1.1.45); K00560 thymidylate syn	
hypothetical protein		hypothetical protein	328906029	Prop022_229	238818	239288 +	C	folA; dihydrofolate reductase (EC:1.5.1.3); K00287 dihydrofolate reduct	
transcriptional regulator, RpiR family	HMPREF0675_4719	transcriptional regulator, RpiR family	328906028						
thrombospondin type 3 repeat protein	HMPREF0675_4718	thrombospondin type 3 repeat protein	328906027	Prop022_230	239285	240700 +	B	1670 DNA polymerase IV (EC:2.7.7.7); K02346 DNA polymerase IV [EC:	
hypothetical protein	HMPREF0675_4717	hypothetical protein	328906026						
hypothetical protein	HMPREF0675_4716	hypothetical protein	328906025						
hypothetical protein	HMPREF0675_4715	hypothetical protein	328906024						
hypothetical protein	HMPREF0675_4714	hypothetical protein	328906023	Prop022_231	241389	241985 +	C	hypothetical protein (db=KEGG evalua=2.0e-53 bit_score=211.0 identity	
hypothetical protein	HMPREF0675_4713	hypothetical protein	328906022	Prop022_232	242116	243609 +	D	IPRSCAN: seg (db=Seg db_id=seg from=16 to=31)	
hypothetical protein	HMPREF0675_4712	hypothetical protein	328906021						
hypothetical protein	HMPREF0675_4711	hypothetical protein	328906020						
hypothetical protein	HMPREF0675_4710	hypothetical protein	328906019	Prop022_233	243679	244689 +	D	IPRSCAN: seg (db=Seg db_id=seg from=16 to=31)	
hypothetical protein	HMPREF0675_4709	hypothetical protein	328906018						
hypothetical protein	HMPREF0675_4708	hypothetical protein	328906017	Prop022_234	244751	245299 +	D	IPRSCAN: seg (db=Seg db_id=seg from=17 to=46)	
hypothetical protein	HMPREF0675_4707	hypothetical protein	328906016						
hypothetical protein	HMPREF0675_4706	hypothetical protein	328906015	Prop022_235	245399	246424 +	D	IPRSCAN: seg (db=Seg db_id=seg from=10 to=25)	
hypothetical protein	HMPREF0675_4705	hypothetical protein	328906014	Prop022_236	246568	247437 +	D	IPRSCAN: seg (db=Seg db_id=seg from=10 to=37)	
hypothetical protein	HMPREF0675_4704	hypothetical protein	328906013	Prop022_237	247424	248896 +	C	ABC transporter related protein; K02006 cobalt/nickel transport system A	
hypothetical protein	HMPREF0675_4703	hypothetical protein	328906012	Prop022_238	248880	249767 +	C	transport system permease protein (db=KEGG evalua=3.0e-11 bit_score	
hypothetical protein	HMPREF0675_4702	hypothetical protein	328906011	Prop022_239	249764	250906 +	C	achAcl_2131 ATPase associated with various cellular activities (db=KEG	
hypothetical protein	HMPREF0675_4701	hypothetical protein	328906010	Prop022_240	250966	251796 +	C	hypothetical protein (db=KEGG evalua=3.0e-33 bit_score=145.0 identity	
hypothetical protein	HMPREF0675_4700	hypothetical protein	328906009	Prop022_241	251780	252286 +	D	IPRSCAN: TPKK_C (db=HMMPfam db_id=PF12555 from=16 to=41)	
hypothetical protein	HMPREF0675_4699	hypothetical protein	328906008	Prop022_242	252277	253248 +	C	von Willebrand factor, type A (db=KEGG evalua=2.0e-28 bit_score=	
hypothetical protein	HMPREF0675_4698	hypothetical protein	328906007	Prop022_243	253245	254195 +	C	von Willebrand factor, type A precursor; K07114 (db=KEGG evalua	
hypothetical protein	HMPREF0675_4697	hypothetical protein	328906006	Prop022_244	254192	255007 +	D	IPRSCAN: coiled-coil (db=Coil db_id=coil from=97 to=118 evalua	
hypothetical protein	HMPREF0675_4696	hypothetical protein	328906005	Prop022_245	255062	256015 +	C	hypothetical protein (db=KEGG evalua=1.0e-24 bit_score=117.0 identity	
hypothetical protein	HMPREF0675_4695	hypothetical protein	328906004						
hypothetical protein	HMPREF0675_4694	hypothetical protein	328906003						
hypothetical protein	HMPREF0675_4693	hypothetical protein	328906002						
hypothetical protein	HMPREF0675_4692	hypothetical protein	328906001						
hypothetical protein	HMPREF0675_4691	hypothetical protein	328906000						
hypothetical protein	HMPREF0675_4690	hypothetical protein	328905999						
hypothetical protein	HMPREF0675_4689	hypothetical protein	328905998						
hypothetical protein	HMPREF0675_4688	hypothetical protein	328905997						
hypothetical protein	HMPREF0675_4687	hypothetical protein	328905996						
hypothetical protein	HMPREF0675_4686	hypothetical protein	328905995						
hypothetical protein	HMPREF0675_4685	hypothetical protein	328905994						
hypothetical protein	HMPREF0675_4684	hypothetical protein	328905993						
hypothetical protein	HMPREF0675_4683	hypothetical protein	328905992						
hypothetical protein	HMPREF0675_4682	hypothetical protein	328905991						
hypothetical protein	HMPREF0675_4681	hypothetical protein	328905990						
hypothetical protein	HMPREF0675_4680	hypothetical protein	328905989						
hypothetical protein	HMPREF0675_4679	hypothetical protein	328905988						
hypothetical protein	HMPREF0675_4678	hypothetical protein	328905987						
hypothetical protein	HMPREF0675_4677	hypothetical protein	328905986						
hypothetical protein	HMPREF0675_4676	hypothetical protein	328905985						
hypothetical protein	HMPREF0675_4675	hypothetical protein	328905984						
hypothetical protein	HMPREF0675_4674	hypothetical protein	328905983						
hypothetical protein	HMPREF0675_4673	hypothetical protein	328905982						
hypothetical protein	HMPREF0675_4672	hypothetical protein	328905981						
hypothetical protein	HMPREF0675_4671	hypothetical protein	328905980						
hypothetical protein	HMPREF0675_4670	hypothetical protein	328905979						
hypothetical protein	HMPREF0675_4669	hypothetical protein	328905978						
hypothetical protein	HMPREF0675_4668	hypothetical protein	328905977						
hypothetical protein	HMPREF0675_4667	hypothetical protein	328905976						
hypothetical protein	HMPREF0675_4666	hypothetical protein	328905975						
hypothetical protein	HMPREF0675_4665	hypothetical protein	328905974						
hypothetical protein	HMPREF0675_4664	hypothetical protein	328905973						
hypothetical protein	HMPREF0675_4663	hypothetical protein	328905972						
hypothetical protein	HMPREF0675_4662	hypothetical protein	328905971						
hypothetical protein	HMPREF0675_4661	hypothetical protein	328905970						
hypothetical protein	HMPREF0675_4660	hypothetical protein	328905969						
hypothetical protein	HMPREF0675_4659	hypothetical protein	328905968						
hypothetical protein	HMPREF0675_4658	hypothetical protein	328905967						
hypothetical protein	HMPREF0675_4657	hypothetical protein	328905966						
hypothetical protein	HMPREF0675_4656	hypothetical protein	328905965						
hypothetical protein	HMPREF0675_4655	hypothetical protein	328905964						
hypothetical protein	HMPREF0675_4654	hypothetical protein	328905963						
hypothetical protein	HMPREF0675_4653	hypothetical protein	328905962						
hypothetical protein									

		Prop099_11	13183	13692 +		hypothetical protein STP_0944 [Streptococcus parauberis KCTC 1
		Prop099_12	13745	15001 +		putative major facilitator family transporter (Streptomyces collini
		Prop099_13	14991	16676 +		antibiotic dehydratase domain-containing protein [Micromonospora
		Prop099_14	16789	17265 +		antibiotic dehydratase domain-containing protein [Micromonospora
		Prop099_15	17256	18434 +		Hypothetical protein
		Prop099_16	18477	19055 -		4"-phosphopantetheinyl transferase [Frankia sp. Eu1c1] gb ADP71
		Prop099_17	19060	19344 -		Hypothetical protein
		Prop099_18	19349	20614 -		type III restriction system endonuclease [Actinomyces urogenitalis
		Prop099_19	20611	21264 -		hypothetical protein Asphe3_22290 [Arthrobacter phenanthrenivorus
		Prop099_20	21261	21515 -		prophage regulatory protein (Streptomyces sp. SPB78) gb EFL001
		Prop099_21	21747	22628 +		putative AraC family transcriptional regulator [Microbacterium phos
		Prop099_22	22831	23910 +		hypothetical protein Asphe3_22350 [Arthrobacter phenanthrenivorus
		Prop099_23	23910	24473 +		hypothetical protein BinB_03562 [Brevibacterium linens BL2]
(tRNA)	HMPREF0675_4684	Prop019_1	/length=269924 /%G+C=62.77 /description=[Propionibacterium]			
		Prop019_2	351	716 +	C	putative bifunctional primase/DNA polymerase protein (db=KEGG
		Prop019_3	617	997 +	D	IPRSCAN: seg (db=Seg db_id=seg from:10 to=39)
		Prop019_4	1714	1878 +	D	IPRSCAN: seg (db=Seg db_id=seg from:10 to=31)
		Prop019_5	1976	2836 +	C	hypothetical protein (db=KEGG eval=1.0e-85 bit_score=319.0
		Prop019_6	2843	3853 +	B	kse:Ksed_06610 ParB-like nuclease; K03497 chromosome partic
ABC transporter, ATP-binding protein	HMPREF0675_5002	Prop019_7	3885	4574 +	C	hypothetical protein (db=KEGG eval=6.0e-53 bit_score=210.0
hypothetical protein	HMPREF0675_3179	Prop019_8	8758	9036 +	D	IPRSCAN: seg (db=Seg db_id=seg from:59 to=77)
hypothetical protein	HMPREF0675_3696	Prop019_9	5858	6229 +	C	metalloendopeptidase-like membrane protein (db=KEGG eval=
		Prop019_10	6226	6492 +	D	IPRSCAN: seg (db=Seg db_id=seg from:19 to=41)
		Prop019_11	7306	7626 +	C	hypothetical protein (db=KEGG eval=7.0e-37 bit_score=155.0
		Prop019_12	7657	8763 +	B	kse:Ksed_06740 hypothetical protein (db=KEGG
		Prop019_13	8758	9036 +	D	IPRSCAN: seg (db=Seg db_id=seg from:1 to=21)
		Prop019_14	9043	10503 +	B	kse:Ksed_06750 hypothetical protein (db=KEGG
		Prop019_15	10507	11361 +	C	hypothetical protein (db=KEGG eval=1.0e-34 bit_score=150.0
		Prop019_16	11445	12224 +	C	hypothetical protein (db=KEGG eval=3.0e-61 bit_score=238.0
		Prop019_17	12221	13705 +	B	mlu:Mut_00150 hypothetical protein (db=KEGG
		Prop019_18	14266	14666 +	C	hypothetical protein with heat repeat (db=KEGG eval=4.0e-26
		Prop019_19	14263	16044 +	B	mlu:Mut_00130 hypothetical protein (db=KEGG
		Prop019_20	16127	16567 +	C	single-strand binding protein family (db=KEGG eval=2.0e-50 bi
		Prop019_21	16579	17148 +	C	hypothetical protein (db=KEGG eval=1.0e-64 bit_score=248.0
		Prop019_22	17154	17363 +	E	GENE: 8399-8608 + (rbs_motif=GGAG/GAGG rbs_spacer=5-10bp
		Prop019_23	17541	19316 +	B	pfr:PFREUD_17960 recombinase (db=KEGG
		Prop019_24	19414	20022 +	B	1642 oligoribonuclease (EC:3.1.1.~); K13288 oligoribonuclease (Ei
		Prop019_25	20096	21223 +	B	4682 transporter, major facilitator family protein (db=KEGG)
		Prop019_26	21561	22871 +	B	1640 hypothetical protein (db=KEGG)
		Prop019_27	22894	24759 +	B	1639 putative ABC transporter (db=KEGG)
		Prop019_28	24756	26366 +	B	1638 putative ABC transporter (db=KEGG)
		Prop019_29	26512	26979 +	C	single-strand binding family protein; K03111 single-strand DNA-binding p
		Prop019_30	27100	28785 +	B	1636 putative ABC transporter ATP-binding protein (db=KEGG)
		Prop019_31	29153	31244 +	B	1634 FAD-linked oxidoreductase/iron-sulfur cluster-binding protein; K069
		Prop019_32	32061	32609 +	C	MarR family transcriptional regulator (db=KEGG eval=6.0e-72 bit_scor
		Prop019_33	32761	34668 +	B	1632 putative long-chain fatty-acid CoA ligase (AMP-binding enzyme); KI
		Prop019_34	34665	35510 +	B	4670 acyl-CoA thioester hydrolase, YbgC/YbaW fami
		Prop019_35	35518	37191 +	B	1630 alpha-glucosidase/amyase family protein; K01187 alpha-glucosidas
		Prop019_36	37284	38732 +	B	1629 6-phosphogluconate dehydrogenase (EC:1.1.1.44); K00033 6-phos
		Prop019_37	39000	40118 +	C	hypothetical protein (db=KEGG eval=4.0e-91 bit_score=338.0
		Prop019_38	40305	40487 +	C	hypothetical protein (db=KEGG eval=8.0e-21 bit_score=102.0 identity
		Prop019_39	40574	43168 +	B	1627 aminopeptidase N (EC:3.4.11.2); K01256 aminopeptidase N (EC:3.
		Prop019_40	43410	44961 +	B	DsbA-like thioredoxin (db=KEGG eval=7.0e-69 bit_score=262.1
		Prop019_41	44088	45662 +	B	cmi:CMH_0460 hypothetical protein (db=KEGG)
		Prop019_42	45780	48002 +	B	1626 ligA; NAD-dependent DNA ligase LigA (EC:6.5.1.2); K01972 DNA lig
		Prop019_43	48103	49392 +	B	4662 hypothetical protein (db=KEGG)
		Prop019_44	49464	49937 +	C	ribose 5-phosphate isomerase (EC:5.3.1.6); K01808 ribose 5-phosphat
		Prop019_45	49926	50165 +	C	hypothetical protein (db=KEGG eval=8.0e-21 bit_score=102.0 identity
		Prop019_46	50263	51081 +	B	4659 putative formamido-pyrimidine-DNA glycosylase; K05522 endonucle
		Prop019_47	51108	52457 +	B	1622 hypothetical protein (db=KEGG)
		Prop019_48	52719	55964 +	B	1621 lysS; lysyl-tRNA synthetase (EC:6.1.1.6); K04567 lysyl-tRNA synth
		Prop019_49	56002	56943 +	B	1620 putative poly(3-hydroxyalkanoate) depolymerase (EC:3.1.1.~); K01
		Prop019_50	57361	57804 +	C	hypothetical protein (db=KEGG eval=5.0e-21 bit_score=103.0 identity
		Prop019_51	58079	59326 +	B	afn:Acrer_2043 peptidase T (EC:3.4.11.4); K01258 tripeptide ami
		Prop019_52	59570	61183 +	B	4642 tig; trigger factor (EC:5.2.1.8); K03545 trigger factor (db=KEGG)
		Prop019_53	61288	62631 +	B	4641 hypothetical protein (db=KEGG)
		Prop019_54	62848	63318 +	B	1573 ATP-dependent Clp protease proteolytic subunit 1 (EC:3.4.21.92);
		Prop019_55	63326	64015 +	B	1572 ATP-dependent Clp protease proteolytic subunit 2 (EC:3.4.21.92);
		Prop019_56	64220	65512 +	B	4638 ctpX; ATP-dependent Clp protease, ATP-binding subunit ClpX; K035-
		Prop019_57	65515	65898 +	E	GENE: 56683..57266 - (rbs_motif=AGGAGG rbs_spacer=5-10bp)
		Prop019_58	65949	69209 +	B	4637 WD40-like protein (db=KEGG)
		Prop019_59	69678	72293 +	B	1568 valS; valyl-tRNA synthetase (EC:6.1.1.9); K01873 valyl-tRNA synth
		Prop019_60	72404	73198 +	B	1567 hypothetical protein (db=KEGG)
		Prop019_61	73284	73778 +	C	hypothetical protein (db=KEGG eval=4.0e-76 bit_score=286.0 identity
		Prop019_62	73888	74706 +	C	hypothetical protein (db=KEGG eval=4.0e-73 bit_score=278.0
		Prop019_63	74794	75510 +	B	1565 6-phosphogluconolactonase (EC:3.1.1.31); K01057 6-phosphogluc
		Prop019_64	75528	76457 +	B	4631 putative OpcA protein (db=KEGG)
		Prop019_65	76467	78071 +	B	1563 glucose-6-phosphate 1-dehydrogenase (EC:1.1.1.49); K00036 gluc
		Prop019_66	78180	79289 +	B	1561 membrane protein, putative heme O synthase; K02301 protoheme
		Prop019_67	79668	80813 +	B	krh:KRH_21570 cytochrome P450 (EC:1.14.~) (db=KEGG)
		Prop019_68	81804	82478 +	C	putative ABC transporter-associated permease; K09686 antibiotic transp
		Prop019_69	82570	83310 +	C	4624 ABC transporter, ATP-binding protein; K09687 antibiotic transport s
		Prop019_70	83354	85837 +	B	4623 putative V-type H(+)-translocating pyrophosphatase; K01507 inorg
		Prop019_71	86354	87376 +	B	1555 MalR repressor protein (db=KEGG)
		Prop019_72	87404	88309 +	B	4621 putative type IV conjugative transfer system protein TraI; K
		Prop019_73	88309	89913 +	B	4620 ABC transporter, permease protein; K01009 maltose/maltodextrin t
		Prop019_74	90017	91258 +	B	1552 putative periplasmic maltose-binding protein; K01008 malte
		Prop019_75	91570	92310 +	B	1550 ArsR family transcriptional regulator (db=KEGG)
		Prop019_76	92307	92755 +	B	1549 hypothetical protein; K09014 Fe-S cluster assembly protein SuB (d
		Prop019_77	93807	95015 +	B	1548 hypothetical protein; K09015 Fe-S cluster assembly protein SuD (d
		Prop019_78	95015	95338 +	C	Rieske (2Fe-2S) domain protein; K05710 ferredoxin subunit of phenylpro
		Prop019_79	95338	95338 +	C	Rieske (2Fe-2S) domain protein; K05710 ferredoxin subunit of phenylpro

Fe assembly ATPase SuFC	HMMPREF0675_4613	Fe assembly ATPase SuFC	328907698	Prop019_79	95345	96112 +	B	4613 sufc; Fe assembly ATPase SuFC; K09013 Fe-5 cluster assembly A
cytosine desulfurase(EC:2.8.1.7; EC:4.4.1.16)	HMMPREF0675_4612	cytosine desulfurase, SuFS family protein	328907697	Prop019_80	96115	97356 +	B	4612 cytosine desulfurase(EC:2.8.1.7); K11717 cytosine desulfurase / su
SUF system FeS assembly protein, NiUF family	HMMPREF0675_4611	SUF system FeS assembly protein, NiUF family	328907696	Prop019_81	97353	97844 +	C	SUF system FeS assembly protein, NiUF family; K04488 iron/nitrogen fixation
PAa-like protein involved in Fe-S cluster assembly	HMMPREF0675_4610	hypothetical protein	328907695	Prop019_82	97844	98200 +	C	hypothetical protein (db=KEGG evalua=6.0e-57 bit_score=224.0 identity
Dicarboxylate carrier MatC domain protein Dicarboxylate carrier MatC domain protein hypothetical protein sodium ion-translocating decarboxylase, I putative acyl-CoA carboxylase, alpha sub hypothetical protein hypothetical protein carboxyl transferase			328907694					
			328907693					
			328907692					
			328907691					
			328907690					
			328907689					
			328907688					
			328907687					
			328907686	Prop019_83	98275	100287 +	B	4609 pyridine nucleotide-disulfide oxidoreductase; K10797 2-enoate red
			328907685	Prop019_84	100443	101315 +	C	hypothetical protein; K07054 (db=KEGG evalua=3.0e-54 bit_scor
pyridine nucleotide-disulfide oxidoreductase	HMMPREF0675_4609	putative 2-enoate reductase	328907684					
hypothetical protein acetyltransferase, GNAT family ABC transporter, ATP-binding protein hypothetical protein methyltransferase domain protein(EC:2.1.1.51) hypothetical protein hypothetical protein 3-oxoacyl-[acyl-carrier-protein] reductase(EC:1.1.1.100) enoyl-[acyl carrier protein] reductase(EC:1.3.1.19) hypothetical protein ABC transporter, ATP-binding protein(EC:3.6.3.34) modulation efficiency protein D putative stomatin/prohibitin-family membrane protease sub			328907683					
			328907682	Prop019_85	101327	102200 +	C	hypothetical protein (db=KEGG evalua=6.0e-48 bit_score=194.0 identity
			328907681	Prop019_86	102257	103855 +	B	1538 ABC transporter ATP binding protein (db=KEGG)
			328907680	Prop019_87	103924	104427 +	C	hypothetical protein (db=KEGG evalua=6.0e-35 bit_score=149.0
			328907679	Prop019_88	104450	105196 +	B	1536 putative resistance protein (db=KEGG)
			328907678	Prop019_89	105268	106039 +	B	4602 hypothetical protein (db=KEGG)
			328907677	Prop019_90	106131	106379 +	C	hypothetical protein (db=KEGG evalua=4.0e-36 bit_score=153.0 identity
			328907676	Prop019_91	106752	107273 +	C	3-oxoacyl-[acyl-carrier-protein] reductase(EC:1.1.1.100); K00509 3-oxo
			328907675	Prop019_92	107315	108088 +	E	4599 enoyl-[acyl carrier protein] reductase(EC:1.3.1.19); K02008 enoyl- GENE: 3.155 + (rbs_motif=None rbs_spacer=None)
			328907674	Prop019_93	108543	108826 +	D	IPRSKAN; seq (db=Seq db_id=seq from 38 to 49)
ABC transporter, ATP-binding protein(EC:3.6.3.34) modulation efficiency protein D putative stomatin/prohibitin-family membrane protease sub			328907673	Prop019_94	109049	109729 +	C	4597 ABC transporter, ATP-binding protein; K02013 iron complex transpo
			328907672	Prop019_95	109755	110219 +	C	hypothetical protein (db=KEGG evalua=6.0e-44 bit_score=179.0 identity
			328907671	Prop019_96	109755	110219 +	C	4595 putative stomatin/prohibitin-family membrane protease subunit Yst
			328907670	Prop019_97	110305	111573 +	B	
			328907669	Prop019_98	111744	112085 +	C	ArsR family transcriptional regulator (db=KEGG evalua=2.0e-18) major facilitator superfamily protein (db=KEGG evalua=1.0e-10)
			328907668	Prop019_99	112140	113093 +	C	4594 sodium bile acid symporter family protein; K14347 solute carrier fa
			328907667	Prop019_100	113998	114058 +	B	1526 RNA methylase family protein; K00599 [EC:2.1.1.-] (db=KEGG)
			328907666	Prop019_102	114940	115542 +	B	1525 polypeptide deformylase (EC:3.5.1.31); K01462 [EC:3.5.1.88] (db=
			328907665	Prop019_103	115669	116733 +	B	4591 hypothetical protein (db=KEGG)
	hypothetical protein	HMMPREF0675_4591	hypothetical protein	328907662	Prop019_104	116967	117593 +	C
hypothetical protein site-specific recombinase, phase integrase family			328907661	Prop019_105	117555	118490 +	B	1522 xerC; site-specific tyrosine recombinase XerC; K03733 integrase/re
			328907660	Prop019_106	118808	119662 +	B	1521 rpsB; 30S ribosomal protein S2; K02967 small subunit ribosomal pr
ribosomal protein S2	HMMPREF0675_4588	30S ribosomal protein S2	328907659	Prop019_106	118808	119662 +	B	1521 rpsB; 30S ribosomal protein S2; K02967 small subunit ribosomal pr
ribosomal binding factor Ts	HMMPREF0675_4587	ribosomal factor EF1B	328907657	Prop019_107	12510	12510 +	C	4597 tsf; translation initiation factor Ts; K02357 elongation factor Ts
UMP kinase(EC:2.7.4.22)	HMMPREF0675_4586	UMP kinase	328907656	Prop019_108	120746	121459 +	B	4586 pyrH; UMP kinase (EC:2.7.4.22); K09093 uridylyl transferase (EC:2.7
ribosome recycling factor	HMMPREF0675_4585	ribosome recycling factor	328907655	Prop019_109	121493	122942 +	C	1518 ribosome recycling factor; K02838 ribosome recycling factor (db=KE
phosphatidate cytidyltransferase(EC:2.7.7.41)	HMMPREF0675_4584	phosphatidate cytidyltransferase	328907654	Prop019_110	122059	122922 +	C	UniRef90_D4HDH0 Phosphatidate cytidyltransferase n=5 Tax=Propionib
hypothetical protein	HMMPREF0675_4583	hypothetical protein	328907653	Prop019_111	123006	123179 +	C	hypothetical protein (db=KEGG evalua=9.0e-11 bit_score=68.9 identity=
putative ABC transporter-annotated protein	HMMPREF0675_4582	putative ABC transporter-annotated protein	328907652	Prop019_112	140336	142906 +	B	1510 dihydroadipoyl transfer reductase (EC:1.3.1.26); K00215 dihydroadip
23S rRNA m2A2503 methyltransferase(EC:2.1.1.-)	HMMPREF0675_4581	crf family radical SAM enzyme	328907651	Prop019_113	123873	125120 +	B	4581 rlmN; 23S rRNA m2A2503 methyltransferase (EC:2.1.1.-); K06941
Glu/Leu/Phe/Val dehydrogenase, dimeric glutamate dehydrogenase hypothetical protein			328907650					
			328907649	Prop019_114	125207	126544 +	C	4580 NADP-specific glutamate dehydrogenase (EC:1.4.1.4); K00262 glut
NADP-specific glutamate dehydrogenase(EC:1.4.1.4)	HMMPREF0675_4580	glutamate dehydrogenase	328907648	Prop019_114	125207	126544 +	C	4580 NADP-specific glutamate dehydrogenase (EC:1.4.1.4); K00262 glut
hypothetical protein beta-lactamase			328907647	Prop019_115	126617	126706 +	E	GENE: 18494...18583 (- rbs_motif=None rbs_spacer=None)
			328907646	Prop019_116	126703	128073 +	B	1511 putative 6-aminohexanoate-dimer hydrolase (EC:3.5.1.46); K0145
1-deoxy-D-xylulose 5-phosphate reductoisomerase(EC:1.1.1.267)	HMMPREF0675_4577	1-deoxy-D-xylulose 5-phosphate reductoisomerase	328907645	Prop019_117	128172	129395 +	B	1510 1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC:1.1.1.267);
putative RIP metalloprotease RseP	HMMPREF0675_4576	putative RIP metalloprotease RseP	328907644	Prop019_118	129392	130669 +	B	4576 putative RIP metalloprotease RseP; K01417 [EC:3.4.24.-] (db=KEG
hypothetical protein putative transcriptional regulator			328907643					
			328907642	Prop019_119	130826	133432 +	B	cjkJk1043 nuch; putative extracellular nuclease; K07004 (db=KE
hypothetical protein	HMMPREF0675_4575	hypothetical protein	328907641	Prop019_120	133558	134700 +	B	1506 ispG, gcpE; 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthet
TENA/THI-4 family protein	HMMPREF0675_4574	hypothetical protein	328907640	Prop019_121	134702	135541 +	C	acetyltransferase, GNAT family; K06976 [EC:2.3.1.16] (db=KEGG
4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase(EC:2.3.1.16)	HMMPREF0675_4573	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	328907639	Prop019_121	134702	135541 +	C	1506 ispG, gcpE; 4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthet
acetyltransferase, GNAT family	HMMPREF0675_4572	acetyltransferase family protein	328907638	Prop019_122	136077	136934 +	B	1504 ABC transporter ATP-binding protein; K09819 manganese/iron tran
hypothetical protein putative lipoprotein			328907637					
			328907636	Prop019_122	136077	136934 +	B	1504 ABC transporter ATP-binding protein; K09819 manganese/iron tran
anchored repeat-type ABC transporter, permease subunit	HMMPREF0675_4571	anchored repeat-type ABC transporter, ATP-binding subunit	328907635	Prop019_123	136948	137791 +	B	1502 anchored repeat-type ABC transporter, ATP-binding subunit (db=KE
anchored repeat-type ABC transporter, ATP-binding subunit	HMMPREF0675_4570	anchored repeat-type ABC transporter, ATP-binding subunit	328907634	Prop019_124	137714	138823 +	C	4570 hypothetical protein (db=KEGG)
actinobacterial surface-anchored protein domain	HMMPREF0675_4569	actinobacterial surface-anchored protein domain	328907633	Prop019_125	138813	140339 +	B	1501 periplasmic solute binding protein (db=KEGG)
anchored repeat ABC transporter, substrate-binding protein	HMMPREF0675_4568	periplasmic solute binding protein	328907632	Prop019_126	140336	142906 +	B	1500 hypothetical protein (db=KEGG evalua=9.0e-11 bit_score=68.9 identity=
putative ABC transporter-annotated protein	HMMPREF0675_4567	putative ABC transporter-annotated protein	328907631	Prop019_127	143413	145158 +	B	1499 prolyl-tRNA synthetase (EC:6.1.1.15); K01881 prolyl-tRNA synthet
proline-tRNA ligase(EC:6.1.1.15)	HMMPREF0675_4566	proline-tRNA ligase	328907630	Prop019_128	145261	147022 +	B	1498 hypothetical protein (db=KEGG)
putative metallophosphoesterase	HMMPREF0675_4565	putative metallophosphoesterase	328907629	Prop019_129	147202	149727 +	C	1497 hypothetical protein; K07090 (db=KEGG)
hypothetical protein	HMMPREF0675_4564	putative membrane protein	328907628	Prop019_130	147959	148903 +	C	1494 nusA; transcription elongation factor NusA (db=KEGG)
hypothetical protein	HMMPREF0675_4563	putative lipoprotein	328907627	Prop019_131	149408	149564 +	B	1495 hypothetical protein; K07048 hypothetical protein (db=KEGG)
transcription termination factor NusA	HMMPREF0675_4562	transcription elongation factor NusA	328907626	Prop019_132	149586	150557 +	C	1494 nusA; transcription elongation factor NusA; K02600 N utilization su
hypothetical protein	HMMPREF0675_4560	hypothetical protein	328907625					
translation initiation factor IF-2	HMMPREF0675_4559	translation initiation factor IF-2	328907624	Prop019_133	151115	154015 +	B	4559 infB; translation initiation factor IF-2; K02519 translation initiation f
3-dehydroquinate synthase arabinose operon protein AraM phosphocarrier, HPr family			328907623					
			328907622	Prop019_134	154184	154705 +	E	GENE: 46061...46582 + (rbs_motif=None rbs_spacer=None)
PTS system, glucitol/sorbitol-specific IIA	HMMPREF0675_4557	PTS system, glucitol/sorbitol-specific IIA	328907614	Prop019_135	155065	155484 +	C	ABC transporter, ATP-binding protein (db=KEGG evalua=1.0e-73 bit_scor
PTS system, glucitol/sorbitol-specific IIB	HMMPREF0675_4556	PTS system, glucitol/sorbitol-specific IIB	328907613	Prop019_136	155342	155869 +	C	ABC transporter, permease protein (db=KEGG evalua=1.0e-73 bit_scor
PTS system, glucitol/sorbitol-specific IIC component	HMMPREF0675_4555	PTS system, glucitol/sorbitol-specific IIC component	328907612	Prop019_137	155964	156653 +	C	4556 putative type IV conjugative transfer system protein TrlA (db=KEGG
glucitol operon activator protein	HMMPREF0675_4554	putative membrane protein	328907611	Prop019_138	156650	157261 +	C	hypothetical protein (db=KEGG evalua=7.0e-76 bit_score=286.0 identity
PSD domain protein	HMMPREF0675_4553	ribosome-binding factor A	328907610	Prop019_139	157342	157779 +	C	rhfA; ribosome-binding factor A; K02834 ribosome-binding factor A (db=
hypothetical protein								
3-dehydroquinate synthase(EC:1.1.1.261)	HMMPREF0675_4552	3-dehydroquinate synthase	328907609	Prop019_140	157814	158710 +	B	1478 trfB; tRNA pseudouridine synthase B (EC:4.2.1.7); K03177 tRNA i
phosphocarrier, HPr family	HMMPREF0675_4551	phosphocarrier, HPr family	328907608	Prop019_141	159050	160393 +	C	4543 proV; glycine betaine/proline transporter ATP binding subunit; K02
PTS system, glucitol/sorbitol-specific IIA component	HMMPREF0675_4550	PTS system, glucitol/sorbitol-specific IIA component	328907607	Prop019_142	160393	161869 +	C	1476 glcX; glycine betaine transport system permease protein; K02001 glyci
PTS system, glucitol/sorbitol-specific IIC component	HMMPREF0675_4549	PTS system, glucitol/sorbitol-specific IIC component	328907606	Prop019_143	161308	162366 +	B	1475 putative substrate binding component of glycine/betaine transport syst
glucitol operon activator protein	HMMPREF0675_4548	glucitol operon activator protein	328907605	Prop019_144	162476	163407 +	C	1474 riboflavin biosynthesis protein RibF (riboflavin kinase); K11753 rib
hypothetical protein	HMMPREF0675_4547	hypothetical protein	328907604	Prop019_145	163904	164168 +	C	rpsD; ribosomal protein S15; K02956 small subunit ribosomal protein S1
cupin domain protein	HMMPREF0675_4546	cupin domain protein	328907603	Prop019_146	164623	166830 +	B	1471 polynucleotide phosphorylase/polyadenylase (EC:2.7.7.8); K09062
RNA pseudouridine synthase B(EC:4.5.99.12)	HMMPREF0675_4545	RNA pseudouridine synthase B	328907602	Prop019_147	167010	167750 +	B	1469 dihydroadipoyl transfer reductase (EC:1.3.1.26); K00215 dihydroadip
glycine betaine/L-proline transporter ATP binding subunit(EC:2.7.1.26; EC:2.7.2.2H)	HMMPREF0675_4544	putative glycine betaine/proline ABC transport	328907601	Prop019_148	167687	168587 +	C	1469 hypothetical protein (db=KEGG)
ABC transporter, substrate-binding protein, QAT family	HMMPREF0675_4543	substrate binding component of glycine/betaine	328907600	Prop019_149	168690	170429 +	C	4535 thiamine pyrophosphate enzyme; K00156 pyruvate dehydrogenase
riboflavin biosynthesis protein RibF(EC:2.7.1.26; EC:2.7.2.2H)	HMMPREF0675_4542	riboflavin biosynthesis protein RibF	328907599	Prop019_150	170550	171704 +	C	glyoxyl transferase, group 1 (db=KEGG evalua=1.0e-72 bit_scor
ribosomal protein S15	HMMPREF0675_4541	30S ribosomal protein S15	328907598	Prop019_151	171701	172053 +	C	1-lyxyl-sn-glycerol-3-phosphate acyltransferase(EC:2.3.1.51); K0
guanosine pentaphosphate synthetase I/polyribonucleotide diphosphocytidyl reductase(EC:1.3.1.26)	HMMPREF0675_4540	guanosine pentaphosphate synthetase I/polyri	328907597	Prop019_152	172302	174731 +	C	4534 Zn-dependent hydrolase, RNA-metabolizing, CpsF 100 kDa a
hypothetical protein	HMMPREF0675_4539	hypothetical protein	328907596	Prop019_153	174111	177605 +	B	kase=K22960 hypothetical protein (db=KEGG)
thiamine pyrophosphate enzyme(EC:1.2.2.2)	HMMPREF0675_4538	pyruvate dehydrogenase	328907595	Prop019_154	177806	180580 +	C	pfrPREUD_02950 helicase (db=KEGG)
hypothetical protein glyoxyl transferase, group 1 (db=KEGG evalua=1.0e-72 bit_scor			328907594	Prop019_155	180850	181056 +	D	hypothetical protein (db=KEGG evalua=4.0e-21 bit_score=103.0
			328907593	Prop019_156	181080	183749 +	C	amtAmet_4058 N-6 DNA methylase (db=KEGG)
Zn-dependent hydrolase, RNA-metabolizing, CpsF 100 kDa	HMMPREF0675_4537	Zn-dependent hydrolase	328907592	Prop019_157	183743	184972 +	C	type I restriction modification DNA specificity domain protein; K0
hypothetical protein hypothetical protein			328907591	Prop019_158	184969	188124 +	C	amtAmet_4056 HsdR family type I site-specific deoxyribonuclease
			328907590	Prop019_159	188117	188863 +	C	hypothetical protein; K07043 (db=KEGG evalua=2.0e-79 bit_scor
			328907589	Prop019_160	188856	190424 +	C	amtAmet_4054 hypothetical protein (db=KEGG)
			328907588	Prop019_161	190966	191655 +	C	Putative uncharacterized protein n=1Tax=Mobiliunz mulieris A1
			328907587	Prop019_162	191661	191906 +	C	hypothetical protein (db=KEGG evalua=1.0e-09 bit_score=65.5

[illegible]

NAD(+)/NADH kinase (EC:2.7.1.23)	HMPREF0675_4444	inorganic polyphosphate/ATP-NAD kinase	328907881	Prop017_287	312583	313518 +	B	1395 pgnK; inorganic polyphosphate/ATP-NAD kinase (EC:2.7.1.23); K00
DNA repair protein RecN	HMPREF0675_4443	DNA repair protein RecN	328907880	Prop017_286	310907	312586 +	B	1394 DNA repair protein RecN; K03631 DNA repair protein RecN (Recom
hypothetical protein	HMPREF0675_4442	hypothetical protein	328907879					
hypothetical protein	HMPREF0675_4441	hypothetical protein	328907878					
hypothetical protein	HMPREF0675_4440	hypothetical protein	328907877					
CTP synthase(EC:6.3.4.2)	HMPREF0675_4439	CTP synthase	328907876	Prop017_285	309145	310941 +	B	1390 pyrG; CTP synthetase (EC:6.3.4.2); K01937 CTP synthetase (EC:6.3.
hydrolase, NUDIX family	HMPREF0675_4438	putative ADP-ribose pyrophosphatase	328907875	Prop017_284	308489	309148 +	B	4438 hydrolase, NUDIX family; K01515 ADP-ribose pyrophosphatase (EC.
tyrosine recombinase XerD	HMPREF0675_4437	site-specific tyrosine recombinase XerD	328907874	Prop017_283	307572	308492 +	B	4437 xerD; tyrosine recombinase XerD; K04763 integrase/recombinase X
ColQ/ColB/Mind/ParA nucleotide binding domain protein	HMPREF0675_4436	sporulation initiation inhibitor protein Soj	328907873	Prop017_282	306558	307475 +	B	1387 chromosome partitioning protein; K03496 chromosome partitioning
hypothetical protein	HMPREF0675_4435	Smu178	328907872	Prop017_281	306211	306573 +	C	hypothetical protein (db=KEGG evalua=2.0e-38 bit_score=160.0 identity
pseudouridylate synthase(EC:5.4.99.12)	HMPREF0675_4434	pseudouridylate synthase	328907871	Prop017_280	305456	306193 +	B	4434 pseudouridylate synthase; K06178 ribosomal large subunit pseudou
peptidyl-prolyl cis-trans isomerase, FKBP-type(EC:5.2.1.8)	HMPREF0675_4433	peptidyl-prolyl cis-trans isomerase, FKBP-type	328907870	Prop017_279	304370	305446 +	B	1384 putative peptidyl-prolyl cis-trans isomerase (EC:5.2.1.8); K01802 p
putative glutamyl-queuosine tRNA(Asp) synthetase(EC:6.1.1.17)	HMPREF0675_4432	glutamyl-tRNA synthetase class Ic family prot	328907869	Prop017_278	303469	304308 +	B	1383 glutamyl-tRNA synthetase (EC:6.1.1.17); K01885 glutamyl-tRNA sy
hypothetical protein	HMPREF0675_4431	DeoR family transcriptional regulator	328907868	Prop017_277	302629	303231 +	B	1382 DeoR family transcriptional regulator; K13572 proteasome accesso
hypothetical protein	HMPREF0675_4430	transcriptional regulator	328907867	Prop017_276	301304	302272 +	B	1381 regulatory protein; K13573 proteasome accessory factor C (db=KE
hypothetical protein	HMPREF0675_4429	hypothetical protein	328907866	Prop017_275	301099	301302 +	C	hypothetical protein (db=KEGG evalua=7.0e-10 bit_score=66.2 identity=
twin arginine-targeting protein translocase, TatA/E family	HMPREF0675_4428	twin arginine-targeting protein translocase, Tat	328907865	Prop017_274	300772	301005 +	C	tatA; twin arginine-targeting protein translocase, TatA/E family; K03116
twin arginine-targeting protein translocase TatC	HMPREF0675_4427	twin arginine-targeting protein translocase Tat	328907864	Prop017_273	299870	300763 +	B	4427 tatC; twin arginine-targeting protein translocase TatC; K03118 sec
hypothetical protein	HMPREF0675_4426	diacylglycerol kinase catalytic region	328907863	Prop017_272	298938	299831 +	C	diacylglycerol kinase catalytic region; K07029 (db=KEGG evalua=
putative helicase(EC:3.6.1.-)	HMPREF0675_4425	putative helicase	328907862	Prop017_271	296149	298908 +	B	4425 putative helicase; K03727 ATP-dependent RNA helicase HelY (EC:3.
imidazoleglycerol phosphate synthase, cyclase subunit(EC:3.6.1.22)	HMPREF0675_4424	imidazoleglycerol phosphate synthase, cyclase	328907861	Prop017_270	295325	296086 +	B	4424 hisF; imidazoleglycerol phosphate synthase, cyclase subunit (EC:4.
histidine triad domain protein	HMPREF0675_4423	putative cell-cycle regulation histidine triad pr	328907860	Prop017_269	294870	295280 +	C	histidine triad domain protein; K02503 Hit-like protein involved in cell-cy
thiosulfine pyrophosphatase enzyme(EC:1.2.2.2)	HMPREF0675_4422	acetolactate synthase I large subunit	328907859	Prop017_268	292845	294650 +	C	aceA; acetolactate synthase I large subunit (EC:1.2.2.2)
hypothetical protein	HMPREF0675_4421	acetolactate synthase 1 catalytic subunit	328907858					
acetolactate synthase-like protein(EC:2.2.1.6)	HMPREF0675_4420	acetolactate synthase 3 regulatory subunit	328907857	Prop017_267	292337	292843 +	C	ilvI; acetolactate synthase 3 regulatory subunit (EC:2.2.1.6); K01653 ac
keto-alcohol reductoisomerase(EC:1.1.1.86)	HMPREF0675_4419	keto-alcohol reductoisomerase	328907856	Prop017_266	291247	292275 +	C	1359 ilvC; keto-alcohol reductoisomerase (EC:1.1.1.86); K00053 keto-
hypothetical protein	HMPREF0675_4418	cytidine/deoxycytidylate deaminase/NUDIX/mu	328907855	Prop017_265	290533	291162 +	B	1371 putative transferase (db=KEGG)
3-isopropylmalate dehydrogenase(EC:1.1.1.85)	HMPREF0675_4417	putative 3-isopropylmalate dehydrogenase	328907854	Prop017_264	289425	290483 +	B	pfr:PFREUD_13360 leuB; 3-isopropylmalate dehydrogenase (EC:1.1.1.85
putative 3-isopropylmalate dehydrogenase	HMPREF0675_4416	branched-chain-amino-acid transaminase	328907853	Prop017_263	288244	289335 +	B	1368 branched-chain amino acid aminotransferase (EC:2.6.1.42); K0082
branched-chain-amino-acid transaminase	HMPREF0675_4415	thymidine phosphorylase	328907852	Prop017_262	286864	288147 +	B	1367 dea; thymidine phosphorylase (EC:3.2.2.1); K01921 D-alanine-D-alan
pyrimidine nucleoside phosphorylase(EC:2.4.2.4)	HMPREF0675_4414	putative 2-hydroxyhepta-2,4-diene-1,7-dioate	328907851	Prop017_261	285982	286782 +	B	4414 FAH family protein (db=KEGG)
FAH family protein	HMPREF0675_4413	CAAX amino terminal protease family protein	328907850	Prop017_260	285020	285982 +	B	4413 CAAX amino terminal protease family protein; K07052 (db=KEGG)
CAAX amino terminal protease family protein	HMPREF0675_4412							
(rRNA)	HMPREF0675_4411							
transcriptional regulator, IctR family, C-terminal domain protein	HMPREF0675_4410	putative transcriptional regulator	328907849	Prop017_259	283803	284522 +	B	1364 putative transcriptional regulator (db=KEGG)
putative 3-isopropylmalate dehydratase large subunit	HMPREF0675_4409	3-isopropylmalate dehydratase, large subunit	328907848	Prop017_258	282261	283682 +	B	kfi:KflA_4859 3-isopropylmalate dehydratase, large subunit; K01703 3-is
hypothetical protein(EC:4.2.1.35,EC:4.2.1.33)	HMPREF0675_4407	3-isopropylmalate dehydratase small subunit	328907847	Prop017_257	281669	282259 +	C	leuD; 3-isopropylmalate dehydratase small subunit (3-isopropylmalate isom
acylttransferase	HMPREF0675_4406	acylttransferase	328907846	Prop017_256	280804	281580 +	B	1360 putative acyltransferase (db=KEGG)
D-alia D-alia ligase N-terminal domain protein(EC:6.3.2.4)	HMPREF0675_4405	D-alanine-D-alanine ligase	328907845	Prop017_255	279558	280275 +	B	1359 D-alanine-D-alanine ligase (EC:6.3.2.4); K01755 argininosuccin
hypothetical protein	HMPREF0675_4404	secreted protein	328907844	Prop017_254	279233	279648 +	C	hypothetical protein (db=KEGG evalua=5.0e-59 bit_score=229.0 identity
thiamine-phosphate kinase(EC:2.7.4.16)	HMPREF0675_4403	thiamine-phosphate kinase	328907843	Prop017_253	278174	279136 +	B	1357 thiamine monophosphate kinase (EC:2.7.4.16); K00946 thiamine-n
Cell division protein FtsK	HMPREF0675_4402	putative stage III sporulation protein E	328907841	Prop017_252	275477	277849 +	B	1356 FtsK/SpoIIIE protein; K03466 DNA segregation ATPase FtsK/SpoIII
hypothetical protein	HMPREF0675_4401	putative membrane protein	328907840	Prop017_251	275065	275343 +	C	protein of unknown function DUF805 (db=KEGG evalua=2.0e-08 bit_scor
			Prop017_250	274829	274993 +		E	GENE: 270474..270638 + (rbs_motif=AGGAG rbs_spacer=5-10bp
(rRNA)	HMPREF0675_4400							
peptide chain release factor 2	HMPREF0675_4399	peptide chain release factor 2	328907839	Prop017_249	273398	274579 +	B	4399 prfB; peptide chain release factor 2; K02836 peptide chain release f
cell division ATP-binding protein FtsE	HMPREF0675_4398	cell division ATP-binding protein FtsE	328907838	Prop017_248	272701	273387 +	B	4398 ftsE; cell division ATP-binding protein FtsE; K09812 cell division tra
efflux ABC transporter, permease protein	HMPREF0675_4397	cell division protein	328907837	Prop017_247	271766	272668 +	B	1352 cell division protein; K09811 cell division transport system permeas
SecA-binding protein	HMPREF0675_4396	SecA-binding protein	328907836	Prop017_246	271237	271719 +	B	1351 smbB; SecA-binding protein; K03654 SecA-binding protein (db=Keg
N-acetyl-gamma-glutamyl-phosphate reductase(EC:1.2.1.1)	HMPREF0675_4395	N-acetyl-gamma-glutamyl-phosphate reductas	328907835	Prop017_245	270083	271138 +	B	4395 argC; N-acetyl-gamma-glutamyl-phosphate reductase (EC:1.2.1.38
ArgJ family protein(EC:2.3.1.35,EC:2.3.1.1)	HMPREF0675_4394	glutamate N-acetyltransferase/amino-acid ace	328907834	Prop017_244	268905	270071 +	B	bfa:BfaE_21730 glutamate N-acetyltransferase/amino-acid acetyltransfer
acetylglutamate kinase(EC:2.7.2.8)	HMPREF0675_4393	acetylglutamate kinase	328907833	Prop017_243	267958	268908 +	B	4393 argB; acetylglutamate kinase (EC:2.7.2.8); K00930 acetylglutamin
acetylornithine transaminase(EC:2.6.1.11)	HMPREF0675_4392	aminotransferase, acetylornithine/succinylornit	328907832	Prop017_242	266766	267965 +	B	4392 acetylornithine transaminase (EC:2.6.1.11); K00818 acetylornithin
argininosuccinate lyase(EC:4.3.2.1)	HMPREF0675_4391	argininosuccinate lyase	328907831	Prop017_241	265934	266918 +	C	4391 argC; argininosuccinate lyase (EC:4.3.2.1); K01755 argininosuccin
hypothetical protein	HMPREF0675_4390	hypothetical protein	328907830	Prop017_240	264684	265217 +	C	hypothetical protein (db=KEGG evalua=3.0e-56 bit_score=220.0 identity
hypothetical protein	HMPREF0675_4389	hypothetical protein	328907829	Prop017_239	263975	264598 +	C	hypothetical protein (db=KEGG evalua=2.0e-75 bit_score=284.0 identity
hypothetical protein	HMPREF0675_4388	hypothetical protein	328907828					
hypothetical protein	HMPREF0675_4387	putative membrane protein	328907827					
hypothetical protein	HMPREF0675_4386	putative bacitracin transport ATP-binding	328907826					
hypothetical protein	HMPREF0675_4385	hypothetical protein	328907824					
hypothetical protein	HMPREF0675_4384	hypothetical protein	328907823					
hypothetical protein	HMPREF0675_4383	hypothetical protein	328907822					
hypothetical protein	HMPREF0675_4382	DNA restriction-modification system, DNA	328907821					
hypothetical protein	HMPREF0675_4381	putative type III restriction enzyme	328907820					
hypothetical protein	HMPREF0675_4380	putative type III restriction enzyme	328907819					
hypothetical protein	HMPREF0675_4379	hypothetical protein	328907818					
hypothetical protein	HMPREF0675_4378	hypothetical protein	328907817					
hypothetical protein	HMPREF0675_4377	hypothetical protein	328907816					
hypothetical protein	HMPREF0675_4376	hypothetical protein	328907815					
hypothetical protein	HMPREF0675_4375	hypothetical protein	328907814					
hypothetical protein	HMPREF0675_4374	hypothetical protein	328907813					
hypothetical protein	HMPREF0675_4373	hypothetical protein	328907812					
hypothetical protein	HMPREF0675_4372	hypothetical protein	328907811					
hypothetical protein	HMPREF0675_4371	hypothetical protein	Prop017_238	261967	263610 +		B	bbp:BBPR_0309 recombinase family protein (db=KEGG)
hypothetical protein	HMPREF0675_4370	hypothetical protein	Prop017_237	261219	261779 +		B	antirestriction ArdA family protein (db=KEGG evalua=2.0e-31 bit
hypothetical protein	HMPREF0675_4369	hypothetical protein	Prop017_236	260752	261174 +		B	GENE: 256397..256819 + (rbs_motif=GGAG/GAGG rbs_spacer=5-
hypothetical protein	HMPREF0675_4368	hypothetical protein	Prop017_235	259718	260170 +		D	IPRSCAN: seg (db=Seg db_id=seg from:14 to=28)
hypothetical protein	HMPREF0675_4367	hypothetical protein	Prop017_234	259503	259718 +		C	K063 family transcriptional regulator; K07222 putative transcrip
hypothetical protein	HMPREF0675_4366	hypothetical protein	Prop017_233	258786	259286 +		C	protein-tyrosine phosphatase, low molecular weight (db=KEGG e
hypothetical protein	HMPREF0675_4365	hypothetical protein	Prop017_232	257978	258643 +		C	hypothetical protein (db=KEGG evalua=3.0e-44 bit_score=181.0
hypothetical protein	HMPREF0675_4364	hypothetical protein						
hypothetical protein	HMPREF0675_4363	hypothetical protein						
hypothetical protein	HMPREF0675_4362	hypothetical protein						
hypothetical protein	HMPREF0675_4361	hypothetical protein						
hypothetical protein	HMPREF0675_4360	hypothetical protein						
hypothetical protein	HMPREF0675_4359	hypothetical protein						
hypothetical protein	HMPREF0675_4358	hypothetical protein						
hypothetical protein	HMPREF0675_4357	hypothetical protein						
hypothetical protein	HMPREF0675_4356	hypothetical protein						
hypothetical protein	HMPREF0675_4355	hypothetical protein						
hypothetical protein	HMPREF0675_4354	hypothetical protein						
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hypothetical protein	HMPREF0675_4339	hypothetical protein						
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hypothetical protein	HMPREF0675_4332	hypothetical protein						
hypothetical protein	HMPREF0675_4331	hypothetical protein						
hypothetical protein	HMPREF0675_4330	hypothetical protein						
hypothetical protein	HMPREF0675_4329	hypothetical protein						
hypothetical protein	HMPREF0675_4328	hypothetical protein						
hypothetical protein	HMPREF0675_4327	hypothetical protein						
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hypothetical protein	HMPREF0675_4325	hypothetical protein						
hypothetical protein	HMPREF0675_4324	hypothetical protein						
hypothetical protein	HMPREF0675_4323	hypothetical protein						
hypothetical protein	HMPREF0675_4322	hypothetical protein						
hypothetical protein	HMPREF0675_4321	hypothetical protein						
hypothetical protein	HMPREF0675_4320	hypothetical protein						
hypothetical protein	HMPREF0675_4319	hypothetical						

[illegible]

[illegible]

methylmalonyl-CoA epimerase(EC:5.1.99.1)	HMPREF0675_4166	methylmalonyl-CoA epimerase	328907374	Prop017_16	13672	14130	+	B	4166 mce; methylmalonyl-CoA epimerase (EC:5.1.99.1) (db=KEGG)
hypothetical protein	HMPREF0675_4165	putative adhesion/surface protein	328907373	Prop017_15	12191	13534	+	B	4165 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_4164	hypothetical protein	328907372	Prop017_14	11043	12077	+	B	1102 hypothetical protein; K07503 hypothetical protein (db=KEGG)
hydrolase, alpha/beta domain protein	HMPREF0675_4163	putative esterase/lipase YbFf	328907371	Prop017_13	10156	10968	+	B	1101 putative esterase/lipase YbFf (EC:3.1.1.-); K01175 [EC:3.1.1.-] (db=KEGG)
hypothetical protein(EC:5.2.1.8)	HMPREF0675_4162	peptidyl-prolyl cis-trans isomerase B	328907370	Prop017_12	9643	10146	+	C	hypothetical protein; K03768 peptidyl-prolyl cis-trans isomerase B (cydO) (db=KEGG)
hypothetical protein	HMPREF0675_4161	hypothetical protein	328907369						
hypothetical protein	HMPREF0675_4160	hypothetical protein	328907368	Prop017_11	8236	9255	+	B	4161 hypothetical protein (db=KEGG)
hypothetical protein	HMPREF0675_4159	molecular chaperone, HSP70 family	328907367	Prop017_10	6713	8200	+	B	cgI:NgI2295 gI2378; molecular chaperone (db=KEGG)
hypothetical protein	HMPREF0675_4158	putative membrane protein	328907366	Prop017_9	6412	6762	+	D	IPRSCAN: seq (db=Seq db, id=seq from=33 to=52)
putative uncharacterized protein, YigZ family	HMPREF0675_4157	putative membrane protein	328907365	Prop017_8	4962	6188	+	B	4159 hypothetical protein (db=KEGG)
putative uncharacterized protein, YigZ family	HMPREF0675_4156	hypothetical protein	328907365	Prop017_7	4621	4965	+	C	putative uncharacterized protein, YigZ family (db=KEGG eval=4.0e-28)
diacylglycerol kinase catalytic domain (presumed)	HMPREF0675_4155	hypothetical protein	328907365	Prop017_6	4318	4521	+	E	GENE: 43702..43905 + (rbs_motif=None rbs_spacer=None)
MTA/SAH nucleosidase(EC:3.2.2.9)	HMPREF0675_4154	diacylglycerol kinase catalytic region	328907364	Prop017_5	3359	4246	+	B	4157 diacylglycerol kinase catalytic domain (presumed); K07029 (db=KEGG)
Sua5/YciO/YrdC/YwIc family protein	HMPREF0675_4153	5'-methylthioadenosine/S-adenosylhomocysteine lyase	328907363	Prop017_4	2655	3329	+	B	1093 5'-methylthioadenosine/S-adenosylhomocysteine nucleoside; K01175
hypothetical protein	HMPREF0675_4152	Sua5/YciO/YrdC domain-containing protein	328907362	Prop017_3	1971	2591	+	B	4155 SUA5/YciO/YrdC/YwIc family protein; K07566 putative translation factor
pyrophosphate--fructose-6-phosphate 1-phosphotransferase	HMPREF0675_4151	hypothetical protein	328907361	Prop017_2	1739	1894	+	E	GENE: 41123..41278 - (rbs_motif=None rbs_spacer=None)
		pyrophosphate--fructose-6-phosphate 1-phosphotransferase	328907360	Prop017_1	152	1351	+	B	4153 pyrophosphate--fructose-6-phosphate 1-phosphotransferase (EC:2.7.1.12) (db=KEGG)

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Unplaced fragments:

						Prop009 /length=1133 /%G+C=64.34 /description=[Propionibacterium]												
Prop009_1						252	1133	+	B	mjI:mjIs_3211 integrase catalytic subunit (db=KEGG)								
										Prop011 /length=1403 /%G+C=68.49 /description=[Propionibacterium]								
transposase						328908013	Prop011_1	883	1395	+	C	tnpA; transposase (db=KEGG eval=6.0e-57 bit_score=222.0 id=100%)						
										Prop014 /length=9443 /%G+C=54.11 /Phase:								
methionine adenosyltransferase(EC:2.5.1.6)						HMPREF0675_4253	methionine adenosyltransferase		328907465	Prop014_1	45	1202	+	C	S-adenosylmethionine synthetase (EC:2.5.1.6); K00789 S-adenosylmethionine synthetase (db=KEGG eval=1.0e-96 bit_score=355.0)			
drug resistance MFS transporter, drug:H+ antiporter-2 (14:HMPREF0675_3896)							Prop014_2	1291	1863	+	C	hypothetical protein (db=KEGG eval=1.0e-96 bit_score=355.0)						
							Prop014_3	2094	4154	+	C	hypothetical protein; K09136 hypothetical protein (db=KEGG eval=1.0e-96 bit_score=355.0)						
							Prop014_4	4165	5517	+	B	UniRef90_D6L6Y0 Transporter, major facilitator family n=1 Tax=Parascarcinoma (db=KEGG eval=1.0e-96 bit_score=355.0)						
							Prop014_5	6225	6686	+	C	phage-associated protein (db=KEGG eval=1.0e-60 bit_score=2.0)						
							Prop014_6	6677	8053	+	C	phage-associated protein (db=KEGG eval=0.0 bit_score=761.0)						
							Prop014_7	8034	8312	+	C	hypothetical protein (db=KEGG eval=4.0e-34 bit_score=146.0)						
							Prop014_8	8452	9441	+	C	phage-associated protein (db=KEGG eval=4.0e-117 bit_score=94.0 id=100%)						
										Prop001 /length=3133 /%G+C=62.27 /description=[Propionibacterium]								
						putative lipoprotein	328906655	Prop001_1	244	1374	+	B	bbp:BBPR_1244 hypothetical protein (db=KEGG)					
						hypothetical protein	328906656	Prop001_2	1367	1819	+	B	hypothetical protein (db=KEGG eval=3.0e-25 bit_score=116.0)					
							Prop001_3	2073	2375	+	C	transposase for IS2404 (db=KEGG eval=2.0e-17 bit_score=91.0)						
							Prop001_4	2403	2723	+	C	transposase, IS4 (db=KEGG eval=3.0e-18 bit_score=94.0 id=100%)						

Prop004 /length=6779 /%G+C=58.45 /SEE MAIN CONTIG:

deoxyribose-phosphate aldolase(EC:4.1.2.4)	HMPREF0675_4279	deoxyribose-phosphate aldolase	328906416	Prop004_1	581	1231	+	C	deoxyribose-phosphate aldolase 1; K01619 deoxyribose-phosphate aldolase 1 (db=KEGG)
putative L-fucose:H+ symporter permease	HMPREF0675_4278	putative L-fucose:H+ symporter permease	328907491	Prop004_2	1233	2564	+	B	ahc:Arch_1731 L-fucose transporter; K02429 MFS transporter, FHS family (db=KEGG)
hypothetical protein	HMPREF0675_4277	hypothetical protein	328907490	Prop004_3	2592	3608	+	B	ahc:Arch_1730 hypothetical protein (db=KEGG)
ribokinase(EC:2.7.1.15)	HMPREF0675_4276	ribokinase	328907489	Prop004_4	3611	4537	+	B	ahc:Arch_1729 ribokinase; K00852 ribokinase (EC:2.7.1.15) (db=KEGG)
hypothetical protein	HMPREF0675_4281	hypothetical protein	328905738	Prop004_5	4627	5571	+	B	Prop004_5 [328905738] transcriptional repressor, CopG family (db=KEGG)
		#REF!	328907596	Prop004_6	5883	6227	+	C	Drug resistance transporter EmrB/QacA subfamily protein n=1 Tax=EmrB/QacA subfamily drug resistance transporter (db=KEGG eval=1.0e-96 bit_score=355.0)
			Prop004_7	6267	6602	+	C	EmrB/QacA subfamily drug resistance transporter (db=KEGG eval=1.0e-96 bit_score=355.0)	
			Prop004_8	6714	6779	+	C	GENE: 6714..6779 - (rbs_motif=None rbs_spacer=None)	

P. humerusii genome fragment - possibly a phage/plasmid?

hypothetical protein	328905702	
hypothetical protein	328905701	
hypothetical protein	328905700	
hypothetical protein	328905698	
hypothetical protein	328905697	
hypothetical protein	328905696	
hypothetical protein	328905695	
hypothetical protein	328905694	
putative integral membrane sensor protein	328905693	
putative peptidase	328905692	
transposase	328905691	
resolvase	328905690	
hypothetical protein	328905689	
hypothetical protein	328905688	
hypothetical protein	328905687	
hypothetical protein	328905686	
hypothetical protein	328905685	
hypothetical protein	328905684	
transcriptional regulator, CopG family	328905683	
hypothetical protein	328905682	
hypothetical protein	328905681	
toxin-antitoxin system, toxin component,	328905680	
hypothetical protein	328905679	
hypothetical protein	328905678	
hypothetical protein	328905677	
hypothetical protein	328905676	
putative permease	328905675	
hypothetical protein	328905674	
hypothetical protein	328905673	
hypothetical protein	328905672	
hypothetical protein	328905671	
hypothetical protein	328905670	
hypothetical protein	328905669	
hypothetical protein	328905668	
4'-phosphopantetheinyl transferase family	328905667	
2,3-diaminopropionate biosynthesis protein	328905666	
2,3-diaminopropionate biosynthesis protein	328905665	
AMP-binding enzyme	328905664	
AMP-binding enzyme	328905663	
putative thioesterase	328905662	
putative biotin carboxylase	328905661	
hypothetical protein	328905660	
hypothetical protein	328905659	
putative membrane protein	328905658	
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hypothetical protein	328905656	
hypothetical protein	328905655	
toxin-antitoxin system, toxin component,	328905654	
hypothetical protein	328905653	
hypothetical protein	328905652	
hypothetical protein	328905651	
plasmid partition protein ParA	328905650	
hypothetical protein	328905649	
plasmid stabilization system protein	328905648	
putative toxin-antitoxin system, antitoxin	328905647	
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hypothetical protein	328905643	
hypothetical protein	328905642	