

Supplementary Table 1. Protein encoding genes (PEGs) in the *Pectobacterium carotovorum* subsp. *carotovorum* ICMP 5702 genome

Protein encoding gene (peg)	Contig_id	Start	Stop	Strand	Function
<i>Pcc</i> ICMP5702_peg1	AODT01000001.1	220	2	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2	AODT01000003.1	1198	677	-	Molybdopterin-guanine dinucleotide biosynthesis protein MobB
<i>Pcc</i> ICMP5702_peg3	AODT01000003.1	1766	1188	-	Molybdenum cofactor guanylyltransferase (EC 2.7.7.77)
<i>Pcc</i> ICMP5702_peg4	AODT01000003.1	1980	2249	+	Protein YihD
<i>Pcc</i> ICMP5702_peg5	AODT01000003.1	2328	3314	+	YihE protein, a ser/thr kinase implicated in LPS synthesis and Cpx signalling
<i>Pcc</i> ICMP5702_peg6	AODT01000003.1	3339	3962	+	Periplasmic thiol:disulfide interchange protein DsbA
<i>Pcc</i> ICMP5702_peg7	AODT01000003.1	4341	7130	+	DNA polymerase I (EC 2.7.7.7)
<i>Pcc</i> ICMP5702_peg8	AODT01000003.1	8182	7547	-	GTP-binding protein EngB
<i>Pcc</i> ICMP5702_peg9	AODT01000003.1	8184	8375	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg10	AODT01000003.1	8386	8940	+	Der GTPase-activating protein YihI
<i>Pcc</i> ICMP5702_peg11	AODT01000003.1	8944	9114	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg12	AODT01000003.1	9262	10635	+	Coproporphyrinogen III oxidase, oxygen-independent (EC 1.3.99.22)
<i>Pcc</i> ICMP5702_peg13	AODT01000003.1	10695	10943	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg14	AODT01000003.1	11018	11131	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg15	AODT01000003.1	11246	11124	-	Uncharacterized protein YshB
<i>Pcc</i> ICMP5702_peg16	AODT01000003.1	12802	11390	-	Nitrogen regulation protein NR(I), GlnG (=NtrC)
<i>Pcc</i> ICMP5702_peg17	AODT01000003.1	13859	12810	-	Nitrogen regulation protein NtrB (EC 2.7.13.3)
<i>Pcc</i> ICMP5702_peg18	AODT01000003.1	13896	14039	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg19	AODT01000003.1	15561	14152	-	Glutamine synthetase type I (EC 6.3.1.2)
<i>Pcc</i> ICMP5702_peg20	AODT01000003.1	15931	17754	+	GTP-binding protein TypA/BipA
<i>Pcc</i> ICMP5702_peg21	AODT01000003.1	17917	18528	+	alpha-D-glucose 1-phosphate phosphatase YihX (EC 3.1.3.10)
<i>Pcc</i> ICMP5702_peg22	AODT01000003.1	18593	19030	+	D-aminoacyl-tRNA deacylase (EC 3.1.1.96)
<i>Pcc</i> ICMP5702_peg23	AODT01000003.1	19169	20110	+	Uncharacterized GNAT family acetyltransferase YiiD
<i>Pcc</i> ICMP5702_peg24	AODT01000003.1	21997	20306	-	Uncharacterized protein YicH
<i>Pcc</i> ICMP5702_peg25	AODT01000003.1	23543	22155	-	Xanthine permease @ Xanthine:proton symporter XanP
<i>Pcc</i> ICMP5702_peg26	AODT01000003.1	25790	23709	-	ATP-dependent DNA helicase RecG (EC 3.6.4.12)
<i>Pcc</i> ICMP5702_peg27	AODT01000003.1	26482	25790	-	tRNA (guanosine(18)-2'-O)-methyltransferase (EC 2.1.1.34)
<i>Pcc</i> ICMP5702_peg28	AODT01000003.1	28587	26488	-	Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase (EC 3.1.7.2) / GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase II
<i>Pcc</i> ICMP5702_peg29	AODT01000003.1	28881	28606	-	DNA-directed RNA polymerase omega subunit (EC 2.7.7.6)
<i>Pcc</i> ICMP5702_peg30	AODT01000003.1	29558	28935	-	Guanylate kinase (EC 2.7.4.8)
<i>Pcc</i> ICMP5702_peg31	AODT01000003.1	29880	31571	+	DNA ligase (NAD(+)) (EC 6.5.1.2)
<i>Pcc</i> ICMP5702_peg32	AODT01000003.1	31825	31691	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg33	AODT01000003.1	31827	33506	+	Kdo2-lipid A phosphoethanolamine transferase EptB (EC 2.7.8.42)

<i>Pcc</i> ICMP5702_peg34	AODT01000003.1	34132	34680	+	Outer membrane protein X precursor
<i>Pcc</i> ICMP5702_peg35	AODT01000003.1	36328	34724	-	Rtn protein
<i>Pcc</i> ICMP5702_peg36	AODT01000003.1	37466	36510	-	Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg37	AODT01000003.1	38890	37688	-	Uncharacterized protein YhiN
<i>Pcc</i> ICMP5702_peg38	AODT01000003.1	38905	39045	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg39	AODT01000003.1	39168	40673	+	Low-affinity inorganic phosphate transporter
<i>Pcc</i> ICMP5702_peg40	AODT01000003.1	41137	40802	-	Universal stress protein B
<i>Pcc</i> ICMP5702_peg41	AODT01000003.1	41691	42128	+	Universal stress protein A
<i>Pcc</i> ICMP5702_peg42	AODT01000003.1	42420	43763	+	NADP-specific glutamate dehydrogenase (EC 1.4.1.4)
<i>Pcc</i> ICMP5702_peg43	AODT01000003.1	43938	45251	+	Oxidoreductase
<i>Pcc</i> ICMP5702_peg44	AODT01000003.1	47105	45258	-	5'-nucleotidase (EC 3.1.3.5); 2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16); Putative UDP-sugar hydrolase (EC 3.6.1.45)
<i>Pcc</i> ICMP5702_peg45	AODT01000003.1	48052	47306	-	16S rRNA (guanine(1516)-N(2))-methyltransferase (EC 2.1.1.242)
<i>Pcc</i> ICMP5702_peg46	AODT01000003.1	50091	48049	-	Oligopeptidase A (EC 3.4.24.70)
<i>Pcc</i> ICMP5702_peg47	AODT01000003.1	50415	52964	+	Putative Ton-B dependent hemine receptor
<i>Pcc</i> ICMP5702_peg48	AODT01000003.1	53146	53658	+	RNA polymerase ECF-type sigma factor
<i>Pcc</i> ICMP5702_peg49	AODT01000003.1	53655	54644	+	Fe ²⁺ -dicitrate sensor, membrane component
<i>Pcc</i> ICMP5702_peg50	AODT01000003.1	54848	55669	+	putative TonB-dependent receptor
<i>Pcc</i> ICMP5702_peg51	AODT01000003.1	55973	55680	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg52	AODT01000003.1	56193	57884	+	Chaperone protein HscC
<i>Pcc</i> ICMP5702_peg53	AODT01000003.1	60658	57929	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg54	AODT01000003.1	61362	60658	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg55	AODT01000003.1	61770	63125	+	Alkyl sulfatase and related hydrolases, MBL-fold metallo-hydrolase superfamily
<i>Pcc</i> ICMP5702_peg56	AODT01000003.1	63248	63631	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg57	AODT01000003.1	63912	64754	+	23S rRNA (adenine(2030)-N(6))-methyltransferase (EC 2.1.1.266)
<i>Pcc</i> ICMP5702_peg58	AODT01000003.1	64883	66235	+	Glutathione reductase (EC 1.8.1.7)
<i>Pcc</i> ICMP5702_peg59	AODT01000003.1	66618	66331	-	mRNA interferase RelE
<i>Pcc</i> ICMP5702_peg60	AODT01000003.1	66866	66615	-	RelB/StbD replicon stabilization protein (antitoxin to RelE/StbE)
<i>Pcc</i> ICMP5702_peg61	AODT01000003.1	67067	68029	+	Iron-chelator utilization protein
<i>Pcc</i> ICMP5702_peg62	AODT01000003.1	68819	68064	-	Thiol:disulfide interchange protein DsbG precursor
<i>Pcc</i> ICMP5702_peg63	AODT01000003.1	69098	69721	+	Homoserine/homoserine lactone efflux protein
<i>Pcc</i> ICMP5702_peg64	AODT01000003.1	70822	69782	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg65	AODT01000003.1	71133	70819	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg66	AODT01000003.1	71444	71118	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg67	AODT01000003.1	72765	71632	-	Alkylhydroperoxidase AhpD domain protein

<i>Pcc</i> ICMP5702_peg68	AODT01000003.1	73796	72762	-	Coenzyme F420-dependent N5,N10-methylene tetrahydromethanopterin reductase and related flavin-dependent oxidoreductases
<i>Pcc</i> ICMP5702_peg69	AODT01000003.1	75501	73798	-	ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines) / ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg70	AODT01000003.1	76358	75498	-	ABC transporter, permease protein 2 (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg71	AODT01000003.1	77299	76355	-	ABC transporter, permease protein 1 (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg72	AODT01000003.1	78964	77327	-	ABC transporter, substrate-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg73	AODT01000003.1	78985	79104	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg74	AODT01000003.1	80275	79268	-	Glyoxylate reductase (EC 1.1.1.79) / Hydroxypyruvate reductase (EC 1.1.1.81) / 2-ketoaldonate reductase, broad specificity (EC 1.1.1.215)
<i>Pcc</i> ICMP5702_peg75	AODT01000003.1	80590	82551	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg76	AODT01000003.1	83047	82619	-	Uncharacterized N-acetyltransferase YiaC
<i>Pcc</i> ICMP5702_peg77	AODT01000003.1	83607	83044	-	DNA-3-methyladenine glycosylase (EC 3.2.2.20)
<i>Pcc</i> ICMP5702_peg78	AODT01000003.1	83904	84710	+	Uncharacterized UPF0721 integral membrane protein
<i>Pcc</i> ICMP5702_peg79	AODT01000003.1	84838	85752	+	Glycyl-tRNA synthetase alpha chain (EC 6.1.1.14)
<i>Pcc</i> ICMP5702_peg80	AODT01000003.1	85762	87831	+	Glycyl-tRNA synthetase beta chain (EC 6.1.1.14)
<i>Pcc</i> ICMP5702_peg81	AODT01000003.1	88765	87890	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg82	AODT01000003.1	89499	88765	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg83	AODT01000003.1	90882	89503	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg84	AODT01000003.1	91285	92001	+	Uncharacterized protein YiaF
<i>Pcc</i> ICMP5702_peg85	AODT01000003.1	92438	94345	+	component (EC 2.7.1.197) / PTS system, mannitol-specific IIA component (EC 2.7.1.197)
<i>Pcc</i> ICMP5702_peg86	AODT01000003.1	94407	95555	+	Mannitol-1-phosphate 5-dehydrogenase (EC 1.1.1.17)
<i>Pcc</i> ICMP5702_peg87	AODT01000003.1	95709	96239	+	Mannitol operon repressor
<i>Pcc</i> ICMP5702_peg88	AODT01000003.1	96366	96728	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg89	AODT01000003.1	98714	96828	-	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg90	AODT01000003.1	98980	98864	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg91	AODT01000003.1	99646	99020	-	Superoxide dismutase [Mn] (EC 1.15.1.1)
<i>Pcc</i> ICMP5702_peg92	AODT01000003.1	100715	99882	-	Sulfur carrier protein FdhD
<i>Pcc</i> ICMP5702_peg93	AODT01000003.1	100936	102471	+	Aldehyde dehydrogenase (EC 1.2.1.3)
<i>Pcc</i> ICMP5702_peg94	AODT01000003.1	102684	103676	+	Inner membrane protein YiaH
<i>Pcc</i> ICMP5702_peg95	AODT01000003.1	105148	103691	-	Xylulose kinase (EC 2.7.1.17)
<i>Pcc</i> ICMP5702_peg96	AODT01000003.1	106540	105221	-	Xylose isomerase (EC 5.3.1.5)
<i>Pcc</i> ICMP5702_peg97	AODT01000003.1	107012	108010	+	D-xylose ABC transporter, substrate-binding protein XylF
<i>Pcc</i> ICMP5702_peg98	AODT01000003.1	108127	109668	+	D-xylose ABC transporter, ATP-binding protein XylG
<i>Pcc</i> ICMP5702_peg99	AODT01000003.1	109646	110827	+	D-xylose ABC transporter, permease protein XylH

<i>Pcc</i> ICMP5702_peg100	AODT01000003.1	110832	110948	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg101	AODT01000003.1	110964	112142	+	Xylose activator XylR (AraC family)
<i>Pcc</i> ICMP5702_peg102	AODT01000003.1	112784	112209	-	DJ-1/YajL/PfpI superfamily, includes chaperone protein YajL (former ThiJ), parkinsonism-associated protein DJ-1, peptidases PfpI, Hsp31
<i>Pcc</i> ICMP5702_peg103	AODT01000003.1	113197	114543	+	Argininosuccinate synthase (EC 6.3.4.5)
<i>Pcc</i> ICMP5702_peg104	AODT01000003.1	114813	115463	+	N-(3-oxohexanoyl)-L-homoserine lactone synthase @ N-acyl-L-homoserine lactone synthase, LuxI family (EC 2.3.1.184)
<i>Pcc</i> ICMP5702_peg105	AODT01000003.1	116175	115447	-	N-(3-oxohexanoyl)-L-homoserine lactone-binding transcriptional activator @ Acyl-homoserine lactone-binding transcriptional activator, LuxR family
<i>Pcc</i> ICMP5702_peg106	AODT01000003.1	117727	116525	-	pectin methylesterase(EC:3.1.1.11)
<i>Pcc</i> ICMP5702_peg107	AODT01000003.1	118727	117732	-	Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg108	AODT01000003.1	118847	119236	+	Rhodanese-related sulfurtransferase
<i>Pcc</i> ICMP5702_peg109	AODT01000003.1	119622	119281	-	Inner membrane protein YdgC
<i>Pcc</i> ICMP5702_peg110	AODT01000003.1	120089	121102	+	3-oxoacyl-[acyl-carrier-protein] synthase (EC 2.3.1.41)
<i>Pcc</i> ICMP5702_peg111	AODT01000003.1	121099	122127	+	FIG036672: Nucleoside-diphosphate-sugar epimerase
<i>Pcc</i> ICMP5702_peg112	AODT01000003.1	122120	122926	+	MBL-fold metallo-hydrolase superfamily
<i>Pcc</i> ICMP5702_peg113	AODT01000003.1	122923	124209	+	Adenylate-forming enzyme
<i>Pcc</i> ICMP5702_peg114	AODT01000003.1	124206	124862	+	Ser/Thr and Tyr protein phosphatase (dual specificity)
<i>Pcc</i> ICMP5702_peg115	AODT01000003.1	124867	125991	+	Fatty acid hydroxylase family (carotene hydroxylase/sterol desaturase)
<i>Pcc</i> ICMP5702_peg116	AODT01000003.1	125984	127111	+	Linoleoyl-CoA desaturase (EC 1.14.19.3)
<i>Pcc</i> ICMP5702_peg117	AODT01000003.1	127111	128208	+	Linoleoyl-CoA desaturase (EC 1.14.19.3)
<i>Pcc</i> ICMP5702_peg118	AODT01000003.1	128269	129198	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg119	AODT01000003.1	129488	130927	+	1.2.1.21)
<i>Pcc</i> ICMP5702_peg120	AODT01000003.1	131127	132287	+	L-lactate dehydrogenase
<i>Pcc</i> ICMP5702_peg121	AODT01000003.1	132411	133646	+	Uncharacterized UPF0118 membrane protein
<i>Pcc</i> ICMP5702_peg122	AODT01000003.1	134019	133657	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg123	AODT01000003.1	134447	134061	-	FIG00905008: Hypothetical protein
<i>Pcc</i> ICMP5702_peg124	AODT01000003.1	134561	135106	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg125	AODT01000003.1	135711	135154	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg126	AODT01000003.1	136033	136338	+	HipB protein @ Antitoxin HigA
<i>Pcc</i> ICMP5702_peg127	AODT01000003.1	136335	137585	+	Toxin HigB / Protein kinase domain of HipA
<i>Pcc</i> ICMP5702_peg128	AODT01000003.1	138030	137728	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg129	AODT01000003.1	138238	138354	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg130	AODT01000003.1	138363	140207	+	5-methylcytosine-specific restriction related enzyme
<i>Pcc</i> ICMP5702_peg131	AODT01000003.1	140226	142706	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg132	AODT01000003.1	143026	143550	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg133	AODT01000003.1	143580	144467	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg134	AODT01000003.1	145424	144561	-	UPF0701 protein YicC
<i>Pcc</i> ICMP5702_peg135	AODT01000003.1	146431	145523	-	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg136	AODT01000003.1	147775	146828	-	Isoaspartyl aminopeptidase (EC 3.4.19.5) @ Asp-X dipeptidase
<i>Pcc</i> ICMP5702_peg137	AODT01000003.1	148657	147836	-	D-aminopeptidase dipeptide-binding protein DppA (EC 3.4.11.-)
<i>Pcc</i> ICMP5702_peg138	AODT01000003.1	149760	148684	-	D-aminopeptidase (EC 3.4.11.19)
<i>Pcc</i> ICMP5702_peg139	AODT01000003.1	150668	149769	-	Oligopeptide transport permease protein OppC-like
<i>Pcc</i> ICMP5702_peg140	AODT01000003.1	151597	150677	-	Oligopeptide transport permease protein OppB-like
<i>Pcc</i> ICMP5702_peg141	AODT01000003.1	153157	151616	-	Oligopeptide transport substrate-binding protein
<i>Pcc</i> ICMP5702_peg142	AODT01000003.1	155117	153246	-	Oligopeptide transport ATP-binding protein
<i>Pcc</i> ICMP5702_peg143	AODT01000003.1	156130	155162	-	L-alanine-DL-glutamate epimerase (EC 5.1.1.n1)
<i>Pcc</i> ICMP5702_peg144	AODT01000003.1	156332	157048	+	Ribonuclease PH (EC 2.7.7.56)
<i>Pcc</i> ICMP5702_peg145	AODT01000003.1	157106	157747	+	Orotate phosphoribosyltransferase (EC 2.4.2.10)
<i>Pcc</i> ICMP5702_peg146	AODT01000003.1	158407	157811	-	Transcriptional regulator SlmA, TetR family
<i>Pcc</i> ICMP5702_peg147	AODT01000003.1	158994	158536	-	Deoxyuridine 5'-triphosphate nucleotidohydrolase (EC 3.6.1.23)
<i>Pcc</i> ICMP5702_peg148	AODT01000003.1	160249	158972	-	Phosphopantothenoylcysteine decarboxylase (EC 4.1.1.36) / Phosphopantothenoylcysteine synthetase (EC 6.3.2.5)
<i>Pcc</i> ICMP5702_peg149	AODT01000003.1	160403	161068	+	UPF0758 protein YicR
<i>Pcc</i> ICMP5702_peg150	AODT01000003.1	161306	161542	+	LSU ribosomal protein L28p @ LSU ribosomal protein L28p, zinc-independent
<i>Pcc</i> ICMP5702_peg151	AODT01000003.1	161554	161721	+	LSU ribosomal protein L33p @ LSU ribosomal protein L33p, zinc-independent
<i>Pcc</i> ICMP5702_peg152	AODT01000003.1	161955	162764	+	Formamidopyrimidine-DNA glycosylase (EC 3.2.2.23)
<i>Pcc</i> ICMP5702_peg153	AODT01000003.1	162822	163811	+	Glycosyltransferase
<i>Pcc</i> ICMP5702_peg154	AODT01000003.1	164305	163817	-	Phosphopantetheine adenylyltransferase (EC 2.7.7.3)
<i>Pcc</i> ICMP5702_peg155	AODT01000003.1	165621	164344	-	3-deoxy-D-manno-octulosonic acid transferase (EC 2.4.99.12)(EC 2.4.99.13)
<i>Pcc</i> ICMP5702_peg156	AODT01000003.1	166708	165848	-	putative glycosyltransferase
<i>Pcc</i> ICMP5702_peg157	AODT01000003.1	167542	166868	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg158	AODT01000003.1	167691	167837	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg159	AODT01000003.1	169167	168055	-	dTDP-3-amino-3,6-dideoxy-alpha-D-galactopyranose transaminase (EC 2.6.1.90)
<i>Pcc</i> ICMP5702_peg160	AODT01000003.1	169731	169201	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg161	AODT01000003.1	170131	169724	-	FIG01210424: Hypothetical protein
<i>Pcc</i> ICMP5702_peg162	AODT01000003.1	171654	170182	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg163	AODT01000003.1	171942	171772	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg164	AODT01000003.1	172093	172218	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg165	AODT01000003.1	173211	172309	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg166	AODT01000003.1	174082	173297	-	Putative two-domain glycosyltransferase
<i>Pcc</i> ICMP5702_peg167	AODT01000003.1	175211	174189	-	UDP-glucose:(glucosyl)lipopolysaccharide alpha-1,2-glycosyltransferase (EC 2.4.1.58)

<i>Pcc</i> ICMP5702_peg168	AODT01000003.1	176274	175264	-	Lipopolysaccharide 1,3-galactosyltransferase (EC 2.4.1.44)
<i>Pcc</i> ICMP5702_peg169	AODT01000003.1	177467	176352	-	UDP-glucose:(heptosyl) LPS alpha1,3-glucosyltransferase WaaG
<i>Pcc</i> ICMP5702_peg170	AODT01000003.1	178534	177464	-	Lipopolysaccharide core heptosyltransferase III
<i>Pcc</i> ICMP5702_peg171	AODT01000003.1	180010	178727	-	O-antigen ligase
<i>Pcc</i> ICMP5702_peg172	AODT01000003.1	180990	180007	-	Lipopolysaccharide core heptosyltransferase I
<i>Pcc</i> ICMP5702_peg173	AODT01000003.1	182090	180987	-	ADP-heptose--lipooligosaccharide heptosyltransferase II
<i>Pcc</i> ICMP5702_peg174	AODT01000003.1	183046	182114	-	ADP-L-glycero-D-manno-heptose-6-epimerase (EC 5.1.3.20)
<i>Pcc</i> ICMP5702_peg175	AODT01000003.1	183045	183176	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg176	AODT01000003.1	183289	184485	+	2-amino-3-ketobutyrate coenzyme A ligase (EC 2.3.1.29)
<i>Pcc</i> ICMP5702_peg177	AODT01000003.1	184496	185527	+	L-threonine 3-dehydrogenase (EC 1.1.1.103)
<i>Pcc</i> ICMP5702_peg178	AODT01000003.1	186526	185579	-	Putative periplasmic protein YibQ, distant homology with nucleoside diphosphatase and polysaccharide deacetylase
<i>Pcc</i> ICMP5702_peg179	AODT01000003.1	187830	186529	-	Murein hydrolase activator EnvC
<i>Pcc</i> ICMP5702_peg180	AODT01000003.1	188076	188507	+	Rhodanese-related sulfurtransferase YibN
<i>Pcc</i> ICMP5702_peg181	AODT01000003.1	188727	189197	+	Protein-export protein SecB (maintains pre-export unfolded state)
<i>Pcc</i> ICMP5702_peg182	AODT01000003.1	189197	190216	+	Glycerol-3-phosphate dehydrogenase [NAD(P)+] (EC 1.1.1.94)
<i>Pcc</i> ICMP5702_peg183	AODT01000003.1	190359	191180	+	Serine acetyltransferase (EC 2.3.1.30)
<i>Pcc</i> ICMP5702_peg184	AODT01000003.1	191487	192140	+	Lipid A palmitoyltransferase PagP (EC 2.3.1.251)
<i>Pcc</i> ICMP5702_peg185	AODT01000003.1	194129	193194	-	Transcriptional activator MetR
<i>Pcc</i> ICMP5702_peg186	AODT01000003.1	194234	196498	+	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14)
<i>Pcc</i> ICMP5702_peg187	AODT01000003.1	197300	198922	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg188	AODT01000003.1	199610	201271	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg189	AODT01000003.1	202201	201374	-	Dienelactone hydrolase family protein
<i>Pcc</i> ICMP5702_peg190	AODT01000003.1	202533	203303	+	Uridine phosphorylase (EC 2.4.2.3)
<i>Pcc</i> ICMP5702_peg191	AODT01000003.1	203453	204235	+	Protein tyrosine phosphatase (EC 3.1.3.48)
<i>Pcc</i> ICMP5702_peg192	AODT01000003.1	207016	204377	-	Phosphoenolpyruvate carboxylase (EC 4.1.1.31)
<i>Pcc</i> ICMP5702_peg193	AODT01000003.1	208648	207260	-	PTS system, beta-glucoside-specific IIB component / PTS system, beta-glucoside-specific IIC component
<i>Pcc</i> ICMP5702_peg194	AODT01000003.1	208970	210169	+	Starvation sensing protein RspA
<i>Pcc</i> ICMP5702_peg195	AODT01000003.1	210891	210178	-	Transcriptional regulator, GntR family
<i>Pcc</i> ICMP5702_peg196	AODT01000003.1	212097	210946	-	N-acetylmethionine deacetylase (EC 3.5.1.16)
<i>Pcc</i> ICMP5702_peg197	AODT01000003.1	212300	213304	+	N-acetyl-gamma-glutamyl-phosphate reductase (EC 1.2.1.38)
<i>Pcc</i> ICMP5702_peg198	AODT01000003.1	213342	214115	+	N-acetylglutamate kinase (EC 2.7.2.8)
<i>Pcc</i> ICMP5702_peg199	AODT01000003.1	214178	215551	+	Argininosuccinate lyase (EC 4.3.2.1)
<i>Pcc</i> ICMP5702_peg200	AODT01000003.1	215773	217332	+	DNA recombination protein RmuC
<i>Pcc</i> ICMP5702_peg201	AODT01000003.1	217527	217634	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg202	AODT01000003.1	217652	218407	+	2-methoxy-6-polyprenyl-1,4-benzoquinol methylase (EC 2.1.1.201) @
<i>Pcc</i> ICMP5702_peg203	AODT01000003.1	218420	219043	+	Demethylmenaquinone methyltransferase (EC 2.1.1.163)
<i>Pcc</i> ICMP5702_peg204	AODT01000003.1	219040	220680	+	Ubiquinone biosynthesis protein UbiJ
<i>Pcc</i> ICMP5702_peg205	AODT01000003.1	220763	221023	+	Ubiquinone biosynthesis regulatory protein kinase UbiB
<i>Pcc</i> ICMP5702_peg206	AODT01000003.1	221027	221638	+	Twin-arginine translocation protein TatA
<i>Pcc</i> ICMP5702_peg207	AODT01000003.1	221642	222394	+	Twin-arginine translocation protein TatB
<i>Pcc</i> ICMP5702_peg208	AODT01000003.1	222473	223255	+	Twin-arginine translocation protein TatC
<i>Pcc</i> ICMP5702_peg209	AODT01000003.1	223273	224295	+	Deoxyribonuclease TatD
<i>Pcc</i> ICMP5702_peg210	AODT01000003.1	224895	224407	-	Porphobilinogen synthase (EC 4.2.1.24)
<i>Pcc</i> ICMP5702_peg211	AODT01000003.1	225096	226592	+	Transcriptional activator RfaH
<i>Pcc</i> ICMP5702_peg212	AODT01000003.1	226645	227346	+	3-polyprenyl-4-hydroxybenzoate carboxy-lyase (EC 4.1.1.98)
<i>Pcc</i> ICMP5702_peg213	AODT01000003.1	228600	227437	+	NAD(P)H-flavin reductase (EC 1.5.1.41) (EC 1.16.1.3)
				-	3-ketoacyl-CoA thiolase (EC 2.3.1.16)
				-	Enoyl-CoA hydratase (EC 4.2.1.17) / Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)
<i>Pcc</i> ICMP5702_peg214	AODT01000003.1	230801	228612	-	
<i>Pcc</i> ICMP5702_peg215	AODT01000003.1	230987	232318	+	Xaa-Pro dipeptidase PepQ (EC 3.4.13.9)
<i>Pcc</i> ICMP5702_peg216	AODT01000003.1	232318	232929	+	FIG000605: protein co-occurring with transport systems (COG1739)
<i>Pcc</i> ICMP5702_peg217	AODT01000003.1	232972	234423	+	Trk potassium uptake system protein TrkH
<i>Pcc</i> ICMP5702_peg218	AODT01000003.1	234445	234984	+	Protoporphyrinogen IX oxidase, oxygen-independent, HemG
<i>Pcc</i> ICMP5702_peg219	AODT01000004.1	156	1469	+	UDP-N-acetylenolpyruvoylglucosamine reductase (EC 1.3.1.98)
				+	Biotin operon repressor / Biotin--protein ligase (EC 6.3.4.9)(EC 6.3.4.10)(EC 6.3.4.11)(EC 6.3.4.15)
<i>Pcc</i> ICMP5702_peg220	AODT01000004.1	1466	2425	+	
<i>Pcc</i> ICMP5702_peg221	AODT01000004.1	3414	2464	-	Pantothenate kinase (EC 2.7.1.33)
<i>Pcc</i> ICMP5702_peg222	AODT01000004.1	4174	3626	-	Acetyltransferase
<i>Pcc</i> ICMP5702_peg223	AODT01000004.1	5076	5663	+	Translation elongation factor Tu
<i>Pcc</i> ICMP5702_peg224	AODT01000005.1	1	684	+	Translation elongation factor Tu
<i>Pcc</i> ICMP5702_peg225	AODT01000006.1	2	91	+	Translation elongation factor Tu
<i>Pcc</i> ICMP5702_peg226	AODT01000006.1	329	712	+	Protein translocase subunit SecE
<i>Pcc</i> ICMP5702_peg227	AODT01000006.1	714	1259	+	Transcription antitermination protein NusG
<i>Pcc</i> ICMP5702_peg228	AODT01000006.1	1422	1850	+	LSU ribosomal protein L11p (L12e)
<i>Pcc</i> ICMP5702_peg229	AODT01000006.1	1854	2558	+	LSU ribosomal protein L1p (L10Ae)
<i>Pcc</i> ICMP5702_peg230	AODT01000006.1	2876	3373	+	LSU ribosomal protein L10p (P0)
<i>Pcc</i> ICMP5702_peg231	AODT01000006.1	3440	3805	+	LSU ribosomal protein L7p/L12p (P1/P2)
<i>Pcc</i> ICMP5702_peg232	AODT01000006.1	4133	8161	+	DNA-directed RNA polymerase beta subunit (EC 2.7.7.6)
<i>Pcc</i> ICMP5702_peg233	AODT01000006.1	8268	12491	+	DNA-directed RNA polymerase beta' subunit (EC 2.7.7.6)

<i>Pcc</i> ICMP5702_peg234	AODT01000006.1	12811	14208	+	Shikimate transporter
<i>Pcc</i> ICMP5702_peg235	AODT01000006.1	14495	14304	-	Uncharacterized protein YjiS
<i>Pcc</i> ICMP5702_peg236	AODT01000006.1	14670	16106	+	DNA-binding transcriptional regulator, MocR family / aminotransferase domain
<i>Pcc</i> ICMP5702_peg237	AODT01000006.1	17523	16402	-	2-iminoacetate synthase (ThiH) (EC 4.1.99.19)
<i>Pcc</i> ICMP5702_peg238	AODT01000006.1	18305	17520	-	Thiazole synthase (EC 2.8.1.10)
<i>Pcc</i> ICMP5702_peg239	AODT01000006.1	18507	18307	-	Sulfur carrier protein ThiS
<i>Pcc</i> ICMP5702_peg240	AODT01000006.1	19282	18488	-	Sulfur carrier protein ThiS adenylyltransferase (EC 2.7.7.73)
<i>Pcc</i> ICMP5702_peg241	AODT01000006.1	19925	19284	-	Thiamin-phosphate pyrophosphorylase (EC 2.5.1.3)
<i>Pcc</i> ICMP5702_peg242	AODT01000006.1	21901	19922	-	Phosphomethylpyrimidine synthase ThiC (EC 4.1.99.17)
<i>Pcc</i> ICMP5702_peg243	AODT01000006.1	22753	22292	-	Regulator of sigma D
<i>Pcc</i> ICMP5702_peg244	AODT01000006.1	22862	23644	+	NADH pyrophosphatase (EC 3.6.1.22), decaps 5'-NAD modified RNA
<i>Pcc</i> ICMP5702_peg245	AODT01000006.1	23744	24808	+	Uroporphyrinogen III decarboxylase (EC 4.1.1.37)
<i>Pcc</i> ICMP5702_peg246	AODT01000006.1	24824	25513	+	Endonuclease V (EC 3.1.21.7)
<i>Pcc</i> ICMP5702_peg247	AODT01000006.1	25591	26181	+	Uncharacterized protein YjaG
<i>Pcc</i> ICMP5702_peg248	AODT01000006.1	26386	26658	+	DNA-binding protein HU-alpha
<i>Pcc</i> ICMP5702_peg249	AODT01000006.1	26663	27349	+	Uncharacterized protein YjaH
<i>Pcc</i> ICMP5702_peg250	AODT01000006.1	28726	27440	-	Phosphoribosylamine--glycine ligase (EC 6.3.4.13)
					IMP cyclohydrolase (EC 3.5.4.10) / Phosphoribosylaminoimidazolecarboxamide
<i>Pcc</i> ICMP5702_peg251	AODT01000006.1	30333	28744	-	formyltransferase (EC 2.1.2.3)
<i>Pcc</i> ICMP5702_peg252	AODT01000006.1	30955	30428	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg253	AODT01000007.1	1268	507	-	Amino acid ABC transporter, ATP-binding protein YhdZ
<i>Pcc</i> ICMP5702_peg254	AODT01000007.1	2371	1277	-	Amino acid ABC transporter, permease protein 2, YhdY
<i>Pcc</i> ICMP5702_peg255	AODT01000007.1	3559	2381	-	Amino acid ABC transporter, permease protein 1, YhdX
<i>Pcc</i> ICMP5702_peg256	AODT01000007.1	4651	3626	-	Amino acid ABC transporter, substrate-binding protein YhdW
<i>Pcc</i> ICMP5702_peg257	AODT01000007.1	5682	5017	-	L-cystine ABC transporter, permease protein TcyB
<i>Pcc</i> ICMP5702_peg258	AODT01000007.1	6539	5772	-	L-cystine ABC transporter, substrate-binding protein TcyA
<i>Pcc</i> ICMP5702_peg259	AODT01000007.1	6858	8003	+	Endonuclease/exonuclease/phosphatase family protein
<i>Pcc</i> ICMP5702_peg260	AODT01000007.1	8072	8476	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg261	AODT01000007.1	9491	8745	-	Protein phosphatase 2C-like
<i>Pcc</i> ICMP5702_peg262	AODT01000007.1	10225	9494	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg263	AODT01000007.1	10819	10634	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg264	AODT01000007.1	11006	11194	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg265	AODT01000007.1	11187	11378	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg266	AODT01000007.1	11813	11517	-	DNA-binding protein Fis
<i>Pcc</i> ICMP5702_peg267	AODT01000007.1	12754	11837	-	tRNA-dihydrouridine synthase DusB
<i>Pcc</i> ICMP5702_peg268	AODT01000007.1	13894	13160	-	Carbonic anhydrase, alpha class (EC 4.2.1.1)

<i>Pcc</i> ICMP5702_peg269	AODT01000007.1	15080	14193	-	Ribosomal protein L11 methyltransferase
<i>Pcc</i> ICMP5702_peg270	AODT01000007.1	16549	15098	-	Pantothenate:Na ⁺ symporter (TC 2.A.21.1.1)
<i>Pcc</i> ICMP5702_peg271	AODT01000007.1	16781	16539	-	Uncharacterized protein YhdT
<i>Pcc</i> ICMP5702_peg272	AODT01000007.1	16819	16929	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg273	AODT01000007.1	16943	17059	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg274	AODT01000007.1	17207	17635	+	Molybdate-binding domain of ModE
<i>Pcc</i> ICMP5702_peg275	AODT01000007.1	19158	17815	-	Biotin carboxylase of acetyl-CoA carboxylase (EC 6.3.4.14)
<i>Pcc</i> ICMP5702_peg276	AODT01000007.1	19637	19170	-	Biotin carboxyl carrier protein of acetyl-CoA carboxylase
<i>Pcc</i> ICMP5702_peg277	AODT01000007.1	20114	19662	-	3-dehydroquinone dehydratase II (EC 4.2.1.10)
<i>Pcc</i> ICMP5702_peg278	AODT01000007.1	20968	20369	-	Protein-methionine-sulfoxide reductase heme-binding subunit MsrQ
<i>Pcc</i> ICMP5702_peg279	AODT01000007.1	22048	21047	-	Protein-methionine-sulfoxide reductase catalytic subunit MsrP
<i>Pcc</i> ICMP5702_peg280	AODT01000007.1	23196	22219	-	Acryloyl-CoA reductase AcuI/YhdH (EC 1.3.1.84)
<i>Pcc</i> ICMP5702_peg281	AODT01000007.1	23374	25311	+	RNase E specificity factor CsrD
<i>Pcc</i> ICMP5702_peg282	AODT01000007.1	25628	26671	+	Rod shape-determining protein MreB
<i>Pcc</i> ICMP5702_peg283	AODT01000007.1	26834	27817	+	Rod shape-determining protein MreC
<i>Pcc</i> ICMP5702_peg284	AODT01000007.1	27814	28302	+	Rod shape-determining protein MreD
<i>Pcc</i> ICMP5702_peg285	AODT01000007.1	28311	28904	+	Septum formation protein Maf
<i>Pcc</i> ICMP5702_peg286	AODT01000007.1	28894	30363	+	Ribonuclease G
<i>Pcc</i> ICMP5702_peg287	AODT01000007.1	30405	34235	+	Uncharacterized protein YhdP
<i>Pcc</i> ICMP5702_peg288	AODT01000007.1	34292	35737	+	TldD protein, part of TldE/TldD proteolytic complex
<i>Pcc</i> ICMP5702_peg289	AODT01000007.1	36719	35778	-	Transcriptional regulator AaeR, LysR family
<i>Pcc</i> ICMP5702_peg290	AODT01000007.1	37054	37257	+	AaeX protein, function unknown
<i>Pcc</i> ICMP5702_peg291	AODT01000007.1	37265	38230	+	AaeAB efflux system for hydroxylated, aromatic carboxylic acids, membrane fusion component AaeA
<i>Pcc</i> ICMP5702_peg292	AODT01000007.1	38242	40230	+	AaeAB efflux system for hydroxylated, aromatic carboxylic acids, inner membrane subunit AaeB
<i>Pcc</i> ICMP5702_peg293	AODT01000007.1	40378	41832	+	Succinate-semialdehyde dehydrogenase [NAD(P) ⁺] (EC 1.2.1.16)
<i>Pcc</i> ICMP5702_peg294	AODT01000007.1	42481	41930	-	UPF0307 protein YjgA
<i>Pcc</i> ICMP5702_peg295	AODT01000007.1	42777	44117	+	TldE protein, part of TldE/TldD proteolytic complex
<i>Pcc</i> ICMP5702_peg296	AODT01000007.1	44592	44182	-	Regulator of nucleoside diphosphate kinase
<i>Pcc</i> ICMP5702_peg297	AODT01000007.1	45036	44764	-	Phosphocarrier protein, nitrogen regulation associated
<i>Pcc</i> ICMP5702_peg298	AODT01000007.1	45925	45068	-	RNase adapter protein RapZ
<i>Pcc</i> ICMP5702_peg299	AODT01000007.1	46586	46086	-	PTS IIA-like nitrogen-regulatory protein PtsN
<i>Pcc</i> ICMP5702_peg300	AODT01000007.1	46943	46656	-	Ribosome hibernation promoting factor Hpf
<i>Pcc</i> ICMP5702_peg301	AODT01000007.1	48400	46967	-	RNA polymerase sigma-54 factor RpoN
<i>Pcc</i> ICMP5702_peg302	AODT01000007.1	49175	48450	-	Lipopolysaccharide ABC transporter, ATP-binding protein LptB

<i>Pcc</i> ICMP5702_peg303	AODT01000007.1	49751	49179	-	Lipopolysaccharide export system protein LptA
<i>Pcc</i> ICMP5702_peg304	AODT01000007.1	50298	49732	-	Lipopolysaccharide export system protein LptC
<i>Pcc</i> ICMP5702_peg305	AODT01000007.1	50861	50295	-	3-deoxy-D-manno-octulosonate 8-phosphate phosphatase (EC 3.1.3.45)
<i>Pcc</i> ICMP5702_peg306	AODT01000007.1	51972	50881	-	D-arabinose-5-phosphate isomerase (EC 5.3.1.13)
<i>Pcc</i> ICMP5702_peg307	AODT01000007.1	52993	52028	-	Inner membrane protein YrbG, predicted calcium/sodium:proton antiporter
<i>Pcc</i> ICMP5702_peg308	AODT01000007.1	53283	54095	+	Phospholipid ABC transporter ATP-binding protein MlaF
<i>Pcc</i> ICMP5702_peg309	AODT01000007.1	54103	54885	+	Phospholipid ABC transporter permease protein MlaE
<i>Pcc</i> ICMP5702_peg310	AODT01000007.1	54890	55456	+	Phospholipid ABC transporter substrate-binding protein MlaD
<i>Pcc</i> ICMP5702_peg311	AODT01000007.1	55469	56098	+	Phospholipid ABC transporter shuttle protein MlaC
<i>Pcc</i> ICMP5702_peg312	AODT01000007.1	56112	56402	+	Phospholipid ABC transporter-binding protein MlaB
<i>Pcc</i> ICMP5702_peg313	AODT01000007.1	56537	56791	+	Acid stress protein IbaG
<i>Pcc</i> ICMP5702_peg314	AODT01000007.1	56876	58138	+	UDP-N-acetylglucosamine 1-carboxyvinyltransferase (EC 2.5.1.7)
<i>Pcc</i> ICMP5702_peg315	AODT01000007.1	59333	58236	-	Outer membrane stress sensor protease DegS
<i>Pcc</i> ICMP5702_peg316	AODT01000007.1	60841	59471	-	Outer membrane stress sensor protease DegQ, serine protease
<i>Pcc</i> ICMP5702_peg317	AODT01000007.1	61502	61098	-	Putative cytochrome d ubiquinol oxidase subunit III (EC 1.10.3.-) (Cytochrome bd-I oxidase subunit III)
<i>Pcc</i> ICMP5702_peg318	AODT01000007.1	61717	62874	+	Cell division protein ZapE
<i>Pcc</i> ICMP5702_peg319	AODT01000007.1	63113	63541	+	LSU ribosomal protein L13p (L13Ae)
<i>Pcc</i> ICMP5702_peg320	AODT01000007.1	63557	63949	+	SSU ribosomal protein S9p (S16e)
<i>Pcc</i> ICMP5702_peg321	AODT01000007.1	65441	64113	-	Uncharacterized MFS-type transporter YdfJ
<i>Pcc</i> ICMP5702_peg322	AODT01000007.1	66702	65656	-	L-idonate 5-dehydrogenase (EC 1.1.1.264)
<i>Pcc</i> ICMP5702_peg323	AODT01000007.1	67586	66813	-	5-keto-D-gluconate 5-reductase (EC 1.1.1.69)
<i>Pcc</i> ICMP5702_peg324	AODT01000007.1	67767	68471	+	Transcriptional regulator, GntR family
<i>Pcc</i> ICMP5702_peg325	AODT01000007.1	68811	70055	+	Starvation sensing protein RspA
<i>Pcc</i> ICMP5702_peg326	AODT01000007.1	70474	71115	+	Stringent starvation protein A
<i>Pcc</i> ICMP5702_peg327	AODT01000007.1	71121	71624	+	Stringent starvation protein B
<i>Pcc</i> ICMP5702_peg328	AODT01000007.1	72476	71703	-	2,3-butanediol dehydrogenase, S-alcohol forming, (R)-acetoin-specific (EC 1.1.1.4) / Acetoin (diacetyl) reductase (EC 1.1.1.304)
<i>Pcc</i> ICMP5702_peg329	AODT01000007.1	72857	73285	+	Gfa-like protein
<i>Pcc</i> ICMP5702_peg330	AODT01000007.1	74751	73333	-	Glutamate synthase [NADPH] small chain (EC 1.4.1.13)
<i>Pcc</i> ICMP5702_peg331	AODT01000007.1	79221	74761	-	Glutamate synthase [NADPH] large chain (EC 1.4.1.13)
<i>Pcc</i> ICMP5702_peg332	AODT01000007.1	79873	80802	+	[4Fe-4S]-AdoMet protein YhcC
<i>Pcc</i> ICMP5702_peg333	AODT01000007.1	80922	83285	+	Aerobic respiration control sensor protein ArcB (EC 2.7.13.3)
<i>Pcc</i> ICMP5702_peg334	AODT01000007.1	83784	84437	+	Enhancing lycopene biosynthesis protein 2
<i>Pcc</i> ICMP5702_peg335	AODT01000007.1	84434	85168	+	Monofunctional biosynthetic peptidoglycan transglycosylase
<i>Pcc</i> ICMP5702_peg336	AODT01000007.1	85258	86553	+	probable exported protein YPO3473

<i>Pcc</i> ICMP5702_peg337	AODT01000007.1	87251	86679	-	Uncharacterized protein YraP
<i>Pcc</i> ICMP5702_peg338	AODT01000007.1	87853	87263	-	DnaA initiator-associating protein DiaA
<i>Pcc</i> ICMP5702_peg339	AODT01000007.1	88278	88042	-	UPF0102 protein YraN
<i>Pcc</i> ICMP5702_peg340	AODT01000007.1	90413	88395	-	Penicillin-binding protein activator LpoA
<i>Pcc</i> ICMP5702_peg341	AODT01000007.1	90475	91362	+	16S rRNA (cytidine(1402)-2'-O)-methyltransferase (EC 2.1.1.198)
<i>Pcc</i> ICMP5702_peg342	AODT01000007.1	91931	92185	+	RelB/StbD replicon stabilization protein (antitoxin to RelE/StbE)
<i>Pcc</i> ICMP5702_peg343	AODT01000007.1	92175	92462	+	mRNA interferase RelE
<i>Pcc</i> ICMP5702_peg344	AODT01000007.1	92639	93424	+	4,5-DOPA dioxygenase extradiol (EC 1.13.11.29), but not physiological substrate
<i>Pcc</i> ICMP5702_peg345	AODT01000007.1	94844	93684	-	Putative acid-amine ligase YgiC
<i>Pcc</i> ICMP5702_peg346	AODT01000007.1	95529	94855	-	UPF0441 protein YgiB
<i>Pcc</i> ICMP5702_peg347	AODT01000007.1	97194	95800	-	Outer membrane channel TolC (OpmH)
<i>Pcc</i> ICMP5702_peg348	AODT01000007.1	97531	98163	+	ADP-ribose pyrophosphatase (EC 3.6.1.13)
<i>Pcc</i> ICMP5702_peg349	AODT01000007.1	98168	98599	+	Uncharacterized protein YqiB
<i>Pcc</i> ICMP5702_peg350	AODT01000007.1	98707	99534	+	3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17)
<i>Pcc</i> ICMP5702_peg351	AODT01000007.1	99534	100115	+	Esterase YqiA
<i>Pcc</i> ICMP5702_peg352	AODT01000007.1	100200	102095	+	DNA topoisomerase IV subunit B (EC 5.99.1.3)
<i>Pcc</i> ICMP5702_peg353	AODT01000007.1	102136	103032	+	Transcriptional regulator PA1859, LysR family
<i>Pcc</i> ICMP5702_peg354	AODT01000007.1	103654	103073	-	Modulator of drug activity B
<i>Pcc</i> ICMP5702_peg355	AODT01000007.1	103796	103915	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg356	AODT01000007.1	106324	103922	-	TonB-dependent hemin, ferrichrome receptor
<i>Pcc</i> ICMP5702_peg357	AODT01000007.1	106576	106911	+	FIG00905655: Hypothetical protein
<i>Pcc</i> ICMP5702_peg358	AODT01000007.1	106961	107611	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg359	AODT01000007.1	107647	108150	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg360	AODT01000007.1	108338	110608	+	DNA topoisomerase IV subunit A (EC 5.99.1.3)
<i>Pcc</i> ICMP5702_peg361	AODT01000007.1	110759	111496	+	Acyl-CoA:1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51) @ Acyl-ACP:1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.n4)
<i>Pcc</i> ICMP5702_peg362	AODT01000007.1	111596	113011	+	Cell division protein FtsP
<i>Pcc</i> ICMP5702_peg363	AODT01000007.1	113162	113284	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg364	AODT01000007.1	113352	114089	+	Transcriptional regulator, GntR family
<i>Pcc</i> ICMP5702_peg365	AODT01000007.1	114966	114139	-	Methylglyoxal reductase, dihydroxyacetone producing @ 2,5-didehydrogluconate reductase (2-dehydro-D-gluconate-forming) (EC 1.1.1.274)
<i>Pcc</i> ICMP5702_peg366	AODT01000007.1	116412	115249	-	NADPH-dependent broad range aldehyde dehydrogenase YqhD
<i>Pcc</i> ICMP5702_peg367	AODT01000007.1	117156	116416	-	FMN reductase [NAD(P)H] (EC 1.5.1.39)
<i>Pcc</i> ICMP5702_peg368	AODT01000007.1	117410	118399	+	Transcriptional regulator YqhC, positively regulates YqhD and DkgA
<i>Pcc</i> ICMP5702_peg369	AODT01000007.1	119089	118430	-	DedA family inner membrane protein YghB
<i>Pcc</i> ICMP5702_peg370	AODT01000007.1	120744	119554	-	Cystathionine beta-lyase (EC 4.4.1.8)

<i>Pcc</i> ICMP5702_peg371	AODT01000007.1	122299	121007	-	TRAP-type C4-dicarboxylate transport system, large permease component
<i>Pcc</i> ICMP5702_peg372	AODT01000007.1	122821	122315	-	TRAP-type C4-dicarboxylate transport system, small permease component
<i>Pcc</i> ICMP5702_peg373	AODT01000007.1	123913	122936	-	TRAP-type C4-dicarboxylate transport system, periplasmic component
<i>Pcc</i> ICMP5702_peg374	AODT01000007.1	124412	124287	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg375	AODT01000007.1	124619	125629	+	TonB-ExbBD energy transducing system, ExbB subunit
<i>Pcc</i> ICMP5702_peg376	AODT01000007.1	125633	126058	+	TonB-ExbBD energy transducing system, ExbD subunit
<i>Pcc</i> ICMP5702_peg377	AODT01000007.1	127186	126167	-	Sucrose operon repressor ScrR, LacI family
<i>Pcc</i> ICMP5702_peg378	AODT01000007.1	128626	127217	-	Sucrose-6-phosphate hydrolase (EC 3.2.1.26)
<i>Pcc</i> ICMP5702_peg379	AODT01000007.1	129996	128626	-	PTS system, sucrose-specific IIB component (EC 2.7.1.211) / PTS system, sucrose-specific IIC component
<i>Pcc</i> ICMP5702_peg380	AODT01000007.1	131602	130067	-	Sucrose outer membrane porin
<i>Pcc</i> ICMP5702_peg381	AODT01000007.1	132725	131802	-	Fructokinase (EC 2.7.1.4)
<i>Pcc</i> ICMP5702_peg382	AODT01000007.1	133049	133237	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg383	AODT01000007.1	133230	133958	+	Polymer-forming bactofilin
<i>Pcc</i> ICMP5702_peg384	AODT01000007.1	133990	136707	+	CRISPR-associated helicase Cas3
<i>Pcc</i> ICMP5702_peg385	AODT01000007.1	137170	136697	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg386	AODT01000007.1	137536	137174	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg387	AODT01000007.1	137732	137869	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg388	AODT01000007.1	138150	139718	+	CRISPR-associated protein, Cse1 family
<i>Pcc</i> ICMP5702_peg389	AODT01000007.1	139702	140349	+	CRISPR-associated protein, Cse2 family
<i>Pcc</i> ICMP5702_peg390	AODT01000007.1	140353	141420	+	CRISPR-associated protein, Cse4 family
<i>Pcc</i> ICMP5702_peg391	AODT01000007.1	141430	142164	+	CRISPR-associated protein, Cas5e family
<i>Pcc</i> ICMP5702_peg392	AODT01000007.1	142164	142811	+	CRISPR-associated protein, Cse3 family
<i>Pcc</i> ICMP5702_peg393	AODT01000007.1	142839	143756	+	CRISPR-associated protein Cas1
<i>Pcc</i> ICMP5702_peg394	AODT01000007.1	143757	144050	+	CRISPR-associated protein Cas2
<i>Pcc</i> ICMP5702_peg395	AODT01000007.1	144314	144030	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg396	AODT01000007.1	144733	144551	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg397	AODT01000007.1	145283	144912	-	Transcriptional regulator, Xre family
<i>Pcc</i> ICMP5702_peg398	AODT01000007.1	145617	145357	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg399	AODT01000007.1	145854	146270	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg400	AODT01000007.1	146991	146482	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg401	AODT01000007.1	147413	147574	+	CRISPR-associated protein Cas2
<i>Pcc</i> ICMP5702_peg402	AODT01000007.1	148419	148877	+	FIG00905442: Hypothetical protein
<i>Pcc</i> ICMP5702_peg403	AODT01000007.1	150324	148972	-	Aromatic-L-amino-acid decarboxylase (EC 4.1.1.28)
<i>Pcc</i> ICMP5702_peg404	AODT01000007.1	151646	150375	-	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg405	AODT01000007.1	151785	152231	+	Transcriptional regulator, HxlR family

<i>Pcc</i> ICMP5702_peg406	AODT01000007.1	152241	152708	+	UPF0306 protein YhbP
<i>Pcc</i> ICMP5702_peg407	AODT01000007.1	152797	153450	+	Uncharacterized protein YraR
<i>Pcc</i> ICMP5702_peg408	AODT01000007.1	153926	153462	-	Ribonucleotide reductase of class III (anaerobic), activating protein (EC 1.97.1.4)
<i>Pcc</i> ICMP5702_peg409	AODT01000007.1	156145	154007	-	Ribonucleotide reductase of class III (anaerobic), large subunit (EC 1.17.4.2)
<i>Pcc</i> ICMP5702_peg410	AODT01000007.1	156932	156546	-	2-iminobutanoate/2-iminopropanoate deaminase RidA/TdcF (EC 3.5.99.10)
<i>Pcc</i> ICMP5702_peg411	AODT01000007.1	157495	157031	-	Aspartate carbamoyltransferase regulatory chain (PyrI)
<i>Pcc</i> ICMP5702_peg412	AODT01000007.1	158446	157511	-	Aspartate carbamoyltransferase (EC 2.1.3.2)
<i>Pcc</i> ICMP5702_peg413	AODT01000007.1	158643	158521	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg414	AODT01000007.1	158896	159363	+	Protein YjgK, linked to biofilm formation
<i>Pcc</i> ICMP5702_peg415	AODT01000007.1	160418	159411	-	Ornithine carbamoyltransferase (EC 2.1.3.3)
<i>Pcc</i> ICMP5702_peg416	AODT01000007.1	160580	161005	+	Ribonuclease E inhibitor RraB
<i>Pcc</i> ICMP5702_peg417	AODT01000007.1	161618	161115	-	Uncharacterized N-acetyltransferase YjgM
<i>Pcc</i> ICMP5702_peg418	AODT01000007.1	161654	161770	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg419	AODT01000007.1	162038	163219	+	FIG018993: membrane protein
<i>Pcc</i> ICMP5702_peg420	AODT01000007.1	163229	164266	+	Zn-dependent protease with chaperone function
<i>Pcc</i> ICMP5702_peg421	AODT01000007.1	164867	165967	+	Homoserine O-acetyltransferase (EC 2.3.1.31)
<i>Pcc</i> ICMP5702_peg422	AODT01000007.1	166180	167799	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg423	AODT01000007.1	168442	167879	-	RNA:NAD 2'-phosphotransferase
<i>Pcc</i> ICMP5702_peg424	AODT01000007.1	171451	168581	-	Valyl-tRNA synthetase (EC 6.1.1.9)
<i>Pcc</i> ICMP5702_peg425	AODT01000007.1	171913	171464	-	DNA polymerase III chi subunit (EC 2.7.7.7)
<i>Pcc</i> ICMP5702_peg426	AODT01000007.1	173529	172018	-	Cytosol aminopeptidase PepA (EC 3.4.11.1)
<i>Pcc</i> ICMP5702_peg427	AODT01000007.1	173812	174927	+	Lipopolysaccharide export system permease protein LptF
<i>Pcc</i> ICMP5702_peg428	AODT01000007.1	174927	176003	+	Lipopolysaccharide export system permease protein LptG
<i>Pcc</i> ICMP5702_peg429	AODT01000007.1	176519	177778	+	Integrase
<i>Pcc</i> ICMP5702_peg430	AODT01000007.1	177915	180695	+	Type I restriction-modification system, restriction subunit R (EC 3.1.21.3)
<i>Pcc</i> ICMP5702_peg431	AODT01000007.1	180695	182509	+	Type I restriction-modification system, specificity subunit S
<i>Pcc</i> ICMP5702_peg432	AODT01000007.1	182513	184243	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg433	AODT01000007.1	184240	185043	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg434	AODT01000007.1	185045	186565	+	2.1.1.72)
<i>Pcc</i> ICMP5702_peg435	AODT01000007.1	187748	186978	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg436	AODT01000007.1	188184	187957	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg437	AODT01000007.1	188246	188404	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg438	AODT01000007.1	189506	188550	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg439	AODT01000007.1	191713	190256	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg440	AODT01000007.1	192104	192835	+	FIG00711288: Hypothetical protein
<i>Pcc</i> ICMP5702_peg441	AODT01000007.1	192890	193567	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg442	AODT01000007.1	193665	194030	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg443	AODT01000007.1	194073	194480	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg444	AODT01000007.1	194513	194725	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg445	AODT01000007.1	194807	195628	+	UPF0380 proteins YafZ and homologs
<i>Pcc</i> ICMP5702_peg446	AODT01000007.1	195681	196154	+	UPF0758 family protein
<i>Pcc</i> ICMP5702_peg447	AODT01000007.1	196194	196529	+	YafW protein (antitoxin to YkfI)
<i>Pcc</i> ICMP5702_peg448	AODT01000007.1	196599	196811	+	YkfI toxin protein
<i>Pcc</i> ICMP5702_peg449	AODT01000007.1	197037	197870	+	Z1226 protein
<i>Pcc</i> ICMP5702_peg450	AODT01000007.1	197980	198231	+	FIG00634356: Hypothetical protein
<i>Pcc</i> ICMP5702_peg451	AODT01000007.1	198285	198680	+	Hypothetical protein; Some similarities with unknown protein
<i>Pcc</i> ICMP5702_peg452	AODT01000007.1	198994	198875	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg453	AODT01000007.1	199082	199216	+	Integrase
<i>Pcc</i> ICMP5702_peg454	AODT01000007.1	199298	200272	+	Integrase
<i>Pcc</i> ICMP5702_peg455	AODT01000007.1	200309	200518	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg456	AODT01000007.1	201049	200765	-	Antitoxin HigA
<i>Pcc</i> ICMP5702_peg457	AODT01000007.1	201359	201039	-	Toxin HigB
<i>Pcc</i> ICMP5702_peg458	AODT01000007.1	201620	201474	-	Replicative helicase RepA
<i>Pcc</i> ICMP5702_peg459	AODT01000007.1	201762	201941	+	Integrase
<i>Pcc</i> ICMP5702_peg460	AODT01000007.1	202405	202073	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg461	AODT01000007.1	202657	203532	+	Putative transcriptional regulator STM3175
<i>Pcc</i> ICMP5702_peg462	AODT01000007.1	204098	204517	+	Acetyltransferase
<i>Pcc</i> ICMP5702_peg463	AODT01000007.1	204617	205738	+	LSU ribosomal protein L16p arginine hydroxylase
<i>Pcc</i> ICMP5702_peg464	AODT01000007.1	205780	205965	+	putative exported lipase
<i>Pcc</i> ICMP5702_peg465	AODT01000007.1	206026	206154	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg466	AODT01000007.1	207675	206236	-	Aspartate ammonia-lyase (EC 4.3.1.1)
<i>Pcc</i> ICMP5702_peg467	AODT01000007.1	207781	207653	-	Aspartate ammonia-lyase (EC 4.3.1.1)
<i>Pcc</i> ICMP5702_peg468	AODT01000007.1	208922	207927	-	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg469	AODT01000007.1	209851	209516	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg470	AODT01000007.1	210454	212532	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg471	AODT01000007.1	212525	213838	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg472	AODT01000007.1	213854	214048	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg473	AODT01000007.1	215723	214128	-	Transcriptional regulatory protein RtcR
<i>Pcc</i> ICMP5702_peg474	AODT01000007.1	215915	217150	+	RNA-2',3'-PO4:RNA-5'-OH ligase
<i>Pcc</i> ICMP5702_peg475	AODT01000007.1	217167	218510	+	FIG00906026: Hypothetical protein
<i>Pcc</i> ICMP5702_peg476	AODT01000007.1	218590	218874	+	Antitoxin DinJ (binds YafQ toxin)
<i>Pcc</i> ICMP5702_peg477	AODT01000007.1	218871	219176	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg478	AODT01000007.1	219973	219182	-	Possible restriction endonuclease
<i>Pcc</i> ICMP5702_peg479	AODT01000007.1	220127	221224	+	Uncharacterized outer membrane protein YaiW
<i>Pcc</i> ICMP5702_peg480	AODT01000007.1	222743	221274	-	Na(+)-dependent bicarbonate transporter BicA
<i>Pcc</i> ICMP5702_peg481	AODT01000007.1	223441	222740	-	Carbonic anhydrase, beta class (EC 4.2.1.1)
<i>Pcc</i> ICMP5702_peg482	AODT01000007.1	225941	223992	-	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg483	AODT01000007.1	229092	226381	-	Mg(2+) transport ATPase, P-type (EC 3.6.3.2)
<i>Pcc</i> ICMP5702_peg484	AODT01000007.1	231111	229534	-	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg485	AODT01000007.1	231271	231393	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg486	AODT01000007.1	231887	231573	-	L-rhamnose mutarotase (EC 5.1.3.32)
<i>Pcc</i> ICMP5702_peg487	AODT01000007.1	232821	231997	-	Rhamnulose-1-phosphate aldolase (EC 4.1.2.19)
<i>Pcc</i> ICMP5702_peg488	AODT01000007.1	234088	232826	-	L-rhamnose isomerase (EC 5.3.1.14)
<i>Pcc</i> ICMP5702_peg489	AODT01000007.1	235575	234085	-	Rhamnulokinase (EC 2.7.1.5)
<i>Pcc</i> ICMP5702_peg490	AODT01000007.1	235644	235757	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg491	AODT01000007.1	235912	236751	+	L-rhamnose operon regulatory protein RhaS
<i>Pcc</i> ICMP5702_peg492	AODT01000007.1	236776	237630	+	L-rhamnose operon transcriptional activator RhaR
<i>Pcc</i> ICMP5702_peg493	AODT01000007.1	237692	237982	+	Prevent host death protein, Phd antitoxin
<i>Pcc</i> ICMP5702_peg494	AODT01000007.1	237970	238275	+	Death on curing protein, Doc toxin
<i>Pcc</i> ICMP5702_peg495	AODT01000007.1	240101	238395	-	ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines) / ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg496	AODT01000007.1	240964	240098	-	ABC transporter, permease protein 2 (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg497	AODT01000007.1	241913	240957	-	ABC transporter, permease protein 1 (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg498	AODT01000007.1	243507	241894	-	ABC transporter, substrate-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg499	AODT01000007.1	243648	244238	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg500	AODT01000007.1	244451	244777	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg501	AODT01000007.1	244920	245066	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg502	AODT01000007.1	245186	245800	+	DUF1440 domain-containing membrane protein
<i>Pcc</i> ICMP5702_peg503	AODT01000007.1	246470	246009	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg504	AODT01000007.1	246972	246586	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg505	AODT01000007.1	247501	247124	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg506	AODT01000007.1	247961	247554	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg507	AODT01000007.1	248410	248027	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg508	AODT01000007.1	249561	248527	-	L-rhamnose-proton symporter
<i>Pcc</i> ICMP5702_peg509	AODT01000007.1	249887	250393	+	Putative inner membrane protein (Fragment)
<i>Pcc</i> ICMP5702_peg510	AODT01000007.1	250488	251525	+	Putative oxidoreductase YncB
<i>Pcc</i> ICMP5702_peg511	AODT01000007.1	251878	251576	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg512	AODT01000007.1	252145	251969	-	Hypothetical protein

<i>Pcc</i> ICMP5702_peg513	AODT01000007.1	252270	252157	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg514	AODT01000007.1	252805	252377	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg515	AODT01000007.1	252930	252802	-	T6SS component Hcp
<i>Pcc</i> ICMP5702_peg516	AODT01000007.1	254492	253281	-	2-polyprenylphenol hydroxylase
<i>Pcc</i> ICMP5702_peg517	AODT01000007.1	255698	254520	-	2-polyprenyl-6-methoxyphenol hydroxylase
<i>Pcc</i> ICMP5702_peg518	AODT01000007.1	257069	255744	-	Xaa-Pro aminopeptidase (EC 3.4.11.9)
<i>Pcc</i> ICMP5702_peg519	AODT01000007.1	257731	257144	-	UPF0149 exported protein YgfB
<i>Pcc</i> ICMP5702_peg520	AODT01000007.1	257924	258253	+	Z-ring-associated protein ZapA
<i>Pcc</i> ICMP5702_peg521	AODT01000007.1	258452	259198	+	5-formyltetrahydrofolate cyclo-ligase (EC 6.3.3.2)
					NadR transcriptional regulator / Nicotinamide-nucleotide adenylyltransferase, NadR family (EC 2.7.7.1) / Ribosylnicotinamide kinase (EC 2.7.1.22)
<i>Pcc</i> ICMP5702_peg522	AODT01000007.1	260448	259195	-	
<i>Pcc</i> ICMP5702_peg523	AODT01000007.1	261948	260566	-	DNA repair protein RadA
<i>Pcc</i> ICMP5702_peg524	AODT01000007.1	262943	261966	-	Phosphoserine phosphatase (EC 3.1.3.3)
<i>Pcc</i> ICMP5702_peg525	AODT01000007.1	263100	263798	+	Protein Smp
<i>Pcc</i> ICMP5702_peg526	AODT01000007.1	264767	263853	-	FIG00905227: Hypothetical protein
<i>Pcc</i> ICMP5702_peg527	AODT01000007.1	265061	266650	+	Peptide chain release factor 3
<i>Pcc</i> ICMP5702_peg528	AODT01000007.1	267151	267759	+	Osmotically inducible protein OsmY
<i>Pcc</i> ICMP5702_peg529	AODT01000007.1	267905	268066	+	UPF0391 membrane protein YtjA
<i>Pcc</i> ICMP5702_peg530	AODT01000007.1	268205	268393	+	UPF0337 family protein
<i>Pcc</i> ICMP5702_peg531	AODT01000007.1	268508	269305	+	Putative deoxyribonuclease YjjV
<i>Pcc</i> ICMP5702_peg532	AODT01000007.1	269621	270898	+	Na ⁺ dependent nucleoside transporter NupC
<i>Pcc</i> ICMP5702_peg533	AODT01000007.1	271048	271764	+	4'-phosphopantetheinyl transferase (EC 2.7.8.-) [enterobactin] siderophore
<i>Pcc</i> ICMP5702_peg534	AODT01000007.1	273844	271814	-	Colicin I receptor
<i>Pcc</i> ICMP5702_peg535	AODT01000007.1	275137	273875	-	Uncharacterized MFS-type transporter
					Isochorismate synthase (EC 5.4.4.2) @ Isochorismate synthase (EC 5.4.4.2) of siderophore biosynthesis
<i>Pcc</i> ICMP5702_peg536	AODT01000007.1	275469	276665	+	
<i>Pcc</i> ICMP5702_peg537	AODT01000007.1	276662	278287	+	2,3-dihydroxybenzoate-AMP ligase (EC 2.7.7.58) of siderophore biosynthesis
<i>Pcc</i> ICMP5702_peg538	AODT01000007.1	278298	279173	+	Isochorismatase (EC 3.3.2.1) of siderophore biosynthesis
<i>Pcc</i> ICMP5702_peg539	AODT01000007.1	279170	282313	+	Siderophore biosynthesis non-ribosomal peptide synthetase modules
					2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase (EC 1.3.1.28) of siderophore biosynthesis
<i>Pcc</i> ICMP5702_peg540	AODT01000007.1	282322	283089	+	
<i>Pcc</i> ICMP5702_peg541	AODT01000007.1	283112	289429	+	Siderophore biosynthesis non-ribosomal peptide synthetase modules
<i>Pcc</i> ICMP5702_peg542	AODT01000007.1	289426	291540	+	Siderophore biosynthesis non-ribosomal peptide synthetase modules
<i>Pcc</i> ICMP5702_peg543	AODT01000007.1	293122	291614	-	Outer membrane protein
<i>Pcc</i> ICMP5702_peg544	AODT01000007.1	301799	293229	-	Hypothetical protein formerly called flagellar hook-length control protein FliK
<i>Pcc</i> ICMP5702_peg545	AODT01000007.1	302748	302008	-	Phage tail collar domain

<i>Pcc</i> ICMP5702_peg546	AODT01000007.1	305350	303242	-	Peptidase M50
<i>Pcc</i> ICMP5702_peg547	AODT01000007.1	306672	305347	-	Probable membrane-fusion protein
<i>Pcc</i> ICMP5702_peg548	AODT01000007.1	307472	306669	-	Membrane-fusion protein
<i>Pcc</i> ICMP5702_peg549	AODT01000007.1	309844	307763	-	probable membrane protein YPO1990
<i>Pcc</i> ICMP5702_peg550	AODT01000007.1	309954	310556	+	Phosphonates utilization ATP-binding protein PhnK
<i>Pcc</i> ICMP5702_peg551	AODT01000007.1	310553	310840	+	Alpha-D-ribose 1-methylphosphonate 5-triphosphate diphosphatase (EC 3.6.1.63)
<i>Pcc</i> ICMP5702_peg552	AODT01000007.1	310884	311453	+	Ribose 1,5-bisphosphate phosphokinase PhnN (EC 2.7.4.23)
<i>Pcc</i> ICMP5702_peg553	AODT01000007.1	311492	312265	+	Metal-dependent hydrolases of the beta-lactamase superfamily I; PhnP protein
<i>Pcc</i> ICMP5702_peg554	AODT01000007.1	312621	312358	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg555	AODT01000007.1	312756	313652	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg556	AODT01000007.1	314869	313940	-	Ync
<i>Pcc</i> ICMP5702_peg557	AODT01000007.1	315638	314856	-	Ynd
<i>Pcc</i> ICMP5702_peg558	AODT01000007.1	315801	315920	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg559	AODT01000007.1	316104	316565	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg560	AODT01000007.1	316562	316771	+	Ner-like regulatory protein
<i>Pcc</i> ICMP5702_peg561	AODT01000007.1	317086	317931	+	Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg562	AODT01000007.1	317967	318557	+	Transporter, LysE family
<i>Pcc</i> ICMP5702_peg563	AODT01000007.1	319129	318554	-	Transcriptional regulator YjdC, AcrR family
<i>Pcc</i> ICMP5702_peg564	AODT01000007.1	320894	319164	-	Cytochrome c-type biogenesis protein DsbD, protein-disulfide reductase (EC 1.8.1.8)
<i>Pcc</i> ICMP5702_peg565	AODT01000007.1	321202	320870	-	Periplasmic divalent cation tolerance protein CutA
<i>Pcc</i> ICMP5702_peg566	AODT01000007.1	322635	321334	-	Anaerobic C4-dicarboxylate transporter DcuA
<i>Pcc</i> ICMP5702_peg567	AODT01000007.1	324459	323020	-	Aspartate ammonia-lyase (EC 4.3.1.1)
<i>Pcc</i> ICMP5702_peg568	AODT01000007.1	324941	325417	+	UPF0716 protein FxsA
<i>Pcc</i> ICMP5702_peg569	AODT01000007.1	325655	325948	+	Heat shock protein 10 kDa family chaperone GroES
<i>Pcc</i> ICMP5702_peg570	AODT01000007.1	325994	327640	+	Heat shock protein 60 kDa family chaperone GroEL
<i>Pcc</i> ICMP5702_peg571	AODT01000007.1	327906	328415	+	Chorismate--pyruvate lyase (EC 4.1.3.40)
<i>Pcc</i> ICMP5702_peg572	AODT01000007.1	328450	329313	+	4-hydroxybenzoate polyprenyltransferase (EC 2.5.1.39)
<i>Pcc</i> ICMP5702_peg573	AODT01000007.1	331970	329457	-	Glycerol-3-phosphate acyltransferase (EC 2.3.1.15)
<i>Pcc</i> ICMP5702_peg574	AODT01000007.1	332223	332588	+	Diacylglycerol kinase (EC 2.7.1.107)
<i>Pcc</i> ICMP5702_peg575	AODT01000007.1	332699	333307	+	SOS-response repressor and protease LexA (EC 3.4.21.88)
<i>Pcc</i> ICMP5702_peg576	AODT01000007.1	333753	333962	+	UPF0337 protein YjBJ
<i>Pcc</i> ICMP5702_peg577	AODT01000007.1	334522	334007	-	Zinc uptake regulation protein Zur
<i>Pcc</i> ICMP5702_peg578	AODT01000007.1	335337	334639	-	Quercetin 2,3-dioxygenase (EC 1.13.11.24) => YhhW
<i>Pcc</i> ICMP5702_peg579	AODT01000007.1	335451	336347	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg580	AODT01000007.1	337401	336406	-	Glutathione S-transferase, omega (EC 2.5.1.18)
<i>Pcc</i> ICMP5702_peg581	AODT01000007.1	337904	337509	-	Inner membrane protein YqjF

<i>Pcc</i> ICMP5702_peg582	AODT01000007.1	338468	338178	-	Inner membrane protein YqjK
<i>Pcc</i> ICMP5702_peg583	AODT01000007.1	338860	338465	-	Phage holin
<i>Pcc</i> ICMP5702_peg584	AODT01000007.1	339179	338874	-	ElaB protein
<i>Pcc</i> ICMP5702_peg585	AODT01000007.1	339758	339354	-	Periplasmic protein YqjC
<i>Pcc</i> ICMP5702_peg586	AODT01000007.1	340159	339764	-	Uncharacterized protein YqjB
<i>Pcc</i> ICMP5702_peg587	AODT01000007.1	340845	340162	-	DedA family inner membrane protein YqjA
<i>Pcc</i> ICMP5702_peg588	AODT01000007.1	342123	341347	-	Hexuronate utilization operon transcriptional repressor ExuR
<i>Pcc</i> ICMP5702_peg589	AODT01000007.1	343634	342333	-	Hexuronate transporter
<i>Pcc</i> ICMP5702_peg590	AODT01000007.1	344049	345458	+	Uronate isomerase (EC 5.3.1.12)
<i>Pcc</i> ICMP5702_peg591	AODT01000007.1	345571	347037	+	Altronate oxidoreductase (EC 1.1.1.58)
<i>Pcc</i> ICMP5702_peg592	AODT01000007.1	347057	348547	+	Altronate dehydratase (EC 4.2.1.7)
<i>Pcc</i> ICMP5702_peg593	AODT01000007.1	348637	349167	+	Inner membrane protein ygiV
<i>Pcc</i> ICMP5702_peg594	AODT01000007.1	350505	349258	-	Serine/threonine:Na ⁺ symporter SstT
<i>Pcc</i> ICMP5702_peg595	AODT01000007.1	351811	350858	-	Alkaline induced inner membrane protein Alx
<i>Pcc</i> ICMP5702_peg596	AODT01000007.1	353063	352065	-	Uncharacterized oxidoreductase YgjR
<i>Pcc</i> ICMP5702_peg597	AODT01000007.1	353225	354364	+	23S rRNA (guanine(1835)-N(2))-methyltransferase (EC 2.1.1.174)
<i>Pcc</i> ICMP5702_peg598	AODT01000007.1	356701	354647	-	2,4-dienoyl-CoA reductase [NADPH] (EC 1.3.1.34)
<i>Pcc</i> ICMP5702_peg599	AODT01000007.1	356917	357213	+	FIG00614148: Hypothetical protein
<i>Pcc</i> ICMP5702_peg600	AODT01000007.1	357441	357929	+	Spheroplast protein Y
<i>Pcc</i> ICMP5702_peg601	AODT01000007.1	358139	359608	+	GGDEF domain protein
<i>Pcc</i> ICMP5702_peg602	AODT01000007.1	359680	360039	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg603	AODT01000007.1	360311	362275	+	PTS system, beta-glucoside-specific IIB component / PTS system, beta-glucoside-specific IIC component / PTS system, beta-glucoside-specific IIA component
<i>Pcc</i> ICMP5702_peg604	AODT01000007.1	362300	363523	+	Putative arylsulfatase regulatory protein
<i>Pcc</i> ICMP5702_peg605	AODT01000007.1	363580	365259	+	Arylsulfatase (EC 3.1.6.1)
<i>Pcc</i> ICMP5702_peg606	AODT01000007.1	366722	365334	-	6-phospho-beta-glucosidase (EC 3.2.1.86)
<i>Pcc</i> ICMP5702_peg607	AODT01000007.1	366794	366991	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg608	AODT01000007.1	367114	367617	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg609	AODT01000007.1	368115	372341	+	Assimilatory nitrate reductase large subunit (EC 1.7.99.4)
<i>Pcc</i> ICMP5702_peg610	AODT01000007.1	373216	372452	-	Intracellular protease
<i>Pcc</i> ICMP5702_peg611	AODT01000007.1	373396	374298	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg612	AODT01000007.1	374705	376696	+	O-antigen acetylase
<i>Pcc</i> ICMP5702_peg613	AODT01000007.1	377277	377780	+	G/U mismatch-specific uracil DNA glycosylase (EC 3.2.2.28)
<i>Pcc</i> ICMP5702_peg614	AODT01000007.1	379713	377878	-	RNA polymerase sigma factor RpoD
<i>Pcc</i> ICMP5702_peg615	AODT01000007.1	381622	379868	-	DNA primase DnaG
<i>Pcc</i> ICMP5702_peg616	AODT01000007.1	381992	381777	-	SSU ribosomal protein S21p

<i>Pcc</i> ICMP5702_peg617	AODT01000007.1	382105	381983	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg618	AODT01000007.1	382220	383233	+	N(6)-L-threonylcarbamoyladenine synthase (EC 2.3.1.234)
<i>Pcc</i> ICMP5702_peg619	AODT01000007.1	383814	383344	-	Arginine pathway regulatory protein ArgR, repressor of arg regulon
<i>Pcc</i> ICMP5702_peg620	AODT01000007.1	384284	385222	+	Malate dehydrogenase (EC 1.1.1.37)
<i>Pcc</i> ICMP5702_peg621	AODT01000007.1	385556	385293	-	Ner-like regulatory protein
<i>Pcc</i> ICMP5702_peg622	AODT01000007.1	385879	386130	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg623	AODT01000007.1	386380	386754	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg624	AODT01000007.1	387803	386832	-	Octaprenyl diphosphate synthase (EC 2.5.1.90)
<i>Pcc</i> ICMP5702_peg625	AODT01000007.1	388060	388371	+	LSU ribosomal protein L21p
<i>Pcc</i> ICMP5702_peg626	AODT01000007.1	388391	388648	+	LSU ribosomal protein L27p
<i>Pcc</i> ICMP5702_peg627	AODT01000007.1	388738	389700	+	Uncharacterized inner membrane transporter YhbE
<i>Pcc</i> ICMP5702_peg628	AODT01000007.1	389960	391132	+	GTP-binding protein Obg
<i>Pcc</i> ICMP5702_peg629	AODT01000007.1	392633	391200	-	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)
<i>Pcc</i> ICMP5702_peg630	AODT01000007.1	392902	393378	+	Transcription elongation factor GreA
<i>Pcc</i> ICMP5702_peg631	AODT01000007.1	393800	393507	-	RNA-binding protein YhbY
<i>Pcc</i> ICMP5702_peg632	AODT01000007.1	393944	394573	+	23S rRNA (uridine(2552)-2'-O)-methyltransferase (EC 2.1.1.166)
<i>Pcc</i> ICMP5702_peg633	AODT01000007.1	394621	396570	+	Cell division-associated, ATP-dependent zinc metalloprotease FtsH
<i>Pcc</i> ICMP5702_peg634	AODT01000007.1	396692	397525	+	Dihydropteroate synthase (EC 2.5.1.15)
<i>Pcc</i> ICMP5702_peg635	AODT01000007.1	397533	398870	+	Phosphoglucosamine mutase (EC 5.4.2.10)
<i>Pcc</i> ICMP5702_peg636	AODT01000007.1	399120	399452	+	Protein translocase membrane subunit SecG
<i>Pcc</i> ICMP5702_peg637	AODT01000007.1	400642	399626	-	Putative oxidoreductase YncB
<i>Pcc</i> ICMP5702_peg638	AODT01000007.1	401321	400695	-	FIG00905929: Hypothetical protein
<i>Pcc</i> ICMP5702_peg639	AODT01000007.1	405459	401386	-	Polyketide synthase modules and related proteins
<i>Pcc</i> ICMP5702_peg640	AODT01000007.1	411038	405537	-	Polyketide synthase type I
<i>Pcc</i> ICMP5702_peg641	AODT01000007.1	411451	411179	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg642	AODT01000007.1	411823	411551	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg643	AODT01000007.1	413345	411834	-	Polyketide synthase modules and related proteins
<i>Pcc</i> ICMP5702_peg644	AODT01000007.1	414106	413477	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg645	AODT01000007.1	414435	417530	+	Polyketide synthase modules and related proteins
<i>Pcc</i> ICMP5702_peg646	AODT01000007.1	418160	417729	-	FIG00904614: Hypothetical protein
<i>Pcc</i> ICMP5702_peg647	AODT01000007.1	418678	418217	-	Phage lysozyme R (EC 3.2.1.17)
<i>Pcc</i> ICMP5702_peg648	AODT01000007.1	419264	418671	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg649	AODT01000007.1	419699	420313	+	Two-component transcriptional response regulator, LuxR family
<i>Pcc</i> ICMP5702_peg650	AODT01000007.1	420919	421371	+	Bacterial ribosome SSU maturation protein RimP
<i>Pcc</i> ICMP5702_peg651	AODT01000007.1	421393	422922	+	Transcription termination protein NusA
<i>Pcc</i> ICMP5702_peg652	AODT01000007.1	422948	425647	+	Translation initiation factor 2

<i>Pcc</i> ICMP5702_peg653	AODT01000007.1	425722	426120	+	Ribosome-binding factor A
<i>Pcc</i> ICMP5702_peg654	AODT01000007.1	426120	427064	+	tRNA pseudouridine(55) synthase (EC 5.4.99.25)
<i>Pcc</i> ICMP5702_peg655	AODT01000007.1	427187	427456	+	SSU ribosomal protein S15p (S13e)
<i>Pcc</i> ICMP5702_peg656	AODT01000007.1	427706	429826	+	Polyribonucleotide nucleotidyltransferase (EC 2.7.7.8)
<i>Pcc</i> ICMP5702_peg657	AODT01000007.1	429967	430851	+	Lipoprotein NlpI
<i>Pcc</i> ICMP5702_peg658	AODT01000007.1	431026	432924	+	DEAD-box ATP-dependent RNA helicase DeaD (= CshA) (EC 3.6.4.13)
<i>Pcc</i> ICMP5702_peg659	AODT01000007.1	434043	433012	-	Luciferase-like monooxygenase YhbW
<i>Pcc</i> ICMP5702_peg660	AODT01000007.1	435062	434184	-	Uncharacterized peptidase U32 family member YhbV
<i>Pcc</i> ICMP5702_peg661	AODT01000007.1	436069	435074	-	Uncharacterized protease YhbU
<i>Pcc</i> ICMP5702_peg662	AODT01000007.1	436426	436950	+	Uncharacterized protein YhbT
<i>Pcc</i> ICMP5702_peg663	AODT01000007.1	436944	437486	+	Uncharacterized N-acetyltransferase YhbS
<i>Pcc</i> ICMP5702_peg664	AODT01000007.1	437810	437511	-	UPF0213 protein YhbQ
<i>Pcc</i> ICMP5702_peg665	AODT01000007.1	438014	439492	+	Aminobenzoyl-glutamate utilization protein B
<i>Pcc</i> ICMP5702_peg666	AODT01000007.1	439541	439663	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg667	AODT01000007.1	439885	440010	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg668	AODT01000007.1	440259	441038	+	Deoxyribose-phosphate aldolase (EC 4.1.2.4)
<i>Pcc</i> ICMP5702_peg669	AODT01000007.1	441132	442460	+	Thymidine phosphorylase (EC 2.4.2.4)
<i>Pcc</i> ICMP5702_peg670	AODT01000007.1	442550	443773	+	Phosphopentomutase (EC 5.4.2.7)
<i>Pcc</i> ICMP5702_peg671	AODT01000007.1	443821	444540	+	Purine nucleoside phosphorylase (EC 2.4.2.1)
<i>Pcc</i> ICMP5702_peg672	AODT01000007.1	446341	444593	-	Efflux ABC transporter, permease/ATP-binding protein
<i>Pcc</i> ICMP5702_peg673	AODT01000007.1	448885	446390	-	Ferrichrome-iron receptor
<i>Pcc</i> ICMP5702_peg674	AODT01000007.1	449968	449006	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg675	AODT01000007.1	450507	449965	-	RNA polymerase sigma-70 factor, ECF subfamily
<i>Pcc</i> ICMP5702_peg676	AODT01000007.1	451227	450748	-	Putative exported protein precursor
<i>Pcc</i> ICMP5702_peg677	AODT01000007.1	451882	451439	-	Ribosomal-protein-S18p-alanine acetyltransferase (EC 2.3.1.128)
<i>Pcc</i> ICMP5702_peg678	AODT01000007.1	452264	451833	-	DNA polymerase III psi subunit (EC 2.7.7.7)
<i>Pcc</i> ICMP5702_peg679	AODT01000007.1	452424	453473	+	16S rRNA (guanine(1207)-N(2))-methyltransferase (EC 2.1.1.172)
<i>Pcc</i> ICMP5702_peg680	AODT01000007.1	454502	453510	-	Oxidoreductase, aldo/keto reductase family
<i>Pcc</i> ICMP5702_peg681	AODT01000007.1	454604	455521	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg682	AODT01000007.1	456438	456148	-	putative membrane protein
<i>Pcc</i> ICMP5702_peg683	AODT01000007.1	457446	456544	-	Transcriptional regulator of alpha-acetolactate operon AlsR
<i>Pcc</i> ICMP5702_peg684	AODT01000007.1	457576	458358	+	Alpha-acetolactate decarboxylase (EC 4.1.1.5)
<i>Pcc</i> ICMP5702_peg685	AODT01000007.1	458380	460059	+	Acetolactate synthase, catabolic (EC 2.2.1.6)
<i>Pcc</i> ICMP5702_peg686	AODT01000007.1	460194	461657	+	putative membrane protein
<i>Pcc</i> ICMP5702_peg687	AODT01000007.1	462856	461705	-	Lactaldehyde reductase (EC 1.1.1.77)
<i>Pcc</i> ICMP5702_peg688	AODT01000007.1	463419	464534	+	Aminomethyltransferase (glycine cleavage system T protein) (EC 2.1.2.10)

<i>Pcc</i> ICMP5702_peg689	AODT01000007.1	464594	464986	+	Glycine cleavage system H protein
<i>Pcc</i> ICMP5702_peg690	AODT01000007.1	465105	467978	+	1.4.4.2)
<i>Pcc</i> ICMP5702_peg691	AODT01000007.1	468123	468593	+	Acetyltransferase
<i>Pcc</i> ICMP5702_peg692	AODT01000007.1	469354	468728	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg693	AODT01000007.1	470315	469368	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg694	AODT01000007.1	470776	471648	+	ABC transporter, permease protein 1 (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg695	AODT01000007.1	471638	472558	+	ABC transporter, permease protein 2 (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg696	AODT01000007.1	472596	473420	+	3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17)
<i>Pcc</i> ICMP5702_peg697	AODT01000007.1	473420	474508	+	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg698	AODT01000007.1	474501	475808	+	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg699	AODT01000007.1	477116	475854	-	Lactose permease
<i>Pcc</i> ICMP5702_peg700	AODT01000007.1	479532	477388	-	alpha-galactosidase (EC 3.2.1.22)
<i>Pcc</i> ICMP5702_peg701	AODT01000007.1	480760	479756	-	Putative ThuR, regulatory protein for trehalosemaltose transport
<i>Pcc</i> ICMP5702_peg702	AODT01000007.1	481423	480815	-	Uncharacterized hydrolase DSY2054
<i>Pcc</i> ICMP5702_peg703	AODT01000007.1	481702	482349	+	FIG01964566: Predicted membrane protein, hemolysin III homolog
<i>Pcc</i> ICMP5702_peg704	AODT01000007.1	483405	482404	-	tRNA-modifying protein YgfZ
<i>Pcc</i> ICMP5702_peg705	AODT01000007.1	483447	483578	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg706	AODT01000007.1	483641	483907	+	Succinate dehydrogenase flavin-adding protein, antitoxin of CptAB toxin-antitoxin
<i>Pcc</i> ICMP5702_peg707	AODT01000007.1	483927	484301	+	Putative inner membrane protein
<i>Pcc</i> ICMP5702_peg708	AODT01000007.1	484370	485305	+	23S rRNA (adenine(1618)-N(6))-methyltransferase (EC 2.1.1.181)
<i>Pcc</i> ICMP5702_peg709	AODT01000007.1	485694	485371	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg710	AODT01000007.1	486241	485723	-	Flavodoxin 2
<i>Pcc</i> ICMP5702_peg711	AODT01000007.1	486967	486581	-	FIG00906030: Hypothetical protein
<i>Pcc</i> ICMP5702_peg712	AODT01000007.1	488503	487175	-	Uncharacterized MFS-type transporter YhjE
<i>Pcc</i> ICMP5702_peg713	AODT01000007.1	488681	488800	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg714	AODT01000007.1	488815	489714	+	Site-specific tyrosine recombinase XerD
<i>Pcc</i> ICMP5702_peg715	AODT01000007.1	489853	490569	+	Thiol:disulfide interchange protein DsbC
<i>Pcc</i> ICMP5702_peg716	AODT01000007.1	490582	492339	+	Single-stranded-DNA-specific exonuclease RecJ
<i>Pcc</i> ICMP5702_peg717	AODT01000007.1	492498	493544	+	Peptide chain release factor 2 @ programmed frameshift-containing
<i>Pcc</i> ICMP5702_peg718	AODT01000007.1	493553	495070	+	Lysyl-tRNA synthetase (class II) (EC 6.1.1.6)
<i>Pcc</i> ICMP5702_peg719	AODT01000007.1	495421	495233	-	Alcohol dehydrogenase (EC 1.1.1.1)
<i>Pcc</i> ICMP5702_peg720	AODT01000007.1	495570	495424	-	Alcohol dehydrogenase (EC 1.1.1.1)
<i>Pcc</i> ICMP5702_peg721	AODT01000007.1	495695	496090	+	Redox-sensing transcriptional regulator QorR
<i>Pcc</i> ICMP5702_peg722	AODT01000007.1	496257	497012	+	Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg723	AODT01000007.1	497075	497758	+	Transporter, LysE family

<i>Pcc</i> ICMP5702_peg724	AODT01000007.1	498113	499327	+	Phage integrase, Phage P4-associated
<i>Pcc</i> ICMP5702_peg725	AODT01000007.1	499345	499992	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg726	AODT01000007.1	500316	500537	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg727	AODT01000007.1	500802	500617	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg728	AODT01000007.1	500908	501195	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg729	AODT01000007.1	501188	501376	+	FIG00613435: Hypothetical protein
<i>Pcc</i> ICMP5702_peg730	AODT01000007.1	501369	501557	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg731	AODT01000007.1	501547	501894	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg732	AODT01000007.1	501887	502180	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg733	AODT01000007.1	502197	502508	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg734	AODT01000007.1	502749	505427	+	Phage protein
<i>Pcc</i> ICMP5702_peg735	AODT01000007.1	506088	506687	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg736	AODT01000007.1	506701	507816	+	Zn peptidase with DNA binding
<i>Pcc</i> ICMP5702_peg737	AODT01000007.1	507969	507850	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg738	AODT01000007.1	508585	508352	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg739	AODT01000007.1	508748	509560	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg740	AODT01000007.1	509568	509774	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg741	AODT01000007.1	510211	509960	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg742	AODT01000007.1	510334	512097	+	IS, phage, Tn; Transposon-related functions
<i>Pcc</i> ICMP5702_peg743	AODT01000007.1	513149	513706	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg744	AODT01000007.1	513935	514225	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg745	AODT01000007.1	514439	514873	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg746	AODT01000007.1	514979	516133	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg747	AODT01000007.1	516518	516348	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg748	AODT01000007.1	517484	517963	+	T6SS component Hcp
<i>Pcc</i> ICMP5702_peg749	AODT01000007.1	518183	517983	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg750	AODT01000007.1	518836	518180	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg751	AODT01000007.1	519788	519153	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg752	AODT01000007.1	520061	520453	+	Uncharacterized protein YybH
<i>Pcc</i> ICMP5702_peg753	AODT01000007.1	521654	520587	-	DUF1176 domain-containing protein
<i>Pcc</i> ICMP5702_peg754	AODT01000007.1	521995	522954	+	Lipid A biosynthesis palmitoleoyltransferase (EC 2.3.1.242)
<i>Pcc</i> ICMP5702_peg755	AODT01000007.1	524501	523017	-	Cytosine/purine/uracil/thiamine/allantoin permease family protein
<i>Pcc</i> ICMP5702_peg756	AODT01000007.1	524653	525375	+	Transcriptional regulator, GntR family
<i>Pcc</i> ICMP5702_peg757	AODT01000007.1	525372	526109	+	Allantoin racemase (EC 5.1.99.3)
<i>Pcc</i> ICMP5702_peg758	AODT01000007.1	526124	527083	+	Uricase (urate oxidase) (EC 1.7.3.3)
<i>Pcc</i> ICMP5702_peg759	AODT01000007.1	527293	527159	-	Hypothetical protein

<i>Pcc</i> ICMP5702_peg760	AODT01000007.1	527540	527274	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg761	AODT01000007.1	527918	529273	+	Guanine/hypoxanthine permease GhxP
<i>Pcc</i> ICMP5702_peg762	AODT01000007.1	529556	531202	+	Uncharacterized Na(+)/H(+) exchanger YjcE
<i>Pcc</i> ICMP5702_peg763	AODT01000007.1	531390	531527	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg764	AODT01000007.1	531561	532271	+	Two-component transcriptional response regulator, LuxR family
<i>Pcc</i> ICMP5702_peg765	AODT01000007.1	532249	533748	+	Two-component system sensor histidine kinase
<i>Pcc</i> ICMP5702_peg766	AODT01000007.1	533764	533880	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg767	AODT01000007.1	534062	534283	+	Flp pilus assembly protein, pilin Flp
<i>Pcc</i> ICMP5702_peg768	AODT01000007.1	534291	534842	+	Type IV prepilin peptidase TadV/CpaA
<i>Pcc</i> ICMP5702_peg769	AODT01000007.1	534889	535833	+	Flp pilus assembly protein RcpC/CpaB
<i>Pcc</i> ICMP5702_peg770	AODT01000007.1	535913	537352	+	Type II/IV secretion system secretin RcpA/CpaC, associated with Flp pilus assembly
<i>Pcc</i> ICMP5702_peg771	AODT01000007.1	537374	538060	+	Flp pilus assembly protein CpaD
<i>Pcc</i> ICMP5702_peg772	AODT01000007.1	538075	539274	+	Type II/IV secretion system ATPase TadZ/CpaE, associated with Flp pilus assembly
<i>Pcc</i> ICMP5702_peg773	AODT01000007.1	539338	540738	+	Type II/IV secretion system ATP hydrolase Tada/VirB11/CpaF, Tada subfamily
<i>Pcc</i> ICMP5702_peg774	AODT01000007.1	540756	541736	+	Flp pilus assembly protein TadB
<i>Pcc</i> ICMP5702_peg775	AODT01000007.1	541751	542710	+	Type II/IV secretion system protein TadC, associated with Flp pilus assembly
<i>Pcc</i> ICMP5702_peg776	AODT01000007.1	542814	543665	+	Flp pilus assembly protein TadD, contains TPR repeat
<i>Pcc</i> ICMP5702_peg777	AODT01000007.1	543734	544237	+	FIG00904721: Hypothetical protein
<i>Pcc</i> ICMP5702_peg778	AODT01000007.1	544230	544862	+	FIG00904883: Hypothetical protein
<i>Pcc</i> ICMP5702_peg779	AODT01000007.1	545043	546662	+	Mlr7847 protein
<i>Pcc</i> ICMP5702_peg780	AODT01000007.1	546721	556458	+	Hemagglutinin
<i>Pcc</i> ICMP5702_peg781	AODT01000007.1	556713	558503	+	Outer membrane protein
<i>Pcc</i> ICMP5702_peg782	AODT01000007.1	558503	559258	+	RND efflux system, membrane fusion protein
<i>Pcc</i> ICMP5702_peg783	AODT01000007.1	559255	560610	+	probable membrane-fusion protein
<i>Pcc</i> ICMP5702_peg784	AODT01000007.1	560613	562742	+	cAMP-dependent protein kinase regulatory chain
<i>Pcc</i> ICMP5702_peg785	AODT01000007.1	563072	564802	+	Rhamnogalacturonate lyase (EC 4.2.2.-)
<i>Pcc</i> ICMP5702_peg786	AODT01000007.1	565842	564946	-	Transposase
<i>Pcc</i> ICMP5702_peg787	AODT01000007.1	567752	566094	-	Acetate permease ActP (cation/acetate symporter)
<i>Pcc</i> ICMP5702_peg788	AODT01000007.1	568060	567749	-	Inner membrane protein YjcH, clustering with ActP
<i>Pcc</i> ICMP5702_peg789	AODT01000007.1	570147	568186	-	Acetyl-CoA synthetase (EC 6.2.1.1)
<i>Pcc</i> ICMP5702_peg790	AODT01000007.1	571050	571442	+	global regulatory protein
<i>Pcc</i> ICMP5702_peg791	AODT01000007.1	571484	571600	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg792	AODT01000007.1	572180	574549	+	Ferrichrome-iron receptor
<i>Pcc</i> ICMP5702_peg793	AODT01000007.1	574722	575246	+	RNA polymerase ECF-type sigma factor
<i>Pcc</i> ICMP5702_peg794	AODT01000007.1	575243	576190	+	sigma factor regulatory protein, FecR/PupR family
<i>Pcc</i> ICMP5702_peg795	AODT01000007.1	576360	577370	+	putative membrane protein

<i>Pcc</i> ICMP5702_peg796	AODT01000007.1	579079	577553	-	Oligogalacturonide transporter
<i>Pcc</i> ICMP5702_peg797	AODT01000007.1	579463	579837	+	FIG00905046: Hypothetical protein
<i>Pcc</i> ICMP5702_peg798	AODT01000007.1	581317	579830	-	D-mannonate oxidoreductase (EC 1.1.1.57)
<i>Pcc</i> ICMP5702_peg799	AODT01000007.1	581521	581637	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg800	AODT01000007.1	581639	582919	+	O-acetylhomoserine sulfhydrylase (EC 2.5.1.49) @ O-succinylhomoserine sulfhydrylase (EC 2.5.1.48)
<i>Pcc</i> ICMP5702_peg801	AODT01000007.1	584050	582983	-	L,D-transpeptidase => YbiS
<i>Pcc</i> ICMP5702_peg802	AODT01000007.1	585032	584235	-	Aliphatic amidase AmiE (EC 3.5.1.4)
<i>Pcc</i> ICMP5702_peg803	AODT01000007.1	585590	585054	-	Cytochrome b561
<i>Pcc</i> ICMP5702_peg804	AODT01000007.1	589368	585835	-	Pyruvate-flavodoxin oxidoreductase
<i>Pcc</i> ICMP5702_peg805	AODT01000007.1	589430	589651	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg806	AODT01000007.1	589781	590206	+	FIG00613065: Hypothetical protein
<i>Pcc</i> ICMP5702_peg807	AODT01000007.1	590425	590937	+	GCN5-related N-acetyltransferase
<i>Pcc</i> ICMP5702_peg808	AODT01000007.1	591607	590981	-	Homoserine/homoserine lactone efflux protein
<i>Pcc</i> ICMP5702_peg809	AODT01000007.1	592645	591863	-	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg810	AODT01000007.1	593601	592930	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg811	AODT01000007.1	593855	593733	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg812	AODT01000007.1	594198	594689	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg813	AODT01000007.1	594682	595266	+	Cell filamentation protein Fic
<i>Pcc</i> ICMP5702_peg814	AODT01000007.1	595627	595376	-	mRNA interferase RelE
<i>Pcc</i> ICMP5702_peg815	AODT01000007.1	596466	596795	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg816	AODT01000007.1	596814	596954	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg817	AODT01000007.1	597972	597490	-	tmRNA-binding protein SmpB
<i>Pcc</i> ICMP5702_peg818	AODT01000007.1	598128	598574	+	Ribosome association toxin RatA
<i>Pcc</i> ICMP5702_peg819	AODT01000007.1	598555	598845	+	UPF0125 protein RatB
<i>Pcc</i> ICMP5702_peg820	AODT01000007.1	599419	599084	-	Outer membrane beta-barrel assembly protein BamE
<i>Pcc</i> ICMP5702_peg821	AODT01000007.1	601233	599572	-	DNA repair protein RecN
<i>Pcc</i> ICMP5702_peg822	AODT01000007.1	602211	601315	-	NAD kinase (EC 2.7.1.23)
<i>Pcc</i> ICMP5702_peg823	AODT01000007.1	602343	602930	+	Heat shock protein GrpE
<i>Pcc</i> ICMP5702_peg824	AODT01000007.1	603162	604400	+	Manganese transport protein MntH
<i>Pcc</i> ICMP5702_peg825	AODT01000007.1	604653	604450	-	2-hydroxymuconate tautomerase-like protein
<i>Pcc</i> ICMP5702_peg826	AODT01000007.1	605833	604667	-	Uncharacterized integral membrane protein YjiJ
<i>Pcc</i> ICMP5702_peg827	AODT01000007.1	606065	606646	+	GDP-mannose pyrophosphatase NudK
<i>Pcc</i> ICMP5702_peg828	AODT01000007.1	607028	608293	+	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg829	AODT01000007.1	608357	609238	+	ABC transporter, permease protein 1 (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg830	AODT01000007.1	609240	610052	+	ABC transporter, permease protein 2 (cluster 1, maltose/g3p/polyamine/iron)

<i>Pcc</i> ICMP5702_peg831	AODT01000007.1	610089	611174	+	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg832	AODT01000007.1	611391	612914	+	Arabinogalactan endo-1,4-beta-galactanase (EC 3.2.1.89)
<i>Pcc</i> ICMP5702_peg833	AODT01000007.1	614022	612985	-	Transcriptional regulator, LacI family
<i>Pcc</i> ICMP5702_peg834	AODT01000007.1	615064	614303	-	ABC transporter, ATP-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg835	AODT01000007.1	616062	615118	-	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg836	AODT01000007.1	616955	616059	-	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg837	AODT01000007.1	617149	617262	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg838	AODT01000007.1	618270	617368	-	Beta-glucoside bgl operon antiterminator, BglG family
<i>Pcc</i> ICMP5702_peg839	AODT01000007.1	619825	618365	-	6-phospho-beta-glucosidase (EC 3.2.1.86)
<i>Pcc</i> ICMP5702_peg840	AODT01000007.1	621788	619857	-	PTS system, beta-glucoside-specific IIB component / PTS system, beta-glucoside-specific IIC component / PTS system, beta-glucoside-specific IIA component
<i>Pcc</i> ICMP5702_peg841	AODT01000007.1	621877	622020	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg842	AODT01000007.1	624097	622103	-	Transketolase (EC 2.2.1.1)
<i>Pcc</i> ICMP5702_peg843	AODT01000007.1	625063	624113	-	Transaldolase (EC 2.2.1.2)
<i>Pcc</i> ICMP5702_peg844	AODT01000007.1	625734	625276	-	Ribose-5-phosphate isomerase B (EC 5.3.1.6)
<i>Pcc</i> ICMP5702_peg845	AODT01000007.1	626125	626280	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg846	AODT01000007.1	626277	627659	+	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg847	AODT01000007.1	627661	629433	+	Dihydroxyacetone kinase, ATP-dependent (EC 2.7.1.29)
<i>Pcc</i> ICMP5702_peg848	AODT01000007.1	629430	630209	+	Triosephosphate isomerase (EC 5.3.1.1)
<i>Pcc</i> ICMP5702_peg849	AODT01000007.1	630226	631062	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg850	AODT01000007.1	631100	631957	+	Putative oxidoreductase
<i>Pcc</i> ICMP5702_peg851	AODT01000007.1	632159	633121	+	Transcriptional regulator, SorC family
<i>Pcc</i> ICMP5702_peg852	AODT01000007.1	633393	635672	+	NADP-dependent malic enzyme (EC 1.1.1.40)
<i>Pcc</i> ICMP5702_peg853	AODT01000007.1	635851	635726	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg854	AODT01000007.1	635868	637142	+	Tryptophan-specific transport protein
<i>Pcc</i> ICMP5702_peg855	AODT01000007.1	637779	637327	-	Protein YaiI
<i>Pcc</i> ICMP5702_peg856	AODT01000007.1	638715	637783	-	Coproporphyrinogen III oxidase, aerobic (EC 1.3.3.3)
<i>Pcc</i> ICMP5702_peg857	AODT01000007.1	638885	639322	+	Acetyltransferase YpeA
<i>Pcc</i> ICMP5702_peg858	AODT01000007.1	639453	639974	+	RNA polymerase ECF-type sigma factor
<i>Pcc</i> ICMP5702_peg859	AODT01000007.1	639964	640911	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg860	AODT01000007.1	641031	643847	+	Putative Ton-B dependent hemine receptor
<i>Pcc</i> ICMP5702_peg861	AODT01000007.1	643873	646644	+	Probable zinc protease pqqL (EC 3.4.99.-)
<i>Pcc</i> ICMP5702_peg862	AODT01000007.1	646641	648314	+	Efflux ABC transporter, permease/ATP-binding protein
<i>Pcc</i> ICMP5702_peg863	AODT01000007.1	648502	649101	+	Predicted outer membrane lipoprotein YfeY
<i>Pcc</i> ICMP5702_peg864	AODT01000007.1	649244	650143	+	Predicted dye-decolorizing peroxidase (DyP), YfeX-like subgroup

<i>Pcc</i> ICMP5702_peg865	AODT01000007.1	650461	651489	+	Sulfate and thiosulfate binding protein CysP
<i>Pcc</i> ICMP5702_peg866	AODT01000007.1	651489	652343	+	Sulfate transport system permease protein CysT
<i>Pcc</i> ICMP5702_peg867	AODT01000007.1	652343	653236	+	Sulfate transport system permease protein CysW
<i>Pcc</i> ICMP5702_peg868	AODT01000007.1	653410	654291	+	Cysteine synthase B (EC 2.5.1.47)
<i>Pcc</i> ICMP5702_peg869	AODT01000007.1	656247	654295	-	Macrolide export ATP-binding/permease protein MacB
<i>Pcc</i> ICMP5702_peg870	AODT01000007.1	657450	656251	-	Macrolide-specific efflux protein MacA
<i>Pcc</i> ICMP5702_peg871	AODT01000007.1	657701	658381	+	Transcriptional regulatory protein cpxR
<i>Pcc</i> ICMP5702_peg872	AODT01000007.1	658381	659748	+	Two-component system sensor histidine kinase
<i>Pcc</i> ICMP5702_peg873	AODT01000007.1	660323	659814	-	PTS system, glucose-specific IIA component (EC 2.7.1.199)
<i>Pcc</i> ICMP5702_peg874	AODT01000007.1	662199	660472	-	Phosphoenolpyruvate-protein phosphotransferase of PTS system (EC 2.7.3.9)
<i>Pcc</i> ICMP5702_peg875	AODT01000007.1	662502	662245	-	Phosphotransferase system, phosphocarrier protein HPr
<i>Pcc</i> ICMP5702_peg876	AODT01000007.1	662618	662815	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg877	AODT01000007.1	663902	662934	-	Cysteine synthase (EC 2.5.1.47)
<i>Pcc</i> ICMP5702_peg878	AODT01000007.1	664892	664065	-	Sulfate transporter, CysZ-type
<i>Pcc</i> ICMP5702_peg879	AODT01000007.1	665117	666154	+	Cell division protein ZipA
<i>Pcc</i> ICMP5702_peg880	AODT01000007.1	666284	667537	+	L-methionine and branched-chain amino acid export protein YjeH
<i>Pcc</i> ICMP5702_peg881	AODT01000007.1	667963	667673	-	Uncharacterized protein YqiC
<i>Pcc</i> ICMP5702_peg882	AODT01000007.1	668449	669102	+	3,4-dihydroxy-2-butanone 4-phosphate synthase (EC 4.1.99.12)
<i>Pcc</i> ICMP5702_peg883	AODT01000007.1	670066	669206	-	Tellurite methyltransferase (EC 2.1.1.265)
<i>Pcc</i> ICMP5702_peg884	AODT01000007.1	671321	670173	-	Nitric oxide reductase FIRd-NAD(+) reductase
<i>Pcc</i> ICMP5702_peg885	AODT01000007.1	672861	671332	-	Anaerobic nitric oxide reductase flavorubredoxin
<i>Pcc</i> ICMP5702_peg886	AODT01000007.1	673027	674565	+	Anaerobic nitric oxide reductase transcription regulator NorR
<i>Pcc</i> ICMP5702_peg887	AODT01000007.1	676419	674776	-	Fumarate hydratase class I (EC 4.2.1.2)
<i>Pcc</i> ICMP5702_peg888	AODT01000007.1	676739	676903	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg889	AODT01000007.1	677787	676909	-	LysR-family transcriptional regulator STM3020
<i>Pcc</i> ICMP5702_peg890	AODT01000007.1	677927	678397	+	putative membrane protein
<i>Pcc</i> ICMP5702_peg891	AODT01000007.1	679097	678435	-	DNA-3-methyladenine glycosylase II (EC 3.2.2.21)
<i>Pcc</i> ICMP5702_peg892	AODT01000007.1	680073	679294	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg893	AODT01000007.1	680356	681438	+	ADA regulatory protein / Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63)
<i>Pcc</i> ICMP5702_peg894	AODT01000007.1	681453	682109	+	Alpha-ketoglutarate-dependent dioxygenase AlkB (EC 1.14.11.33)
<i>Pcc</i> ICMP5702_peg895	AODT01000007.1	683691	682162	-	redox proteins related to the succinate dehydrogenases and fumarate reductases
<i>Pcc</i> ICMP5702_peg896	AODT01000007.1	684137	683733	-	redox proteins related to the succinate dehydrogenases and fumarate reductases
<i>Pcc</i> ICMP5702_peg897	AODT01000007.1	685522	684146	-	Putative transport protein
<i>Pcc</i> ICMP5702_peg898	AODT01000007.1	686485	685523	-	NrfD protein
<i>Pcc</i> ICMP5702_peg899	AODT01000007.1	687176	686478	-	NrfC protein

<i>Pcc</i> ICMP5702_peg900	AODT01000007.1	688663	687698	-	Putative lipase/esterase
<i>Pcc</i> ICMP5702_peg901	AODT01000007.1	689135	690037	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg902	AODT01000007.1	690472	690194	-	bacteriocin immunity protein
<i>Pcc</i> ICMP5702_peg903	AODT01000007.1	692285	690489	-	T6SS PAAR-repeat protein / RhaS protein
<i>Pcc</i> ICMP5702_peg904	AODT01000007.1	692603	693817	+	Mannonate dehydratase (EC 4.2.1.8)
<i>Pcc</i> ICMP5702_peg905	AODT01000007.1	693847	694869	+	Starvation sensing protein RspB
<i>Pcc</i> ICMP5702_peg906	AODT01000007.1	695069	696439	+	Uncharacterized MFS-type transporter YdfJ
<i>Pcc</i> ICMP5702_peg907	AODT01000007.1	696543	698009	+	D-mannonate oxidoreductase (EC 1.1.1.57)
<i>Pcc</i> ICMP5702_peg908	AODT01000007.1	698212	698898	+	Transcriptional regulator YdfH, GntR family
<i>Pcc</i> ICMP5702_peg909	AODT01000007.1	700326	698965	-	3-phytase precursor (EC 3.1.3.8)
<i>Pcc</i> ICMP5702_peg910	AODT01000007.1	701694	700360	-	putative phospholipase
<i>Pcc</i> ICMP5702_peg911	AODT01000007.1	702370	701687	-	Ferric siderophore transport system, biopolymer transport protein ExbB
<i>Pcc</i> ICMP5702_peg912	AODT01000007.1	704696	702456	-	TonB-dependent receptor
<i>Pcc</i> ICMP5702_peg913	AODT01000007.1	705545	704787	-	putative TonB-dependent receptor
<i>Pcc</i> ICMP5702_peg914	AODT01000007.1	705951	705547	-	Biopolymer transport protein ExbD/TolR
<i>Pcc</i> ICMP5702_peg915	AODT01000007.1	707454	706261	-	Multidrug-efflux transporter, major facilitator superfamily (MFS)
<i>Pcc</i> ICMP5702_peg916	AODT01000007.1	709922	708057	-	Avirulence protein
<i>Pcc</i> ICMP5702_peg917	AODT01000007.1	711544	710228	-	Cytosine permease
<i>Pcc</i> ICMP5702_peg918	AODT01000007.1	712248	711559	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg919	AODT01000007.1	712691	712278	-	Acetyltransferase
<i>Pcc</i> ICMP5702_peg920	AODT01000007.1	712844	713014	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg921	AODT01000007.1	713530	713264	-	bacteriocin immunity protein
<i>Pcc</i> ICMP5702_peg922	AODT01000007.1	715338	713527	-	T6SS PAAR-repeat protein / RhaS protein
<i>Pcc</i> ICMP5702_peg923	AODT01000007.1	715716	716609	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg924	AODT01000007.1	716698	717858	+	Aspartate aminotransferase (EC 2.6.1.1)
<i>Pcc</i> ICMP5702_peg925	AODT01000007.1	717855	718781	+	Auxin efflux carrier family protein
<i>Pcc</i> ICMP5702_peg926	AODT01000007.1	718990	721209	+	Putative OMR family iron-siderophore receptor precursor
<i>Pcc</i> ICMP5702_peg927	AODT01000007.1	722663	721314	-	Glucarate dehydratase related protein YgcY
<i>Pcc</i> ICMP5702_peg928	AODT01000007.1	724002	722656	-	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg929	AODT01000007.1	724284	725033	+	ABC transporter, ATP-binding protein
<i>Pcc</i> ICMP5702_peg930	AODT01000007.1	725615	725046	-	Fimbrial subunit
<i>Pcc</i> ICMP5702_peg931	AODT01000007.1	726677	725643	-	probable exported protein YPO4040
<i>Pcc</i> ICMP5702_peg932	AODT01000007.1	727444	726695	-	Periplasmic fimbrial chaperone
<i>Pcc</i> ICMP5702_peg933	AODT01000007.1	730076	727482	-	Outer membrane usher protein
<i>Pcc</i> ICMP5702_peg934	AODT01000007.1	730678	730130	-	PapA
<i>Pcc</i> ICMP5702_peg935	AODT01000007.1	730832	730954	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg936	AODT01000007.1	731389	732162	+	FIG00905021: Hypothetical protein
<i>Pcc</i> ICMP5702_peg937	AODT01000007.1	732149	732619	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg938	AODT01000007.1	733251	732679	-	Transcriptional regulator, AcrR family
<i>Pcc</i> ICMP5702_peg939	AODT01000007.1	733345	734238	+	probable integral membrane protein NMA1777
<i>Pcc</i> ICMP5702_peg940	AODT01000007.1	734879	734328	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg941	AODT01000007.1	735070	734951	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg942	AODT01000007.1	735496	735095	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg943	AODT01000007.1	736147	735554	-	Transcriptional regulator, AcrR family
<i>Pcc</i> ICMP5702_peg944	AODT01000007.1	736279	736812	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg945	AODT01000007.1	737583	737017	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg946	AODT01000007.1	738460	737861	-	Transcriptional regulator, AcrR family
<i>Pcc</i> ICMP5702_peg947	AODT01000007.1	738578	739165	+	NAD(P)H oxidoreductase YrkL @ Putative NADPH-quinone reductase (modulator of drug activity B) @ Flavodoxin 2
<i>Pcc</i> ICMP5702_peg948	AODT01000007.1	739399	740436	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg949	AODT01000007.1	742213	741116	-	Lipase
<i>Pcc</i> ICMP5702_peg950	AODT01000007.1	742296	742718	+	transcriptional regulator, MarR family
<i>Pcc</i> ICMP5702_peg951	AODT01000007.1	744018	742786	-	Transcription regulatory protein opdE
<i>Pcc</i> ICMP5702_peg952	AODT01000007.1	744089	745045	+	Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg953	AODT01000007.1	745238	745531	+	Uncharacterized protein STM4317
<i>Pcc</i> ICMP5702_peg954	AODT01000007.1	745528	745653	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg955	AODT01000007.1	745753	746016	+	FIG001353: Acetyltransferase
<i>Pcc</i> ICMP5702_peg956	AODT01000007.1	746222	747370	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg957	AODT01000007.1	747763	747503	-	CcdB toxin protein
<i>Pcc</i> ICMP5702_peg958	AODT01000007.1	748021	747803	-	CcdA protein (antitoxin to CcdB)
<i>Pcc</i> ICMP5702_peg959	AODT01000007.1	748284	748036	-	DNA-binding protein
<i>Pcc</i> ICMP5702_peg960	AODT01000007.1	748624	748370	-	DNA-binding protein
<i>Pcc</i> ICMP5702_peg961	AODT01000007.1	748729	748938	+	Ner-like regulatory protein
<i>Pcc</i> ICMP5702_peg962	AODT01000007.1	749308	749601	+	Uncharacterized protein STM4317
<i>Pcc</i> ICMP5702_peg963	AODT01000007.1	749598	750086	+	FIG001353: Acetyltransferase
<i>Pcc</i> ICMP5702_peg964	AODT01000008.1	3	1097	+	Modification methylase EcoRI (EC 2.1.1.72)
<i>Pcc</i> ICMP5702_peg965	AODT01000008.1	1097	2176	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg966	AODT01000008.1	2185	2319	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg967	AODT01000008.1	2338	2481	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg968	AODT01000008.1	2906	2601	-	CcdB toxin protein
<i>Pcc</i> ICMP5702_peg969	AODT01000008.1	3127	2909	-	CcdA protein (antitoxin to CcdB)
<i>Pcc</i> ICMP5702_peg970	AODT01000008.1	3929	3186	-	TriL protein

<i>Pcc</i> ICMP5702_peg971	AODT01000008.1	4664	3984	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg972	AODT01000008.1	5174	4833	-	FIG00613582: Hypothetical protein
<i>Pcc</i> ICMP5702_peg973	AODT01000008.1	5315	5485	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg974	AODT01000008.1	6885	5626	-	Integrase
<i>Pcc</i> ICMP5702_peg975	AODT01000008.1	7799	9952	+	Ornithine decarboxylase (EC 4.1.1.17)
<i>Pcc</i> ICMP5702_peg976	AODT01000008.1	11480	10029	-	L-asparagine permease
<i>Pcc</i> ICMP5702_peg977	AODT01000008.1	11680	11823	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg978	AODT01000008.1	12605	11862	-	Putative oxidoreductase
<i>Pcc</i> ICMP5702_peg979	AODT01000008.1	13311	12682	-	Transcriptional regulator, AcrR family
<i>Pcc</i> ICMP5702_peg980	AODT01000008.1	13600	14823	+	Transcriptional regulator
<i>Pcc</i> ICMP5702_peg981	AODT01000008.1	14839	15669	+	TIM-barrel signal transduction protein
<i>Pcc</i> ICMP5702_peg982	AODT01000008.1	15884	16927	+	Probable lipoprotein signal peptide
<i>Pcc</i> ICMP5702_peg983	AODT01000008.1	17972	16890	-	Transcriptional regulator
<i>Pcc</i> ICMP5702_peg984	AODT01000008.1	19140	18067	-	Membrane-bound lytic murein transglycosylase C (EC 3.2.1.n1)
<i>Pcc</i> ICMP5702_peg985	AODT01000008.1	19465	19193	-	FIG001341: Probable Fe(2+)-trafficking protein YggX
<i>Pcc</i> ICMP5702_peg986	AODT01000008.1	20568	19462	-	A/G-specific adenine glycosylase (EC 3.2.2.-)
<i>Pcc</i> ICMP5702_peg987	AODT01000008.1	20734	21453	+	tRNA (guanine(46)-N(7))-methyltransferase (EC 2.1.1.33)
<i>Pcc</i> ICMP5702_peg988	AODT01000008.1	21455	21799	+	FIG002060: uncharacterized protein YggL
<i>Pcc</i> ICMP5702_peg989	AODT01000008.1	21914	22627	+	FIG004016: Uncharacterized protein YggN
<i>Pcc</i> ICMP5702_peg990	AODT01000008.1	22842	25934	+	Extracellular serine protease precursor (EC 3.4.21.-)
<i>Pcc</i> ICMP5702_peg991	AODT01000008.1	26185	26901	+	Transcriptional regulator PhnF
<i>Pcc</i> ICMP5702_peg992	AODT01000008.1	26902	27348	+	2.7.8.37)
<i>Pcc</i> ICMP5702_peg993	AODT01000008.1	27348	27923	+	2.7.8.37)
<i>Pcc</i> ICMP5702_peg994	AODT01000008.1	27923	28999	+	2.7.8.37)
<i>Pcc</i> ICMP5702_peg995	AODT01000008.1	28992	29846	+	Alpha-D-ribose 1-methylphosphonate 5-phosphate C-P lyase (EC 4.7.1.1)
<i>Pcc</i> ICMP5702_peg996	AODT01000008.1	29833	30597	+	Phosphonates utilization ATP-binding protein PhnK
<i>Pcc</i> ICMP5702_peg997	AODT01000008.1	30597	31373	+	2.7.8.37)
<i>Pcc</i> ICMP5702_peg998	AODT01000008.1	31360	32496	+	Alpha-D-ribose 1-methylphosphonate 5-triphosphate diphosphatase (EC 3.6.1.63)
<i>Pcc</i> ICMP5702_peg999	AODT01000008.1	32649	33476	+	Phosphonate ABC transporter ATP-binding protein PhnC (TC 3.A.1.9.1)
<i>Pcc</i> ICMP5702_peg1000	AODT01000008.1	33543	34475	+	Phosphonate ABC transporter substrate-binding protein PhnD (TC 3.A.1.9.1)
<i>Pcc</i> ICMP5702_peg1001	AODT01000008.1	34602	35462	+	Phosphonate ABC transporter permease protein PhnE2 (TC 3.A.1.9.1)
<i>Pcc</i> ICMP5702_peg1002	AODT01000008.1	35464	36360	+	Phosphonate ABC transporter permease protein PhnE1 (TC 3.A.1.9.1)
<i>Pcc</i> ICMP5702_peg1003	AODT01000008.1	37806	36766	-	Tas protein, an NADP(H)-dependent aldo-keto reductase
<i>Pcc</i> ICMP5702_peg1004	AODT01000008.1	38213	38013	-	Uncharacterized lipoprotein YgdR
<i>Pcc</i> ICMP5702_peg1005	AODT01000008.1	39122	38406	-	UPF0053 inner membrane protein YgdQ
<i>Pcc</i> ICMP5702_peg1006	AODT01000008.1	40188	39541	-	DNA mismatch repair endonuclease MutH

<i>Pcc</i> ICMP5702_peg1007	AODT01000008.1	40495	40611	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1008	AODT01000008.1	40933	41466	+	Adenosine (5')-pentaphospho-(5'')-adenosine pyrophosphohydrolase
<i>Pcc</i> ICMP5702_peg1009	AODT01000008.1	41479	43725	+	associated
<i>Pcc</i> ICMP5702_peg1010	AODT01000008.1	43952	44818	+	Prolipoprotein diacylglyceryl transferase
<i>Pcc</i> ICMP5702_peg1011	AODT01000008.1	44855	45649	+	Thymidylate synthase (EC 2.1.1.45)
<i>Pcc</i> ICMP5702_peg1012	AODT01000008.1	45866	46333	+	Prepilin peptidase dependent protein A precursor
<i>Pcc</i> ICMP5702_peg1013	AODT01000008.1	46375	46953	+	FIG004819: Prepilin peptidase dependent protein B precursor
<i>Pcc</i> ICMP5702_peg1014	AODT01000008.1	46989	47405	+	Uncharacterized protein YgdB
<i>Pcc</i> ICMP5702_peg1015	AODT01000008.1	47410	47787	+	FIG004136: Prepilin peptidase dependent protein C precursor
<i>Pcc</i> ICMP5702_peg1016	AODT01000008.1	47844	51242	+	Exodeoxyribonuclease V gamma chain (EC 3.1.11.5)
<i>Pcc</i> ICMP5702_peg1017	AODT01000008.1	51339	54275	+	Protease III precursor (EC 3.4.24.55)
<i>Pcc</i> ICMP5702_peg1018	AODT01000008.1	54272	57853	+	Exodeoxyribonuclease V beta chain (EC 3.1.11.5)
<i>Pcc</i> ICMP5702_peg1019	AODT01000008.1	57850	59709	+	Exodeoxyribonuclease V alpha chain (EC 3.1.11.5)
<i>Pcc</i> ICMP5702_peg1020	AODT01000008.1	60744	59722	-	Possible L-talarate utilization transcriptional regulator, LacI family
<i>Pcc</i> ICMP5702_peg1021	AODT01000008.1	60917	61045	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1022	AODT01000008.1	61070	62266	+	L-talarate dehydratase @ Galactarate dehydratase (EC 4.2.1.42)
<i>Pcc</i> ICMP5702_peg1023	AODT01000008.1	63655	62330	-	N-acetylglutamate synthase (EC 2.3.1.1)
<i>Pcc</i> ICMP5702_peg1024	AODT01000008.1	63934	65178	+	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)
<i>Pcc</i> ICMP5702_peg1025	AODT01000008.1	66007	65882	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1026	AODT01000008.1	66106	67236	+	Membrane-bound lytic murein transglycosylase A
<i>Pcc</i> ICMP5702_peg1027	AODT01000008.1	68242	67325	-	Dihydrodipicolinate synthase family
<i>Pcc</i> ICMP5702_peg1028	AODT01000008.1	68987	68286	-	Transcriptional regulator, AcrR family
<i>Pcc</i> ICMP5702_peg1029	AODT01000008.1	70324	69071	-	N-acyl-L-amino acid amidohydrolase (EC 3.5.1.14)
<i>Pcc</i> ICMP5702_peg1030	AODT01000008.1	72038	70317	-	ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines) / ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg1031	AODT01000008.1	72970	72035	-	ABC transporter, permease protein 2 (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg1032	AODT01000008.1	73958	72972	-	ABC transporter, permease protein 1 (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg1033	AODT01000008.1	75597	74011	-	ABC transporter, substrate-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg1034	AODT01000008.1	75844	75731	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1035	AODT01000008.1	76012	78270	+	Biotin sulfoxide reductase (EC 1.-.-.) / Free methionine-(S)-sulfoxide reductase
<i>Pcc</i> ICMP5702_peg1036	AODT01000008.1	78339	79157	+	HesA/MoeB/ThiF family protein => sulfur transfer pathway protein CsdL
<i>Pcc</i> ICMP5702_peg1037	AODT01000008.1	79628	79173	-	Sulfur acceptor protein => sulfur transfer pathway protein CsdE
<i>Pcc</i> ICMP5702_peg1038	AODT01000008.1	80837	79632	-	Cysteine desulfurase (EC 2.8.1.7) => sulfur transfer pathway protein CsdA
<i>Pcc</i> ICMP5702_peg1039	AODT01000008.1	81021	81242	+	Uncharacterized lipoprotein YgdI
<i>Pcc</i> ICMP5702_peg1040	AODT01000008.1	81474	81259	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1041	AODT01000008.1	81780	82703	+	Glycine cleavage system transcriptional activator GcvA

<i>Pcc</i> ICMP5702_peg1042	AODT01000008.1	82806	83201	+	FIG00018398: hypothetical regulator
<i>Pcc</i> ICMP5702_peg1043	AODT01000008.1	83194	84294	+	23S rRNA (cytidine(2498)-2'-O)-methyltransferase (EC 2.1.1.186)
<i>Pcc</i> ICMP5702_peg1044	AODT01000008.1	85130	84348	-	Flap endonuclease Xni
<i>Pcc</i> ICMP5702_peg1045	AODT01000008.1	86674	85202	-	Pyrimidine/purine nucleotide 5'-monophosphate nucleosidase PpnN (EC 3.2.2.4) (EC 3.2.2.10)
<i>Pcc</i> ICMP5702_peg1046	AODT01000008.1	87732	86884	-	NADPH-dependent 7-cyano-7-deazaguanine reductase (EC 1.7.1.13)
<i>Pcc</i> ICMP5702_peg1047	AODT01000008.1	87803	88351	+	Syd protein
<i>Pcc</i> ICMP5702_peg1048	AODT01000008.1	89274	90950	+	Exoenzymes regulatory protein AepA precursor
<i>Pcc</i> ICMP5702_peg1049	AODT01000008.1	91214	91660	+	Transcriptional regulator, MarR family
<i>Pcc</i> ICMP5702_peg1050	AODT01000008.1	91752	92102	+	Uncharacterized protein YqcC
<i>Pcc</i> ICMP5702_peg1051	AODT01000008.1	92095	92883	+	tRNA pseudouridine(65) synthase (EC 5.4.99.26)
<i>Pcc</i> ICMP5702_peg1052	AODT01000008.1	92951	93406	+	Hypothetical flavoprotein YqcA (clustered with tRNA pseudouridine synthase C)
<i>Pcc</i> ICMP5702_peg1053	AODT01000008.1	93869	93480	-	UPF0325 protein YaeH
<i>Pcc</i> ICMP5702_peg1054	AODT01000008.1	94852	94025	-	2,3,4,5-tetrahydropyridine-2,6-dicarboxylate N-succinyltransferase (EC 2.3.1.117)
<i>Pcc</i> ICMP5702_peg1055	AODT01000008.1	97595	94881	-	[Protein-P _{II}] uridylyltransferase (EC 2.7.7.59) / [Protein-P _{II}]-UMP uridylyl-removing enzyme
<i>Pcc</i> ICMP5702_peg1056	AODT01000008.1	98503	97709	-	Methionine aminopeptidase (EC 3.4.11.18)
<i>Pcc</i> ICMP5702_peg1057	AODT01000008.1	98848	99573	+	SSU ribosomal protein S2p (SAe)
<i>Pcc</i> ICMP5702_peg1058	AODT01000008.1	99708	100559	+	Translation elongation factor Ts
<i>Pcc</i> ICMP5702_peg1059	AODT01000008.1	100715	101440	+	Uridylate kinase (EC 2.7.4.22)
<i>Pcc</i> ICMP5702_peg1060	AODT01000008.1	101576	102133	+	Ribosome recycling factor
<i>Pcc</i> ICMP5702_peg1061	AODT01000008.1	102378	103574	+	1-deoxy-D-xylulose 5-phosphate reductoisomerase (EC 1.1.1.267)
<i>Pcc</i> ICMP5702_peg1062	AODT01000008.1	103773	104534	+	Undecaprenyl diphosphate synthase (EC 2.5.1.31)
<i>Pcc</i> ICMP5702_peg1063	AODT01000008.1	104544	105401	+	Phosphatidate cytidylyltransferase (EC 2.7.7.41)
<i>Pcc</i> ICMP5702_peg1064	AODT01000008.1	105423	106778	+	Intramembrane protease RasP/YluC, implicated in cell division based on FtsL cleavage
<i>Pcc</i> ICMP5702_peg1065	AODT01000008.1	106814	109258	+	Outer membrane protein assembly factor YaeT
<i>Pcc</i> ICMP5702_peg1066	AODT01000008.1	109402	109899	+	Periplasmic chaperone of outer membrane proteins Skp @ Outer membrane protein H precursor
<i>Pcc</i> ICMP5702_peg1067	AODT01000008.1	109903	110925	+	UDP-3-O-[3-hydroxymyristoyl] glucosamine N-acyltransferase (EC 2.3.1.191)
<i>Pcc</i> ICMP5702_peg1068	AODT01000008.1	111010	111483	+	3-hydroxyacyl-[acyl-carrier-protein] dehydratase, FabZ form (EC 4.2.1.59)
<i>Pcc</i> ICMP5702_peg1069	AODT01000008.1	111488	112276	+	2.3.1.129)
<i>Pcc</i> ICMP5702_peg1070	AODT01000008.1	112280	113431	+	Lipid-A-disaccharide synthase (EC 2.4.1.182)
<i>Pcc</i> ICMP5702_peg1071	AODT01000008.1	113425	114048	+	Ribonuclease HII (EC 3.1.26.4)
<i>Pcc</i> ICMP5702_peg1072	AODT01000008.1	114152	117634	+	DNA polymerase III alpha subunit (EC 2.7.7.7)
<i>Pcc</i> ICMP5702_peg1073	AODT01000008.1	117647	118606	+	Acetyl-coenzyme A carboxyl transferase alpha chain (EC 6.4.1.2)
<i>Pcc</i> ICMP5702_peg1074	AODT01000008.1	118714	119103	+	Uncharacterized protein YaeR with similarity to glyoxylase family

<i>Pcc</i> ICMP5702_peg1075	AODT01000008.1	119108	120484	+	tRNA(Ile)-lysine synthetase (EC 6.3.4.19)
<i>Pcc</i> ICMP5702_peg1076	AODT01000008.1	120865	120605	-	Rho-specific inhibitor of transcription termination (YaeO)
<i>Pcc</i> ICMP5702_peg1077	AODT01000008.1	121052	120852	-	UPF0253 protein YaeP
<i>Pcc</i> ICMP5702_peg1078	AODT01000008.1	121293	121847	+	YaeQ protein
<i>Pcc</i> ICMP5702_peg1079	AODT01000008.1	121918	122619	+	Copper homeostasis protein CutF precursor / Lipoprotein NlpE involved in surface adhesion
<i>Pcc</i> ICMP5702_peg1080	AODT01000008.1	125245	122681	-	DNA mismatch repair protein MutS
<i>Pcc</i> ICMP5702_peg1081	AODT01000008.1	125811	126605	+	probable membrane protein YPO4049
<i>Pcc</i> ICMP5702_peg1082	AODT01000008.1	126958	126620	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1083	AODT01000008.1	127292	126951	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1084	AODT01000008.1	127844	127365	-	T6SS component Hcp
<i>Pcc</i> ICMP5702_peg1085	AODT01000008.1	128814	128185	-	Glutathione S-transferase family protein
<i>Pcc</i> ICMP5702_peg1086	AODT01000008.1	129150	129019	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1087	AODT01000008.1	129306	130928	+	Rtn protein
<i>Pcc</i> ICMP5702_peg1088	AODT01000008.1	131049	131390	+	Protein PhnA
<i>Pcc</i> ICMP5702_peg1089	AODT01000008.1	131398	131529	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1090	AODT01000008.1	131529	132599	+	Membrane-bound lytic murein transglycosylase B
<i>Pcc</i> ICMP5702_peg1091	AODT01000008.1	132674	132802	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1092	AODT01000008.1	133111	133836	+	putative membrane protein
<i>Pcc</i> ICMP5702_peg1093	AODT01000008.1	134726	133833	-	Transcriptional regulator RSp1267, LysR family
<i>Pcc</i> ICMP5702_peg1094	AODT01000008.1	135512	134805	-	FIG066100: Diguanylate cyclase (GGDEF domain) with PAS/PAC sensor
<i>Pcc</i> ICMP5702_peg1095	AODT01000008.1	135951	135499	-	FIG057251: Fe-S oxidoreductase
<i>Pcc</i> ICMP5702_peg1096	AODT01000008.1	136507	135953	-	FIG062788: Hypothetical protein
<i>Pcc</i> ICMP5702_peg1097	AODT01000008.1	137765	136521	-	FIG017431: Sigma factor-like phosphatase with CBS pair domains
<i>Pcc</i> ICMP5702_peg1098	AODT01000008.1	139154	137961	-	putative lipoprotein
<i>Pcc</i> ICMP5702_peg1099	AODT01000008.1	139365	140099	+	Hexuronate utilization operon transcriptional repressor ExuR
<i>Pcc</i> ICMP5702_peg1100	AODT01000008.1	140387	141583	+	Mannonate dehydratase (EC 4.2.1.8)
<i>Pcc</i> ICMP5702_peg1101	AODT01000008.1	142730	141687	-	Pectate lyase (EC 4.2.2.2)
<i>Pcc</i> ICMP5702_peg1102	AODT01000008.1	143307	144515	+	Polygalacturonase (EC 3.2.1.15)
<i>Pcc</i> ICMP5702_peg1103	AODT01000008.1	145998	144829	-	Type I secretion membrane fusion protein, HlyD family @ Type I secretion system, membrane fusion protein LapC
<i>Pcc</i> ICMP5702_peg1104	AODT01000008.1	148147	146009	-	Type I secretion system ATPase, LssB family LapB
<i>Pcc</i> ICMP5702_peg1105	AODT01000008.1	149638	148187	-	Type I secretion system, outer membrane component LapE
<i>Pcc</i> ICMP5702_peg1106	AODT01000008.1	164703	150109	-	T1SS secreted agglutinin RTX
<i>Pcc</i> ICMP5702_peg1107	AODT01000008.1	165118	165249	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1108	AODT01000008.1	165322	165486	+	FIG00904457: Hypothetical protein

<i>Pcc</i> ICMP5702_peg1109	AODT01000008.1	165489	167069	+	ATP-binding protein syrD
<i>Pcc</i> ICMP5702_peg1110	AODT01000008.1	167276	168325	+	L-asparaginase (EC 3.5.1.1)
<i>Pcc</i> ICMP5702_peg1111	AODT01000008.1	168607	169128	+	Shikimate kinase III (EC 2.7.1.71)
<i>Pcc</i> ICMP5702_peg1112	AODT01000008.1	169269	169553	+	Pyrimidine/purine nucleoside phosphorylase PpnP
<i>Pcc</i> ICMP5702_peg1113	AODT01000008.1	169714	169601	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1114	AODT01000008.1	169815	171095	+	Putative nucleoside transporter YegT
<i>Pcc</i> ICMP5702_peg1115	AODT01000008.1	171092	172093	+	ADP-ribosylglycohydrolase family protein YegU
<i>Pcc</i> ICMP5702_peg1116	AODT01000008.1	172093	173070	+	Uncharacterized sugar kinase YegV, PfkB family
<i>Pcc</i> ICMP5702_peg1117	AODT01000008.1	173790	173044	-	Uncharacterized HTH-type transcriptional regulator YegW
<i>Pcc</i> ICMP5702_peg1118	AODT01000008.1	174327	176117	+	Methyl-accepting chemotaxis protein
<i>Pcc</i> ICMP5702_peg1119	AODT01000008.1	177171	176242	-	DNA recombination-dependent growth factor RdgC
<i>Pcc</i> ICMP5702_peg1120	AODT01000008.1	177458	178369	+	Cryptic sugar kinase Mak
<i>Pcc</i> ICMP5702_peg1121	AODT01000008.1	182056	178373	-	Exonuclease SbcC
<i>Pcc</i> ICMP5702_peg1122	AODT01000008.1	183279	182053	-	Exonuclease SbcD
<i>Pcc</i> ICMP5702_peg1123	AODT01000008.1	183525	183370	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1124	AODT01000008.1	183574	184263	+	Phosphate regulon transcriptional regulatory protein PhoB (SphR)
<i>Pcc</i> ICMP5702_peg1125	AODT01000008.1	184291	185613	+	Phosphate regulon sensor protein PhoR (SphS) (EC 2.7.13.3)
<i>Pcc</i> ICMP5702_peg1126	AODT01000008.1	185629	186567	+	Phosphate-binding protein
<i>Pcc</i> ICMP5702_peg1127	AODT01000008.1	186808	187914	+	Methionine synthase II (cobalamin-independent)
<i>Pcc</i> ICMP5702_peg1128	AODT01000008.1	188287	188496	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1129	AODT01000008.1	188518	189837	+	Na(+)-dependent branched-chain amino acid transporter
<i>Pcc</i> ICMP5702_peg1130	AODT01000008.1	189979	191355	+	Proline-specific permease ProY
<i>Pcc</i> ICMP5702_peg1131	AODT01000008.1	192689	191415	-	Miniconductance mechanosensitive channel YbdG
<i>Pcc</i> ICMP5702_peg1132	AODT01000008.1	193515	192913	-	Alkyl hydroperoxide reductase subunit C-like protein
<i>Pcc</i> ICMP5702_peg1133	AODT01000008.1	194307	193726	-	Acyl carrier protein phosphodiesterase (EC 3.1.4.14)
<i>Pcc</i> ICMP5702_peg1134	AODT01000008.1	194487	195554	+	S-adenosylmethionine:tRNA ribosyltransferase-isomerase (EC 2.4.99.17)
<i>Pcc</i> ICMP5702_peg1135	AODT01000008.1	195651	196796	+	Queuine tRNA-ribosyltransferase (EC 2.4.2.29)
<i>Pcc</i> ICMP5702_peg1136	AODT01000008.1	196923	197255	+	Protein translocase subunit YajC
<i>Pcc</i> ICMP5702_peg1137	AODT01000008.1	197316	199130	+	Protein translocase subunit SecD
<i>Pcc</i> ICMP5702_peg1138	AODT01000008.1	199140	200114	+	Protein translocase subunit SecF
<i>Pcc</i> ICMP5702_peg1139	AODT01000008.1	200881	200312	-	Putative outer membrane lipoprotein
<i>Pcc</i> ICMP5702_peg1140	AODT01000008.1	201099	201548	+	Ribonucleotide reductase transcriptional regulator NrdR
<i>Pcc</i> ICMP5702_peg1141	AODT01000008.1	201584	202720	+	Diaminohydroxyphosphoribosylaminopyrimidine deaminase (EC 3.5.4.26) / 5-amino-6-(5-phosphoribosylamino)uracil reductase (EC 1.1.1.193)
<i>Pcc</i> ICMP5702_peg1142	AODT01000008.1	202831	203307	+	6,7-dimethyl-8-ribityllumazine synthase (EC 2.5.1.78)
<i>Pcc</i> ICMP5702_peg1143	AODT01000008.1	203332	203751	+	Transcription termination protein NusB

<i>Pcc</i> ICMP5702_peg1144	AODT01000008.1	203820	204800	+	Thiamine-monophosphate kinase (EC 2.7.4.16)
<i>Pcc</i> ICMP5702_peg1145	AODT01000008.1	204775	205311	+	Phosphatidylglycerophosphatase A (EC 3.1.3.27)
<i>Pcc</i> ICMP5702_peg1146	AODT01000008.1	207245	205380	-	1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7)
<i>Pcc</i> ICMP5702_peg1147	AODT01000008.1	208175	207264	-	(2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10) @ Dimethylallyltransferase (EC 2.5.1.1)
<i>Pcc</i> ICMP5702_peg1148	AODT01000008.1	208420	208172	-	Exodeoxyribonuclease VII small subunit (EC 3.1.11.6)
<i>Pcc</i> ICMP5702_peg1149	AODT01000008.1	208498	208653	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1150	AODT01000008.1	208673	210121	+	tRNA 4-thiouridine synthase (EC 2.8.1.4) / Rhodanese-like domain required for thiamine synthesis
<i>Pcc</i> ICMP5702_peg1151	AODT01000008.1	210755	210165	-	DJ-1/YajL/PfpI superfamily, includes chaperone protein YajL (former ThiJ), parkinsonism-associated protein DJ-1, peptidases PfpI, Hsp31
<i>Pcc</i> ICMP5702_peg1152	AODT01000008.1	211626	210718	-	2-dehydropantoate 2-reductase (EC 1.1.1.169)
<i>Pcc</i> ICMP5702_peg1153	AODT01000008.1	211816	212307	+	UPF0234 protein Yitk
<i>Pcc</i> ICMP5702_peg1154	AODT01000008.1	213727	212363	-	Inner membrane transport protein YajR
<i>Pcc</i> ICMP5702_peg1155	AODT01000008.1	214781	213891	-	Heme O synthase, protoheme IX farnesyltransferase, COX10-CtaB
<i>Pcc</i> ICMP5702_peg1156	AODT01000008.1	215128	214796	-	Cytochrome O ubiquinol oxidase subunit IV (EC 1.10.3.-)
<i>Pcc</i> ICMP5702_peg1157	AODT01000008.1	215742	215128	-	Cytochrome O ubiquinol oxidase subunit III (EC 1.10.3.-)
<i>Pcc</i> ICMP5702_peg1158	AODT01000008.1	217723	215732	-	Cytochrome O ubiquinol oxidase subunit I (EC 1.10.3.-)
<i>Pcc</i> ICMP5702_peg1159	AODT01000008.1	218690	217728	-	Cytochrome O ubiquinol oxidase subunit II (EC 1.10.3.-)
<i>Pcc</i> ICMP5702_peg1160	AODT01000008.1	220602	219115	-	AmpG permease
<i>Pcc</i> ICMP5702_peg1161	AODT01000008.1	221240	220662	-	Hypothetical lipoprotein YajG precursor
<i>Pcc</i> ICMP5702_peg1162	AODT01000008.1	221578	221892	+	Cell division protein Bola
<i>Pcc</i> ICMP5702_peg1163	AODT01000008.1	222207	223511	+	Cell division trigger factor (EC 5.2.1.8)
<i>Pcc</i> ICMP5702_peg1164	AODT01000008.1	224047	224670	+	ATP-dependent Clp protease proteolytic subunit ClpP (EC 3.4.21.92)
<i>Pcc</i> ICMP5702_peg1165	AODT01000008.1	224834	226108	+	ATP-dependent Clp protease ATP-binding subunit ClpX
<i>Pcc</i> ICMP5702_peg1166	AODT01000008.1	226300	228681	+	ATP-dependent protease La (EC 3.4.21.53) Type I
<i>Pcc</i> ICMP5702_peg1167	AODT01000008.1	228879	229151	+	DNA-binding protein HU-beta
<i>Pcc</i> ICMP5702_peg1168	AODT01000008.1	229547	231427	+	Peptidyl-prolyl cis-trans isomerase PpiD (EC 5.2.1.8)
<i>Pcc</i> ICMP5702_peg1169	AODT01000008.1	231566	231931	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1170	AODT01000008.1	232037	232435	+	4-hydroxybenzoyl-CoA thioesterase family active site
<i>Pcc</i> ICMP5702_peg1171	AODT01000008.1	233210	232515	-	7-cyano-7-deazaguanine synthase (EC 6.3.4.20)
<i>Pcc</i> ICMP5702_peg1172	AODT01000008.1	234386	233310	-	Pyridoxal-5'-phosphate-dependent enzyme beta superfamily (fold type II)
<i>Pcc</i> ICMP5702_peg1173	AODT01000008.1	234754	235215	+	DNA-binding transcriptional activator DecR, AsnC family
<i>Pcc</i> ICMP5702_peg1174	AODT01000008.1	235294	237063	+	Efflux ABC transporter, permease/ATP-binding protein MdlA
<i>Pcc</i> ICMP5702_peg1175	AODT01000008.1	237056	238834	+	Efflux ABC transporter, permease/ATP-binding protein MdlB
<i>Pcc</i> ICMP5702_peg1176	AODT01000008.1	238966	239082	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg1177	AODT01000008.1	239195	239533	+	Nitrogen regulatory protein P-II, GlnK
<i>Pcc</i> ICMP5702_peg1178	AODT01000008.1	239573	240859	+	Ammonium transporter
<i>Pcc</i> ICMP5702_peg1179	AODT01000008.1	241860	240997	-	Acyl-CoA thioesterase II (EC 3.1.2.-)
<i>Pcc</i> ICMP5702_peg1180	AODT01000008.1	242073	242654	+	glycoprotein/polysaccharide metabolism
<i>Pcc</i> ICMP5702_peg1181	AODT01000008.1	242994	242674	-	DNA base-flipping protein
<i>Pcc</i> ICMP5702_peg1182	AODT01000008.1	243398	243216	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1183	AODT01000008.1	243941	243738	-	Haemolysin expression modulating protein
<i>Pcc</i> ICMP5702_peg1184	AODT01000008.1	244363	243995	-	Hha toxicity modulator TomB
<i>Pcc</i> ICMP5702_peg1185	AODT01000008.1	245105	244962	-	LSU ribosomal protein L36p @ LSU ribosomal protein L36p, zinc-independent
<i>Pcc</i> ICMP5702_peg1186	AODT01000008.1	245371	245123	-	LSU ribosomal protein L31p @ LSU ribosomal protein L31p, zinc-independent
<i>Pcc</i> ICMP5702_peg1187	AODT01000008.1	248730	245602	-	Multidrug efflux system AcrAB-TolC, inner-membrane proton/drug antiporter AcrB (RND type)
<i>Pcc</i> ICMP5702_peg1188	AODT01000008.1	249952	248759	-	Multidrug efflux system AcrAB-TolC, membrane fusion component AcrA
<i>Pcc</i> ICMP5702_peg1189	AODT01000008.1	250118	250759	+	Transcriptional regulator of <i>acrAB</i> operon, AcrR
<i>Pcc</i> ICMP5702_peg1190	AODT01000008.1	250987	250817	-	Uncharacterized protein YbaM
<i>Pcc</i> ICMP5702_peg1191	AODT01000008.1	251559	251023	-	Primosomal replication protein N prime prime
<i>Pcc</i> ICMP5702_peg1192	AODT01000008.1	251789	252184	+	Inner membrane protein YbaN
<i>Pcc</i> ICMP5702_peg1193	AODT01000008.1	252397	252954	+	Adenine phosphoribosyltransferase (EC 2.4.2.7)
<i>Pcc</i> ICMP5702_peg1194	AODT01000008.1	253029	255092	+	DNA polymerase III subunits gamma and tau (EC 2.7.7.7)
<i>Pcc</i> ICMP5702_peg1195	AODT01000008.1	255133	255462	+	Nucleoid-associated protein YaaK
<i>Pcc</i> ICMP5702_peg1196	AODT01000008.1	255462	256067	+	Recombination protein RecR
<i>Pcc</i> ICMP5702_peg1197	AODT01000008.1	256242	258131	+	Chaperone protein HtpG
<i>Pcc</i> ICMP5702_peg1198	AODT01000008.1	258225	258368	+	Adenylate kinase (EC 2.7.4.3)
<i>Pcc</i> ICMP5702_peg1199	AODT01000008.1	258396	259040	+	Adenylate kinase (EC 2.7.4.3)
<i>Pcc</i> ICMP5702_peg1200	AODT01000008.1	259072	259197	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1201	AODT01000008.1	259262	260224	+	Ferrochelatase, protoheme ferro-lyase (EC 4.99.1.1)
<i>Pcc</i> ICMP5702_peg1202	AODT01000008.1	262017	260332	-	Inner membrane protein YbaL, KefB/KefC family
<i>Pcc</i> ICMP5702_peg1203	AODT01000008.1	262472	262290	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1204	AODT01000008.1	262686	264335	+	UDP-sugar hydrolase (EC 3.6.1.45); 5'-nucleotidase (EC 3.1.3.5)
<i>Pcc</i> ICMP5702_peg1205	AODT01000008.1	264572	266587	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1206	AODT01000008.1	266749	268737	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1207	AODT01000008.1	269029	271182	+	Pyruvate:H ⁺ symporter BtsT
<i>Pcc</i> ICMP5702_peg1208	AODT01000008.1	271328	271531	+	Uncharacterized proteins YbdD and YjiX
<i>Pcc</i> ICMP5702_peg1209	AODT01000008.1	271548	272534	+	Metal-binding GTPase YjiA
<i>Pcc</i> ICMP5702_peg1210	AODT01000008.1	272801	274183	+	Polygalacturonase (EC 3.2.1.15)
<i>Pcc</i> ICMP5702_peg1211	AODT01000008.1	274771	274292	-	Cys-tRNA(Pro) deacylase YbaK

<i>Pcc</i> ICMP5702_peg1212	AODT01000008.1	275660	274842	-	Uncharacterized protein YbaP
<i>Pcc</i> ICMP5702_peg1213	AODT01000008.1	276041	276472	+	DNA-binding protein, CopG family
<i>Pcc</i> ICMP5702_peg1214	AODT01000008.1	279290	276567	-	Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5); Copper-translocating P-type ATPase (EC 3.6.3.4)
<i>Pcc</i> ICMP5702_peg1215	AODT01000008.1	279407	279808	+	Copper resistance transcriptional regulator CueR (MerR family)
<i>Pcc</i> ICMP5702_peg1216	AODT01000008.1	280320	279865	-	Putative activity regulator of membrane protease YbbK
<i>Pcc</i> ICMP5702_peg1217	AODT01000008.1	281234	280320	-	Protein QmcA (possibly involved in integral membrane quality control) YfaE: ferredoxin involved with ribonucleotide reductase diferric-tyrosyl radical (Y*) cofactor maintenance
<i>Pcc</i> ICMP5702_peg1218	AODT01000008.1	281635	281375	-	Ribonucleotide reductase of class Ia (aerobic), beta subunit (EC 1.17.4.1)
<i>Pcc</i> ICMP5702_peg1219	AODT01000008.1	282769	281639	-	Ribonucleotide reductase of class Ia (aerobic), alpha subunit (EC 1.17.4.1)
<i>Pcc</i> ICMP5702_peg1220	AODT01000008.1	285177	282892	-	3-demethylubiquinol 3-O-methyltransferase (EC 2.1.1.64) @ 2-polyprenyl-6- hydroxyphenyl methylase (EC 2.1.1.222)
<i>Pcc</i> ICMP5702_peg1221	AODT01000008.1	286246	285527	-	DNA gyrase subunit A (EC 5.99.1.3)
<i>Pcc</i> ICMP5702_peg1222	AODT01000008.1	286508	289147	+	Sensor histidine kinase RcsC (EC 2.7.13.3)
<i>Pcc</i> ICMP5702_peg1223	AODT01000008.1	289263	292118	+	DNA-binding capsular synthesis response regulator RcsB
<i>Pcc</i> ICMP5702_peg1224	AODT01000008.1	292806	292156	-	Phosphotransferase RcsD
<i>Pcc</i> ICMP5702_peg1225	AODT01000008.1	295499	292815	-	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg1226	AODT01000008.1	296685	295516	-	Isochorismate synthase (EC 5.4.4.2) @ Menaquinone-specific isochorismate synthase (EC 5.4.4.2)
<i>Pcc</i> ICMP5702_peg1227	AODT01000008.1	297028	298350	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1228	AODT01000008.1	298364	298477	+	2.2.1.9)
<i>Pcc</i> ICMP5702_peg1229	AODT01000008.1	298596	300278	+	2-succinyl-6-hydroxy-2,4-cyclohexadiene-1-carboxylate synthase (EC 4.2.99.20)
<i>Pcc</i> ICMP5702_peg1230	AODT01000008.1	300266	301081	+	Naphthoate synthase (EC 4.1.3.36)
<i>Pcc</i> ICMP5702_peg1231	AODT01000008.1	301087	301944	+	O-succinylbenzoate synthase (EC 4.2.1.113)
<i>Pcc</i> ICMP5702_peg1232	AODT01000008.1	301944	302915	+	O-succinylbenzoic acid--CoA ligase (EC 6.2.1.26)
<i>Pcc</i> ICMP5702_peg1233	AODT01000008.1	302903	304336	+	FIG00904705: Hypothetical protein
<i>Pcc</i> ICMP5702_peg1234	AODT01000008.1	304547	304338	-	Uncharacterized outer membrane protein YfaZ
<i>Pcc</i> ICMP5702_peg1235	AODT01000008.1	304800	305339	+	Tyrosine-specific transport protein
<i>Pcc</i> ICMP5702_peg1236	AODT01000008.1	306705	305497	-	ADP-ribose pyrophosphatase of COG1058 family (EC 3.6.1.13) / Nicotinamide- nucleotide amidase paralog YfaY, no functional activity
<i>Pcc</i> ICMP5702_peg1237	AODT01000008.1	306926	308119	+	FIG000875: Thioredoxin domain-containing protein EC-YbbN
<i>Pcc</i> ICMP5702_peg1238	AODT01000008.1	309413	308553	-	Putative NAD(P)-dependent oxidoreductase EC-YbbO
<i>Pcc</i> ICMP5702_peg1239	AODT01000008.1	310294	309524	-	Multifunctional acyl-CoA thioesterase I, protease I, lysophospholipase L1
<i>Pcc</i> ICMP5702_peg1240	AODT01000008.1	310916	310323	-	Uncharacterized metabolite ABC transporter in Enterobacteriaceae, ATP-binding protein EC-YbbA
<i>Pcc</i> ICMP5702_peg1241	AODT01000008.1	310929	311660	+	

<i>Pcc</i> ICMP5702_peg1242	AODT01000008.1	311657	314086	+	Uncharacterized metabolite ABC transporter in Enterobacteriaceae, permease protein EC-YbbP
<i>Pcc</i> ICMP5702_peg1243	AODT01000008.1	315133	314558	-	Spermidine N1-acetyltransferase (EC 2.3.1.57)
<i>Pcc</i> ICMP5702_peg1244	AODT01000008.1	317443	315302	-	Ferrichrome-iron receptor
<i>Pcc</i> ICMP5702_peg1245	AODT01000008.1	318542	317436	-	ABC transporter, substrate-binding protein (cluster 8, B12/iron complex)
<i>Pcc</i> ICMP5702_peg1246	AODT01000008.1	318620	318739	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1247	AODT01000008.1	319460	318822	-	Phosphoribosylglycinamide formyltransferase (EC 2.1.2.2)
<i>Pcc</i> ICMP5702_peg1248	AODT01000008.1	320497	319460	-	Phosphoribosylformylglycinamide cyclo-ligase (EC 6.3.3.1)
<i>Pcc</i> ICMP5702_peg1249	AODT01000008.1	320652	320530	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1250	AODT01000008.1	320835	321461	+	Uracil phosphoribosyltransferase (EC 2.4.2.9)
<i>Pcc</i> ICMP5702_peg1251	AODT01000008.1	321691	322980	+	Uracil permease @ Uracil:proton symporter UraA
<i>Pcc</i> ICMP5702_peg1252	AODT01000008.1	323040	323786	+	DnaA inactivator Hda (shorter homolog of DnaA)
<i>Pcc</i> ICMP5702_peg1253	AODT01000008.1	324214	323843	-	Uncharacterized protein YfgD, not an arsenate reductase
<i>Pcc</i> ICMP5702_peg1254	AODT01000008.1	325692	324229	-	Exported zinc metalloprotease YfgC precursor
<i>Pcc</i> ICMP5702_peg1255	AODT01000008.1	326330	325863	-	Thiol peroxidase, Bcp-type (EC 1.11.1.15)
<i>Pcc</i> ICMP5702_peg1256	AODT01000008.1	326935	326384	-	Glycine cleavage system transcriptional antiactivator GcvR
<i>Pcc</i> ICMP5702_peg1257	AODT01000008.1	327306	328184	+	4-hydroxy-tetrahydrodipicolinate synthase (EC 4.3.3.7)
<i>Pcc</i> ICMP5702_peg1258	AODT01000008.1	328201	329238	+	Outer membrane beta-barrel assembly protein BamC
<i>Pcc</i> ICMP5702_peg1259	AODT01000008.1	329382	330095	+	Phosphoribosylaminoimidazole-succinocarboxamide synthase (EC 6.3.2.6)
<i>Pcc</i> ICMP5702_peg1260	AODT01000008.1	330315	330767	+	UPF0756 membrane protein YeaL
<i>Pcc</i> ICMP5702_peg1261	AODT01000008.1	330785	332827	+	tRNA cytosine(34) acetyltransferase (EC 2.3.1.193)
<i>Pcc</i> ICMP5702_peg1262	AODT01000008.1	333273	332902	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1263	AODT01000008.1	334729	333464	-	Thioredoxin / Domain of unknown function
<i>Pcc</i> ICMP5702_peg1264	AODT01000008.1	335279	334857	-	Biopolymer transport protein ExbD/TolR
<i>Pcc</i> ICMP5702_peg1265	AODT01000008.1	336034	335294	-	MotA/TolQ/ExbB proton channel family protein
<i>Pcc</i> ICMP5702_peg1266	AODT01000008.1	336994	336113	-	putative TonB-dependent receptor
<i>Pcc</i> ICMP5702_peg1267	AODT01000008.1	338179	337211	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1268	AODT01000008.1	338710	338189	-	RNA polymerase ECF-type sigma factor
<i>Pcc</i> ICMP5702_peg1269	AODT01000008.1	338785	339024	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1270	AODT01000008.1	339121	341499	+	Ferrichrome-iron receptor
<i>Pcc</i> ICMP5702_peg1271	AODT01000008.1	341561	343342	+	Efflux ABC transporter, permease/ATP-binding protein
<i>Pcc</i> ICMP5702_peg1272	AODT01000008.1	343376	346090	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1273	AODT01000008.1	349156	346193	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1274	AODT01000008.1	349385	349612	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1275	AODT01000008.1	349776	350393	+	Esterase YpfH
<i>Pcc</i> ICMP5702_peg1276	AODT01000008.1	350762	352432	+	Methyl-accepting chemotaxis sensor/transducer protein

<i>Pcc</i> ICMP5702_peg1277	AODT01000008.1	352735	352541	-	UPF0370 protein YpfN
<i>Pcc</i> ICMP5702_peg1278	AODT01000008.1	353412	352738	-	FIG009095: D,D-carboxypeptidase family protein
<i>Pcc</i> ICMP5702_peg1279	AODT01000008.1	354536	353409	-	N-succinyl-L,L-diaminopimelate desuccinylase (EC 3.5.1.18)
<i>Pcc</i> ICMP5702_peg1280	AODT01000008.1	354915	354538	-	FIG138056: a glutathione-dependent thiol reductase
<i>Pcc</i> ICMP5702_peg1281	AODT01000008.1	356089	355379	-	Uncharacterized protein YgeA of aspartate/glutamate/hydantoin racemase family
<i>Pcc</i> ICMP5702_peg1282	AODT01000008.1	356307	356516	+	Cold shock protein of CSP family => CspE (naming convention as in E.coli)
<i>Pcc</i> ICMP5702_peg1283	AODT01000008.1	356981	356598	-	Fluoride ion transporter CrcB
<i>Pcc</i> ICMP5702_peg1284	AODT01000008.1	357675	357872	+	Twin-arginine translocation protein TatE
<i>Pcc</i> ICMP5702_peg1285	AODT01000008.1	358920	357955	-	Lipoyl synthase (EC 2.8.1.8)
<i>Pcc</i> ICMP5702_peg1286	AODT01000008.1	359831	359148	-	Octanoate-[acyl-carrier-protein]-protein-N-octanoyltransferase (EC 2.3.1.181)
<i>Pcc</i> ICMP5702_peg1287	AODT01000008.1	360260	359997	-	Proposed lipoate regulatory protein YbeD
<i>Pcc</i> ICMP5702_peg1288	AODT01000008.1	361607	360396	-	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)
<i>Pcc</i> ICMP5702_peg1289	AODT01000008.1	362895	361774	-	Septum-associated rare lipoprotein A
<i>Pcc</i> ICMP5702_peg1290	AODT01000008.1	364021	362909	-	Rod shape-determining protein RodA
<i>Pcc</i> ICMP5702_peg1291	AODT01000008.1	365935	364031	-	Peptidoglycan D,D-transpeptidase MrdA (EC 3.4.16.4)
<i>Pcc</i> ICMP5702_peg1292	AODT01000008.1	366439	365969	-	23S rRNA (pseudouridine(1915)-N(3))-methyltransferase (EC 2.1.1.177)
<i>Pcc</i> ICMP5702_peg1293	AODT01000008.1	366758	366441	-	Ribosomal silencing factor RsfA
<i>Pcc</i> ICMP5702_peg1294	AODT01000008.1	366903	366769	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1295	AODT01000008.1	367642	366953	-	Nicotinate-nucleotide adenyltransferase (EC 2.7.7.18)
<i>Pcc</i> ICMP5702_peg1296	AODT01000008.1	368634	367609	-	DNA polymerase III delta subunit (EC 2.7.7.7)
<i>Pcc</i> ICMP5702_peg1297	AODT01000008.1	369185	368631	-	LPS-assembly lipoprotein LptE
<i>Pcc</i> ICMP5702_peg1298	AODT01000008.1	371782	369200	-	Leucyl-tRNA synthetase (EC 6.1.1.4)
<i>Pcc</i> ICMP5702_peg1299	AODT01000008.1	371950	371801	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1300	AODT01000008.1	372092	372574	+	Uncharacterized protein YbeL
<i>Pcc</i> ICMP5702_peg1301	AODT01000008.1	373349	372624	-	Glutamate/aspartate ABC transporter, ATP-binding protein GltL (TC 3.A.1.3.4)
<i>Pcc</i> ICMP5702_peg1302	AODT01000008.1	374023	373349	-	Glutamate/aspartate ABC transporter, permease protein GltK (TC 3.A.1.3.4)
<i>Pcc</i> ICMP5702_peg1303	AODT01000008.1	374767	374027	-	Glutamate/aspartate ABC transporter, permease protein GltJ (TC 3.A.1.3.4)
<i>Pcc</i> ICMP5702_peg1304	AODT01000008.1	375883	374987	-	Glutamate/aspartate ABC transporter, substrate-binding protein GltI (TC 3.A.1.3.4)
<i>Pcc</i> ICMP5702_peg1305	AODT01000008.1	377865	376336	-	Apolipoprotein N-acyltransferase / Copper homeostasis protein CutE
<i>Pcc</i> ICMP5702_peg1306	AODT01000008.1	378751	377873	-	Magnesium and cobalt efflux protein CorC
<i>Pcc</i> ICMP5702_peg1307	AODT01000008.1	379358	378879	-	Metal-dependent hydrolase YbeY, involved in rRNA and/or ribosome maturation and assembly
<i>Pcc</i> ICMP5702_peg1308	AODT01000008.1	380413	379355	-	Phosphate starvation-inducible protein PhoH, predicted ATPase
<i>Pcc</i> ICMP5702_peg1309	AODT01000008.1	382168	380744	-	tRNA-i(6)A37 methylthiotransferase (EC 2.8.4.3)
<i>Pcc</i> ICMP5702_peg1310	AODT01000008.1	382401	382183	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1311	AODT01000008.1	382396	383562	+	2-polyprenyl-3-methyl-6-methoxy-1,4-benzoquinol hydroxylase

<i>Pcc</i> ICMP5702_peg1312	AODT01000008.1	384199	383585	-	FIG00905542: Hypothetical protein
<i>Pcc</i> ICMP5702_peg1313	AODT01000008.1	386839	385175	-	Asparagine synthetase [glutamine-hydrolyzing] (EC 6.3.5.4)
<i>Pcc</i> ICMP5702_peg1314	AODT01000008.1	388266	387043	-	N-acetylglucosamine-6P-responsive transcriptional repressor NagC, ROK family
<i>Pcc</i> ICMP5702_peg1315	AODT01000008.1	389507	388362	-	N-acetylglucosamine-6-phosphate deacetylase (EC 3.5.1.25)
<i>Pcc</i> ICMP5702_peg1316	AODT01000008.1	390326	389526	-	Glucosamine-6-phosphate deaminase (EC 3.5.99.6)
<i>Pcc</i> ICMP5702_peg1317	AODT01000008.1	390685	392181	+	PTS system, N-acetylglucosamine-specific IIC component / PTS system, N-acetylglucosamine-specific IIB component (EC 2.7.1.193)
<i>Pcc</i> ICMP5702_peg1318	AODT01000008.1	392372	394030	+	Glutaminyl-tRNA synthetase (EC 6.1.1.18)
<i>Pcc</i> ICMP5702_peg1319	AODT01000008.1	394543	394094	-	Ferric uptake regulation protein FUR
<i>Pcc</i> ICMP5702_peg1320	AODT01000008.1	395400	394873	-	Flavodoxin 1
<i>Pcc</i> ICMP5702_peg1321	AODT01000008.1	396036	396185	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1322	AODT01000008.1	396290	397957	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg1323	AODT01000008.1	398371	398090	-	Uncharacterized protein YbfE
<i>Pcc</i> ICMP5702_peg1324	AODT01000008.1	399441	398662	-	Esterase ybfF (EC 3.1.-.-)
<i>Pcc</i> ICMP5702_peg1325	AODT01000008.1	399703	400242	+	SeqA protein, negative modulator of initiation of replication
<i>Pcc</i> ICMP5702_peg1326	AODT01000008.1	400290	401933	+	Phosphoglucomutase (EC 5.4.2.2)
<i>Pcc</i> ICMP5702_peg1327	AODT01000008.1	402425	401997	-	putative membrane protein
<i>Pcc</i> ICMP5702_peg1328	AODT01000008.1	403188	402508	-	DNA-binding response regulator KdpE
<i>Pcc</i> ICMP5702_peg1329	AODT01000008.1	405956	403194	-	Osmosensitive K ⁺ channel histidine kinase KdpD
<i>Pcc</i> ICMP5702_peg1330	AODT01000008.1	406634	406059	-	Potassium-transporting ATPase C chain (EC 3.6.3.12) (TC 3.A.3.7.1)
<i>Pcc</i> ICMP5702_peg1331	AODT01000008.1	408798	406654	-	Potassium-transporting ATPase B chain (EC 3.6.3.12) (TC 3.A.3.7.1)
<i>Pcc</i> ICMP5702_peg1332	AODT01000008.1	410502	408814	-	Potassium-transporting ATPase A chain (EC 3.6.3.12) (TC 3.A.3.7.1)
<i>Pcc</i> ICMP5702_peg1333	AODT01000008.1	410654	410502	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1334	AODT01000008.1	411014	411220	+	Uncharacterized protein YbfA
<i>Pcc</i> ICMP5702_peg1335	AODT01000008.1	411497	412456	+	YbgA
<i>Pcc</i> ICMP5702_peg1336	AODT01000008.1	412478	413944	+	Deoxyribodipyrimidine photolyase (EC 4.1.99.3)
<i>Pcc</i> ICMP5702_peg1337	AODT01000008.1	413937	414680	+	GTP cyclohydrolase 1 type 2 homolog YbgI
<i>Pcc</i> ICMP5702_peg1338	AODT01000008.1	414837	415493	+	Allophanate hydrolase 2 subunit 1 (EC 3.5.1.54)
<i>Pcc</i> ICMP5702_peg1339	AODT01000008.1	415487	416431	+	Allophanate hydrolase 2 subunit 2 (EC 3.5.1.54)
<i>Pcc</i> ICMP5702_peg1340	AODT01000008.1	416421	417158	+	Lactam utilization protein LamB
<i>Pcc</i> ICMP5702_peg1341	AODT01000008.1	417188	417835	+	Pyrrolidone-carboxylate peptidase (EC 3.4.19.3)
<i>Pcc</i> ICMP5702_peg1342	AODT01000008.1	417879	418670	+	Endonuclease VIII
<i>Pcc</i> ICMP5702_peg1343	AODT01000008.1	418686	419111	+	Glyoxalase/bleomycin resistance protein/dioxygenase
<i>Pcc</i> ICMP5702_peg1344	AODT01000008.1	420455	419169	-	Citrate synthase (si) (EC 2.3.3.1)
<i>Pcc</i> ICMP5702_peg1345	AODT01000008.1	421128	421517	+	Succinate dehydrogenase cytochrome b-556 subunit
<i>Pcc</i> ICMP5702_peg1346	AODT01000008.1	421511	421858	+	Succinate dehydrogenase hydrophobic membrane anchor protein

<i>Pcc</i> ICMP5702_peg1347	AODT01000008.1	421858	423624	+	Succinate dehydrogenase flavoprotein subunit (EC 1.3.5.1)
<i>Pcc</i> ICMP5702_peg1348	AODT01000008.1	423641	424357	+	Succinate dehydrogenase iron-sulfur protein (EC 1.3.5.1)
<i>Pcc</i> ICMP5702_peg1349	AODT01000008.1	424633	427440	+	2-oxoglutarate dehydrogenase E1 component (EC 1.2.4.2)
<i>Pcc</i> ICMP5702_peg1350	AODT01000008.1	427456	428682	+	Dihydrolipoamide succinyltransferase component (E2) of 2-oxoglutarate dehydrogenase complex (EC 2.3.1.61)
<i>Pcc</i> ICMP5702_peg1351	AODT01000008.1	428742	428873	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1352	AODT01000008.1	428880	430046	+	Succinyl-CoA ligase [ADP-forming] beta chain (EC 6.2.1.5)
<i>Pcc</i> ICMP5702_peg1353	AODT01000008.1	430046	430918	+	Succinyl-CoA ligase [ADP-forming] alpha chain (EC 6.2.1.5)
<i>Pcc</i> ICMP5702_peg1354	AODT01000008.1	431146	432315	+	TPR domain protein
<i>Pcc</i> ICMP5702_peg1355	AODT01000008.1	433041	434609	+	Cytochrome d ubiquinol oxidase subunit I (EC 1.10.3.-)
<i>Pcc</i> ICMP5702_peg1356	AODT01000008.1	434623	435762	+	Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-)
<i>Pcc</i> ICMP5702_peg1357	AODT01000008.1	435779	435895	+	Cytochrome d ubiquinol oxidase subunit X (EC 1.10.3.-)
<i>Pcc</i> ICMP5702_peg1358	AODT01000008.1	435892	436185	+	Cyd operon protein YbgE
<i>Pcc</i> ICMP5702_peg1359	AODT01000008.1	436319	436723	+	Tol-Pal system-associated acyl-CoA thioesterase
<i>Pcc</i> ICMP5702_peg1360	AODT01000008.1	436720	437406	+	Tol-Pal system protein TolQ
<i>Pcc</i> ICMP5702_peg1361	AODT01000008.1	437419	437844	+	Tol biopolymer transport system, TolR protein
<i>Pcc</i> ICMP5702_peg1362	AODT01000008.1	437909	439084	+	TolA protein
<i>Pcc</i> ICMP5702_peg1363	AODT01000008.1	439224	440516	+	Tol-Pal system beta propeller repeat protein TolB
<i>Pcc</i> ICMP5702_peg1364	AODT01000008.1	440557	441066	+	Tol-Pal system peptidoglycan-associated lipoprotein PAL
<i>Pcc</i> ICMP5702_peg1365	AODT01000008.1	441413	441892	+	Cell division coordinator CpoB
<i>Pcc</i> ICMP5702_peg1366	AODT01000008.1	442507	443223	+	Uncharacterized DUF554 membrane protein
<i>Pcc</i> ICMP5702_peg1367	AODT01000008.1	443636	443238	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1368	AODT01000008.1	443859	444920	+	Quinolate synthetase (EC 2.5.1.72)
<i>Pcc</i> ICMP5702_peg1369	AODT01000008.1	444980	445705	+	Ribosyl nicotinamide transporter, PnuC-like
<i>Pcc</i> ICMP5702_peg1370	AODT01000008.1	446663	445713	-	Cobalt/zinc/cadmium resistance protein CzcD
<i>Pcc</i> ICMP5702_peg1371	AODT01000008.1	446947	448014	+	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I alpha (EC 2.5.1.54)
<i>Pcc</i> ICMP5702_peg1372	AODT01000009.1	908	156	-	Phosphoglycerate mutase (EC 5.4.2.11)
<i>Pcc</i> ICMP5702_peg1373	AODT01000009.1	4183	1046	-	Copper/silver efflux RND transporter, transmembrane protein CusA
<i>Pcc</i> ICMP5702_peg1374	AODT01000009.1	5682	4180	-	Copper/silver efflux RND transporter, membrane fusion protein CusB
<i>Pcc</i> ICMP5702_peg1375	AODT01000009.1	6938	5679	-	Copper/silver efflux RND transporter, outer membrane protein CusC
<i>Pcc</i> ICMP5702_peg1376	AODT01000009.1	7304	6951	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1377	AODT01000009.1	7831	7379	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1378	AODT01000009.1	9016	7970	-	Aldose 1-epimerase (EC 5.1.3.3)
<i>Pcc</i> ICMP5702_peg1379	AODT01000009.1	10155	9136	-	UDP-glucose 4-epimerase (EC 5.1.3.2)
<i>Pcc</i> ICMP5702_peg1380	AODT01000009.1	11829	10354	-	Putative molybdenum transport ATP-binding protein modF
<i>Pcc</i> ICMP5702_peg1381	AODT01000009.1	12715	11870	-	DNA-binding domain of ModE / Molybdate-binding domain of ModE

<i>Pcc</i> ICMP5702_peg1382	AODT01000009.1	12982	13137	+	AcrZ membrane protein associated with AcrAB-TolC multidrug efflux pump
<i>Pcc</i> ICMP5702_peg1383	AODT01000009.1	13284	14054	+	Molybdenum ABC transporter, substrate-binding protein ModA
<i>Pcc</i> ICMP5702_peg1384	AODT01000009.1	14054	14743	+	Molybdenum ABC transporter permease protein ModB
<i>Pcc</i> ICMP5702_peg1385	AODT01000009.1	14743	15801	+	Molybdenum ABC transporter ATP-binding protein ModC
<i>Pcc</i> ICMP5702_peg1386	AODT01000009.1	16039	16902	+	Sugar phosphate isomerases/epimerases
<i>Pcc</i> ICMP5702_peg1387	AODT01000009.1	17956	16976	-	Transcriptional regulator KPN_00542, LacI family
<i>Pcc</i> ICMP5702_peg1388	AODT01000009.1	19233	18082	-	Oxidoreductase
<i>Pcc</i> ICMP5702_peg1389	AODT01000009.1	20300	19230	-	Xylose isomerase-like TIM-barrel protein KPN_00539
<i>Pcc</i> ICMP5702_peg1390	AODT01000009.1	21681	20437	-	Uncharacterized transporter KPN_00538, MFS-type
<i>Pcc</i> ICMP5702_peg1391	AODT01000009.1	21869	22834	+	Glucokinase (EC 2.7.1.2)
<i>Pcc</i> ICMP5702_peg1392	AODT01000009.1	23725	22904	-	Hydrolase, HAD superfamily
<i>Pcc</i> ICMP5702_peg1393	AODT01000009.1	24383	25381	+	6-phosphogluconolactonase (EC 3.1.1.31)
<i>Pcc</i> ICMP5702_peg1394	AODT01000009.1	26686	25436	-	Uncharacterized protein KPN_00625
<i>Pcc</i> ICMP5702_peg1395	AODT01000009.1	27777	26701	-	5-methylthioribose ABC transporter, substrate-binding protein
<i>Pcc</i> ICMP5702_peg1396	AODT01000009.1	28103	27957	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1397	AODT01000009.1	28869	28234	-	Formate dehydrogenase N gamma subunit (EC 1.2.1.2)
<i>Pcc</i> ICMP5702_peg1398	AODT01000009.1	29770	28862	-	Formate dehydrogenase N beta subunit (EC 1.2.1.2)
<i>Pcc</i> ICMP5702_peg1399	AODT01000009.1	32830	29783	-	Formate dehydrogenase O alpha subunit (EC 1.2.1.2)
<i>Pcc</i> ICMP5702_peg1400	AODT01000009.1	35243	33111	-	Methionyl-tRNA synthetase (EC 6.1.1.10)
<i>Pcc</i> ICMP5702_peg1401	AODT01000009.1	35365	36474	+	[4Fe-4S] cluster assembly scaffold protein Mrp (=ApcC)
<i>Pcc</i> ICMP5702_peg1402	AODT01000009.1	36848	37489	+	Uridine kinase (EC 2.7.1.48)
<i>Pcc</i> ICMP5702_peg1403	AODT01000009.1	37597	38178	+	Deoxycytidine triphosphate deaminase (EC 3.5.4.13)
<i>Pcc</i> ICMP5702_peg1404	AODT01000009.1	38242	40077	+	AsmA protein
<i>Pcc</i> ICMP5702_peg1405	AODT01000009.1	40342	41694	+	C4-dicarboxylate transporter DcuC (TC 2.A.61.1.1)
<i>Pcc</i> ICMP5702_peg1406	AODT01000009.1	42157	41738	-	Protein of unknown function DUF86, SO_3166 group
<i>Pcc</i> ICMP5702_peg1407	AODT01000009.1	42537	42154	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1408	AODT01000009.1	44237	42651	-	Putative capsular polysaccharide transport protein YegH
<i>Pcc</i> ICMP5702_peg1409	AODT01000009.1	44296	44508	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1410	AODT01000009.1	44632	44730	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1411	AODT01000009.1	44966	46063	+	2.7.8.33)
<i>Pcc</i> ICMP5702_peg1412	AODT01000009.1	46214	47317	+	Putative polysaccharide export protein YccZ precursor
<i>Pcc</i> ICMP5702_peg1413	AODT01000009.1	47326	47760	+	Low molecular weight protein-tyrosine-phosphatase (EC 3.1.3.48) => Etp
<i>Pcc</i> ICMP5702_peg1414	AODT01000009.1	47776	49941	+	Tyrosine-protein kinase (EC 2.7.10.2)
<i>Pcc</i> ICMP5702_peg1415	AODT01000009.1	50245	51120	+	Glucose-1-phosphate thymidyltransferase (EC 2.7.7.24)
<i>Pcc</i> ICMP5702_peg1416	AODT01000009.1	51129	52001	+	dTDP-4-dehydrorhamnose reductase (EC 1.1.1.133)
<i>Pcc</i> ICMP5702_peg1417	AODT01000009.1	52012	52557	+	dTDP-4-dehydrorhamnose 3,5-epimerase (EC 5.1.3.13)

<i>Pcc</i> ICMP5702_peg1418	AODT01000009.1	52611	54227	+	4-hydroxy-2-oxovalerate aldolase (EC 4.1.3.39)
<i>Pcc</i> ICMP5702_peg1419	AODT01000009.1	54211	54858	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1420	AODT01000009.1	54866	55591	+	3-deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38)
<i>Pcc</i> ICMP5702_peg1421	AODT01000009.1	55671	56903	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1422	AODT01000009.1	56939	58213	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1423	AODT01000009.1	58210	58857	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1424	AODT01000009.1	58865	59995	+	UDP-glucose 4-epimerase (EC 5.1.3.2)
<i>Pcc</i> ICMP5702_peg1425	AODT01000009.1	59992	60960	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1426	AODT01000009.1	61006	62127	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1427	AODT01000009.1	62130	63035	+	dTDP-rhamnosyl transferase RfbF (EC 2.-.-.-)
<i>Pcc</i> ICMP5702_peg1428	AODT01000009.1	63049	64158	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1429	AODT01000009.1	64317	65213	+	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)
<i>Pcc</i> ICMP5702_peg1430	AODT01000009.1	65444	66850	+	6-phosphogluconate dehydrogenase, decarboxylating (EC 1.1.1.44)
<i>Pcc</i> ICMP5702_peg1431	AODT01000009.1	67021	66881	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1432	AODT01000009.1	67318	67611	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1433	AODT01000009.1	67687	68364	+	Uncharacterized lipoprotein YjbF
<i>Pcc</i> ICMP5702_peg1434	AODT01000009.1	68374	69156	+	YjbG polysaccharide synthesis-related protein
<i>Pcc</i> ICMP5702_peg1435	AODT01000009.1	69153	71276	+	Uncharacterized lipoprotein YjbH
<i>Pcc</i> ICMP5702_peg1436	AODT01000009.1	71668	72225	+	Periplasmic chorismate mutase I precursor (EC 5.4.99.5)
<i>Pcc</i> ICMP5702_peg1437	AODT01000009.1	72244	73872	+	Kumamolysin
<i>Pcc</i> ICMP5702_peg1438	AODT01000009.1	74198	75622	+	6-phospho-beta-glucosidase (EC 3.2.1.86)
<i>Pcc</i> ICMP5702_peg1439	AODT01000009.1	75733	76569	+	Beta-glucoside bgl operon antiterminator, BglG family
<i>Pcc</i> ICMP5702_peg1440	AODT01000009.1	76803	77864	+	Response regulator protein
<i>Pcc</i> ICMP5702_peg1441	AODT01000009.1	78224	77937	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1442	AODT01000009.1	79129	78272	-	Predicted transcriptional regulator of the myo-inositol catabolic operon
<i>Pcc</i> ICMP5702_peg1443	AODT01000009.1	79228	79356	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1444	AODT01000009.1	79457	80968	+	Malonate-semialdehyde dehydrogenase [inositol] (EC 1.2.1.18)
<i>Pcc</i> ICMP5702_peg1445	AODT01000009.1	81031	81342	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1446	AODT01000009.1	81445	83376	+	3D-(3,5/4)-trihydroxycyclohexane-1,2-dione hydrolase (EC 3.7.1.22)
<i>Pcc</i> ICMP5702_peg1447	AODT01000009.1	84091	85077	+	Myo-inositol 2-dehydrogenase 1 (EC 1.1.1.18)
<i>Pcc</i> ICMP5702_peg1448	AODT01000009.1	85158	86096	+	Inositol transport system sugar-binding protein
<i>Pcc</i> ICMP5702_peg1449	AODT01000009.1	86163	87710	+	Inositol transport system ATP-binding protein
<i>Pcc</i> ICMP5702_peg1450	AODT01000009.1	87723	88754	+	Inositol transport system permease protein
<i>Pcc</i> ICMP5702_peg1451	AODT01000009.1	88795	89928	+	Myo-inositol 2-dehydrogenase 2 (EC 1.1.1.18)
<i>Pcc</i> ICMP5702_peg1452	AODT01000009.1	89973	91877	+	5-keto-2-deoxygluconokinase (EC 2.7.1.92) / uncharacterized domain
<i>Pcc</i> ICMP5702_peg1453	AODT01000009.1	91911	92801	+	Inosose dehydratase (EC 4.2.1.44)

<i>Pcc</i> ICMP5702_peg1454	AODT01000009.1	92889	93725	+	5-deoxy-glucuronate isomerase (EC 5.3.1.30)
<i>Pcc</i> ICMP5702_peg1455	AODT01000009.1	94104	93826	-	KluA
<i>Pcc</i> ICMP5702_peg1456	AODT01000009.1	94871	94182	-	3.A.1.11.1)
<i>Pcc</i> ICMP5702_peg1457	AODT01000009.1	96557	94893	-	Ferric iron ABC transporter, permease protein
<i>Pcc</i> ICMP5702_peg1458	AODT01000009.1	97623	96574	-	Ferric iron ABC transporter, iron-binding protein
<i>Pcc</i> ICMP5702_peg1459	AODT01000009.1	98697	97858	-	Beta-glucoside bgl operon antiterminator, BglG family
<i>Pcc</i> ICMP5702_peg1460	AODT01000009.1	100255	98792	-	6-phospho-beta-glucosidase (EC 3.2.1.86)
<i>Pcc</i> ICMP5702_peg1461	AODT01000009.1	102120	100255	-	PTS system, beta-glucoside-specific IIB component / PTS system, beta-glucoside-specific IIC component / PTS system, beta-glucoside-specific IIA component
<i>Pcc</i> ICMP5702_peg1462	AODT01000009.1	102562	103626	+	Probable diguanylate cyclase YeaP
<i>Pcc</i> ICMP5702_peg1463	AODT01000009.1	104454	103648	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1464	AODT01000009.1	105015	104563	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1465	AODT01000009.1	105927	105589	-	Protein YoaG
<i>Pcc</i> ICMP5702_peg1466	AODT01000009.1	106270	105938	-	Uncharacterized protein YeaR
<i>Pcc</i> ICMP5702_peg1467	AODT01000009.1	106668	107258	+	Flavoredoxin
<i>Pcc</i> ICMP5702_peg1468	AODT01000009.1	108377	107469	-	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg1469	AODT01000009.1	108503	109438	+	Hypothetical protein; Some similarities with different peroxydase
<i>Pcc</i> ICMP5702_peg1470	AODT01000009.1	110086	109517	-	Transcriptional regulator, AcrR family
<i>Pcc</i> ICMP5702_peg1471	AODT01000009.1	110224	111315	+	NADH:flavin oxidoreductases, Old Yellow Enzyme family
<i>Pcc</i> ICMP5702_peg1472	AODT01000009.1	111391	112173	+	Oxidoreductase, short-chain dehydrogenase/reductase family
<i>Pcc</i> ICMP5702_peg1473	AODT01000009.1	112268	113086	+	Oxidoreductase
<i>Pcc</i> ICMP5702_peg1474	AODT01000009.1	113094	114113	+	Zinc-type alcohol dehydrogenase-like protein
<i>Pcc</i> ICMP5702_peg1475	AODT01000009.1	114215	114370	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1476	AODT01000009.1	115868	114606	-	Lactose permease
<i>Pcc</i> ICMP5702_peg1477	AODT01000009.1	115967	116158	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1478	AODT01000009.1	119277	116146	-	beta-galactosidase (EC 3.2.1.23)
<i>Pcc</i> ICMP5702_peg1479	AODT01000009.1	120667	119591	-	Transcriptional repressor of the lac operon
<i>Pcc</i> ICMP5702_peg1480	AODT01000009.1	122105	121056	-	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg1481	AODT01000009.1	124198	122120	-	ABC transporter, permease protein 1 (cluster 1, maltose/g3p/polyamine/iron) / ABC transporter, permease protein 2 (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg1482	AODT01000009.1	125627	124593	-	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg1483	AODT01000009.1	126990	125665	-	Possible sugar-phosphate sensor or MFS family transporter KOX_12270
<i>Pcc</i> ICMP5702_peg1484	AODT01000009.1	128657	127080	-	Two-component system sensor histidine kinase KOX_12275
<i>Pcc</i> ICMP5702_peg1485	AODT01000009.1	129290	128661	-	Two-component transcriptional response regulator KOX_12280, LuxR family
<i>Pcc</i> ICMP5702_peg1486	AODT01000009.1	129521	130336	+	Lipoprotein 28 (NlpA)

<i>Pcc</i> ICMP5702_peg1487	AODT01000009.1	130561	131505	+	Pectin lyase (EC 4.2.2.10)
<i>Pcc</i> ICMP5702_peg1488	AODT01000009.1	132391	131675	-	Aspartate racemase (EC 5.1.1.13)
<i>Pcc</i> ICMP5702_peg1489	AODT01000009.1	132631	133530	+	LysR-family transcriptional regulator YjiE
<i>Pcc</i> ICMP5702_peg1490	AODT01000009.1	134922	133618	-	Proton/sodium-glutamate symport protein
<i>Pcc</i> ICMP5702_peg1491	AODT01000009.1	134943	135101	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1492	AODT01000009.1	136477	135584	-	Transcriptional regulator, GntR family
<i>Pcc</i> ICMP5702_peg1493	AODT01000009.1	137899	136586	-	Citrate/H ⁺ symporter of CitMHS family
<i>Pcc</i> ICMP5702_peg1494	AODT01000009.1	140739	138589	-	Formate dehydrogenase H (EC 1.2.1.2)
<i>Pcc</i> ICMP5702_peg1495	AODT01000009.1	140861	140742	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1496	AODT01000009.1	141275	142954	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg1497	AODT01000009.1	143461	145365	+	High-affinity Fe ²⁺ /Pb ²⁺ permease precursor
<i>Pcc</i> ICMP5702_peg1498	AODT01000009.1	145471	146013	+	Periplasmic protein p19 involved in high-affinity Fe ²⁺ transport
<i>Pcc</i> ICMP5702_peg1499	AODT01000009.1	146171	147565	+	putative membrane protein
<i>Pcc</i> ICMP5702_peg1500	AODT01000009.1	147568	148857	+	Fe ²⁺ ABC transporter, permease protein 1
<i>Pcc</i> ICMP5702_peg1501	AODT01000009.1	148847	149986	+	Fe ²⁺ ABC transporter, permease protein 2
<i>Pcc</i> ICMP5702_peg1502	AODT01000009.1	149991	150707	+	Fe ²⁺ ABC transporter, ATP-binding subunit
<i>Pcc</i> ICMP5702_peg1503	AODT01000009.1	150694	151191	+	Possible periplasmic thiredoxin
<i>Pcc</i> ICMP5702_peg1504	AODT01000009.1	152205	151228	-	Inner membrane protein Ytff
<i>Pcc</i> ICMP5702_peg1505	AODT01000009.1	153287	152454	-	Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg1506	AODT01000009.1	153774	154727	+	Alkanesulfonate utilization operon LysR-family regulator Cbl
<i>Pcc</i> ICMP5702_peg1507	AODT01000009.1	154899	154744	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1508	AODT01000009.1	155234	155713	+	T6SS component Hcp
<i>Pcc</i> ICMP5702_peg1509	AODT01000009.1	155930	155733	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1510	AODT01000009.1	156622	155927	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1511	AODT01000009.1	156995	156837	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1512	AODT01000009.1	157197	158552	+	Proton/glutamate symporter @ Proton/aspartate symporter
<i>Pcc</i> ICMP5702_peg1513	AODT01000009.1	159732	158629	-	Glycerol dehydrogenase (EC 1.1.1.6)
<i>Pcc</i> ICMP5702_peg1514	AODT01000009.1	160727	159861	-	Taurine ABC transporter, permease protein TauC
<i>Pcc</i> ICMP5702_peg1515	AODT01000009.1	161553	160687	-	Taurine ABC transporter, ATP-binding protein TauB
<i>Pcc</i> ICMP5702_peg1516	AODT01000009.1	162632	161610	-	Taurine ABC transporter, substrate-binding protein TauA
<i>Pcc</i> ICMP5702_peg1517	AODT01000009.1	162952	163974	+	Hydroxycarboxylate dehydrogenase (NADP ⁺) HcxB
<i>Pcc</i> ICMP5702_peg1518	AODT01000009.1	164040	165053	+	ABC transporter, substrate-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg1519	AODT01000009.1	165060	165833	+	ABC transporter, permease protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg1520	AODT01000009.1	165830	166633	+	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg1521	AODT01000009.1	166655	167668	+	D-cysteine desulfhydrase (EC 4.4.1.15)

<i>Pcc</i> ICMP5702_peg1522	AODT01000009.1	167665	168381	+	Aspartate racemase (EC 5.1.1.13)
<i>Pcc</i> ICMP5702_peg1523	AODT01000009.1	169765	168425	-	Anaerobic C4-dicarboxylate transporter DcuB
<i>Pcc</i> ICMP5702_peg1524	AODT01000009.1	171968	170613	-	Type I secretion outer membrane protein, TolC family @ ABC exporter for hemopore HasA, outer membrane component HasF
<i>Pcc</i> ICMP5702_peg1525	AODT01000009.1	173329	171971	-	Type I secretion membrane fusion protein, HlyD family @ ABC exporter for hemopore HasA, membrane fusion protein (MFP) family component HasE
<i>Pcc</i> ICMP5702_peg1526	AODT01000009.1	175241	173394	-	Type I secretion system ATPase @ ABC exporter for hemopore HasA, ATP-binding component HasD
<i>Pcc</i> ICMP5702_peg1527	AODT01000009.1	176113	175496	-	Hemophore HasA
<i>Pcc</i> ICMP5702_peg1528	AODT01000009.1	178909	176231	-	Hemophore HasA outer membrane receptor HasR / Iron siderophore receptor protein
<i>Pcc</i> ICMP5702_peg1529	AODT01000009.1	180122	179169	-	Iron siderophore sensor protein
<i>Pcc</i> ICMP5702_peg1530	AODT01000009.1	180731	180222	-	FIG006045: Sigma factor, ECF subfamily
<i>Pcc</i> ICMP5702_peg1531	AODT01000009.1	181115	181285	+	FIG00904518: Hypothetical protein
<i>Pcc</i> ICMP5702_peg1532	AODT01000009.1	181406	182830	+	4-aminobutyraldehyde dehydrogenase (EC 1.2.1.19)
<i>Pcc</i> ICMP5702_peg1533	AODT01000009.1	183158	184564	+	Putrescine aminotransferase (EC 2.6.1.82)
<i>Pcc</i> ICMP5702_peg1534	AODT01000009.1	185377	187044	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg1535	AODT01000009.1	188198	187212	-	SAM-dependent methyltransferase
<i>Pcc</i> ICMP5702_peg1536	AODT01000009.1	188265	189257	+	Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg1537	AODT01000009.1	189520	189383	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1538	AODT01000009.1	189532	191034	+	L-Proline/Glycine betaine transporter ProP
<i>Pcc</i> ICMP5702_peg1539	AODT01000009.1	191168	192487	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1540	AODT01000009.1	192796	192557	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1541	AODT01000009.1	194364	192904	-	AMP nucleosidase (EC 3.2.2.4)
<i>Pcc</i> ICMP5702_peg1542	AODT01000009.1	196263	194485	-	ABC transporter, permease protein 1 (cluster 5, nickel/peptides/opines) / ABC transporter, permease protein 2 (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg1543	AODT01000009.1	197812	196301	-	ABC transporter, substrate-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg1544	AODT01000009.1	199070	197823	-	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg1545	AODT01000009.1	199991	199155	-	ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg1546	AODT01000009.1	200869	199988	-	ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg1547	AODT01000009.1	201946	201014	-	Transposase
<i>Pcc</i> ICMP5702_peg1548	AODT01000009.1	203913	202120	-	Putative PQQ enzyme repeat
<i>Pcc</i> ICMP5702_peg1549	AODT01000009.1	204739	203930	-	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg1550	AODT01000009.1	206337	204736	-	Alkanesulfonates transport system permease protein
<i>Pcc</i> ICMP5702_peg1551	AODT01000009.1	206575	207711	+	ABC transporter, substrate-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg1552	AODT01000009.1	208662	207724	-	Transcriptional regulator, LysR family

<i>Pcc</i> ICMP5702_peg1553	AODT01000009.1	209566	208808	-	CDP-diacylglycerol pyrophosphatase (EC 3.6.1.26)
<i>Pcc</i> ICMP5702_peg1554	AODT01000009.1	211846	209837	-	iron aquisition outermembrane yersiniabactin receptor (FyuA, Psn, pesticin receptor) @
<i>Pcc</i> ICMP5702_peg1555	AODT01000009.1	213311	212040	-	Outer membrane receptor for ferric siderophore
<i>Pcc</i> ICMP5702_peg1556	AODT01000009.1	213421	213308	-	Putative signal transducer
<i>Pcc</i> ICMP5702_peg1557	AODT01000009.1	214503	213535	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1558	AODT01000009.1	214734	216572	+	iron aquisition regulator (YbtA, AraC-like, required for transcription of FyuA/psn, Irp2)
<i>Pcc</i> ICMP5702_peg1559	AODT01000009.1	216569	218359	+	Iron siderophore ABC transporter, permease/ATP-binding protein YbtP
					Iron siderophore ABC transporter, permease/ATP-binding protein YbtQ
					N-(3-oxohexanoyl)-L-homoserine lactone-binding transcriptional activator @ N-(3-oxooctanoyl)-L-homoserine lactone-binding transcriptional activator @ Acyl-
<i>Pcc</i> ICMP5702_peg1560	AODT01000009.1	219114	218377	-	homoserine lactone-binding transcriptional activator, LuxR family
<i>Pcc</i> ICMP5702_peg1561	AODT01000009.1	219608	220222	+	Transcriptional regulator, AcrR family
<i>Pcc</i> ICMP5702_peg1562	AODT01000009.1	220844	220200	-	ortholog of Bordetella pertussis (BX470248) BP2750
<i>Pcc</i> ICMP5702_peg1563	AODT01000009.1	222484	220841	-	Paraquat-inducible protein B
<i>Pcc</i> ICMP5702_peg1564	AODT01000009.1	223098	222481	-	Paraquat-inducible protein A
<i>Pcc</i> ICMP5702_peg1565	AODT01000009.1	223726	223088	-	Paraquat-inducible protein A
<i>Pcc</i> ICMP5702_peg1566	AODT01000009.1	224421	223759	-	putative lipoprotein
<i>Pcc</i> ICMP5702_peg1567	AODT01000009.1	224962	225933	+	Chemotaxis protein CheV (EC 2.7.3.-)
<i>Pcc</i> ICMP5702_peg1568	AODT01000009.1	226888	226049	-	Glutathione S-transferase (EC 2.5.1.18)
<i>Pcc</i> ICMP5702_peg1569	AODT01000009.1	227789	227178	-	Rrf2-linked NADH-flavin reductase
<i>Pcc</i> ICMP5702_peg1570	AODT01000009.1	227913	228332	+	Transcriptional regulator, HxlR family
<i>Pcc</i> ICMP5702_peg1571	AODT01000009.1	228559	228681	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1572	AODT01000009.1	228686	228988	+	Antitoxin HlgA
<i>Pcc</i> ICMP5702_peg1573	AODT01000009.1	230029	229025	-	pyridoxal-phosphate dependent enzyme family protein
<i>Pcc</i> ICMP5702_peg1574	AODT01000009.1	230082	230420	+	Transcriptional regulator, ArsR family
<i>Pcc</i> ICMP5702_peg1575	AODT01000009.1	230839	230435	-	Transcriptional regulator, HxlR family
<i>Pcc</i> ICMP5702_peg1576	AODT01000009.1	230917	231342	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1577	AODT01000009.1	231462	232097	+	NmrA family protein
<i>Pcc</i> ICMP5702_peg1578	AODT01000009.1	232192	232305	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1579	AODT01000009.1	233516	232317	-	Multidrug resistance transporter, Bcr/CflA family
<i>Pcc</i> ICMP5702_peg1580	AODT01000009.1	234920	233685	-	Multidrug resistance protein ErmB
<i>Pcc</i> ICMP5702_peg1581	AODT01000009.1	234987	235442	+	Transcriptional regulator, MerR family
<i>Pcc</i> ICMP5702_peg1582	AODT01000009.1	235642	237078	+	6-phospho-beta-glucosidase (EC 3.2.1.86)
<i>Pcc</i> ICMP5702_peg1583	AODT01000009.1	237240	237722	+	Putative cold-shock protein
<i>Pcc</i> ICMP5702_peg1584	AODT01000009.1	237899	238438	+	Nucleoprotein/polynucleotide-associated enzyme
<i>Pcc</i> ICMP5702_peg1585	AODT01000009.1	239990	238578	-	Diguanylate cyclase (EC 2.7.7.65) => DgcJ

<i>Pcc</i> ICMP5702_peg1586	AODT01000009.1	240323	240568	+	Uncharacterized protein YmjA
<i>Pcc</i> ICMP5702_peg1587	AODT01000009.1	241823	240792	-	5-methyltetrahydropteroyltriglutamate--homocysteine methyltransferase (EC 2.1.1.14)
<i>Pcc</i> ICMP5702_peg1588	AODT01000009.1	242831	241854	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1589	AODT01000009.1	243673	243329	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1590	AODT01000009.1	243979	245181	+	Tyrosyl-tRNA synthetase (EC 6.1.1.1)
<i>Pcc</i> ICMP5702_peg1591	AODT01000009.1	245306	246196	+	2-dehydropantoate 2-reductase (EC 1.1.1.169)
<i>Pcc</i> ICMP5702_peg1592	AODT01000009.1	248404	246554	-	Conjugative transfer ATP-dependent DNA helicase
<i>Pcc</i> ICMP5702_peg1593	AODT01000009.1	250265	248394	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1594	AODT01000009.1	250456	250569	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1595	AODT01000009.1	251035	251277	+	Antirestriction protein
<i>Pcc</i> ICMP5702_peg1596	AODT01000009.1	251288	251464	+	Antirestriction protein
<i>Pcc</i> ICMP5702_peg1597	AODT01000009.1	251586	251822	+	CcdA protein (antitoxin to CcdB)
<i>Pcc</i> ICMP5702_peg1598	AODT01000009.1	251825	252139	+	CcdB toxin protein
<i>Pcc</i> ICMP5702_peg1599	AODT01000009.1	253598	252801	-	Protein MtfA
<i>Pcc</i> ICMP5702_peg1600	AODT01000009.1	254219	253833	-	Putative secreted protein
<i>Pcc</i> ICMP5702_peg1601	AODT01000009.1	254462	254941	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1602	AODT01000009.1	255592	254996	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1603	AODT01000009.1	256180	256347	+	UPF0057 membrane protein YqaE
<i>Pcc</i> ICMP5702_peg1604	AODT01000009.1	257856	256435	-	2-oxoglutarate/malate translocator
<i>Pcc</i> ICMP5702_peg1605	AODT01000009.1	259352	258003	-	3-carboxy-cis,cis-muconate cycloisomerase (EC 5.5.1.2)
<i>Pcc</i> ICMP5702_peg1606	AODT01000009.1	259579	260319	+	Transcriptional regulator, GntR family
<i>Pcc</i> ICMP5702_peg1607	AODT01000009.1	261918	260446	-	Putative two-component response regulator and GGDEF family protein YeaJ
<i>Pcc</i> ICMP5702_peg1608	AODT01000009.1	262200	263108	+	Transcription regulator [contains diacylglycerol kinase catalytic domain]
<i>Pcc</i> ICMP5702_peg1609	AODT01000009.1	263778	263179	-	Nitroreductase family protein
<i>Pcc</i> ICMP5702_peg1610	AODT01000009.1	264637	263879	-	Molybdopterin-synthase adenylyltransferase (EC 2.7.7.80)
<i>Pcc</i> ICMP5702_peg1611	AODT01000009.1	265875	264640	-	Molybdopterin molybdenumtransferase (EC 2.10.1.1)
<i>Pcc</i> ICMP5702_peg1612	AODT01000009.1	266354	268255	+	Oligopeptide transport ATP-binding protein @ Glutathione ABC transporter, ATP-binding protein GsiA
<i>Pcc</i> ICMP5702_peg1613	AODT01000009.1	268281	269825	+	Oligopeptide transport substrate-binding protein @ Glutathione ABC transporter, substrate-binding protein GsiB
<i>Pcc</i> ICMP5702_peg1614	AODT01000009.1	269934	270854	+	Oligopeptide transport permease protein OppB-like @ Glutathione ABC transporter, permease protein GsiC
<i>Pcc</i> ICMP5702_peg1615	AODT01000009.1	270864	271769	+	Oligopeptide transport permease protein OppC-like @ Glutathione ABC transporter, permease protein GsiD
<i>Pcc</i> ICMP5702_peg1616	AODT01000009.1	273512	271815	-	NAD-dependent malic enzyme (EC 1.1.1.38)
<i>Pcc</i> ICMP5702_peg1617	AODT01000009.1	274611	273721	-	Cytidine deaminase (EC 3.5.4.5)

<i>Pcc</i> ICMP5702_peg1618	AODT01000009.1	275479	274784	-	Inner membrane protein YohK
<i>Pcc</i> ICMP5702_peg1619	AODT01000009.1	275886	275479	-	UPF0299 membrane protein YohJ
<i>Pcc</i> ICMP5702_peg1620	AODT01000009.1	276902	276108	-	Endoglucanase
<i>Pcc</i> ICMP5702_peg1621	AODT01000009.1	278484	277180	-	Adenosylmethionine-8-amino-7-oxonanoate aminotransferase (EC 2.6.1.62)
<i>Pcc</i> ICMP5702_peg1622	AODT01000009.1	278580	279617	+	Biotin synthase (EC 2.8.1.6)
<i>Pcc</i> ICMP5702_peg1623	AODT01000009.1	279657	280814	+	8-amino-7-oxonanoate synthase (EC 2.3.1.47)
<i>Pcc</i> ICMP5702_peg1624	AODT01000009.1	280795	281556	+	Malonyl-[acyl-carrier protein] O-methyltransferase (EC 2.1.1.197)
<i>Pcc</i> ICMP5702_peg1625	AODT01000009.1	281549	282229	+	Dethiobiotin synthase BioD (EC 6.3.3.3)
<i>Pcc</i> ICMP5702_peg1626	AODT01000009.1	282266	282388	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1627	AODT01000009.1	282505	282984	+	T6SS component Hcp
<i>Pcc</i> ICMP5702_peg1628	AODT01000009.1	283066	283758	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1629	AODT01000009.1	283759	284190	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1630	AODT01000009.1	284227	284652	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1631	AODT01000009.1	284652	284768	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1632	AODT01000009.1	285378	285256	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1633	AODT01000009.1	285417	287429	+	Excinuclease ABC subunit B
<i>Pcc</i> ICMP5702_peg1634	AODT01000009.1	287458	287889	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1635	AODT01000009.1	288797	287865	-	Putative structural protein
<i>Pcc</i> ICMP5702_peg1636	AODT01000009.1	289187	290209	+	GTP 3',8-cyclase (EC 4.1.99.22)
<i>Pcc</i> ICMP5702_peg1637	AODT01000009.1	290244	290762	+	Molybdenum cofactor biosynthesis protein MoaB
<i>Pcc</i> ICMP5702_peg1638	AODT01000009.1	290781	291275	+	Cyclic pyranopterin monophosphate synthase (EC 4.6.1.17)
<i>Pcc</i> ICMP5702_peg1639	AODT01000009.1	291272	291517	+	Molybdopterin synthase sulfur carrier subunit
<i>Pcc</i> ICMP5702_peg1640	AODT01000009.1	291520	291972	+	Molybdopterin synthase catalytic subunit MoaE (EC 2.8.1.12)
<i>Pcc</i> ICMP5702_peg1641	AODT01000009.1	292085	292792	+	Inner membrane protein YbhL
<i>Pcc</i> ICMP5702_peg1642	AODT01000009.1	294000	292864	-	ABC-type efflux pump permease component YbhR
<i>Pcc</i> ICMP5702_peg1643	AODT01000009.1	295185	294010	-	ABC-type efflux pump permease component YbhS
<i>Pcc</i> ICMP5702_peg1644	AODT01000009.1	296920	295178	-	ABC-type efflux pump, duplicated ATPase component YbhF
<i>Pcc</i> ICMP5702_peg1645	AODT01000009.1	297941	296913	-	ABC-type efflux pump membrane fusion component YbhG
<i>Pcc</i> ICMP5702_peg1646	AODT01000009.1	298118	298234	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1647	AODT01000009.1	298495	300618	+	Ferric aerobactin receptor precursor
<i>Pcc</i> ICMP5702_peg1648	AODT01000009.1	300677	301627	+	3.A.1.14.1)
<i>Pcc</i> ICMP5702_peg1649	AODT01000009.1	301624	302613	+	Iron compound ABC transporter, permease protein
<i>Pcc</i> ICMP5702_peg1650	AODT01000009.1	302606	303637	+	Iron(III) dicitrate transport system permease protein FecD (TC 3.A.1.14.1)
<i>Pcc</i> ICMP5702_peg1651	AODT01000009.1	303647	304501	+	Iron compound ABC transporter, ATP-binding protein
<i>Pcc</i> ICMP5702_peg1652	AODT01000009.1	304491	305300	+	unknown conserved protein in bacilli
<i>Pcc</i> ICMP5702_peg1653	AODT01000009.1	305598	307037	+	ATP-dependent RNA helicase RhlE (EC 3.6.4.13)

<i>Pcc</i> ICMP5702_peg1654	AODT01000010.1	1615	308	-	Outer membrane porin KPN_00433
<i>Pcc</i> ICMP5702_peg1655	AODT01000010.1	3109	2099	-	Galactose operon repressor, GalR-LacI family of transcriptional regulators
<i>Pcc</i> ICMP5702_peg1656	AODT01000010.1	3574	4614	+	Galactose-1-phosphate uridylyltransferase (EC 2.7.7.10)
<i>Pcc</i> ICMP5702_peg1657	AODT01000010.1	4624	5787	+	Galactokinase (EC 2.7.1.6)
<i>Pcc</i> ICMP5702_peg1658	AODT01000010.1	6266	5829	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1659	AODT01000010.1	6613	6431	-	Probable mRNA interferase HicA
<i>Pcc</i> ICMP5702_peg1660	AODT01000010.1	8207	6729	-	Mg/Co/Ni transporter MgtE, CBS domain-containing
<i>Pcc</i> ICMP5702_peg1661	AODT01000010.1	8425	8874	+	Organic hydroperoxide resistance transcriptional regulator
<i>Pcc</i> ICMP5702_peg1662	AODT01000010.1	9061	9486	+	Organic hydroperoxide resistance protein
<i>Pcc</i> ICMP5702_peg1663	AODT01000010.1	9992	9777	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1664	AODT01000010.1	10415	10227	-	FIG00613750: Hypothetical protein
<i>Pcc</i> ICMP5702_peg1665	AODT01000010.1	10491	10616	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1666	AODT01000010.1	12182	10647	-	Exopolyphosphatase (EC 3.6.1.11)
<i>Pcc</i> ICMP5702_peg1667	AODT01000010.1	14254	12182	-	Polyphosphate kinase (EC 2.7.4.1)
<i>Pcc</i> ICMP5702_peg1668	AODT01000010.1	14472	16640	+	Phosphate ABC transporter, permease protein PstC (TC 3.A.1.7.1)
<i>Pcc</i> ICMP5702_peg1669	AODT01000010.1	16637	18283	+	Phosphate ABC transporter, permease protein PstA (TC 3.A.1.7.1)
<i>Pcc</i> ICMP5702_peg1670	AODT01000010.1	18299	19114	+	Phosphate ABC transporter, ATP-binding protein PstB (TC 3.A.1.7.1)
<i>Pcc</i> ICMP5702_peg1671	AODT01000010.1	19135	19332	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1672	AODT01000010.1	19348	19911	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1673	AODT01000010.1	20421	19957	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1674	AODT01000010.1	20643	20789	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1675	AODT01000010.1	20811	21248	+	Putative DNA-binding protein
<i>Pcc</i> ICMP5702_peg1676	AODT01000010.1	22707	21340	-	L-serine dehydratase, beta subunit (EC 4.3.1.17) / L-serine dehydratase, alpha subunit (EC 4.3.1.17)
<i>Pcc</i> ICMP5702_peg1677	AODT01000010.1	24064	22775	-	Serine transporter
<i>Pcc</i> ICMP5702_peg1678	AODT01000010.1	24125	24259	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1679	AODT01000010.1	24522	24382	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1680	AODT01000010.1	25652	24582	-	N5-carboxyaminoimidazole ribonucleotide synthase (EC 6.3.4.18)
<i>Pcc</i> ICMP5702_peg1681	AODT01000010.1	26158	25649	-	N5-carboxyaminoimidazole ribonucleotide mutase (EC 5.4.99.18)
<i>Pcc</i> ICMP5702_peg1682	AODT01000010.1	27059	26337	-	UDP-2,3-diacetylglucosamine diphosphatase (EC 3.6.1.54)
<i>Pcc</i> ICMP5702_peg1683	AODT01000010.1	27564	27070	-	Peptidyl-prolyl cis-trans isomerase PpiB (EC 5.2.1.8)
<i>Pcc</i> ICMP5702_peg1684	AODT01000010.1	27986	28417	+	putative membrane protein
<i>Pcc</i> ICMP5702_peg1685	AODT01000010.1	28688	30073	+	CysteinyI-tRNA synthetase (EC 6.1.1.16)
<i>Pcc</i> ICMP5702_peg1686	AODT01000010.1	30377	30165	-	Uncharacterized S4 RNA-binding-domain protein YbcJ
<i>Pcc</i> ICMP5702_peg1687	AODT01000010.1	31402	30539	-	Methenyltetrahydrofolate cyclohydrolase (EC 3.5.4.9) / Methylenetetrahydrofolate dehydrogenase (NADP+) (EC 1.5.1.5)

<i>Pcc</i> ICMP5702_peg1688	AODT01000010.1	33067	31520	-	Putative regulatory protein
<i>Pcc</i> ICMP5702_peg1689	AODT01000010.1	33622	34788	+	UDP-glucose 6-dehydrogenase (EC 1.1.1.22)
<i>Pcc</i> ICMP5702_peg1690	AODT01000010.1	35000	36148	+	UDP-4-amino-4-deoxy-L-arabinose--oxoglutarate aminotransferase (EC 2.6.1.87)
<i>Pcc</i> ICMP5702_peg1691	AODT01000010.1	36141	37124	+	Undecaprenyl-phosphate 4-deoxy-4-formamido-L-arabinose transferase (EC 2.4.2.53)
<i>Pcc</i> ICMP5702_peg1692	AODT01000010.1	37121	39121	+	UDP-4-amino-4-deoxy-L-arabinose formyltransferase (EC 2.1.2.13) / UDP-glucuronic acid oxidase (UDP-4-keto-hexauronic acid decarboxylating) (EC 1.1.1.305)
<i>Pcc</i> ICMP5702_peg1693	AODT01000010.1	39118	40011	+	3.5.1.n3)
<i>Pcc</i> ICMP5702_peg1694	AODT01000010.1	40029	41699	+	Undecaprenyl phosphate-alpha-4-amino-4-deoxy-L-arabinose arabinosyl transferase (EC 2.4.2.43) @ Polymyxin resistance protein PmrK
<i>Pcc</i> ICMP5702_peg1695	AODT01000010.1	41696	42037	+	Undecaprenyl phosphate-aminoarabinose flippase subunit ArnE
<i>Pcc</i> ICMP5702_peg1696	AODT01000010.1	42037	42429	+	Undecaprenyl phosphate-aminoarabinose flippase subunit ArnF
<i>Pcc</i> ICMP5702_peg1697	AODT01000010.1	43502	42447	-	Ferric iron ABC transporter, ATP-binding protein
<i>Pcc</i> ICMP5702_peg1698	AODT01000010.1	45082	43505	-	Ferric iron ABC transporter, permease protein
<i>Pcc</i> ICMP5702_peg1699	AODT01000010.1	46254	45238	-	Ferric iron ABC transporter, iron-binding protein
<i>Pcc</i> ICMP5702_peg1700	AODT01000010.1	46753	47076	+	PTS system, cellobiose-specific IIA component (EC 2.7.1.205)
<i>Pcc</i> ICMP5702_peg1701	AODT01000010.1	47626	47177	-	Transcriptional regulator
<i>Pcc</i> ICMP5702_peg1702	AODT01000010.1	47722	47850	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1703	AODT01000010.1	47939	48832	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg1704	AODT01000010.1	49009	49482	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1705	AODT01000010.1	49985	51121	+	Poly(glycerophosphate chain) D-alanine transfer protein DltD
<i>Pcc</i> ICMP5702_peg1706	AODT01000010.1	51118	51240	+	Component involved in D-alanylation of teichoic acids
<i>Pcc</i> ICMP5702_peg1707	AODT01000010.1	51251	52369	+	D-alanyl transfer protein DltB
<i>Pcc</i> ICMP5702_peg1708	AODT01000010.1	52366	53799	+	D-alanine--poly(phosphoribitol) ligase subunit 1 (EC 6.1.1.13)
<i>Pcc</i> ICMP5702_peg1709	AODT01000010.1	53816	54037	+	D-alanine--poly(phosphoribitol) ligase ACP subunit (EC 6.1.1.13)
<i>Pcc</i> ICMP5702_peg1710	AODT01000010.1	54134	54262	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1711	AODT01000010.1	54386	55588	+	Chloramphenicol resistance, MFS efflux pump => CmlA family
<i>Pcc</i> ICMP5702_peg1712	AODT01000010.1	56234	55758	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1713	AODT01000010.1	56918	57772	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1714	AODT01000010.1	57874	58242	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1715	AODT01000010.1	58832	59038	+	Putative DNA-binding protein
<i>Pcc</i> ICMP5702_peg1716	AODT01000010.1	59331	60542	+	Integrase/recombinase (XerC/CodV family)
<i>Pcc</i> ICMP5702_peg1717	AODT01000010.1	60535	61896	+	Phage integrase
<i>Pcc</i> ICMP5702_peg1718	AODT01000010.1	61889	63778	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1719	AODT01000010.1	63819	64223	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1720	AODT01000010.1	64326	64739	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1721	AODT01000010.1	65571	65197	-	putative lipoprotein

<i>Pcc</i> ICMP5702_peg1722	AODT01000010.1	66265	65600	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1723	AODT01000010.1	66732	66583	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1724	AODT01000010.1	67219	66923	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1725	AODT01000010.1	67797	67384	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1726	AODT01000010.1	68074	68271	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1727	AODT01000010.1	68683	68300	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1728	AODT01000010.1	69171	68680	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1729	AODT01000010.1	71039	69171	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1730	AODT01000010.1	72186	71032	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1731	AODT01000010.1	72673	72203	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1732	AODT01000010.1	73035	73274	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1733	AODT01000010.1	73300	74904	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1734	AODT01000010.1	75203	75033	-	putative phage-related protein
<i>Pcc</i> ICMP5702_peg1735	AODT01000010.1	75309	75193	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1736	AODT01000010.1	75450	75644	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1737	AODT01000010.1	75681	76580	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1738	AODT01000010.1	77701	76826	-	Toll-Interleukin receptor
<i>Pcc</i> ICMP5702_peg1739	AODT01000010.1	79368	78163	-	Phage integrase, Phage P4-associated
<i>Pcc</i> ICMP5702_peg1740	AODT01000010.1	80007	82460	+	Potassium efflux system KefA protein / Small-conductance mechanosensitive channel
<i>Pcc</i> ICMP5702_peg1741	AODT01000010.1	83401	82541	-	D-alanine aminotransferase (EC 2.6.1.21)
<i>Pcc</i> ICMP5702_peg1742	AODT01000010.1	84424	83444	-	L-alanine-DL-glutamate epimerase (EC 5.1.1.n1)
<i>Pcc</i> ICMP5702_peg1743	AODT01000010.1	84825	86066	+	Glutamate-pyruvate aminotransferase AlaC (EC 2.6.1.2)
<i>Pcc</i> ICMP5702_peg1744	AODT01000010.1	86152	86601	+	OutS lipoprotein precursor
<i>Pcc</i> ICMP5702_peg1745	AODT01000010.1	87167	86598	-	General secretion pathway protein B
<i>Pcc</i> ICMP5702_peg1746	AODT01000010.1	87696	89264	+	Pectate lyase precursor (EC 4.2.2.2)
<i>Pcc</i> ICMP5702_peg1747	AODT01000010.1	89391	91370	+	Exo-poly-alpha-D-galacturonosidase (EC 3.2.1.82)
<i>Pcc</i> ICMP5702_peg1748	AODT01000010.1	91421	92284	+	General secretion pathway protein C
<i>Pcc</i> ICMP5702_peg1749	AODT01000010.1	92286	94325	+	General secretion pathway protein D
<i>Pcc</i> ICMP5702_peg1750	AODT01000010.1	94322	95818	+	General secretion pathway protein E
<i>Pcc</i> ICMP5702_peg1751	AODT01000010.1	95820	97046	+	General secretion pathway protein F
<i>Pcc</i> ICMP5702_peg1752	AODT01000010.1	97079	97549	+	General secretion pathway protein G
<i>Pcc</i> ICMP5702_peg1753	AODT01000010.1	97826	98389	+	General secretion pathway protein H
<i>Pcc</i> ICMP5702_peg1754	AODT01000010.1	98386	98751	+	General secretion pathway protein I
<i>Pcc</i> ICMP5702_peg1755	AODT01000010.1	98751	99401	+	General secretion pathway protein J
<i>Pcc</i> ICMP5702_peg1756	AODT01000010.1	99398	100384	+	General secretion pathway protein K
<i>Pcc</i> ICMP5702_peg1757	AODT01000010.1	100381	101658	+	General secretion pathway protein L

<i>Pcc</i> ICMP5702_peg1758	AODT01000010.1	101655	102149	+	General secretion pathway protein M
<i>Pcc</i> ICMP5702_peg1759	AODT01000010.1	102139	102885	+	General secretion pathway protein N
<i>Pcc</i> ICMP5702_peg1760	AODT01000010.1	102975	103820	+	Leader peptidase (Prepilin peptidase) (EC 3.4.23.43) / N-methyltransferase (EC 2.1.1.-)
<i>Pcc</i> ICMP5702_peg1761	AODT01000010.1	105437	104412	-	Alkanal monooxygenase alpha chain (EC 1.14.14.3)
<i>Pcc</i> ICMP5702_peg1762	AODT01000010.1	105760	106824	+	Iron(III) ABC transporter, solute-binding protein
<i>Pcc</i> ICMP5702_peg1763	AODT01000010.1	106821	107858	+	ABC-type Fe ³⁺ -siderophore transport system, permease component
<i>Pcc</i> ICMP5702_peg1764	AODT01000010.1	107860	108630	+	ABC transporter, ATP-binding protein (cluster 8, B12/iron complex)
<i>Pcc</i> ICMP5702_peg1765	AODT01000010.1	108627	109361	+	Molybdenum-binding periplasmic protein
<i>Pcc</i> ICMP5702_peg1766	AODT01000010.1	109482	110864	+	ATP-dependent 23S rRNA helicase DbpA
<i>Pcc</i> ICMP5702_peg1767	AODT01000010.1	110925	111497	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1768	AODT01000010.1	112141	111602	-	FIG00904919: Hypothetical protein
<i>Pcc</i> ICMP5702_peg1769	AODT01000010.1	112666	112932	+	FIG00904950: Hypothetical protein
<i>Pcc</i> ICMP5702_peg1770	AODT01000010.1	113055	113816	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1771	AODT01000010.1	114055	114846	+	putative secreted protein
<i>Pcc</i> ICMP5702_peg1772	AODT01000010.1	115286	115086	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1773	AODT01000010.1	115393	115283	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1774	AODT01000010.1	116426	115494	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1775	AODT01000010.1	118047	117244	-	FIG00905678: Hypothetical protein
<i>Pcc</i> ICMP5702_peg1776	AODT01000010.1	118847	118044	-	FIG00905334: Hypothetical protein
<i>Pcc</i> ICMP5702_peg1777	AODT01000010.1	119496	118870	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1778	AODT01000010.1	120055	119603	-	Acetyltransferase, GNAT family
<i>Pcc</i> ICMP5702_peg1779	AODT01000010.1	120160	120465	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1780	AODT01000010.1	120477	120614	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1781	AODT01000010.1	121319	121537	+	Transcriptional regulator, AlpA like
<i>Pcc</i> ICMP5702_peg1782	AODT01000010.1	121542	122393	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1783	AODT01000010.1	122431	123429	+	Phage major capsid protein GpN
<i>Pcc</i> ICMP5702_peg1784	AODT01000010.1	123438	123947	+	Phage capsid scaffolding protein GpO
<i>Pcc</i> ICMP5702_peg1785	AODT01000010.1	124190	124059	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1786	AODT01000010.1	124393	124590	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1787	AODT01000010.1	124583	124765	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1788	AODT01000010.1	124758	124994	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1789	AODT01000010.1	124981	125391	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1790	AODT01000010.1	125388	127973	+	DNA primase, phage associated
<i>Pcc</i> ICMP5702_peg1791	AODT01000010.1	128282	128623	+	putative phage gene
<i>Pcc</i> ICMP5702_peg1792	AODT01000010.1	129257	128733	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1793	AODT01000010.1	129400	130959	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg1794	AODT01000010.1	132140	130965	-	Phage integrase, Phage P4-associated
<i>Pcc</i> ICMP5702_peg1795	AODT01000010.1	133391	132453	-	Inner membrane protein YfdC
<i>Pcc</i> ICMP5702_peg1796	AODT01000010.1	133932	134693	+	Outer-membrane-phospholipid-binding lipoprotein MlaA
<i>Pcc</i> ICMP5702_peg1797	AODT01000010.1	134891	135004	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1798	AODT01000010.1	135056	136636	+	Malate:quinone oxidoreductase (EC 1.1.5.4)
<i>Pcc</i> ICMP5702_peg1799	AODT01000010.1	137605	136709	-	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg1800	AODT01000010.1	137747	138499	+	Oxidoreductase, short-chain dehydrogenase/reductase family
<i>Pcc</i> ICMP5702_peg1801	AODT01000010.1	139958	138657	-	Long-chain fatty acid transport protein
<i>Pcc</i> ICMP5702_peg1802	AODT01000010.1	140088	140207	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1803	AODT01000010.1	140347	140643	+	UPF0381 protein YfcZ
<i>Pcc</i> ICMP5702_peg1804	AODT01000010.1	140908	142221	+	3-ketoacyl-CoA thiolase (EC 2.3.1.16)
<i>Pcc</i> ICMP5702_peg1805	AODT01000010.1	142218	144434	+	Enoyl-CoA hydratase (EC 4.2.1.17) / Delta(3)-cis-delta(2)-trans-enoyl-CoA isomerase (EC 5.3.3.8) / 3-hydroxyacyl-CoA dehydrogenase (EC 1.1.1.35) / 3-hydroxybutyryl-CoA epimerase (EC 5.1.2.3)
<i>Pcc</i> ICMP5702_peg1806	AODT01000010.1	145437	144427	-	Sigma-fimbriae tip adhesin
<i>Pcc</i> ICMP5702_peg1807	AODT01000010.1	147823	145442	-	Sigma-fimbriae usher protein
<i>Pcc</i> ICMP5702_peg1808	AODT01000010.1	148652	147867	-	Sigma-fimbriae chaperone protein
<i>Pcc</i> ICMP5702_peg1809	AODT01000010.1	149212	148676	-	Sigma-fimbriae tip adhesin
<i>Pcc</i> ICMP5702_peg1810	AODT01000010.1	150006	149395	-	Sigma-fimbriae uncharacterized paralogous subunit
<i>Pcc</i> ICMP5702_peg1811	AODT01000010.1	151077	151559	+	Phosphohistidine phosphatase SixA
<i>Pcc</i> ICMP5702_peg1812	AODT01000010.1	152189	151647	-	UPF0115 protein YfcN
<i>Pcc</i> ICMP5702_peg1813	AODT01000010.1	152361	153293	+	Ribosomal protein L3 N(5)-glutamine methyltransferase (EC 2.1.1.298)
<i>Pcc</i> ICMP5702_peg1814	AODT01000010.1	153381	154466	+	Chorismate synthase (EC 4.2.3.5)
<i>Pcc</i> ICMP5702_peg1815	AODT01000010.1	154473	155318	+	Penicillin-insensitive murein endopeptidase
<i>Pcc</i> ICMP5702_peg1816	AODT01000010.1	155352	156152	+	Transmembrane protein YfcA
<i>Pcc</i> ICMP5702_peg1817	AODT01000010.1	156159	156725	+	Translation elongation factor P Lys34 hydroxylase
<i>Pcc</i> ICMP5702_peg1818	AODT01000010.1	156759	157043	+	Uncharacterized protein YfcL
<i>Pcc</i> ICMP5702_peg1819	AODT01000010.1	159478	157454	-	tRNA (5-methylaminomethyl-2-thiouridylate)-methyltransferase (EC 2.1.1.61) / FAD-dependent cmnm(5)s(2)U34 oxidoreductase
<i>Pcc</i> ICMP5702_peg1820	AODT01000010.1	159652	160869	+	3-oxoacyl-[acyl-carrier-protein] synthase, KASI (EC 2.3.1.41)
<i>Pcc</i> ICMP5702_peg1821	AODT01000010.1	161047	160892	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1822	AODT01000010.1	162288	161032	-	Flagellar regulator flk
<i>Pcc</i> ICMP5702_peg1823	AODT01000010.1	163365	162394	-	Permease of the drug/metabolite transporter (DMT) superfamily
<i>Pcc</i> ICMP5702_peg1824	AODT01000010.1	163478	164614	+	Erythronate-4-phosphate dehydrogenase (EC 1.1.1.290)
<i>Pcc</i> ICMP5702_peg1825	AODT01000010.1	164745	165755	+	Semialdehyde dehydrogenase, USG-1 protein
<i>Pcc</i> ICMP5702_peg1826	AODT01000010.1	165755	166606	+	tRNA pseudouridine(38-40) synthase (EC 5.4.99.12)

<i>Pcc</i> ICMP5702_peg1827	AODT01000010.1	166801	167463	+	DedA protein
<i>Pcc</i> ICMP5702_peg1828	AODT01000010.1	167688	168605	+	Acetyl-coenzyme A carboxyl transferase beta chain (EC 6.4.1.2)
<i>Pcc</i> ICMP5702_peg1829	AODT01000010.1	168711	169979	+	Dihydrofolate synthase (EC 6.3.2.12) @ Folylpolylglutamate synthase (EC 6.3.2.17)
<i>Pcc</i> ICMP5702_peg1830	AODT01000010.1	169969	170736	+	Septum-associated cell division protein DedD
<i>Pcc</i> ICMP5702_peg1831	AODT01000010.1	171030	170896	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1832	AODT01000010.1	171052	171552	+	Colicin V production protein
<i>Pcc</i> ICMP5702_peg1833	AODT01000010.1	171574	173091	+	Amidophosphoribosyltransferase (EC 2.4.2.14)
<i>Pcc</i> ICMP5702_peg1834	AODT01000010.1	173307	173879	+	Flavin prenyltransferase UbiX
<i>Pcc</i> ICMP5702_peg1835	AODT01000010.1	174287	175066	+	Histidine ABC transporter, substrate-binding protein HisJ (TC 3.A.1.3.1)
<i>Pcc</i> ICMP5702_peg1836	AODT01000010.1	175207	175896	+	Histidine ABC transporter, permease protein HisQ (TC 3.A.1.3.1)
<i>Pcc</i> ICMP5702_peg1837	AODT01000010.1	175889	176605	+	Histidine ABC transporter, permease protein HisM (TC 3.A.1.3.1)
<i>Pcc</i> ICMP5702_peg1838	AODT01000010.1	176623	177396	+	Histidine ABC transporter, ATP-binding protein HisP (TC 3.A.1.3.1)
<i>Pcc</i> ICMP5702_peg1839	AODT01000010.1	178469	177564	-	Cell division inhibitor Slr1223 (YfcH in EC), contains epimerase/dehydratase and DUF1731 domains
<i>Pcc</i> ICMP5702_peg1840	AODT01000010.1	178856	178485	-	D-erythro-7,8-dihydroneopterin triphosphate epimerase
<i>Pcc</i> ICMP5702_peg1841	AODT01000010.1	179608	178982	-	Probable glutathione S-transferase (EC 2.5.1.18), YfcG homolog
<i>Pcc</i> ICMP5702_peg1842	AODT01000010.1	179871	180422	+	Phosphodiesterase YfcE
<i>Pcc</i> ICMP5702_peg1843	AODT01000010.1	180546	181214	+	Uncharacterized Nudix hydrolase YfcD
<i>Pcc</i> ICMP5702_peg1844	AODT01000010.1	182147	181287	-	Uncharacterized membrane protein YoaT
<i>Pcc</i> ICMP5702_peg1845	AODT01000010.1	184405	182267	-	BioD-like N-terminal domain / Phosphate acetyltransferase (EC 2.3.1.8)
<i>Pcc</i> ICMP5702_peg1846	AODT01000010.1	185687	184485	-	Acetate kinase (EC 2.7.2.1)
<i>Pcc</i> ICMP5702_peg1847	AODT01000010.1	186117	186572	+	UPF0208 membrane protein YfbV
<i>Pcc</i> ICMP5702_peg1848	AODT01000010.1	186737	187231	+	UPF0304 protein yfbU
<i>Pcc</i> ICMP5702_peg1849	AODT01000010.1	187235	187909	+	Hexitol phosphatase HxpA (EC 3.1.3.22) (EC 3.1.3.23) (EC 3.1.3.50)
<i>Pcc</i> ICMP5702_peg1850	AODT01000010.1	188033	189865	+	Uncharacterized transporter YfbS
<i>Pcc</i> ICMP5702_peg1851	AODT01000010.1	190494	189895	-	5'-deoxynucleotidase YfbR (EC 3.1.3.89)
<i>Pcc</i> ICMP5702_peg1852	AODT01000010.1	191851	190637	-	Alanine transaminase (EC 2.6.1.2)
<i>Pcc</i> ICMP5702_peg1853	AODT01000010.1	192353	193303	+	LysR family transcriptional regulator LrhA
<i>Pcc</i> ICMP5702_peg1854	AODT01000010.1	193981	194421	+	NADH ubiquinone oxidoreductase chain A (EC 1.6.5.3)
<i>Pcc</i> ICMP5702_peg1855	AODT01000010.1	194439	195113	+	NADH-ubiquinone oxidoreductase chain B (EC 1.6.5.3)
<i>Pcc</i> ICMP5702_peg1856	AODT01000010.1	195212	197011	+	NADH-ubiquinone oxidoreductase chain C (EC 1.6.5.3) / NADH-ubiquinone oxidoreductase chain D (EC 1.6.5.3)
<i>Pcc</i> ICMP5702_peg1857	AODT01000010.1	197014	197559	+	NADH-ubiquinone oxidoreductase chain E (EC 1.6.5.3)
<i>Pcc</i> ICMP5702_peg1858	AODT01000010.1	197556	198905	+	NADH-ubiquinone oxidoreductase chain F (EC 1.6.5.3)
<i>Pcc</i> ICMP5702_peg1859	AODT01000010.1	199092	201818	+	NADH-ubiquinone oxidoreductase chain G (EC 1.6.5.3)
<i>Pcc</i> ICMP5702_peg1860	AODT01000010.1	201815	202789	+	NADH-ubiquinone oxidoreductase chain H (EC 1.6.5.3)

<i>Pcc</i> ICMP5702_peg1861	AODT01000010.1	202807	203349	+	NADH-ubiquinone oxidoreductase chain I (EC 1.6.5.3)
<i>Pcc</i> ICMP5702_peg1862	AODT01000010.1	203359	203919	+	NADH-ubiquinone oxidoreductase chain J (EC 1.6.5.3)
<i>Pcc</i> ICMP5702_peg1863	AODT01000010.1	203916	204218	+	NADH-ubiquinone oxidoreductase chain K (EC 1.6.5.3)
<i>Pcc</i> ICMP5702_peg1864	AODT01000010.1	204215	206062	+	NADH-ubiquinone oxidoreductase chain L (EC 1.6.5.3)
<i>Pcc</i> ICMP5702_peg1865	AODT01000010.1	206163	207698	+	NADH-ubiquinone oxidoreductase chain M (EC 1.6.5.3)
<i>Pcc</i> ICMP5702_peg1866	AODT01000010.1	207705	209162	+	NADH-ubiquinone oxidoreductase chain N (EC 1.6.5.3)
<i>Pcc</i> ICMP5702_peg1867	AODT01000010.1	209424	209735	+	ElaB protein
<i>Pcc</i> ICMP5702_peg1868	AODT01000010.1	211512	209815	-	Trehalose-6-phosphate hydrolase (EC 3.2.1.93)
<i>Pcc</i> ICMP5702_peg1869	AODT01000010.1	212998	211580	-	PTS system, trehalose-specific IIB component (EC 2.7.1.201) / PTS system, trehalose-specific IIC component
<i>Pcc</i> ICMP5702_peg1870	AODT01000010.1	213366	213268	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1871	AODT01000010.1	214132	213572	-	Ribosomal-protein-L7p-serine acetyltransferase
<i>Pcc</i> ICMP5702_peg1872	AODT01000010.1	215041	214145	-	Phenazine biosynthesis protein PhzF like
<i>Pcc</i> ICMP5702_peg1873	AODT01000010.1	215159	216751	+	Bis-ABC ATPase YbiT
<i>Pcc</i> ICMP5702_peg1874	AODT01000010.1	217121	216867	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1875	AODT01000010.1	217156	218469	+	Radical SAM family protein HutW, similar to coproporphyrinogen III oxidase, oxygen-independent, associated with heme uptake
<i>Pcc</i> ICMP5702_peg1876	AODT01000010.1	218484	218984	+	Putative heme iron utilization protein
<i>Pcc</i> ICMP5702_peg1877	AODT01000010.1	218981	219610	+	Flavin reductase (EC 1.5.1.30)
<i>Pcc</i> ICMP5702_peg1878	AODT01000010.1	219729	220247	+	Inner membrane protein YlaC
<i>Pcc</i> ICMP5702_peg1879	AODT01000010.1	220497	221219	+	Glutamine amidotransferase, class I
<i>Pcc</i> ICMP5702_peg1880	AODT01000010.1	221328	222779	+	DNA-binding transcriptional regulator, MocR family / aminotransferase domain
<i>Pcc</i> ICMP5702_peg1881	AODT01000010.1	222790	222915	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1882	AODT01000010.1	223016	223945	+	Formate dehydrogenase formation protein FdhE
<i>Pcc</i> ICMP5702_peg1883	AODT01000010.1	224325	223999	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1884	AODT01000010.1	224727	224329	-	Inner membrane protein YidH
<i>Pcc</i> ICMP5702_peg1885	AODT01000010.1	224937	224833	-	Cytochrome d ubiquinol oxidase subunit X (EC 1.10.3.-)
<i>Pcc</i> ICMP5702_peg1886	AODT01000010.1	226096	224957	-	Cytochrome d ubiquinol oxidase subunit II (EC 1.10.3.-)
<i>Pcc</i> ICMP5702_peg1887	AODT01000010.1	227688	226111	-	Cytochrome d ubiquinol oxidase subunit I (EC 1.10.3.-)
<i>Pcc</i> ICMP5702_peg1888	AODT01000010.1	228970	228353	-	Tail fiber assembly protein
<i>Pcc</i> ICMP5702_peg1889	AODT01000010.1	230796	228970	-	Phage tail fiber protein
<i>Pcc</i> ICMP5702_peg1890	AODT01000010.1	231022	232311	+	Response regulator NasT
<i>Pcc</i> ICMP5702_peg1891	AODT01000010.1	233255	233073	-	FIG00904954: Hypothetical protein
<i>Pcc</i> ICMP5702_peg1892	AODT01000010.1	233242	234501	+	Nitrate ABC transporter, substrate-binding protein
<i>Pcc</i> ICMP5702_peg1893	AODT01000010.1	234514	235428	+	Nitrate ABC transporter, permease protein
<i>Pcc</i> ICMP5702_peg1894	AODT01000010.1	235439	236233	+	Nitrate ABC transporter, ATP-binding protein

<i>Pcc</i> ICMP5702_peg1895	AODT01000010.1	236250	240440	+	Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4)
<i>Pcc</i> ICMP5702_peg1896	AODT01000010.1	240437	243145	+	Assimilatory nitrate reductase large subunit (EC 1.7.99.4)
<i>Pcc</i> ICMP5702_peg1897	AODT01000010.1	243171	244004	+	Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)
<i>Pcc</i> ICMP5702_peg1898	AODT01000010.1	244097	244498	+	Transposase
<i>Pcc</i> ICMP5702_peg1899	AODT01000010.1	245062	244598	-	Uncharacterized protein YehS
<i>Pcc</i> ICMP5702_peg1900	AODT01000010.1	245668	245147	-	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase (EC 1.13.11.54)
<i>Pcc</i> ICMP5702_peg1901	AODT01000010.1	245905	246888	+	ABC transporter, substrate-binding protein KPN_00641
<i>Pcc</i> ICMP5702_peg1902	AODT01000010.1	246893	248440	+	ABC transporter, dimeric ATP-binding protein KPN_00640
<i>Pcc</i> ICMP5702_peg1903	AODT01000010.1	248437	249429	+	ABC transporter, permease protein 1 KPN_00639
<i>Pcc</i> ICMP5702_peg1904	AODT01000010.1	249426	250424	+	ABC transporter, permease protein 2 KPN_00638
<i>Pcc</i> ICMP5702_peg1905	AODT01000010.1	250485	251426	+	Ribokinase-like protein
<i>Pcc</i> ICMP5702_peg1906	AODT01000010.1	252522	251494	-	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
<i>Pcc</i> ICMP5702_peg1907	AODT01000010.1	254066	252519	-	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
<i>Pcc</i> ICMP5702_peg1908	AODT01000010.1	254533	254228	-	Transcriptional regulator, ArsR family
<i>Pcc</i> ICMP5702_peg1909	AODT01000010.1	254619	255707	+	NADH-dependent flavin oxidoreductase
<i>Pcc</i> ICMP5702_peg1910	AODT01000010.1	257253	256096	-	Cystathionine gamma-lyase (EC 4.4.1.1)
<i>Pcc</i> ICMP5702_peg1911	AODT01000010.1	258666	257299	-	Cystathionine beta-synthase (EC 4.2.1.22)
<i>Pcc</i> ICMP5702_peg1912	AODT01000010.1	259847	259194	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1913	AODT01000010.1	259995	259864	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1914	AODT01000010.1	260255	260070	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1915	AODT01000010.1	260560	261027	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1916	AODT01000010.1	261658	261885	+	Prevent host death protein, Phd antitoxin
<i>Pcc</i> ICMP5702_peg1917	AODT01000010.1	261909	262256	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1918	AODT01000010.1	263469	262633	-	Outer membrane protein V
<i>Pcc</i> ICMP5702_peg1919	AODT01000010.1	263673	264350	+	Two-component transcriptional response regulator, LuxR family
<i>Pcc</i> ICMP5702_peg1920	AODT01000010.1	264350	265747	+	integral membrane sensor signal transduction histidine kinase
<i>Pcc</i> ICMP5702_peg1921	AODT01000010.1	266650	265733	-	aminotransferase, class IV
<i>Pcc</i> ICMP5702_peg1922	AODT01000010.1	267491	266679	-	Cystine ABC transporter, ATP-binding protein
<i>Pcc</i> ICMP5702_peg1923	AODT01000010.1	268180	267515	-	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg1924	AODT01000010.1	268866	268189	-	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg1925	AODT01000010.1	269141	270550	+	Immune-responsive protein 1
<i>Pcc</i> ICMP5702_peg1926	AODT01000010.1	271418	270585	-	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg1927	AODT01000010.1	272969	271737	-	Two-component system sensor histidine kinase
<i>Pcc</i> ICMP5702_peg1928	AODT01000010.1	273655	272966	-	Two-component transcriptional response regulator, LuxR family
<i>Pcc</i> ICMP5702_peg1929	AODT01000010.1	273837	274652	+	outer membrane protein V
<i>Pcc</i> ICMP5702_peg1930	AODT01000010.1	274675	275757	+	HlyD family secretion protein

<i>Pcc</i> ICMP5702_peg1931	AODT01000010.1	275757	278834	+	RND efflux system, inner membrane transporter
<i>Pcc</i> ICMP5702_peg1932	AODT01000010.1	280074	278893	-	Mandelate racemase/muconate lactonizing enzyme-like protein
<i>Pcc</i> ICMP5702_peg1933	AODT01000010.1	280850	280116	-	salicylate esterase
<i>Pcc</i> ICMP5702_peg1934	AODT01000010.1	282584	281085	-	Sulfate permease
<i>Pcc</i> ICMP5702_peg1935	AODT01000010.1	284583	282784	-	Translation elongation factor LepA
<i>Pcc</i> ICMP5702_peg1936	AODT01000010.1	285221	284895	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1937	AODT01000010.1	285540	286451	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg1938	AODT01000010.1	287570	286452	-	NADH:flavin oxidoreductases, Old Yellow Enzyme family
<i>Pcc</i> ICMP5702_peg1939	AODT01000010.1	288955	287681	-	Membrane-bound lytic murein transglycosylase B
<i>Pcc</i> ICMP5702_peg1940	AODT01000010.1	290749	289247	-	Efflux transport system, outer membrane factor (OMF) lipoprotein XCC0419
<i>Pcc</i> ICMP5702_peg1941	AODT01000010.1	290836	291450	+	Transcriptional regulator KPN_02146, AcrR family
<i>Pcc</i> ICMP5702_peg1942	AODT01000010.1	291543	292652	+	RND efflux system, membrane fusion protein KPN_02145
<i>Pcc</i> ICMP5702_peg1943	AODT01000010.1	292649	295738	+	RND efflux system, inner membrane transporter KPN_02144
<i>Pcc</i> ICMP5702_peg1944	AODT01000010.1	295850	297097	+	Multidrug resistance transporter, Bcr/CflA family
<i>Pcc</i> ICMP5702_peg1945	AODT01000010.1	298355	297168	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1946	AODT01000010.1	299096	298944	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1947	AODT01000010.1	299214	299489	+	Nitrogen assimilation regulatory protein Nac amino-terminal domain
<i>Pcc</i> ICMP5702_peg1948	AODT01000010.1	299874	300140	+	FIG00905150: Hypothetical protein
<i>Pcc</i> ICMP5702_peg1949	AODT01000010.1	301723	300311	-	D-serine/D-alanine/glycine transporter
<i>Pcc</i> ICMP5702_peg1950	AODT01000010.1	302144	302284	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1951	AODT01000010.1	302601	302888	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1952	AODT01000010.1	303206	302982	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1953	AODT01000010.1	303850	304506	+	BarA-associated response regulator UvrY (= GacA = SirA)
<i>Pcc</i> ICMP5702_peg1954	AODT01000010.1	304499	306331	+	Excinuclease ABC subunit C
<i>Pcc</i> ICMP5702_peg1955	AODT01000010.1	306390	306938	+	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase (EC 2.7.8.5)
<i>Pcc</i> ICMP5702_peg1956	AODT01000010.1	307690	307478	-	Phage integrase, site-specific tyrosine recombinase
<i>Pcc</i> ICMP5702_peg1957	AODT01000010.1	308651	307776	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1958	AODT01000010.1	309285	308740	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1959	AODT01000010.1	310791	309337	-	Flagellin
<i>Pcc</i> ICMP5702_peg1960	AODT01000010.1	311832	311987	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1961	AODT01000010.1	312267	313001	+	Lipid A biosynthesis palmitoleoyltransferase (EC 2.3.1.242)
<i>Pcc</i> ICMP5702_peg1962	AODT01000010.1	313267	321900	+	Cyclic beta-1,2-glucan synthase (EC 2.4.1.-)
<i>Pcc</i> ICMP5702_peg1963	AODT01000010.1	322312	322094	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1964	AODT01000010.1	324000	322588	-	DgcO
<i>Pcc</i> ICMP5702_peg1965	AODT01000010.1	324211	324414	+	DsrB protein
<i>Pcc</i> ICMP5702_peg1966	AODT01000010.1	326191	324482	-	Methyl-accepting chemotaxis protein III (ribose and galactose chemoreceptor protein)

<i>Pcc</i> ICMP5702_peg1967	AODT01000010.1	326501	327433	+	Permease of the drug/metabolite transporter (DMT) superfamily
<i>Pcc</i> ICMP5702_peg1968	AODT01000010.1	327748	327936	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1969	AODT01000010.1	328254	328604	+	Flagellar transcriptional activator FlhD
<i>Pcc</i> ICMP5702_peg1970	AODT01000010.1	328608	329186	+	Flagellar transcriptional activator FlhC
<i>Pcc</i> ICMP5702_peg1971	AODT01000010.1	329321	330208	+	Flagellar motor rotation protein MotA
<i>Pcc</i> ICMP5702_peg1972	AODT01000010.1	330205	331260	+	Flagellar motor rotation protein MotB
<i>Pcc</i> ICMP5702_peg1973	AODT01000010.1	331300	333303	+	Signal transduction histidine kinase CheA
<i>Pcc</i> ICMP5702_peg1974	AODT01000010.1	333335	333832	+	Positive regulator of CheA protein activity (CheW)
<i>Pcc</i> ICMP5702_peg1975	AODT01000010.1	333859	333975	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1976	AODT01000010.1	333968	335653	+	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)
<i>Pcc</i> ICMP5702_peg1977	AODT01000010.1	336167	337039	+	Chemotaxis protein methyltransferase CheR (EC 2.1.1.80)
<i>Pcc</i> ICMP5702_peg1978	AODT01000010.1	337039	338091	+	Chemotaxis response regulator protein-glutamate methylesterase CheB (EC 3.1.1.61)
<i>Pcc</i> ICMP5702_peg1979	AODT01000010.1	338130	338519	+	CheY
<i>Pcc</i> ICMP5702_peg1980	AODT01000010.1	338529	339173	+	Chemotaxis response - phosphatase CheZ
<i>Pcc</i> ICMP5702_peg1981	AODT01000010.1	339173	339271	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg1982	AODT01000010.1	339418	340569	+	Flagellar biosynthesis protein FlhB
<i>Pcc</i> ICMP5702_peg1983	AODT01000010.1	340562	342646	+	Flagellar biosynthesis protein FlhA
<i>Pcc</i> ICMP5702_peg1984	AODT01000010.1	342655	343062	+	Flagellar protein FlhE
<i>Pcc</i> ICMP5702_peg1985	AODT01000010.1	343555	343118	-	Flagellar biosynthesis protein FlgN
<i>Pcc</i> ICMP5702_peg1986	AODT01000010.1	343857	343561	-	Negative regulator of flagellin synthesis FlgM (anti-sigma28)
<i>Pcc</i> ICMP5702_peg1987	AODT01000010.1	344667	343999	-	Flagellar basal-body P-ring formation protein FlgA
<i>Pcc</i> ICMP5702_peg1988	AODT01000010.1	344833	345249	+	Flagellar basal-body rod protein FlgB
<i>Pcc</i> ICMP5702_peg1989	AODT01000010.1	345278	345682	+	Flagellar basal-body rod protein FlgC
<i>Pcc</i> ICMP5702_peg1990	AODT01000010.1	345698	346372	+	Flagellar basal-body rod modification protein FlgD
<i>Pcc</i> ICMP5702_peg1991	AODT01000010.1	346447	347649	+	Flagellar hook protein FlgE
<i>Pcc</i> ICMP5702_peg1992	AODT01000010.1	347671	348426	+	Flagellar basal-body rod protein FlgF
<i>Pcc</i> ICMP5702_peg1993	AODT01000010.1	348454	349236	+	Flagellar basal-body rod protein FlgG
<i>Pcc</i> ICMP5702_peg1994	AODT01000010.1	349417	350130	+	Flagellar L-ring protein FlgH
<i>Pcc</i> ICMP5702_peg1995	AODT01000010.1	350147	351256	+	Flagellar P-ring protein FlgI
<i>Pcc</i> ICMP5702_peg1996	AODT01000010.1	351256	352218	+	Flagellar protein FlgJ [peptidoglycan hydrolase]
<i>Pcc</i> ICMP5702_peg1997	AODT01000010.1	352345	354039	+	Flagellar hook-associated protein FlgK
<i>Pcc</i> ICMP5702_peg1998	AODT01000010.1	354071	355024	+	Flagellar hook-associated protein FlgL
<i>Pcc</i> ICMP5702_peg1999	AODT01000010.1	355172	355050	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2000	AODT01000010.1	356180	355395	-	Flagellar biosynthesis protein FliR
<i>Pcc</i> ICMP5702_peg2001	AODT01000010.1	356452	356183	-	Flagellar biosynthesis protein FliQ
<i>Pcc</i> ICMP5702_peg2002	AODT01000010.1	357249	356473	-	Flagellar biosynthesis protein FliP

<i>Pcc</i> ICMP5702_peg2003	AODT01000010.1	357668	357246	-	Flagellar biosynthesis protein FliO
<i>Pcc</i> ICMP5702_peg2004	AODT01000010.1	358081	357668	-	Flagellar motor switch protein FliN
<i>Pcc</i> ICMP5702_peg2005	AODT01000010.1	359087	358074	-	Flagellar motor switch protein FliM
<i>Pcc</i> ICMP5702_peg2006	AODT01000010.1	359572	359093	-	Flagellar basal body-associated protein FliL
<i>Pcc</i> ICMP5702_peg2007	AODT01000010.1	361023	359728	-	Flagellar hook-length control protein FliK
<i>Pcc</i> ICMP5702_peg2008	AODT01000010.1	361466	361020	-	Flagellar protein FliJ
<i>Pcc</i> ICMP5702_peg2009	AODT01000010.1	362845	361475	-	Flagellum-specific ATP synthase FliI
<i>Pcc</i> ICMP5702_peg2010	AODT01000010.1	363570	362845	-	Flagellar assembly protein FliH
<i>Pcc</i> ICMP5702_peg2011	AODT01000010.1	364555	363563	-	Flagellar motor switch protein FliG
<i>Pcc</i> ICMP5702_peg2012	AODT01000010.1	366276	364552	-	Flagellar M-ring protein FliF
<i>Pcc</i> ICMP5702_peg2013	AODT01000010.1	366323	366445	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2014	AODT01000010.1	366537	366851	+	Flagellar hook-basal body complex protein FliE
<i>Pcc</i> ICMP5702_peg2015	AODT01000010.1	367508	367128	-	Flagellar biosynthesis protein FliT
<i>Pcc</i> ICMP5702_peg2016	AODT01000010.1	367918	367508	-	Flagellar biosynthesis protein FliS
<i>Pcc</i> ICMP5702_peg2017	AODT01000010.1	369337	367949	-	Flagellar cap protein FliD
<i>Pcc</i> ICMP5702_peg2018	AODT01000010.1	369618	369776	+	Flagellin FliC
<i>Pcc</i> ICMP5702_peg2019	AODT01000011.1	1	513	+	Flagellin FliC
<i>Pcc</i> ICMP5702_peg2020	AODT01000011.1	510	1058	+	Flagellin FliC
<i>Pcc</i> ICMP5702_peg2021	AODT01000011.1	1450	5133	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2022	AODT01000011.1	5279	8782	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2023	AODT01000011.1	8805	9926	+	Aminotransferase, DegT/DnrJ/EryC1/StrS family
<i>Pcc</i> ICMP5702_peg2024	AODT01000011.1	10044	10637	+	Putative o-acyltransferase, CysE/LacA/LpxA/NodL family
<i>Pcc</i> ICMP5702_peg2025	AODT01000011.1	10839	11681	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2026	AODT01000011.1	12812	11754	-	Glycosyl transferase, group 2 family
<i>Pcc</i> ICMP5702_peg2027	AODT01000011.1	13276	13998	+	RNA polymerase sigma factor for flagellar operon
<i>Pcc</i> ICMP5702_peg2028	AODT01000011.1	14203	14718	+	Regulator of sigma S factor FliZ
<i>Pcc</i> ICMP5702_peg2029	AODT01000011.1	15250	16038	+	Phosphate starvation-inducible protein PhoH, predicted ATPase
<i>Pcc</i> ICMP5702_peg2030	AODT01000011.1	17073	16435	-	predicted 4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17)
<i>Pcc</i> ICMP5702_peg2031	AODT01000011.1	19323	17290	-	High-affinity choline uptake protein BetT
<i>Pcc</i> ICMP5702_peg2032	AODT01000011.1	19677	20264	+	Transcriptional regulator BetI, TetR family
<i>Pcc</i> ICMP5702_peg2033	AODT01000011.1	20334	21806	+	Betaine aldehyde dehydrogenase (EC 1.2.1.8)
<i>Pcc</i> ICMP5702_peg2034	AODT01000011.1	21826	23505	+	Choline dehydrogenase (EC 1.1.99.1)
<i>Pcc</i> ICMP5702_peg2035	AODT01000011.1	23665	24318	+	FIG004088: inner membrane protein YebE
<i>Pcc</i> ICMP5702_peg2036	AODT01000011.1	24931	24413	-	3-hydroxyacyl-[acyl-carrier-protein] dehydratase, FabA form (EC 4.2.1.59) @ Trans-2-decenoyl-[acyl-carrier-protein] isomerase (EC 5.3.3.14)
<i>Pcc</i> ICMP5702_peg2037	AODT01000011.1	26750	25023	-	Lon protease homolog YcbZ

<i>Pcc</i> ICMP5702_peg2038	AODT01000011.1	26970	27428	+	Putative dehydrogenase
<i>Pcc</i> ICMP5702_peg2039	AODT01000011.1	28668	27583	-	Outer membrane protein A precursor
<i>Pcc</i> ICMP5702_peg2040	AODT01000011.1	29537	29031	-	Cell division inhibitor Sula
<i>Pcc</i> ICMP5702_peg2041	AODT01000011.1	29761	30381	+	DNA transformation protein TfoX
<i>Pcc</i> ICMP5702_peg2042	AODT01000011.1	32531	30396	-	Putative efflux (PET) family inner membrane protein YccS
<i>Pcc</i> ICMP5702_peg2043	AODT01000011.1	32998	32552	-	Inner membrane protein YccF
<i>Pcc</i> ICMP5702_peg2044	AODT01000011.1	33196	35253	+	DNA helicase IV (EC 3.6.4.12)
<i>Pcc</i> ICMP5702_peg2045	AODT01000011.1	35789	35331	-	Methylglyoxal synthase (EC 4.2.3.3)
<i>Pcc</i> ICMP5702_peg2046	AODT01000011.1	36451	35927	-	UPF0319 protein YccT precursor
<i>Pcc</i> ICMP5702_peg2047	AODT01000011.1	36646	37059	+	Succinyl-CoA synthetase, alpha subunit-related enzymes
<i>Pcc</i> ICMP5702_peg2048	AODT01000011.1	37450	37142	-	Heat shock protein HspQ
<i>Pcc</i> ICMP5702_peg2049	AODT01000011.1	37676	37954	+	Acylphosphate phosphohydrolase (EC 3.6.1.7)
<i>Pcc</i> ICMP5702_peg2050	AODT01000011.1	38296	37967	-	tRNA 2-thiouridine synthesis protein TusE
<i>Pcc</i> ICMP5702_peg2051	AODT01000011.1	39065	38406	-	Putative TEGT family carrier/transport protein
<i>Pcc</i> ICMP5702_peg2052	AODT01000011.1	40085	39831	-	FIG00905364: Hypothetical protein
<i>Pcc</i> ICMP5702_peg2053	AODT01000011.1	40552	40974	+	MutT/Nudix family protein
<i>Pcc</i> ICMP5702_peg2054	AODT01000011.1	41064	41588	+	Isochorismatase (EC 3.3.2.1)
<i>Pcc</i> ICMP5702_peg2055	AODT01000011.1	41593	42048	+	Acetyltransferase
<i>Pcc</i> ICMP5702_peg2056	AODT01000011.1	42213	42641	+	Universal stress protein G
<i>Pcc</i> ICMP5702_peg2057	AODT01000011.1	43202	42696	-	Uncharacterized protein YbbK
<i>Pcc</i> ICMP5702_peg2058	AODT01000011.1	43471	43286	-	Orphan toxin OrtT
<i>Pcc</i> ICMP5702_peg2059	AODT01000011.1	43627	43926	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2060	AODT01000011.1	44085	44366	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2061	AODT01000011.1	44536	44423	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2062	AODT01000011.1	45218	46882	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg2063	AODT01000011.1	48517	46994	-	Uncharacterized iron-regulated membrane protein; Iron-uptake factor PiuB
<i>Pcc</i> ICMP5702_peg2064	AODT01000011.1	49114	48620	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2065	AODT01000011.1	49492	51060	+	Glucans biosynthesis protein G precursor
<i>Pcc</i> ICMP5702_peg2066	AODT01000011.1	51053	53632	+	Glucans biosynthesis glucosyltransferase H
<i>Pcc</i> ICMP5702_peg2067	AODT01000011.1	54672	53752	-	Lipid A biosynthesis lauroyl acyltransferase (EC 2.3.1.241)
<i>Pcc</i> ICMP5702_peg2068	AODT01000011.1	56028	54934	-	NADH-dependent flavin oxidoreductase
<i>Pcc</i> ICMP5702_peg2069	AODT01000011.1	56264	57331	+	Rhodanese domain protein, Enterobacterial subgroup, YceA homolog
<i>Pcc</i> ICMP5702_peg2070	AODT01000011.1	57983	57405	-	Protein yceI precursor
<i>Pcc</i> ICMP5702_peg2071	AODT01000011.1	58564	58010	-	Cytochrome b561 homolog 2
<i>Pcc</i> ICMP5702_peg2072	AODT01000011.1	59279	59025	-	Biofilm regulator BssS
<i>Pcc</i> ICMP5702_peg2073	AODT01000011.1	59770	59513	-	FIG00905936: Hypothetical protein

<i>Pcc</i> ICMP5702_peg2074	AODT01000011.1	60098	59859	-	DNA-damage-inducible protein I
<i>Pcc</i> ICMP5702_peg2075	AODT01000011.1	61248	60205	-	Dihydroorotase (EC 3.5.2.3)
<i>Pcc</i> ICMP5702_peg2076	AODT01000011.1	61433	61720	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2077	AODT01000011.1	65136	61783	-	Ribonuclease E (EC 3.1.26.12)
<i>Pcc</i> ICMP5702_peg2078	AODT01000011.1	65275	65144	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2079	AODT01000011.1	65707	66687	+	LSU rRNA pseudouridine(955/2504/2580) synthase (EC 5.4.99.24)
<i>Pcc</i> ICMP5702_peg2080	AODT01000011.1	67351	66767	-	Maf-like protein YceF
<i>Pcc</i> ICMP5702_peg2081	AODT01000011.1	67492	68013	+	FIG01269488: protein, clustered with ribosomal protein L32p
<i>Pcc</i> ICMP5702_peg2082	AODT01000011.1	68030	68200	+	LSU ribosomal protein L32p @ LSU ribosomal protein L32p, zinc-independent
<i>Pcc</i> ICMP5702_peg2083	AODT01000011.1	68230	69276	+	Phosphate:acyl-ACP acyltransferase PlsX (EC 2.3.1.n2)
<i>Pcc</i> ICMP5702_peg2084	AODT01000011.1	69283	70236	+	3-oxoacyl-[acyl-carrier-protein] synthase, KASIII (EC 2.3.1.180)
<i>Pcc</i> ICMP5702_peg2085	AODT01000011.1	70254	71183	+	Malonyl CoA-acyl carrier protein transacylase (EC 2.3.1.39)
<i>Pcc</i> ICMP5702_peg2086	AODT01000011.1	71198	71932	+	3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100), FadG
<i>Pcc</i> ICMP5702_peg2087	AODT01000011.1	72087	72323	+	Acyl carrier protein
<i>Pcc</i> ICMP5702_peg2088	AODT01000011.1	72405	73646	+	3-oxoacyl-[acyl-carrier-protein] synthase, KASII (EC 2.3.1.179)
<i>Pcc</i> ICMP5702_peg2089	AODT01000011.1	73751	74572	+	Aminodeoxychorismate lyase (EC 4.1.3.38)
<i>Pcc</i> ICMP5702_peg2090	AODT01000011.1	74587	75606	+	Murein endolytic transglycosylase MltG
<i>Pcc</i> ICMP5702_peg2091	AODT01000011.1	75596	76255	+	Thymidylate kinase (EC 2.7.4.9)
<i>Pcc</i> ICMP5702_peg2092	AODT01000011.1	76255	77265	+	DNA polymerase III delta prime subunit (EC 2.7.7.7)
<i>Pcc</i> ICMP5702_peg2093	AODT01000011.1	77285	78082	+	Uncharacterized metal-dependent hydrolase YcfH
<i>Pcc</i> ICMP5702_peg2094	AODT01000011.1	78396	79829	+	PTS system, glucose-specific IIC component / PTS system, glucose-specific IIB component (EC 2.7.1.199)
<i>Pcc</i> ICMP5702_peg2095	AODT01000011.1	80687	79890	-	Putative DNA-binding protein
<i>Pcc</i> ICMP5702_peg2096	AODT01000011.1	80812	82266	+	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg2097	AODT01000011.1	82496	82314	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2098	AODT01000011.1	82495	82845	+	YcfF/hinT protein: a purine nucleoside phosphoramidase
<i>Pcc</i> ICMP5702_peg2099	AODT01000011.1	82945	83325	+	YcfL protein: an outer membrane lipoprotein that is part of a salvage cluster
<i>Pcc</i> ICMP5702_peg2100	AODT01000011.1	83347	83928	+	Lipoprotein YcfM, part of a salvage pathway of unknown substrate
<i>Pcc</i> ICMP5702_peg2101	AODT01000011.1	83909	84793	+	Thiamine kinase (EC 2.7.1.89) @ Adenosylcobinamide kinase (EC 2.7.1.156)
<i>Pcc</i> ICMP5702_peg2102	AODT01000011.1	84866	85885	+	beta-N-acetylglucosaminidase (EC 3.2.1.52)
<i>Pcc</i> ICMP5702_peg2103	AODT01000011.1	86048	86590	+	YcfP protein: probably an esterase that is part of a salvage cluster
<i>Pcc</i> ICMP5702_peg2104	AODT01000011.1	86957	88261	+	NADH dehydrogenase (EC 1.6.99.3)
<i>Pcc</i> ICMP5702_peg2105	AODT01000011.1	88719	89258	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2106	AODT01000011.1	90535	89339	-	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg2107	AODT01000011.1	91782	90574	-	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg2108	AODT01000011.1	91918	92508	+	Transcriptional regulator, AcrR family

<i>Pcc</i> ICMP5702_peg2109	AODT01000011.1	93924	92560	-	Uncharacterized chaperone protein YegD
<i>Pcc</i> ICMP5702_peg2110	AODT01000011.1	94204	95214	+	Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg2111	AODT01000011.1	95402	96241	+	dehydrogenases)
<i>Pcc</i> ICMP5702_peg2112	AODT01000011.1	99820	96368	-	Transcription-repair coupling factor
<i>Pcc</i> ICMP5702_peg2113	AODT01000011.1	99963	101165	+	Lipoprotein releasing system transmembrane protein LolC
<i>Pcc</i> ICMP5702_peg2114	AODT01000011.1	101158	101865	+	Lipoprotein-releasing system ATP-binding protein LolD
<i>Pcc</i> ICMP5702_peg2115	AODT01000011.1	101862	103109	+	Lipoprotein releasing system transmembrane protein LolE
<i>Pcc</i> ICMP5702_peg2116	AODT01000011.1	103194	104108	+	N-acetyl-D-glucosamine kinase (EC 2.7.1.59)
<i>Pcc</i> ICMP5702_peg2117	AODT01000011.1	104120	104950	+	NAD-dependent protein deacetylase of SIR2 family
<i>Pcc</i> ICMP5702_peg2118	AODT01000011.1	105208	104993	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2119	AODT01000011.1	106228	105512	-	Hcp transcriptional regulator HcpR (Crp/Fnr family)
<i>Pcc</i> ICMP5702_peg2120	AODT01000011.1	106345	106686	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2121	AODT01000011.1	106747	107511	+	SAM-dependent methyltransferase HI0095 (UbiE paralog)
<i>Pcc</i> ICMP5702_peg2122	AODT01000011.1	107644	108639	+	Vitamin B12 ABC transporter, permease protein BtuC
<i>Pcc</i> ICMP5702_peg2123	AODT01000011.1	108691	109242	+	Glutathione peroxidase (EC 1.11.1.9) @ Thioredoxin peroxidase (EC 1.11.1.15)
<i>Pcc</i> ICMP5702_peg2124	AODT01000011.1	109243	110019	+	Vitamin B12 ABC transporter, ATP-binding protein BtuD
<i>Pcc</i> ICMP5702_peg2125	AODT01000011.1	110151	110636	+	Probable endopeptidase NlpC
<i>Pcc</i> ICMP5702_peg2126	AODT01000011.1	110682	111698	+	Lipoate-protein ligase A
<i>Pcc</i> ICMP5702_peg2127	AODT01000011.1	111875	113326	+	UPF0061 protein YdiU
<i>Pcc</i> ICMP5702_peg2128	AODT01000011.1	114145	113348	-	ABC-type hemin transport system, ATPase component
<i>Pcc</i> ICMP5702_peg2129	AODT01000011.1	115142	114138	-	Hemin ABC transporter, permease protein
<i>Pcc</i> ICMP5702_peg2130	AODT01000011.1	115957	115139	-	Periplasmic hemin-binding protein
<i>Pcc</i> ICMP5702_peg2131	AODT01000011.1	117003	115954	-	Hemin transport protein HmuS
<i>Pcc</i> ICMP5702_peg2132	AODT01000011.1	118267	117221	-	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I alpha (EC 2.5.1.54)
<i>Pcc</i> ICMP5702_peg2133	AODT01000011.1	119328	118471	-	Phosphoenolpyruvate synthase regulatory protein
<i>Pcc</i> ICMP5702_peg2134	AODT01000011.1	119593	121971	+	Phosphoenolpyruvate synthase (EC 2.7.9.2)
<i>Pcc</i> ICMP5702_peg2135	AODT01000011.1	123231	122185	-	FAD:protein FMN transferase (EC 2.7.1.180)
<i>Pcc</i> ICMP5702_peg2136	AODT01000011.1	124859	123750	-	UPF0118 inner membrane protein YdiK
<i>Pcc</i> ICMP5702_peg2137	AODT01000011.1	125005	124871	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2138	AODT01000011.1	125157	128210	+	Uncharacterized protein YdiJ
<i>Pcc</i> ICMP5702_peg2139	AODT01000011.1	128210	128626	+	1,4-dihydroxy-2-naphthoyl-CoA hydrolase (EC 3.1.2.28) in menaquinone biosynthesis
<i>Pcc</i> ICMP5702_peg2140	AODT01000011.1	129100	128699	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2141	AODT01000011.1	129527	129898	+	Iron-sulfur cluster assembly iron binding protein SufA
<i>Pcc</i> ICMP5702_peg2142	AODT01000011.1	129912	131411	+	Iron-sulfur cluster assembly protein SufB
<i>Pcc</i> ICMP5702_peg2143	AODT01000011.1	131509	132255	+	Iron-sulfur cluster assembly ATPase protein SufC
<i>Pcc</i> ICMP5702_peg2144	AODT01000011.1	132230	133576	+	Iron-sulfur cluster assembly protein SufD

<i>Pcc</i> ICMP5702_peg2145	AODT01000011.1	133576	134799	+	Cysteine desulfurase (EC 2.8.1.7) => SufS
<i>Pcc</i> ICMP5702_peg2146	AODT01000011.1	134833	135249	+	Sulfur acceptor protein => iron-sulfur cluster assembly SufE
<i>Pcc</i> ICMP5702_peg2147	AODT01000011.1	135660	135511	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2148	AODT01000011.1	135919	136941	+	L,D-transpeptidase
<i>Pcc</i> ICMP5702_peg2149	AODT01000011.1	137357	137121	-	Major outer membrane lipoprotein Lpp
<i>Pcc</i> ICMP5702_peg2150	AODT01000011.1	139084	137672	-	Pyruvate kinase (EC 2.7.1.40)
<i>Pcc</i> ICMP5702_peg2151	AODT01000011.1	139381	139479	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2152	AODT01000011.1	139727	140590	+	Beta-glucoside bgl operon antiterminator, BglG family
<i>Pcc</i> ICMP5702_peg2153	AODT01000011.1	141028	142929	+	PTS system, beta-glucoside-specific IIB component / PTS system, beta-glucoside-specific IIC component / PTS system, beta-glucoside-specific IIA component
<i>Pcc</i> ICMP5702_peg2154	AODT01000011.1	142965	144359	+	6-phospho-beta-glucosidase (EC 3.2.1.86)
<i>Pcc</i> ICMP5702_peg2155	AODT01000011.1	144610	146250	+	Outer membrane porin
<i>Pcc</i> ICMP5702_peg2156	AODT01000011.1	146337	147527	+	Uncharacterized glycosyl hydrolase YieL
<i>Pcc</i> ICMP5702_peg2157	AODT01000011.1	147634	148647	+	Inosine-uridine nucleoside N-ribohydrolase
<i>Pcc</i> ICMP5702_peg2158	AODT01000011.1	148935	148675	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2159	AODT01000011.1	149086	150519	+	Cytochrome c552 precursor (EC 1.7.2.2)
<i>Pcc</i> ICMP5702_peg2160	AODT01000011.1	150568	151137	+	Cytochrome c-type protein NrfB precursor
<i>Pcc</i> ICMP5702_peg2161	AODT01000011.1	151134	151805	+	NrfC protein
<i>Pcc</i> ICMP5702_peg2162	AODT01000011.1	151802	152764	+	NrfD protein
<i>Pcc</i> ICMP5702_peg2163	AODT01000011.1	152786	154660	+	Cytochrome c-type heme lyase subunit nrfE, nitrite reductase complex assembly
<i>Pcc</i> ICMP5702_peg2164	AODT01000011.1	154653	155054	+	Formate-dependent nitrite reductase complex subunit NrfF
<i>Pcc</i> ICMP5702_peg2165	AODT01000011.1	155051	155911	+	Cytochrome c-type heme lyase subunit nrfG, nitrite reductase complex assembly
<i>Pcc</i> ICMP5702_peg2166	AODT01000011.1	156115	156747	+	ABC transporter involved in cytochrome c biogenesis, ATPase component CcmA
<i>Pcc</i> ICMP5702_peg2167	AODT01000011.1	156735	157391	+	ABC transporter involved in cytochrome c biogenesis, CcmB subunit
<i>Pcc</i> ICMP5702_peg2168	AODT01000011.1	157460	158200	+	Cytochrome c-type biogenesis protein CcmC, putative heme lyase for CcmE
<i>Pcc</i> ICMP5702_peg2169	AODT01000011.1	158197	158418	+	Cytochrome c-type biogenesis protein CcmD, interacts with CcmCE
<i>Pcc</i> ICMP5702_peg2170	AODT01000011.1	158415	158897	+	Cytochrome c-type biogenesis protein CcmE, heme chaperone
<i>Pcc</i> ICMP5702_peg2171	AODT01000011.1	158894	160849	+	Cytochrome c heme lyase subunit CcmF
<i>Pcc</i> ICMP5702_peg2172	AODT01000011.1	160846	161403	+	Cytochrome c-type biogenesis protein CcmG/DsbE, thiol:disulfide oxidoreductase
<i>Pcc</i> ICMP5702_peg2173	AODT01000011.1	161400	161858	+	Cytochrome c heme lyase subunit CcmL
<i>Pcc</i> ICMP5702_peg2174	AODT01000011.1	161855	162724	+	Cytochrome c heme lyase subunit CcmH
<i>Pcc</i> ICMP5702_peg2175	AODT01000011.1	163907	163305	-	Cytochrome c-type protein NapC
<i>Pcc</i> ICMP5702_peg2176	AODT01000011.1	164353	163916	-	Nitrate reductase cytochrome c550-type subunit
<i>Pcc</i> ICMP5702_peg2177	AODT01000011.1	165213	164350	-	Polyferredoxin NapH (periplasmic nitrate reductase)
<i>Pcc</i> ICMP5702_peg2178	AODT01000011.1	165892	165200	-	Ferredoxin-type protein NapG (periplasmic nitrate reductase)
<i>Pcc</i> ICMP5702_peg2179	AODT01000011.1	168384	165898	-	Periplasmic nitrate reductase (EC 1.7.99.4)

<i>Pcc</i> ICMP5702_peg2180	AODT01000011.1	168701	168381	-	Periplasmic nitrate reductase component NapD
<i>Pcc</i> ICMP5702_peg2181	AODT01000011.1	169234	168698	-	Ferredoxin-type protein NapF (periplasmic nitrate reductase)
<i>Pcc</i> ICMP5702_peg2182	AODT01000011.1	169481	171202	+	Nitrate/nitrite sensor protein NarQ
<i>Pcc</i> ICMP5702_peg2183	AODT01000011.1	171290	171922	+	Nitrate/nitrite response regulator protein NarP
<i>Pcc</i> ICMP5702_peg2184	AODT01000011.1	172953	171991	-	Auxin efflux carrier family protein
<i>Pcc</i> ICMP5702_peg2185	AODT01000011.1	173094	173981	+	Transcriptional regulator
<i>Pcc</i> ICMP5702_peg2186	AODT01000011.1	174528	174154	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2187	AODT01000011.1	175228	175542	+	small multidrug resistance family (SMR) protein
<i>Pcc</i> ICMP5702_peg2188	AODT01000011.1	176070	176861	+	Putative hydrolase
<i>Pcc</i> ICMP5702_peg2189	AODT01000011.1	177682	176909	-	Transcriptional regulator, DeoR family
<i>Pcc</i> ICMP5702_peg2190	AODT01000011.1	177762	179027	+	Phosphoesterase
<i>Pcc</i> ICMP5702_peg2191	AODT01000011.1	179471	181645	+	Catalase-peroxidase KatG (EC 1.11.1.21)
<i>Pcc</i> ICMP5702_peg2192	AODT01000011.1	181981	181718	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2193	AODT01000011.1	182063	182476	+	Transcriptional regulator, MarR family
<i>Pcc</i> ICMP5702_peg2194	AODT01000011.1	182641	182528	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2195	AODT01000011.1	182821	183879	+	Urea carboxylase-related ABC transporter, substrate-binding protein
<i>Pcc</i> ICMP5702_peg2196	AODT01000011.1	183902	184717	+	Urea carboxylase-related ABC transporter, permease protein
<i>Pcc</i> ICMP5702_peg2197	AODT01000011.1	184714	185505	+	Urea carboxylase-related ABC transporter, ATP-binding protein
<i>Pcc</i> ICMP5702_peg2198	AODT01000011.1	185519	186265	+	Urea carboxylase-related aminomethyltransferase
<i>Pcc</i> ICMP5702_peg2199	AODT01000011.1	186277	186912	+	Urea carboxylase-related aminomethyltransferase
<i>Pcc</i> ICMP5702_peg2200	AODT01000011.1	186903	187046	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2201	AODT01000011.1	187155	190760	+	Urea carboxylase (EC 6.3.4.6)
<i>Pcc</i> ICMP5702_peg2202	AODT01000011.1	190768	190881	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2203	AODT01000011.1	192581	191208	-	Multidrug efflux transporter MdtK/NorM (MATE family)
<i>Pcc</i> ICMP5702_peg2204	AODT01000011.1	192825	193460	+	Riboflavin synthase eubacterial/eukaryotic (EC 2.5.1.9)
<i>Pcc</i> ICMP5702_peg2205	AODT01000011.1	194674	193523	-	Cyclopropane-fatty-acyl-phospholipid synthase (EC 2.1.1.79)
<i>Pcc</i> ICMP5702_peg2206	AODT01000011.1	195906	194881	-	Purine nucleotide synthesis repressor
<i>Pcc</i> ICMP5702_peg2207	AODT01000011.1	196300	196389	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2208	AODT01000011.1	197342	196491	-	Murein DD-endopeptidase MepH
<i>Pcc</i> ICMP5702_peg2209	AODT01000011.1	197416	197571	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2210	AODT01000011.1	197684	198034	+	Monothiol glutaredoxin GrxD
<i>Pcc</i> ICMP5702_peg2211	AODT01000011.1	198809	198138	-	Ribonuclease T
<i>Pcc</i> ICMP5702_peg2212	AODT01000011.1	199366	198959	-	Lactoylglutathione lyase (EC 4.4.1.5)
<i>Pcc</i> ICMP5702_peg2213	AODT01000011.1	199656	199895	+	Uncharacterized protein YdhL
<i>Pcc</i> ICMP5702_peg2214	AODT01000011.1	200124	200561	+	Transcriptional regulator SlyA
<i>Pcc</i> ICMP5702_peg2215	AODT01000011.1	201160	200693	-	Outer membrane lipoprotein pcp precursor

<i>Pcc</i> ICMP5702_peg2216	AODT01000011.1	201510	202622	+	Anhydro-N-acetylmuramic acid kinase (EC 2.7.1.170)
<i>Pcc</i> ICMP5702_peg2217	AODT01000011.1	202720	203037	+	Inhibitor of vertebrate c-type lysozyme, outer membrane => MliC
<i>Pcc</i> ICMP5702_peg2218	AODT01000011.1	203097	203828	+	Pyridoxamine 5'-phosphate oxidase (EC 1.4.3.5)
<i>Pcc</i> ICMP5702_peg2219	AODT01000011.1	203918	204049	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2220	AODT01000011.1	204064	205341	+	Tyrosyl-tRNA synthetase (EC 6.1.1.1)
<i>Pcc</i> ICMP5702_peg2221	AODT01000011.1	205426	206286	+	Pyridoxal kinase (EC 2.7.1.35)
<i>Pcc</i> ICMP5702_peg2222	AODT01000011.1	206933	206325	-	Glutathione S-transferase (EC 2.5.1.18)
<i>Pcc</i> ICMP5702_peg2223	AODT01000011.1	207525	207647	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2224	AODT01000011.1	207788	209092	+	Proton/sodium-glutamate symport protein
<i>Pcc</i> ICMP5702_peg2225	AODT01000011.1	209253	209414	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2226	AODT01000011.1	209436	212108	+	Aconitate hydratase (EC 4.2.1.3)
<i>Pcc</i> ICMP5702_peg2227	AODT01000011.1	212413	214047	+	ABC transporter, substrate-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg2228	AODT01000011.1	214713	214120	-	GTP cyclohydrolase II (EC 3.5.4.25)
<i>Pcc</i> ICMP5702_peg2229	AODT01000011.1	214779	214898	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2230	AODT01000011.1	215006	215782	+	Phosphatidylglycerophosphatase B (EC 3.1.3.27)
<i>Pcc</i> ICMP5702_peg2231	AODT01000011.1	215889	216053	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2232	AODT01000011.1	216110	217051	+	ABC transporter, substrate-binding protein KPN_00600
<i>Pcc</i> ICMP5702_peg2233	AODT01000011.1	217096	217728	+	putative lipoprotein
<i>Pcc</i> ICMP5702_peg2234	AODT01000011.1	217725	219281	+	ABC transporter, ATP-binding protein KPN_00598
<i>Pcc</i> ICMP5702_peg2235	AODT01000011.1	219283	220380	+	ABC transporter, permease protein KPN_00597
<i>Pcc</i> ICMP5702_peg2236	AODT01000011.1	220543	221373	+	Transketolase, N-terminal section (EC 2.2.1.1)
<i>Pcc</i> ICMP5702_peg2237	AODT01000011.1	221366	222310	+	Transketolase, C-terminal section (EC 2.2.1.1)
<i>Pcc</i> ICMP5702_peg2238	AODT01000011.1	222313	223809	+	Unknown pentose kinase TM0952
<i>Pcc</i> ICMP5702_peg2239	AODT01000011.1	224040	225038	+	Unknown pentose isomerase ECA1953
<i>Pcc</i> ICMP5702_peg2240	AODT01000011.1	226182	225127	-	Unknown pentose utilization regulator 2, DeoR family
<i>Pcc</i> ICMP5702_peg2241	AODT01000011.1	226256	226561	+	Inner membrane protein yciS
<i>Pcc</i> ICMP5702_peg2242	AODT01000011.1	226574	227743	+	Lipopolysaccharide assembly protein LapB
<i>Pcc</i> ICMP5702_peg2243	AODT01000011.1	227928	228671	+	Orotidine 5'-phosphate decarboxylase (EC 4.1.1.23)
<i>Pcc</i> ICMP5702_peg2244	AODT01000011.1	228668	229003	+	Translation initiation factor SUI1-related protein
<i>Pcc</i> ICMP5702_peg2245	AODT01000011.1	229270	229055	-	Osmotically-inducible lipoprotein OsmB
<i>Pcc</i> ICMP5702_peg2246	AODT01000011.1	229604	230299	+	L-ribulose-5-phosphate 4-epimerase (EC 5.1.3.4)
<i>Pcc</i> ICMP5702_peg2247	AODT01000011.1	232547	230484	-	Carbon starvation protein A
<i>Pcc</i> ICMP5702_peg2248	AODT01000011.1	233717	232800	-	Putative oxidoreductase SCO7655
<i>Pcc</i> ICMP5702_peg2249	AODT01000011.1	235711	233777	-	Exoribonuclease II (EC 3.1.13.1)
<i>Pcc</i> ICMP5702_peg2250	AODT01000011.1	238430	236118	-	Putative formate dehydrogenase oxidoreductase protein
<i>Pcc</i> ICMP5702_peg2251	AODT01000011.1	238738	239634	+	LysR-family transcriptional regulator PA5179

<i>Pcc</i> ICMP5702_peg2252	AODT01000011.1	240908	239838	-	Transcriptional regulator, LacI family
<i>Pcc</i> ICMP5702_peg2253	AODT01000011.1	241229	242539	+	Hexuronate transporter
<i>Pcc</i> ICMP5702_peg2254	AODT01000011.1	242574	244940	+	Alpha-glucosidase (EC 3.2.1.20)
<i>Pcc</i> ICMP5702_peg2255	AODT01000011.1	245548	248424	+	redox proteins related to the succinate dehydrogenases and fumarate reductases
<i>Pcc</i> ICMP5702_peg2256	AODT01000011.1	248540	249520	+	FAD:protein FMN transferase (EC 2.7.1.180)
<i>Pcc</i> ICMP5702_peg2257	AODT01000011.1	250247	249690	-	AidA
<i>Pcc</i> ICMP5702_peg2258	AODT01000011.1	251351	250563	-	Enoyl-[acyl-carrier-protein] reductase [NADH] (EC 1.3.1.9)
<i>Pcc</i> ICMP5702_peg2259	AODT01000011.1	252360	251545	-	Peptide ABC transporter, ATP-binding protein SapF
<i>Pcc</i> ICMP5702_peg2260	AODT01000011.1	253352	252360	-	Peptide ABC transporter, ATP-binding protein SapD
<i>Pcc</i> ICMP5702_peg2261	AODT01000011.1	254259	253369	-	Peptide ABC transporter, permease protein SapC
<i>Pcc</i> ICMP5702_peg2262	AODT01000011.1	255211	254246	-	Peptide ABC transporter, permease protein SapB
<i>Pcc</i> ICMP5702_peg2263	AODT01000011.1	256950	255208	-	Peptide ABC transporter, substrate-binding protein SapA
<i>Pcc</i> ICMP5702_peg2264	AODT01000011.1	257334	257215	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2265	AODT01000011.1	257431	258957	+	beta-1,4-glucanase (cellulase) (EC 3.2.1.4)
<i>Pcc</i> ICMP5702_peg2266	AODT01000011.1	260021	259032	-	Psp operon transcriptional activator
<i>Pcc</i> ICMP5702_peg2267	AODT01000011.1	260247	260912	+	Phage shock protein A @ Suppressor of sigma54-dependent transcription, PspA-like
<i>Pcc</i> ICMP5702_peg2268	AODT01000011.1	261003	261227	+	Phage shock protein B
<i>Pcc</i> ICMP5702_peg2269	AODT01000011.1	261227	261592	+	Phage shock protein C
<i>Pcc</i> ICMP5702_peg2270	AODT01000011.1	262239	261685	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2271	AODT01000011.1	262866	262384	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2272	AODT01000011.1	270714	262879	-	family
<i>Pcc</i> ICMP5702_peg2273	AODT01000011.1	271257	270742	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2274	AODT01000011.1	273011	271269	-	Channel-forming transporter/cytolysins activator of TpsB family
<i>Pcc</i> ICMP5702_peg2275	AODT01000011.1	273387	274784	+	Conserved protein YcjX with nucleoside triphosphate hydrolase domain
<i>Pcc</i> ICMP5702_peg2276	AODT01000011.1	274781	275824	+	Membrane protein YcjF
<i>Pcc</i> ICMP5702_peg2277	AODT01000011.1	276130	277290	+	Gluconate dehydratase (EC 4.2.1.39)
<i>Pcc</i> ICMP5702_peg2278	AODT01000011.1	277314	277619	+	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)
<i>Pcc</i> ICMP5702_peg2279	AODT01000011.1	277647	278936	+	PTS system, cellobiose-specific IIC component
<i>Pcc</i> ICMP5702_peg2280	AODT01000011.1	278968	279273	+	PTS system, cellobiose-specific IIA component (EC 2.7.1.69)
<i>Pcc</i> ICMP5702_peg2281	AODT01000011.1	279346	280350	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2282	AODT01000011.1	280457	282001	+	N-acyl-L-amino acid amidohydrolase (EC 3.5.1.14)
<i>Pcc</i> ICMP5702_peg2283	AODT01000011.1	282138	283706	+	Transcriptional repressor protein TyrR
<i>Pcc</i> ICMP5702_peg2284	AODT01000011.1	284261	283758	-	Thiol peroxidase, Tpx-type (EC 1.11.1.15)
<i>Pcc</i> ICMP5702_peg2285	AODT01000011.1	285060	284341	-	Gamma-D-Glutamyl-meso-Diaminopimelate Amidase
<i>Pcc</i> ICMP5702_peg2286	AODT01000011.1	285225	286841	+	Murein peptide ABC transporter, substrate-binding protein (requires DppBCDF)
<i>Pcc</i> ICMP5702_peg2287	AODT01000011.1	286966	287949	+	Magnesium and cobalt transport protein CorA

<i>Pcc</i> ICMP5702_peg2288	AODT01000011.1	288107	287979	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2289	AODT01000011.1	288514	288690	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2290	AODT01000011.1	289747	288812	-	tRNA-(cytosine32)-2-thiocytidine synthetase TtcA
<i>Pcc</i> ICMP5702_peg2291	AODT01000011.1	290391	290122	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2292	AODT01000011.1	290948	291100	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2293	AODT01000011.1	291137	291487	+	soluble [2Fe-2S] ferredoxin
<i>Pcc</i> ICMP5702_peg2294	AODT01000011.1	292066	292356	+	Uncharacterized protein YdbJ
<i>Pcc</i> ICMP5702_peg2295	AODT01000011.1	293382	292390	-	D-lactate dehydrogenase (EC 1.1.1.28)
<i>Pcc</i> ICMP5702_peg2296	AODT01000011.1	295047	293494	-	Aerotaxis sensor receptor protein
<i>Pcc</i> ICMP5702_peg2297	AODT01000011.1	296970	295417	-	Aerotaxis sensor receptor protein
<i>Pcc</i> ICMP5702_peg2298	AODT01000011.1	297343	299934	+	Putative uncharacterized protein ydbH
<i>Pcc</i> ICMP5702_peg2299	AODT01000011.1	299950	300183	+	Uncharacterized protein YnbE
<i>Pcc</i> ICMP5702_peg2300	AODT01000011.1	300832	300227	-	FMN-dependent NADH-azoreductase (EC 1.7.1.6)
<i>Pcc</i> ICMP5702_peg2301	AODT01000011.1	301138	305025	+	ATP-dependent helicase HrpA
<i>Pcc</i> ICMP5702_peg2302	AODT01000011.1	305881	305042	-	STAPHYLOLYTIC protease PREPROENZYME LASA
<i>Pcc</i> ICMP5702_peg2303	AODT01000011.1	307706	305928	-	Sensory box/GGDEF family protein
<i>Pcc</i> ICMP5702_peg2304	AODT01000011.1	309039	308179	-	Uncharacterized serine protease YdgD
<i>Pcc</i> ICMP5702_peg2305	AODT01000011.1	309576	309274	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2306	AODT01000011.1	309694	309810	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2307	AODT01000011.1	310452	309982	-	Acid shock protein precursor
<i>Pcc</i> ICMP5702_peg2308	AODT01000011.1	311941	310628	-	Sensory histidine kinase in two-component regulatory system with RstA
<i>Pcc</i> ICMP5702_peg2309	AODT01000011.1	312675	311938	-	Two-component transcriptional response regulator RstA
<i>Pcc</i> ICMP5702_peg2310	AODT01000011.1	312895	314097	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2311	AODT01000011.1	314308	314883	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2312	AODT01000011.1	315736	314933	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2313	AODT01000011.1	316023	315733	-	RNA polymerase ECF-type sigma factor
<i>Pcc</i> ICMP5702_peg2314	AODT01000011.1	317001	316279	-	FolM Alternative dihydrofolate reductase 1
<i>Pcc</i> ICMP5702_peg2315	AODT01000011.1	317140	317556	+	Uncharacterized protein VC1189
<i>Pcc</i> ICMP5702_peg2316	AODT01000011.1	319298	317595	-	Putative sulfate permease
<i>Pcc</i> ICMP5702_peg2317	AODT01000011.1	320562	319462	-	Calcium/proton antiporter
<i>Pcc</i> ICMP5702_peg2318	AODT01000011.1	321695	320892	-	Iron-chelator utilization protein
<i>Pcc</i> ICMP5702_peg2319	AODT01000011.1	322137	322820	+	Cation transport protein ChaC
<i>Pcc</i> ICMP5702_peg2320	AODT01000011.1	323939	322899	-	Peptide chain release factor RF-3
<i>Pcc</i> ICMP5702_peg2321	AODT01000011.1	323974	324087	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2322	AODT01000011.1	325516	324242	-	Acyltransferase
<i>Pcc</i> ICMP5702_peg2323	AODT01000011.1	325761	325630	-	Hypothetical protein

<i>Pcc</i> ICMP5702_peg2324	AODT01000011.1	326492	325842	-	Nitrate/nitrite response regulator protein NarL
<i>Pcc</i> ICMP5702_peg2325	AODT01000011.1	328356	326485	-	Nitrate/nitrite sensor protein NarX
<i>Pcc</i> ICMP5702_peg2326	AODT01000011.1	328473	328598	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2327	AODT01000011.1	328630	330018	+	Nitrate/nitrite transporter NarK/U
<i>Pcc</i> ICMP5702_peg2328	AODT01000011.1	330735	334496	+	Respiratory nitrate reductase alpha chain (EC 1.7.99.4)
<i>Pcc</i> ICMP5702_peg2329	AODT01000011.1	334496	336061	+	Respiratory nitrate reductase beta chain (EC 1.7.99.4)
<i>Pcc</i> ICMP5702_peg2330	AODT01000011.1	336054	336773	+	Respiratory nitrate reductase delta chain (EC 1.7.99.4)
<i>Pcc</i> ICMP5702_peg2331	AODT01000011.1	336773	337462	+	Respiratory nitrate reductase gamma chain (EC 1.7.99.4)
<i>Pcc</i> ICMP5702_peg2332	AODT01000011.1	338603	337731	-	Permease of the drug/metabolite transporter (DMT) superfamily
<i>Pcc</i> ICMP5702_peg2333	AODT01000011.1	338666	339211	+	Transcriptional regulator, MarR family
<i>Pcc</i> ICMP5702_peg2334	AODT01000011.1	339309	339776	+	OsmC/Ohr family protein
<i>Pcc</i> ICMP5702_peg2335	AODT01000011.1	341022	339880	-	D-threo-3-hydroxyaspartate ammonia-lyase (EC 4.3.1.-)
<i>Pcc</i> ICMP5702_peg2336	AODT01000011.1	341960	341019	-	Ornithine cyclodeaminase (EC 4.3.1.12)
<i>Pcc</i> ICMP5702_peg2337	AODT01000011.1	342945	341971	-	L-threo-3-hydroxyaspartate ammonia-lyase (EC 4.3.1.16)
<i>Pcc</i> ICMP5702_peg2338	AODT01000011.1	343253	343876	+	YheO-like PAS domain
<i>Pcc</i> ICMP5702_peg2339	AODT01000011.1	344047	345129	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2340	AODT01000011.1	345438	345686	+	UPF0410 protein YeaQ
<i>Pcc</i> ICMP5702_peg2341	AODT01000011.1	346282	345734	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2342	AODT01000011.1	346932	346279	-	SanC
<i>Pcc</i> ICMP5702_peg2343	AODT01000011.1	348231	346987	-	Putative aminotransferase
<i>Pcc</i> ICMP5702_peg2344	AODT01000011.1	349264	348215	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2345	AODT01000011.1	350093	349278	-	Probable taurine catabolism dioxygenase
<i>Pcc</i> ICMP5702_peg2346	AODT01000011.1	351038	350259	-	Oxidoreductase, short-chain dehydrogenase/reductase family
<i>Pcc</i> ICMP5702_peg2347	AODT01000011.1	351256	351113	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2348	AODT01000011.1	351284	351409	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2349	AODT01000011.1	352500	351406	-	3.A.1.11.1) Transcriptional regulator GabR of GABA utilization (GntR family with aminotransferase-like domain)
<i>Pcc</i> ICMP5702_peg2350	AODT01000011.1	354186	352693	-	
<i>Pcc</i> ICMP5702_peg2351	AODT01000011.1	354368	355633	+	Gamma-aminobutyrate:alpha-ketoglutarate aminotransferase (EC 2.6.1.19)
<i>Pcc</i> ICMP5702_peg2352	AODT01000011.1	355644	357116	+	Succinate-semialdehyde dehydrogenase [NAD(P)+] (EC 1.2.1.16)
<i>Pcc</i> ICMP5702_peg2353	AODT01000011.1	357135	357272	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2354	AODT01000011.1	357458	358537	+	Spermidine/putrescine import ABC transporter substrate-binding protein PotD (TC 3.A.1.11.1)
<i>Pcc</i> ICMP5702_peg2355	AODT01000011.1	358580	359848	+	Spermidine/putrescine import ABC transporter permease protein PotB (TC 3.A.1.11.1)
<i>Pcc</i> ICMP5702_peg2356	AODT01000011.1	359875	360693	+	Spermidine/putrescine import ABC transporter permease protein PotC (TC 3.A.1.11.1)
<i>Pcc</i> ICMP5702_peg2357	AODT01000011.1	360932	360807	-	Hypothetical protein

<i>Pcc</i> ICMP5702_peg2358	AODT01000011.1	361195	361929	+	Oxidoreductase, short-chain dehydrogenase/reductase family
<i>Pcc</i> ICMP5702_peg2359	AODT01000011.1	361922	363046	+	Aminotransferase, class III
<i>Pcc</i> ICMP5702_peg2360	AODT01000011.1	363043	364341	+	Putative aminotransferase
<i>Pcc</i> ICMP5702_peg2361	AODT01000011.1	365905	364379	-	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg2362	AODT01000011.1	366273	366118	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2363	AODT01000011.1	367658	366327	-	putative membrane-associated phospholipid phosphatase, PAP2 superfamily
<i>Pcc</i> ICMP5702_peg2364	AODT01000011.1	368002	368115	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2365	AODT01000011.1	368252	369274	+	Methionine ABC transporter ATP-binding protein
<i>Pcc</i> ICMP5702_peg2366	AODT01000011.1	369267	369926	+	Methionine ABC transporter permease protein
<i>Pcc</i> ICMP5702_peg2367	AODT01000011.1	369968	371080	+	N-acylamino acid racemase
<i>Pcc</i> ICMP5702_peg2368	AODT01000011.1	371641	372465	+	Methionine ABC transporter substrate-binding protein
<i>Pcc</i> ICMP5702_peg2369	AODT01000011.1	372544	372933	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2370	AODT01000011.1	372926	373246	+	Transcriptional regulator, Xre family
<i>Pcc</i> ICMP5702_peg2371	AODT01000011.1	374757	373339	-	N-acyl-L-amino acid amidohydrolase (EC 3.5.1.14)
<i>Pcc</i> ICMP5702_peg2372	AODT01000011.1	374900	375832	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg2373	AODT01000011.1	377027	375948	-	Type III secretion inner membrane protein (YscU,SpaS,EscU,HrcU,SsaU, homologous to flagellar export components)
<i>Pcc</i> ICMP5702_peg2374	AODT01000011.1	377841	377041	-	Type III secretion inner membrane protein (YscT,HrcT,SpaR,EscT,EpaR1,homologous to flagellar export components)
<i>Pcc</i> ICMP5702_peg2375	AODT01000011.1	378108	377848	-	Type III secretion inner membrane protein (YscS,homologous to flagellar export components)
<i>Pcc</i> ICMP5702_peg2376	AODT01000011.1	378769	378116	-	Type III secretion inner membrane protein (YscR,SpaR,HrcR,EscR,homologous to flagellar export components)
<i>Pcc</i> ICMP5702_peg2377	AODT01000011.1	379905	378766	-	Type III secretion inner membrane protein (YscQ,homologous to flagellar export components)
<i>Pcc</i> ICMP5702_peg2378	AODT01000011.1	380435	379902	-	type III secretion protein HrpP
<i>Pcc</i> ICMP5702_peg2379	AODT01000011.1	380869	380432	-	Type III secretion spans bacterial envelope protein (YscO)
<i>Pcc</i> ICMP5702_peg2380	AODT01000011.1	382226	380859	-	YscN,SpaL,MxiB,HrcN,EscN)
<i>Pcc</i> ICMP5702_peg2381	AODT01000011.1	383161	382226	-	type III secretion protein HrpQ
<i>Pcc</i> ICMP5702_peg2382	AODT01000011.1	385272	383170	-	Type III secretion inner membrane channel protein (LcrD,HrcV,EscV,SsaV)
<i>Pcc</i> ICMP5702_peg2383	AODT01000011.1	386477	385269	-	type III secretion protein HrpJ
<i>Pcc</i> ICMP5702_peg2384	AODT01000011.1	386806	387351	+	RNA polymerase sigma factor RpoE
<i>Pcc</i> ICMP5702_peg2385	AODT01000011.1	387596	389062	+	Probable two-component sensor, near polyamine transporter
<i>Pcc</i> ICMP5702_peg2386	AODT01000011.1	389099	389740	+	Two-component transcriptional response regulator, LuxR family
<i>Pcc</i> ICMP5702_peg2387	AODT01000011.1	389958	390110	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2388	AODT01000011.1	390110	391195	+	Formate hydrogenlyase transcriptional activator

<i>Pcc</i> ICMP5702_peg2389	AODT01000011.1	392846	391257	-	C-di-GMP phosphodiesterase A-related protein
<i>Pcc</i> ICMP5702_peg2390	AODT01000011.1	393181	393387	+	Hrp pili protein hrpA (TTSS pilin hrpA)
<i>Pcc</i> ICMP5702_peg2391	AODT01000011.1	393456	393827	+	type III secretion protein HrpB(Pto)
					Type III secretion bridge between inner and outermembrane lipoprotein
<i>Pcc</i> ICMP5702_peg2392	AODT01000011.1	393834	394601	+	(YscJ,HrcJ,EscJ, PscJ)
<i>Pcc</i> ICMP5702_peg2393	AODT01000011.1	394598	395230	+	type III secretion protein HrpD
<i>Pcc</i> ICMP5702_peg2394	AODT01000011.1	395264	395863	+	Type III secretion cytoplasmic protein (YscL)
<i>Pcc</i> ICMP5702_peg2395	AODT01000011.1	396010	396234	+	HrpF
<i>Pcc</i> ICMP5702_peg2396	AODT01000011.1	396245	396655	+	type III secretion protein HrpG
<i>Pcc</i> ICMP5702_peg2397	AODT01000011.1	396648	398717	+	Type III secretion outermembrane pore forming protein (YscC,MxiD,HrcC, InvG)
<i>Pcc</i> ICMP5702_peg2398	AODT01000011.1	398745	398936	+	type III secretion protein HrpT
<i>Pcc</i> ICMP5702_peg2399	AODT01000011.1	398929	399276	+	negative regulator of hrp expression HrpV
<i>Pcc</i> ICMP5702_peg2400	AODT01000011.1	399421	400491	+	Harpin hrpN (Harpin-Ech)
<i>Pcc</i> ICMP5702_peg2401	AODT01000011.1	400861	400700	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2402	AODT01000011.1	400990	403017	+	VgrG protein
<i>Pcc</i> ICMP5702_peg2403	AODT01000011.1	403014	403811	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2404	AODT01000011.1	403811	405805	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2405	AODT01000011.1	405805	406509	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2406	AODT01000011.1	406633	406520	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2407	AODT01000011.1	406657	407364	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2408	AODT01000011.1	407414	407680	+	T6SS PAAR-repeat protein
<i>Pcc</i> ICMP5702_peg2409	AODT01000011.1	408101	407778	-	potential HrpW-specific chaperone
<i>Pcc</i> ICMP5702_peg2410	AODT01000011.1	409578	408103	-	Type III effector HrpW, hairpin with pectate lyase domain
<i>Pcc</i> ICMP5702_peg2411	AODT01000011.1	409759	414642	+	Type III effector protein AvrE1
<i>Pcc</i> ICMP5702_peg2412	AODT01000011.1	414678	415100	+	putative avirulence protein
<i>Pcc</i> ICMP5702_peg2413	AODT01000011.1	415786	415121	-	Transcriptional regulator, GntR family
<i>Pcc</i> ICMP5702_peg2414	AODT01000011.1	416122	417786	+	Channel-forming transporter/cytolysins activator of TpsB family
<i>Pcc</i> ICMP5702_peg2415	AODT01000011.1	417837	435410	+	family
<i>Pcc</i> ICMP5702_peg2416	AODT01000011.1	435412	435699	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2417	AODT01000011.1	436053	436298	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2418	AODT01000011.1	436302	436433	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2419	AODT01000011.1	436543	437013	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2420	AODT01000011.1	437229	437104	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2421	AODT01000011.1	437309	437464	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2422	AODT01000011.1	437632	437489	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2423	AODT01000011.1	437913	438218	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg2424	AODT01000011.1	438255	438359	+	family
<i>Pcc</i> ICMP5702_peg2425	AODT01000011.1	438364	438735	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2426	AODT01000011.1	439359	440480	+	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg2427	AODT01000011.1	442389	440683	-	Exopolysaccharide lyase (EC 4.2.2.9)
<i>Pcc</i> ICMP5702_peg2428	AODT01000011.1	443271	442507	-	putative secreted protein
<i>Pcc</i> ICMP5702_peg2429	AODT01000011.1	444210	443392	-	Putative outer membrane protein
<i>Pcc</i> ICMP5702_peg2430	AODT01000011.1	444338	444207	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2431	AODT01000011.1	444972	446735	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2432	AODT01000011.1	446951	446775	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2433	AODT01000011.1	447097	448104	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2434	AODT01000011.1	448650	450356	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2435	AODT01000011.1	450734	452536	+	Allophanate hydrolase (EC 3.5.1.54)
<i>Pcc</i> ICMP5702_peg2436	AODT01000011.1	452529	456143	+	Urea carboxylase (EC 6.3.4.6)
<i>Pcc</i> ICMP5702_peg2437	AODT01000011.1	456193	456981	+	Transcriptional regulator, GntR family
<i>Pcc</i> ICMP5702_peg2438	AODT01000011.1	456978	458246	+	Urea ABC transporter, substrate-binding protein UrtA
<i>Pcc</i> ICMP5702_peg2439	AODT01000011.1	458318	459892	+	Urea ABC transporter, permease protein UrtB
<i>Pcc</i> ICMP5702_peg2440	AODT01000011.1	459892	460980	+	Urea ABC transporter, permease protein UrtC
<i>Pcc</i> ICMP5702_peg2441	AODT01000011.1	460973	461830	+	Urea ABC transporter, ATPase protein UrtD
<i>Pcc</i> ICMP5702_peg2442	AODT01000011.1	461832	462530	+	Urea ABC transporter, ATPase protein UrtE
<i>Pcc</i> ICMP5702_peg2443	AODT01000011.1	462624	463364	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2444	AODT01000011.1	463361	463810	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2445	AODT01000011.1	463934	464254	+	Arsenical resistance operon repressor
<i>Pcc</i> ICMP5702_peg2446	AODT01000011.1	464301	465593	+	Arsenite/antimonite:H ⁺ antiporter ArsB
<i>Pcc</i> ICMP5702_peg2447	AODT01000011.1	465603	466028	+	Arsenate reductase (EC 1.20.4.1) glutaredoxin-coupled, glutaredoxin-like family
<i>Pcc</i> ICMP5702_peg2448	AODT01000011.1	466936	466112	-	ABC transporter, ATP-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg2449	AODT01000011.1	467904	466960	-	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg2450	AODT01000011.1	468536	467982	-	Acetyltransferase, GNAT family
<i>Pcc</i> ICMP5702_peg2451	AODT01000011.1	469593	468622	-	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg2452	AODT01000011.1	470603	469668	-	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg2453	AODT01000011.1	471954	470626	-	Nitrilotriacetate monooxygenase component A (EC 1.14.13.-)
<i>Pcc</i> ICMP5702_peg2454	AODT01000011.1	472275	472820	+	NADH-FMN oxidoreductase
<i>Pcc</i> ICMP5702_peg2455	AODT01000011.1	474354	473158	-	N-acetyl-L,L-diaminopimelate deacetylase homolog
<i>Pcc</i> ICMP5702_peg2456	AODT01000011.1	474648	475628	+	Luciferase-like monooxygenase YhbW
<i>Pcc</i> ICMP5702_peg2457	AODT01000011.1	475705	476214	+	DUF1706 domain-containing protein
<i>Pcc</i> ICMP5702_peg2458	AODT01000011.1	476397	476624	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2459	AODT01000011.1	476859	477641	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg2460	AODT01000011.1	478885	477881	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2461	AODT01000011.1	479974	478988	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2462	AODT01000011.1	480158	479985	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2463	AODT01000011.1	481347	480322	-	AscBF operon repressor
<i>Pcc</i> ICMP5702_peg2464	AODT01000011.1	481738	483198	+	PTS system, arbutin-, cellobiose-, and salicin-specific IIB component / PTS system, arbutin-, cellobiose-, and salicin-specific IIC component
<i>Pcc</i> ICMP5702_peg2465	AODT01000011.1	483233	484663	+	6-phospho-beta-glucosidase (EC 3.2.1.86)
<i>Pcc</i> ICMP5702_peg2466	AODT01000011.1	484898	485698	+	Histidinol-phosphatase [alternative form] (EC 3.1.3.15)
<i>Pcc</i> ICMP5702_peg2467	AODT01000011.1	485748	486134	+	Possible glyoxylase family protein (Lactoylglutathione lyase) (EC 4.4.1.5)
<i>Pcc</i> ICMP5702_peg2468	AODT01000011.1	486152	486559	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2469	AODT01000011.1	486728	487951	+	Zinc-binding GTPase YciC
<i>Pcc</i> ICMP5702_peg2470	AODT01000011.1	487990	488115	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2471	AODT01000011.1	489269	488133	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2472	AODT01000011.1	490207	489284	-	Homolog of eukaryotic DNA ligase III
<i>Pcc</i> ICMP5702_peg2473	AODT01000011.1	490657	491250	+	FIG00904989: Hypothetical protein
<i>Pcc</i> ICMP5702_peg2474	AODT01000011.1	491496	492560	+	Putative outer membrane protein
<i>Pcc</i> ICMP5702_peg2475	AODT01000011.1	493496	492609	-	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg2476	AODT01000011.1	493600	495162	+	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg2477	AODT01000011.1	496323	495223	-	Inner membrane protein YbiR, putative anion permease
<i>Pcc</i> ICMP5702_peg2478	AODT01000011.1	497815	496724	-	GTP-binding and nucleic acid-binding protein YchF
<i>Pcc</i> ICMP5702_peg2479	AODT01000011.1	498532	497945	-	Peptidyl-tRNA hydrolase (EC 3.1.1.29)
<i>Pcc</i> ICMP5702_peg2480	AODT01000011.1	498847	499116	+	Putative membrane protein YchH
<i>Pcc</i> ICMP5702_peg2481	AODT01000011.1	500234	499287	-	Ribose-phosphate pyrophosphokinase (EC 2.7.6.1)
<i>Pcc</i> ICMP5702_peg2482	AODT01000011.1	501244	500372	-	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase (EC 2.7.1.148)
<i>Pcc</i> ICMP5702_peg2483	AODT01000011.1	501871	501248	-	Outer membrane lipoprotein component of lipoprotein transport system LolB
<i>Pcc</i> ICMP5702_peg2484	AODT01000011.1	501903	502049	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2485	AODT01000011.1	502104	503360	+	Glutamyl-tRNA reductase (EC 1.2.1.70)
<i>Pcc</i> ICMP5702_peg2486	AODT01000011.1	503394	504476	+	Peptide chain release factor 1
<i>Pcc</i> ICMP5702_peg2487	AODT01000011.1	504476	505321	+	Peptide chain release factor N(5)-glutamine methyltransferase (EC 2.1.1.297)
<i>Pcc</i> ICMP5702_peg2488	AODT01000011.1	505333	505728	+	FIG002082: Protein SirB2
<i>Pcc</i> ICMP5702_peg2489	AODT01000011.1	505731	506540	+	FIG002708: Protein SirB1
<i>Pcc</i> ICMP5702_peg2490	AODT01000011.1	506616	507470	+	2-Keto-3-deoxy-D-manno-octulosonate-8-phosphate synthase (EC 2.5.1.55)
<i>Pcc</i> ICMP5702_peg2491	AODT01000011.1	508527	507574	-	Protein YdgH
<i>Pcc</i> ICMP5702_peg2492	AODT01000011.1	509107	510636	+	NAD(P) transhydrogenase N-domain of subunit alpha (EC 1.6.1.2) / NAD(P) transhydrogenase C-domain of subunit alpha (EC 1.6.1.2)
<i>Pcc</i> ICMP5702_peg2493	AODT01000011.1	510647	512035	+	NAD(P) transhydrogenase subunit beta (EC 1.6.1.2)

<i>Pcc</i> ICMP5702_peg2494	AODT01000011.1	513121	512171	-	Universal stress protein E
<i>Pcc</i> ICMP5702_peg2495	AODT01000011.1	514059	513313	-	Fumarate and nitrate reduction regulatory protein
<i>Pcc</i> ICMP5702_peg2496	AODT01000011.1	514878	514342	-	Methylated-DNA--protein-cysteine methyltransferase (EC 2.1.1.63)
<i>Pcc</i> ICMP5702_peg2497	AODT01000011.1	514967	515251	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2498	AODT01000011.1	515536	516831	+	Myo-inositol 2-dehydrogenase 1 (EC 1.1.1.18)
<i>Pcc</i> ICMP5702_peg2499	AODT01000011.1	516942	518261	+	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg2500	AODT01000011.1	518863	518339	-	Superoxide dismutase [Cu-Zn] precursor (EC 1.15.1.1)
<i>Pcc</i> ICMP5702_peg2501	AODT01000011.1	520147	518918	-	S-adenosyl-L-methionine dependent methyltransferase, similar to cyclopropane-fatty-acyl-phospholipid synthase
<i>Pcc</i> ICMP5702_peg2502	AODT01000011.1	520869	520144	-	FIG001571: Hypothetical protein
<i>Pcc</i> ICMP5702_peg2503	AODT01000011.1	522130	520862	-	Amine oxidase, flavin-containing
<i>Pcc</i> ICMP5702_peg2504	AODT01000011.1	522852	522136	-	Oxidoreductase, short-chain dehydrogenase/reductase family
<i>Pcc</i> ICMP5702_peg2505	AODT01000011.1	523328	522849	-	FIG002994: Putative transcriptional regulator
<i>Pcc</i> ICMP5702_peg2506	AODT01000011.1	526046	523584	-	Virulence factor SrfC homolog
<i>Pcc</i> ICMP5702_peg2507	AODT01000011.1	529030	526043	-	SrfB
<i>Pcc</i> ICMP5702_peg2508	AODT01000011.1	530448	529033	-	putative virulence factor
<i>Pcc</i> ICMP5702_peg2509	AODT01000011.1	531426	530737	-	Expansin-YoaJ
<i>Pcc</i> ICMP5702_peg2510	AODT01000011.1	531735	532163	+	Peroxiredoxin OsmC (EC 1.11.1.15)
<i>Pcc</i> ICMP5702_peg2511	AODT01000011.1	532479	532874	+	Soluble cytochrome b562
<i>Pcc</i> ICMP5702_peg2512	AODT01000011.1	532980	533534	+	Transcriptional regulator, AcrR family
<i>Pcc</i> ICMP5702_peg2513	AODT01000011.1	533673	534869	+	Inner membrane protein YbjJ
<i>Pcc</i> ICMP5702_peg2514	AODT01000011.1	535007	535495	+	Histone acetyltransferase HPA2 and related acetyltransferases
<i>Pcc</i> ICMP5702_peg2515	AODT01000011.1	535665	537638	+	Methyl-accepting chemotaxis protein
<i>Pcc</i> ICMP5702_peg2516	AODT01000011.1	537860	538708	+	Transcriptional regulator ArgP, LysR family
<i>Pcc</i> ICMP5702_peg2517	AODT01000011.1	539015	538749	-	Uncharacterized protein YjbD
<i>Pcc</i> ICMP5702_peg2518	AODT01000011.1	539176	539511	+	steroid delta-isomerase domain protein
<i>Pcc</i> ICMP5702_peg2519	AODT01000011.1	539875	540162	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2520	AODT01000011.1	540306	541460	+	COG1649 predicted glycoside hydrolase
<i>Pcc</i> ICMP5702_peg2521	AODT01000011.1	541751	541524	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2522	AODT01000011.1	542274	543656	+	Diaminobutyrate--2-oxoglutarate aminotransferase (EC 2.6.1.76)
<i>Pcc</i> ICMP5702_peg2523	AODT01000011.1	543675	545177	+	L-2,4-diaminobutyrate decarboxylase (EC 4.1.1.86)
<i>Pcc</i> ICMP5702_peg2524	AODT01000011.1	545557	545327	-	Tautomerase PptA
<i>Pcc</i> ICMP5702_peg2525	AODT01000011.1	545801	546691	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2526	AODT01000011.1	546720	548558	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2527	AODT01000011.1	548910	549158	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2528	AODT01000011.1	549203	549802	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg2529	AODT01000011.1	549802	550926	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2530	AODT01000011.1	551166	551023	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2531	AODT01000011.1	551247	552431	+	Periplasmic aromatic amino acid aminotransferase beta precursor (EC 2.6.1.57)
<i>Pcc</i> ICMP5702_peg2532	AODT01000011.1	552638	553387	+	NADP-dependent 3-hydroxy acid dehydrogenase YdfG (EC 1.1.1.381) @ 3-hydroxypropionate dehydrogenase (EC 1.1.1.298)
<i>Pcc</i> ICMP5702_peg2533	AODT01000011.1	553693	555210	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2534	AODT01000011.1	555228	555434	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2535	AODT01000011.1	555713	556063	+	UPF0482 protein YnfB
<i>Pcc</i> ICMP5702_peg2536	AODT01000011.1	556229	556849	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2537	AODT01000011.1	556952	557251	+	Putative outer membrane protein
<i>Pcc</i> ICMP5702_peg2538	AODT01000011.1	558801	557314	-	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg2539	AODT01000011.1	559569	558904	-	Dethiobiotin synthase BioD (EC 6.3.3.3)
<i>Pcc</i> ICMP5702_peg2540	AODT01000011.1	560920	559703	-	Mlc, transcriptional repressor of MalT (the transcriptional activator of maltose regulon) and manXYZ operon
<i>Pcc</i> ICMP5702_peg2541	AODT01000011.1	561998	561102	-	LysR family transcriptional regulator YnfL
<i>Pcc</i> ICMP5702_peg2542	AODT01000011.1	562113	563381	+	Uncharacterized MFS-type transporter YnfM
<i>Pcc</i> ICMP5702_peg2543	AODT01000011.1	563447	564484	+	DNA replication terminus site-binding protein
<i>Pcc</i> ICMP5702_peg2544	AODT01000011.1	565903	564548	-	Fumarate hydratase class II (EC 4.2.1.2)
<i>Pcc</i> ICMP5702_peg2545	AODT01000011.1	566186	567358	+	Mannose-6-phosphate isomerase (EC 5.3.1.8)
<i>Pcc</i> ICMP5702_peg2546	AODT01000011.1	567447	569006	+	Putative GTP-binding protein YdgA
<i>Pcc</i> ICMP5702_peg2547	AODT01000011.1	569105	570082	+	Putative sodium-dependent transporter
<i>Pcc</i> ICMP5702_peg2548	AODT01000011.1	570204	571220	+	Adenosine deaminase (EC 3.5.4.4)
<i>Pcc</i> ICMP5702_peg2549	AODT01000011.1	571764	571300	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2550	AODT01000011.1	573001	572009	-	Putative membrane protein precursor
<i>Pcc</i> ICMP5702_peg2551	AODT01000011.1	574375	573329	-	Uncharacterized oxidoreductase YdgJ
<i>Pcc</i> ICMP5702_peg2552	AODT01000011.1	575421	574489	-	Arabinose operon regulatory protein AraC
<i>Pcc</i> ICMP5702_peg2553	AODT01000011.1	576471	575485	-	L-arabinose ABC transporter, permease protein AraH
<i>Pcc</i> ICMP5702_peg2554	AODT01000011.1	578013	576490	-	L-arabinose ABC transporter, ATP-binding protein AraG
<i>Pcc</i> ICMP5702_peg2555	AODT01000011.1	579108	578125	-	L-arabinose ABC transporter, substrate-binding protein AraF
<i>Pcc</i> ICMP5702_peg2556	AODT01000011.1	579481	581166	+	Ribulokinase (EC 2.7.1.16)
<i>Pcc</i> ICMP5702_peg2557	AODT01000011.1	581204	582709	+	L-arabinose isomerase (EC 5.3.1.4)
<i>Pcc</i> ICMP5702_peg2558	AODT01000011.1	582873	582733	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2559	AODT01000011.1	582983	583198	+	Cnu protein
<i>Pcc</i> ICMP5702_peg2560	AODT01000011.1	583415	583996	+	Electron transport complex protein RnfA
<i>Pcc</i> ICMP5702_peg2561	AODT01000011.1	583996	584574	+	Electron transport complex protein RnfB
<i>Pcc</i> ICMP5702_peg2562	AODT01000011.1	584567	586843	+	Electron transport complex protein RnfC

<i>Pcc</i> ICMP5702_peg2563	AODT01000011.1	586844	587899	+	Electron transport complex protein RnfD
<i>Pcc</i> ICMP5702_peg2564	AODT01000011.1	587910	588539	+	Electron transport complex protein RnfG
<i>Pcc</i> ICMP5702_peg2565	AODT01000011.1	588536	589243	+	Electron transport complex protein RnfE
<i>Pcc</i> ICMP5702_peg2566	AODT01000011.1	589240	589875	+	Endonuclease III (EC 4.2.99.18)
<i>Pcc</i> ICMP5702_peg2567	AODT01000011.1	590553	592070	+	Di-tripeptide/H ⁺ symporter DtpA
<i>Pcc</i> ICMP5702_peg2568	AODT01000011.1	593177	592203	-	Cys regulon transcriptional activator CysB
<i>Pcc</i> ICMP5702_peg2569	AODT01000011.1	593337	593504	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2570	AODT01000011.1	596157	593557	-	DNA topoisomerase I (EC 5.99.1.2)
<i>Pcc</i> ICMP5702_peg2571	AODT01000011.1	596354	596482	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2572	AODT01000011.1	596527	596796	+	Protein YciN
<i>Pcc</i> ICMP5702_peg2573	AODT01000011.1	597901	596855	-	Possible protease sohB (EC 3.4.21.-)
<i>Pcc</i> ICMP5702_peg2574	AODT01000011.1	598260	599021	+	Putative oxidoreductase
<i>Pcc</i> ICMP5702_peg2575	AODT01000011.1	599040	599630	+	Cob(I)alamin adenosyltransferase (EC 2.5.1.17)
<i>Pcc</i> ICMP5702_peg2576	AODT01000011.1	600596	599712	-	LSU rRNA pseudouridine(2605) synthase (EC 5.4.99.22)
<i>Pcc</i> ICMP5702_peg2577	AODT01000011.1	601395	600775	-	YciO protein, TsaC/YrdC paralog
<i>Pcc</i> ICMP5702_peg2578	AODT01000011.1	602410	601538	-	FIG00031715: Predicted metal-dependent phosphoesterases (PHP family)
<i>Pcc</i> ICMP5702_peg2579	AODT01000011.1	602767	604329	+	Anthranilate synthase, aminase component (EC 4.1.3.27)
<i>Pcc</i> ICMP5702_peg2580	AODT01000011.1	604329	604907	+	Anthranilate synthase, amidotransferase component (EC 4.1.3.27)
<i>Pcc</i> ICMP5702_peg2581	AODT01000011.1	604922	605989	+	Anthranilate phosphoribosyltransferase (EC 2.4.2.18)
<i>Pcc</i> ICMP5702_peg2582	AODT01000011.1	605997	607364	+	Indole-3-glycerol phosphate synthase (EC 4.1.1.48) / Phosphoribosylanthranilate isomerase (EC 5.3.1.24)
<i>Pcc</i> ICMP5702_peg2583	AODT01000011.1	607381	608571	+	Tryptophan synthase beta chain (EC 4.2.1.20)
<i>Pcc</i> ICMP5702_peg2584	AODT01000011.1	608571	609377	+	Tryptophan synthase alpha chain (EC 4.2.1.20)
<i>Pcc</i> ICMP5702_peg2585	AODT01000011.1	609764	610483	+	Oligogalacturonate-specific porin protein KdgM
<i>Pcc</i> ICMP5702_peg2586	AODT01000011.1	611250	610618	-	Outer membrane protein W precursor
<i>Pcc</i> ICMP5702_peg2587	AODT01000011.1	611507	611382	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2588	AODT01000011.1	611600	612352	+	Membrane protein YciC, linked to IspA
<i>Pcc</i> ICMP5702_peg2589	AODT01000011.1	612551	613120	+	Intracellular septation protein IspA
<i>Pcc</i> ICMP5702_peg2590	AODT01000011.1	613140	613562	+	Acyl-CoA thioesterase YciA, involved in membrane biogenesis
<i>Pcc</i> ICMP5702_peg2591	AODT01000011.1	614440	613685	-	TonB-ExbBD energy transducing system, TonB subunit
<i>Pcc</i> ICMP5702_peg2592	AODT01000011.1	614704	615000	+	YciL protein
<i>Pcc</i> ICMP5702_peg2593	AODT01000011.1	615132	616805	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg2594	AODT01000011.1	617046	616870	-	FIG00613881: Hypothetical protein
<i>Pcc</i> ICMP5702_peg2595	AODT01000011.1	617360	618820	+	Cardiolipin synthase, bacterial type ClsA
<i>Pcc</i> ICMP5702_peg2596	AODT01000011.1	618876	619199	+	dsDNA mimic protein, highly acidic
<i>Pcc</i> ICMP5702_peg2597	AODT01000011.1	620552	619518	-	Oligopeptide ABC transporter, ATP-binding protein OppF (TC 3.A.1.5.1)

<i>Pcc</i> ICMP5702_peg2598	AODT01000011.1	621544	620549	-	Oligopeptide ABC transporter, ATP-binding protein OppD (TC 3.A.1.5.1)
<i>Pcc</i> ICMP5702_peg2599	AODT01000011.1	622464	621556	-	Oligopeptide ABC transporter, permease protein OppC (TC 3.A.1.5.1)
<i>Pcc</i> ICMP5702_peg2600	AODT01000011.1	623396	622476	-	Oligopeptide ABC transporter, permease protein OppB (TC 3.A.1.5.1)
<i>Pcc</i> ICMP5702_peg2601	AODT01000011.1	625087	623450	-	Oligopeptide ABC transporter, substrate-binding protein OppA (TC 3.A.1.5.1)
<i>Pcc</i> ICMP5702_peg2602	AODT01000011.1	626949	625279	-	Oligopeptide ABC transporter, substrate-binding protein OppA (TC 3.A.1.5.1)
<i>Pcc</i> ICMP5702_peg2603	AODT01000011.1	627958	630633	+	Acetaldehyde dehydrogenase (EC 1.2.1.10) / Alcohol dehydrogenase (EC 1.1.1.1)
<i>Pcc</i> ICMP5702_peg2604	AODT01000011.1	631384	630788	-	Thymidine kinase (EC 2.7.1.21)
<i>Pcc</i> ICMP5702_peg2605	AODT01000011.1	631779	632186	+	DNA-binding protein H-NS
<i>Pcc</i> ICMP5702_peg2606	AODT01000011.1	633244	632333	-	UTP--glucose-1-phosphate uridylyltransferase (EC 2.7.7.9)
<i>Pcc</i> ICMP5702_peg2607	AODT01000011.1	634466	633450	-	Regulator of RpoS
<i>Pcc</i> ICMP5702_peg2608	AODT01000011.1	635490	634585	-	FIG00613342: Bacterial patatin-like phospholipase domain containing protein
<i>Pcc</i> ICMP5702_peg2609	AODT01000011.1	635623	636090	+	UPF0225 protein YchJ
<i>Pcc</i> ICMP5702_peg2610	AODT01000011.1	636174	637022	+	Formyltetrahydrofolate deformylase (EC 3.5.1.10)
<i>Pcc</i> ICMP5702_peg2611	AODT01000011.1	638052	637426	-	UPF0126 inner membrane protein YicG
<i>Pcc</i> ICMP5702_peg2612	AODT01000011.1	638480	639286	+	Exodeoxyribonuclease III (EC 3.1.11.2)
<i>Pcc</i> ICMP5702_peg2613	AODT01000011.1	639692	639402	-	Uncharacterized protein YnjH
<i>Pcc</i> ICMP5702_peg2614	AODT01000011.1	641614	639689	-	DNA topoisomerase III (EC 5.99.1.2)
<i>Pcc</i> ICMP5702_peg2615	AODT01000011.1	642262	641711	-	Putative NAD(P)H nitroreductase YdjA
<i>Pcc</i> ICMP5702_peg2616	AODT01000011.1	642547	644397	+	Signal peptide peptidase SppA (protease 4)
<i>Pcc</i> ICMP5702_peg2617	AODT01000011.1	644631	645650	+	L-asparaginase I, cytoplasmic (EC 3.5.1.1)
<i>Pcc</i> ICMP5702_peg2618	AODT01000011.1	645670	646317	+	Nicotinamidase (EC 3.5.1.19)
<i>Pcc</i> ICMP5702_peg2619	AODT01000011.1	646648	646370	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2620	AODT01000011.1	647199	646780	-	Peptide-methionine (R)-S-oxide reductase MsrB (EC 1.8.4.12)
<i>Pcc</i> ICMP5702_peg2621	AODT01000011.1	647544	648539	+	NAD-dependent glyceraldehyde-3-phosphate dehydrogenase (EC 1.2.1.12)
<i>Pcc</i> ICMP5702_peg2622	AODT01000011.1	648647	649516	+	Aldose 1-epimerase family protein YeaD
<i>Pcc</i> ICMP5702_peg2623	AODT01000011.1	650443	649592	-	Putative oxidoreductase YeaE, aldo/keto reductase family
<i>Pcc</i> ICMP5702_peg2624	AODT01000011.1	650580	650464	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2625	AODT01000011.1	651351	650602	-	MltA-interacting protein MipA
<i>Pcc</i> ICMP5702_peg2626	AODT01000011.1	651807	653741	+	Uncharacterized protein YeaG
<i>Pcc</i> ICMP5702_peg2627	AODT01000011.1	653751	655052	+	UPF0229 protein YeaH
<i>Pcc</i> ICMP5702_peg2628	AODT01000011.1	655191	655601	+	FIG00904844: Hypothetical protein
<i>Pcc</i> ICMP5702_peg2629	AODT01000011.1	655799	656998	+	Multidrug resistance transporter, Bcr/CflA family
<i>Pcc</i> ICMP5702_peg2630	AODT01000011.1	658274	657021	-	D-amino acid dehydrogenase (EC 1.4.99.6)
<i>Pcc</i> ICMP5702_peg2631	AODT01000011.1	658759	659739	+	6-phosphofructokinase (EC 2.7.1.11)
<i>Pcc</i> ICMP5702_peg2632	AODT01000011.1	659750	660043	+	PTS system, IIB component
<i>Pcc</i> ICMP5702_peg2633	AODT01000011.1	660057	661394	+	PTS system, IIC component, UlaA-type

<i>Pcc</i> ICMP5702_peg2634	AODT01000011.1	661439	661717	+	FIG00904613: Hypothetical protein
<i>Pcc</i> ICMP5702_peg2635	AODT01000011.1	661724	662161	+	PTS system, IIA component
<i>Pcc</i> ICMP5702_peg2636	AODT01000011.1	662158	662691	+	Putative kinase
<i>Pcc</i> ICMP5702_peg2637	AODT01000011.1	662728	663627	+	Tagatose 1,6-bisphosphate aldolase (EC 4.1.2.40)
<i>Pcc</i> ICMP5702_peg2638	AODT01000011.1	663884	665425	+	FIG004684: SpoVR-like protein
<i>Pcc</i> ICMP5702_peg2639	AODT01000011.1	666242	665523	-	Transcriptional regulator for fatty acid degradation FadR, GntR family
<i>Pcc</i> ICMP5702_peg2640	AODT01000011.1	666473	668053	+	Na ⁺ /H ⁺ antiporter NhaB
<i>Pcc</i> ICMP5702_peg2641	AODT01000011.1	668248	668778	+	Periplasmic thiol:disulfide oxidoreductase DsbB, required for DsbA reoxidation
<i>Pcc</i> ICMP5702_peg2642	AODT01000011.1	669051	668854	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2643	AODT01000011.1	669477	669262	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2644	AODT01000011.1	669864	669643	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2645	AODT01000011.1	670128	669925	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2646	AODT01000011.1	670661	670215	-	UPF0260 protein YcgN
<i>Pcc</i> ICMP5702_peg2647	AODT01000011.1	671437	670781	-	Uncharacterized fumarylacetoacetase-like protein YcgM
<i>Pcc</i> ICMP5702_peg2648	AODT01000011.1	672192	671905	-	Protein YcgL
<i>Pcc</i> ICMP5702_peg2649	AODT01000011.1	672299	672985	+	Septum site-determining protein MinC
<i>Pcc</i> ICMP5702_peg2650	AODT01000011.1	673006	673818	+	Septum site-determining protein MinD
<i>Pcc</i> ICMP5702_peg2651	AODT01000011.1	673822	674091	+	Cell division topological specificity factor MinE
<i>Pcc</i> ICMP5702_peg2652	AODT01000011.1	675435	674311	-	Ribonuclease D (EC 3.1.26.3)
<i>Pcc</i> ICMP5702_peg2653	AODT01000011.1	677365	675647	-	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)
<i>Pcc</i> ICMP5702_peg2654	AODT01000011.1	678162	677533	-	Uncharacterized lipoprotein YeaY
<i>Pcc</i> ICMP5702_peg2655	AODT01000011.1	678963	678262	-	tRNA threonylcarbamoyladenine biosynthesis protein TsaB
<i>Pcc</i> ICMP5702_peg2656	AODT01000011.1	680998	679079	-	DinG family ATP-dependent helicase YoaA
<i>Pcc</i> ICMP5702_peg2657	AODT01000011.1	681208	681552	+	RidA/YER057c/UK114 superfamily, group 2, YoaB-like protein
<i>Pcc</i> ICMP5702_peg2658	AODT01000011.1	681838	681590	-	UPF0181 protein YoaH
<i>Pcc</i> ICMP5702_peg2659	AODT01000011.1	681983	681870	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2660	AODT01000011.1	681982	683424	+	Para-aminobenzoate synthase, aminase component (EC 2.6.1.85)
<i>Pcc</i> ICMP5702_peg2661	AODT01000011.1	683421	684014	+	Uncharacterized Nudix hydrolase NudL
<i>Pcc</i> ICMP5702_peg2662	AODT01000011.1	684410	685774	+	L-serine dehydratase, beta subunit (EC 4.3.1.17) / L-serine dehydratase, alpha subunit (EC 4.3.1.17)
<i>Pcc</i> ICMP5702_peg2663	AODT01000011.1	687456	685900	-	UPF0053 inner membrane protein YoaE
<i>Pcc</i> ICMP5702_peg2664	AODT01000011.1	688027	688989	+	PTS system, mannose-specific IIA component (EC 2.7.1.191) / PTS system, mannose-specific IIB component (EC 2.7.1.191)
<i>Pcc</i> ICMP5702_peg2665	AODT01000011.1	689145	689942	+	PTS system, mannose-specific IIC component
<i>Pcc</i> ICMP5702_peg2666	AODT01000011.1	689957	690799	+	PTS system, mannose-specific IID component
<i>Pcc</i> ICMP5702_peg2667	AODT01000011.1	690867	691319	+	UPF0266 membrane protein YobD

<i>Pcc</i> ICMP5702_peg2668	AODT01000011.1	691744	692316	+	Putative manganese efflux pump MntP
<i>Pcc</i> ICMP5702_peg2669	AODT01000011.1	693211	692381	-	23S rRNA (guanine(745)-N(1))-methyltransferase (EC 2.1.1.187)
<i>Pcc</i> ICMP5702_peg2670	AODT01000011.1	693528	693319	-	Cold shock protein of CSP family => CspC (naming convention as in E.coli)
<i>Pcc</i> ICMP5702_peg2671	AODT01000011.1	693686	693570	-	Uncharacterized protein YobF
<i>Pcc</i> ICMP5702_peg2672	AODT01000011.1	694635	695549	+	Manganese ABC transporter, periplasmic-binding protein SitA
<i>Pcc</i> ICMP5702_peg2673	AODT01000011.1	695546	696436	+	Manganese ABC transporter, ATP-binding protein SitB
<i>Pcc</i> ICMP5702_peg2674	AODT01000011.1	696436	697299	+	Manganese ABC transporter, inner membrane permease protein SitC
<i>Pcc</i> ICMP5702_peg2675	AODT01000011.1	697296	698153	+	Manganese ABC transporter, inner membrane permease protein SitD
<i>Pcc</i> ICMP5702_peg2676	AODT01000011.1	698425	699285	+	Ribulosamine/erythrosamine 3-kinase potentially involved in protein deglycation
<i>Pcc</i> ICMP5702_peg2677	AODT01000011.1	699920	699372	-	putative membrane protein
<i>Pcc</i> ICMP5702_peg2678	AODT01000011.1	700107	700772	+	2-deoxyglucose-6-phosphate hydrolase (EC 3.1.3.68) @ Mannitol-1-phosphatase (EC 3.1.3.22) @ Sorbitol-6-phosphatase (EC 3.1.3.50)
<i>Pcc</i> ICMP5702_peg2679	AODT01000011.1	701206	700874	-	Pectin degradation protein KdgF
<i>Pcc</i> ICMP5702_peg2680	AODT01000011.1	701404	701285	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2681	AODT01000011.1	701595	701723	+	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17)
<i>Pcc</i> ICMP5702_peg2682	AODT01000011.1	701807	702568	+	2-dehydro-3-deoxy-D-gluconate 5-dehydrogenase (EC 1.1.1.127) @ 2-deoxy-D-gluconate 3-dehydrogenase (EC 1.1.1.125)
<i>Pcc</i> ICMP5702_peg2683	AODT01000011.1	702843	704474	+	Exopolygalacturonate lyase (EC 4.2.2.9)
<i>Pcc</i> ICMP5702_peg2684	AODT01000011.1	704522	705412	+	ABC transporter, permease protein 1 (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg2685	AODT01000011.1	705405	706310	+	ABC transporter, permease protein 2 (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg2686	AODT01000011.1	706324	707451	+	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg2687	AODT01000011.1	707467	708759	+	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg2688	AODT01000011.1	709007	709735	+	Oligogalacturonate-specific porin protein KdgM
<i>Pcc</i> ICMP5702_peg2689	AODT01000011.1	710080	711033	+	Endo-1,4-beta-xylanase (EC 3.2.1.8)
<i>Pcc</i> ICMP5702_peg2690	AODT01000011.1	711114	711689	+	Membrane-bound metal-dependent hydrolase YdjM, induced during SOS response
<i>Pcc</i> ICMP5702_peg2691	AODT01000011.1	711861	713255	+	L-cystine uptake protein TcyP, sodium:anion symporter family
<i>Pcc</i> ICMP5702_peg2692	AODT01000011.1	713682	713353	-	Osmotically-inducible lipoprotein E
<i>Pcc</i> ICMP5702_peg2693	AODT01000011.1	713908	714732	+	NAD synthetase (EC 6.3.1.5)
<i>Pcc</i> ICMP5702_peg2694	AODT01000011.1	714815	715708	+	Permease of the drug/metabolite transporter (DMT) superfamily
<i>Pcc</i> ICMP5702_peg2695	AODT01000011.1	715840	717558	+	Afflux ABC transporter, permease/ATP-binding protein YwjA
<i>Pcc</i> ICMP5702_peg2696	AODT01000011.1	717695	718120	+	Uncharacterized protein YgbA
<i>Pcc</i> ICMP5702_peg2697	AODT01000011.1	718478	718182	-	Integration host factor alpha subunit
<i>Pcc</i> ICMP5702_peg2698	AODT01000011.1	720870	718483	-	Phenylalanyl-tRNA synthetase beta chain (EC 6.1.1.20)
<i>Pcc</i> ICMP5702_peg2699	AODT01000011.1	721868	720885	-	Phenylalanyl-tRNA synthetase alpha chain (EC 6.1.1.20)
<i>Pcc</i> ICMP5702_peg2700	AODT01000011.1	722543	722187	-	LSU ribosomal protein L20p

<i>Pcc</i> ICMP5702_peg2701	AODT01000011.1	722784	722587	-	LSU ribosomal protein L35p
<i>Pcc</i> ICMP5702_peg2702	AODT01000011.1	723221	722880	-	Translation initiation factor 3
<i>Pcc</i> ICMP5702_peg2703	AODT01000011.1	725353	723425	-	Threonyl-tRNA synthetase (EC 6.1.1.3)
<i>Pcc</i> ICMP5702_peg2704	AODT01000011.1	727011	725611	-	Phenylalanine-specific permease
<i>Pcc</i> ICMP5702_peg2705	AODT01000011.1	727402	727139	-	Uncharacterized protein YebO
<i>Pcc</i> ICMP5702_peg2706	AODT01000011.1	728378	727587	-	Transcriptional regulator KdgR, KDG operon repressor
<i>Pcc</i> ICMP5702_peg2707	AODT01000011.1	729759	728593	-	Oligogalacturonate lyase (EC 4.2.2.6)
<i>Pcc</i> ICMP5702_peg2708	AODT01000011.1	730996	730115	-	Protease HtpX
<i>Pcc</i> ICMP5702_peg2709	AODT01000011.1	732007	731159	-	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)
<i>Pcc</i> ICMP5702_peg2710	AODT01000011.1	733375	732038	-	Glycerol-3-phosphate ABC transporter, substrate-binding protein UgpB
<i>Pcc</i> ICMP5702_peg2711	AODT01000011.1	734859	733636	-	Oxalate/formate antiporter
<i>Pcc</i> ICMP5702_peg2712	AODT01000011.1	735793	735044	-	Two-component transcriptional response regulator YpdB
<i>Pcc</i> ICMP5702_peg2713	AODT01000011.1	737535	735790	-	Sensor histidine kinase YpdA
<i>Pcc</i> ICMP5702_peg2714	AODT01000011.1	739866	737698	-	Sensory box/GGDEF family protein
<i>Pcc</i> ICMP5702_peg2715	AODT01000011.1	740517	740260	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2716	AODT01000011.1	740919	741653	+	Repressor protein CI
<i>Pcc</i> ICMP5702_peg2717	AODT01000011.1	742155	742505	+	Phage protein Mup21, positive regulator of late transcription protein C
<i>Pcc</i> ICMP5702_peg2718	AODT01000011.1	742965	744074	+	Hypothetical iron-sulfur cluster binding protein YccM
<i>Pcc</i> ICMP5702_peg2719	AODT01000011.1	745148	744270	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2720	AODT01000011.1	745585	745259	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2721	AODT01000011.1	747223	745970	-	Isocitrate dehydrogenase [NADP] (EC 1.1.1.42)
<i>Pcc</i> ICMP5702_peg2722	AODT01000011.1	747351	747980	+	LSU rRNA pseudouridine(2457) synthase (EC 5.4.99.20)
<i>Pcc</i> ICMP5702_peg2723	AODT01000011.1	747973	748419	+	Nudix-like NDP and NTP phosphohydrolase NudJ
<i>Pcc</i> ICMP5702_peg2724	AODT01000011.1	748559	749665	+	tRNA-specific 2-thiouridylase MnmA (EC 2.8.1.13)
<i>Pcc</i> ICMP5702_peg2725	AODT01000011.1	749668	750306	+	High frequency lysogenization protein HflD
<i>Pcc</i> ICMP5702_peg2726	AODT01000011.1	750436	751806	+	Adenylosuccinate lyase (EC 4.3.2.2) @ SAICAR lyase (EC 4.3.2.2)
<i>Pcc</i> ICMP5702_peg2727	AODT01000011.1	752049	752738	+	Transcriptional regulatory protein PhoP
<i>Pcc</i> ICMP5702_peg2728	AODT01000011.1	752735	754189	+	Sensor histidine kinase PhoQ (EC 2.7.13.3)
<i>Pcc</i> ICMP5702_peg2729	AODT01000011.1	754327	755448	+	LSU ribosomal protein L16p arginine hydroxylase
<i>Pcc</i> ICMP5702_peg2730	AODT01000011.1	756756	755524	-	Tripeptide aminopeptidase (EC 3.4.11.4)
<i>Pcc</i> ICMP5702_peg2731	AODT01000011.1	757127	758242	+	3.A.1.11.1)
<i>Pcc</i> ICMP5702_peg2732	AODT01000011.1	758226	759086	+	Spermidine/putrescine import ABC transporter permease protein PotB (TC 3.A.1.11.1)
<i>Pcc</i> ICMP5702_peg2733	AODT01000011.1	759083	759859	+	Spermidine/putrescine import ABC transporter permease protein PotC (TC 3.A.1.11.1)
					Spermidine/putrescine import ABC transporter substrate-binding protein PotD (TC
<i>Pcc</i> ICMP5702_peg2734	AODT01000011.1	760094	761137	+	3.A.1.11.1)
<i>Pcc</i> ICMP5702_peg2735	AODT01000011.1	761289	761981	+	Phospholipid-binding protein

<i>Pcc</i> ICMP5702_peg2736	AODT01000011.1	762026	762892	+	Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg2737	AODT01000011.1	765071	763056	-	Tail-specific protease precursor (EC 3.4.21.102)
<i>Pcc</i> ICMP5702_peg2738	AODT01000011.1	765849	765091	-	RNA chaperone ProQ
<i>Pcc</i> ICMP5702_peg2739	AODT01000011.1	766440	765934	-	Free methionine-(R)-sulfoxide reductase, contains GAF domain
<i>Pcc</i> ICMP5702_peg2740	AODT01000011.1	766722	768002	+	Inner membrane protein YebS
<i>Pcc</i> ICMP5702_peg2741	AODT01000011.1	768005	770644	+	Uncharacterized protein YebT
<i>Pcc</i> ICMP5702_peg2742	AODT01000011.1	770789	772243	+	16S rRNA (cytosine(1407)-C(5))-methyltransferase (EC 2.1.1.178)
<i>Pcc</i> ICMP5702_peg2743	AODT01000011.1	772366	772557	+	Uncharacterized protein YebW
<i>Pcc</i> ICMP5702_peg2744	AODT01000011.1	773272	772577	-	RNA binding S1 domain protein
<i>Pcc</i> ICMP5702_peg2745	AODT01000011.1	774379	773312	-	Malate dehydrogenase (EC 1.1.1.37)
<i>Pcc</i> ICMP5702_peg2746	AODT01000011.1	774615	775097	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2747	AODT01000011.1	775286	775140	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2748	AODT01000011.1	775922	775641	-	E.coli)
<i>Pcc</i> ICMP5702_peg2749	AODT01000011.1	776767	776414	-	Putative periplasmic or exported protein
<i>Pcc</i> ICMP5702_peg2750	AODT01000011.1	777558	777052	-	Bacterial non-heme ferritin (EC 1.16.3.2)
<i>Pcc</i> ICMP5702_peg2751	AODT01000011.1	777931	778161	+	DNA polymerase III theta subunit (EC 2.7.7.7)
<i>Pcc</i> ICMP5702_peg2752	AODT01000011.1	778325	778435	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2753	AODT01000011.1	780571	778520	-	Protease II (EC 3.4.21.83)
<i>Pcc</i> ICMP5702_peg2754	AODT01000011.1	780772	781950	+	Formate-dependent phosphoribosylglycinamide formyltransferase
<i>Pcc</i> ICMP5702_peg2755	AODT01000011.1	782646	782005	-	4-hydroxy-2-oxoglutarate aldolase (EC 4.1.3.16) @ 2-dehydro-3-deoxyphosphogluconate aldolase (EC 4.1.2.14)
<i>Pcc</i> ICMP5702_peg2756	AODT01000011.1	784294	782819	-	Glucose-6-phosphate 1-dehydrogenase (EC 1.1.1.49)
<i>Pcc</i> ICMP5702_peg2757	AODT01000011.1	784694	785563	+	Phosphogluconate repressor HexR, RpiR family
<i>Pcc</i> ICMP5702_peg2758	AODT01000011.1	785948	787390	+	Pyruvate kinase (EC 2.7.1.40)
<i>Pcc</i> ICMP5702_peg2759	AODT01000011.1	788486	787515	-	Lipid A biosynthesis myristoyltransferase (EC 2.3.1.243)
<i>Pcc</i> ICMP5702_peg2760	AODT01000011.1	790123	788801	-	Murein DD-endopeptidase MepM
<i>Pcc</i> ICMP5702_peg2761	AODT01000011.1	791155	790136	-	Zinc ABC transporter, substrate-binding protein ZnuA
<i>Pcc</i> ICMP5702_peg2762	AODT01000011.1	791233	791991	+	Zinc ABC transporter, ATP-binding protein ZnuC
<i>Pcc</i> ICMP5702_peg2763	AODT01000011.1	791988	792773	+	Zinc ABC transporter, permease protein ZnuB
<i>Pcc</i> ICMP5702_peg2764	AODT01000011.1	793830	792868	-	Catabolite control protein A
<i>Pcc</i> ICMP5702_peg2765	AODT01000011.1	794287	795615	+	PTS system, cellobiose-specific IIC component
<i>Pcc</i> ICMP5702_peg2766	AODT01000011.1	795782	796087	+	PTS system, cellobiose-specific IIA component (EC 2.7.1.205)
<i>Pcc</i> ICMP5702_peg2767	AODT01000011.1	796255	797634	+	Outer membrane porin KPN_04057/KPN_04724
<i>Pcc</i> ICMP5702_peg2768	AODT01000011.1	798720	797710	-	Holliday junction ATP-dependent DNA helicase RuvB (EC 3.6.4.12)
<i>Pcc</i> ICMP5702_peg2769	AODT01000011.1	799345	798728	-	Holliday junction ATP-dependent DNA helicase RuvA (EC 3.6.4.12)
<i>Pcc</i> ICMP5702_peg2770	AODT01000011.1	799958	799437	-	Crossover junction endodeoxyribonuclease RuvC (EC 3.1.22.4)

<i>Pcc</i> ICMP5702_peg2771	AODT01000011.1	800765	800022	-	Probable transcriptional regulatory protein YebC
<i>Pcc</i> ICMP5702_peg2772	AODT01000011.1	801256	800789	-	Dihydroneopterin triphosphate pyrophosphohydrolase type 2
<i>Pcc</i> ICMP5702_peg2773	AODT01000011.1	803030	801234	-	Aspartyl-tRNA synthetase (EC 6.1.1.12)
<i>Pcc</i> ICMP5702_peg2774	AODT01000011.1	803489	804709	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2775	AODT01000011.1	804785	805600	+	UPF0759 protein YecE
<i>Pcc</i> ICMP5702_peg2776	AODT01000011.1	805756	806151	+	Inner membrane protein YecN
<i>Pcc</i> ICMP5702_peg2777	AODT01000011.1	806307	807050	+	Carboxy-S-adenosyl-L-methionine synthase
<i>Pcc</i> ICMP5702_peg2778	AODT01000011.1	807047	808033	+	tRNA ho5U(34) carboxymethyltransferase
<i>Pcc</i> ICMP5702_peg2779	AODT01000011.1	808948	808190	-	Cytoplasmic copper homeostasis protein CutC
<i>Pcc</i> ICMP5702_peg2780	AODT01000011.1	809781	809233	-	Protein YecM
<i>Pcc</i> ICMP5702_peg2781	AODT01000011.1	810439	812169	+	Arginyl-tRNA synthetase (EC 6.1.1.19)
<i>Pcc</i> ICMP5702_peg2782	AODT01000011.1	813878	812343	-	Peptidoglycan lipid II flippase MurJ
<i>Pcc</i> ICMP5702_peg2783	AODT01000011.1	815001	814006	-	Virulence factor MviM
<i>Pcc</i> ICMP5702_peg2784	AODT01000011.1	815665	815027	-	Protein of unknown function YceH
<i>Pcc</i> ICMP5702_peg2785	AODT01000011.1	816259	815675	-	Ribosomal-protein-S5p-alanine acetyltransferase (EC 2.3.1.128)
<i>Pcc</i> ICMP5702_peg2786	AODT01000011.1	816575	817780	+	Multidrug resistance protein MdtH
<i>Pcc</i> ICMP5702_peg2787	AODT01000011.1	817963	818610	+	Glutaredoxin 2
<i>Pcc</i> ICMP5702_peg2788	AODT01000011.1	818810	819376	+	Uncharacterized lipoprotein yceB precursor
<i>Pcc</i> ICMP5702_peg2789	AODT01000011.1	820015	819434	-	Anaerobic respiratory reductase chaperone
<i>Pcc</i> ICMP5702_peg2790	AODT01000011.1	820814	820077	-	Putative hydrolase YcdX (EC 3.1.-.-)
<i>Pcc</i> ICMP5702_peg2791	AODT01000011.1	822858	821299	-	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg2792	AODT01000011.1	823069	823191	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2793	AODT01000011.1	823319	823462	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2794	AODT01000011.1	824288	823722	-	Uncharacterized lipoprotein YmbA
<i>Pcc</i> ICMP5702_peg2795	AODT01000011.1	825928	824288	-	Paraquat-inducible protein B
<i>Pcc</i> ICMP5702_peg2796	AODT01000011.1	827222	825915	-	Paraquat-inducible protein A
<i>Pcc</i> ICMP5702_peg2797	AODT01000011.1	829246	827318	-	Bis-ABC ATPase Uup
<i>Pcc</i> ICMP5702_peg2798	AODT01000011.1	831397	829250	-	23S rRNA (guanine(2445)-N(2))-methyltransferase (EC 2.1.1.173) / 23S rRNA (guanine(2069)-N(7))-methyltransferase (EC 2.1.1.264)
<i>Pcc</i> ICMP5702_peg2799	AODT01000011.1	831478	832581	+	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1
<i>Pcc</i> ICMP5702_peg2800	AODT01000011.1	833233	832646	-	Cell division protein ZapC
<i>Pcc</i> ICMP5702_peg2801	AODT01000011.1	834445	833435	-	Dihydroorotate dehydrogenase (quinone) (EC 1.3.5.2)
<i>Pcc</i> ICMP5702_peg2802	AODT01000011.1	837264	834649	-	Membrane alanine aminopeptidase N (EC 3.4.11.2)
<i>Pcc</i> ICMP5702_peg2803	AODT01000011.1	837434	837324	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2804	AODT01000011.1	837488	838693	+	Nicotinate phosphoribosyltransferase (EC 6.3.4.21)
<i>Pcc</i> ICMP5702_peg2805	AODT01000011.1	838886	840286	+	Asparaginyl-tRNA synthetase (EC 6.1.1.22)

<i>Pcc</i> ICMP5702_peg2806	AODT01000011.1	840582	841658	+	Outer membrane porin OmpF
<i>Pcc</i> ICMP5702_peg2807	AODT01000011.1	841949	843139	+	Aspartate aminotransferase (EC 2.6.1.1)
<i>Pcc</i> ICMP5702_peg2808	AODT01000011.1	843884	843237	-	Hypothetical metal-binding enzyme, YcbL homolog
<i>Pcc</i> ICMP5702_peg2809	AODT01000011.1	844515	843967	-	FIG001587: exported protein
<i>Pcc</i> ICMP5702_peg2810	AODT01000011.1	846433	844694	-	L,D-transpeptidase YcbB
<i>Pcc</i> ICMP5702_peg2811	AODT01000011.1	846861	846718	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2812	AODT01000011.1	851307	846868	-	Chromosome partition protein MukB
<i>Pcc</i> ICMP5702_peg2813	AODT01000011.1	852049	851327	-	Chromosome partition protein MukE
<i>Pcc</i> ICMP5702_peg2814	AODT01000011.1	853355	852030	-	Chromosome partition protein MukF
<i>Pcc</i> ICMP5702_peg2815	AODT01000011.1	854137	853352	-	tRNA uridine 5-oxyacetic acid(34) methyltransferase (EC 2.1.1.-)
<i>Pcc</i> ICMP5702_peg2816	AODT01000011.1	854305	855153	+	Membrane Protein Functionally coupled to the MukBEF Chromosome Partitioning Mechanism
<i>Pcc</i> ICMP5702_peg2817	AODT01000011.1	855998	855105	-	Uncharacterized protein YcbJ
<i>Pcc</i> ICMP5702_peg2818	AODT01000011.1	857513	856200	-	Pectate lyase L precursor (EC 4.2.2.2)
<i>Pcc</i> ICMP5702_peg2819	AODT01000011.1	858571	857819	-	3-deoxy-manno-octulosonate cytidyltransferase (EC 2.7.7.38)
<i>Pcc</i> ICMP5702_peg2820	AODT01000011.1	858750	858568	-	FIG002473: Protein YcaR in KDO2-Lipid A biosynthesis cluster
<i>Pcc</i> ICMP5702_peg2821	AODT01000011.1	859863	858862	-	Tetraacyldisaccharide 4'-kinase (EC 2.7.1.130)
<i>Pcc</i> ICMP5702_peg2822	AODT01000011.1	861653	859860	-	Lipid A export permease/ATP-binding protein MsbA
<i>Pcc</i> ICMP5702_peg2823	AODT01000011.1	863940	861646	-	DNA internalization-related competence protein ComEC/Rec2
<i>Pcc</i> ICMP5702_peg2824	AODT01000011.1	865097	864150	-	Choline binding ABC transport system substrate-binding protein ChoX
<i>Pcc</i> ICMP5702_peg2825	AODT01000011.1	866704	865097	-	Choline-sulfatase (EC 3.1.6.6)
<i>Pcc</i> ICMP5702_peg2826	AODT01000011.1	866748	867671	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg2827	AODT01000011.1	867782	868618	+	Glycine betaine/L-proline transport ATP-binding protein ProV (TC 3.A.1.12.1)
<i>Pcc</i> ICMP5702_peg2828	AODT01000011.1	868631	869461	+	Choline binding ABC transport system permease protein ChoW
<i>Pcc</i> ICMP5702_peg2829	AODT01000011.1	869914	869597	-	UPF0265 protein YeeX
<i>Pcc</i> ICMP5702_peg2830	AODT01000011.1	870806	870048	-	Iron compound ABC transporter, ATP-binding protein
<i>Pcc</i> ICMP5702_peg2831	AODT01000011.1	871810	870803	-	Iron compound ABC transporter, permease protein
<i>Pcc</i> ICMP5702_peg2832	AODT01000011.1	872759	871797	-	Iron compound ABC transporter, permease protein
<i>Pcc</i> ICMP5702_peg2833	AODT01000011.1	873747	872782	-	ABC transporter, substrate-binding protein (cluster 8, B12/iron complex)
<i>Pcc</i> ICMP5702_peg2834	AODT01000011.1	874011	873895	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2835	AODT01000011.1	874030	875457	+	Exodeoxyribonuclease I (EC 3.1.11.1)
<i>Pcc</i> ICMP5702_peg2836	AODT01000011.1	877077	875707	-	Low-affinity putrescine importer PlaP
<i>Pcc</i> ICMP5702_peg2837	AODT01000011.1	877227	877096	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2838	AODT01000011.1	878465	877701	-	Flagellar brake protein YcgR
<i>Pcc</i> ICMP5702_peg2839	AODT01000011.1	878501	878629	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2840	AODT01000011.1	879803	878898	-	Triphosphoribosyl-dephospho-CoA synthase (EC 2.4.2.52)

<i>Pcc</i> ICMP5702_peg2841	AODT01000011.1	880311	879781	-	Citrate lyase holo-[acyl-carrier-protein] synthase (EC 2.7.7.61)
<i>Pcc</i> ICMP5702_peg2842	AODT01000011.1	881863	880334	-	Citrate lyase alpha chain (EC 4.1.3.6)
<i>Pcc</i> ICMP5702_peg2843	AODT01000011.1	882792	881917	-	Citrate lyase beta chain (EC 4.1.3.6)
<i>Pcc</i> ICMP5702_peg2844	AODT01000011.1	883082	882792	-	Citrate lyase gamma chain, acyl carrier protein
<i>Pcc</i> ICMP5702_peg2845	AODT01000011.1	884170	883106	-	[Citrate [pro-3S]-lyase] ligase (EC 6.2.1.22)
<i>Pcc</i> ICMP5702_peg2846	AODT01000011.1	885142	884258	-	Fumarylacetoacetate hydrolase family protein
<i>Pcc</i> ICMP5702_peg2847	AODT01000011.1	886629	885259	-	Citrate-sodium symporter (TC 2.A.24.1.1)
<i>Pcc</i> ICMP5702_peg2848	AODT01000011.1	887049	888644	+	Tricarboxylate transport sensor protein TctE => Citrate response regulator CitA
<i>Pcc</i> ICMP5702_peg2849	AODT01000011.1	888737	889438	+	CitB
<i>Pcc</i> ICMP5702_peg2850	AODT01000011.1	889910	891844	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg2851	AODT01000011.1	892147	894099	+	Methyl-accepting chemotaxis protein
<i>Pcc</i> ICMP5702_peg2852	AODT01000011.1	895040	894204	-	Protein YeeZ
<i>Pcc</i> ICMP5702_peg2853	AODT01000011.1	895732	896631	+	ATP phosphoribosyltransferase (EC 2.4.2.17) => HisGI
<i>Pcc</i> ICMP5702_peg2854	AODT01000011.1	896637	897965	+	Histidinol dehydrogenase (EC 1.1.1.23)
<i>Pcc</i> ICMP5702_peg2855	AODT01000011.1	897962	899035	+	Histidinol-phosphate aminotransferase (EC 2.6.1.9)
<i>Pcc</i> ICMP5702_peg2856	AODT01000011.1	899051	900118	+	Histidinol-phosphatase (EC 3.1.3.15) / Imidazoleglycerol-phosphate dehydratase (EC 4.2.1.19)
<i>Pcc</i> ICMP5702_peg2857	AODT01000011.1	900118	900708	+	Imidazole glycerol phosphate synthase amidotransferase subunit HisH
<i>Pcc</i> ICMP5702_peg2858	AODT01000011.1	900715	901452	+	5.3.1.16)
<i>Pcc</i> ICMP5702_peg2859	AODT01000011.1	901434	902210	+	Imidazole glycerol phosphate synthase cyclase subunit
<i>Pcc</i> ICMP5702_peg2860	AODT01000011.1	902204	902836	+	Phosphoribosyl-AMP cyclohydrolase (EC 3.5.4.19) / Phosphoribosyl-ATP pyrophosphatase (EC 3.6.1.31)
<i>Pcc</i> ICMP5702_peg2861	AODT01000011.1	903280	902996	-	Integration host factor beta subunit
<i>Pcc</i> ICMP5702_peg2862	AODT01000011.1	905079	903370	-	SSU ribosomal protein S1p
<i>Pcc</i> ICMP5702_peg2863	AODT01000011.1	905837	905160	-	Cytidylate kinase (EC 2.7.4.25)
<i>Pcc</i> ICMP5702_peg2864	AODT01000011.1	905881	906051	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2865	AODT01000011.1	907348	906059	-	3-phosphoshikimate 1-carboxyvinyltransferase (EC 2.5.1.19)
<i>Pcc</i> ICMP5702_peg2866	AODT01000011.1	908515	907430	-	Phosphoserine aminotransferase (EC 2.6.1.52)
<i>Pcc</i> ICMP5702_peg2867	AODT01000011.1	908845	910608	+	Ribosomal protein S12p methylthiotransferase accessory factor YcaO
<i>Pcc</i> ICMP5702_peg2868	AODT01000011.1	910754	910879	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2869	AODT01000011.1	911048	911908	+	Formate efflux transporter FocA
<i>Pcc</i> ICMP5702_peg2870	AODT01000011.1	911966	914248	+	Pyruvate formate-lyase (EC 2.3.1.54)
<i>Pcc</i> ICMP5702_peg2871	AODT01000011.1	914518	915258	+	Pyruvate formate-lyase activating enzyme (EC 1.97.1.4)
<i>Pcc</i> ICMP5702_peg2872	AODT01000011.1	916917	915349	-	Hydantoinase/oxoprolinase family protein
<i>Pcc</i> ICMP5702_peg2873	AODT01000011.1	918037	916928	-	utilization
<i>Pcc</i> ICMP5702_peg2874	AODT01000011.1	919395	918064	-	Cytosine/purine/uracil/thiamine/allantoin permease family protein

<i>Pcc</i> ICMP5702_peg2875	AODT01000011.1	919669	920610	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg2876	AODT01000011.1	921795	920596	-	Hypothetical MFS-type transporter protein YcaD
<i>Pcc</i> ICMP5702_peg2877	AODT01000011.1	923361	922066	-	Seryl-tRNA synthetase (EC 6.1.1.11)
<i>Pcc</i> ICMP5702_peg2878	AODT01000011.1	924808	923465	-	Replication-associated recombination protein RarA
<i>Pcc</i> ICMP5702_peg2879	AODT01000011.1	925427	924816	-	Outer membrane lipoprotein carrier protein LolA
<i>Pcc</i> ICMP5702_peg2880	AODT01000011.1	929171	925677	-	DNA translocase FtsK
<i>Pcc</i> ICMP5702_peg2881	AODT01000011.1	929780	929286	-	Leucine-responsive regulatory protein, regulator for leucine (or Irp) regulon and high-affinity branched-chain amino acid transport system
<i>Pcc</i> ICMP5702_peg2882	AODT01000011.1	930366	931328	+	Thioredoxin reductase (EC 1.8.1.9)
<i>Pcc</i> ICMP5702_peg2883	AODT01000011.1	931566	933332	+	Efflux ABC transporter for glutathione/L-cysteine, essential for assembly of bd-type respiratory oxidases => CydD subunit
<i>Pcc</i> ICMP5702_peg2884	AODT01000011.1	933332	935071	+	Efflux ABC transporter for glutathione/L-cysteine, essential for assembly of bd-type respiratory oxidases => CydC subunit
<i>Pcc</i> ICMP5702_peg2885	AODT01000011.1	935105	935809	+	Leucyl/phenylalanyl-tRNA--protein transferase (EC 2.3.2.6)
<i>Pcc</i> ICMP5702_peg2886	AODT01000011.1	935923	936141	+	Translation initiation factor 1
<i>Pcc</i> ICMP5702_peg2887	AODT01000011.1	936279	937724	+	2.6.1.1)
<i>Pcc</i> ICMP5702_peg2888	AODT01000011.1	938204	937725	-	4-carboxymuconolactone decarboxylase domain/alkylhydroperoxidase AhpD family core domain protein
<i>Pcc</i> ICMP5702_peg2889	AODT01000011.1	940713	938440	-	ATP-dependent Clp protease ATP-binding subunit ClpA
<i>Pcc</i> ICMP5702_peg2890	AODT01000011.1	941063	940743	-	ATP-dependent Clp protease adaptor protein ClpS
<i>Pcc</i> ICMP5702_peg2891	AODT01000011.1	941486	941707	+	Cold shock protein of CSP family => CspD (naming convention as in E.coli)
<i>Pcc</i> ICMP5702_peg2892	AODT01000011.1	943489	941825	-	Predicted ATP-dependent endonuclease of the OLD family, YbjD subgroup
<i>Pcc</i> ICMP5702_peg2893	AODT01000011.1	943828	944730	+	Lysine exporter LysO
<i>Pcc</i> ICMP5702_peg2894	AODT01000011.1	944919	946571	+	Hydroxylamine reductase (EC 1.7.99.1)
<i>Pcc</i> ICMP5702_peg2895	AODT01000011.1	946711	947736	+	NADH oxidoreductase for hydroxylamine reductase
<i>Pcc</i> ICMP5702_peg2896	AODT01000011.1	947937	947797	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2897	AODT01000011.1	947938	949374	+	Putative nucleoside-diphosphate-sugar epimerase
<i>Pcc</i> ICMP5702_peg2898	AODT01000011.1	950198	949371	-	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28) @ 1,6-anhydro-N-acetylmuramyl-L-alanine amidase
<i>Pcc</i> ICMP5702_peg2899	AODT01000011.1	950576	950253	-	UPF0145 protein YbjQ
<i>Pcc</i> ICMP5702_peg2900	AODT01000011.1	950785	951534	+	Arginine ABC transporter, ATP-binding protein ArtP
<i>Pcc</i> ICMP5702_peg2901	AODT01000011.1	951555	952286	+	Arginine ABC transporter, substrate-binding protein ArtI
<i>Pcc</i> ICMP5702_peg2902	AODT01000011.1	952298	953014	+	Arginine ABC transporter, permease protein ArtQ
<i>Pcc</i> ICMP5702_peg2903	AODT01000011.1	953014	953682	+	Arginine ABC transporter, permease protein ArtM
<i>Pcc</i> ICMP5702_peg2904	AODT01000011.1	954011	954742	+	Arginine ABC transporter, substrate-binding protein ArtJ
<i>Pcc</i> ICMP5702_peg2905	AODT01000011.1	954985	954794	-	Hypothetical protein

<i>Pcc</i> ICMP5702_peg2906	AODT01000012.1	399	274	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2907	AODT01000012.1	1553	420	-	23S rRNA (uracil(747)-C(5))-methyltransferase (EC 2.1.1.189)
<i>Pcc</i> ICMP5702_peg2908	AODT01000012.1	2130	1678	-	Inner membrane protein YbjO
<i>Pcc</i> ICMP5702_peg2909	AODT01000012.1	3165	2320	-	Putrescine transport system permease protein PotI (TC 3.A.1.11.2)
<i>Pcc</i> ICMP5702_peg2910	AODT01000012.1	4127	3162	-	Putrescine transport system permease protein PotH (TC 3.A.1.11.2)
<i>Pcc</i> ICMP5702_peg2911	AODT01000012.1	5413	4142	-	Putrescine transport ATP-binding protein PotG (TC 3.A.1.11.2)
<i>Pcc</i> ICMP5702_peg2912	AODT01000012.1	6587	5478	-	Putrescine ABC transporter putrescine-binding protein PotF (TC 3.A.1.11.2)
<i>Pcc</i> ICMP5702_peg2913	AODT01000012.1	6775	6894	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2914	AODT01000012.1	7441	6959	-	Uncharacterized sensory transduction regulator YbjN
<i>Pcc</i> ICMP5702_peg2915	AODT01000012.1	7588	7722	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2916	AODT01000012.1	8630	7719	-	Ribosomal protein S6--L-glutamate ligase
<i>Pcc</i> ICMP5702_peg2917	AODT01000012.1	9366	8647	-	Oxygen-insensitive NADPH nitroreductase (EC 1.-.-.)
<i>Pcc</i> ICMP5702_peg2918	AODT01000012.1	9675	9941	+	Glutaredoxin 1
<i>Pcc</i> ICMP5702_peg2919	AODT01000012.1	10467	10033	-	Inner membrane protein YbjM
<i>Pcc</i> ICMP5702_peg2920	AODT01000012.1	10466	10609	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2921	AODT01000012.1	10736	12469	+	Putative transport protein YbjL
<i>Pcc</i> ICMP5702_peg2922	AODT01000012.1	12932	13600	+	Deoxyribose-phosphate aldolase (EC 4.1.2.4)
<i>Pcc</i> ICMP5702_peg2923	AODT01000012.1	13632	14405	+	Deoxyribose operon repressor DeoR
<i>Pcc</i> ICMP5702_peg2924	AODT01000012.1	15755	14550	-	D-alanyl-D-alanine carboxypeptidase (EC 3.4.16.4)
<i>Pcc</i> ICMP5702_peg2925	AODT01000012.1	16702	16043	-	Methionine ABC transporter permease protein
<i>Pcc</i> ICMP5702_peg2926	AODT01000012.1	17711	16695	-	Methionine ABC transporter ATP-binding protein
<i>Pcc</i> ICMP5702_peg2927	AODT01000012.1	18638	17793	-	Methionine ABC transporter substrate-binding protein
<i>Pcc</i> ICMP5702_peg2928	AODT01000012.1	18781	19398	+	Uncharacterized glutathione S-transferase-like protein
<i>Pcc</i> ICMP5702_peg2929	AODT01000012.1	20596	19430	-	Soluble aldose sugar dehydrogenase, PQQ-dependent (EC 1.1.5.-)
<i>Pcc</i> ICMP5702_peg2930	AODT01000012.1	20821	22134	+	Ribosomal protein S12p Asp88 (<i>E. coli</i>) methylthiotransferase (EC 2.8.4.4)
<i>Pcc</i> ICMP5702_peg2931	AODT01000012.1	22317	23096	+	SanA protein
<i>Pcc</i> ICMP5702_peg2932	AODT01000012.1	24281	23106	-	Uncharacterized protein YeiB
<i>Pcc</i> ICMP5702_peg2933	AODT01000012.1	24408	24295	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2934	AODT01000012.1	25082	24420	-	GTP cyclohydrolase I (EC 3.5.4.16) type 1
<i>Pcc</i> ICMP5702_peg2935	AODT01000012.1	25107	25298	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2936	AODT01000012.1	27110	25428	-	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg2937	AODT01000012.1	27812	28702	+	LysR family transcriptional regulator YneJ
<i>Pcc</i> ICMP5702_peg2938	AODT01000012.1	28816	29937	+	S-(hydroxymethyl)glutathione dehydrogenase (EC 1.1.1.284)
<i>Pcc</i> ICMP5702_peg2939	AODT01000012.1	29980	30822	+	S-formylglutathione hydrolase (EC 3.1.2.12)
<i>Pcc</i> ICMP5702_peg2940	AODT01000012.1	31004	31648	+	Glutathione S-transferase (EC 2.5.1.18)
<i>Pcc</i> ICMP5702_peg2941	AODT01000012.1	31887	32099	+	FIG00613542: Hypothetical protein

<i>Pcc</i> ICMP5702_peg2942	AODT01000012.1	33268	32180	-	Hydroxycarboxylate dehydrogenase (NADP+) HcxA
<i>Pcc</i> ICMP5702_peg2943	AODT01000012.1	33535	35046	+	5-methylthioribose ABC transporter, ATP-binding protein
<i>Pcc</i> ICMP5702_peg2944	AODT01000012.1	35043	36038	+	5-methylthioribose ABC transporter, permease protein
<i>Pcc</i> ICMP5702_peg2945	AODT01000012.1	36184	36068	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2946	AODT01000012.1	37447	36458	-	Hydroxypyruvate reductase (EC 1.1.1.81)
<i>Pcc</i> ICMP5702_peg2947	AODT01000012.1	40030	37910	-	TonB-dependent receptor; Outer membrane receptor for ferrienterochelin and colicins
<i>Pcc</i> ICMP5702_peg2948	AODT01000012.1	41823	40348	-	Lysine-specific permease
<i>Pcc</i> ICMP5702_peg2949	AODT01000012.1	42831	41959	-	Transcriptional regulator YeiE, LysR family
<i>Pcc</i> ICMP5702_peg2950	AODT01000012.1	42952	44025	+	UPF0324 inner membrane protein YeiH
<i>Pcc</i> ICMP5702_peg2951	AODT01000012.1	44094	44939	+	Endonuclease IV (EC 3.1.21.2)
<i>Pcc</i> ICMP5702_peg2952	AODT01000012.1	46762	45071	-	PTS system, inactive IIB catalytic domain / PTS system, fructose-specific IIB component (EC 2.7.1.202) / PTS system, fructose-specific IIC component
<i>Pcc</i> ICMP5702_peg2953	AODT01000012.1	47719	46781	-	1-phosphofructokinase (EC 2.7.1.56)
<i>Pcc</i> ICMP5702_peg2954	AODT01000012.1	48849	47716	-	PTS system, fructose-specific IIA component (EC 2.7.1.202) / Fructose-specific phosphocarrier protein HPr
<i>Pcc</i> ICMP5702_peg2955	AODT01000012.1	49027	48914	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2956	AODT01000012.1	49034	50362	+	Sugar efflux transporter B
<i>Pcc</i> ICMP5702_peg2957	AODT01000012.1	50627	50373	-	UPF0153 protein YeiW
<i>Pcc</i> ICMP5702_peg2958	AODT01000012.1	50790	51362	+	Elongation factor P-like protein
<i>Pcc</i> ICMP5702_peg2959	AODT01000012.1	51449	52435	+	Zinc-binding GTPase YeiR
<i>Pcc</i> ICMP5702_peg2960	AODT01000012.1	52474	53175	+	Lipid A 1-diphosphate synthase
<i>Pcc</i> ICMP5702_peg2961	AODT01000012.1	53498	54079	+	Murein DD-endopeptidase MepS @ Murein LD-carboxypeptidase (EC 3.4.17.13)
<i>Pcc</i> ICMP5702_peg2962	AODT01000012.1	54548	56356	+	ABC transporter, substrate-binding protein YejA
<i>Pcc</i> ICMP5702_peg2963	AODT01000012.1	56366	57463	+	ABC transporter, permease protein YejB
<i>Pcc</i> ICMP5702_peg2964	AODT01000012.1	57460	58485	+	ABC transporter, permease protein YejE
<i>Pcc</i> ICMP5702_peg2965	AODT01000012.1	58487	60103	+	ABC transporter, ATP-binding protein YejF
<i>Pcc</i> ICMP5702_peg2966	AODT01000012.1	60488	60144	-	Uncharacterized protein YejG
<i>Pcc</i> ICMP5702_peg2967	AODT01000012.1	62062	60872	-	Multidrug resistance transporter => Bicyclomycin resistance protein Bcr-1
<i>Pcc</i> ICMP5702_peg2968	AODT01000012.1	62798	62103	-	SSU rRNA pseudouridine(516) synthase (EC 5.4.99.19)
<i>Pcc</i> ICMP5702_peg2969	AODT01000012.1	63023	63262	+	FIG00613847: Hypothetical protein
<i>Pcc</i> ICMP5702_peg2970	AODT01000012.1	63265	65043	+	ATP-dependent RNA helicase YejH
<i>Pcc</i> ICMP5702_peg2971	AODT01000012.1	65179	65463	+	LSU ribosomal protein L25p
<i>Pcc</i> ICMP5702_peg2972	AODT01000012.1	65563	66711	+	putative membrane protein
<i>Pcc</i> ICMP5702_peg2973	AODT01000012.1	67796	66789	-	Nucleoid-associated protein NdpA
<i>Pcc</i> ICMP5702_peg2974	AODT01000012.1	68038	68268	+	UPF0352 protein YejL
<i>Pcc</i> ICMP5702_peg2975	AODT01000012.1	68283	70031	+	Inner membrane protein YejM, alkaline phosphatase superfamily

<i>Pcc</i> ICMP5702_peg2976	AODT01000012.1	70404	71633	+	Phage integrase
<i>Pcc</i> ICMP5702_peg2977	AODT01000012.1	71917	72558	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2978	AODT01000012.1	72551	72754	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2979	AODT01000012.1	73217	75640	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2980	AODT01000012.1	76323	76126	-	Putative DNA-binding protein
<i>Pcc</i> ICMP5702_peg2981	AODT01000012.1	77262	76408	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2982	AODT01000012.1	77843	77505	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2983	AODT01000012.1	78062	78193	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2984	AODT01000012.1	79519	78650	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2985	AODT01000012.1	80099	79656	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2986	AODT01000012.1	80200	80892	+	Phage integrase
<i>Pcc</i> ICMP5702_peg2987	AODT01000012.1	81039	81230	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2988	AODT01000012.1	81620	81261	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2989	AODT01000012.1	82392	81922	-	DNA gyrase inhibitory protein
<i>Pcc</i> ICMP5702_peg2990	AODT01000012.1	83263	82541	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2991	AODT01000012.1	83837	83508	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg2992	AODT01000012.1	84440	83904	-	Rhodanese-domain-containing inner membrane protein YgaP
<i>Pcc</i> ICMP5702_peg2993	AODT01000012.1	84845	86245	+	Uncharacterized transporter YeeO
<i>Pcc</i> ICMP5702_peg2994	AODT01000012.1	87458	86289	-	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg2995	AODT01000012.1	88259	87744	-	Outer membrane protein X precursor
<i>Pcc</i> ICMP5702_peg2996	AODT01000012.1	88636	89523	+	Threonine/homoserine exporter RhtA
<i>Pcc</i> ICMP5702_peg2997	AODT01000012.1	90062	89511	-	Uncharacterized protein PA4799
<i>Pcc</i> ICMP5702_peg2998	AODT01000012.1	90421	90924	+	DNA protection during starvation protein
<i>Pcc</i> ICMP5702_peg2999	AODT01000012.1	91315	92061	+	Glutamine ABC transporter, substrate-binding protein GlnH
<i>Pcc</i> ICMP5702_peg3000	AODT01000012.1	92179	92748	+	Glutamine ABC transporter, permease protein GlnP
<i>Pcc</i> ICMP5702_peg3001	AODT01000012.1	92745	93467	+	Glutamine ABC transporter, ATP-binding protein GlnQ
<i>Pcc</i> ICMP5702_peg3002	AODT01000012.1	95387	93519	-	Putative peptidase
<i>Pcc</i> ICMP5702_peg3003	AODT01000012.1	96441	95473	-	Anthranilate phosphoribosyltransferase-like protein
<i>Pcc</i> ICMP5702_peg3004	AODT01000012.1	97186	96551	-	Phage DNA invertase
<i>Pcc</i> ICMP5702_peg3005	AODT01000013.1	61	189	+	Phage tail fiber protein
<i>Pcc</i> ICMP5702_peg3006	AODT01000013.1	306	1349	+	Phage tail fiber protein GpH
<i>Pcc</i> ICMP5702_peg3007	AODT01000013.1	1349	1969	+	Tail fiber assembly protein
<i>Pcc</i> ICMP5702_peg3008	AODT01000013.1	2495	1971	-	Phage tail fiber assembly protein
<i>Pcc</i> ICMP5702_peg3009	AODT01000013.1	3216	2497	-	Phage tail fiber protein
<i>Pcc</i> ICMP5702_peg3010	AODT01000013.1	4631	3354	-	Phage tail fiber Mup49, S
<i>Pcc</i> ICMP5702_peg3011	AODT01000013.1	5215	4634	-	Phage tail formation protein GpI

<i>Pcc</i> ICMP5702_peg3012	AODT01000013.1	6311	5208	-	Phage protein Mup47, W
<i>Pcc</i> ICMP5702_peg3013	AODT01000013.1	6649	6302	-	Phage baseplate assembly protein
<i>Pcc</i> ICMP5702_peg3014	AODT01000013.1	7289	6708	-	Phage baseplate assembly protein V
<i>Pcc</i> ICMP5702_peg3015	AODT01000013.1	8446	7286	-	Phage tail formation protein GpD
<i>Pcc</i> ICMP5702_peg3016	AODT01000013.1	8646	8434	-	Phage tail protein GpX
<i>Pcc</i> ICMP5702_peg3017	AODT01000013.1	9565	8636	-	Phage tail protein U
<i>Pcc</i> ICMP5702_peg3018	AODT01000013.1	11976	9565	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3019	AODT01000013.1	12612	12292	-	Phage tail protein E
<i>Pcc</i> ICMP5702_peg3020	AODT01000013.1	13048	12752	-	soluble [2Fe-2S] ferredoxin
<i>Pcc</i> ICMP5702_peg3021	AODT01000013.1	13629	13105	-	Phage tail tube protein FII
<i>Pcc</i> ICMP5702_peg3022	AODT01000013.1	15056	13629	-	Phage tail sheath monomer GpFI
<i>Pcc</i> ICMP5702_peg3023	AODT01000013.1	15243	15046	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3024	AODT01000013.1	15584	15240	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3025	AODT01000013.1	15657	15785	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3026	AODT01000013.1	16264	15953	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3027	AODT01000013.1	16586	16257	-	putative membrane protein
<i>Pcc</i> ICMP5702_peg3028	AODT01000013.1	17250	16576	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3029	AODT01000013.1	17851	17240	-	putative lytic murein transglycosylase precursor
<i>Pcc</i> ICMP5702_peg3030	AODT01000013.1	18182	17853	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3031	AODT01000013.1	19769	18402	-	Type I secretion outer membrane protein, TolC family @ ABC-type protease exporter, outer membrane component PrtF/AprF
<i>Pcc</i> ICMP5702_peg3032	AODT01000013.1	21100	19772	-	Type I secretion membrane fusion protein, HlyD family @ ABC-type protease exporter, membrane fusion protein (MFP) family component PrtE/AprE
<i>Pcc</i> ICMP5702_peg3033	AODT01000013.1	22855	21128	-	Type I secretion system ATPase @ ABC-type protease exporter, ATP-binding component PrtD/AprD
<i>Pcc</i> ICMP5702_peg3034	AODT01000013.1	23235	22873	-	Alkaline proteinase inhibitor precursor
<i>Pcc</i> ICMP5702_peg3035	AODT01000013.1	24720	23290	-	Secreted alkaline metalloproteinase (EC 3.4.24.-), PrtA/B/C/G homolog
<i>Pcc</i> ICMP5702_peg3036	AODT01000013.1	25138	24962	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3037	AODT01000013.1	27341	25242	-	ATP-dependent helicase DinG/Rad3
<i>Pcc</i> ICMP5702_peg3038	AODT01000013.1	27521	28366	+	Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg3039	AODT01000013.1	28419	29066	+	Threonine efflux protein
<i>Pcc</i> ICMP5702_peg3040	AODT01000013.1	29203	29310	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3041	AODT01000013.1	29951	29412	-	Isopentenyl-diphosphate Delta-isomerase (EC 5.3.3.2)
<i>Pcc</i> ICMP5702_peg3042	AODT01000013.1	32358	30052	-	Periplasmic beta-glucosidase (EC 3.2.1.21)
<i>Pcc</i> ICMP5702_peg3043	AODT01000013.1	32556	32440	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3044	AODT01000013.1	32752	33438	+	Glutathione S-transferase

<i>Pcc</i> ICMP5702_peg3045	AODT01000013.1	34460	33513	-	Murein-DD-endopeptidase (EC 3.4.99.-)
<i>Pcc</i> ICMP5702_peg3046	AODT01000013.1	35121	34603	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3047	AODT01000013.1	35559	35200	-	Polyferredoxin
<i>Pcc</i> ICMP5702_peg3048	AODT01000013.1	36159	35617	-	Adenylate cyclase (EC 4.6.1.1)
<i>Pcc</i> ICMP5702_peg3049	AODT01000013.1	37091	36543	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3050	AODT01000013.1	38055	37108	-	Homocysteine S-methyltransferase (EC 2.1.1.10)
<i>Pcc</i> ICMP5702_peg3051	AODT01000013.1	39460	38048	-	S-methylmethionine permease
<i>Pcc</i> ICMP5702_peg3052	AODT01000013.1	40743	39811	-	tRNA-dihydrouridine(16) synthase
<i>Pcc</i> ICMP5702_peg3053	AODT01000013.1	40956	41627	+	Epoxyqueuosine reductase (EC 1.17.99.6) QueH
<i>Pcc</i> ICMP5702_peg3054	AODT01000013.1	43273	41678	-	Possible tripeptide-binding ABC transporter, periplasmic substrate-binding component
<i>Pcc</i> ICMP5702_peg3055	AODT01000013.1	43468	44697	+	Tripeptide aminopeptidase (EC 3.4.11.4)
<i>Pcc</i> ICMP5702_peg3056	AODT01000013.1	45612	44740	-	Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg3057	AODT01000013.1	45728	46627	+	Permease of the drug/metabolite transporter (DMT) superfamily
<i>Pcc</i> ICMP5702_peg3058	AODT01000014.1	1479	397	-	Maltose/maltodextrin transport ATP-binding protein MalK (EC 3.6.3.19)
<i>Pcc</i> ICMP5702_peg3059	AODT01000014.1	1972	3204	+	Maltodextrin ABC transporter, substrate-binding protein MdxE
<i>Pcc</i> ICMP5702_peg3060	AODT01000014.1	3305	4609	+	Maltodextrin ABC transporter, permease protein MdxF
<i>Pcc</i> ICMP5702_peg3061	AODT01000014.1	4622	5470	+	Maltodextrin ABC transporter, permease protein MdxG
<i>Pcc</i> ICMP5702_peg3062	AODT01000014.1	5506	6720	+	Arabinogalactan endo-1,4-beta-galactanase (EC 3.2.1.89)
<i>Pcc</i> ICMP5702_peg3063	AODT01000014.1	6767	8827	+	beta-galactosidase (EC 3.2.1.23)
<i>Pcc</i> ICMP5702_peg3064	AODT01000014.1	8979	9320	+	Phosphotransferase system EIIB, cysteine phosphorylation domain
<i>Pcc</i> ICMP5702_peg3065	AODT01000014.1	9642	9526	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3066	AODT01000014.1	10692	9727	-	Aldo/keto reductase, SCO4109 family
<i>Pcc</i> ICMP5702_peg3067	AODT01000014.1	10950	12146	+	Na ⁺ dependent nucleoside transporter NupC
<i>Pcc</i> ICMP5702_peg3068	AODT01000014.1	12392	13627	+	Multidrug efflux system MdtABC-ToIC, membrane fusion component MdtA
<i>Pcc</i> ICMP5702_peg3069	AODT01000014.1	13627	16749	+	Multidrug efflux system MdtABC-ToIC, inner-membrane proton/drug antiporter MdtB (RND type)
<i>Pcc</i> ICMP5702_peg3070	AODT01000014.1	16746	19826	+	Multidrug efflux system MdtABC-ToIC, inner-membrane proton/drug antiporter MdtC (RND type)
<i>Pcc</i> ICMP5702_peg3071	AODT01000014.1	20250	21650	+	Uncharacterized transporter MdtD of major facilitator superfamily (MFS)
<i>Pcc</i> ICMP5702_peg3072	AODT01000014.1	21658	23025	+	Sensory histidine kinase BaeS
<i>Pcc</i> ICMP5702_peg3073	AODT01000014.1	23051	23779	+	Response regulator BaeR
<i>Pcc</i> ICMP5702_peg3074	AODT01000014.1	23813	24454	+	Xenobiotic acyltransferase XAT family
<i>Pcc</i> ICMP5702_peg3075	AODT01000014.1	24508	25059	+	Acetyltransferase, GNAT family
<i>Pcc</i> ICMP5702_peg3076	AODT01000014.1	25427	26386	+	Glutathione S-transferase, omega (EC 2.5.1.18)
<i>Pcc</i> ICMP5702_peg3077	AODT01000014.1	26600	27961	+	Uncharacterized protease YegQ
<i>Pcc</i> ICMP5702_peg3078	AODT01000014.1	28297	28142	-	Hypothetical protein

<i>Pcc</i> ICMP5702_peg3079	AODT01000014.1	28376	29275	+	Lipid kinase YegS
<i>Pcc</i> ICMP5702_peg3080	AODT01000014.1	29711	29304	-	PsiE protein
<i>Pcc</i> ICMP5702_peg3081	AODT01000014.1	30693	29890	-	Hydroxymethylpyrimidine phosphate kinase ThiD (EC 2.7.4.7)
<i>Pcc</i> ICMP5702_peg3082	AODT01000014.1	31478	30690	-	Hydroxyethylthiazole kinase (EC 2.7.1.50)
<i>Pcc</i> ICMP5702_peg3083	AODT01000014.1	31776	32795	+	Cinnamyl alcohol dehydrogenase/reductase (EC 1.1.1.195) @ Alcohol dehydrogenase (EC 1.1.1.1)
<i>Pcc</i> ICMP5702_peg3084	AODT01000014.1	32949	33872	+	GGDEF domain protein
<i>Pcc</i> ICMP5702_peg3085	AODT01000014.1	33839	34000	+	Alcohol dehydrogenase (EC 1.1.1.1)
<i>Pcc</i> ICMP5702_peg3086	AODT01000014.1	34881	34063	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3087	AODT01000014.1	35844	35077	-	Putative transmembrane protein
<i>Pcc</i> ICMP5702_peg3088	AODT01000014.1	36304	35918	-	probable ring-cleaving dioxygenase PA0880
<i>Pcc</i> ICMP5702_peg3089	AODT01000014.1	36518	37420	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg3090	AODT01000014.1	38210	37437	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3091	AODT01000014.1	38614	39744	+	Choloylglycine hydrolase (EC 3.5.1.24)
<i>Pcc</i> ICMP5702_peg3092	AODT01000014.1	39946	41991	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3093	AODT01000014.1	42447	42139	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3094	AODT01000014.1	43107	42487	-	FMN-dependent NADH-azoreductase (EC 1.7.1.6)
<i>Pcc</i> ICMP5702_peg3095	AODT01000014.1	43915	43142	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3096	AODT01000014.1	44082	45110	+	Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg3097	AODT01000014.1	45216	46673	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3098	AODT01000014.1	47141	46926	-	Ner-like regulatory protein
<i>Pcc</i> ICMP5702_peg3099	AODT01000014.1	47248	47478	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3100	AODT01000014.1	47549	47785	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3101	AODT01000014.1	47805	48503	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3102	AODT01000014.1	49108	48656	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3103	AODT01000014.1	49381	49112	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3104	AODT01000014.1	49703	50041	+	COG3636: Predicted transcriptional regulator
<i>Pcc</i> ICMP5702_peg3105	AODT01000014.1	50109	50333	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3106	AODT01000014.1	52196	50358	-	Putative DNA helicase
<i>Pcc</i> ICMP5702_peg3107	AODT01000014.1	54303	52210	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3108	AODT01000014.1	54553	54437	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3109	AODT01000014.1	56208	54631	-	GMP synthase [glutamine-hydrolyzing], amidotransferase subunit (EC 6.3.5.2) / GMP synthase [glutamine-hydrolyzing], ATP pyrophosphatase subunit (EC 6.3.5.2)
<i>Pcc</i> ICMP5702_peg3110	AODT01000014.1	57793	56327	-	Inosine-5'-monophosphate dehydrogenase (EC 1.1.1.205) / CBS domain
<i>Pcc</i> ICMP5702_peg3111	AODT01000014.1	57965	59359	+	Exodeoxyribonuclease VII large subunit (EC 3.1.11.6)
<i>Pcc</i> ICMP5702_peg3112	AODT01000014.1	59588	60631	+	Extracellular metalloprotease precursor (EC 3.4.24.-)

<i>Pcc</i> ICMP5702_peg3113	AODT01000014.1	60628	60975	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3114	AODT01000014.1	61205	60981	-	Uncharacterized protein YfgJ
<i>Pcc</i> ICMP5702_peg3115	AODT01000014.1	61651	61208	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3116	AODT01000014.1	62723	61764	-	Possible AEC family malate permease
<i>Pcc</i> ICMP5702_peg3117	AODT01000014.1	64284	62797	-	GTP-binding protein EngA
<i>Pcc</i> ICMP5702_peg3118	AODT01000014.1	65608	64427	-	Outer membrane beta-barrel assembly protein BamB
<i>Pcc</i> ICMP5702_peg3119	AODT01000014.1	66239	65619	-	UPF0070 protein YfgM
<i>Pcc</i> ICMP5702_peg3120	AODT01000014.1	67527	66253	-	Histidyl-tRNA synthetase (EC 6.1.1.21)
<i>Pcc</i> ICMP5702_peg3121	AODT01000014.1	68786	67665	-	(E)-4-hydroxy-3-methylbut-2-enyl-diphosphate synthase (flavodoxin) (EC 1.17.7.3)
<i>Pcc</i> ICMP5702_peg3122	AODT01000014.1	69825	68827	-	Cytoskeleton protein RodZ
<i>Pcc</i> ICMP5702_peg3123	AODT01000014.1	70612	69815	-	Type IV pilus biogenesis protein PilF
<i>Pcc</i> ICMP5702_peg3124	AODT01000014.1	72058	70802	-	23S rRNA (adenine(2503)-C(2))-methyltransferase @ tRNA (adenine(37)-C(2))-methyltransferase (EC 2.1.1.192)
<i>Pcc</i> ICMP5702_peg3125	AODT01000014.1	72728	72300	-	Nucleoside diphosphate kinase (EC 2.7.4.6)
<i>Pcc</i> ICMP5702_peg3126	AODT01000014.1	72987	73130	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3127	AODT01000014.1	73284	74864	+	PTS system, maltose and glucose-specific IIC component / PTS system, maltose and glucose-specific IIB component (EC 2.7.1.208)
<i>Pcc</i> ICMP5702_peg3128	AODT01000014.1	74878	76239	+	Maltose-6'-phosphate glucosidase (EC 3.2.1.122)
<i>Pcc</i> ICMP5702_peg3129	AODT01000014.1	76343	77212	+	3-mercaptopyruvate sulfurtransferase (EC 2.8.1.2)
<i>Pcc</i> ICMP5702_peg3130	AODT01000014.1	77254	78042	+	Transcriptional regulator, RpiR family
<i>Pcc</i> ICMP5702_peg3131	AODT01000014.1	78871	78077	-	Protein SseB
<i>Pcc</i> ICMP5702_peg3132	AODT01000014.1	80231	78924	-	Peptidase B (EC 3.4.11.23)
<i>Pcc</i> ICMP5702_peg3133	AODT01000014.1	80646	80446	-	Protein IscX, believed to be involved in assembly of Fe-S clusters
<i>Pcc</i> ICMP5702_peg3134	AODT01000014.1	81003	80668	-	Ferredoxin, 2Fe-2S
<i>Pcc</i> ICMP5702_peg3135	AODT01000014.1	82855	81005	-	Chaperone protein HscA
<i>Pcc</i> ICMP5702_peg3136	AODT01000014.1	83449	82931	-	Chaperone protein HscB
<i>Pcc</i> ICMP5702_peg3137	AODT01000014.1	83844	83521	-	Iron-sulfur cluster assembly iron binding protein IscA
<i>Pcc</i> ICMP5702_peg3138	AODT01000014.1	84311	83925	-	Iron-sulfur cluster assembly scaffold protein IscU
<i>Pcc</i> ICMP5702_peg3139	AODT01000014.1	85550	84336	-	Cysteine desulfurase (EC 2.8.1.7) => IscS
<i>Pcc</i> ICMP5702_peg3140	AODT01000014.1	86296	85802	-	Iron-sulfur cluster regulator IscR
<i>Pcc</i> ICMP5702_peg3141	AODT01000014.1	87141	86416	-	tRNA (cytidine(32)/uridine(32)-2'-O)-methyltransferase (EC 2.1.1.200)
<i>Pcc</i> ICMP5702_peg3142	AODT01000014.1	87277	88080	+	Inositol-1-monophosphatase (EC 3.1.3.25)
<i>Pcc</i> ICMP5702_peg3143	AODT01000014.1	88236	89354	+	ABC transporter, substrate-binding protein (cluster 8, B12/iron complex)
<i>Pcc</i> ICMP5702_peg3144	AODT01000014.1	89361	90443	+	ABC transporter, permease protein (cluster 8, B12/iron complex)
<i>Pcc</i> ICMP5702_peg3145	AODT01000014.1	90440	91240	+	ABC transporter, ATP-binding protein (cluster 8, B12/iron complex)
<i>Pcc</i> ICMP5702_peg3146	AODT01000014.1	91689	91366	-	FIG00904755: Hypothetical protein

<i>Pcc</i> ICMP5702_peg3147	AODT01000014.1	93441	91774	-	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg3148	AODT01000014.1	93566	93438	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3149	AODT01000014.1	93818	93678	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3150	AODT01000014.1	95015	93888	-	ABC transporter, substrate-binding protein (cluster 8, B12/iron complex)
<i>Pcc</i> ICMP5702_peg3151	AODT01000014.1	96237	95134	-	Nickel/cobalt efflux system STM2551
<i>Pcc</i> ICMP5702_peg3152	AODT01000014.1	96836	96228	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3153	AODT01000014.1	98091	96931	-	Probable 3-phenylpropionic acid transporter
<i>Pcc</i> ICMP5702_peg3154	AODT01000014.1	99612	98359	-	Serine hydroxymethyltransferase (EC 2.1.2.1)
<i>Pcc</i> ICMP5702_peg3155	AODT01000014.1	99973	101163	+	Flavohemoglobin / Nitric oxide dioxygenase (EC 1.14.12.17)
<i>Pcc</i> ICMP5702_peg3156	AODT01000014.1	101658	103298	+	rhamnogalacturonan acetyltransferase
<i>Pcc</i> ICMP5702_peg3157	AODT01000014.1	103397	104503	+	Pectinesterase (EC 3.1.1.11)
<i>Pcc</i> ICMP5702_peg3158	AODT01000014.1	104899	104561	-	Nitrogen regulatory protein P-II
<i>Pcc</i> ICMP5702_peg3159	AODT01000014.1	106373	105036	-	Transcriptional response regulatory protein GlrR
<i>Pcc</i> ICMP5702_peg3160	AODT01000014.1	107221	106370	-	Uncharacterized protein YfhG
<i>Pcc</i> ICMP5702_peg3161	AODT01000014.1	108676	107240	-	Sensor histidine kinase GlrK
<i>Pcc</i> ICMP5702_peg3162	AODT01000014.1	108943	109065	+	Hypothetical protein
					Phosphoribosylformylglycinamide synthase, synthetase subunit (EC 6.3.5.3) / Phosphoribosylformylglycinamide synthase, glutamine amidotransferase subunit (EC 6.3.5.3)
<i>Pcc</i> ICMP5702_peg3163	AODT01000014.1	113284	109397	-	
<i>Pcc</i> ICMP5702_peg3164	AODT01000014.1	113564	115009	+	Membrane-bound lytic murein transglycosylase F (EC 4.2.2.n1)
<i>Pcc</i> ICMP5702_peg3165	AODT01000014.1	115662	115156	-	tRNA-specific adenosine-34 deaminase (EC 3.5.4.33)
<i>Pcc</i> ICMP5702_peg3166	AODT01000014.1	116368	115730	-	Phosphatidylglycerophosphatase C (EC 3.1.3.27)
<i>Pcc</i> ICMP5702_peg3167	AODT01000014.1	117326	116400	-	N-acetylmuramic acid 6-phosphate etherase (EC 4.2.1.126)
<i>Pcc</i> ICMP5702_peg3168	AODT01000014.1	117479	118168	+	T1SS associated transglutaminase-like cysteine proteinase LapP
<i>Pcc</i> ICMP5702_peg3169	AODT01000014.1	118178	120130	+	Membrane bound c-di-GMP receptor LapD
<i>Pcc</i> ICMP5702_peg3170	AODT01000014.1	120618	120274	-	Tryptophan synthase (indole-salvaging) (EC 4.2.1.122)
<i>Pcc</i> ICMP5702_peg3171	AODT01000014.1	135080	120684	-	T1SS secreted agglutinin RTX @ RTX toxins and related Ca ²⁺ -binding proteins
<i>Pcc</i> ICMP5702_peg3172	AODT01000014.1	135169	135306	+	Hypothetical protein
					Type I secretion outer membrane protein, TolC family @ Type I secretion system, outer membrane component LapE
<i>Pcc</i> ICMP5702_peg3173	AODT01000014.1	135463	136815	+	
<i>Pcc</i> ICMP5702_peg3174	AODT01000014.1	136894	139143	+	Type I secretion system ATPase @ Type I secretion system ATPase, LssB family LapB
					Type I secretion membrane fusion protein, HlyD family @ Type I secretion system, membrane fusion protein LapC
<i>Pcc</i> ICMP5702_peg3175	AODT01000014.1	139130	140491	+	
<i>Pcc</i> ICMP5702_peg3176	AODT01000014.1	142047	140533	-	Membrane bound c-di-GMP receptor LapD
<i>Pcc</i> ICMP5702_peg3177	AODT01000014.1	143470	142835	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3178	AODT01000014.1	144097	144357	+	Uncharacterized ferredoxin-like protein YfhL

<i>Pcc</i> ICMP5702_peg3179	AODT01000014.1	144756	144376	-	Holo-[acyl-carrier-protein] synthase (EC 2.7.8.7)
<i>Pcc</i> ICMP5702_peg3180	AODT01000014.1	145487	144756	-	Pyridoxine 5'-phosphate synthase (EC 2.6.99.2)
<i>Pcc</i> ICMP5702_peg3181	AODT01000014.1	146305	145568	-	DNA recombination and repair protein RecO
<i>Pcc</i> ICMP5702_peg3182	AODT01000014.1	147222	146317	-	GTP-binding protein Era
<i>Pcc</i> ICMP5702_peg3183	AODT01000014.1	147899	147219	-	Ribonuclease III (EC 3.1.26.3)
<i>Pcc</i> ICMP5702_peg3184	AODT01000014.1	149155	148190	-	Signal peptidase I (EC 3.4.21.89)
<i>Pcc</i> ICMP5702_peg3185	AODT01000014.1	151070	149172	-	Translation elongation factor LepA
<i>Pcc</i> ICMP5702_peg3186	AODT01000014.1	151720	151268	-	Sigma factor RpoE regulatory protein RseC
<i>Pcc</i> ICMP5702_peg3187	AODT01000014.1	152679	151717	-	Sigma factor RpoE negative regulatory protein RseB precursor
<i>Pcc</i> ICMP5702_peg3188	AODT01000014.1	153329	152679	-	Sigma factor RpoE negative regulatory protein RseA
<i>Pcc</i> ICMP5702_peg3189	AODT01000014.1	153964	153389	-	RNA polymerase sigma factor RpoE
<i>Pcc</i> ICMP5702_peg3190	AODT01000014.1	154297	155964	+	L-aspartate oxidase (EC 1.4.3.16)
<i>Pcc</i> ICMP5702_peg3191	AODT01000014.1	156781	156035	-	tRNA(1)(Val) (adenine(37)-N(6))-methyltransferase (EC 2.1.1.223)
<i>Pcc</i> ICMP5702_peg3192	AODT01000014.1	156916	158241	+	ATP-dependent RNA helicase SrmB
<i>Pcc</i> ICMP5702_peg3193	AODT01000014.1	158695	158312	-	Autonomous glycyl radical cofactor
<i>Pcc</i> ICMP5702_peg3194	AODT01000014.1	159072	159758	+	Uracil-DNA glycosylase, family 1 (EC 3.2.2.27)
<i>Pcc</i> ICMP5702_peg3195	AODT01000014.1	160383	161252	+	IroE protein
<i>Pcc</i> ICMP5702_peg3196	AODT01000014.1	162737	161322	-	Glutamyl-tRNA synthetase (EC 6.1.1.17)
<i>Pcc</i> ICMP5702_peg3197	AODT01000014.1	165008	163902	-	FMN oxidoreductase
<i>Pcc</i> ICMP5702_peg3198	AODT01000014.1	165212	166261	+	Oxidoreductase
<i>Pcc</i> ICMP5702_peg3199	AODT01000014.1	166346	166927	+	Transcriptional regulator, AcrR family
<i>Pcc</i> ICMP5702_peg3200	AODT01000014.1	167273	167707	+	putative membrane protein
<i>Pcc</i> ICMP5702_peg3201	AODT01000014.1	168781	167789	-	Sulfate and thiosulfate import ATP-binding protein CysA (EC 3.6.3.25)
<i>Pcc</i> ICMP5702_peg3202	AODT01000014.1	169652	168771	-	Sulfate transport system permease protein CysW
<i>Pcc</i> ICMP5702_peg3203	AODT01000014.1	170477	169665	-	Sulfate transport system permease protein CysT
<i>Pcc</i> ICMP5702_peg3204	AODT01000014.1	171644	170634	-	Sulfate and thiosulfate binding protein CysP
<i>Pcc</i> ICMP5702_peg3205	AODT01000014.1	173181	171985	-	Sugar diacid utilization regulator SdaR
<i>Pcc</i> ICMP5702_peg3206	AODT01000014.1	174823	173375	-	HtrA protease/chaperone protein
<i>Pcc</i> ICMP5702_peg3207	AODT01000014.1	176524	175013	-	Deoxyguanosinetriphosphate triphosphohydrolase (EC 3.1.5.1), subgroup 1
<i>Pcc</i> ICMP5702_peg3208	AODT01000014.1	176646	177344	+	5'-methylthioadenosine nucleosidase (EC 3.2.2.16) @ S-adenosylhomocysteine nucleosidase (EC 3.2.2.9)
<i>Pcc</i> ICMP5702_peg3209	AODT01000014.1	177350	178177	+	Vitamin B12 ABC transporter, substrate-binding protein BtuF
<i>Pcc</i> ICMP5702_peg3210	AODT01000014.1	178409	178687	+	FIG00634617: Hypothetical protein
<i>Pcc</i> ICMP5702_peg3211	AODT01000014.1	179184	178837	-	Iron-sulfur cluster insertion protein ErpA
<i>Pcc</i> ICMP5702_peg3212	AODT01000014.1	179452	180732	+	Glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8)
<i>Pcc</i> ICMP5702_peg3213	AODT01000014.1	180892	181515	+	Uncharacterized glutathione S-transferase-like protein

<i>Pcc</i> ICMP5702_peg3214	AODT01000014.1	182990	181530	-	DNA-binding transcriptional regulator, MocR family / aminotransferase domain
<i>Pcc</i> ICMP5702_peg3215	AODT01000014.1	183127	183717	+	Transporter, LysE family
<i>Pcc</i> ICMP5702_peg3216	AODT01000014.1	185778	183760	-	Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), permease component FhuB
					Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), periplasmic substrate binding protein FhuD
<i>Pcc</i> ICMP5702_peg3217	AODT01000014.1	186697	185771	-	
<i>Pcc</i> ICMP5702_peg3218	AODT01000014.1	187511	186714	-	Ferric hydroxamate ABC transporter (TC 3.A.1.14.3), ATP-binding protein FhuC
<i>Pcc</i> ICMP5702_peg3219	AODT01000014.1	190587	188107	-	Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
<i>Pcc</i> ICMP5702_peg3220	AODT01000014.1	193152	190690	-	ATP-dependent helicase HrpB
<i>Pcc</i> ICMP5702_peg3221	AODT01000014.1	193245	193775	+	2'-5' RNA ligase
<i>Pcc</i> ICMP5702_peg3222	AODT01000014.1	193810	194514	+	Sugar fermentation stimulation protein SfsA
<i>Pcc</i> ICMP5702_peg3223	AODT01000014.1	194782	195237	+	RNA polymerase-binding transcription factor DksA
<i>Pcc</i> ICMP5702_peg3224	AODT01000014.1	195366	196298	+	Glutamyl-Q tRNA(Asp) synthetase
<i>Pcc</i> ICMP5702_peg3225	AODT01000014.1	196492	197850	+	Poly(A) polymerase (EC 2.7.7.19)
<i>Pcc</i> ICMP5702_peg3226	AODT01000014.1	197850	198395	+	2-amino-4-hydroxy-6-hydroxymethylidihydropteridine pyrophosphokinase (EC 2.7.6.3)
<i>Pcc</i> ICMP5702_peg3227	AODT01000014.1	198501	199298	+	3-methyl-2-oxobutanoate hydroxymethyltransferase (EC 2.1.2.11)
<i>Pcc</i> ICMP5702_peg3228	AODT01000014.1	199362	200216	+	Pantoate--beta-alanine ligase (EC 6.3.2.1)
<i>Pcc</i> ICMP5702_peg3229	AODT01000014.1	200234	200614	+	Aspartate 1-decarboxylase (EC 4.1.1.11)
<i>Pcc</i> ICMP5702_peg3230	AODT01000014.1	201447	200677	-	Uncharacterized efflux ABC transporter, permease protein YadH
<i>Pcc</i> ICMP5702_peg3231	AODT01000014.1	202382	201444	-	Uncharacterized efflux ABC transporter, ATP-binding protein YadG
<i>Pcc</i> ICMP5702_peg3232	AODT01000014.1	202716	203357	+	Carbonic anhydrase, beta class (EC 4.2.1.1)
<i>Pcc</i> ICMP5702_peg3233	AODT01000014.1	203995	203417	-	Hypoxanthine-guanine phosphoribosyltransferase (EC 2.4.2.8)
<i>Pcc</i> ICMP5702_peg3234	AODT01000014.1	204103	204534	+	Acetyltransferase, GNAT family
<i>Pcc</i> ICMP5702_peg3235	AODT01000014.1	205620	204535	-	ABC-type spermidine/putrescine transport systems, ATPase components
<i>Pcc</i> ICMP5702_peg3236	AODT01000014.1	207247	205625	-	Ferric iron ABC transporter, permease protein
<i>Pcc</i> ICMP5702_peg3237	AODT01000014.1	207329	207505	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3238	AODT01000014.1	207542	207889	+	Predicted chaperone lipoprotein YacC, potentially involved in protein secretion
<i>Pcc</i> ICMP5702_peg3239	AODT01000014.1	207998	208861	+	Spermidine synthase (EC 2.5.1.16)
<i>Pcc</i> ICMP5702_peg3240	AODT01000014.1	208907	209701	+	S-adenosylmethionine decarboxylase proenzyme (EC 4.1.1.50), prokaryotic class 1A
<i>Pcc</i> ICMP5702_peg3241	AODT01000014.1	210217	210456	+	class Ib
<i>Pcc</i> ICMP5702_peg3242	AODT01000014.1	210466	210873	+	Ribonucleotide reduction protein NrdI
<i>Pcc</i> ICMP5702_peg3243	AODT01000014.1	210852	213032	+	Ribonucleotide reductase of class Ib (aerobic), alpha subunit (EC 1.17.4.1)
<i>Pcc</i> ICMP5702_peg3244	AODT01000014.1	213057	214019	+	Ribonucleotide reductase of class Ib (aerobic), beta subunit (EC 1.17.4.1)
<i>Pcc</i> ICMP5702_peg3245	AODT01000014.1	215115	214378	-	DNA polymerase III epsilon subunit (EC 2.7.7.7)
<i>Pcc</i> ICMP5702_peg3246	AODT01000014.1	215172	215636	+	Ribonuclease HI (EC 3.1.26.4)
<i>Pcc</i> ICMP5702_peg3247	AODT01000014.1	216366	215656	-	FIG005121: SAM-dependent methyltransferase (EC 2.1.1.-)
<i>Pcc</i> ICMP5702_peg3248	AODT01000014.1	216410	217165	+	Hydroxyacylglutathione hydrolase (EC 3.1.2.6)

<i>Pcc</i> ICMP5702_peg3249	AODT01000014.1	217251	218609	+	Membrane-bound lytic murein transglycosylase D
<i>Pcc</i> ICMP5702_peg3250	AODT01000014.1	219465	218677	-	UPF0294 protein YafD
<i>Pcc</i> ICMP5702_peg3251	AODT01000015.1	3108	532	-	Chaperone protein ClpB (ATP-dependent unfoldase)
<i>Pcc</i> ICMP5702_peg3252	AODT01000015.1	3967	3242	-	FIG00003370: Multicopper polyphenol oxidase
<i>Pcc</i> ICMP5702_peg3253	AODT01000015.1	4988	4011	-	LSU rRNA pseudouridine(1911/1915/1917) synthase (EC 5.4.99.23)
<i>Pcc</i> ICMP5702_peg3254	AODT01000015.1	5123	5857	+	Outer membrane beta-barrel assembly protein BamD
<i>Pcc</i> ICMP5702_peg3255	AODT01000015.1	6180	6518	+	Ribosome-associated inhibitor A
<i>Pcc</i> ICMP5702_peg3256	AODT01000015.1	6867	8027	+	Chorismate mutase I (EC 5.4.99.5) / Prephenate dehydratase (EC 4.2.1.51)
					Chorismate mutase I (EC 5.4.99.5) / Cyclohexadienyl dehydrogenase (EC 1.3.1.12)(EC
<i>Pcc</i> ICMP5702_peg3257	AODT01000015.1	9230	8109	-	1.3.1.43)
<i>Pcc</i> ICMP5702_peg3258	AODT01000015.1	10310	9237	-	2-keto-3-deoxy-D-arabino-heptulosonate-7-phosphate synthase I alpha (EC 2.5.1.54)
<i>Pcc</i> ICMP5702_peg3259	AODT01000015.1	10560	11276	+	Two-component transcriptional response regulator BtsR
<i>Pcc</i> ICMP5702_peg3260	AODT01000015.1	11323	11670	+	Uncharacterized protein YfiL
<i>Pcc</i> ICMP5702_peg3261	AODT01000015.1	11933	12871	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3262	AODT01000015.1	14375	13317	-	Phage integrase
<i>Pcc</i> ICMP5702_peg3263	AODT01000015.1	15001	14396	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3264	AODT01000015.1	15877	15014	-	Phage repressor protein cI
<i>Pcc</i> ICMP5702_peg3265	AODT01000015.1	15999	16334	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3266	AODT01000015.1	16373	16882	+	Phage activator protein cII
<i>Pcc</i> ICMP5702_peg3267	AODT01000015.1	16896	17084	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3268	AODT01000015.1	17278	17108	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3269	AODT01000015.1	17411	17587	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3270	AODT01000015.1	17584	18084	+	Phage replication protein GpB
<i>Pcc</i> ICMP5702_peg3271	AODT01000015.1	18147	18395	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3272	AODT01000015.1	18395	18703	+	Phage Orf81 protein
<i>Pcc</i> ICMP5702_peg3273	AODT01000015.1	18703	18927	+	Putative transcriptional regulator DksA, TraR, DnaK (ACLAME 75)
<i>Pcc</i> ICMP5702_peg3274	AODT01000015.1	18924	19937	+	Uncharacterized 37.8 kDa protein in gpa 5'region
<i>Pcc</i> ICMP5702_peg3275	AODT01000015.1	19934	22231	+	Phage replication protein GpA, endonuclease
<i>Pcc</i> ICMP5702_peg3276	AODT01000015.1	22234	22629	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3277	AODT01000015.1	22629	22967	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3278	AODT01000015.1	23126	23347	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3279	AODT01000015.1	24688	23669	-	Phage portal vertex protein GpQ
<i>Pcc</i> ICMP5702_peg3280	AODT01000015.1	25434	24685	-	Phage terminase, ATPase subunit GpP
<i>Pcc</i> ICMP5702_peg3281	AODT01000015.1	27200	25431	-	Phage terminase, ATPase subunit GpP
<i>Pcc</i> ICMP5702_peg3282	AODT01000015.1	27340	28194	+	Phage capsid scaffolding protein GpO
<i>Pcc</i> ICMP5702_peg3283	AODT01000015.1	28242	29354	+	Phage major capsid protein GpN

<i>Pcc</i> ICMP5702_peg3284	AODT01000015.1	29358	30017	+	Phage terminase, endonuclease subunit GpM
<i>Pcc</i> ICMP5702_peg3285	AODT01000015.1	30109	30612	+	Phage head completion-stabilization protein GpL
<i>Pcc</i> ICMP5702_peg3286	AODT01000015.1	30612	30815	+	Phage tail protein GpX
<i>Pcc</i> ICMP5702_peg3287	AODT01000015.1	30818	31027	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3288	AODT01000015.1	31011	31520	+	Phage lysozyme R (EC 3.2.1.17)
<i>Pcc</i> ICMP5702_peg3289	AODT01000015.1	31517	31960	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3290	AODT01000015.1	32050	32505	+	Phage tail completion protein GpR
<i>Pcc</i> ICMP5702_peg3291	AODT01000015.1	32498	32950	+	Phage tail completion protein GpS
<i>Pcc</i> ICMP5702_peg3292	AODT01000015.1	33050	33682	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3293	AODT01000015.1	33675	33872	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3294	AODT01000015.1	34258	33890	-	Secreted protein Hcp
<i>Pcc</i> ICMP5702_peg3295	AODT01000015.1	34423	35127	+	Phage baseplate assembly protein GpV
<i>Pcc</i> ICMP5702_peg3296	AODT01000015.1	35124	35468	+	Phage baseplate assembly protein GpW
<i>Pcc</i> ICMP5702_peg3297	AODT01000015.1	35473	36381	+	Phage baseplate assembly protein GpJ
<i>Pcc</i> ICMP5702_peg3298	AODT01000015.1	36374	36985	+	Phage tail formation protein GpI
<i>Pcc</i> ICMP5702_peg3299	AODT01000015.1	36982	39465	+	Phage tail fiber protein GpH
<i>Pcc</i> ICMP5702_peg3300	AODT01000015.1	39704	39561	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3301	AODT01000015.1	39753	40922	+	Phage tail sheath monomer GpFI
<i>Pcc</i> ICMP5702_peg3302	AODT01000015.1	40937	41458	+	Phage major tail tube protein GpFII
<i>Pcc</i> ICMP5702_peg3303	AODT01000015.1	41525	41821	+	Phage tail protein GpE
<i>Pcc</i> ICMP5702_peg3304	AODT01000015.1	41836	41955	+	Phage P2 GpE family protein
<i>Pcc</i> ICMP5702_peg3305	AODT01000015.1	41948	44776	+	Phage tail length tape-measure protein GpT
<i>Pcc</i> ICMP5702_peg3306	AODT01000015.1	44778	45263	+	Phage tail protein GpU
<i>Pcc</i> ICMP5702_peg3307	AODT01000015.1	45260	46420	+	Phage tail formation protein GpD
<i>Pcc</i> ICMP5702_peg3308	AODT01000015.1	46541	46428	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3309	AODT01000015.1	47235	46888	-	LSU ribosomal protein L19p
<i>Pcc</i> ICMP5702_peg3310	AODT01000015.1	48054	47299	-	tRNA (guanine(37)-N(1))-methyltransferase (EC 2.1.1.228)
<i>Pcc</i> ICMP5702_peg3311	AODT01000015.1	48641	48093	-	16S rRNA processing protein RimM
<i>Pcc</i> ICMP5702_peg3312	AODT01000015.1	48908	48660	-	SSU ribosomal protein S16p
<i>Pcc</i> ICMP5702_peg3313	AODT01000015.1	50427	49066	-	Signal recognition particle protein Ffh
<i>Pcc</i> ICMP5702_peg3314	AODT01000015.1	50433	50573	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3315	AODT01000015.1	50597	51391	+	Inner membrane protein YpjD
<i>Pcc</i> ICMP5702_peg3316	AODT01000015.1	51976	51461	-	S-ribosylhomocysteine lyase (EC 4.4.1.21) @ Autoinducer-2 production protein LuxS
<i>Pcc</i> ICMP5702_peg3317	AODT01000015.1	53682	52129	-	Glutamate--cysteine ligase (EC 6.3.2.2)
<i>Pcc</i> ICMP5702_peg3318	AODT01000015.1	54193	53765	-	putative membrane protein
<i>Pcc</i> ICMP5702_peg3319	AODT01000015.1	54756	54190	-	Fructose-1-phosphate phosphatase YqaB (EC 3.1.3.-)

<i>Pcc</i> ICMP5702_peg3320	AODT01000015.1	56224	56039	-	Carbon storage regulator
<i>Pcc</i> ICMP5702_peg3321	AODT01000015.1	56492	56361	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3322	AODT01000015.1	59176	56549	-	Alanyl-tRNA synthetase (EC 6.1.1.7)
<i>Pcc</i> ICMP5702_peg3323	AODT01000015.1	59809	59315	-	Regulatory protein RecX
<i>Pcc</i> ICMP5702_peg3324	AODT01000015.1	60928	59855	-	RecA protein
<i>Pcc</i> ICMP5702_peg3325	AODT01000015.1	61530	61036	-	Nicotinamide-nucleotide amidase (EC 3.5.1.42)
<i>Pcc</i> ICMP5702_peg3326	AODT01000015.1	62102	61767	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3327	AODT01000015.1	62542	62426	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3328	AODT01000015.1	62584	63072	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3329	AODT01000015.1	63155	63829	+	UPF0056 inner membrane protein MarC
<i>Pcc</i> ICMP5702_peg3330	AODT01000015.1	64009	65607	+	Putative two-component response regulator and GGDEF family protein YeaJ
<i>Pcc</i> ICMP5702_peg3331	AODT01000015.1	67064	65874	-	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg3332	AODT01000015.1	68067	67186	-	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg3333	AODT01000015.1	68283	68918	+	Glutaredoxin 2
<i>Pcc</i> ICMP5702_peg3334	AODT01000015.1	69629	69207	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3335	AODT01000015.1	71104	69764	-	N-glycosyltransferase
<i>Pcc</i> ICMP5702_peg3336	AODT01000015.1	71967	71116	-	PvcB protein, related to amino acid oxidizing enzymes
<i>Pcc</i> ICMP5702_peg3337	AODT01000015.1	72432	72022	-	PvcA protein, related to known isonitrile synthases
<i>Pcc</i> ICMP5702_peg3338	AODT01000015.1	73575	72586	-	Mobile element protein
<i>Pcc</i> ICMP5702_peg3339	AODT01000015.1	73784	73629	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3340	AODT01000016.1	654	82	-	PvcA protein, related to known isonitrile synthases
<i>Pcc</i> ICMP5702_peg3341	AODT01000016.1	1798	1433	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3342	AODT01000016.1	2395	2057	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3343	AODT01000016.1	2634	2494	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3344	AODT01000016.1	3224	3364	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3345	AODT01000016.1	3761	3432	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3346	AODT01000016.1	4726	3764	-	Rhs-family protein
<i>Pcc</i> ICMP5702_peg3347	AODT01000016.1	5605	4739	-	Rhs-family protein
<i>Pcc</i> ICMP5702_peg3348	AODT01000016.1	5585	5761	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3349	AODT01000016.1	6193	5822	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3350	AODT01000016.1	11319	6202	-	Rhs-family protein
<i>Pcc</i> ICMP5702_peg3351	AODT01000016.1	12257	11340	-	FIG00613785: Hypothetical protein
<i>Pcc</i> ICMP5702_peg3352	AODT01000016.1	13210	12254	-	FIG00614279: Hypothetical protein
<i>Pcc</i> ICMP5702_peg3353	AODT01000016.1	14148	13369	-	Ankyrin-like protein
<i>Pcc</i> ICMP5702_peg3354	AODT01000016.1	15518	14148	-	T6SS PAAR-repeat protein / RhaS protein
<i>Pcc</i> ICMP5702_peg3355	AODT01000016.1	17564	15528	-	VgrG protein

<i>Pcc</i> ICMP5702_peg3356	AODT01000016.1	18279	17761	-	T6SS component Hcp
<i>Pcc</i> ICMP5702_peg3357	AODT01000016.1	18664	18843	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3358	AODT01000016.1	20255	18903	-	FIG00613524: Hypothetical protein
<i>Pcc</i> ICMP5702_peg3359	AODT01000016.1	21723	20287	-	Type VI secretion-related protein VasL
<i>Pcc</i> ICMP5702_peg3360	AODT01000016.1	25338	21772	-	T6SS component TssM (IcmF/VasK)
<i>Pcc</i> ICMP5702_peg3361	AODT01000016.1	26787	25363	-	T6SS component TssA (ImpA)
<i>Pcc</i> ICMP5702_peg3362	AODT01000016.1	27359	26799	-	Type VI secretion protein VasI
<i>Pcc</i> ICMP5702_peg3363	AODT01000016.1	28897	27359	-	T6SS sigma-54-dependent regulator VasH
<i>Pcc</i> ICMP5702_peg3364	AODT01000016.1	31497	28900	-	T6SS AAA+ chaperone ClpV (TssH)
<i>Pcc</i> ICMP5702_peg3365	AODT01000016.1	32287	31511	-	T6SS outer membrane component TssL (ImpK/VasF)
<i>Pcc</i> ICMP5702_peg3366	AODT01000016.1	33640	32303	-	T6SS component TssK (ImpJ/VasE)
<i>Pcc</i> ICMP5702_peg3367	AODT01000016.1	34164	33643	-	T6SS secretion lipoprotein TssJ (VasD)
<i>Pcc</i> ICMP5702_peg3368	AODT01000016.1	35384	34164	-	T6SS forkhead associated domain protein Impl/VasC
<i>Pcc</i> ICMP5702_peg3369	AODT01000016.1	36385	35387	-	T6SS component TssG (ImpH/VasB)
<i>Pcc</i> ICMP5702_peg3370	AODT01000016.1	38115	36349	-	T6SS component TssF (ImpG/VasA)
<i>Pcc</i> ICMP5702_peg3371	AODT01000016.1	38549	38118	-	T6SS lysozyme-like component TssE
<i>Pcc</i> ICMP5702_peg3372	AODT01000016.1	40033	38555	-	T6SS component TssC (ImpC/VipB)
<i>Pcc</i> ICMP5702_peg3373	AODT01000016.1	40559	40056	-	T6SS component TssB (ImpB/VipA)
<i>Pcc</i> ICMP5702_peg3374	AODT01000016.1	42524	41496	-	Dienelactone hydrolase and related enzymes
<i>Pcc</i> ICMP5702_peg3375	AODT01000016.1	43734	42538	-	Transcriptional regulator
<i>Pcc</i> ICMP5702_peg3376	AODT01000016.1	43971	44876	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg3377	AODT01000016.1	45806	45078	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3378	AODT01000016.1	47388	45811	-	TPR domain protein
<i>Pcc</i> ICMP5702_peg3379	AODT01000016.1	47693	47550	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3380	AODT01000016.1	48278	47742	-	Phage integrase
<i>Pcc</i> ICMP5702_peg3381	AODT01000016.1	48465	48292	-	Phage integrase, Phage P4-associated
<i>Pcc</i> ICMP5702_peg3382	AODT01000016.1	49420	49839	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3383	AODT01000016.1	51397	50144	-	Gamma-glutamyl phosphate reductase (EC 1.2.1.41)
<i>Pcc</i> ICMP5702_peg3384	AODT01000016.1	52511	51408	-	Glutamate 5-kinase (EC 2.7.2.11) / RNA-binding C-terminal domain PUA
<i>Pcc</i> ICMP5702_peg3385	AODT01000016.1	53009	52635	-	Curlin genes transcriptional activator
<i>Pcc</i> ICMP5702_peg3386	AODT01000016.1	53192	53527	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3387	AODT01000016.1	54855	53608	-	Fermentation/respiration switch protein
<i>Pcc</i> ICMP5702_peg3388	AODT01000016.1	55555	55097	-	Xanthine-guanine phosphoribosyltransferase (EC 2.4.2.22)
<i>Pcc</i> ICMP5702_peg3389	AODT01000016.1	55844	55659	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3390	AODT01000016.1	55887	57347	+	Cytosol nonspecific dipeptidase (EC 3.4.13.18)
<i>Pcc</i> ICMP5702_peg3391	AODT01000016.1	58472	57414	-	DNA polymerase IV (EC 2.7.7.7)

<i>Pcc</i> ICMP5702_peg3392	AODT01000016.1	59348	58548	-	Putative DNA-binding protein
<i>Pcc</i> ICMP5702_peg3393	AODT01000016.1	59581	60351	+	SAM-dependent methyltransferase YafE (UbiE paralog)
<i>Pcc</i> ICMP5702_peg3394	AODT01000016.1	60606	60439	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3395	AODT01000016.1	60608	61342	+	Putative L,D-transpeptidase YafK
<i>Pcc</i> ICMP5702_peg3396	AODT01000016.1	62080	61313	-	Putative glutamine amidotransferase YafJ
<i>Pcc</i> ICMP5702_peg3397	AODT01000016.1	62895	62314	-	D-sedoheptulose 7-phosphate isomerase (EC 5.3.1.28)
<i>Pcc</i> ICMP5702_peg3398	AODT01000016.1	63021	62905	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3399	AODT01000016.1	63245	65692	+	Acyl-coenzyme A dehydrogenase FadE (EC 1.3.8.-)
<i>Pcc</i> ICMP5702_peg3400	AODT01000016.1	65789	66139	+	Uncharacterized protein YajD
<i>Pcc</i> ICMP5702_peg3401	AODT01000016.1	67403	66201	-	5-methylthioribose kinase (EC 2.7.1.100)
<i>Pcc</i> ICMP5702_peg3402	AODT01000016.1	67540	68568	+	S-methyl-5-thioribose-1-phosphate isomerase (EC 5.3.1.23)
<i>Pcc</i> ICMP5702_peg3403	AODT01000016.1	68894	68628	-	T6SS PAAR-repeat protein
<i>Pcc</i> ICMP5702_peg3404	AODT01000016.1	70669	68954	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3405	AODT01000016.1	71187	70666	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3406	AODT01000016.1	71823	71305	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3407	AODT01000016.1	72545	71820	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3408	AODT01000016.1	74574	72547	-	VgrG protein
<i>Pcc</i> ICMP5702_peg3409	AODT01000016.1	74639	74761	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3410	AODT01000016.1	75640	75095	-	1,2-dihydroxy-3-keto-5-methylthiopentene dioxygenase (EC 1.13.11.54)
<i>Pcc</i> ICMP5702_peg3411	AODT01000016.1	76326	75637	-	2,3-diketo-5-methylthiopentyl-1-phosphate enolase-phosphatase (EC 3.1.3.77)
<i>Pcc</i> ICMP5702_peg3412	AODT01000016.1	76940	76323	-	Methylthioribulose-1-phosphate dehydratase (EC 4.2.1.109)
<i>Pcc</i> ICMP5702_peg3413	AODT01000016.1	77131	78288	+	Glutamine-dependent 2-keto-4-methylthiobutyrate transaminase
<i>Pcc</i> ICMP5702_peg3414	AODT01000016.1	78276	79043	+	Aliphatic amidase AmiE (EC 3.5.1.4)
<i>Pcc</i> ICMP5702_peg3415	AODT01000016.1	80341	79079	-	N-carbamoyl-L-amino acid hydrolase (EC 3.5.1.87)
<i>Pcc</i> ICMP5702_peg3416	AODT01000016.1	81582	80338	-	Serine--pyruvate aminotransferase (EC 2.6.1.51) / L-alanine:glyoxylate aminotransferase (EC 2.6.1.44)
<i>Pcc</i> ICMP5702_peg3417	AODT01000016.1	82419	81676	-	ABC transporter, ATP-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg3418	AODT01000016.1	83056	82400	-	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg3419	AODT01000016.1	83718	83053	-	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg3420	AODT01000016.1	84537	83731	-	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg3421	AODT01000016.1	85998	85159	-	Transcriptional regulator, RpiR family
<i>Pcc</i> ICMP5702_peg3422	AODT01000016.1	86196	87800	+	Gamma-glutamyltranspeptidase (EC 2.3.2.2) @ Glutathione hydrolase (EC 3.4.19.13)
<i>Pcc</i> ICMP5702_peg3423	AODT01000016.1	87826	88023	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3424	AODT01000016.1	88020	89438	+	Oxamate carbamoyltransferase (EC 2.1.3.5)
<i>Pcc</i> ICMP5702_peg3425	AODT01000016.1	89428	89811	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3426	AODT01000016.1	90049	89867	-	Hypothetical protein

<i>Pcc</i> ICMP5702_peg3427	AODT01000016.1	90297	90431	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3428	AODT01000016.1	91203	92405	+	Glycine betaine/L-proline transport ATP-binding protein ProV (TC 3.A.1.12.1)
<i>Pcc</i> ICMP5702_peg3429	AODT01000016.1	92398	93666	+	Glycine betaine/L-proline transport system permease protein ProW (TC 3.A.1.12.1)
<i>Pcc</i> ICMP5702_peg3430	AODT01000016.1	93901	94908	+	Glycine betaine/L-proline transport substrate-binding protein ProX (TC 3.A.1.12.1)
<i>Pcc</i> ICMP5702_peg3431	AODT01000016.1	96126	94969	-	Hypothetical protein, not 6-phosphogluconolactonase
<i>Pcc</i> ICMP5702_peg3432	AODT01000016.1	96285	97505	+	Uncharacterized MFS-type transporter STM2812
<i>Pcc</i> ICMP5702_peg3433	AODT01000016.1	97689	98429	+	Inner membrane protein YgaZ
<i>Pcc</i> ICMP5702_peg3434	AODT01000016.1	98426	98755	+	Uncharacterized protein YgaH
<i>Pcc</i> ICMP5702_peg3435	AODT01000016.1	98945	99460	+	Multidrug resistance regulator EmrR (MprA)
<i>Pcc</i> ICMP5702_peg3436	AODT01000016.1	99736	99590	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3437	AODT01000016.1	99735	100910	+	Multidrug efflux system EmrAB-OMF, membrane fusion component EmrA Multidrug efflux system EmrAB-OMF, inner-membrane proton/drug antiporter EmrB (MFS type)
<i>Pcc</i> ICMP5702_peg3438	AODT01000016.1	100928	102463	+	
<i>Pcc</i> ICMP5702_peg3439	AODT01000016.1	102670	103854	+	Na ⁺ dependent nucleoside transporter NupC
<i>Pcc</i> ICMP5702_peg3440	AODT01000016.1	104339	103905	-	Uncharacterized protein KPN_01043
<i>Pcc</i> ICMP5702_peg3441	AODT01000016.1	105560	104409	-	Uncharacterized tRNA/rRNA methyltransferase YfiF
<i>Pcc</i> ICMP5702_peg3442	AODT01000016.1	105810	106229	+	Thioredoxin 2
<i>Pcc</i> ICMP5702_peg3443	AODT01000016.1	106376	107125	+	Uncharacterized conserved protein YfiP, contains DTW domain
<i>Pcc</i> ICMP5702_peg3444	AODT01000016.1	107158	109806	+	Protein lysine acetyltransferase Pat (EC 2.3.1.-)
<i>Pcc</i> ICMP5702_peg3445	AODT01000016.1	110007	111362	+	CDP-diacylglycerol--serine O-phosphatidyltransferase (EC 2.7.8.8)
<i>Pcc</i> ICMP5702_peg3446	AODT01000016.1	112751	111471	-	Alpha-ketoglutarate permease
<i>Pcc</i> ICMP5702_peg3447	AODT01000017.1	2891	2328	-	D-glycero-beta-D-manno-heptose-1,7-bisphosphate 7-phosphatase (EC 3.1.3.82)
<i>Pcc</i> ICMP5702_peg3448	AODT01000017.1	3071	4102	+	Methionine ABC transporter ATP-binding protein
<i>Pcc</i> ICMP5702_peg3449	AODT01000017.1	4095	4748	+	Methionine ABC transporter permease protein
<i>Pcc</i> ICMP5702_peg3450	AODT01000017.1	4814	5629	+	Methionine ABC transporter substrate-binding protein
<i>Pcc</i> ICMP5702_peg3451	AODT01000017.1	5873	6283	+	Protein RcsF
<i>Pcc</i> ICMP5702_peg3452	AODT01000017.1	6280	6996	+	tRNA (adenine(37)-N6)-methyltransferase
<i>Pcc</i> ICMP5702_peg3453	AODT01000017.1	7142	8860	+	Prolyl-tRNA synthetase (EC 6.1.1.15), bacterial type
<i>Pcc</i> ICMP5702_peg3454	AODT01000017.1	9955	8966	-	RNA polymerase sigma factor RpoS
<i>Pcc</i> ICMP5702_peg3455	AODT01000017.1	11043	10009	-	Murein hydrolase activator NlpD
<i>Pcc</i> ICMP5702_peg3456	AODT01000017.1	12016	11390	-	Protein-L-isoaspartate O-methyltransferase (EC 2.1.1.77)
<i>Pcc</i> ICMP5702_peg3457	AODT01000017.1	12156	12010	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3458	AODT01000017.1	13202	12156	-	tRNA pseudouridine(13) synthase (EC 5.4.99.27)
<i>Pcc</i> ICMP5702_peg3459	AODT01000017.1	13804	13307	-	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase (EC 4.6.1.12)
<i>Pcc</i> ICMP5702_peg3460	AODT01000017.1	14571	13858	-	2-C-methyl-D-erythritol 4-phosphate cytidyltransferase (EC 2.7.7.60)
<i>Pcc</i> ICMP5702_peg3461	AODT01000017.1	14910	14575	-	Cell division protein DivIC (FtsB), stabilizes FtsL against RasP cleavage

<i>Pcc</i> ICMP5702_peg3462	AODT01000017.1	15059	14931	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3463	AODT01000017.1	15242	16012	+	Glutamine ABC transporter, substrate-binding protein GlnH
<i>Pcc</i> ICMP5702_peg3464	AODT01000017.1	16146	16910	+	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg3465	AODT01000017.1	16897	17619	+	ABC transporter, ATP-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg3466	AODT01000017.1	18035	17688	-	Inner membrane protein YgbE
<i>Pcc</i> ICMP5702_peg3467	AODT01000017.1	18696	18079	-	Adenylylsulfate kinase (EC 2.7.1.25)
<i>Pcc</i> ICMP5702_peg3468	AODT01000017.1	20188	18698	-	Sulfate adenylyltransferase subunit 1 (EC 2.7.7.4)
<i>Pcc</i> ICMP5702_peg3469	AODT01000017.1	21108	20200	-	Sulfate adenylyltransferase subunit 2 (EC 2.7.7.4)
<i>Pcc</i> ICMP5702_peg3470	AODT01000017.1	22560	21118	-	Precorrin-2 oxidase (EC 1.3.1.76) @ Sirohydrochlorin ferrochelatase activity of CysG (EC 4.99.1.4) / Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)
<i>Pcc</i> ICMP5702_peg3471	AODT01000017.1	22986	24365	+	Acetaldehyde dehydrogenase (EC 1.2.1.10) @ Acetaldehyde dehydrogenase (EC 1.2.1.10), ethanolamine utilization cluster
<i>Pcc</i> ICMP5702_peg3472	AODT01000017.1	24487	25527	+	Ethanolamine operon regulatory protein
<i>Pcc</i> ICMP5702_peg3473	AODT01000017.1	25677	26714	+	Alcohol dehydrogenase (EC 1.1.1.1)
<i>Pcc</i> ICMP5702_peg3474	AODT01000017.1	26888	27001	+	BioD-like N-terminal domain / Phosphate acetyltransferase (EC 2.3.1.8)
<i>Pcc</i> ICMP5702_peg3475	AODT01000017.1	27776	27042	-	Phosphoadenylyl-sulfate reductase [thioredoxin] (EC 1.8.4.8)
<i>Pcc</i> ICMP5702_peg3476	AODT01000017.1	29522	27789	-	Sulfite reductase [NADPH] hemoprotein beta-component (EC 1.8.1.2)
<i>Pcc</i> ICMP5702_peg3477	AODT01000017.1	31351	29522	-	Sulfite reductase [NADPH] flavoprotein alpha-component (EC 1.8.1.2)
<i>Pcc</i> ICMP5702_peg3478	AODT01000017.1	33365	31641	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3479	AODT01000017.1	33908	34648	+	Sensory box/GGDEF family protein
<i>Pcc</i> ICMP5702_peg3480	AODT01000017.1	34898	36577	+	FIG00614028: Hypothetical protein
<i>Pcc</i> ICMP5702_peg3481	AODT01000017.1	38001	36628	-	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg3482	AODT01000017.1	38412	38206	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3483	AODT01000017.1	38500	39834	+	Polygalacturonase (EC 3.2.1.15)
<i>Pcc</i> ICMP5702_peg3484	AODT01000017.1	39929	40291	+	6-carboxy-5,6,7,8-tetrahydropterin synthase (EC 4.1.2.50)
<i>Pcc</i> ICMP5702_peg3485	AODT01000017.1	41047	40376	-	7-carboxy-7-deazaguanine synthase (EC 4.3.99.3)
<i>Pcc</i> ICMP5702_peg3486	AODT01000017.1	41251	42234	+	MBL-fold metallo-hydrolase superfamily
<i>Pcc</i> ICMP5702_peg3487	AODT01000017.1	43254	42250	-	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg3488	AODT01000017.1	43281	44270	+	MBL-fold metallo-hydrolase superfamily
<i>Pcc</i> ICMP5702_peg3489	AODT01000017.1	44279	45025	+	Oxidoreductase, short-chain dehydrogenase/reductase family
<i>Pcc</i> ICMP5702_peg3490	AODT01000017.1	46493	45354	-	Rhamnogalacturonides degradation protein RhiN
<i>Pcc</i> ICMP5702_peg3491	AODT01000017.1	48096	46537	-	Rhamnogalacturonide transporter RhiT
<i>Pcc</i> ICMP5702_peg3492	AODT01000017.1	49290	48400	-	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg3493	AODT01000017.1	49461	50879	+	Coniferyl aldehyde dehydrogenase (EC 1.2.1.68)
<i>Pcc</i> ICMP5702_peg3494	AODT01000017.1	50924	51604	+	Intracellular protease
<i>Pcc</i> ICMP5702_peg3495	AODT01000017.1	53080	51785	-	Enolase (EC 4.2.1.11)

<i>Pcc</i> ICMP5702_peg3496	AODT01000017.1	54816	53179	-	CTP synthase (EC 6.3.4.2)
<i>Pcc</i> ICMP5702_peg3497	AODT01000017.1	55855	55043	-	Nucleoside triphosphate pyrophosphohydrolase MazG (EC 3.6.1.8)
<i>Pcc</i> ICMP5702_peg3498	AODT01000017.1	56062	55937	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3499	AODT01000017.1	58477	56243	-	Inactive (p)ppGpp 3'-pyrophosphohydrolase domain / GTP pyrophosphokinase (EC 2.7.6.5), (p)ppGpp synthetase I
<i>Pcc</i> ICMP5702_peg3500	AODT01000017.1	59880	58531	-	23S rRNA (uracil(1939)-C(5))-methyltransferase (EC 2.1.1.190)
<i>Pcc</i> ICMP5702_peg3501	AODT01000017.1	59998	62793	+	Signal transduction histidine-protein kinase BarA (EC 2.7.13.3)
<i>Pcc</i> ICMP5702_peg3502	AODT01000017.1	64318	63173	-	Glycerate kinase (EC 2.7.1.31)
<i>Pcc</i> ICMP5702_peg3503	AODT01000017.1	65380	64496	-	2-hydroxy-3-oxopropionate reductase (EC 1.1.1.60)
<i>Pcc</i> ICMP5702_peg3504	AODT01000017.1	66240	65470	-	2-dehydro-3-deoxyglucarate aldolase (EC 4.1.2.20)
<i>Pcc</i> ICMP5702_peg3505	AODT01000017.1	67650	66310	-	Glucarate dehydratase (EC 4.2.1.40)
<i>Pcc</i> ICMP5702_peg3506	AODT01000017.1	69024	67687	-	Glucarate dehydratase related protein YgcY
<i>Pcc</i> ICMP5702_peg3507	AODT01000017.1	71116	69764	-	D-glucarate transporter
<i>Pcc</i> ICMP5702_peg3508	AODT01000017.1	71403	71540	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3509	AODT01000017.1	71660	73234	+	D-galactarate dehydratase (EC 4.2.1.42)
<i>Pcc</i> ICMP5702_peg3510	AODT01000017.1	73378	73235	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3511	AODT01000017.1	74009	75559	+	Aerotaxis sensor receptor protein
<i>Pcc</i> ICMP5702_peg3512	AODT01000017.1	75728	76135	+	probable exported protein YPO2987
<i>Pcc</i> ICMP5702_peg3513	AODT01000017.1	76334	76696	+	probable exported protein YPO2987
<i>Pcc</i> ICMP5702_peg3514	AODT01000017.1	77010	76789	-	Uncharacterized protein YpeB
<i>Pcc</i> ICMP5702_peg3515	AODT01000017.1	79060	77015	-	DNA ligase (NAD(+)) (EC 6.5.1.2)
<i>Pcc</i> ICMP5702_peg3516	AODT01000017.1	80642	79206	-	D-glycero-beta-D-manno-heptose 1-phosphate adenylyltransferase (EC 2.7.7.70) / D-glycero-beta-D-manno-heptose-7-phosphate kinase (EC 2.7.1.167)
<i>Pcc</i> ICMP5702_peg3517	AODT01000017.1	83618	80763	-	Glutamine synthetase adenylyl-L-tyrosine phosphorylase (EC 2.7.7.89) / Glutamate-ammonia-ligase adenylyltransferase (EC 2.7.7.42)
<i>Pcc</i> ICMP5702_peg3518	AODT01000017.1	85008	83671	-	Inorganic triphosphatase (EC 3.6.1.25)
<i>Pcc</i> ICMP5702_peg3519	AODT01000017.1	85273	85893	+	Arylsulfatase (EC 3.1.6.1)
<i>Pcc</i> ICMP5702_peg3520	AODT01000017.1	86002	87246	+	CCA tRNA nucleotidyltransferase (EC 2.7.7.72)
<i>Pcc</i> ICMP5702_peg3521	AODT01000017.1	88136	87318	-	Undecaprenyl-diphosphatase (EC 3.6.1.27)
<i>Pcc</i> ICMP5702_peg3522	AODT01000017.1	88637	88284	-	Dihydroneopterin aldolase (EC 4.1.2.25)
<i>Pcc</i> ICMP5702_peg3523	AODT01000017.1	88766	89401	+	Acyl-ACP:glycerol-3-phosphate O-acyltransferase (EC 2.3.1.n5)
<i>Pcc</i> ICMP5702_peg3524	AODT01000017.1	91229	89643	-	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg3525	AODT01000017.1	91299	91463	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3526	AODT01000017.1	91479	92009	+	Inorganic pyrophosphatase (EC 3.6.1.1)
<i>Pcc</i> ICMP5702_peg3527	AODT01000017.1	92484	92125	-	UPF0131 protein YtfP
<i>Pcc</i> ICMP5702_peg3528	AODT01000017.1	96524	92487	-	Inner membrane component of TAM transport system

<i>Pcc</i> ICMP5702_peg3529	AODT01000017.1	98362	96521	-	Outer membrane component of TAM transport system
<i>Pcc</i> ICMP5702_peg3530	AODT01000017.1	98821	99459	+	Peptide-methionine (S)-S-oxide reductase MsrA (EC 1.8.4.11)
<i>Pcc</i> ICMP5702_peg3531	AODT01000017.1	99631	100956	+	UPF0053 inner membrane protein YtfL
<i>Pcc</i> ICMP5702_peg3532	AODT01000017.1	101222	101016	-	Uncharacterized protein YtfK
<i>Pcc</i> ICMP5702_peg3533	AODT01000017.1	101568	102137	+	Uncharacterized protein YtfJ
<i>Pcc</i> ICMP5702_peg3534	AODT01000017.1	102889	102149	-	3'(2'),5'-bisphosphate nucleotidase (EC 3.1.3.7)
<i>Pcc</i> ICMP5702_peg3535	AODT01000017.1	103104	105056	+	2',3'-cyclic-nucleotide 2'-phosphodiesterase (EC 3.1.4.16) / 3'-nucleotidase (EC 3.1.3.6)
<i>Pcc</i> ICMP5702_peg3536	AODT01000017.1	105499	105116	-	Transcriptional regulator, HxlR family
<i>Pcc</i> ICMP5702_peg3537	AODT01000017.1	105691	106245	+	Trp repressor binding protein
<i>Pcc</i> ICMP5702_peg3538	AODT01000017.1	106720	106298	-	Uncharacterized protein YaaX/YpeC
<i>Pcc</i> ICMP5702_peg3539	AODT01000017.1	107024	108691	+	Pyruvate decarboxylase (EC 4.1.1.1); Alpha-keto-acid decarboxylase (EC 4.1.1.-)
<i>Pcc</i> ICMP5702_peg3540	AODT01000017.1	108794	109459	+	Repair of Iron Centers di-iron protein
<i>Pcc</i> ICMP5702_peg3541	AODT01000017.1	110170	109550	-	FKBP-type peptidyl-prolyl cis-trans isomerase FklB (EC 5.2.1.8)
<i>Pcc</i> ICMP5702_peg3542	AODT01000017.1	110173	110307	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3543	AODT01000017.1	110575	111288	+	Uncharacterized protein YtfB
<i>Pcc</i> ICMP5702_peg3544	AODT01000017.1	111647	111285	-	FIG016027: protein of unknown function YeaO
<i>Pcc</i> ICMP5702_peg3545	AODT01000017.1	112229	111777	-	LSU ribosomal protein L9p
<i>Pcc</i> ICMP5702_peg3546	AODT01000017.1	112498	112271	-	SSU ribosomal protein S18p @ SSU ribosomal protein S18p, zinc-independent
<i>Pcc</i> ICMP5702_peg3547	AODT01000017.1	112823	112503	-	Primosomal replication protein N
<i>Pcc</i> ICMP5702_peg3548	AODT01000017.1	113221	112829	-	SSU ribosomal protein S6p
<i>Pcc</i> ICMP5702_peg3549	AODT01000017.1	114155	113403	-	YjfP protein
<i>Pcc</i> ICMP5702_peg3550	AODT01000017.1	114450	116390	+	Methyl-accepting chemotaxis protein
<i>Pcc</i> ICMP5702_peg3551	AODT01000017.1	116752	117873	+	Protein with similarity to RtcB
<i>Pcc</i> ICMP5702_peg3552	AODT01000017.1	117870	118493	+	Peptide chain release factor homolog
<i>Pcc</i> ICMP5702_peg3553	AODT01000017.1	118985	118527	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3554	AODT01000017.1	119301	118966	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3555	AODT01000017.1	119479	119787	+	Lipoprotein BsmA
<i>Pcc</i> ICMP5702_peg3556	AODT01000017.1	120249	119851	-	UPF0719 inner membrane protein YjfL
<i>Pcc</i> ICMP5702_peg3557	AODT01000017.1	120616	122148	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg3558	AODT01000017.1	122936	122205	-	23S rRNA (guanosine(2251)-2'-O)-methyltransferase (EC 2.1.1.185)
<i>Pcc</i> ICMP5702_peg3559	AODT01000017.1	125478	123022	-	3'-to-5' exoribonuclease RNase R
<i>Pcc</i> ICMP5702_peg3560	AODT01000017.1	125945	125520	-	Nitrite-sensitive transcriptional repressor NsrR
<i>Pcc</i> ICMP5702_peg3561	AODT01000017.1	126241	127812	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg3562	AODT01000017.1	128346	130178	+	Methyl-accepting chemotaxis protein
<i>Pcc</i> ICMP5702_peg3563	AODT01000017.1	131163	130147	-	Twitching motility protein PilT
<i>Pcc</i> ICMP5702_peg3564	AODT01000017.1	131185	131898	+	Pyridoxal phosphate-containing protein YggS

<i>Pcc</i> ICMP5702_peg3565	AODT01000017.1	131990	132817	+	Pyrroline-5-carboxylate reductase (EC 1.5.1.2)
<i>Pcc</i> ICMP5702_peg3566	AODT01000017.1	132867	133421	+	Cell division integral membrane protein, YggT and half-length relatives
<i>Pcc</i> ICMP5702_peg3567	AODT01000017.1	133418	133708	+	UPF0235 protein VC0458
<i>Pcc</i> ICMP5702_peg3568	AODT01000017.1	133740	134333	+	Nucleoside 5-triphosphatase RdgB (dHATP, dITP, XTP-specific) (EC 3.6.1.66)
<i>Pcc</i> ICMP5702_peg3569	AODT01000017.1	134326	135465	+	Oxygen-independent coproporphyrinogen-III oxidase-like protein YggW
<i>Pcc</i> ICMP5702_peg3570	AODT01000017.1	137104	135560	-	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg3571	AODT01000017.1	137206	137111	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3572	AODT01000017.1	137474	137605	+	Entericidin A
<i>Pcc</i> ICMP5702_peg3573	AODT01000017.1	137875	137991	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3574	AODT01000017.1	138520	138065	-	N-acetyltransferase ElaA
<i>Pcc</i> ICMP5702_peg3575	AODT01000017.1	139794	138565	-	Lysophospholipid transporter LpIT
<i>Pcc</i> ICMP5702_peg3576	AODT01000017.1	141962	139791	-	2-acylglycerophosphoethanolamine acyltransferase (EC 2.3.1.40) / Acyl-[acyl-carrier-protein] synthetase (EC 6.2.1.20)
<i>Pcc</i> ICMP5702_peg3577	AODT01000017.1	142842	142369	-	Acetyltransferase, GNAT family
<i>Pcc</i> ICMP5702_peg3578	AODT01000017.1	143612	142845	-	Hexuronate utilization operon transcriptional repressor ExuR
<i>Pcc</i> ICMP5702_peg3579	AODT01000017.1	144064	143747	-	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)
<i>Pcc</i> ICMP5702_peg3580	AODT01000017.1	145530	144094	-	beta-glucosidase (EC 3.2.1.21)
<i>Pcc</i> ICMP5702_peg3581	AODT01000017.1	146892	145555	-	PTS system, cellobiose-specific IIC component
<i>Pcc</i> ICMP5702_peg3582	AODT01000017.1	147147	147491	+	PTS system, cellobiose-specific IIA component (EC 2.7.1.205)
<i>Pcc</i> ICMP5702_peg3583	AODT01000017.1	147625	148638	+	Transcriptional regulator STM3012, LacI family
<i>Pcc</i> ICMP5702_peg3584	AODT01000017.1	149297	148692	-	Transcriptional regulator
<i>Pcc</i> ICMP5702_peg3585	AODT01000017.1	149423	150319	+	Permease of the drug/metabolite transporter (DMT) superfamily
<i>Pcc</i> ICMP5702_peg3586	AODT01000017.1	151601	150339	-	Diaminopimelate decarboxylase (EC 4.1.1.20)
<i>Pcc</i> ICMP5702_peg3587	AODT01000017.1	151753	152676	+	Transcriptional activator protein LysR
<i>Pcc</i> ICMP5702_peg3588	AODT01000017.1	153617	152709	-	Transcriptional regulator clustered with PA0057, LysR family
<i>Pcc</i> ICMP5702_peg3589	AODT01000017.1	153725	154606	+	Metallo-beta-lactamase superfamily protein PA0057
<i>Pcc</i> ICMP5702_peg3590	AODT01000017.1	154594	155250	+	Thioredoxin-like protein clustered with PA0057
<i>Pcc</i> ICMP5702_peg3591	AODT01000017.1	155418	155981	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3592	AODT01000017.1	156017	156310	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3593	AODT01000017.1	156784	156404	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3594	AODT01000017.1	157291	157881	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3595	AODT01000017.1	158057	159079	+	tRNA-dihydrouridine(20/20a) synthase (EC 1.3.1.91)
<i>Pcc</i> ICMP5702_peg3596	AODT01000017.1	159245	159532	+	Phage shock protein G
<i>Pcc</i> ICMP5702_peg3597	AODT01000017.1	159853	159737	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3598	AODT01000017.1	161395	160007	-	Putative cytochrome
<i>Pcc</i> ICMP5702_peg3599	AODT01000017.1	161571	161750	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg3600	AODT01000017.1	162733	161747	-	Quinone oxidoreductase (EC 1.6.5.5)
<i>Pcc</i> ICMP5702_peg3601	AODT01000017.1	162981	164387	+	Replicative DNA helicase (DnaB) (EC 3.6.4.12)
<i>Pcc</i> ICMP5702_peg3602	AODT01000017.1	164429	165511	+	Alanine racemase (EC 5.1.1.1)
<i>Pcc</i> ICMP5702_peg3603	AODT01000017.1	165504	166142	+	FIG00904952: Hypothetical protein
<i>Pcc</i> ICMP5702_peg3604	AODT01000017.1	166457	166936	+	Transcriptional regulator, AsnC family
<i>Pcc</i> ICMP5702_peg3605	AODT01000017.1	166938	167063	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3606	AODT01000017.1	167176	167799	+	Uncharacterized UPF0750 membrane protein
<i>Pcc</i> ICMP5702_peg3607	AODT01000017.1	167863	169056	+	Biosynthetic Aromatic amino acid aminotransferase alpha (EC 2.6.1.57)
<i>Pcc</i> ICMP5702_peg3608	AODT01000017.1	169225	169722	+	UTP pyrophosphatase (EC 3.6.1.9)
<i>Pcc</i> ICMP5702_peg3609	AODT01000017.1	169929	169810	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3610	AODT01000017.1	170109	170339	+	T6SS component Hcp
<i>Pcc</i> ICMP5702_peg3611	AODT01000017.1	170796	170392	-	putative membrane protein
<i>Pcc</i> ICMP5702_peg3612	AODT01000017.1	171075	170842	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3613	AODT01000017.1	171095	171388	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3614	AODT01000017.1	172146	171742	-	putative membrane protein
<i>Pcc</i> ICMP5702_peg3615	AODT01000017.1	172448	172191	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3616	AODT01000017.1	173445	172588	-	probable membrane protein YPO2863
<i>Pcc</i> ICMP5702_peg3617	AODT01000017.1	173741	173610	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3618	AODT01000017.1	175207	174788	-	UPF0047 protein YjbQ
<i>Pcc</i> ICMP5702_peg3619	AODT01000017.1	178057	175223	-	Excinuclease ABC subunit A
<i>Pcc</i> ICMP5702_peg3620	AODT01000017.1	178308	178853	+	Single-stranded DNA-binding protein
<i>Pcc</i> ICMP5702_peg3621	AODT01000017.1	179621	179010	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3622	AODT01000017.1	179872	180327	+	Histone acetyltransferase HPA2 and related acetyltransferases
<i>Pcc</i> ICMP5702_peg3623	AODT01000017.1	181431	180394	-	Transcriptional regulator, LacI family
<i>Pcc</i> ICMP5702_peg3624	AODT01000017.1	182480	181431	-	Domain of unknown function / ABC transporter, permease protein 2 (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg3625	AODT01000017.1	183490	182492	-	ABC transporter, permease protein 1 (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg3626	AODT01000017.1	184605	183514	-	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg3627	AODT01000017.1	185714	184608	-	Rhamnolacturonides degradation protein RhiN
<i>Pcc</i> ICMP5702_peg3628	AODT01000017.1	188178	185716	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3629	AODT01000017.1	188621	189928	+	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg3630	AODT01000017.1	189925	190476	+	Glucosamine kinase GpsK (EC 2.7.1.8)
<i>Pcc</i> ICMP5702_peg3631	AODT01000017.1	190473	191387	+	N-acetylglucosamine kinase of eukaryotic type (EC 2.7.1.59)
<i>Pcc</i> ICMP5702_peg3632	AODT01000017.1	191413	193236	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3633	AODT01000017.1	193724	193840	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg3634	AODT01000017.1	193837	194547	+	Zinc ABC transporter, ATP-binding protein ZnuC
<i>Pcc</i> ICMP5702_peg3635	AODT01000017.1	194544	195398	+	Zinc ABC transporter, permease protein ZnuB
<i>Pcc</i> ICMP5702_peg3636	AODT01000017.1	195439	196317	+	Zinc ABC transporter, substrate-binding protein ZnuA
<i>Pcc</i> ICMP5702_peg3637	AODT01000017.1	196424	196894	+	conserved Hypothetical protein
<i>Pcc</i> ICMP5702_peg3638	AODT01000017.1	197736	196921	-	D-threonate utilization transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg3639	AODT01000017.1	198860	197880	-	D-threonate 4-phosphate dehydrogenase [decarboxylating]
<i>Pcc</i> ICMP5702_peg3640	AODT01000017.1	200181	198853	-	D-threonate kinase
<i>Pcc</i> ICMP5702_peg3641	AODT01000017.1	200418	201554	+	Alcohol dehydrogenase (EC 1.1.1.1)
<i>Pcc</i> ICMP5702_peg3642	AODT01000017.1	201623	202507	+	Dihydrodipicolinate synthase family protein APECO1_1389
<i>Pcc</i> ICMP5702_peg3643	AODT01000017.1	202546	203961	+	Na ⁺ /solute symporter
<i>Pcc</i> ICMP5702_peg3644	AODT01000017.1	203965	205152	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3645	AODT01000017.1	205341	205811	+	Protein YjgK, linked to biofilm formation
<i>Pcc</i> ICMP5702_peg3646	AODT01000017.1	205856	206545	+	Oxidoreductase, short-chain dehydrogenase/reductase family
<i>Pcc</i> ICMP5702_peg3647	AODT01000017.1	207781	206591	-	Transcriptional regulator, LacI family
<i>Pcc</i> ICMP5702_peg3648	AODT01000017.1	208100	208543	+	PTS system, IIA component
<i>Pcc</i> ICMP5702_peg3649	AODT01000017.1	208566	208853	+	PTS system, IIB component
<i>Pcc</i> ICMP5702_peg3650	AODT01000017.1	208868	210127	+	PTS system, IIC component, UlaA-type
<i>Pcc</i> ICMP5702_peg3651	AODT01000017.1	210181	210846	+	Fructose-6-phosphate aldolase
<i>Pcc</i> ICMP5702_peg3652	AODT01000017.1	211288	210929	-	UPF0231 protein YacL
<i>Pcc</i> ICMP5702_peg3653	AODT01000017.1	214198	211475	-	Aconitate hydratase 2 (EC 4.2.1.3)
<i>Pcc</i> ICMP5702_peg3654	AODT01000017.1	214518	215024	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3655	AODT01000017.1	216574	215174	-	RtcB-like protein
<i>Pcc</i> ICMP5702_peg3656	AODT01000017.1	216834	217145	+	Transcriptional regulator, ArsR family
<i>Pcc</i> ICMP5702_peg3657	AODT01000017.1	219535	217241	-	TonB-dependent receptor; Outer membrane receptor for ferric enterobactin and colicins B, D
<i>Pcc</i> ICMP5702_peg3658	AODT01000017.1	219755	219621	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3659	AODT01000017.1	219958	220941	+	Transcriptional regulator of AraC family, enterobactin-dependent, predicted
<i>Pcc</i> ICMP5702_peg3660	AODT01000017.1	221052	222380	+	MmgE/PrpD family protein
<i>Pcc</i> ICMP5702_peg3661	AODT01000017.1	224217	222505	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3662	AODT01000017.1	225633	224455	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3663	AODT01000017.1	226483	225860	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3664	AODT01000017.1	228638	226731	-	Rhamnogalacturonan endolyase (EC 4.2.2.23)
<i>Pcc</i> ICMP5702_peg3665	AODT01000017.1	230021	228837	-	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg3666	AODT01000017.1	231211	230018	-	Beta-lactamase class C-like and penicillin binding proteins (PBPs) superfamily
<i>Pcc</i> ICMP5702_peg3667	AODT01000017.1	231329	232225	+	Transcriptional regulator, LysR family

<i>Pcc</i> ICMP5702_peg3668	AODT01000017.1	233711	232287	-	Dihydrolipoamide dehydrogenase of pyruvate dehydrogenase complex (EC 1.8.1.4) @ Dihydrolipoamide dehydrogenase (EC 1.8.1.4)
<i>Pcc</i> ICMP5702_peg3669	AODT01000017.1	235812	233926	-	Dihydrolipoamide acetyltransferase component of pyruvate dehydrogenase complex (EC 2.3.1.12)
<i>Pcc</i> ICMP5702_peg3670	AODT01000017.1	238490	235827	-	Pyruvate dehydrogenase E1 component (EC 1.2.4.1)
<i>Pcc</i> ICMP5702_peg3671	AODT01000017.1	239396	238632	-	Transcriptional repressor for pyruvate dehydrogenase complex
<i>Pcc</i> ICMP5702_peg3672	AODT01000017.1	239548	239682	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3673	AODT01000017.1	240079	241437	+	Aromatic amino acid transport protein AroP
<i>Pcc</i> ICMP5702_peg3674	AODT01000017.1	241626	243059	+	Possible GPH family transporter (TC 2.A.2) for arabinosides
<i>Pcc</i> ICMP5702_peg3675	AODT01000017.1	243037	243993	+	alpha-L-arabinofuranosidase II (EC 3.2.1.55)
<i>Pcc</i> ICMP5702_peg3676	AODT01000017.1	244884	244030	-	AmpE protein
<i>Pcc</i> ICMP5702_peg3677	AODT01000017.1	245456	244884	-	1,6-anhydro-N-acetylmuramyl-L-alanine amidase
<i>Pcc</i> ICMP5702_peg3678	AODT01000017.1	245848	246735	+	Nucleoside-specific channel-forming protein Tsx precursor
<i>Pcc</i> ICMP5702_peg3679	AODT01000017.1	246880	247770	+	Quinolate phosphoribosyltransferase [decarboxylating] (EC 2.4.2.19)
<i>Pcc</i> ICMP5702_peg3680	AODT01000017.1	248093	248539	+	Type IV pilin PilA
<i>Pcc</i> ICMP5702_peg3681	AODT01000017.1	248542	250026	+	Type IV fimbrial assembly, ATPase PilB
<i>Pcc</i> ICMP5702_peg3682	AODT01000017.1	250023	251228	+	Type IV fimbrial assembly protein PilC
<i>Pcc</i> ICMP5702_peg3683	AODT01000017.1	252353	251313	-	GMP reductase (EC 1.7.1.7)
<i>Pcc</i> ICMP5702_peg3684	AODT01000017.1	252773	253399	+	Dephospho-CoA kinase (EC 2.7.1.24)
<i>Pcc</i> ICMP5702_peg3685	AODT01000017.1	253392	254144	+	Cell division protein ZapD
<i>Pcc</i> ICMP5702_peg3686	AODT01000017.1	254202	254396	+	DNA gyrase inhibitor YacG
<i>Pcc</i> ICMP5702_peg3687	AODT01000017.1	254856	254461	-	Mutator MutT protein (7,8-dihydro-8-oxoguanine-triphosphatase) (EC 3.6.1.-)
<i>Pcc</i> ICMP5702_peg3688	AODT01000017.1	257649	254947	-	Protein translocase subunit SecA
<i>Pcc</i> ICMP5702_peg3689	AODT01000017.1	258277	257762	-	Secretion monitor SecM
<i>Pcc</i> ICMP5702_peg3690	AODT01000017.1	258304	258831	+	Zn-ribbon-containing, possibly RNA-binding protein and truncated derivatives
<i>Pcc</i> ICMP5702_peg3691	AODT01000017.1	259782	258850	-	UDP-3-O-[3-hydroxymyristoyl] N-acetylglucosamine deacetylase (EC 3.5.1.108)
<i>Pcc</i> ICMP5702_peg3692	AODT01000017.1	261023	259872	-	Cell division protein FtsZ
<i>Pcc</i> ICMP5702_peg3693	AODT01000017.1	262348	261092	-	Cell division protein FtsA
<i>Pcc</i> ICMP5702_peg3694	AODT01000017.1	263226	262402	-	Cell division protein FtsQ
<i>Pcc</i> ICMP5702_peg3695	AODT01000017.1	264148	263228	-	D-alanine--D-alanine ligase (EC 6.3.2.4)
<i>Pcc</i> ICMP5702_peg3696	AODT01000017.1	265617	264157	-	UDP-N-acetylmuramate--L-alanine ligase (EC 6.3.2.8)
<i>Pcc</i> ICMP5702_peg3697	AODT01000017.1	266771	265680	-	UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide) pyrophosphoryl- undecaprenol N-acetylglucosamine transferase (EC 2.4.1.227)
<i>Pcc</i> ICMP5702_peg3698	AODT01000017.1	267970	266768	-	Peptidoglycan glycosyltransferase FtsW (EC 2.4.1.129)
<i>Pcc</i> ICMP5702_peg3699	AODT01000017.1	269286	267970	-	UDP-N-acetylmuramoyl-L-alanine--D-glutamate ligase (EC 6.3.2.9)
<i>Pcc</i> ICMP5702_peg3700	AODT01000017.1	270372	269290	-	Phospho-N-acetylmuramoyl-pentapeptide-transferase (EC 2.7.8.13)

<i>Pcc</i> ICMP5702_peg3701	AODT01000017.1	271727	270366	-	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase (EC 6.3.2.10)
<i>Pcc</i> ICMP5702_peg3702	AODT01000017.1	273211	271724	-	UDP-N-acetylmuramoyl-dipeptide--2,6-diaminopimelate ligase (EC 6.3.2.13)
<i>Pcc</i> ICMP5702_peg3703	AODT01000017.1	274961	273198	-	Cell division protein FtsI [Peptidoglycan synthetase] (EC 2.4.1.129)
<i>Pcc</i> ICMP5702_peg3704	AODT01000017.1	275305	274985	-	Cell division protein FtsL
<i>Pcc</i> ICMP5702_peg3705	AODT01000017.1	276246	275302	-	16S rRNA (cytosine(1402)-N(4))-methyltransferase (EC 2.1.1.199)
<i>Pcc</i> ICMP5702_peg3706	AODT01000017.1	276707	276249	-	Transcriptional regulator MraZ
<i>Pcc</i> ICMP5702_peg3707	AODT01000017.1	277594	278031	+	L-alanine exporter AlaE
<i>Pcc</i> ICMP5702_peg3708	AODT01000017.1	279102	278098	-	Fructose repressor FruR, LacI family
<i>Pcc</i> ICMP5702_peg3709	AODT01000017.1	279861	279370	-	Acetolactate synthase small subunit (EC 2.2.1.6)
<i>Pcc</i> ICMP5702_peg3710	AODT01000017.1	281582	279864	-	Acetolactate synthase large subunit (EC 2.2.1.6)
<i>Pcc</i> ICMP5702_peg3711	AODT01000017.1	283832	281943	-	Long-chain-fatty-acid--CoA ligase (EC 6.2.1.3)
<i>Pcc</i> ICMP5702_peg3712	AODT01000017.1	284159	285757	+	2-isopropylmalate synthase (EC 2.3.3.13)
<i>Pcc</i> ICMP5702_peg3713	AODT01000017.1	285757	286848	+	3-isopropylmalate dehydrogenase (EC 1.1.1.85)
<i>Pcc</i> ICMP5702_peg3714	AODT01000017.1	286851	288251	+	3-isopropylmalate dehydratase large subunit (EC 4.2.1.33)
<i>Pcc</i> ICMP5702_peg3715	AODT01000017.1	288265	288867	+	3-isopropylmalate dehydratase small subunit (EC 4.2.1.33)
<i>Pcc</i> ICMP5702_peg3716	AODT01000017.1	289250	288939	-	FIG023406: Hypothetical protein
<i>Pcc</i> ICMP5702_peg3717	AODT01000017.1	289981	289247	-	FIG006238: AzlC family protein
<i>Pcc</i> ICMP5702_peg3718	AODT01000017.1	290922	290086	-	FIG229276: Transcriptional regulator, AraC family
<i>Pcc</i> ICMP5702_peg3719	AODT01000017.1	292766	291147	-	Methyl-accepting chemotaxis protein III (ribose and galactose chemoreceptor protein)
<i>Pcc</i> ICMP5702_peg3720	AODT01000017.1	292929	292783	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3721	AODT01000017.1	293021	293140	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3722	AODT01000017.1	293355	293239	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3723	AODT01000017.1	293457	293684	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3724	AODT01000017.1	293713	294273	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3725	AODT01000017.1	294583	294419	-	Sugar-phosphate stress protein SgrT (embedded in SgrS)
<i>Pcc</i> ICMP5702_peg3726	AODT01000017.1	294674	296332	+	SgrR, sugar-phosphate stress, transcriptional activator of SgrS small RNA
<i>Pcc</i> ICMP5702_peg3727	AODT01000017.1	296514	297530	+	Thiamin ABC transporter, substrate-binding component
<i>Pcc</i> ICMP5702_peg3728	AODT01000017.1	297506	299113	+	Thiamin ABC transporter, transmembrane component
<i>Pcc</i> ICMP5702_peg3729	AODT01000017.1	299100	299810	+	Thiamin ABC transporter, ATPase component
<i>Pcc</i> ICMP5702_peg3730	AODT01000017.1	301437	299815	-	Xylan 1,4-beta-xylosidase (EC 3.2.1.37)
<i>Pcc</i> ICMP5702_peg3731	AODT01000017.1	301952	303616	+	Acetolactate synthase large subunit (EC 2.2.1.6)
<i>Pcc</i> ICMP5702_peg3732	AODT01000017.1	303622	303933	+	Acetolactate synthase small subunit (EC 2.2.1.6)
<i>Pcc</i> ICMP5702_peg3733	AODT01000017.1	304739	303969	-	DedA family inner membrane protein YabI
<i>Pcc</i> ICMP5702_peg3734	AODT01000017.1	305168	306748	+	GGDEF domain protein
<i>Pcc</i> ICMP5702_peg3735	AODT01000017.1	307059	309425	+	DNA polymerase II (EC 2.7.7.7)
<i>Pcc</i> ICMP5702_peg3736	AODT01000017.1	309652	312555	+	RNA polymerase associated protein RapA

<i>Pcc</i> ICMP5702_peg3737	AODT01000017.1	312908	313561	+	LSU rRNA pseudouridine(746) synthase (EC 5.4.99.29) @ tRNA pseudouridine(32) synthase (EC 5.4.99.28)
<i>Pcc</i> ICMP5702_peg3738	AODT01000017.1	314535	313645	-	DnaJ-like protein DjlA
<i>Pcc</i> ICMP5702_peg3739	AODT01000017.1	314688	317084	+	LPS-assembly protein LptD @ Organic solvent tolerance protein precursor
<i>Pcc</i> ICMP5702_peg3740	AODT01000017.1	317187	318482	+	Periplasmic chaperone and peptidyl-prolyl cis-trans isomerase of outer membrane proteins SurA (EC 5.2.1.8)
<i>Pcc</i> ICMP5702_peg3741	AODT01000017.1	318498	319499	+	4-hydroxythreonine-4-phosphate dehydrogenase (EC 1.1.1.262)
<i>Pcc</i> ICMP5702_peg3742	AODT01000017.1	319492	320310	+	2.1.1.182)
<i>Pcc</i> ICMP5702_peg3743	AODT01000017.1	320323	320700	+	ApaG protein
<i>Pcc</i> ICMP5702_peg3744	AODT01000017.1	320703	321560	+	Bis(5'-nucleosyl)-tetrphosphatase, symmetrical (EC 3.6.1.41)
<i>Pcc</i> ICMP5702_peg3745	AODT01000017.1	321795	321601	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3746	AODT01000017.1	322462	321938	-	Integral membrane protein
<i>Pcc</i> ICMP5702_peg3747	AODT01000017.1	322574	323479	+	Transcriptional regulator
<i>Pcc</i> ICMP5702_peg3748	AODT01000017.1	324051	323569	-	Dihydrofolate reductase (EC 1.5.1.3)
<i>Pcc</i> ICMP5702_peg3749	AODT01000017.1	324620	324150	-	FIG001826: putative inner membrane protein
<i>Pcc</i> ICMP5702_peg3750	AODT01000017.1	325450	324611	-	FIG023911: putative membrane protein
<i>Pcc</i> ICMP5702_peg3751	AODT01000017.1	325605	326219	+	Transporter, LysE family
<i>Pcc</i> ICMP5702_peg3752	AODT01000017.1	326687	326319	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3753	AODT01000017.1	327474	326785	-	Transcriptional regulator, DeoR family
<i>Pcc</i> ICMP5702_peg3754	AODT01000017.1	330861	327637	-	Carbamoyl-phosphate synthase large chain (EC 6.3.5.5)
<i>Pcc</i> ICMP5702_peg3755	AODT01000017.1	332024	330876	-	Carbamoyl-phosphate synthase small chain (EC 6.3.5.5)
<i>Pcc</i> ICMP5702_peg3756	AODT01000017.1	332425	332237	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3757	AODT01000017.1	333333	332470	-	4-hydroxy-tetrahydrodipicolinate reductase (EC 1.17.1.8)
<i>Pcc</i> ICMP5702_peg3758	AODT01000017.1	334578	333628	-	4-hydroxy-3-methylbut-2-enyl diphosphate reductase (EC 1.17.7.4)
<i>Pcc</i> ICMP5702_peg3759	AODT01000017.1	335032	334559	-	FKBP-type peptidyl-prolyl cis-trans isomerase SlpA (EC 5.2.1.8)
<i>Pcc</i> ICMP5702_peg3760	AODT01000017.1	335544	335032	-	Lipoprotein signal peptidase (EC 3.4.23.36)
<i>Pcc</i> ICMP5702_peg3761	AODT01000017.1	338357	335544	-	Isoleucyl-tRNA synthetase (EC 6.1.1.5)
<i>Pcc</i> ICMP5702_peg3762	AODT01000017.1	339330	338389	-	FMN adenylyltransferase (EC 2.7.7.2) / Riboflavin kinase (EC 2.7.1.26)
<i>Pcc</i> ICMP5702_peg3763	AODT01000017.1	339757	340020	+	SSU ribosomal protein S20p
<i>Pcc</i> ICMP5702_peg3764	AODT01000017.1	341005	340058	-	Transcriptional activator NhaR
<i>Pcc</i> ICMP5702_peg3765	AODT01000017.1	342201	341005	-	Na ⁺ /H ⁺ antiporter NhaA type
<i>Pcc</i> ICMP5702_peg3766	AODT01000017.1	343624	342488	-	Chaperone protein DnaJ
<i>Pcc</i> ICMP5702_peg3767	AODT01000017.1	345640	343733	-	Chaperone protein DnaK
<i>Pcc</i> ICMP5702_peg3768	AODT01000017.1	345828	345712	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3769	AODT01000017.1	346124	346699	+	Succinate-acetate/proton symporter SatP
<i>Pcc</i> ICMP5702_peg3770	AODT01000017.1	348150	346813	-	L-Proline/Glycine betaine transporter ProP

<i>Pcc</i> ICMP5702_peg3771	AODT01000017.1	348865	348278	-	Molybdopterin adenylyltransferase (EC 2.7.7.75)
<i>Pcc</i> ICMP5702_peg3772	AODT01000017.1	349138	348947	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3773	AODT01000017.1	349233	350321	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3774	AODT01000017.1	351352	350399	-	Transaldolase (EC 2.2.1.2)
<i>Pcc</i> ICMP5702_peg3775	AODT01000017.1	351666	352439	+	UPF0246 protein YaaA
<i>Pcc</i> ICMP5702_peg3776	AODT01000017.1	353775	352486	-	Threonine synthase (EC 4.2.3.1)
<i>Pcc</i> ICMP5702_peg3777	AODT01000017.1	354708	353779	-	Homoserine kinase (EC 2.7.1.39)
<i>Pcc</i> ICMP5702_peg3778	AODT01000017.1	357170	354711	-	Aspartokinase (EC 2.7.2.4) / Homoserine dehydrogenase (EC 1.1.1.3)
<i>Pcc</i> ICMP5702_peg3779	AODT01000017.1	357585	357430	-	FIG00905955: Hypothetical protein
<i>Pcc</i> ICMP5702_peg3780	AODT01000017.1	358282	357596	-	Uncharacterized tRNA/rRNA methyltransferase LasT
<i>Pcc</i> ICMP5702_peg3781	AODT01000017.1	358459	358322	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3782	AODT01000017.1	358851	358735	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3783	AODT01000017.1	359017	359733	+	Aerobic respiration control response regulator ArcA
<i>Pcc</i> ICMP5702_peg3784	AODT01000017.1	360271	359789	-	Conserved uncharacterized protein CreA
<i>Pcc</i> ICMP5702_peg3785	AODT01000017.1	360477	361364	+	DNA-binding transcriptional dual regulator Rob
<i>Pcc</i> ICMP5702_peg3786	AODT01000017.1	362003	361353	-	Phosphoglycerate mutase (EC 5.4.2.11)
<i>Pcc</i> ICMP5702_peg3787	AODT01000017.1	362054	362593	+	Inosine/xanthosine triphosphatase
<i>Pcc</i> ICMP5702_peg3788	AODT01000017.1	362944	362597	-	Transcriptional repressor protein TrpR
<i>Pcc</i> ICMP5702_peg3789	AODT01000017.1	364951	363017	-	Soluble lytic murein transglycosylase (EC 4.2.2.n1)
<i>Pcc</i> ICMP5702_peg3790	AODT01000017.1	365435	367102	+	Energy-dependent translational throttle protein EttA
<i>Pcc</i> ICMP5702_peg3791	AODT01000017.1	368882	367179	-	Methyl-accepting chemotaxis protein III (ribose and galactose chemoreceptor protein)
<i>Pcc</i> ICMP5702_peg3792	AODT01000017.1	370047	369136	-	Transcriptional regulator EAM_0627, LysR family
<i>Pcc</i> ICMP5702_peg3793	AODT01000017.1	370167	371168	+	Zinc-type alcohol dehydrogenase-like protein
<i>Pcc</i> ICMP5702_peg3794	AODT01000017.1	372471	371239	-	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)
<i>Pcc</i> ICMP5702_peg3795	AODT01000017.1	372656	372540	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3796	AODT01000017.1	373482	372766	-	Ribose-5-phosphate isomerase A (EC 5.3.1.6)
<i>Pcc</i> ICMP5702_peg3797	AODT01000017.1	373631	373512	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3798	AODT01000017.1	373652	374545	+	Transcriptional regulator ArgP, LysR family
<i>Pcc</i> ICMP5702_peg3799	AODT01000017.1	375377	374637	-	Protein of unknown function DUF541
<i>Pcc</i> ICMP5702_peg3800	AODT01000017.1	375504	375391	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3801	AODT01000017.1	376195	375581	-	Arginine exporter protein ArgO
<i>Pcc</i> ICMP5702_peg3802	AODT01000017.1	377296	376448	-	Protein involved in stability of MscS mechanosensitive channel
<i>Pcc</i> ICMP5702_peg3803	AODT01000017.1	378703	377627	-	Fructose-bisphosphate aldolase class II (EC 4.1.2.13)
<i>Pcc</i> ICMP5702_peg3804	AODT01000017.1	380004	378841	-	Phosphoglycerate kinase (EC 2.7.2.3)
<i>Pcc</i> ICMP5702_peg3805	AODT01000017.1	381093	380077	-	D-erythrose-4-phosphate dehydrogenase (EC 1.2.1.72)
<i>Pcc</i> ICMP5702_peg3806	AODT01000017.1	383402	381408	-	Transketolase (EC 2.2.1.1)

<i>Pcc</i> ICMP5702_peg3807	AODT01000017.1	383814	384566	+	Putative metalloprotease yggG (EC 3.4.24.-)
<i>Pcc</i> ICMP5702_peg3808	AODT01000017.1	385241	385786	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3809	AODT01000017.1	387826	385844	-	Biosynthetic arginine decarboxylase (EC 4.1.1.19)
<i>Pcc</i> ICMP5702_peg3810	AODT01000017.1	387977	387819	-	FIG00905173: Hypothetical protein
<i>Pcc</i> ICMP5702_peg3811	AODT01000017.1	388536	389687	+	S-adenosylmethionine synthetase (EC 2.5.1.6)
<i>Pcc</i> ICMP5702_peg3812	AODT01000017.1	389853	390323	+	Protein SprT
<i>Pcc</i> ICMP5702_peg3813	AODT01000017.1	390420	391118	+	Endonuclease I precursor (EC 3.1.21.1)
<i>Pcc</i> ICMP5702_peg3814	AODT01000017.1	391236	391970	+	16S rRNA (uracil(1498)-N(3))-methyltransferase (EC 2.1.1.193)
<i>Pcc</i> ICMP5702_peg3815	AODT01000017.1	391982	392941	+	Glutathione synthetase (EC 6.3.2.3)
<i>Pcc</i> ICMP5702_peg3816	AODT01000017.1	393025	393588	+	UPF0301 protein YqgE
<i>Pcc</i> ICMP5702_peg3817	AODT01000017.1	393588	394007	+	Putative pre-16S rRNA nuclease YqgF
<i>Pcc</i> ICMP5702_peg3818	AODT01000017.1	395093	394089	-	Fructose-1,6-bisphosphatase, type I (EC 3.1.3.11)
<i>Pcc</i> ICMP5702_peg3819	AODT01000017.1	395263	396648	+	UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelate ligase (EC 6.3.2.-)
<i>Pcc</i> ICMP5702_peg3820	AODT01000017.1	398056	396758	-	Adenylosuccinate synthetase (EC 6.3.4.4)
<i>Pcc</i> ICMP5702_peg3821	AODT01000017.1	398356	398156	-	Putative inner membrane protein YjeT (clustered with HflC)
<i>Pcc</i> ICMP5702_peg3822	AODT01000017.1	399477	398482	-	HflC protein
<i>Pcc</i> ICMP5702_peg3823	AODT01000017.1	400740	399481	-	HflK protein
<i>Pcc</i> ICMP5702_peg3824	AODT01000017.1	402117	400837	-	Ribosome LSU-associated GTP-binding protein HflX
<i>Pcc</i> ICMP5702_peg3825	AODT01000017.1	402511	402212	-	RNA-binding protein Hfq
<i>Pcc</i> ICMP5702_peg3826	AODT01000017.1	403566	402625	-	tRNA dimethylallyltransferase (EC 2.5.1.75)
<i>Pcc</i> ICMP5702_peg3827	AODT01000017.1	405568	403559	-	DNA mismatch repair protein MutL
<i>Pcc</i> ICMP5702_peg3828	AODT01000017.1	407308	405620	-	N-acetylmuramoyl-L-alanine amidase (EC 3.5.1.28)
<i>Pcc</i> ICMP5702_peg3829	AODT01000017.1	407787	407305	-	tRNA threonylcarbamoyladenosine biosynthesis protein TsaE
<i>Pcc</i> ICMP5702_peg3830	AODT01000017.1	409358	407793	-	NAD(P)H-hydrate epimerase (EC 5.1.99.6) / ADP-dependent (S)-NAD(P)H-hydrate dehydratase (EC 4.2.1.136)
<i>Pcc</i> ICMP5702_peg3831	AODT01000017.1	409504	410643	+	Epoxyqueuosine reductase (EC 1.17.99.6) QueG
<i>Pcc</i> ICMP5702_peg3832	AODT01000017.1	412733	411171	-	Alkyl hydroperoxide reductase protein F
<i>Pcc</i> ICMP5702_peg3833	AODT01000017.1	413440	412877	-	Alkyl hydroperoxide reductase protein C (EC 1.11.1.15)
<i>Pcc</i> ICMP5702_peg3834	AODT01000017.1	415199	413535	-	putative transport
<i>Pcc</i> ICMP5702_peg3835	AODT01000017.1	416625	415357	-	ABC transporter, RND-adaptor-like protein
<i>Pcc</i> ICMP5702_peg3836	AODT01000017.1	418084	416618	-	Efflux transport system, outer membrane factor (OMF) lipoprotein
<i>Pcc</i> ICMP5702_peg3837	AODT01000017.1	419324	418077	-	ABC-type antimicrobial peptide transport system, permease component
<i>Pcc</i> ICMP5702_peg3838	AODT01000017.1	420018	419317	-	ABC-type antimicrobial peptide transport system, ATPase component
<i>Pcc</i> ICMP5702_peg3839	AODT01000017.1	422165	420690	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3840	AODT01000017.1	423315	422389	-	D-3-phosphoglycerate dehydrogenase (EC 1.1.1.95)

<i>Pcc</i> ICMP5702_peg3841	AODT01000017.1	425091	423385	-	Hypothetical protein Cinnamyl alcohol dehydrogenase/reductase (EC 1.1.1.195) @ Alcohol dehydrogenase (EC 1.1.1.1)
<i>Pcc</i> ICMP5702_peg3842	AODT01000017.1	426525	425476	-	
<i>Pcc</i> ICMP5702_peg3843	AODT01000017.1	427282	426665	-	Threonine efflux protein
<i>Pcc</i> ICMP5702_peg3844	AODT01000017.1	427534	428418	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg3845	AODT01000017.1	428437	429603	+	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg3846	AODT01000017.1	430493	429675	-	ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg3847	AODT01000017.1	431254	430490	-	ABC transporter, permease protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg3848	AODT01000017.1	432289	431270	-	ABC transporter, substrate-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg3849	AODT01000017.1	432627	434282	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3850	AODT01000017.1	435065	434370	-	Pyrimidine 5'-nucleotidase YjjG (EC 3.1.3.5)
<i>Pcc</i> ICMP5702_peg3851	AODT01000017.1	436258	435062	-	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg3852	AODT01000017.1	436444	437049	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3853	AODT01000017.1	437689	437144	-	BsmB
<i>Pcc</i> ICMP5702_peg3854	AODT01000017.1	437874	437987	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3855	AODT01000017.1	439148	438606	-	3'-to-5' oligoribonuclease (orn)
<i>Pcc</i> ICMP5702_peg3856	AODT01000017.1	439332	440381	+	Ribosome small subunit biogenesis RbfA-release protein RsgA
<i>Pcc</i> ICMP5702_peg3857	AODT01000017.1	440529	441557	+	Phosphatidylserine decarboxylase (EC 4.1.1.65)
<i>Pcc</i> ICMP5702_peg3858	AODT01000017.1	441615	444938	+	Miniconductance mechanosensitive channel MscM
<i>Pcc</i> ICMP5702_peg3859	AODT01000017.1	445967	444990	-	Translation elongation factor P Lys34--(R)-beta-lysine ligase
<i>Pcc</i> ICMP5702_peg3860	AODT01000017.1	446442	448238	+	Fumarate reductase flavoprotein subunit (EC 1.3.5.4)
<i>Pcc</i> ICMP5702_peg3861	AODT01000017.1	448231	448968	+	Fumarate reductase iron-sulfur protein (EC 1.3.5.4)
<i>Pcc</i> ICMP5702_peg3862	AODT01000017.1	448979	449377	+	Fumarate reductase subunit C
<i>Pcc</i> ICMP5702_peg3863	AODT01000017.1	449392	449748	+	Fumarate reductase subunit D
<i>Pcc</i> ICMP5702_peg3864	AODT01000017.1	449870	450454	+	Lipocalin Blc
<i>Pcc</i> ICMP5702_peg3865	AODT01000017.1	450720	450448	-	Uncharacterized membrane protein PA1577
<i>Pcc</i> ICMP5702_peg3866	AODT01000017.1	450968	450837	-	Entericidin B
<i>Pcc</i> ICMP5702_peg3867	AODT01000017.1	451718	451152	-	Translation elongation factor P
<i>Pcc</i> ICMP5702_peg3868	AODT01000017.1	451760	452812	+	Lysine 2,3-aminomutase (EC 5.4.3.2)
<i>Pcc</i> ICMP5702_peg3869	AODT01000017.1	453222	452875	-	probable membrane protein yjeI
<i>Pcc</i> ICMP5702_peg3870	AODT01000017.1	454915	453266	-	Glucose-6-phosphate isomerase (EC 5.3.1.9)
<i>Pcc</i> ICMP5702_peg3871	AODT01000017.1	455425	456801	+	Aspartokinase (EC 2.7.2.4)
<i>Pcc</i> ICMP5702_peg3872	AODT01000017.1	458490	456844	-	Sodium-dependent phosphate transporter
<i>Pcc</i> ICMP5702_peg3873	AODT01000017.1	458797	460251	+	2-oxoglutarate/malate translocator
<i>Pcc</i> ICMP5702_peg3874	AODT01000017.1	462424	460322	-	Ferrichrome-iron receptor
<i>Pcc</i> ICMP5702_peg3875	AODT01000017.1	463585	462629	-	Transcriptional regulator, AraC family

<i>Pcc</i> ICMP5702_peg3876	AODT01000017.1	467781	464098	-	5-methyltetrahydrofolate--homocysteine methyltransferase (EC 2.1.1.13)
<i>Pcc</i> ICMP5702_peg3877	AODT01000017.1	468167	468997	+	Acetate operon repressor IclR
<i>Pcc</i> ICMP5702_peg3878	AODT01000017.1	471116	469341	-	Isocitrate dehydrogenase phosphatase (EC 2.7.11.5)/kinase (EC 3.1.3.-)
<i>Pcc</i> ICMP5702_peg3879	AODT01000017.1	472472	471165	-	Isocitrate lyase (EC 4.1.3.1)
<i>Pcc</i> ICMP5702_peg3880	AODT01000017.1	474099	472504	-	Malate synthase (EC 2.3.3.9)
<i>Pcc</i> ICMP5702_peg3881	AODT01000017.1	475316	474387	-	Homoserine O-succinyltransferase (EC 2.3.1.46)
<i>Pcc</i> ICMP5702_peg3882	AODT01000020.1	576	1124	+	Protein YrdA
<i>Pcc</i> ICMP5702_peg3883	AODT01000020.1	1366	1109	-	Uncharacterized protein YrdB
<i>Pcc</i> ICMP5702_peg3884	AODT01000020.1	2190	1363	-	Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)
<i>Pcc</i> ICMP5702_peg3885	AODT01000020.1	2779	2210	-	Threonylcarbamoyl-AMP synthase (EC 2.7.7.87)
<i>Pcc</i> ICMP5702_peg3886	AODT01000020.1	3329	2772	-	Uncharacterized protein YrdD / Threonylcarbamoyl-AMP synthase (EC 2.7.7.87)
<i>Pcc</i> ICMP5702_peg3887	AODT01000020.1	3823	3350	-	Protein of unknown function Smg
<i>Pcc</i> ICMP5702_peg3888	AODT01000020.1	4922	3795	-	Rossmann fold nucleotide-binding protein Smf possibly involved in DNA uptake
<i>Pcc</i> ICMP5702_peg3889	AODT01000020.1	5045	5557	+	Peptide deformylase (EC 3.5.1.88)
<i>Pcc</i> ICMP5702_peg3890	AODT01000020.1	5581	6528	+	Methionyl-tRNA formyltransferase (EC 2.1.2.9)
<i>Pcc</i> ICMP5702_peg3891	AODT01000020.1	6596	7885	+	16S rRNA (cytosine(967)-C(5))-methyltransferase (EC 2.1.1.176)
<i>Pcc</i> ICMP5702_peg3892	AODT01000020.1	7942	9318	+	Trk potassium uptake system protein TrkA
<i>Pcc</i> ICMP5702_peg3893	AODT01000020.1	9410	9823	+	Large-conductance mechanosensitive channel
<i>Pcc</i> ICMP5702_peg3894	AODT01000020.1	10066	9854	-	Alternative ribosome-rescue factor A
<i>Pcc</i> ICMP5702_peg3895	AODT01000020.1	10669	10277	-	LSU ribosomal protein L17p
<i>Pcc</i> ICMP5702_peg3896	AODT01000020.1	11699	10710	-	DNA-directed RNA polymerase alpha subunit (EC 2.7.7.6)
<i>Pcc</i> ICMP5702_peg3897	AODT01000020.1	12345	11725	-	independent
<i>Pcc</i> ICMP5702_peg3898	AODT01000020.1	12765	12376	-	SSU ribosomal protein S11p (S14e)
<i>Pcc</i> ICMP5702_peg3899	AODT01000020.1	13138	12782	-	SSU ribosomal protein S13p (S18e)
<i>Pcc</i> ICMP5702_peg3900	AODT01000020.1	13401	13285	-	LSU ribosomal protein L36p @ LSU ribosomal protein L36p, zinc-dependent
<i>Pcc</i> ICMP5702_peg3901	AODT01000020.1	14766	13435	-	Protein translocase subunit SecY
<i>Pcc</i> ICMP5702_peg3902	AODT01000020.1	15208	14774	-	LSU ribosomal protein L15p (L27Ae)
<i>Pcc</i> ICMP5702_peg3903	AODT01000020.1	15391	15212	-	LSU ribosomal protein L30p (L7e)
<i>Pcc</i> ICMP5702_peg3904	AODT01000020.1	15897	15397	-	SSU ribosomal protein S5p (S2e)
<i>Pcc</i> ICMP5702_peg3905	AODT01000020.1	16265	15912	-	LSU ribosomal protein L18p (L5e)
<i>Pcc</i> ICMP5702_peg3906	AODT01000020.1	16808	16275	-	LSU ribosomal protein L6p (L9e)
<i>Pcc</i> ICMP5702_peg3907	AODT01000020.1	17213	16821	-	SSU ribosomal protein S8p (S15Ae)
<i>Pcc</i> ICMP5702_peg3908	AODT01000020.1	17552	17247	-	SSU ribosomal protein S14p (S29e) @ SSU ribosomal protein S14p (S29e), zinc-independent
<i>Pcc</i> ICMP5702_peg3909	AODT01000020.1	18105	17566	-	LSU ribosomal protein L5p (L11e)
<i>Pcc</i> ICMP5702_peg3910	AODT01000020.1	18434	18120	-	LSU ribosomal protein L24p (L26e)

<i>Pcc</i> ICMP5702_peg3911	AODT01000020.1	18816	18445	-	LSU ribosomal protein L14p (L23e)
<i>Pcc</i> ICMP5702_peg3912	AODT01000020.1	19232	18978	-	SSU ribosomal protein S17p (S11e)
<i>Pcc</i> ICMP5702_peg3913	AODT01000020.1	19423	19232	-	LSU ribosomal protein L29p (L35e)
<i>Pcc</i> ICMP5702_peg3914	AODT01000020.1	19833	19423	-	LSU ribosomal protein L16p (L10e)
<i>Pcc</i> ICMP5702_peg3915	AODT01000020.1	20547	19846	-	SSU ribosomal protein S3p (S3e)
<i>Pcc</i> ICMP5702_peg3916	AODT01000020.1	20897	20565	-	LSU ribosomal protein L22p (L17e)
<i>Pcc</i> ICMP5702_peg3917	AODT01000020.1	21190	20912	-	SSU ribosomal protein S19p (S15e)
<i>Pcc</i> ICMP5702_peg3918	AODT01000020.1	22028	21207	-	LSU ribosomal protein L2p (L8e)
<i>Pcc</i> ICMP5702_peg3919	AODT01000020.1	22348	22046	-	LSU ribosomal protein L23p (L23Ae)
<i>Pcc</i> ICMP5702_peg3920	AODT01000020.1	22950	22345	-	LSU ribosomal protein L4p (L1e)
<i>Pcc</i> ICMP5702_peg3921	AODT01000020.1	23590	22961	-	LSU ribosomal protein L3p (L3e)
<i>Pcc</i> ICMP5702_peg3922	AODT01000020.1	23934	23623	-	SSU ribosomal protein S10p (S20e)
<i>Pcc</i> ICMP5702_peg3923	AODT01000020.1	24057	24212	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3924	AODT01000020.1	24712	24239	-	Bacterioferritin (EC 1.16.3.1)
<i>Pcc</i> ICMP5702_peg3925	AODT01000020.1	24979	24785	-	Bacterioferritin-associated ferredoxin
<i>Pcc</i> ICMP5702_peg3926	AODT01000020.1	25273	25184	-	Translation elongation factor Tu
<i>Pcc</i> ICMP5702_peg3927	AODT01000021.1	589	2	-	Translation elongation factor Tu
<i>Pcc</i> ICMP5702_peg3928	AODT01000021.1	2773	659	-	Translation elongation factor G
<i>Pcc</i> ICMP5702_peg3929	AODT01000021.1	3340	2870	-	SSU ribosomal protein S7p (S5e)
<i>Pcc</i> ICMP5702_peg3930	AODT01000021.1	3811	3437	-	SSU ribosomal protein S12p (S23e)
<i>Pcc</i> ICMP5702_peg3931	AODT01000021.1	4230	3943	-	tRNA 5-methylaminomethyl-2-thiouridine synthase subunit TusB
<i>Pcc</i> ICMP5702_peg3932	AODT01000021.1	4607	4248	-	tRNA 5-methylaminomethyl-2-thiouridine synthase subunit TusC
<i>Pcc</i> ICMP5702_peg3933	AODT01000021.1	5006	4617	-	tRNA 5-methylaminomethyl-2-thiouridine synthase subunit TusD
<i>Pcc</i> ICMP5702_peg3934	AODT01000021.1	5728	5006	-	YheO-like PAS domain
<i>Pcc</i> ICMP5702_peg3935	AODT01000021.1	5907	7553	+	Lipid A phosphoethanolamine transferase EptA/PmrC (EC 2.7.8.43)
<i>Pcc</i> ICMP5702_peg3936	AODT01000021.1	7550	8218	+	BasS/PmrB)
<i>Pcc</i> ICMP5702_peg3937	AODT01000021.1	8215	9309	+	Sensor protein BasS/PmrB (activates BasR/PmrA)
<i>Pcc</i> ICMP5702_peg3938	AODT01000021.1	10669	9398	-	Serine hydroxymethyltransferase (EC 2.1.2.1)
<i>Pcc</i> ICMP5702_peg3939	AODT01000021.1	11517	10705	-	Pyridoxal phosphate-containing protein YggS
<i>Pcc</i> ICMP5702_peg3940	AODT01000021.1	11621	13114	+	2.6.1.1)
<i>Pcc</i> ICMP5702_peg3941	AODT01000021.1	14084	13251	-	FKBP-type peptidyl-prolyl cis-trans isomerase FkpA precursor (EC 5.2.1.8)
<i>Pcc</i> ICMP5702_peg3942	AODT01000021.1	14352	14570	+	Protein SlyX
<i>Pcc</i> ICMP5702_peg3943	AODT01000021.1	15266	14670	-	FKBP-type peptidyl-prolyl cis-trans isomerase SlyD (EC 5.2.1.8)
<i>Pcc</i> ICMP5702_peg3944	AODT01000021.1	15581	15387	-	Cytoplasmic protein, probably associated with glutathione-regulated potassium-efflux
<i>Pcc</i> ICMP5702_peg3945	AODT01000021.1	17455	15644	-	Glutathione-regulated potassium-efflux system protein KefB
<i>Pcc</i> ICMP5702_peg3946	AODT01000021.1	18008	17457	-	Glutathione-regulated potassium-efflux system ancillary protein KefG

<i>Pcc</i> ICMP5702_peg3947	AODT01000021.1	18134	20047	+	Bis-ABC ATPase YheS
<i>Pcc</i> ICMP5702_peg3948	AODT01000021.1	20711	20109	-	Transporter, LysE family
<i>Pcc</i> ICMP5702_peg3949	AODT01000021.1	20818	21858	+	Putative esterase YheT functionally coupled to phosphoribulokinase homolog
<i>Pcc</i> ICMP5702_peg3950	AODT01000021.1	21855	22091	+	UPF0270 protein YheU
<i>Pcc</i> ICMP5702_peg3951	AODT01000021.1	22217	23086	+	Phosphoribulokinase homolog, function unknown
<i>Pcc</i> ICMP5702_peg3952	AODT01000021.1	23606	23199	-	Protein YhfA
<i>Pcc</i> ICMP5702_peg3953	AODT01000021.1	23777	23905	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3954	AODT01000021.1	23980	24612	+	Cyclic AMP receptor protein
<i>Pcc</i> ICMP5702_peg3955	AODT01000021.1	25997	24771	-	N-acetylmethionine aminotransferase (EC 2.6.1.11) @ N-succinyl-L,L-diaminopimelate aminotransferase (EC 2.6.1.17)
<i>Pcc</i> ICMP5702_peg3956	AODT01000021.1	26692	26117	-	Para-aminobenzoate synthase, amidotransferase component (EC 2.6.1.85)
<i>Pcc</i> ICMP5702_peg3957	AODT01000021.1	27373	28497	+	Pectate lyase B precursor (EC 4.2.2.2)
<i>Pcc</i> ICMP5702_peg3958	AODT01000021.1	29166	30290	+	Pectate lyase B precursor (EC 4.2.2.2)
<i>Pcc</i> ICMP5702_peg3959	AODT01000021.1	30657	30788	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3960	AODT01000021.1	31001	32125	+	Pectate lyase B precursor (EC 4.2.2.2)
<i>Pcc</i> ICMP5702_peg3961	AODT01000021.1	32295	33572	+	Pectate lyase (EC 4.2.2.2)
<i>Pcc</i> ICMP5702_peg3962	AODT01000021.1	34237	33653	-	Peptidyl-prolyl cis-trans isomerase PpiA precursor (EC 5.2.1.8)
<i>Pcc</i> ICMP5702_peg3963	AODT01000021.1	35253	34444	-	ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg3964	AODT01000021.1	36089	35265	-	ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg3965	AODT01000021.1	37047	36124	-	ABC transporter, permease protein 2 (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg3966	AODT01000021.1	38084	37044	-	ABC transporter, permease protein 1 (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg3967	AODT01000021.1	39827	38217	-	ABC transporter, substrate-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg3968	AODT01000021.1	41081	39927	-	Galactonate dehydratase (EC 4.2.1.6)
<i>Pcc</i> ICMP5702_peg3969	AODT01000021.1	41466	41567	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3970	AODT01000021.1	41718	44270	+	Nitrite reductase [NAD(P)H] large subunit (EC 1.7.1.4)
<i>Pcc</i> ICMP5702_peg3971	AODT01000021.1	44267	44635	+	Nitrite reductase [NAD(P)H] small subunit (EC 1.7.1.4)
<i>Pcc</i> ICMP5702_peg3972	AODT01000021.1	44662	46041	+	Precorrin-2 oxidase (EC 1.3.1.76) @ Sirohydrochlorin ferrochelatase activity of CysG (EC 4.99.1.4) / Uroporphyrinogen-III methyltransferase (EC 2.1.1.107)
<i>Pcc</i> ICMP5702_peg3973	AODT01000021.1	46530	47246	+	Octopine ABC transporter, permease protein OccQ
<i>Pcc</i> ICMP5702_peg3974	AODT01000021.1	47246	47980	+	Octopine ABC transporter, permease protein OccM
<i>Pcc</i> ICMP5702_peg3975	AODT01000021.1	47977	48741	+	Octopine ABC transporter, ATP-binding protein OccP
<i>Pcc</i> ICMP5702_peg3976	AODT01000021.1	48971	49840	+	Octopine ABC transporter, substrate-binding protein OccT
<i>Pcc</i> ICMP5702_peg3977	AODT01000021.1	49935	51392	+	N-acyl-L-amino acid amidohydrolase (EC 3.5.1.14)
<i>Pcc</i> ICMP5702_peg3978	AODT01000021.1	52472	51468	-	Tryptophanyl-tRNA synthetase (EC 6.1.1.2)
<i>Pcc</i> ICMP5702_peg3979	AODT01000021.1	53173	52469	-	Phosphoglycolate phosphatase (EC 3.1.3.18)
<i>Pcc</i> ICMP5702_peg3980	AODT01000021.1	53843	53166	-	Ribulose-phosphate 3-epimerase (EC 5.1.3.1)

<i>Pcc</i> ICMP5702_peg3981	AODT01000021.1	54768	53956	-	Methyl-directed repair DNA adenine methylase (EC 2.1.1.72)
<i>Pcc</i> ICMP5702_peg3982	AODT01000021.1	55864	54848	-	Septum-associated cell division protein DamX
<i>Pcc</i> ICMP5702_peg3983	AODT01000021.1	57133	56048	-	3-dehydroquinase synthase (EC 4.2.3.4)
<i>Pcc</i> ICMP5702_peg3984	AODT01000021.1	57706	57185	-	Shikimate kinase I (EC 2.7.1.71)
<i>Pcc</i> ICMP5702_peg3985	AODT01000021.1	58037	57939	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3986	AODT01000021.1	59332	58058	-	Type IV pilus biogenesis protein PilQ
<i>Pcc</i> ICMP5702_peg3987	AODT01000021.1	59810	59433	-	Type IV pilus biogenesis protein PilP
<i>Pcc</i> ICMP5702_peg3988	AODT01000021.1	60394	59807	-	Type IV pilus biogenesis protein PilO
<i>Pcc</i> ICMP5702_peg3989	AODT01000021.1	60956	60387	-	Type IV pilus biogenesis protein PilN
<i>Pcc</i> ICMP5702_peg3990	AODT01000021.1	61810	60959	-	Type IV pilus biogenesis protein PilM
<i>Pcc</i> ICMP5702_peg3991	AODT01000021.1	61922	64477	+	Multimodular transpeptidase-transglycosylase (EC 2.4.1.129) (EC 3.4.-.-)
<i>Pcc</i> ICMP5702_peg3992	AODT01000021.1	66022	64598	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3993	AODT01000021.1	66811	66254	-	ADP compounds hydrolase NudE
<i>Pcc</i> ICMP5702_peg3994	AODT01000021.1	67011	66829	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg3995	AODT01000021.1	67249	69396	+	IgaA: a membrane protein that prevents overactivation of the Rcs regulatory system
<i>Pcc</i> ICMP5702_peg3996	AODT01000021.1	69514	70200	+	GMP/IMP nucleotidase YrfG
<i>Pcc</i> ICMP5702_peg3997	AODT01000021.1	70213	70623	+	Ribosome-associated heat shock protein implicated in the recycling of the 50S subunit (S4 paralog)
<i>Pcc</i> ICMP5702_peg3998	AODT01000021.1	70700	71569	+	33 kDa chaperonin HsI0
<i>Pcc</i> ICMP5702_peg3999	AODT01000021.1	71768	73387	+	Phosphoenolpyruvate carboxykinase [ATP] (EC 4.1.1.49)
<i>Pcc</i> ICMP5702_peg4000	AODT01000021.1	74844	73483	-	Osmolarity sensory histidine kinase EnvZ
<i>Pcc</i> ICMP5702_peg4001	AODT01000021.1	75560	74841	-	Two-component system response regulator OmpR
<i>Pcc</i> ICMP5702_peg4002	AODT01000021.1	76303	75893	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4003	AODT01000021.1	77532	76372	-	ABC transporter, substrate-binding protein (cluster 8, B12/iron complex)
<i>Pcc</i> ICMP5702_peg4004	AODT01000021.1	78775	77525	-	Multidrug resistance protein ErmB
<i>Pcc</i> ICMP5702_peg4005	AODT01000021.1	80005	78836	-	Tauropine dehydrogenase
<i>Pcc</i> ICMP5702_peg4006	AODT01000021.1	81032	80016	-	Pyridoxal-5'-phosphate-dependent enzyme beta superfamily (fold type II)
<i>Pcc</i> ICMP5702_peg4007	AODT01000021.1	82449	81046	-	Orn/DAP/Arg family decarboxylase
<i>Pcc</i> ICMP5702_peg4008	AODT01000021.1	84680	82491	-	Ferrichrome-iron receptor
<i>Pcc</i> ICMP5702_peg4009	AODT01000021.1	86664	84763	-	Siderophore synthetase superfamily, group B
<i>Pcc</i> ICMP5702_peg4010	AODT01000021.1	86915	87796	+	Similar to citrate lyase beta chain, 3
<i>Pcc</i> ICMP5702_peg4011	AODT01000021.1	88342	87866	-	Transcription elongation factor GreB
<i>Pcc</i> ICMP5702_peg4012	AODT01000021.1	88517	90232	+	Hemolysin A
<i>Pcc</i> ICMP5702_peg4013	AODT01000021.1	90568	92235	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg4014	AODT01000021.1	92351	92238	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4015	AODT01000021.1	93710	92424	-	Citrate synthase (si) (EC 2.3.3.1)

<i>Pcc</i> ICMP5702_peg4016	AODT01000021.1	94004	96358	+	Transcription accessory protein (S1 RNA-binding domain)
<i>Pcc</i> ICMP5702_peg4017	AODT01000021.1	96586	97374	+	Transcriptional regulator, IclR family
<i>Pcc</i> ICMP5702_peg4018	AODT01000021.1	97716	98672	+	2-keto-3-deoxygluconate permease (KDG permease)
<i>Pcc</i> ICMP5702_peg4019	AODT01000021.1	98685	99521	+	4-deoxy-L-threo-5-hexosulose-uronate ketol-isomerase (EC 5.3.1.17)
<i>Pcc</i> ICMP5702_peg4020	AODT01000021.1	100150	99596	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4021	AODT01000021.1	100680	100147	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4022	AODT01000021.1	101536	100670	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4023	AODT01000021.1	101808	101530	-	Flavodoxin reductases (ferredoxin-NADPH reductases) family 1
<i>Pcc</i> ICMP5702_peg4024	AODT01000021.1	102938	101808	-	CpmD protein involved in carbapenem biosynthesis
<i>Pcc</i> ICMP5702_peg4025	AODT01000021.1	103814	102993	-	CpmC protein involved in carbapenem biosynthesis
<i>Pcc</i> ICMP5702_peg4026	AODT01000021.1	104581	103829	-	Carboxymethylproline synthase (EC 2.3.1.226)
<i>Pcc</i> ICMP5702_peg4027	AODT01000021.1	106095	104584	-	Carbapenam-3-carboxylate synthase (EC 6.3.3.6)
<i>Pcc</i> ICMP5702_peg4028	AODT01000021.1	107017	106283	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4029	AODT01000021.1	108881	107460	-	ABC-type antimicrobial peptide transport system, permease component
<i>Pcc</i> ICMP5702_peg4030	AODT01000021.1	109570	108878	-	ABC-type antimicrobial peptide transport system, ATPase component
<i>Pcc</i> ICMP5702_peg4031	AODT01000021.1	110058	109579	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4032	AODT01000021.1	111816	110071	-	Alkaline phosphatase (EC 3.1.3.1)
<i>Pcc</i> ICMP5702_peg4033	AODT01000021.1	112835	112179	-	Hypothetical protein
					Aminoglycosides efflux system AcrAD-TolC, inner-membrane proton/drug antiporter
<i>Pcc</i> ICMP5702_peg4034	AODT01000021.1	116392	113279	-	AcrD (RND type)
<i>Pcc</i> ICMP5702_peg4035	AODT01000021.1	117342	116575	-	Pimeloyl-[acyl-carrier protein] methyl ester esterase BioH (EC 3.1.1.85)
					Competence protein F homolog, phosphoribosyltransferase domain; protein YhgH
<i>Pcc</i> ICMP5702_peg4036	AODT01000021.1	117442	118143	+	required for utilization of DNA as sole source of carbon and energy
<i>Pcc</i> ICMP5702_peg4037	AODT01000021.1	118204	118779	+	[4Fe-4S] cluster carrier protein NfuA
<i>Pcc</i> ICMP5702_peg4038	AODT01000021.1	120934	118850	-	4-alpha-glucanotransferase (amylomaltase) (EC 2.4.1.25)
<i>Pcc</i> ICMP5702_peg4039	AODT01000021.1	123493	120947	-	Maltodextrin phosphorylase (EC 2.4.1.1)
<i>Pcc</i> ICMP5702_peg4040	AODT01000021.1	124294	123536	-	Glycerol-3-phosphate regulon repressor GlpR
<i>Pcc</i> ICMP5702_peg4041	AODT01000021.1	125152	124319	-	Rhomboid protease GlpG (EC 3.4.21.105)
<i>Pcc</i> ICMP5702_peg4042	AODT01000021.1	125374	126627	+	Glucose-1-phosphatase (EC 3.1.3.10)
<i>Pcc</i> ICMP5702_peg4043	AODT01000021.1	127035	126712	-	Thiosulfate sulfurtransferase GlpE (EC 2.8.1.1)
<i>Pcc</i> ICMP5702_peg4044	AODT01000021.1	127295	127152	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4045	AODT01000021.1	127374	128873	+	Aerobic glycerol-3-phosphate dehydrogenase (EC 1.1.5.3)
<i>Pcc</i> ICMP5702_peg4046	AODT01000021.1	131410	128963	-	Glycogen phosphorylase (EC 2.4.1.1)
<i>Pcc</i> ICMP5702_peg4047	AODT01000021.1	132925	131486	-	Glycogen synthase, ADP-glucose transglucosylase (EC 2.4.1.21)
<i>Pcc</i> ICMP5702_peg4048	AODT01000021.1	134231	132954	-	Glucose-1-phosphate adenylyltransferase (EC 2.7.7.27)
<i>Pcc</i> ICMP5702_peg4049	AODT01000021.1	136243	134267	-	Limit dextrin alpha-1,6-maltotetraose-hydrolase (EC 3.2.1.196)

<i>Pcc</i> ICMP5702_peg4050	AODT01000021.1	138421	136244	-	1,4-alpha-glucan (glycogen) branching enzyme, GH-13-type (EC 2.4.1.18)
<i>Pcc</i> ICMP5702_peg4051	AODT01000021.1	138794	140512	+	Sensor histidine kinase BtsS
<i>Pcc</i> ICMP5702_peg4052	AODT01000021.1	141853	140585	-	HIPA PROTEIN
<i>Pcc</i> ICMP5702_peg4053	AODT01000021.1	142163	141843	-	Transcriptional regulator
<i>Pcc</i> ICMP5702_peg4054	AODT01000021.1	143521	142418	-	Aspartate-semialdehyde dehydrogenase (EC 1.2.1.11)
<i>Pcc</i> ICMP5702_peg4055	AODT01000021.1	143821	144414	+	MarC family integral membrane protein
<i>Pcc</i> ICMP5702_peg4056	AODT01000021.1	146165	144789	-	Low-affinity gluconate/H ⁺ symporter GntU
<i>Pcc</i> ICMP5702_peg4057	AODT01000021.1	146324	146836	+	Gluconokinase (EC 2.7.1.12)
<i>Pcc</i> ICMP5702_peg4058	AODT01000021.1	147841	146846	-	Gluconate utilization system Gnt-I transcriptional repressor
<i>Pcc</i> ICMP5702_peg4059	AODT01000021.1	148698	148003	-	Quercetin 2,3-dioxygenase (EC 1.13.11.24) => YhhW
<i>Pcc</i> ICMP5702_peg4060	AODT01000021.1	150277	149066	-	Anaerobic glycerol-3-phosphate dehydrogenase subunit C (EC 1.1.5.3)
<i>Pcc</i> ICMP5702_peg4061	AODT01000021.1	151536	150274	-	Anaerobic glycerol-3-phosphate dehydrogenase subunit B (EC 1.1.5.3)
<i>Pcc</i> ICMP5702_peg4062	AODT01000021.1	153193	151526	-	Anaerobic glycerol-3-phosphate dehydrogenase subunit A (EC 1.1.5.3)
<i>Pcc</i> ICMP5702_peg4063	AODT01000021.1	153508	154857	+	Glycerol-3-phosphate transporter
<i>Pcc</i> ICMP5702_peg4064	AODT01000021.1	154933	156000	+	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46) periplasmic (secreted in GramPositives)
<i>Pcc</i> ICMP5702_peg4065	AODT01000021.1	156979	156179	-	HAD phosphatase YigL
<i>Pcc</i> ICMP5702_peg4066	AODT01000021.1	158121	157084	-	Lysophospholipase L2 (EC 3.1.1.5)
<i>Pcc</i> ICMP5702_peg4067	AODT01000021.1	158252	158872	+	Homoserine/homoserine lactone efflux protein
<i>Pcc</i> ICMP5702_peg4068	AODT01000021.1	159556	158933	-	Threonine efflux protein RhtC
<i>Pcc</i> ICMP5702_peg4069	AODT01000021.1	161429	159600	-	ATP-dependent DNA helicase RecQ
<i>Pcc</i> ICMP5702_peg4070	AODT01000021.1	162428	161562	-	Phospholipase A1 (EC 3.1.1.32) (EC 3.1.1.4) @ Outer membrane phospholipase A
<i>Pcc</i> ICMP5702_peg4071	AODT01000021.1	162747	163187	+	Uncharacterized protein YigI
<i>Pcc</i> ICMP5702_peg4072	AODT01000021.1	163286	164215	+	Uncharacterized inner membrane protein RarD
<i>Pcc</i> ICMP5702_peg4073	AODT01000021.1	165239	164181	-	AbrB protein
<i>Pcc</i> ICMP5702_peg4074	AODT01000021.1	166656	165706	-	Magnesium and cobalt transport protein CorA
<i>Pcc</i> ICMP5702_peg4075	AODT01000021.1	167814	167068	-	Metal-dependent hydrolase
<i>Pcc</i> ICMP5702_peg4076	AODT01000021.1	170121	167959	-	ATP-dependent DNA helicase UvrD/PcrA (EC 3.6.4.12)
<i>Pcc</i> ICMP5702_peg4077	AODT01000021.1	170916	170200	-	Uncharacterized putative hydrolase YigB
<i>Pcc</i> ICMP5702_peg4078	AODT01000021.1	171851	170916	-	Site-specific tyrosine recombinase XerC
<i>Pcc</i> ICMP5702_peg4079	AODT01000021.1	172552	171848	-	Uncharacterized DUF484 protein YigA
<i>Pcc</i> ICMP5702_peg4080	AODT01000021.1	173373	172549	-	Diaminopimelate epimerase (EC 5.1.1.7)
<i>Pcc</i> ICMP5702_peg4081	AODT01000021.1	173623	173438	-	Diaminopimelate decarboxylase and/or diaminopimelate epimerase leader peptide
<i>Pcc</i> ICMP5702_peg4082	AODT01000021.1	173683	174003	+	Frataxin homolog CyaY, facilitates Fe-S cluster assembly, interacts with IscS
<i>Pcc</i> ICMP5702_peg4083	AODT01000021.1	175209	174037	-	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg4084	AODT01000021.1	177816	175258	-	Adenylate cyclase (EC 4.6.1.1)

<i>Pcc</i> ICMP5702_peg4085	AODT01000021.1	178148	179089	+	Porphobilinogen deaminase (EC 2.5.1.61)
<i>Pcc</i> ICMP5702_peg4086	AODT01000021.1	179086	179826	+	Uroporphyrinogen-III synthase (EC 4.2.1.75)
<i>Pcc</i> ICMP5702_peg4087	AODT01000021.1	179850	180974	+	Uncharacterized protein EC-HemX
<i>Pcc</i> ICMP5702_peg4088	AODT01000021.1	180977	182170	+	Uncharacterized protein EC-HemY in Proteobacteria (unrelated to HemY-type PPO in GramPositives)
<i>Pcc</i> ICMP5702_peg4089	AODT01000021.1	183421	182771	-	Transcriptional regulator, GntR family
<i>Pcc</i> ICMP5702_peg4090	AODT01000021.1	183759	185111	+	Immune-responsive protein 1
<i>Pcc</i> ICMP5702_peg4091	AODT01000021.1	185176	186501	+	Immune-responsive protein 1
<i>Pcc</i> ICMP5702_peg4092	AODT01000021.1	186517	187338	+	Bll7429 protein
<i>Pcc</i> ICMP5702_peg4093	AODT01000021.1	187560	188612	+	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg4094	AODT01000021.1	188738	189961	+	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg4095	AODT01000021.1	189972	191081	+	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg4096	AODT01000021.1	191124	191924	+	ABC transporter, ATP-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg4097	AODT01000021.1	193140	191983	-	N-acetyl-L,L-diaminopimelate deacetylase homolog
<i>Pcc</i> ICMP5702_peg4098	AODT01000021.1	193979	193218	-	Probable amino-acid import ATP-binding protein YxeO
<i>Pcc</i> ICMP5702_peg4099	AODT01000021.1	194660	193989	-	Probable amino-acid permease protein YxeN
<i>Pcc</i> ICMP5702_peg4100	AODT01000021.1	195532	194741	-	Probable amino-acid-binding protein YxeM
<i>Pcc</i> ICMP5702_peg4101	AODT01000021.1	196071	195529	-	Histone acetyltransferase HPA2 and related acetyltransferases
<i>Pcc</i> ICMP5702_peg4102	AODT01000021.1	197445	196081	-	Formerly called adenylosuccinate lyase (similar to archaeal version), but most likely something else
<i>Pcc</i> ICMP5702_peg4103	AODT01000021.1	197694	199001	+	Periplasmic phosphoanhydride phosphohydrolase
<i>Pcc</i> ICMP5702_peg4104	AODT01000021.1	201181	199790	-	Probable transport protein YifK
<i>Pcc</i> ICMP5702_peg4105	AODT01000021.1	202298	201549	-	Lipopolysaccharide N-acetylmannosaminouronosyltransferase (EC 2.4.1.180)
<i>Pcc</i> ICMP5702_peg4106	AODT01000021.1	203677	202295	-	Putative ECA polymerase WzyE
<i>Pcc</i> ICMP5702_peg4107	AODT01000021.1	204759	203674	-	TDP-N-acetylfucosamine:lipid II N-acetylfucosaminyltransferase (EC 2.4.1.325)
<i>Pcc</i> ICMP5702_peg4108	AODT01000021.1	206006	204756	-	Lipid III flippase
<i>Pcc</i> ICMP5702_peg4109	AODT01000021.1	207138	206008	-	dTDP-4-amino-4,6-dideoxygalactose transaminase (EC 2.6.1.59)
<i>Pcc</i> ICMP5702_peg4110	AODT01000021.1	207874	207143	-	dTDP-fucosamine acetyltransferase (EC 2.3.1.210)
<i>Pcc</i> ICMP5702_peg4111	AODT01000021.1	208984	207917	-	dTDP-glucose 4,6-dehydratase (EC 4.2.1.46)
<i>Pcc</i> ICMP5702_peg4112	AODT01000021.1	210243	208981	-	UDP-N-acetyl-D-mannosamine dehydrogenase (EC 1.1.1.336)
<i>Pcc</i> ICMP5702_peg4113	AODT01000021.1	211628	210510	-	UDP-N-acetylglucosamine 2-epimerase (EC 5.1.3.14)
<i>Pcc</i> ICMP5702_peg4114	AODT01000021.1	212742	211696	-	Lipopolysaccharide biosynthesis protein WzzE
<i>Pcc</i> ICMP5702_peg4115	AODT01000021.1	213846	212764	-	2.7.8.33)
<i>Pcc</i> ICMP5702_peg4116	AODT01000021.1	215327	214068	-	Transcription termination factor Rho
<i>Pcc</i> ICMP5702_peg4117	AODT01000021.1	215375	215527	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4118	AODT01000021.1	216149	215823	-	Thioredoxin

<i>Pcc</i> ICMP5702_peg4119	AODT01000021.1	216268	217557	+	ATP-dependent RNA helicase RhlB (EC 3.6.4.13)
					Guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase (EC 3.6.1.40) @
<i>Pcc</i> ICMP5702_peg4120	AODT01000021.1	217564	219060	+	Exopolyphosphatase (EC 3.6.1.11)
<i>Pcc</i> ICMP5702_peg4121	AODT01000021.1	221102	219081	-	ATP-dependent DNA helicase Rep
<i>Pcc</i> ICMP5702_peg4122	AODT01000021.1	221263	221544	+	Peptidyl-prolyl cis-trans isomerase PpiC (EC 5.2.1.8)
					Transcriptional repressor of PutA and PutP / Proline dehydrogenase (EC 1.5.5.2) /
<i>Pcc</i> ICMP5702_peg4123	AODT01000021.1	225609	221641	-	Delta-1-pyrroline-5-carboxylate dehydrogenase (EC 1.2.1.88)
<i>Pcc</i> ICMP5702_peg4124	AODT01000021.1	225806	227290	+	Proline/sodium symporter PutP (TC 2.A.21.2.1) @ Propionate/sodium symporter
<i>Pcc</i> ICMP5702_peg4125	AODT01000021.1	228827	227349	-	Ketol-acid reductoisomerase (NADP(+)) (EC 1.1.1.86)
<i>Pcc</i> ICMP5702_peg4126	AODT01000021.1	228995	229885	+	Transcriptional regulator IlvY, LysR family
<i>Pcc</i> ICMP5702_peg4127	AODT01000021.1	229882	230682	+	Probable exported protein YPO0702
<i>Pcc</i> ICMP5702_peg4128	AODT01000021.1	231444	230701	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4129	AODT01000021.1	232051	231545	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4130	AODT01000021.1	232579	232139	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4131	AODT01000021.1	233166	232576	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4132	AODT01000021.1	233784	233305	-	T6SS component Hcp
<i>Pcc</i> ICMP5702_peg4133	AODT01000021.1	234022	233813	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4134	AODT01000021.1	235844	234300	-	Threonine dehydratase biosynthetic (EC 4.3.1.19)
<i>Pcc</i> ICMP5702_peg4135	AODT01000021.1	237700	235850	-	Dihydroxy-acid dehydratase (EC 4.2.1.9)
<i>Pcc</i> ICMP5702_peg4136	AODT01000021.1	238895	237969	-	Branched-chain amino acid aminotransferase (EC 2.6.1.42)
<i>Pcc</i> ICMP5702_peg4137	AODT01000021.1	239181	238921	-	Acetolactate synthase small subunit (EC 2.2.1.6)
<i>Pcc</i> ICMP5702_peg4138	AODT01000021.1	240906	239260	-	Acetolactate synthase large subunit (EC 2.2.1.6)
<i>Pcc</i> ICMP5702_peg4139	AODT01000021.1	241553	243079	+	AAA+ ATPase superfamily protein YifB/ComM, associated with DNA recombination
<i>Pcc</i> ICMP5702_peg4140	AODT01000021.1	243474	243136	-	UPF0438 protein YifE
<i>Pcc</i> ICMP5702_peg4141	AODT01000021.1	243595	244422	+	LysR family transcriptional regulator HdfR
<i>Pcc</i> ICMP5702_peg4142	AODT01000021.1	245406	244444	-	Galactofuranose ABC transporter, permease protein 2
<i>Pcc</i> ICMP5702_peg4143	AODT01000021.1	246416	245406	-	Galactofuranose ABC transporter, permease protein 1
<i>Pcc</i> ICMP5702_peg4144	AODT01000021.1	247923	246403	-	Galactofuranose ABC transporter, ATP-binding protein
<i>Pcc</i> ICMP5702_peg4145	AODT01000021.1	249070	248114	-	Galactofuranose ABC transporter, substrate-binding protein
<i>Pcc</i> ICMP5702_peg4146	AODT01000022.1	870	232	-	Glutamate racemase (EC 5.1.1.3)
<i>Pcc</i> ICMP5702_peg4147	AODT01000022.1	2911	1034	-	Outer membrane vitamin B12 receptor BtuB
					tRNA (uracil(54)-C5)-methyltransferase (EC 2.1.1.35) @ tmRNA (uracil(341)-C5)-
<i>Pcc</i> ICMP5702_peg4148	AODT01000022.1	3336	4439	+	methyltransferase
<i>Pcc</i> ICMP5702_peg4149	AODT01000022.1	4866	4480	-	Inner membrane protein YijD
<i>Pcc</i> ICMP5702_peg4150	AODT01000022.1	5543	4902	-	Unsaturated fatty acid biosynthesis repressor FabR, TetR family
<i>Pcc</i> ICMP5702_peg4151	AODT01000022.1	5744	7150	+	Soluble pyridine nucleotide transhydrogenase (EC 1.6.1.1)

<i>Pcc</i> ICMP5702_peg4152	AODT01000022.1	8050	7142	-	Hydrogen peroxide-inducible genes activator => OxyR
<i>Pcc</i> ICMP5702_peg4153	AODT01000022.1	9577	8681	-	5,10-methylenetetrahydrofolate reductase (EC 1.5.1.20)
<i>Pcc</i> ICMP5702_peg4154	AODT01000022.1	9590	9721	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4155	AODT01000022.1	10046	9729	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4156	AODT01000022.1	10849	10088	-	3',5'-cyclic-nucleotide phosphodiesterase (EC 3.1.4.17)
<i>Pcc</i> ICMP5702_peg4157	AODT01000022.1	11901	10897	-	Transcriptional regulator, LacI family
<i>Pcc</i> ICMP5702_peg4158	AODT01000022.1	12704	11898	-	ABC transporter, permease protein 2 (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg4159	AODT01000022.1	13540	12701	-	ABC transporter, permease protein
<i>Pcc</i> ICMP5702_peg4160	AODT01000022.1	14745	13612	-	ABC transporter, substrate-binding protein (cluster 1, maltose/g3p/polyamine/iron)
<i>Pcc</i> ICMP5702_peg4161	AODT01000022.1	15934	14768	-	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg4162	AODT01000022.1	18575	16140	-	Aspartokinase (EC 2.7.2.4) / Homoserine dehydrogenase (EC 1.1.1.3)
<i>Pcc</i> ICMP5702_peg4163	AODT01000022.1	19738	18578	-	Cystathionine gamma-synthase (EC 2.5.1.48)
<i>Pcc</i> ICMP5702_peg4164	AODT01000022.1	19926	20243	+	Methionine repressor MetJ
<i>Pcc</i> ICMP5702_peg4165	AODT01000022.1	20461	21258	+	Iron ABC transporter, ATP-binding protein
<i>Pcc</i> ICMP5702_peg4166	AODT01000022.1	21268	22230	+	ABC transporter, substrate-binding protein (cluster 8, B12/iron complex)
<i>Pcc</i> ICMP5702_peg4167	AODT01000022.1	22227	23240	+	ABC transporter, permease protein (cluster 8, B12/iron complex)
<i>Pcc</i> ICMP5702_peg4168	AODT01000022.1	23527	23312	-	LSU ribosomal protein L31p @ LSU ribosomal protein L31p, zinc-dependent
<i>Pcc</i> ICMP5702_peg4169	AODT01000022.1	23800	25998	+	Helicase PriA essential for oriC/DnaA-independent DNA replication
<i>Pcc</i> ICMP5702_peg4170	AODT01000022.1	26307	27350	+	Transcriptional (co)regulator CytR
<i>Pcc</i> ICMP5702_peg4171	AODT01000022.1	27541	28314	+	Cell division protein FtsN
<i>Pcc</i> ICMP5702_peg4172	AODT01000022.1	28398	28928	+	ATP-dependent protease subunit HslV (EC 3.4.25.2)
<i>Pcc</i> ICMP5702_peg4173	AODT01000022.1	28938	30269	+	ATP-dependent hsl protease ATP-binding subunit HslU
<i>Pcc</i> ICMP5702_peg4174	AODT01000022.1	30303	30434	+	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74)
<i>Pcc</i> ICMP5702_peg4175	AODT01000022.1	30415	31332	+	1,4-dihydroxy-2-naphthoate polyprenyltransferase (EC 2.5.1.74)
<i>Pcc</i> ICMP5702_peg4176	AODT01000022.1	31467	31952	+	Ribonuclease E inhibitor RraA
<i>Pcc</i> ICMP5702_peg4177	AODT01000022.1	32311	32072	-	Cell division protein ZapB
<i>Pcc</i> ICMP5702_peg4178	AODT01000022.1	32882	33721	+	Glycerol uptake facilitator protein
<i>Pcc</i> ICMP5702_peg4179	AODT01000022.1	33775	35286	+	Glycerol kinase (EC 2.7.1.30)
<i>Pcc</i> ICMP5702_peg4180	AODT01000022.1	35425	36435	+	Fructose-1,6-bisphosphatase, GlpX type (EC 3.1.3.11)
<i>Pcc</i> ICMP5702_peg4181	AODT01000022.1	36553	37299	+	Ferredoxin--NADP(+) reductase (EC 1.18.1.2) @ Flavodoxin--NADP(+) reductase (EC 1.19.1.1)
<i>Pcc</i> ICMP5702_peg4182	AODT01000022.1	37738	37316	-	Uncharacterized protein YiiR
<i>Pcc</i> ICMP5702_peg4183	AODT01000022.1	37976	38575	+	Uncharacterized protein YiiQ
<i>Pcc</i> ICMP5702_peg4184	AODT01000022.1	38741	39508	+	Triosephosphate isomerase (EC 5.3.1.1)
<i>Pcc</i> ICMP5702_peg4185	AODT01000022.1	39685	39975	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg4186	AODT01000022.1	39962	40276	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4187	AODT01000022.1	41502	40399	-	Agmatine deiminase (EC 3.5.3.12)
<i>Pcc</i> ICMP5702_peg4188	AODT01000022.1	42390	41506	-	N-carbamoylputrescine amidase (EC 3.5.1.53)
<i>Pcc</i> ICMP5702_peg4189	AODT01000022.1	42412	42561	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4190	AODT01000022.1	43480	42722	-	ABC transporter, ATP-binding protein (cluster 1, maltose/g3p/polyamine/iron); ABC transporter, ATP-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg4191	AODT01000022.1	45105	43498	-	ABC transporter, permease protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg4192	AODT01000022.1	45528	45127	-	Biopolymer transport protein ExbD/TolR
<i>Pcc</i> ICMP5702_peg4193	AODT01000022.1	46246	45530	-	MotA/TolQ/ExbB proton channel family protein
<i>Pcc</i> ICMP5702_peg4194	AODT01000022.1	47120	46257	-	putative TonB-dependent receptor
<i>Pcc</i> ICMP5702_peg4195	AODT01000022.1	47578	48585	+	ABC transporter, substrate-binding protein (cluster 10, nitrate/sulfonate/bicarbonate)
<i>Pcc</i> ICMP5702_peg4196	AODT01000022.1	48672	50978	+	TonB-dependent receptor
<i>Pcc</i> ICMP5702_peg4197	AODT01000022.1	50983	53763	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4198	AODT01000022.1	53798	54490	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4199	AODT01000022.1	55406	54477	-	Transcriptional regulator
<i>Pcc</i> ICMP5702_peg4200	AODT01000022.1	55705	55580	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4201	AODT01000022.1	56827	55865	-	6-phosphofructokinase (EC 2.7.1.11)
<i>Pcc</i> ICMP5702_peg4202	AODT01000022.1	57936	57034	-	Ferrous-iron efflux pump FieF
<i>Pcc</i> ICMP5702_peg4203	AODT01000022.1	59185	57998	-	Sugar efflux transporter B
<i>Pcc</i> ICMP5702_peg4204	AODT01000022.1	61564	59492	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4205	AODT01000022.1	62712	61561	-	Mg-chelatase subunit ChlD
<i>Pcc</i> ICMP5702_peg4206	AODT01000022.1	65270	62709	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4207	AODT01000022.1	66439	65330	-	Uncharacterized protein YehL
<i>Pcc</i> ICMP5702_peg4208	AODT01000022.1	70252	66509	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4209	AODT01000022.1	70888	70520	-	Putative regulatory protein
<i>Pcc</i> ICMP5702_peg4210	AODT01000022.1	71219	70959	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4211	AODT01000022.1	72080	71556	-	Periplasmic protein CpxP
<i>Pcc</i> ICMP5702_peg4212	AODT01000022.1	72234	72932	+	Copper-sensing two-component system response regulator CpxR
<i>Pcc</i> ICMP5702_peg4213	AODT01000022.1	72929	74299	+	Copper sensory histidine kinase CpxA
<i>Pcc</i> ICMP5702_peg4214	AODT01000022.1	74493	76667	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4215	AODT01000022.1	76637	77437	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4216	AODT01000022.1	77912	77448	-	tRNA (cytidine(34)-2'-O)-methyltransferase (EC 2.1.1.207)
<i>Pcc</i> ICMP5702_peg4217	AODT01000022.1	78109	78405	+	Uncharacterized protein YhhA
<i>Pcc</i> ICMP5702_peg4218	AODT01000022.1	79375	78419	-	Auxin efflux carrier family protein
<i>Pcc</i> ICMP5702_peg4219	AODT01000022.1	80240	79491	-	Glycerophosphoryl diester phosphodiesterase (EC 3.1.4.46)
<i>Pcc</i> ICMP5702_peg4220	AODT01000022.1	81313	80240	-	Glycerol-3-phosphate ABC transporter, ATP-binding protein UgpC (TC 3.A.1.1.3)

<i>Pcc</i> ICMP5702_peg4221	AODT01000022.1	82184	81339	-	Glycerol-3-phosphate ABC transporter, permease protein UgpE (TC 3.A.1.1.3)
<i>Pcc</i> ICMP5702_peg4222	AODT01000022.1	83068	82181	-	Glycerol-3-phosphate ABC transporter, permease protein UgpA (TC 3.A.1.1.3)
<i>Pcc</i> ICMP5702_peg4223	AODT01000022.1	84475	83141	-	Glycerol-3-phosphate ABC transporter, substrate-binding protein UgpB
<i>Pcc</i> ICMP5702_peg4224	AODT01000022.1	84659	84838	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4225	AODT01000022.1	85246	84905	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4226	AODT01000022.1	86018	85323	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4227	AODT01000022.1	86208	86378	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4228	AODT01000022.1	86505	86930	+	FIG071147: Hypothetical protein
<i>Pcc</i> ICMP5702_peg4229	AODT01000022.1	86881	87210	+	Antitoxin to RelE-like translational repressor toxin
<i>Pcc</i> ICMP5702_peg4230	AODT01000022.1	87995	87234	-	L-threonate/D-erythronate transcriptional regulator, DeoR family
<i>Pcc</i> ICMP5702_peg4231	AODT01000022.1	88334	89248	+	L-threonate dehydrogenase (NAD ⁺)
<i>Pcc</i> ICMP5702_peg4232	AODT01000022.1	89245	90519	+	3-oxo-tetronate kinase
<i>Pcc</i> ICMP5702_peg4233	AODT01000022.1	90516	91172	+	3-oxo-tetronate 4-phosphate decarboxylase
<i>Pcc</i> ICMP5702_peg4234	AODT01000022.1	91206	91988	+	2-dehydrotetronate isomerase (EC 5.3.1.35)
<i>Pcc</i> ICMP5702_peg4235	AODT01000022.1	92183	93541	+	L-threonate/D-erythronate, proton symporter
<i>Pcc</i> ICMP5702_peg4236	AODT01000022.1	93854	95533	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg4237	AODT01000022.1	95547	95705	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4238	AODT01000022.1	95812	97482	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg4239	AODT01000022.1	98164	99834	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg4240	AODT01000022.1	100428	102074	+	Methyl-accepting chemotaxis sensor/transducer protein
<i>Pcc</i> ICMP5702_peg4241	AODT01000022.1	103355	102165	-	Aspartate aminotransferase (AspB-4) (EC 2.6.1.1)
<i>Pcc</i> ICMP5702_peg4242	AODT01000022.1	104185	103484	-	Branched-chain amino acid ABC transporter, ATP-binding protein LivF (TC 3.A.1.4.1)
<i>Pcc</i> ICMP5702_peg4243	AODT01000022.1	104961	104191	-	3.A.1.4.1)
<i>Pcc</i> ICMP5702_peg4244	AODT01000022.1	106232	104958	-	Branched-chain amino acid ABC transporter, permease protein LivM (TC 3.A.1.4.1)
<i>Pcc</i> ICMP5702_peg4245	AODT01000022.1	107155	106229	-	Branched-chain amino acid ABC transporter, permease protein LivH (TC 3.A.1.4.1)
<i>Pcc</i> ICMP5702_peg4246	AODT01000022.1	108425	107313	-	3.A.1.4.1)
<i>Pcc</i> ICMP5702_peg4247	AODT01000022.1	108736	108590	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4248	AODT01000022.1	108830	109276	+	Acetyl-CoA sensor PanM, required for maturation of L-aspartate decarboxylase
<i>Pcc</i> ICMP5702_peg4249	AODT01000022.1	110217	109360	-	RNA polymerase sigma factor RpoH
<i>Pcc</i> ICMP5702_peg4250	AODT01000022.1	110248	110364	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4251	AODT01000022.1	111544	110576	-	Cell-division-associated, ABC-transporter-like signaling protein FtsX
<i>Pcc</i> ICMP5702_peg4252	AODT01000022.1	112205	111534	-	Cell-division-associated, ABC-transporter-like signaling protein FtsE
<i>Pcc</i> ICMP5702_peg4253	AODT01000022.1	113728	112211	-	Signal recognition particle receptor FtsY
<i>Pcc</i> ICMP5702_peg4254	AODT01000022.1	114078	114653	+	16S rRNA (guanine(966)-N(2))-methyltransferase (EC 2.1.1.171)
<i>Pcc</i> ICMP5702_peg4255	AODT01000022.1	114680	114958	+	Uncharacterized protein YhhL
<i>Pcc</i> ICMP5702_peg4256	AODT01000022.1	115321	114962	-	Uncharacterized protein YhhM

<i>Pcc</i> ICMP5702_peg4257	AODT01000022.1	115641	115321	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4258	AODT01000022.1	115833	116462	+	Uncharacterized membrane protein YhhN
					Lead, cadmium, zinc and mercury transporting ATPase (EC 3.6.3.3) (EC 3.6.3.5);
<i>Pcc</i> ICMP5702_peg4259	AODT01000022.1	116761	119115	+	Copper-translocating P-type ATPase (EC 3.6.3.4)
<i>Pcc</i> ICMP5702_peg4260	AODT01000022.1	119417	119175	-	tRNA 5-methylaminomethyl-2-thiouridine synthesis sulfur carrier protein TusA
<i>Pcc</i> ICMP5702_peg4261	AODT01000022.1	119651	120328	+	Putative preQ0 transporter YhhQ
<i>Pcc</i> ICMP5702_peg4262	AODT01000022.1	120516	121082	+	DcrB protein precursor
<i>Pcc</i> ICMP5702_peg4263	AODT01000022.1	122328	121132	-	UPF0226 protein YhhS
<i>Pcc</i> ICMP5702_peg4264	AODT01000022.1	122456	123472	+	Inner membrane protein YhjD
<i>Pcc</i> ICMP5702_peg4265	AODT01000022.1	123640	124572	+	2-dehydro-3-deoxygluconokinase (EC 2.7.1.45)
<i>Pcc</i> ICMP5702_peg4266	AODT01000022.1	126171	124654	-	Protein YhjJ, putative peptidase
<i>Pcc</i> ICMP5702_peg4267	AODT01000022.1	127823	126531	-	Na ⁺ /H ⁺ -dicarboxylate symporter
<i>Pcc</i> ICMP5702_peg4268	AODT01000022.1	129327	128143	-	Protein yhjK
<i>Pcc</i> ICMP5702_peg4269	AODT01000022.1	131324	129663	-	Cellulose biosynthesis protein BcsG
<i>Pcc</i> ICMP5702_peg4270	AODT01000022.1	131544	131326	-	Cellulose biosynthesis protein BcsF
<i>Pcc</i> ICMP5702_peg4271	AODT01000022.1	133145	131541	-	Cellulose biosynthesis protein BcsE
<i>Pcc</i> ICMP5702_peg4272	AODT01000022.1	133486	133695	+	Putative cytoplasmic protein YhjR
<i>Pcc</i> ICMP5702_peg4273	AODT01000022.1	133698	134435	+	Cellulose biosynthesis protein BcsQ
<i>Pcc</i> ICMP5702_peg4274	AODT01000022.1	134432	137131	+	Cellulose synthase catalytic subunit [UDP-forming] (EC 2.4.1.12)
<i>Pcc</i> ICMP5702_peg4275	AODT01000022.1	137173	139533	+	Cyclic di-GMP-binding protein BcsB
<i>Pcc</i> ICMP5702_peg4276	AODT01000022.1	139540	140655	+	beta-1,4-glucanase (cellulase) (EC 3.2.1.4)
<i>Pcc</i> ICMP5702_peg4277	AODT01000022.1	140637	144116	+	Cellulose synthase operon protein C
<i>Pcc</i> ICMP5702_peg4278	AODT01000022.1	145163	144183	-	3-oxoacyl-[acyl-carrier-protein] synthase III
<i>Pcc</i> ICMP5702_peg4279	AODT01000022.1	146182	145205	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4280	AODT01000022.1	147884	146172	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4281	AODT01000022.1	149993	148215	-	Gamma-glutamyltranspeptidase (EC 2.3.2.2) @ Glutathione hydrolase (EC 3.4.19.13)
<i>Pcc</i> ICMP5702_peg4282	AODT01000022.1	151118	150207	-	Probable amino acid metabolite efflux pump
<i>Pcc</i> ICMP5702_peg4283	AODT01000022.1	152489	151281	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4284	AODT01000022.1	152746	152630	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4285	AODT01000022.1	152882	154132	+	Valine--pyruvate aminotransferase (EC 2.6.1.66)
<i>Pcc</i> ICMP5702_peg4286	AODT01000022.1	154671	155189	+	T6SS component Hcp
<i>Pcc</i> ICMP5702_peg4287	AODT01000022.1	155280	156479	+	VgrG protein
<i>Pcc</i> ICMP5702_peg4288	AODT01000022.1	156611	157165	+	VgrG protein
<i>Pcc</i> ICMP5702_peg4289	AODT01000022.1	157174	157581	+	FIG00904992: Hypothetical protein
<i>Pcc</i> ICMP5702_peg4290	AODT01000022.1	157593	161987	+	T6SS PAAR-repeat protein / RhaS protein
<i>Pcc</i> ICMP5702_peg4291	AODT01000022.1	162005	162421	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg4292	AODT01000022.1	162976	162863	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4293	AODT01000022.1	163469	163648	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4294	AODT01000022.1	163678	163965	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4295	AODT01000022.1	164230	164036	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4296	AODT01000022.1	164423	166285	+	T6SS PAAR-repeat protein / RhaS protein
<i>Pcc</i> ICMP5702_peg4297	AODT01000022.1	166289	166819	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4298	AODT01000022.1	167030	166875	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4299	AODT01000022.1	167216	167968	+	T6SS PAAR-repeat protein / RhaS protein
<i>Pcc</i> ICMP5702_peg4300	AODT01000022.1	167971	168360	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4301	AODT01000022.1	168500	168817	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4302	AODT01000022.1	169271	169549	+	T6SS PAAR-repeat protein / RhaS protein
<i>Pcc</i> ICMP5702_peg4303	AODT01000022.1	169668	170147	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4304	AODT01000022.1	171245	170235	-	Dipeptide ABC transporter, ATP-binding protein DppF (TC 3.A.1.5.2)
<i>Pcc</i> ICMP5702_peg4305	AODT01000022.1	172222	171242	-	Dipeptide ABC transporter, ATP-binding protein DppD (TC 3.A.1.5.2)
<i>Pcc</i> ICMP5702_peg4306	AODT01000022.1	173138	172236	-	Dipeptide ABC transporter, permease protein DppC (TC 3.A.1.5.2)
<i>Pcc</i> ICMP5702_peg4307	AODT01000022.1	174171	173152	-	Dipeptide ABC transporter, permease protein DppB (TC 3.A.1.5.2)
<i>Pcc</i> ICMP5702_peg4308	AODT01000022.1	176013	174406	-	Dipeptide ABC transporter, substrate-binding protein DppA (TC 3.A.1.5.2) @
<i>Pcc</i> ICMP5702_peg4309	AODT01000022.1	176957	176772	-	Dipeptide chemoreceptor
<i>Pcc</i> ICMP5702_peg4310	AODT01000022.1	177477	178820	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4311	AODT01000022.1	178808	178960	+	L-malate or citrate/H ⁺ symporter CimH (TC 2.A.24.2.4)
<i>Pcc</i> ICMP5702_peg4312	AODT01000022.1	178808	178960	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4313	AODT01000022.1	179245	178979	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4314	AODT01000022.1	179684	179421	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4315	AODT01000022.1	180576	179671	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4316	AODT01000022.1	181408	180686	-	Fumarate respiration two-component response regulator DcuR
<i>Pcc</i> ICMP5702_peg4317	AODT01000022.1	183029	181401	-	Fumarate respiration sensor kinase protein DcuS
<i>Pcc</i> ICMP5702_peg4318	AODT01000022.1	184630	183218	-	2-oxoglutarate/malate translocator
<i>Pcc</i> ICMP5702_peg4319	AODT01000022.1	184719	184883	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4320	AODT01000022.1	186861	185203	-	Putative transport protein YidE
<i>Pcc</i> ICMP5702_peg4321	AODT01000022.1	186888	187025	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4322	AODT01000022.1	187472	187020	-	16 kDa heat shock protein B
<i>Pcc</i> ICMP5702_peg4323	AODT01000022.1	187513	187626	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4324	AODT01000022.1	188052	187639	-	16 kDa heat shock protein A
<i>Pcc</i> ICMP5702_peg4325	AODT01000022.1	188440	188796	+	Outer membrane lipoprotein YidQ
<i>Pcc</i> ICMP5702_peg4326	AODT01000022.1	190133	188832	-	Uncharacterized protein YidR
<i>Pcc</i> ICMP5702_peg4327	AODT01000022.1	190348	190605	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg4327	AODT01000022.1	192245	190833	-	6-phospho-beta-glucosidase (EC 3.2.1.86)
<i>Pcc</i> ICMP5702_peg4328	AODT01000022.1	193593	192271	-	PTS system, cellobiose-specific IIC component
<i>Pcc</i> ICMP5702_peg4329	AODT01000022.1	193853	193590	-	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)
<i>Pcc</i> ICMP5702_peg4330	AODT01000022.1	194346	195368	+	Alkanesulfonate ABC transporter substrate-binding protein SsuA
<i>Pcc</i> ICMP5702_peg4331	AODT01000022.1	195427	196569	+	FMNH2-dependent alkanesulfonate monooxygenase (EC 1.14.14.5)
<i>Pcc</i> ICMP5702_peg4332	AODT01000022.1	196580	197374	+	Alkanesulfonate ABC transporter permease protein SsuC
<i>Pcc</i> ICMP5702_peg4333	AODT01000022.1	197371	198171	+	Alkanesulfonate ABC transporter ATP-binding protein SsuB
<i>Pcc</i> ICMP5702_peg4334	AODT01000022.1	198344	198601	+	Uncharacterized periplasmic protein YbiJ
<i>Pcc</i> ICMP5702_peg4335	AODT01000022.1	200485	198686	-	ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines) / ABC transporter, ATP-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg4336	AODT01000022.1	201433	200525	-	ABC transporter, permease protein 2 (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg4337	AODT01000022.1	202407	201430	-	ABC transporter, permease protein 1 (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg4338	AODT01000022.1	203396	202407	-	Inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)
<i>Pcc</i> ICMP5702_peg4339	AODT01000022.1	204351	203398	-	Inosine-uridine preferring nucleoside hydrolase (EC 3.2.2.1)
<i>Pcc</i> ICMP5702_peg4340	AODT01000022.1	205337	204453	-	Dihydrodipicolinate synthase family protein bli7272
<i>Pcc</i> ICMP5702_peg4341	AODT01000022.1	206959	205409	-	ABC transporter, substrate-binding protein (cluster 5, nickel/peptides/opines)
<i>Pcc</i> ICMP5702_peg4342	AODT01000022.1	207102	207998	+	Transcriptional regulator, LysR family
<i>Pcc</i> ICMP5702_peg4343	AODT01000022.1	208959	208144	-	Sugar phosphatase YidA (EC 3.1.3.23)
<i>Pcc</i> ICMP5702_peg4344	AODT01000022.1	210557	209115	-	6-phospho-beta-glucosidase (EC 3.2.1.86)
<i>Pcc</i> ICMP5702_peg4345	AODT01000022.1	211073	210717	-	PTS system, cellobiose-specific IIA component (EC 2.7.1.205)
<i>Pcc</i> ICMP5702_peg4346	AODT01000022.1	212376	211063	-	PTS system, cellobiose-specific IIC component
<i>Pcc</i> ICMP5702_peg4347	AODT01000022.1	212698	212393	-	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)
<i>Pcc</i> ICMP5702_peg4348	AODT01000022.1	212910	213923	+	AscBF operon repressor
<i>Pcc</i> ICMP5702_peg4349	AODT01000022.1	214140	216176	+	Methyl-accepting chemotaxis protein I (serine chemoreceptor protein)
<i>Pcc</i> ICMP5702_peg4350	AODT01000022.1	216595	216227	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4351	AODT01000022.1	216758	217948	+	Fosmidomycin resistance protein
<i>Pcc</i> ICMP5702_peg4352	AODT01000022.1	220503	218086	-	DNA gyrase subunit B (EC 5.99.1.3)
<i>Pcc</i> ICMP5702_peg4353	AODT01000022.1	221607	220522	-	DNA recombination and repair protein RecF
<i>Pcc</i> ICMP5702_peg4354	AODT01000022.1	222758	221658	-	DNA polymerase III beta subunit (EC 2.7.7.7)
<i>Pcc</i> ICMP5702_peg4355	AODT01000022.1	224160	222763	-	Chromosomal replication initiator protein DnaA
<i>Pcc</i> ICMP5702_peg4356	AODT01000022.1	224834	224974	+	LSU ribosomal protein L34p
<i>Pcc</i> ICMP5702_peg4357	AODT01000022.1	225226	225029	-	FIG00905621: Hypothetical protein
<i>Pcc</i> ICMP5702_peg4358	AODT01000022.1	225239	225352	+	Ribonuclease P protein component (EC 3.1.26.5)
<i>Pcc</i> ICMP5702_peg4359	AODT01000022.1	225576	227210	+	Inner membrane protein translocase and chaperone YidC, long form
<i>Pcc</i> ICMP5702_peg4360	AODT01000022.1	227338	228702	+	tRNA-5-carboxymethylaminomethyl-2-thiouridine(34) synthesis protein MnmE
<i>Pcc</i> ICMP5702_peg4361	AODT01000022.1	230054	228735	-	Toxin HigB / Protein kinase domain of HipA

<i>Pcc</i> ICMP5702_peg4362	AODT01000022.1	230320	230054	-	HipB protein @ Antitoxin HigA
<i>Pcc</i> ICMP5702_peg4363	AODT01000022.1	230481	231044	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4364	AODT01000022.1	231952	231101	-	NAD(P)H dehydrogenase (quinone) 2 (EC 1.6.5.2)
<i>Pcc</i> ICMP5702_peg4365	AODT01000022.1	232066	232476	+	Redox-sensing transcriptional regulator QorR
<i>Pcc</i> ICMP5702_peg4366	AODT01000022.1	233080	232526	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4367	AODT01000022.1	233184	234686	+	Uncharacterized MFS-type transporter
<i>Pcc</i> ICMP5702_peg4368	AODT01000022.1	235440	234781	-	Putative lipoprotein
<i>Pcc</i> ICMP5702_peg4369	AODT01000022.1	235796	235437	-	Putative lipoprotein
<i>Pcc</i> ICMP5702_peg4370	AODT01000022.1	236486	235815	-	Putative lipoprotein
<i>Pcc</i> ICMP5702_peg4371	AODT01000022.1	236765	236628	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4372	AODT01000022.1	236918	238942	+	Uncharacterized [4Fe4S] protein YgfT
<i>Pcc</i> ICMP5702_peg4373	AODT01000022.1	238939	239460	+	Quad-[4Fe-4S] ferredoxin, HycB/HydN/HyfA family
<i>Pcc</i> ICMP5702_peg4374	AODT01000022.1	239650	240393	+	Uncharacterized protein YieE
<i>Pcc</i> ICMP5702_peg4375	AODT01000022.1	241786	240449	-	Adenine permease AdeP
<i>Pcc</i> ICMP5702_peg4376	AODT01000022.1	242043	242711	+	6-phosphogluconate phosphatase
<i>Pcc</i> ICMP5702_peg4377	AODT01000022.1	243621	242893	-	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg4378	AODT01000022.1	244366	243623	-	ABC transporter, permease protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg4379	AODT01000022.1	245297	244461	-	ABC transporter, substrate-binding protein (cluster 3, basic aa/glutamine/opines)
<i>Pcc</i> ICMP5702_peg4380	AODT01000022.1	246459	245422	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4381	AODT01000022.1	247836	246652	-	Benzoate transport protein
<i>Pcc</i> ICMP5702_peg4382	AODT01000022.1	247928	248494	+	Transcriptional regulator yidN, Cro/CI family
<i>Pcc</i> ICMP5702_peg4383	AODT01000022.1	249302	248574	-	Phosphate transport system regulatory protein PhoU
<i>Pcc</i> ICMP5702_peg4384	AODT01000022.1	250089	249316	-	Phosphate ABC transporter, ATP-binding protein PstB (TC 3.A.1.7.1)
<i>Pcc</i> ICMP5702_peg4385	AODT01000022.1	251063	250176	-	Phosphate ABC transporter, permease protein PstA (TC 3.A.1.7.1)
<i>Pcc</i> ICMP5702_peg4386	AODT01000022.1	252022	251063	-	Phosphate ABC transporter, permease protein PstC (TC 3.A.1.7.1)
<i>Pcc</i> ICMP5702_peg4387	AODT01000022.1	253226	252186	-	Phosphate ABC transporter, substrate-binding protein PstS (TC 3.A.1.7.1)
<i>Pcc</i> ICMP5702_peg4388	AODT01000022.1	254866	253439	-	Bacillus cereus group-specific protein, uncharacterized
<i>Pcc</i> ICMP5702_peg4389	AODT01000022.1	255003	254875	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4390	AODT01000022.1	256863	255031	-	Glutamine--fructose-6-phosphate aminotransferase [isomerizing] (EC 2.6.1.16)
<i>Pcc</i> ICMP5702_peg4391	AODT01000022.1	258418	257048	-	N-acetylglucosamine-1-phosphate uridylyltransferase (EC 2.7.7.23) / Glucosamine-1-phosphate N-acetyltransferase (EC 2.3.1.157)
<i>Pcc</i> ICMP5702_peg4392	AODT01000022.1	258743	260977	+	Exopolysaccharide lyase (EC 4.2.2.9)
<i>Pcc</i> ICMP5702_peg4393	AODT01000022.1	261596	261177	-	ATP synthase epsilon chain (EC 3.6.3.14)
<i>Pcc</i> ICMP5702_peg4394	AODT01000022.1	262998	261616	-	ATP synthase beta chain (EC 3.6.3.14)
<i>Pcc</i> ICMP5702_peg4395	AODT01000022.1	263909	263046	-	ATP synthase gamma chain (EC 3.6.3.14)
<i>Pcc</i> ICMP5702_peg4396	AODT01000022.1	265503	263962	-	ATP synthase alpha chain (EC 3.6.3.14)

<i>Pcc</i> ICMP5702_peg4397	AODT01000022.1	266049	265516	-	ATP synthase delta chain (EC 3.6.3.14)
<i>Pcc</i> ICMP5702_peg4398	AODT01000022.1	266534	266064	-	ATP synthase F0 sector subunit b (EC 3.6.3.14)
<i>Pcc</i> ICMP5702_peg4399	AODT01000022.1	266837	266598	-	ATP synthase F0 sector subunit c (EC 3.6.3.14)
<i>Pcc</i> ICMP5702_peg4400	AODT01000022.1	267687	266887	-	ATP synthase F0 sector subunit a (EC 3.6.3.14)
<i>Pcc</i> ICMP5702_peg4401	AODT01000022.1	268093	267710	-	ATP synthase protein I
<i>Pcc</i> ICMP5702_peg4402	AODT01000022.1	269337	268717	-	16S rRNA (guanine(527)-N(7))-methyltransferase (EC 2.1.1.170)
<i>Pcc</i> ICMP5702_peg4403	AODT01000022.1	271309	269420	-	tRNA-5-carboxymethylaminomethyl-2-thiouridine(34) synthesis protein MnmG
<i>Pcc</i> ICMP5702_peg4404	AODT01000022.1	272143	271700	-	Flavoprotein MioC
<i>Pcc</i> ICMP5702_peg4405	AODT01000022.1	272694	272233	-	Transcriptional regulator AsnC
<i>Pcc</i> ICMP5702_peg4406	AODT01000022.1	272847	273839	+	Aspartate--ammonia ligase (EC 6.3.1.1)
<i>Pcc</i> ICMP5702_peg4407	AODT01000022.1	275314	273836	-	Protein ViaA
<i>Pcc</i> ICMP5702_peg4408	AODT01000022.1	276819	275320	-	ATPase RavA
<i>Pcc</i> ICMP5702_peg4409	AODT01000022.1	277283	279151	+	Kup system potassium uptake protein
<i>Pcc</i> ICMP5702_peg4410	AODT01000022.1	280652	279303	-	Sensory histidine kinase QseC
<i>Pcc</i> ICMP5702_peg4411	AODT01000022.1	281311	280649	-	Two-component system response regulator QseB
<i>Pcc</i> ICMP5702_peg4412	AODT01000022.1	281570	281965	+	Protein ygiW precursor
<i>Pcc</i> ICMP5702_peg4413	AODT01000022.1	282100	282519	+	D-ribose pyranase (EC 5.4.99.62)
<i>Pcc</i> ICMP5702_peg4414	AODT01000022.1	282527	284032	+	Ribose ABC transporter, ATP-binding protein RbsA (TC 3.A.1.2.1)
<i>Pcc</i> ICMP5702_peg4415	AODT01000022.1	284040	285008	+	Ribose ABC transporter, permease protein RbsC (TC 3.A.1.2.1)
<i>Pcc</i> ICMP5702_peg4416	AODT01000022.1	285034	285921	+	Ribose ABC transporter, substrate-binding protein RbsB (TC 3.A.1.2.1)
<i>Pcc</i> ICMP5702_peg4417	AODT01000022.1	285993	286919	+	Ribokinase (EC 2.7.1.15)
<i>Pcc</i> ICMP5702_peg4418	AODT01000022.1	286932	287918	+	Ribose operon repressor
<i>Pcc</i> ICMP5702_peg4419	AODT01000025.1	378	277	-	Uncharacterized lipoprotein YgdR
<i>Pcc</i> ICMP5702_peg4420	AODT01000027.1	347	249	-	PTS system, cellobiose-specific IIB component (EC 2.7.1.205)
<i>Pcc</i> ICMP5702_peg4421	AODT01000029.1	761	159	-	Flagellin FliC
<i>Pcc</i> ICMP5702_peg4422	AODT01000029.1	1044	874	-	Flagellin FliC
<i>Pcc</i> ICMP5702_peg4423	AODT01000029.1	1817	1242	-	Flagellin FliC
<i>Pcc</i> ICMP5702_peg4424	AODT01000032.1	473	988	+	Chaperone protein DnaJ
<i>Pcc</i> ICMP5702_peg4425	AODT01000032.1	1042	1605	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4426	AODT01000032.1	1659	2375	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4427	AODT01000032.1	2372	2734	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4428	AODT01000032.1	3445	3825	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4429	AODT01000032.1	3974	4234	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4430	AODT01000032.1	4231	4524	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4431	AODT01000032.1	4610	4741	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4432	AODT01000032.1	4914	5264	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg4433	AODT01000032.1	5264	5482	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4434	AODT01000032.1	5479	6030	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4435	AODT01000032.1	6276	6079	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4436	AODT01000032.1	7051	6647	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4437	AODT01000032.1	7276	7103	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4438	AODT01000032.1	7503	7754	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4439	AODT01000032.1	7798	8109	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4440	AODT01000032.1	8096	8428	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4441	AODT01000032.1	8581	8967	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4442	AODT01000032.1	9220	9522	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4443	AODT01000032.1	9586	9816	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4444	AODT01000032.1	10149	10436	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4445	AODT01000032.1	10492	10920	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4446	AODT01000032.1	10936	11331	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4447	AODT01000032.1	11344	11451	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4448	AODT01000032.1	11438	11626	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4449	AODT01000032.1	11637	11936	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4450	AODT01000032.1	11945	12136	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4451	AODT01000032.1	12403	12663	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4452	AODT01000032.1	13130	13897	+	Resolvase
<i>Pcc</i> ICMP5702_peg4453	AODT01000032.1	13894	13983	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4454	AODT01000032.1	14157	14816	+	Chromosome partitioning protein ParA
<i>Pcc</i> ICMP5702_peg4455	AODT01000032.1	14901	15197	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4456	AODT01000032.1	15208	15483	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4457	AODT01000032.1	15944	16231	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4458	AODT01000032.1	16952	16485	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4459	AODT01000032.1	17667	16963	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4460	AODT01000032.1	18019	17648	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4461	AODT01000032.1	18354	18707	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4462	AODT01000032.1	18697	22125	+	VirB8
<i>Pcc</i> ICMP5702_peg4463	AODT01000032.1	22308	22571	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4464	AODT01000032.1	22925	23884	+	RepA
<i>Pcc</i> ICMP5702_peg4465	AODT01000032.1	25194	24802	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4466	AODT01000032.1	25514	26038	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4467	AODT01000032.1	26213	26923	+	Peptidoglycan hydrolase VirB1, involved in T-DNA transfer

<i>Pcc</i> ICMP5702_peg4468	AODT01000032.1	27555	30044	+	ATPase required for both assembly of type IV secretion complex and secretion of T-DNA complex, VirB4
<i>Pcc</i> ICMP5702_peg4469	AODT01000032.1	30080	30757	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4470	AODT01000032.1	30787	31188	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4471	AODT01000032.1	31197	32141	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4472	AODT01000032.1	32263	33117	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4473	AODT01000032.1	33117	33926	+	Outer membrane and periplasm component of type IV secretion of T-DNA complex, has secretin-like domain, VirB9
<i>Pcc</i> ICMP5702_peg4474	AODT01000032.1	33923	35230	+	Inner membrane protein of type IV secretion of T-DNA complex, TonB-like, VirB10
<i>Pcc</i> ICMP5702_peg4475	AODT01000032.1	35456	36514	+	ATPase required for both assembly of type IV secretion complex and secretion of T-DNA complex, VirB11
<i>Pcc</i> ICMP5702_peg4476	AODT01000032.1	36887	38500	+	Coupling protein VirD4, ATPase required for T-DNA transfer
<i>Pcc</i> ICMP5702_peg4477	AODT01000032.1	39433	39050	-	Ammonium transporter
<i>Pcc</i> ICMP5702_peg4478	AODT01000032.1	39552	39424	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4479	AODT01000032.1	39675	39905	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4480	AODT01000032.1	39913	41619	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4481	AODT01000032.1	41624	43048	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4482	AODT01000032.1	43038	43469	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4483	AODT01000032.1	43466	44965	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4484	AODT01000032.1	44992	46062	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4485	AODT01000032.1	46079	46585	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4486	AODT01000032.1	46600	47580	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4487	AODT01000032.1	47570	48829	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4488	AODT01000032.1	50262	51404	+	Shufflon-specific DNA recombinase
<i>Pcc</i> ICMP5702_peg4489	AODT01000032.1	51451	51888	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4490	AODT01000032.1	51896	52555	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4491	AODT01000032.1	52653	53021	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4492	AODT01000032.1	53039	53311	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4493	AODT01000032.1	53330	53752	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4494	AODT01000032.1	53755	54705	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4495	AODT01000032.1	54830	54961	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4496	AODT01000032.1	54989	55762	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4497	AODT01000032.1	55776	56048	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4498	AODT01000032.1	56074	56601	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4499	AODT01000032.1	56610	56942	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4500	AODT01000032.1	57003	57272	+	Hypothetical protein

<i>Pcc</i> ICMP5702_peg4501	AODT01000032.1	57361	59697	+	DNA topoisomerase III, TraE-type (EC 5.99.1.2)
<i>Pcc</i> ICMP5702_peg4502	AODT01000032.1	59907	60299	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4503	AODT01000032.1	60650	60841	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4504	AODT01000032.1	60909	61076	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4505	AODT01000032.1	61141	61347	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4506	AODT01000032.1	61397	61702	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4507	AODT01000032.1	61704	61919	+	Haemolysin expression modulating protein
<i>Pcc</i> ICMP5702_peg4508	AODT01000035.1	3	188	+	T1SS secreted agglutinin RTX @ RTX toxins and related Ca ²⁺ -binding proteins
<i>Pcc</i> ICMP5702_peg4509	AODT01000036.1	478	2	-	T6SS PAAR-repeat protein / RhaS protein
<i>Pcc</i> ICMP5702_peg4510	AODT01000039.1	335	3	-	T1SS secreted agglutinin RTX @ RTX toxins and related Ca ²⁺ -binding proteins
<i>Pcc</i> ICMP5702_peg4511	AODT01000040.1	203	3	-	T1SS secreted agglutinin RTX @ RTX toxins and related Ca ²⁺ -binding proteins
<i>Pcc</i> ICMP5702_peg4512	AODT01000040.1	349	200	-	T1SS secreted agglutinin RTX @ RTX toxins and related Ca ²⁺ -binding proteins
<i>Pcc</i> ICMP5702_peg4513	AODT01000041.1	159	1	-	Flagellin FliC
<i>Pcc</i> ICMP5702_peg4514	AODT01000042.1	194	3	-	Transketolase (EC 2.2.1.1)
<i>Pcc</i> ICMP5702_peg4515	AODT01000042.1	379	191	-	Transketolase (EC 2.2.1.1)
<i>Pcc</i> ICMP5702_peg4516	AODT01000043.1	138	251	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4517	AODT01000044.1	2	334	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4518	AODT01000044.1	682	362	-	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4519	AODT01000044.1	2546	2662	+	Hypothetical protein
<i>Pcc</i> ICMP5702_peg4520	AODT01000046.1	1330	14	-	Transposase InsG for insertion sequence element IS4

Supplementary Table 2. Summary of the gene ontology (GO) classifications of the protein encoding genes from *Pectobacterium carotovorum* subsp. *carotovorum* (Pcc) ICMP 5702

GO term	Description	PEGs	%	Associated PEGs
Biological process				
			7.05	peg.25,peg.39,peg.47,peg.50,peg.70,peg.71,peg.72,peg.99,peg.139,peg.140,peg.141,peg.234,peg.254,peg.255,peg.257,peg.291,peg.292,peg.302,peg.307,peg.321,peg.347,peg.356,peg.373,peg.375,peg.376,peg.404,peg.427,peg.428,peg.495,peg.496,peg.497,peg.498,peg.535,peg.543,peg.548,peg.589,peg.672,peg.694,peg.695,peg.697,peg.712,peg.755,peg.761,peg.781,peg.782,peg.796,peg.824,peg.826,peg.829,peg.830,peg.831,peg.835,peg.846,peg.862,peg.870,peg.880,peg.896,peg.897,peg.906,peg.913,peg.914,peg.915,peg.917,peg.925,peg.928,peg.933,peg.939,peg.951,peg.976,peg.1000,peg.1001,peg.1002,peg.1031,peg.1032,peg.1033,peg.1103,peg.1104,peg.1105,peg.1109,peg.1130,peg.1154,peg.1160,peg.1174,peg.1175,peg.1187,peg.1188,peg.1226,peg.1251,peg.1264,peg.1271,peg.1302,peg.1303,peg.1374,peg.1375,peg.1384,peg.1385,peg.1450,peg.1457,peg.1481,peg.1483,peg.1490,peg.1493,peg.1500,peg.1501,peg.1514,peg.1518,peg.1519,peg.1524,peg.1525,peg.1528,peg.1538,peg.1542,peg.1543,peg.1544,peg.1550,peg.1555,peg.1558,peg.1559,peg.1580,peg.1604,peg.1613,peg.1614,peg.1615,peg.1642,peg.1643,peg.1649,peg.1650,peg.1668,peg.1698,peg.1699,peg.1740,peg.1763,peg.1795,peg.1807,peg.1837,peg.1893,peg.1903,peg.1904,peg.1923,peg.1924,peg.1930,peg.1931,peg.1940,peg.1942,peg.1943,peg.1949,peg.2031,peg.2039,peg.2096,peg.2106,peg.2107,peg.2129,peg.2184,peg.2187,peg.2196,peg.2224,peg.2227,peg.2235,peg.2253,peg.2261,peg.2262,peg.2263,peg.2286,peg.2317,peg.2355,peg.2356,peg.2366,peg.2439,peg.2440,peg.2449,peg.2476,peg.2477,peg.2513,peg.2538,peg.2542,peg.2547,peg.2553,peg.2563,peg.2599,peg.2600,peg.2601,peg.2602,peg.2635,peg.2674,peg.2675,peg.2684,peg.2685,peg.2686,peg.2691,peg.2695,peg.2704,peg.2710,peg.2711,peg.2732,peg.2733,peg.2763,peg.2786,peg.2822,peg.2824,peg.2828,peg.2831,peg.2832,peg.2836,peg.2869,peg.2874,peg.2876,peg.2883,peg.2902,peg.2903,peg.2909,peg.2910,peg.2925,peg.2944,peg.2948,peg.2962,peg.2963,peg.2964,peg.2993,peg.2994,peg.3000,peg.3031,peg.3032,peg.3051,peg.3054,peg.3058,peg.3060,peg.3061,peg.3068,peg.3069,peg.3070,peg.3071,peg.3116,peg.3144,peg.3173,peg.3174,peg.3216,peg.3230,peg.3236,peg.3331,peg.3375,peg.3418,peg.3419,peg.3429,peg.3430,peg.3432,peg.3438,peg.3446,peg.3449,peg.3464,peg.3491,peg.3507,peg.3575,peg.3624,peg.3625,peg.3626,peg.3635,peg.3643,peg.3648,peg.3665,peg.3673,peg.3727,peg.3728,peg.3770,peg.3802,peg.3835,peg.3836,peg.3845,peg.3847,peg.3851,peg.3858,peg.3873,peg.3965,peg.3966,peg.3967,peg.3973,peg.3974,peg.4004,peg.4034,peg.4083,peg.4094,peg.4095,peg.4099,peg.4104,peg.4142,peg.4143,peg.4158,peg.4159,peg.4161,peg.4165,peg.4167,peg.4178,peg.4191,peg.4192,peg.4218,peg.4222,peg.4223,peg.4244,peg.4245,peg.4261,peg.4263,peg.4267,peg.4306,peg.4307,peg.4308,peg.4310,peg.4317,peg.4330,peg.4332,peg.4333,peg.4336,peg.4337,peg.4341,peg.4351,peg.4367,peg.4375,peg.4377,peg.4378,peg.4386,peg.4415
GO:0055085	Transmembrane transport	319		
			5.04	peg.36,peg.101,peg.105,peg.107,peg.135,peg.185,peg.195,peg.210,peg.220,peg.236,peg.243,peg.266,peg.289,peg.324,peg.353,peg.364,peg.368,peg.377,peg.385,peg.399,peg.441,peg.450,peg.455,peg.461,peg.468,peg.473,peg.476,peg.493,peg.555,peg.561,peg.577,peg.579,peg.588,peg.611,peg.649,peg.681,peg.683,peg.701,peg.722,peg.756,peg.764,peg.833,peg.838,peg.851,peg.871,peg.886,peg.889,peg.901,peg.908,peg.918,peg.923,peg.936,peg.950,peg.952,peg.953,peg.962,peg.973,peg.983,peg.991,peg.1020,peg.1041,peg.1049,peg.1093,peg.1099,peg.1117,peg.1213,peg.1224,peg.1256,peg.1314,peg.1319,peg.1323,peg.1325,peg.1328,peg.1381,peg.1387,peg.1442,peg.1455,peg.1459,peg.1468,peg.1479,peg.1485,peg.1489,peg.1492,peg.1505,peg.1506,peg.1536,peg.1552,peg.1557,peg.1560,peg.1574,peg.1581,peg.1606,peg.1655,peg.1661,peg.1703,peg.1736,peg.1799,peg.1853,peg.1880,peg.1908,peg.1919,peg.1928,peg.1937,peg.1947,peg.1953,peg.1958,peg.2060,peg.2110,peg.2112,peg.2119,peg.2120,peg.2183,peg.2185,peg.2189,peg.2193,peg.2214,peg.2240,peg.2251,peg.2252,peg.2266,peg.2267,peg.2268,peg.2281,peg.2309,peg.2324,peg.2333,peg.2350,peg.2372,peg.2386,peg.2388,peg.2413,peg.2437,peg.2445,peg.2463,peg.2475,peg.2495,peg.2516,peg.2541,peg.2552,peg.2568,peg.2605,peg.2706,peg.2714,peg.2727,peg.2736,peg.2757,peg.2764,peg.2771,peg.2826,peg.2849,peg.2875,peg.2887,peg.2891,peg.2923,peg.2937,peg.2949,peg.3038,peg.3056,peg.3073,peg.3089,peg.3096,peg.3103,peg.3130,peg.3140,peg.3159,peg.3204,peg.3214,peg.3332,peg.3363,peg.3376,peg.3421,peg.3435,peg.3472,peg.3487,peg.3492,peg.3536,peg.3562,peg.3578,peg.3583,peg.3587,peg.3588,peg.3623,peg.3638,peg.3647,peg.3656,peg.3659,peg.3667,peg.3671,peg.3686,peg.3706,peg.3708,peg.3718,peg.3736,peg.3747,peg.3764,peg.3783,peg.3785,peg.3792,peg.3798,peg.3808,peg.3825,peg.3844,peg.3875,peg.3877,peg.3891,peg.3936,peg.3940,peg.3954,peg.4001,peg.4017,peg.4028,peg.4040,peg.4058,peg.4089,peg.4126,peg.4152,peg.4157,peg.4170,peg.4199,peg.4212,peg.4230,peg.4315,peg.4342,peg.4348,peg.4411,peg.4418,peg.4436,peg.4466
GO:0006355	Regulation of transcription : DNA templated	228		

			peg.46,peg.102,peg.136,peg.137,peg.138,peg.149,peg.179,peg.215,peg.288,peg.295,peg.315,peg.316,peg.327,peg.420,peg.426,peg.446,peg.518,peg.523,peg.546,peg.610,peg.618,peg.629,peg.633,peg.660,peg.661,peg.768,peg.776,peg.784,peg.861,peg.900,peg.982,peg.990,peg.1017,peg.1056,peg.1064,peg.1104,peg.1164,peg.1165,peg.1216,peg.1217,peg.1240,peg.1254,peg.1272,peg.1273,peg.1278,peg.1284,peg.1341,peg.1437,peg.1498,peg.1502,peg.1524,peg.1526,peg.1599,peg.1728,peg.1760,peg.1815,peg.1945,peg.2037,peg.2051,peg.2125,peg.2282,peg.2302,peg.2304,peg.2573,peg.2636,peg.2655,peg.2689,peg.2708,peg.2730,peg.2737,peg.2753,peg.2760,peg.2802,peg.2889,peg.2890,peg.2910,peg.2961,peg.3002,peg.3031,peg.3033,peg.3034,peg.3035,peg.3055,peg.3077,peg.3112,peg.3132,peg.3174,peg.3206,peg.3364,peg.3390,peg.3494,peg.3549,peg.3583,peg.3666,peg.3760,peg.3807,peg.3812,peg.3822,peg.3823,peg.4041,peg.4097,peg.4139,peg.4173,peg.4266,peg.4271,peg.4281
GO:0006508	Proteolysis	106	
			peg.28,peg.49,peg.64,peg.65,peg.127,peg.198,peg.221,peg.296,peg.298,peg.381,peg.419,peg.522,peg.574,peg.674,peg.772,peg.847,peg.874,peg.1009,peg.1023,peg.1050,peg.1116,peg.1338,peg.1452,peg.1454,peg.1608,peg.1667,peg.1846,peg.1905,peg.1907,peg.1932,peg.2119,peg.2195,peg.2196,peg.2221,peg.2238,peg.2277,peg.2341,peg.2359,peg.2375,peg.2385,peg.2391,peg.2393,peg.2395,peg.2471,peg.2540,peg.2636,peg.2676,peg.2735,peg.2774,peg.2817,peg.2821,peg.2840,peg.2997,peg.3330,peg.3384,peg.3499,peg.3630,peg.3631,peg.3640,peg.3684,peg.3776,peg.3816,peg.3830,peg.3949,peg.3951,peg.3999,peg.4052,peg.4057,peg.4232,peg.4265,peg.4268
GO:0016310	Phosphorylation	71	
			peg.150,peg.151,peg.228,peg.229,peg.230,peg.231,peg.319,peg.320,peg.616,peg.625,peg.626,peg.655,peg.1057,peg.1069,peg.1185,peg.1186,peg.1211,peg.1458,peg.2082,peg.2479,peg.2700,peg.2701,peg.2862,peg.2916,peg.2970,peg.2971,peg.3309,peg.3312,peg.3545,peg.3546,peg.3548,peg.3763,peg.3790,peg.3889,peg.3895,peg.3897,peg.3898,peg.3899,peg.3900,peg.3902,peg.3903,peg.3904,peg.3905,peg.3906,peg.3907,peg.3908,peg.3909,peg.3910,peg.3911,peg.3912,peg.3913,peg.3914,peg.3915,peg.3916,peg.3917,peg.3918,peg.3919,peg.3920,peg.3921,peg.3922,peg.3929,peg.3930,peg.4168,peg.4356
GO:0006412	Translation	64	
			peg.178,peg.606,peg.635,peg.758,peg.785,peg.839,peg.843,peg.844,peg.849,peg.850,peg.1102,peg.1210,peg.1315,peg.1326,peg.1340,peg.1438,peg.1460,peg.1478,peg.1549,peg.1582,peg.1747,peg.1906,peg.1907,peg.1962,peg.2030,peg.2154,peg.2156,peg.2238,peg.2239,peg.2254,peg.2465,peg.2545,peg.2622,peg.2870,peg.3042,peg.3128,peg.3447,peg.3483,peg.3490,peg.3580,peg.3627,peg.3639,peg.3640,peg.3651,peg.3675,peg.3730,peg.3774,peg.3951,peg.4039,peg.4046,peg.4057,peg.4197,peg.4231,peg.4232,peg.4233,peg.4234,peg.4276,peg.4327,peg.4344
GO:0005975	Carbohydrate metabolic process	59	
			peg.81,peg.130,peg.246,peg.259,peg.339,peg.394,peg.398,peg.401,peg.430,peg.431,peg.433,peg.449,peg.470,peg.471,peg.478,peg.664,peg.965,peg.1044,peg.1119,peg.1121,peg.1122,peg.1148,peg.1342,peg.1389,peg.1453,peg.1593,peg.1658,peg.1659,peg.1793,peg.1812,peg.1957,peg.2566,peg.2612,peg.2892,peg.2951,peg.3107,peg.3111,peg.3250,peg.3275,peg.3284,peg.3400,peg.3813,peg.3817,peg.3827,peg.4121,peg.4210,peg.4290,peg.4296,peg.4299,peg.4437,peg.4462
GO:0090305	Nucleic acid phosphodiester bond hydrolysis	51	
			peg.75,peg.89,peg.187,peg.188,peg.422,peg.482,peg.484,peg.1118,peg.1276,peg.1322,peg.1496,peg.1534,peg.1738,peg.1966,peg.1974,peg.1976,peg.2062,peg.2296,peg.2297,peg.2361,peg.2515,peg.2593,peg.2791,peg.2850,peg.2851,peg.2936,peg.3147,peg.3169,peg.3511,peg.3524,peg.3550,peg.3557,peg.3561,peg.3570,peg.3719,peg.3791,peg.4013,peg.4236,peg.4238,peg.4239,peg.4240,peg.4268,peg.4349
GO:0007165	Signal transduction	43	

			<p>peg.29,peg.48,peg.66,peg.87,peg.105,peg.126,peg.127,peg.135,peg.185,peg.195,peg.210,peg.220,peg.248,peg.274,peg.289,peg.313,peg.324,peg.352,peg.353,peg.360,peg.364,peg.377,peg.385,peg.393,peg.397,peg.399,peg.405,peg.425,peg.429,peg.430,peg.431,peg.432,peg.441,peg.454,peg.456,peg.468,peg.555,peg.559,peg.560,peg.563,peg.575,peg.577,peg.579,peg.588,peg.611,peg.613,peg.614,peg.621,peg.622,peg.623,peg.649,peg.675,peg.681,peg.683,peg.701,peg.721,peg.724,peg.736,peg.742,peg.756,peg.764,peg.793,peg.817,peg.833,peg.851,peg.858,peg.871,peg.886,peg.889,peg.901,peg.908,peg.918,peg.923,peg.936,peg.938,peg.943,peg.946,peg.950,peg.959,peg.960,peg.961,peg.974,peg.979,peg.988,peg.991,peg.1006,peg.1020,peg.1028,peg.1041,peg.1049,peg.1093,peg.1099,peg.1117,peg.1124,peg.1140,peg.1162,peg.1167,peg.1169,peg.1181,peg.1189,peg.1194,peg.1195,peg.1196,peg.1213,peg.1222,peg.1224,peg.1256,peg.1268,peg.1296,peg.1319,peg.1323,peg.1325,peg.1328,peg.1387,peg.1455,peg.1468,peg.1470,peg.1479,peg.1485,peg.1489,peg.1492,peg.1506,peg.1530,peg.1552,peg.1560,peg.1561,peg.1570,peg.1572,peg.1574,peg.1575,peg.1581,peg.1606,peg.1633,peg.1655,peg.1658,peg.1661,peg.1675,peg.1715,peg.1716,peg.1717,peg.1718,peg.1739,peg.1781,peg.1794,peg.1799,peg.1853,peg.1908,peg.1919,peg.1928,peg.1937,peg.1941,peg.1953,peg.1954,peg.1958,peg.1969,peg.1970,peg.2028,peg.2032,peg.2048,peg.2052,peg.2060,peg.2095,peg.2108,peg.2119,peg.2183,peg.2189,peg.2206,peg.2208,peg.2214,peg.2251,peg.2252,peg.2269,peg.2281,peg.2283,peg.2303,peg.2307,peg.2309,peg.2313,peg.2324,peg.2333,peg.2338,peg.2370,peg.2372,peg.2384,peg.2386,peg.2409,peg.2413,peg.2437,peg.2445,peg.2463,peg.2475,peg.2495,peg.2512,peg.2516,peg.2519,peg.2540,peg.2541,peg.2543,peg.2568,peg.2570,peg.2605,peg.2607,peg.2642,peg.2692,peg.2697,peg.2706,peg.2712,peg.2716,peg.2717,peg.2727,peg.2751,peg.2764,peg.2771,peg.2812,peg.2849,peg.2861,peg.2875,peg.2878,peg.2880,peg.2923,peg.2937,peg.2949,peg.2970,peg.2976,peg.2980,peg.2986,peg.3003,peg.3004,peg.3073,peg.3089,peg.3098,peg.3099,peg.3100,peg.3104,peg.3122,peg.3159,peg.3189,peg.3199,peg.3222,peg.3259,peg.3262,peg.3264,peg.3284,peg.3332,peg.3338,peg.3363,peg.3380,peg.3385,peg.3392,peg.3435,peg.3454,peg.3487,peg.3492,peg.3515,peg.3536,peg.3578,peg.3583,peg.3584,peg.3587,peg.3623,peg.3638,peg.3647,peg.3656,peg.3667,peg.3671,peg.3706,peg.3708,peg.3724,peg.3726,peg.3735,peg.3747,peg.3753,peg.3764,peg.3783,peg.3798,peg.3808,peg.3844,peg.3877,peg.3886,peg.3934,peg.3936,peg.3944,peg.3947,peg.3954,peg.4001,peg.4017,peg.4028,peg.4040,peg.4053,peg.4058,peg.4078,peg.4089,peg.4126,peg.4139,peg.4141,peg.4150,peg.4152,peg.4157,peg.4164,peg.4170,peg.4199,peg.4209,peg.4212,peg.4229,peg.4230,peg.4249,peg.4315,peg.4342,peg.4348,peg.4352,peg.4362,peg.4365,peg.4366,peg.4382,peg.4411,peg.4418,peg.4426,peg.4436,peg.4452,peg.4463,peg.4465,peg.4488,peg.4501,peg.4507,peg.4518,peg.4520</p>
	GO:0003677	DNA Binding	326
Molecular function			
			<p>peg.19,peg.30,peg.52,peg.69,peg.79,peg.95,peg.98,peg.130,peg.142,peg.154,peg.198,peg.204,peg.221,peg.250,peg.253,peg.262,peg.282,peg.302,peg.308,peg.318,peg.333,peg.409,peg.432,peg.470,peg.473,peg.489,peg.495,peg.521,peg.550,peg.552,peg.569,peg.570,peg.574,peg.672,peg.697,peg.773,peg.821,peg.822,peg.831,peg.834,peg.835,peg.847,peg.862,peg.869,peg.886,peg.929,peg.939,peg.980,peg.996,peg.997,peg.999,peg.1030,peg.1059,peg.1075,peg.1120,peg.1174,peg.1175,peg.1197,peg.1199,peg.1220,peg.1223,peg.1233,peg.1241,peg.1248,peg.1259,peg.1271,peg.1295,peg.1301,peg.1308,peg.1313,peg.1318,peg.1330,peg.1338,peg.1339,peg.1340,peg.1380,peg.1385,peg.1401,peg.1404,peg.1449,peg.1456,peg.1480,peg.1502,peg.1515,peg.1520,peg.1526,peg.1545,peg.1546,peg.1549,peg.1558,peg.1559,peg.1593,peg.1612,peg.1644,peg.1651,peg.1667,peg.1697,peg.1725,peg.1750,peg.1764,peg.1838,peg.1873,peg.1894,peg.1902,peg.1922,peg.1973,peg.2029,peg.2091,peg.2101,peg.2109,peg.2112,peg.2114,peg.2124,peg.2126,peg.2128,peg.2134,peg.2143,peg.2166,peg.2197,peg.2201,peg.2234,peg.2259,peg.2260,peg.2266,peg.2283,peg.2301,peg.2365,peg.2388,peg.2436,peg.2441,peg.2442,peg.2448,peg.2482,peg.2554,peg.2575,peg.2597,peg.2598,peg.2650,peg.2673,peg.2686,peg.2695,peg.2713,peg.2762,peg.2773,peg.2781,peg.2805,peg.2812,peg.2821,peg.2827,peg.2830,peg.2840,peg.2863,peg.2877,peg.2878,peg.2880,peg.2883,peg.2884,peg.2889,peg.2900,peg.2911,peg.2916,peg.2926,peg.2943,peg.2965,peg.2997,peg.3001,peg.3033,peg.3058,peg.3120,peg.3125,peg.3135,peg.3145,peg.3159,peg.3163,peg.3218,peg.3220,peg.3228,peg.3231,peg.3235,peg.3243,peg.3251,peg.3254,peg.3281,peg.3317,peg.3363,peg.3364,peg.3401,peg.3417,peg.3428,peg.3444,peg.3448,peg.3465,peg.3467,peg.3469,peg.3496,peg.3563,peg.3626,peg.3634,peg.3640,peg.3676,peg.3684,peg.3688,peg.3695,peg.3696,peg.3699,peg.3729,peg.3754,peg.3755,peg.3767,peg.3777,peg.3804,peg.3815,peg.3819,peg.3826,peg.3827,peg.3829,peg.3837,peg.3838,peg.3846,peg.3871,peg.3937,peg.3947,peg.3951,peg.3963,peg.3964,peg.3975,peg.3978,peg.4030,peg.4048,peg.4051,peg.4057,peg.4084,peg.4096,peg.4098,peg.4139,peg.4144,peg.4161,peg.4165,peg.4173,peg.4179,peg.4190,peg.4207,peg.4220,peg.4232,peg.4242,peg.4243,peg.4252,peg.4290,peg.4304,peg.4305,peg.4333,peg.4335,peg.4353,peg.4355,peg.4393,peg.4395,peg.4406,peg.4408,peg.4414,peg.4417,peg.4468,peg.4474,peg.4475,peg.4483</p>
	GO:0005524	ATP Binding	264

			<p>peg.59,peg.69,peg.97,peg.99,peg.112,peg.136,peg.142,peg.179,peg.207,peg.274,peg.302,peg.308,peg.318,peg.351,peg.392,peg.421,peg.451,peg.495,peg.536,peg.592,peg.612,peg.665,peg.711,peg.765,peg.773,peg.802,peg.814,peg.866,peg.867,peg.868,peg.877,peg.900,peg.929,peg.949,peg.981,peg.1029,peg.1030,peg.1088,peg.1090,peg.1098,peg.1100,peg.1115,peg.1151,peg.1170,peg.1230,peg.1237,peg.1241,peg.1275,peg.1308,peg.1324,peg.1337,peg.1339,peg.1362,peg.1380,peg.1419,peg.1428,peg.1449,peg.1469,peg.1500,peg.1501,peg.1502,peg.1512,peg.1515,peg.1520,peg.1545,peg.1546,peg.1549,peg.1575,peg.1612,peg.1618,peg.1619,peg.1644,peg.1651,peg.1695,peg.1705,peg.1730,peg.1764,peg.1767,peg.1842,peg.1902,peg.1933,peg.1939,peg.1945,peg.2029,peg.2053,peg.2054,peg.2103,peg.2125,peg.2188,peg.2190,peg.2208,peg.2232,peg.2234,peg.2235,peg.2248,peg.2259,peg.2260,peg.2275,peg.2282,peg.2322,peg.2371,peg.2404,peg.2408,peg.2441,peg.2442,peg.2455,peg.2471,peg.2520,peg.2553,peg.2555,peg.2597,peg.2598,peg.2608,peg.2626,peg.2647,peg.2673,peg.2678,peg.2690,peg.2760,peg.2774,peg.2808,peg.2823,peg.2827,peg.2830,peg.2846,peg.2872,peg.2873,peg.2943,peg.2944,peg.2959,peg.2965,peg.2990,peg.3091,peg.3095,peg.3145,peg.3156,peg.3166,peg.3195,peg.3218,peg.3231,peg.3319,peg.3350,peg.3374,peg.3396,peg.3403,peg.3414,peg.3428,peg.3429,peg.3455,peg.3478,peg.3488,peg.3490,peg.3589,peg.3608,peg.3627,peg.3632,peg.3634,peg.3644,peg.3662,peg.3666,peg.3681,peg.3743,peg.3786,peg.3837,peg.3838,peg.3949,peg.3963,peg.3964,peg.3977,peg.3993,peg.4016,peg.4030,peg.4065,peg.4077,peg.4097,peg.4142,peg.4143,peg.4144,peg.4165,peg.4190,peg.4207,peg.4213,peg.4221,peg.4243,peg.4252,peg.4304,peg.4305,peg.4376,peg.4383,peg.4397,peg.4398,peg.4400,peg.4401,peg.4408,peg.4415,peg.4416,peg.4475</p>
GO:0016787	Hydrolase activity	197	
			<p>peg.8,peg.21,peg.44,peg.46,peg.91,peg.137,peg.143,peg.149,peg.160,peg.209,peg.211,peg.217,peg.305,peg.329,peg.332,peg.348,peg.350,peg.366,peg.411,peg.420,peg.446,peg.487,peg.524,peg.602,peg.634,peg.660,peg.661,peg.676,peg.687,peg.696,peg.827,peg.842,peg.861,peg.899,peg.927,peg.1008,peg.1017,peg.1056,peg.1064,peg.1101,peg.1135,peg.1145,peg.1177,peg.1196,peg.1201,peg.1272,peg.1281,peg.1337,peg.1355,peg.1383,peg.1392,peg.1398,peg.1415,peg.1419,peg.1437,peg.1458,peg.1513,peg.1527,peg.1611,peg.1660,peg.1699,peg.1700,peg.1728,peg.1742,peg.1751,peg.1752,peg.1765,peg.1767,peg.1842,peg.1843,peg.1849,peg.1851,peg.1887,peg.2033,peg.2135,peg.2160,peg.2164,peg.2170,peg.2173,peg.2174,peg.2175,peg.2176,peg.2177,peg.2178,peg.2181,peg.2188,peg.2212,peg.2239,peg.2256,peg.2280,peg.2331,peg.2427,peg.2500,peg.2579,peg.2669,peg.2672,peg.2678,peg.2707,peg.2718,peg.2761,peg.2766,peg.2942,peg.3002,peg.3041,peg.3063,peg.3110,peg.3112,peg.3158,peg.3166,peg.3178,peg.3244,peg.3248,peg.3319,peg.3415,peg.3447,peg.3459,peg.3484,peg.3506,peg.3509,peg.3540,peg.3582,peg.3636,peg.3641,peg.3670,peg.3683,peg.3688,peg.3806,peg.3807,peg.3809,peg.3868,peg.3879,peg.3889,peg.3925,peg.3957,peg.3958,peg.3960,peg.3979,peg.3980,peg.3983,peg.3996,peg.4010,peg.4025,peg.4065,peg.4077,peg.4156,peg.4172,peg.4180,peg.4233,peg.4234,peg.4266,peg.4343,peg.4345,peg.4350,peg.4373,peg.4376</p>
GO:0046872	Metal ion binding	155	
			<p>peg.36,peg.101,peg.107,peg.135,peg.185,peg.195,peg.236,peg.266,peg.289,peg.324,peg.353,peg.364,peg.368,peg.441,peg.461,peg.468,peg.473,peg.491,peg.492,peg.555,peg.561,peg.577,peg.579,peg.588,peg.611,peg.619,peg.651,peg.681,peg.683,peg.722,peg.756,peg.889,peg.901,peg.908,peg.923,peg.950,peg.952,peg.983,peg.991,peg.1041,peg.1049,peg.1093,peg.1099,peg.1117,peg.1215,peg.1314,peg.1319,peg.1381,peg.1442,peg.1468,peg.1489,peg.1492,peg.1505,peg.1506,peg.1536,peg.1552,peg.1557,peg.1574,peg.1606,peg.1661,peg.1703,peg.1799,peg.1853,peg.1880,peg.1908,peg.1937,peg.1947,peg.2008,peg.2032,peg.2110,peg.2185,peg.2189,peg.2193,peg.2214,peg.2240,peg.2251,peg.2333,peg.2350,peg.2372,peg.2413,peg.2437,peg.2445,peg.2475,peg.2495,peg.2516,peg.2541,peg.2552,peg.2568,peg.2639,peg.2736,peg.2757,peg.2826,peg.2849,peg.2875,peg.2887,peg.2923,peg.2937,peg.2949,peg.3038,peg.3056,peg.3089,peg.3096,peg.3130,peg.3214,peg.3332,peg.3376,peg.3421,peg.3435,peg.3472,peg.3487,peg.3492,peg.3536,peg.3578,peg.3587,peg.3588,peg.3638,peg.3656,peg.3659,peg.3667,peg.3671,peg.3706,peg.3718,peg.3747,peg.3764,peg.3785,peg.3788,peg.3792,peg.3798,peg.3844,peg.3875,peg.3940,peg.3954,peg.4040,peg.4089,peg.4126,peg.4141,peg.4150,peg.4152,peg.4164,peg.4199,peg.4230,peg.4315,peg.4342</p>
GO:0003700	DNA-binding transcription factor activity	143	

			peg.25,peg.99,peg.234,peg.254,peg.255,peg.257,peg.291,peg.292,peg.321,peg.356,peg.375,peg.376,peg.404,peg.535,peg.548,peg.589,peg.712,peg.755,peg.782,peg.826,peg.835,peg.846,peg.870,peg.880,peg.897,peg.906,peg.914,peg.915,peg.928,peg.951,peg.1154,peg.1160,peg.1188,peg.1226,peg.1251,peg.1264,peg.1302,peg.1303,peg.1361,peg.1374,peg.1450,peg.1483,peg.1500,peg.1501,peg.1518,peg.1538,peg.1544,peg.1555,peg.1580,peg.1604,peg.1649,peg.1650,peg.1695,peg.1696,peg.1763,peg.1795,peg.1836,peg.1837,peg.1903,peg.1904,peg.1923,peg.1924,peg.1930,peg.1931,peg.1942,peg.1943,peg.2031,peg.2096,peg.2106,peg.2107,peg.2129,peg.2187,peg.2235,peg.2253,peg.2439,peg.2449,peg.2476,peg.2513,peg.2538,peg.2542,peg.2553,peg.2711,peg.2786,peg.2824,peg.2831,peg.2832,peg.2836,peg.2876,peg.2902,peg.2903,peg.2944,peg.2994,peg.3000,peg.3068,peg.3069,peg.3070,peg.3071,peg.3144,peg.3216,peg.3331,peg.3375,peg.3418,peg.3419,peg.3430,peg.3432,peg.3438,peg.3446,peg.3464,peg.3507,peg.3665,peg.3728,peg.3770,peg.3845,peg.3851,peg.3873,peg.3973,peg.3974,peg.4004,peg.4083,peg.4094,peg.4095,peg.4099,peg.4142,peg.4143,peg.4161,peg.4167,peg.4192,peg.4245,peg.4261,peg.4263,peg.4317,peg.4333,peg.4351,peg.4367,peg.4377,peg.4378,peg.4415
GO:0022857	Transmembrane transporter activity	137	
			peg.64,peg.127,peg.133,peg.161,peg.162,peg.165,peg.166,peg.180,peg.297,peg.334,peg.411,peg.556,peg.605,peg.610,peg.662,peg.801,peg.813,peg.873,peg.875,peg.916,peg.1085,peg.1407,peg.1418,peg.1427,peg.1567,peg.1568,peg.1589,peg.1700,peg.1841,peg.1879,peg.1962,peg.2021,peg.2022,peg.2024,peg.2026,peg.2050,peg.2069,peg.2119,peg.2135,peg.2148,peg.2256,peg.2275,peg.2280,peg.2344,peg.2359,peg.2402,peg.2580,peg.2635,peg.2655,peg.2766,peg.2810,peg.2817,peg.2838,peg.2867,peg.2928,peg.2940,peg.2947,peg.2954,peg.2992,peg.3044,peg.3069,peg.3074,peg.3091,peg.3213,peg.3309,peg.3395,peg.3396,peg.3494,peg.3527,peg.3582,peg.3648,peg.3829,peg.3882,peg.3931,peg.3932,peg.4052,peg.4260,peg.4269,peg.4345,peg.4407
GO:0016740	Transferase activity	80	1.76
			peg.6,peg.43,peg.61,peg.115,peg.116,peg.227,peg.280,peg.317,peg.322,peg.330,peg.362,peg.367,peg.406,peg.463,peg.580,peg.602,peg.604,peg.850,peg.895,peg.896,peg.905,peg.907,peg.947,peg.978,peg.1035,peg.1085,peg.1218,peg.1239,peg.1356,peg.1357,peg.1471,peg.1472,peg.1473,peg.1474,peg.1503,peg.1517,peg.1568,peg.1800,peg.1817,peg.1841,peg.1857,peg.1886,peg.1936,peg.1938,peg.2111,peg.2255,peg.2314,peg.2318,peg.2345,peg.2358,peg.2433,peg.2503,peg.2504,peg.2551,peg.2560,peg.2563,peg.2565,peg.2574,peg.2615,peg.2657,peg.2729,peg.2745,peg.2750,peg.2783,peg.2895,peg.3076,peg.3083,peg.3197,peg.3489,peg.3590,peg.3641,peg.3646,peg.3793,peg.3842,peg.4025,peg.4372
GO:0016491	Oxidoreductase activity	76	1.68
			peg.334,peg.336,peg.538,peg.550,peg.553,peg.592,peg.849,peg.942,peg.959,peg.960,peg.992,peg.993,peg.994,peg.996,peg.997,peg.998,peg.1022,peg.1026,peg.1074,peg.1090,peg.1211,peg.1343,peg.1371,peg.1462,peg.1585,peg.1634,peg.1681,peg.1830,peg.1834,peg.1925,peg.1939,peg.2090,peg.2164,peg.2165,peg.2173,peg.2174,peg.2467,peg.2637,peg.2660,peg.2716,peg.2717,peg.2818,peg.2841,peg.2844,peg.2859,peg.2870,peg.3029,peg.3088,peg.3169,peg.3249,peg.3642,peg.3660,peg.3664,peg.3734,peg.3961,peg.4010,peg.4090,peg.4091,peg.4198,peg.4208,peg.4340
GO:0016829	Lyase activity	61	1.34
			peg.28,peg.49,peg.65,peg.193,peg.296,peg.379,peg.381,peg.603,peg.674,peg.772,peg.840,peg.874,peg.1009,peg.1050,peg.1116,peg.1328,peg.1461,peg.1905,peg.1907,peg.1932,peg.2153,peg.2195,peg.2196,peg.2216,peg.2238,peg.2277,peg.2278,peg.2339,peg.2341,peg.2375,peg.2391,peg.2393,peg.2395,peg.2464,peg.2471,peg.2636,peg.2664,peg.2676,peg.2735,peg.2774,peg.2997,peg.3127,peg.3226,peg.3330,peg.3499,peg.3579,peg.3630,peg.3631,peg.3640,peg.3816,peg.3949,peg.3999,peg.4232,peg.4265,peg.4268,peg.4329,peg.4347
GO:0016301	Kinase activity	57	1.26

Cellular component

20.9

GO:0016021 Integral component of Membrane 945

peg.9,peg.14,peg.15,peg.23,peg.24,peg.25,peg.27,peg.31,peg.33,peg.35,peg.37,peg.39,peg.40,peg.49,peg.50,peg.53,peg.63,peg.70,peg.71,peg.75,peg.78,peg.82,peg.83,peg.85,peg.89,peg.99,peg.107,peg.109,peg.114,peg.115,peg.116,peg.117,peg.121,peg.139,peg.140,peg.155,peg.156,peg.162,peg.167,peg.171,peg.175,peg.179,peg.180,peg.187,peg.188,peg.193,peg.200,peg.204,peg.217,peg.226,peg.234,peg.240,peg.249,peg.270,peg.271,peg.281,peg.283,peg.284,peg.287,peg.290,peg.291,peg.292,peg.307,peg.310,peg.315,peg.317,peg.321,peg.333,peg.336,peg.356,peg.369,peg.371,peg.372,peg.375,peg.376,peg.379,peg.383,peg.404,peg.419,peg.420,peg.422,peg.440,peg.460,peg.480,peg.482,peg.483,peg.484,peg.496,peg.497,peg.502,peg.508,peg.509,peg.511,peg.514,peg.525,peg.529,peg.532,peg.535,peg.546,peg.547,peg.554,peg.562,peg.564,peg.566,peg.568,peg.572,peg.574,peg.581,peg.582,peg.583,peg.584,peg.587,peg.589,peg.593,peg.594,peg.595,peg.601,peg.603,peg.605,peg.610,peg.612,peg.623,peg.627,peg.633,peg.636,peg.638,peg.645,peg.646,peg.664,peg.672,peg.673,peg.674,peg.682,peg.686,peg.692,peg.694,peg.695,peg.699,peg.703,peg.707,peg.709,peg.712,peg.723,peg.744,peg.749,peg.755,peg.760,peg.761,peg.762,peg.765,peg.767,peg.768,peg.769,peg.774,peg.775,peg.777,peg.778,peg.779,peg.783,peg.784,peg.788,peg.792,peg.795,peg.796,peg.797,peg.803,peg.805,peg.808,peg.810,peg.812,peg.824,peg.826,peg.829,peg.830,peg.832,peg.840,peg.846,peg.859,peg.862,peg.863,peg.866,peg.867,peg.870,peg.872,peg.880,peg.890,peg.897,peg.898,peg.906,peg.911,peg.912,peg.913,peg.914,peg.915,peg.917,peg.925,peg.926,peg.928,peg.933,peg.936,peg.937,peg.939,peg.944,peg.951,peg.968,peg.976,peg.983,peg.990,peg.1005,peg.1012,peg.1013,peg.1014,peg.1015,peg.1017,peg.1031,peg.1032,peg.1036,peg.1040,peg.1042,peg.1063,peg.1064,peg.1075,peg.1079,peg.1081,peg.1082,peg.1083,peg.1084,peg.1087,peg.1089,peg.1092,peg.1098,peg.1103,peg.1104,peg.1105,peg.1109,peg.1114,peg.1118,peg.1125,peg.1129,peg.1130,peg.1131,peg.1136,peg.1137,peg.1138,peg.1145,peg.1154,peg.1155,peg.1156,peg.1157,peg.1158,peg.1160,peg.1168,peg.1174,peg.1175,peg.1181,peg.1187,peg.1192,peg.1193,peg.1202,peg.1207,peg.1214,peg.1216,peg.1226,peg.1242,peg.1244,peg.1251,peg.1264,peg.1265,peg.1267,peg.1270,peg.1271,peg.1276,peg.1277,peg.1304,peg.1305,peg.1312,peg.1322,peg.1327,peg.1329,peg.1333,peg.1334,peg.1345,peg.1346,peg.1356,peg.1358,peg.1362,peg.1364,peg.1366,peg.1369,peg.1370,peg.1373,peg.1382,peg.1384,peg.1390,peg.1398,peg.1404,peg.1405,peg.1408,peg.1414,peg.1426,peg.1428,peg.1432,peg.1433,peg.1436,peg.1440,peg.1450,peg.1455,peg.1457,peg.1461,peg.1473,peg.1476,peg.1481,peg.1483,peg.1490,peg.1493,peg.1496,peg.1498,peg.1499,peg.1500,peg.1501,peg.1504,peg.1509,peg.1512,peg.1514,peg.1519,peg.1523,peg.1524,peg.1525,peg.1526,peg.1529,peg.1534,peg.1538,peg.1542,peg.1544,peg.1550,peg.1553,peg.1554,peg.1555,peg.1558,peg.1559,peg.1563,peg.1564,peg.1565,peg.1576,peg.1579,peg.1580,peg.1585,peg.1600,peg.1603,peg.1604,peg.1607,peg.1614,peg.1615,peg.1617,peg.1618,peg.1619,peg.1629,peg.1630,peg.1641,peg.1645,peg.1648,peg.1649,peg.1650,peg.1660,peg.1663,peg.1668,peg.1676,peg.1677,peg.1684,peg.1688,peg.1691,peg.1694,peg.1698,peg.1705,peg.1706,peg.1707,peg.1711,peg.1720,peg.1722,peg.1727,peg.1731,peg.1733,peg.1737,peg.1740,peg.1742,peg.1745,peg.1756,peg.1760,peg.1763,peg.1765,peg.1787,peg.1795,peg.1806,peg.1807,peg.1808,peg.1816,peg.1823,peg.1827,peg.1832,peg.1835,peg.1844,peg.1847,peg.1850,peg.1854,peg.1860,peg.1862,peg.1863,peg.1864,peg.1865,peg.1866,peg.1867,peg.1869,peg.1878,peg.1883,peg.1884,peg.1886,peg.1892

12.54
peg.33,peg.35,peg.40,peg.50,peg.63,peg.69,peg.70,peg.71,peg.74,peg.78,peg.82,peg.85,peg.98,peg.99,peg.120,peg.139,peg.140,peg.155,peg.187,peg.188,peg.193,peg.204,peg.211,peg.217,peg.218,peg.226,peg.234,peg.253,peg.284,peg.290,peg.291,peg.292,peg.321,peg.333,peg.335,peg.369,peg.371,peg.372,peg.375,peg.376,peg.379,peg.422,peg.483,peg.484,peg.495,peg.496,peg.497,peg.508,peg.509,peg.520,peg.525,peg.529,peg.535,peg.562,peg.564,peg.566,peg.572,peg.573,peg.574,peg.584,peg.587,peg.589,peg.594,peg.603,peg.633,peg.636,peg.657,peg.692,peg.694,peg.695,peg.699,peg.707,peg.712,peg.723,peg.762,peg.765,peg.774,peg.775,peg.803,peg.808,peg.824,peg.829,peg.830,peg.831,peg.834,peg.840,peg.846,peg.866,peg.867,peg.870,peg.872,peg.898,peg.906,peg.911,peg.914,peg.915,peg.928,peg.951,peg.999,peg.1004,peg.1030,peg.1031,peg.1032,peg.1039,peg.1064,peg.1087,peg.1092,peg.1103,peg.1114,peg.1118,peg.1129,peg.1136,peg.1137,peg.1138,peg.1145,peg.1155,peg.1156,peg.1157,peg.1159,peg.1160,peg.1187,peg.1188,peg.1192,peg.1202,peg.1207,peg.1214,peg.1242,peg.1264,peg.1265,peg.1266,peg.1271,peg.1276,peg.1277,peg.1301,peg.1305,peg.1317,peg.1322,peg.1333,peg.1346,peg.1347,peg.1355,peg.1356,peg.1370,peg.1382,peg.1384,peg.1385,peg.1390,peg.1397,peg.1398,peg.1405,peg.1408,peg.1414,peg.1450,peg.1457,peg.1461,peg.1476,peg.1481,peg.1484,peg.1496,peg.1500,peg.1501,peg.1512,peg.1514,peg.1519,peg.1523,peg.1525,peg.1534,peg.1538,peg.1542,peg.1544,peg.1550,peg.1553,peg.1558,peg.1559,peg.1579,peg.1580,peg.1607,peg.1612,peg.1614,peg.1615,peg.1619,peg.1649,peg.1650,peg.1660,peg.1668,peg.1670,peg.1677,peg.1688,peg.1691,peg.1694,peg.1698,peg.1707,peg.1711,peg.1740,peg.1748,peg.1750,peg.1751,peg.1752,peg.1753,peg.1754,peg.1755,peg.1756,peg.1758,peg.1759,peg.1760,peg.1763,peg.1816,peg.1822,peg.1827,peg.1838,peg.1847,peg.1854,peg.1855,peg.1856,peg.1860,peg.1861,peg.1862,peg.1863,peg.1865,peg.1866,peg.1867,peg.1869,peg.1886,peg.1887,peg.1893,peg.1903,peg.1904,peg.1920,peg.1922,peg.1927,peg.1935,peg.1942,peg.1944,peg.1955,peg.1964,peg.1966,peg.1971,peg.1972,peg.1976,peg.1982,peg.1983,peg.2000,peg.2001,peg.2002,peg.2003,peg.2004,peg.2005,peg.2006,peg.2008,peg.2011,peg.2012,peg.2021,peg.2031,peg.2043,peg.2058,peg.2066,peg.2071,peg.2094,peg.2096,peg.2106,peg.2107,peg.2113,peg.2114,peg.2115,peg.2122,peg.2124,peg.2128,peg.2129,peg.2135,peg.2153,peg.2162,peg.2163,peg.2166,peg.2167,peg.2168,peg.2169,peg.2170,peg.2171,peg.2172,peg.2175,peg.2182,peg.2187,peg.2196,peg.2203,peg.2224,peg.2235,peg.2247,peg.2253,peg.2256,peg.2261,peg.2262,peg.2269,peg.2276,peg.2279,peg.2287,peg.2308,peg.2325,peg.2327,peg.2328,peg.2331,peg.2340,peg.2355,peg.2356,peg.2361,peg.2365,peg.2366,peg.2373,peg.2374,peg.2375,peg.2376,peg.2382,peg.2389,peg.2439,peg.2440,peg.2446,peg.2448,peg.2464,peg.2476,peg.2493,peg.2513,peg.2515,peg.2538,peg.2542,peg.2547,peg.2553,peg.2554,peg.2560,peg.2561,peg.2562,peg.2563,peg.2564,peg.2565,peg.2573,peg.2588,peg.2591,peg.2593,peg.2595,peg.2599,peg.2600,peg.2611,peg.2629,peg.2630,peg.2633,peg.2640,peg.2641,peg.2664,peg.2665,peg.2666,peg.2667,peg.2668,peg.2684,peg.2685,peg.2705,peg.2708,peg.2713,peg.2725,peg.2728,peg.2732,peg.2733,peg.2740,peg.2762,peg.2765,peg.2786,peg.2791,peg.2796,peg.2801,peg.2821,peg.2822,peg.2823,peg.2828,peg.2831,peg.2832,peg.2847,peg.2848,peg.2851,peg.2876,peg.2880,peg.2900,peg.2909,peg.2910,peg.2921,peg.2925,peg.2926,peg.2936,peg.2944,peg.2950,peg.2952,peg.2956,peg.2963,peg.2964,peg.2967,peg.3001,peg.3032,peg.3039,peg.3040,peg.3060,peg.3061,peg.3068,peg.3069,peg.3070,peg.3072,peg.3

			<p>peg.3,peg.5,peg.12,peg.16,peg.19,peg.20,peg.22,peg.30,peg.41,peg.45,peg.58,peg.74,peg.79,peg.80,peg.92,peg.96,peg.103,peg.146,peg.154,peg.177,peg.181,peg.183,peg.185,peg.190,peg.196,peg.197,peg.198,peg.199,peg.203,peg.208,peg.213,peg.219,peg.221,peg.224,peg.238,peg.243,peg.245,peg.246,peg.269,peg.282,peg.285,peg.302,peg.314,peg.318,peg.341,peg.378,peg.415,peg.416,peg.424,peg.426,peg.486,peg.487,peg.488,peg.491,peg.492,peg.520,peg.527,peg.565,peg.569,peg.570,peg.571,peg.597,peg.613,peg.614,peg.618,peg.619,peg.628,peg.632,peg.650,peg.651,peg.652,peg.653,peg.656,peg.658,peg.668,peg.670,peg.677,peg.679,peg.704,peg.706,peg.708,peg.714,peg.717,peg.718,peg.817,peg.822,peg.823,peg.843,peg.848,peg.856,peg.874,peg.875,peg.881,peg.883,peg.884,peg.885,peg.975,peg.1006,peg.1009,peg.1011,peg.1023,peg.1043,peg.1046,peg.1054,peg.1058,peg.1059,peg.1060,peg.1068,peg.1069,peg.1071,peg.1072,peg.1075,peg.1111,peg.1119,peg.1134,peg.1148,peg.1150,peg.1163,peg.1164,peg.1166,peg.1193,peg.1195,peg.1197,peg.1199,peg.1201,peg.1222,peg.1248,peg.1256,peg.1257,peg.1261,peg.1282,peg.1285,peg.1286,peg.1292,peg.1293,peg.1298,peg.1307,peg.1309,peg.1316,peg.1318,peg.1319,peg.1325,peg.1337,peg.1344,peg.1368,peg.1391,peg.1400,peg.1402,peg.1484,peg.1590,peg.1599,peg.1621,peg.1625,peg.1633,peg.1635,peg.1653,peg.1657,peg.1682,peg.1685,peg.1766,peg.1804,peg.1805,peg.1811,peg.1819,peg.1824,peg.1845,peg.1846,peg.1851,peg.1868,peg.1882,peg.1906,peg.1919,peg.1928,peg.1932,peg.1948,peg.1954,peg.1969,peg.1970,peg.1973,peg.1978,peg.1980,peg.2009,peg.2010,peg.2027,peg.2036,peg.2038,peg.2048,peg.2050,peg.2056,peg.2077,peg.2080,peg.2083,peg.2084,peg.2087,peg.2102,peg.2112,peg.2117,peg.2126,peg.2145,peg.2146,peg.2180,peg.2181,peg.2220,peg.2239,peg.2249,peg.2272,peg.2273,peg.2285,peg.2290,peg.2295,peg.2380,peg.2479,peg.2481,peg.2486,peg.2490,peg.2495,peg.2496,peg.2524,peg.2539,peg.2543,peg.2552,peg.2557,peg.2575,peg.2583,peg.2604,peg.2605,peg.2630,peg.2631,peg.2637,peg.2639,peg.2652,peg.2664,peg.2670,peg.2683,peg.2693,peg.2698,peg.2699,peg.2702,peg.2703,peg.2724,peg.2725,peg.2730,peg.2738,peg.2742,peg.2748,peg.2750,peg.2755,peg.2771,peg.2773,peg.2779,peg.2781,peg.2797,peg.2798,peg.2800,peg.2801,peg.2805,peg.2812,peg.2813,peg.2814,peg.2819,peg.2844,peg.2849,peg.2853,peg.2856,peg.2857,peg.2858,peg.2859,peg.2860,peg.2863,peg.2865,peg.2866,peg.2870,peg.2871,peg.2877,peg.2882,peg.2885,peg.2886,peg.2891,peg.2894,peg.2922,peg.2930,peg.2954,peg.2958,peg.2973,peg.2989,peg.2998,peg.3041,peg.3079,peg.3111,peg.3120,peg.3124,peg.3125,peg.3132,peg.3139,peg.3141,peg.3154,peg.3155,peg.3163,peg.3179,peg.3180,peg.3182,peg.3183,peg.3190,peg.3191,peg.3192,peg.3194,peg.3196,peg.3212,peg.3223,peg.3227,peg.3228,peg.3229,peg.3233,peg.3239,peg.3246,peg.3250,peg.3251,peg.3254,peg.3256,peg.3257,peg.3310,peg.3311,peg.3320,peg.3322,peg.3323,peg.3324,peg.3344,peg.3348,peg.3383,peg.3384,peg.3385,peg.3391,peg.3397,peg.3412,peg.3447,peg.3453,peg.3454,peg.3456,peg.3475,peg.3490,peg.3526,peg.3540,peg.3558,peg.3559,peg.3565,peg.3569,peg.3619,peg.3651,peg.3684,peg.3685,peg.3688,peg.3692,peg.3695,peg.3696,peg.3699,peg.3701,peg.3702,peg.3705,peg.3706,peg.3713,peg.3741,peg.3742,peg.3757,peg.3761,peg.3766,peg.3774,peg.3777,peg.3780,peg.3788,peg.3790,peg.3794,peg.3804,peg.3805,peg.3811,peg.3812,peg.3814,peg.3817,peg.3818,peg.3820,peg.3824,peg.3829,peg.3831,peg.3833,peg.3855,peg.3856,peg.3859,peg.3867,peg.3870,peg.3878,peg.3880,peg.3881,peg.3885,peg.3891,peg.3928,peg.3931,peg.3932,peg.3933,peg.3936,peg.3938,peg.3955,peg.3978,peg.3994,peg.4171,peg.4175,peg.4221,peg.4261,peg.4263,peg.4385</p>
9.95			
GO:0005737	Cytoplasm	450	
		1.79	
GO:0042597	Periplasmic space	81	
		1.59	
GO:0005887	Integral component of Plasma Membrane	72	
		1.52	
GO:0005840	Ribosome	69	

			peg.72,peg.141,peg.254,peg.255,peg.257,peg.302,peg.309,peg.427,peg.428,peg.498,peg.697,peg.835,peg.1000,peg.1002,peg.1033,peg.1302,peg.1303,peg.1480,peg.1518,peg.1543,peg.1613,peg.1642,peg.1643,peg.1697,peg.1836,peg.1837,peg.1923,peg.1924,peg.2227,peg.2263,peg.2286,peg.2349,peg.2449,peg.2601,peg.2602,peg.2674,peg.2675,peg.2731,peg.2763,peg.2824,peg.2902,peg.2903,peg.2911,peg.2962,peg.3000,peg.3054,peg.3201,peg.3230,peg.3235,peg.3418,peg.3419,peg.3430,peg.3464,peg.3635,peg.3967,peg.3973,peg.3974,peg.4094,peg.4095,peg.4099,peg.4161,peg.4308,peg.4341,peg.4377,peg.4378,peg.4387
		1.46	
GO:0043190	ATP-binding cassette (ABC) transporter complex	66	

Supplementary Table 3. Summary of the cluster of orthologous group (COG) classification of the protein encoding genes (PEGs) from *Pectobacterium carotovorum* subsp. *carotovorum* (Pcc) ICMP 5702

Category	Description	No. of PEGs	Code	Associated PEGs
Information storage and processing				peg.22,peg.27,peg.45,peg.79,peg.80,peg.92,peg.144,peg.150,peg.151,peg.160,peg.223,peg.224,peg.228,peg.229,peg.230,peg.231,peg.267,peg.269,peg.286,peg.300,peg.319,peg.320,peg.410,peg.423,peg.424,peg.527,peg.597,peg.616,peg.618,peg.625,peg.626,peg.631,peg.632,peg.650,peg.652,peg.653,peg.654,peg.655,peg.656,peg.679,peg.704,peg.708,peg.717,peg.718,peg.817,peg.892,peg.987,peg.1043,peg.1051,peg.1057,peg.1058,peg.1060,peg.1185,peg.1186,peg.1243,peg.1261,peg.1292,peg.1293,peg.1298,peg.1300,peg.1307,peg.1309,peg.1318,peg.1400,peg.1590,peg.1685,peg.1721,peg.1813,peg.1819,peg.1826,peg.1871,peg.2077,peg.2079,peg.2082,peg.2220,peg.2244,peg.2249,peg.2290,peg.2435,peg.2478,peg.2479,peg.2486,peg.2487,peg.2576,peg.2577,peg.2652,peg.2657,peg.2692,peg.2698,peg.2699,peg.2700,peg.2701,peg.2702,peg.2703,peg.2724,peg.2742,peg.2773,peg.2778,peg.2781,peg.2785,peg.2798,peg.2805,peg.2815,peg.2862,peg.2877,peg.2886,peg.2907,peg.2958,peg.2968,peg.2971,peg.3075,peg.3120,peg.3124,peg.3141,peg.3183,peg.3191,peg.3196,peg.3221,peg.3224,peg.3255,peg.3309,peg.3310,peg.3311,peg.3312,peg.3322,peg.3402,peg.3424,peg.3453,peg.3456,peg.3458,peg.3500,peg.3545,peg.3546,peg.3548,peg.3552,peg.3558,peg.3559,peg.3705,peg.3737,peg.3742,peg.3761,peg.3763,peg.3780,peg.3814,peg.3817,peg.3825,peg.3859,peg.3867,peg.3889,peg.3890,peg.3891,peg.3895,peg.3897,peg.3898,peg.3899,peg.3900,peg.3902,peg.3903,peg.3904,peg.3905,peg.3906,peg.3907,peg.3908,peg.3909,peg.3910,peg.3911,peg.3912,peg.3913,peg.3914,peg.3915,peg.3916,peg.3917,peg.3918,peg.3919,peg.3920,peg.3921,peg.3922,peg.3927,peg.3928,peg.3929,peg.3930,peg.3931,peg.3932,peg.3933,peg.3978,peg.3997,peg.4148,peg.4168,peg.4216,peg.4254,peg.4260,peg.4356,peg.4358,peg.4360,peg.4402
Translation, ribosomal structure and biogenesis		195	J	peg.23,peg.29,peg.36,peg.48,peg.56,peg.66,peg.76,peg.87,peg.101,peg.105,peg.107,peg.126,peg.132,peg.135,peg.185,peg.195,peg.210,peg.222,peg.227,peg.232,peg.233,peg.236,peg.243,peg.266,peg.289,peg.296,peg.301,peg.313,peg.324,peg.353,peg.364,peg.368,peg.377,peg.385,peg.397,peg.399,peg.405,peg.417,peg.436,peg.441,peg.450,peg.451,peg.455,peg.456,peg.461,peg.462,peg.468,peg.491,peg.492,peg.493,peg.555,peg.557,peg.560,peg.561,peg.563,peg.575,peg.579,peg.588,peg.611,peg.614,peg.619,peg.621,peg.622,peg.623,peg.630,peg.649,peg.651,peg.675,peg.677,peg.681,peg.683,peg.691,peg.701,peg.721,peg.722,peg.726,peg.736,peg.756,peg.764,peg.793,peg.807,peg.833,peg.838,peg.851,peg.857,peg.858,peg.871,peg.886,peg.889,peg.901,peg.908,peg.918,peg.919,peg.923,peg.936,peg.938,peg.943,peg.946,peg.950,peg.952,peg.959,peg.960,peg.961,peg.970,peg.979,peg.983,peg.991,peg.1020,peg.1028,peg.1041,peg.1049,peg.1076,peg.1093,peg.1099,peg.1117,peg.1124,peg.1140,peg.1143,peg.1173,peg.1177,peg.1189,peg.1213,peg.1215,peg.1224,peg.1268,peg.1282,peg.1314,peg.1319,peg.1387,peg.1439,peg.1442,peg.1455,peg.1459,peg.1468,peg.1470,peg.1479,peg.1485,peg.1489,peg.1492,peg.1505,peg.1506,peg.1530,peg.1536,peg.1552,peg.1557,peg.1560,peg.1561,peg.1570,peg.1572,peg.1574,peg.1575,peg.1581,peg.1583,peg.1606,peg.1655,peg.1661,peg.1675,peg.1703,peg.1712,peg.1715,peg.1778,peg.1781,peg.1799,peg.1853,peg.1880,peg.1890,peg.1908,peg.1919,peg.1928,peg.1937,peg.1941,peg.1947,peg.1953,peg.1958,peg.1969,peg.1970,peg.2027,peg.2032,peg.2041,peg.2095,peg.2108,peg.2110,peg.2117,peg.2119,peg.2152,peg.2183,peg.2185,peg.2189,peg.2193,peg.2206,peg.2214,peg.2240,peg.2251,peg.2252,peg.2266,peg.2281,peg.2283,peg.2309,peg.2312,peg.2313,peg.2324,peg.2333,peg.2350,peg.2370,peg.2372,peg.2384,peg.2386,peg.2388,peg.2413,peg.2437,peg.2445,peg.2450,peg.2463,peg.2475,peg.2495,peg.2512,peg.2514,peg.2516,peg.2541,peg.2552,peg.2568,peg.2605,peg.2639,peg.2670,peg.2697,peg.2706,peg.2712,peg.2716,peg.2727,peg.2736,peg.2748,peg.2757,peg.2764,peg.2771,peg.2826,peg.2849,peg.2861,peg.2875,peg.2881,peg.2887,peg.2891,peg.2923,peg.2937,peg.2949,peg.2980,peg.3038,peg.3056,peg.3073,peg.3089,peg.3096,peg.3098,peg.3099,peg.3100,peg.3102,peg.3104,peg.3130,peg.3140,peg.3158,peg.3189,peg.3199,peg.3205,peg.3214,peg.3234,peg.3259,peg.3264,peg.3332,peg.3349,peg.3363,peg.3376,peg.3378,peg.3385,peg.3392,peg.3421,peg.3435,peg.3454,peg.3472,peg.3487,peg.3492,peg.3536,peg.3560,peg.3578,peg.3583,peg.3584,peg.3587,peg.3588,peg.3604,peg.3622,peg.3623,peg.3638,peg.3647,peg.3656,peg.3659,peg.3667,peg.3671,peg.3706,peg.3708,peg.3718,peg.3724,peg.3726,peg.3736,peg.3747,peg.3753,peg.3764,peg.3783,peg.3785,peg.3788,peg.3792,peg.3798,peg.3808,peg.3816,peg.3844,peg.3875,peg.3877,peg.3896,peg.3936,peg.3940,peg.3954,peg.4001,peg.4002,peg.4011,peg.4016,peg.4017,peg.4028,peg.4040,peg.4053,peg.4058,peg.4089,peg.4101,peg.4110,peg.4116,peg.4126,peg.4141,peg.4150,peg.4152,peg.4157,peg.4164,peg.4170,peg.4199,peg.4209,peg.4212,peg.4229,peg.4230,peg.4249,peg.4315,peg.4342,peg.4348,peg.4362,peg.4365,peg.4366,peg.4382,peg.4405,peg.4411,peg.4418,peg.4465,peg.4517
Transcription		355	K	

			peg.7,peg.26,peg.152,peg.208,peg.244,peg.246,peg.248,peg.259,peg.288,peg.339,peg.348,peg.352,peg.360,peg.384,peg.390,peg.393,peg.394,peg.401,peg.425,peg.429,peg.430,peg.431,peg.448,peg.449,peg.453,peg.454,peg.458,peg.478,peg.531,peg.613,peg.615,peg.664,peg.678,peg.716,peg.724,peg.734,peg.742,peg.821,peg.827,peg.891,peg.894,peg.965,peg.974,peg.986,peg.1006,peg.1008,peg.1016,peg.1018,peg.1019,peg.1044,peg.1071,peg.1072,peg.1080,peg.1119,peg.1121,peg.1122,peg.1148,peg.1167,peg.1169,peg.1191,peg.1196,peg.1222,peg.1252,peg.1296,peg.1325,peg.1342,peg.1507,peg.1592,peg.1593,peg.1595,peg.1596,peg.1633,peg.1716,peg.1717,peg.1739,peg.1790,peg.1794,peg.1954,peg.1956,peg.2044,peg.2092,peg.2093,peg.2112,peg.2211,peg.2301,peg.2472,peg.2543,peg.2566,peg.2570,peg.2612,peg.2614,peg.2642,peg.2723,peg.2751,peg.2768,peg.2769,peg.2770,peg.2772,peg.2835,peg.2878,peg.2892,peg.2951,peg.2970,peg.2976,peg.2986,peg.2989,peg.3004,peg.3106,peg.3107,peg.3111,peg.3114,peg.3181,peg.3194,peg.3220,peg.3245,peg.3246,peg.3250,peg.3262,peg.3281,peg.3324,peg.3338,peg.3380,peg.3391,peg.3400,peg.3515,peg.3547,peg.3601,peg.3619,peg.3620,peg.3735,peg.3813,peg.3827,peg.3855,peg.3886,peg.3993,peg.4069,peg.4076,peg.4121,peg.4169,peg.4352,peg.4353,peg.4354,peg.4355,peg.4452,peg.4488,peg.4501,peg.4520
		L	
	Replication, recombination and repair	147	peg.8,peg.60,peg.83,peg.146,peg.179,peg.282,peg.285,peg.318,peg.342,peg.362,peg.520,peg.714,peg.813,peg.879,peg.1075,peg.1163,peg.1283,peg.1365,peg.1401,peg.1414,peg.1830,peg.1916,peg.2038,peg.2040,peg.2080,peg.2526,peg.2589,peg.2628,peg.2649,peg.2650,peg.2651,peg.2800,peg.2812,peg.2813,peg.2814,peg.2880,peg.3461,peg.3540,peg.3685,peg.3692,peg.3693,peg.3694,peg.3698,peg.3704,peg.3982,peg.4078,peg.4171,peg.4177,peg.4251,peg.4252,peg.4253,peg.4273,peg.4403,peg.4454
Cellular process and signalling	Cell cycle control, cell division, chromosome partitioning	54	D
			V
	Defense mechanisms	44	526,peg.1558,peg.1559,peg.1642,peg.1643,peg.1644,peg.1931,peg.1943,peg.1957,peg.2261,peg.2822,peg.2898,peg.2993,peg.3033,peg.3069,peg.3070,peg.3174,peg.3230,peg.3231,peg.3437,peg.3521,peg.3666,peg.3676,peg.3677,peg.3837,peg.4029,peg.4030,peg.4034
			T
	Signal Transduction mechanisms	90	peg.16,peg.17,peg.20,peg.35,peg.41,peg.191,peg.261,peg.262,peg.281,peg.333,peg.601,peg.765,peg.872,peg.944,peg.1009,peg.1087,peg.1094,peg.1125,peg.1162,peg.1207,peg.1223,peg.1225,peg.1308,peg.1328,peg.1329,peg.1413,peg.1440,peg.1462,peg.1484,peg.1567,peg.1585,peg.1607,peg.1688,peg.1811,peg.1920,peg.1927,peg.1964,peg.1979,peg.2029,peg.2056,peg.2059,peg.2182,peg.2247,peg.2296,peg.2297,peg.2303,peg.2308,peg.2325,peg.2381,peg.2385,peg.2389,peg.2494,peg.2626,peg.2713,peg.2714,peg.2728,peg.2738,peg.2739,peg.2774,peg.2848,peg.3072,peg.3084,peg.3159,peg.3161,peg.3169,peg.3176,peg.3177,peg.3186,peg.3187,peg.3188,peg.3223,peg.3273,peg.3320,peg.3330,peg.3368,peg.3479,peg.3501,peg.3511,peg.3519,peg.3562,peg.3734,peg.3744,peg.3773,peg.3937,peg.4000,peg.4051,peg.4213,peg.4268,peg.4316,peg.4410
			M
	Cell wall/membrane/envelope biogenesis	263	peg.6,peg.24,peg.34,peg.50,peg.62,peg.82,peg.94,peg.111,peg.143,peg.153,peg.155,peg.157,peg.159,peg.161,peg.166,peg.167,peg.168,peg.169,peg.170,peg.171,peg.173,peg.184,peg.194,peg.219,peg.283,peg.284,peg.306,peg.314,peg.316,peg.325,peg.335,peg.340,peg.356,peg.380,peg.383,peg.479,peg.534,peg.546,peg.547,peg.548,peg.574,peg.629,peg.673,peg.715,peg.754,peg.782,peg.783,peg.784,peg.785,peg.820,peg.832,peg.870,peg.904,peg.912,peg.913,peg.926,peg.927,peg.984,peg.1004,peg.1010,peg.1022,peg.1024,peg.1026,peg.1039,peg.1064,peg.1065,peg.1066,peg.1067,peg.1069,peg.1070,peg.1090,peg.1101,peg.1102,peg.1103,peg.1131,peg.1139,peg.1161,peg.1188,peg.1210,peg.1244,peg.1258,peg.1278,peg.1288,peg.1289,peg.1290,peg.1291,peg.1297,peg.1305,peg.1362,peg.1364,peg.1374,peg.1379,peg.1386,peg.1404,peg.1411,peg.1412,peg.1416,peg.1420,peg.1423,peg.1428,peg.1429,peg.1433,peg.1435,peg.1486,peg.1522,peg.1525,peg.1566,peg.1618,peg.1645,peg.1647,peg.1654,peg.1690,peg.1705,peg.1707,peg.1740,peg.1742,peg.1744,peg.1760,peg.1796,peg.1808,peg.1815,peg.1918,peg.1929,peg.1930,peg.1932,peg.1935,peg.1939,peg.1940,peg.1942,peg.1961,peg.2023,peg.2026,peg.2031,peg.2039,peg.2066,peg.2067,peg.2100,peg.2102,peg.2113,peg.2115,peg.2125,peg.2149,peg.2155,peg.2156,peg.2157,peg.2208,peg.2215,peg.2245,peg.2277,peg.2304,peg.2320,peg.2368,peg.2398,peg.2427,peg.2428,peg.2429,peg.2483,peg.2501,peg.2520,peg.2549,peg.2585,peg.2586,peg.2606,peg.2625,peg.2654,peg.2688,peg.2719,peg.2737,peg.2759,peg.2760,peg.2788,peg.2806,peg.2818,peg.2838,peg.2852,peg.2879,peg.2924,peg.2927,peg.2947,peg.2961,peg.2984,peg.2995,peg.3029,peg.3032,peg.3045,peg.3062,peg.3068,peg.3091,peg.3097,peg.3118,peg.3157,peg.3164,peg.3175,peg.3185,peg.3206,peg.3219,peg.3249,peg.3254,peg.3346,peg.3347,peg.3350,peg.3367,peg.3440,peg.3450,peg.3451,peg.3455,peg.3505,peg.3506,peg.3529,peg.3543,peg.3662,peg.3678,peg.3691,peg.3696,peg.3697,peg.3699,peg.3700,peg.3701,peg.3702,peg.3703,peg.3730,peg.3739,peg.3740,peg.3760,peg.3789,peg.3802,peg.3819,peg.3828,peg.3835,peg.3864,peg.3869,peg.3874,peg.3893,peg.3941,peg.3961,peg.3962,peg.3968,peg.3991,peg.4064,peg.4070,peg.4111,peg.4113,peg.4114,peg.4115,peg.4131,peg.4146,peg.4274,peg.4275,peg.4276,peg.4281,peg.4290,peg.4296,peg.4299,peg.4302,peg.4369,peg.4370,peg.4390,peg.4391,peg.4392,peg.4419,peg.4467,peg.4491,peg.4509

			peg.771,peg.1659,peg.1730,peg.1822,peg.1959,peg.1971,peg.1972,peg.1982,peg.1983,peg.1984,peg.1985,peg.1986,peg.1987,peg.1988,peg.1989,peg.1990,peg.1991,peg.1992,peg.1993,peg.1994,peg.1995,peg.1996,peg.1997,peg.1998,peg.2000,peg.2001,peg.2002,peg.2003,peg.2004,peg.2005,peg.2006,peg.2007,peg.2008,peg.2010,peg.2011,peg.2012,peg.2014,peg.2015,peg.2016,peg.2017,peg.2018,peg.2019,peg.2020,peg.2028,peg.3092,peg.4081,peg.4421,peg.4422,peg.4423,peg.4437,peg.4513
		N	
Cell motility	51		peg.181,peg.205,peg.206,peg.207,peg.226,peg.292,peg.375,peg.376,peg.636,peg.767,peg.769,peg.770,peg.773,peg.774,peg.776,peg.777,peg.778,peg.779,peg.911,peg.914,peg.1013,peg.1136,peg.1137,peg.1138,peg.1264,peg.1265,peg.1266,peg.1284,peg.1360,peg.1361,peg.1363,peg.1382,peg.1490,peg.1512,peg.1696,peg.1748,peg.1751,peg.1752,peg.1755,peg.1756,peg.1757,peg.1758,peg.1759,peg.1903,peg.1904,peg.2168,peg.2169,peg.2272,peg.2274,peg.2279,peg.2373,peg.2374,peg.2375,peg.2376,peg.2382,peg.2392,peg.2397,peg.2414,peg.2415,peg.2446,peg.2567,peg.2591,peg.2691,peg.2707,peg.2921,peg.3151,peg.3184,peg.3313,peg.3329,peg.3682,peg.3688,peg.3707,peg.3901,peg.3986,peg.4018,peg.4055,peg.4108,peg.4178,peg.4192,peg.4193,peg.4194,peg.4261,peg.4325,peg.4359,peg.4462,peg.4468,peg.4471,peg.4472,peg.4473,peg.4474,peg.4476
Intracellular trafficking, secretion, and vesicular transport	91	U	peg.52,peg.53,peg.67,peg.315,peg.326,peg.420,peg.523,peg.569,peg.570,peg.580,peg.633,peg.660,peg.661,peg.823,peg.990,peg.1017,peg.1115,peg.1132,peg.1164,peg.1165,peg.1166,peg.1168,peg.1197,peg.1217,peg.1238,peg.1255,peg.1263,peg.1273,peg.1341,peg.1437,peg.1548,peg.1662,peg.1841,peg.1882,peg.2109,peg.2142,peg.2143,peg.2144,peg.2163,peg.2165,peg.2166,peg.2167,peg.2170,peg.2171,peg.2174,peg.2222,peg.2273,peg.2284,peg.2334,peg.2342,peg.2510,peg.2620,peg.2655,peg.2708,peg.2787,peg.2885,peg.2888,peg.2889,peg.2918,peg.2940,peg.3044,peg.3076,peg.3077,peg.3135,peg.3136,peg.3241,peg.3251,peg.3333,peg.3364,peg.3442,peg.3590,peg.3738,peg.3766,peg.3767,peg.3807,peg.3822,peg.3823,peg.3833,peg.3952,peg.3998,peg.4118,peg.4139,peg.4172,peg.4173,peg.4321,peg.4323,peg.4424
Posttranslational modification, protein turnover, chaperones	87	O	peg.42,peg.58,peg.68,peg.74,peg.86,peg.91,peg.93,peg.119,peg.120,peg.177,peg.212,peg.237,peg.278,peg.279,peg.280,peg.293,peg.365,peg.366,peg.367,peg.408,peg.475,peg.564,peg.591,peg.598,peg.604,peg.609,peg.620,peg.659,peg.680,peg.687,peg.710,peg.719,peg.798,peg.803,peg.804,peg.852,peg.884,peg.885,peg.887,peg.895,peg.899,peg.905,peg.907,peg.985,peg.1003,peg.1035,peg.1052,peg.1156,peg.1157,peg.1158,peg.1159,peg.1218,peg.1253,peg.1320,peg.1345,peg.1346,peg.1347,peg.1348,peg.1349,peg.1350,peg.1353,peg.1355,peg.1356,peg.1397,peg.1398,peg.1399,peg.1405,peg.1441,peg.1444,peg.1471,peg.1474,peg.1493,peg.1494,peg.1513,peg.1517,peg.1527,peg.1532,peg.1577,peg.1616,peg.1689,peg.1761,peg.1798,peg.1845,peg.1854,peg.1855,peg.1856,peg.1857,peg.1858,peg.1859,peg.1860,peg.1861,peg.1862,peg.1863,peg.1865,peg.1866,peg.1886,peg.1887,peg.1895,peg.1896,peg.1906,peg.1909,peg.1938,peg.2033,peg.2049,peg.2068,peg.2071,peg.2076,peg.2104,peg.2123,peg.2138,peg.2159,peg.2160,peg.2161,peg.2175,peg.2176,peg.2177,peg.2178,peg.2179,peg.2181,peg.2210,peg.2224,peg.2226,peg.2226,peg.2250,peg.2255,peg.2293,peg.2295,peg.2300,peg.2328,peg.2329,peg.2330,peg.2331,peg.2352,peg.2453,peg.2454,peg.2456,peg.2492,peg.2493,peg.2511,peg.2544,peg.2560,peg.2561,peg.2562,peg.2563,peg.2564,peg.2565,peg.2603,peg.2615,peg.2621,peg.2630,peg.2641,peg.2709,peg.2718,peg.2721,peg.2745,peg.2799,peg.2844,peg.2847,peg.2871,peg.2882,peg.2894,peg.2895,peg.2917,peg.2938,peg.2942,peg.2946,peg.3020,peg.3053,peg.3066,peg.3083,peg.3094,peg.3134,peg.3137,peg.3138,peg.3155,peg.3178,peg.3197,peg.3198,peg.3211,peg.3411,peg.3471,peg.3474,peg.3493,peg.3503,peg.3526,peg.3530,peg.3539,peg.3598,peg.3600,peg.3639,peg.3641,peg.3653,peg.3668,peg.3669,peg.3670,peg.3793,peg.3794,peg.3832,peg.3842,peg.3860,peg.3861,peg.3862,peg.3863,peg.3868,peg.3879,peg.3946,peg.3970,peg.3971,peg.4005,peg.4023,peg.4037,peg.4045,peg.4060,peg.4061,peg.4062,peg.4107,peg.4112,peg.4123,peg.4151,peg.4181,peg.4208,peg.4219,peg.4267,peg.4310,peg.4372,peg.4373,peg.4393,peg.4395,peg.4397,peg.4398,peg.4399,peg.4400,peg.4401,peg.4404
Metabolism		C	
Energy production and conversion	233		

		peg.77,peg.85,peg.96,peg.97,peg.99,peg.106,peg.118,peg.193,peg.297,peg.299,peg.338,peg.371,peg.372,peg.373,peg.378,peg.379,peg.381,peg.414,peg.486,peg.487,peg.488,peg.589,peg.590,peg.592,peg.603,peg.606,peg.635,peg.647,peg.698,peg.699,peg.700,peg.758,peg.780,peg.796,peg.825,peg.828,peg.839,peg.840,peg.844,peg.846,peg.847,peg.848,peg.849,peg.873,peg.874,peg.875,peg.928,peg.1114,peg.1116,peg.1205,peg.1281,peg.1315,peg.1316,peg.1317,peg.1326,peg.1378,peg.1389,peg.1390,peg.1395,peg.1417,peg.1438,peg.1448,peg.1449,peg.1450,peg.1452,peg.1453,peg.1454,peg.1460,peg.1461,peg.1476,peg.1478,peg.1483,peg.1487,peg.1488,peg.1582,peg.1620,peg.1683,peg.1693,peg.1700,peg.1746,peg.1747,peg.1868,peg.1869,peg.1901,peg.1902,peg.1905,peg.1907,peg.1962,peg.2030,peg.2094,peg.2150,peg.2153,peg.2154,peg.2232,peg.2234,peg.2235,peg.2236,peg.2237,peg.2238,peg.2239,peg.2246,peg.2253,peg.2254,peg.2265,peg.2278,peg.2280,peg.2395,peg.2410,peg.2464,peg.2465,peg.2466,peg.2499,peg.2509,peg.2513,peg.2545,peg.2553,peg.2555,peg.2557,peg.2622,peg.2632,peg.2635,peg.2637,peg.2664,peg.2665,peg.2666,peg.2676,peg.2681,peg.2687,peg.2710,peg.2722,peg.2755,peg.2758,peg.2765,peg.2766,peg.2767,peg.2929,peg.2943,peg.2944,peg.2952,peg.2954,peg.3042,peg.3059,peg.3063,peg.3064,peg.3115,peg.3127,peg.3128,peg.3142,peg.3253,peg.3288,peg.3386,peg.3397,peg.3431,peg.3480,peg.3481,peg.3483,peg.3491,peg.3502,peg.3507,peg.3509,peg.3541,peg.3579,peg.3580,peg.3581,peg.3582,peg.3591,peg.3629,peg.3630,peg.3631,peg.3644,peg.3645,peg.3648,peg.3664,peg.3674,peg.3675,peg.3759,peg.3786,peg.3796,peg.3803,peg.3818,peg.3943,peg.3951,peg.3957,peg.3958,peg.3960,peg.3980,peg.3992,peg.4019,peg.4038,peg.4049,peg.4050,peg.4063,peg.4122,peg.4142,peg.4143,peg.4145,peg.4180,peg.4184,peg.4221,peg.4223,peg.4228,peg.4233,peg.4234,peg.4265,peg.4283,peg.4327,peg.4329,peg.4344,peg.4345,peg.4346,peg.4347,peg.4351,peg.4413,peg.4416,peg.4420,peg.4514,peg.4515
Carbohydrate transport and metabolism	217	peg.43,peg.46,peg.63,peg.72,peg.136,peg.137,peg.141,peg.149,peg.183,peg.186,peg.196,peg.197,peg.199,peg.215,peg.253,peg.277,peg.322,peg.330,peg.331,peg.345,peg.370,peg.403,peg.415,peg.421,peg.426,peg.446,peg.466,peg.481,peg.498,peg.518,peg.524,peg.562,peg.567,peg.594,peg.688,peg.689,peg.690,peg.723,peg.757,peg.800,peg.808,peg.834,peg.854,peg.868,peg.877,peg.878,peg.880,peg.924,peg.942,peg.975,peg.976,peg.1023,peg.1033,peg.1038,peg.1054,peg.1056,peg.1074,peg.1127,peg.1130,peg.1172,peg.1236,peg.1240,peg.1256,peg.1257,peg.1279,peg.1301,peg.1313,peg.1338,peg.1339,peg.1343,peg.1371,peg.1418,peg.1436,peg.1446,peg.1456,peg.1521,peg.1543,peg.1545,peg.1573,peg.1587,peg.1613,peg.1634,peg.1676,peg.1677,peg.1814,peg.1825,peg.1838,peg.1852,peg.1910,peg.1911,peg.1922,peg.1949,peg.2037,peg.2055,peg.2089,peg.2132,peg.2227,peg.2263,peg.2282,peg.2285,peg.2286,peg.2335,peg.2336,peg.2337,peg.2341,peg.2343,peg.2354,peg.2371,peg.2438,peg.2442,peg.2448,peg.2459,peg.2467,peg.2522,peg.2523,peg.2531,peg.2582,peg.2583,peg.2584,peg.2601,peg.2602,peg.2662,peg.2683,peg.2704,peg.2730,peg.2753,peg.2790,peg.2802,peg.2807,peg.2824,peg.2827,peg.2836,peg.2854,peg.2855,peg.2856,peg.2857,peg.2858,peg.2859,peg.2860,peg.2865,peg.2900,peg.2948,peg.2962,peg.3001,peg.3002,peg.3003,peg.3034,peg.3039,peg.3051,peg.3054,peg.3055,peg.3088,peg.3112,peg.3132,peg.3154,peg.3156,peg.3166,peg.3215,peg.3256,peg.3257,peg.3258,peg.3383,peg.3390,peg.3412,peg.3413,peg.3415,peg.3416,peg.3417,peg.3422,peg.3430,peg.3433,peg.3447,peg.3465,peg.3565,peg.3586,peg.3602,peg.3607,peg.3643,peg.3673,peg.3709,peg.3712,peg.3715,peg.3717,peg.3732,peg.3751,peg.3752,peg.3757,peg.3776,peg.3778,peg.3843,peg.3871,peg.3876,peg.3881,peg.3884,peg.3948,peg.3955,peg.3967,peg.3975,peg.3983,peg.4006,peg.4007,peg.4024,peg.4027,peg.4054,peg.4067,peg.4068,peg.4080,peg.4096,peg.4098,peg.4104,peg.4109,peg.4124,peg.4134,peg.4136,peg.4153,peg.4162,peg.4163,peg.4187,peg.4243,peg.4244,peg.4245,peg.4246,peg.4308,peg.4341
Amino acid transport and metabolism	224	peg.5,peg.25,peg.30,peg.31,peg.44,peg.95,peg.103,peg.145,peg.147,peg.154,peg.174,peg.190,peg.198,peg.221,peg.250,peg.251,peg.350,peg.409,peg.411,peg.412,peg.489,peg.532,peg.552,peg.658,peg.669,peg.670,peg.671,peg.696,peg.822,peg.843,peg.893,peg.917,peg.1011,peg.1046,peg.1055,peg.1059,peg.1111,peg.1134,peg.1135,peg.1146,peg.1171,peg.1193,peg.1199,peg.1204,peg.1219,peg.1220,peg.1247,peg.1248,peg.1250,peg.1251,peg.1259,peg.1352,peg.1368,peg.1372,peg.1391,peg.1393,peg.1402,peg.1403,peg.1541,peg.1605,peg.1617,peg.1653,peg.1657,peg.1680,peg.1681,peg.1687,peg.1766,peg.1833,peg.1846,peg.1851,peg.1879,peg.2034,peg.2053,peg.2075,peg.2091,peg.2116,peg.2126,peg.2133,peg.2216,peg.2228,peg.2243,peg.2481,peg.2482,peg.2490,peg.2548,peg.2556,peg.2581,peg.2604,peg.2610,peg.2631,peg.2656,peg.2661,peg.2693,peg.2726,peg.2754,peg.2801,peg.2804,peg.2819,peg.2821,peg.2840,peg.2853,peg.2863,peg.2874,peg.2916,peg.2922,peg.2934,peg.2997,peg.3037,peg.3048,peg.3067,peg.3079,peg.3082,peg.3109,peg.3110,peg.3125,peg.3163,peg.3165,peg.3207,peg.3208,peg.3233,peg.3239,peg.3240,peg.3242,peg.3243,peg.3244,peg.3317,peg.3384,peg.3388,peg.3401,peg.3439,peg.3459,peg.3467,peg.3495,peg.3496,peg.3516,peg.3520,peg.3535,peg.3568,peg.3683,peg.3684,peg.3687,peg.3695,peg.3754,peg.3755,peg.3774,peg.3777,peg.3787,peg.3804,peg.3820,peg.3826,peg.3870,peg.3878,peg.3979,peg.3984,peg.3999,peg.4035,peg.4039,peg.4046,peg.4047,peg.4048,peg.4084,peg.4102,peg.4105,peg.4119,peg.4120,peg.4125,peg.4156,peg.4179,peg.4201,peg.4338,peg.4339,peg.4394,peg.4396,peg.4406
Nucleotide transport and metabolism	174	

		peg.2,peg.3,peg.12,peg.19,peg.57,peg.104,peg.113,peg.148,peg.156,peg.172,peg.176,peg.192,peg.202,peg.204,peg.209,peg.211,peg.220,peg.238,peg.239,peg.240,peg.241,peg.242,peg.245,peg.270,peg.274,peg.341,peg.521,peg.522,peg.533,peg.537,peg.571,peg.572,peg.624,peg.634,peg.668,peg.684,peg.789,peg.842,peg.856,peg.882,peg.995,peg.1036,peg.1062,peg.1085,peg.1100,peg.1141,peg.1142,peg.1144,peg.1147,peg.1150,peg.1152,peg.1155,peg.1181,peg.1194,peg.1201,peg.1211,peg.1221,peg.1227,peg.1229,peg.1230,peg.1231,peg.1232,peg.1285,peg.1286,peg.1295,peg.1336,peg.1344,peg.1369,peg.1381,peg.1415,peg.1430,peg.1533,peg.1568,peg.1591,peg.1610,peg.1611,peg.1621,peg.1622,peg.1623,peg.1624,peg.1625,peg.1636,peg.1637,peg.1638,peg.1639,peg.1640,peg.1656,peg.1667,peg.1741,peg.1743,peg.1824,peg.1829,peg.1834,peg.1840,peg.1875,peg.1897,peg.1921,peg.1977,peg.2045,peg.2101,peg.2122,peg.2134,peg.2135,peg.2145,peg.2191,peg.2204,peg.2205,peg.2212,peg.2218,peg.2221,peg.2256,peg.2351,peg.2360,peg.2367,peg.2485,peg.2496,peg.2539,peg.2575,peg.2579,peg.2669,peg.2756,peg.2777,peg.2841,peg.2842,peg.2843,peg.2845,peg.2866,peg.2870,peg.2928,peg.2930,peg.2953,peg.3050,peg.3052,peg.3081,peg.3139,peg.3180,peg.3190,peg.3212,peg.3213,peg.3225,peg.3226,peg.3227,peg.3228,peg.3229,peg.3232,peg.3316,peg.3335,peg.3441,peg.3468,peg.3469,peg.3470,peg.3476,peg.3484,peg.3485,peg.3499,peg.3504,peg.3522,peg.3569,peg.3595,peg.3642,peg.3649,peg.3651,peg.3679,peg.3710,peg.3713,peg.3714,peg.3731,peg.3741,peg.3748,peg.3762,peg.3771,peg.3805,peg.3806,peg.3809,peg.3811,peg.3815,peg.3830,peg.3831,peg.3880,peg.3885,peg.3938,peg.3972,peg.3981,peg.4010,peg.4015,peg.4043,peg.4057,peg.4085,peg.4086,peg.4087,peg.4088,peg.4135,peg.4138,peg.4175,peg.4176,peg.4248,peg.4285,peg.4331,peg.4340,peg.4374,peg.4417,peg.110,peg.114,peg.115,peg.116,peg.117,peg.182,peg.213,peg.214,peg.275,peg.276,peg.361,peg.573,peg.612,peg.662,peg.686,peg.818,peg.850,peg.900,peg.910,peg.949,peg.1061,peg.1063,peg.1068,peg.1073,peg.1133,peg.1145,peg.1179,peg.1469,peg.1553,peg.1608,peg.1691,peg.1692,peg.1694,peg.1801,peg.1804,peg.1805,peg.1828,peg.1843,peg.1955,peg.2036,peg.2083,peg.2084,peg.2085,peg.2088,peg.2230,peg.2258,peg.2322,peg.2363,peg.2590,peg.2595,peg.2689,peg.2960,peg.3041,peg.3121,peg.3179,peg.3399,peg.3445,peg.3460,peg.3523,peg.3576,peg.3711,peg.3857,peg.4012,peg.4026,peg.4066,peg.4231,peg.4278,peg.4279
	H	
Coenzyme transport and metabolism	201	
	I	
Lipid transport and metabolism	68	
	P	
Inorganic ion transport and metabolism	338	15

Poorly characterised	Secondary metabolites biosynthesis, transport and catabolism	45	<p>Q</p> <p>peg.55,peg.189,peg.308,peg.309,peg.310,peg.311,peg.334,peg.538,peg.539,peg.541,peg.542,peg.639,peg.640,peg.642,peg.643,peg.645,peg.948,peg.1241,peg.1242,peg.1535,peg.1563,peg.1708,peg.1945,peg.2054,peg.2121,peg.2139,peg.2345,peg.2618,peg.2647,peg.2741,peg.2795,peg.2846,peg.3035,peg.3095,peg.3171,peg.3247,peg.3261,peg.3336,peg.3337,peg.3340,peg.3393,peg.4009,peg.4025,peg.4071,peg.4381</p> <p>S</p> <p>peg.4,peg.10,peg.21,peg.33,peg.37,peg.40,peg.51,peg.54,peg.64,peg.65,peg.78,peg.84,peg.88,peg.102,peg.109,peg.112,peg.121,peg.122,peg.127,peg.131,peg.133,peg.134,peg.178,peg.200,peg.203,peg.216,peg.235,peg.247,peg.249,peg.260,peg.271,peg.287,peg.290,peg.294,peg.295,peg.298,peg.302,peg.303,peg.304,peg.305,peg.312,peg.317,peg.327,peg.329,peg.332,peg.336,peg.337,peg.344,peg.346,peg.349,peg.351,peg.354,peg.359,peg.369,peg.388,peg.389,peg.391,peg.392,peg.406,peg.416,peg.419,peg.427,peg.428,peg.435,peg.439,peg.440,peg.445,peg.447,peg.457,peg.463,peg.472,peg.474,peg.477,peg.494,peg.500,peg.502,peg.503,peg.504,peg.507,peg.509,peg.510,peg.511,peg.515,peg.519,peg.525,peg.528,peg.529,peg.530,peg.545,peg.549,peg.553,peg.554,peg.556,peg.566,peg.568,peg.576,peg.578,peg.581,peg.582,peg.583,peg.584,peg.585,peg.586,peg.587,peg.593,peg.596,peg.602,peg.608,peg.610,peg.628,peg.637,peg.644,peg.648,peg.657,peg.663,peg.665,peg.672,peg.682,peg.702,peg.703,peg.706,peg.707,peg.711,peg.748,peg.752,peg.753,peg.761,peg.786,peg.788,peg.795,peg.801,peg.802,peg.812,peg.815,peg.819,peg.855,peg.861,peg.862,peg.863,peg.881,peg.890,peg.896,peg.902,peg.903,peg.909,peg.916,peg.921,peg.922,peg.925,peg.929,peg.947,peg.953,peg.954,peg.955,peg.957,peg.958,peg.962,peg.963,peg.964,peg.968,peg.969,peg.973,peg.980,peg.981,peg.982,peg.988,peg.989,peg.1014,peg.1029,peg.1037,peg.1042,peg.1045,peg.1047,peg.1048,peg.1050,peg.1053,peg.1077,peg.1078,peg.1081,peg.1084,peg.1092,peg.1095,peg.1098,peg.1106,peg.1112,peg.1151,peg.1153,peg.1170,peg.1180,peg.1183,peg.1184,peg.1190,peg.1192,peg.1195,peg.1206,peg.1208,peg.1209,peg.1212,peg.1235,peg.1237,peg.1239,peg.1254,peg.1260,peg.1272,peg.1274,peg.1275,peg.1277,peg.1287,peg.1323,peg.1324,peg.1327,peg.1334,peg.1335,peg.1337,peg.1340,peg.1354,peg.1357,peg.1358,peg.1359,peg.1366,peg.1376,peg.1388,peg.1392,peg.1394,peg.1406,peg.1407,peg.1419,peg.1427,peg.1434,peg.1447,peg.1451,peg.1465,peg.1467,peg.1472,peg.1473,peg.1499,peg.1508,peg.1523,peg.1539,peg.1547,peg.1562,peg.1564,peg.1565,peg.1569,peg.1576,peg.1584,peg.1586,peg.1588,peg.1589,peg.1597,peg.1598,peg.1599,peg.1600,peg.1602,peg.1603,peg.1609,peg.1619,peg.1627,peg.1635,peg.1641,peg.1652,peg.1663,peg.1664,peg.1672,peg.1682,peg.1684,peg.1686,peg.1701,peg.1718,peg.1736,peg.1738,peg.1745,peg.1767,peg.1775,peg.1776,peg.1783,peg.1784,peg.1786,peg.1791,peg.1793,peg.1803,peg.1806,peg.1809,peg.1810,peg.1812,peg.1816,peg.1817,peg.1818,peg.1827,peg.1832,peg.1839,peg.1842,peg.1844,peg.1847,peg.1848,peg.1849,peg.1867,peg.1872,peg.1873,peg.1878,peg.1883,peg.1884,peg.1885,peg.1888,peg.1889,peg.1898,peg.1899,peg.1900,peg.1917,peg.1925,peg.1933,peg.1936,peg.1948,peg.1952,peg.1963,peg.1965,peg.2021,peg.2022,peg.2024,peg.2035,peg.2042,peg.2043,peg.2046,peg.2047,peg.2048,peg.2051,peg.2052,peg.2057,peg.2058,peg.2063,peg.2064,peg.2069,peg.2070,peg.2072,peg.2074,peg.2081,peg.2090,peg.2099,peg.2103,peg.2105,peg.2111,peg.2120,peg.2127,peg.2136,peg.2141,peg.2146,peg.2148,peg.2184,peg.2188,peg.2190,peg.2192,peg.2198,peg.2199,peg.2213,peg.2217,peg.2233,peg.2241,peg.2248,peg.2257,peg.2268,peg.2275,peg.2276,peg.2294,peg.2298,peg.2299,peg.2302,peg.2307,peg.2310,peg.2311,peg.2338,peg.2339,peg.2340,peg.2344,peg.2359,peg.2369,peg.2379,peg.2383,peg.2391,peg.2393,peg.2400,peg.2402,peg.2403,peg.2404,peg.2405,peg.2407,peg.2408,peg.2411,peg.2412,peg.2423,peg.2431,peg.2433,peg.2434,peg.2441,peg.2455,peg.2457,peg.2460,peg.2461,peg.246</p>
	Function Unknown	791	

Supplementary Table 4. Summary of the KEGG (Kyoto Encyclopedia of Genes and Genomes database) classification of the protein encoding genes (PEGs) from *Pectobacterium carotovorum* subsp. *carotovorum* ^{FC} ICMP 5702

Category	Pathway	No. of PEGs	Associated PEGs
Metabolism			peg.1447,peg.620,peg.1430,peg.182,peg.1906,peg.2086,peg.1416,peg.1152,peg.74,peg.1061,peg.1798,peg.93,peg.197,peg.1349,peg.2258,peg.540,peg.856,peg.218,peg.1347,peg.1348,peg.1345,peg.1346,peg.895,peg.331,peg.330,peg.690,peg.947,peg.186,peg.1221,peg.251,peg.688,peg.415,peg.842,peg.843,peg.573,peg.213,peg.183,peg.421,peg.2085,peg.361,peg.1350,peg.1833,peg.2204,peg.1142,peg.1147,peg.1062,peg.924,peg.2343,peg.1921,peg.1391,peg.381,peg.2150,peg.1111,peg.574,peg.2482,peg.198,peg.1199,peg.2481,peg.1429,peg.1415,peg.1063,peg.2134,peg.524,peg.2254,peg.378,peg.538,peg.1110,peg.196,peg.2228,peg.1553,peg.684,peg.975,peg.1681,peg.1680,peg.245,peg.1371,peg.1344,peg.685,peg.1231,peg.1146,peg.887,peg.2226,peg.209,peg.1027,peg.1814,peg.877,peg.1676,peg.1573,peg.199,peg.1910,peg.370,peg.1201,peg.1805,peg.1378,peg.1417,peg.848,peg.844,peg.214,peg.1372,peg.1326,peg.789,peg.1353,peg.1352,peg.1233,peg.1259,peg.1248,peg.103,peg.250,peg.1313,peg.275,peg.1073,peg.1828,peg.2087,peg.276,peg.1155,peg.1897,peg.536,peg.533,peg.537,peg.689,peg.2485,peg.12,peg.624,peg.1232,peg.1229,peg.1227,peg.882,peg.572,peg.571,peg.211,peg.202,peg.1834,peg.328,peg.2083,peg.804,peg.1234,peg.2191,peg.1436,peg.1608,peg.1393,peg.1230,peg.1112,peg.1247,peg.1204,peg.1141,peg.136,peg.1517,peg.1852,peg.1023,peg.344,peg.1424,peg.516,peg.222,peg.2139,peg.2854,peg.3884,peg.2946,peg.2721,peg.2756,peg.3713,peg.4125,peg.3794,peg.3110,peg.4045,peg.4061,peg.4060,peg.2938,peg.4054,peg.2621,peg.3383,peg.3670,peg.3757,peg.3860,peg.3861,peg.3862,peg.3863,peg.3565,peg.3668,peg.3050,peg.3876,peg.3154,peg.3227,peg.3806,peg.3774,peg.3669,peg.3881,peg.4039,peg.4050,peg.4047,peg.4038,peg.3233,peg.2853,peg.2581,peg.3388,peg.3811,peg.3826,peg.2865,peg.2807,peg.2531,peg.3955,peg.4136,peg.2866,peg.3607,peg.4285,peg.2631,peg.4057,peg.3502,peg.3777,peg.2758,peg.3984,peg.3804,peg.3871,peg.3384,peg.3125,peg.3468,peg.3469,peg.2606,peg.4048,peg.3460,peg.3445,peg.4070,peg.2856,peg.3979,peg.3142,peg.2617,peg.3229,peg.3586,peg.3999,peg.3857,peg.3803,peg.3258,peg.3879,peg.3880,peg.4015,peg.3712,peg.3710,peg.3709,peg.2579,peg.2580,peg.2544,peg.3653,peg.4135,peg.3495,peg.2584,peg.2583,peg.4006,peg.3714,peg.3715,peg.4111,peg.3642,peg.4086,peg.3776,peg.3983,peg.4163,peg.4085,peg.2662,peg.4134,peg.2726,peg.3459,peg.4080,peg.3980,peg.2622,peg.4184,peg.3796,peg.2545,peg.3870,peg.2858,peg.3041,peg.3212,peg.3196,peg.4406,peg.3228,peg.3163,peg.3470,peg.4043,peg.4180,peg.4087,peg.2859,peg.2857,peg.4175,peg.3121,peg.3758,peg.3537,peg.3818,peg.2603,peg.3042,peg.3580,peg.3431,peg.2754,peg.3523,peg.4137,peg.3762,peg.2860,peg.3778,peg.4162,peg.3083,peg.2582,peg.2745,peg.4123,peg.3473,peg.3256,peg.3257,peg.3786,peg.4025,peg.4027,peg.4026,peg.4024,peg.4023,peg.4364,peg.4077,peg.3996,peg.4009
	Biosynthesis of secondary metabolites	312	peg.620,peg.1616,peg.852,peg.1430,peg.1906,peg.1798,peg.1444,peg.1349,peg.1347,peg.1348,peg.1345,peg.1346,peg.895,peg.690,peg.688,peg.842,peg.843,peg.183,peg.1350,peg.1391,peg.2150,peg.1846,peg.2481,peg.2134,peg.524,peg.1687,peg.192,peg.1344,peg.887,peg.2226,peg.877,peg.1676,peg.1573,peg.1805,peg.848,peg.844,peg.214,peg.1372,peg.789,peg.1353,peg.1352,peg.275,peg.1073,peg.1828,peg.276,peg.689,peg.804,peg.1234,peg.1393,peg.1845,peg.1494,peg.2946,peg.2721,peg.2756,peg.3794,peg.2938,peg.2621,peg.3670,peg.3860,peg.3861,peg.3862,peg.3863,peg.4153,peg.3668,peg.3154,peg.3806,peg.3774,peg.3669,peg.2866,peg.2631,peg.4057,peg.3951,peg.2758,peg.4265,peg.3804,peg.2939,peg.3999,peg.3803,peg.2755,peg.3879,peg.3880,peg.4015,peg.2544,peg.3653,peg.3495,peg.2662,peg.4134,peg.3980,peg.4184,peg.3796,peg.3870,peg.4180,peg.3818,peg.3431,peg.3786
	Carbon metabolism	95	

Carbohydrate metabolism

peg.93,peg.1391,peg.2150,peg.2134,peg.606,peg.1378,peg.848,peg.1372,peg.1326,peg.789,peg.2464,peg.873,peg.2094,peg.804,peg.21,peg.620,peg.1798,peg.1349,peg.1347,peg.1348,peg.1345,peg.1346,peg.895,peg.1350,peg.1344,peg.887,peg.2226,peg.1353,peg.1352,peg.804,peg.1430,peg.74,peg.842,peg.843,peg.2481,peg.668,peg.844,peg.1326,peg.670,peg.552,peg.1393,peg.1689,peg.798,peg.591,peg.489,peg.95,peg.1907,peg.1429,peg.106,peg.1102,peg.487,peg.592,peg.1100,peg.1746,peg.96,peg.590,peg.2246,peg.905,peg.194,peg.86,peg.381,peg.489,peg.1116,peg.487,peg.848,peg.96,peg.844,peg.488,peg.85,peg.1849,peg.1391,peg.1657,peg.1429,peg.1656,peg.2254,peg.1478,peg.378,peg.1932,peg.1379,peg.1378,peg.1326,peg.700,peg.1689,peg.1907,peg.2246,peg.1022,peg.1391,peg.381,peg.1429,peg.2265,peg.2254,peg.378,peg.606,peg.1868,peg.1326,peg.1700,peg.2278,peg.2279,peg.873,peg.379,peg.1869,peg.1689,peg.219,peg.314,peg.1391,peg.381,peg.1657,peg.2116,peg.1429,peg.1656,peg.2102,peg.1315,peg.1379,peg.1326,peg.1316,peg.873,peg.2094,peg.1317,peg.635,peg.159,peg.2216,peg.1692,peg.1691,peg.1693,peg.620,peg.1616,peg.852,peg.74,peg.120,peg.1798,peg.93,peg.895,peg.2150,peg.1846,peg.2134,peg.2049,peg.192,peg.887,peg.2212,peg.789,peg.275,peg.1073,peg.1828,peg.276,peg.804,peg.2295,peg.119,peg.1845,peg.620,peg.687,peg.74,peg.690,peg.688,peg.1344,peg.2226,peg.789,peg.19,peg.689,peg.1234,peg.119,peg.687,peg.1444,peg.2351,peg.1846,peg.2045,peg.1805,peg.214,peg.789,peg.1353,peg.1352,peg.275,peg.1073,peg.1828,peg.276,peg.366,peg.1845,peg.280,peg.293,peg.1347,peg.1348,peg.1345,peg.1346,peg.895,peg.2351,peg.684,peg.685,peg.1805,peg.214,peg.328,peg.804,peg.684,peg.685,peg.1353,peg.1352,peg.1447,peg.1444,peg.848,peg.1453,peg.1446,peg.1454,peg.1452,peg.2938,peg.2621,peg.3670,peg.3668,peg.3669,peg.2631,peg.2758,peg.3804,peg.4327,peg.3999,peg.3803,peg.3495,peg.2622,peg.4184,peg.3870,peg.4180,peg.3127,peg.3818,peg.2603,peg.3083,peg.3473,peg.3842,peg.3786,peg.2721,peg.3670,peg.3860,peg.3861,peg.3862,peg.3863,peg.3668,peg.3669,peg.3999,peg.4015,peg.2544,peg.3653,peg.2756,peg.3806,peg.3774,peg.2631,peg.4057,peg.4417,peg.4265,peg.2922,peg.3803,peg.2755,peg.3980,peg.3796,peg.3870,peg.4180,peg.3818,peg.3431,peg.2682,peg.2556,peg.2606,peg.3157,peg.3957,peg.2707,peg.2683,peg.3980,peg.2557,peg.4019,peg.4392,peg.2631,peg.2953,peg.3803,peg.4184,peg.2545,peg.4180,peg.2952,peg.2664,peg.2665,peg.2666,peg.3818,peg.2678,peg.2631,peg.2606,peg.3063,peg.3504,peg.3505,peg.3509,peg.2635,peg.2632,peg.2633,peg.4039,peg.4274,peg.4050,peg.4047,peg.4038,peg.2606,peg.4048,peg.4327,peg.3128,peg.3870,peg.4049,peg.2766,peg.3579,peg.2765,peg.3127,peg.3042,peg.3580,peg.4390,peg.2606,peg.4048,peg.3730,peg.4113,peg.2545,peg.3870,peg.4112,peg.3127,peg.2664,peg.2665,peg.2666,peg.4391,peg.3167,peg.3631,peg.2938,peg.3670,peg.3860,peg.3861,peg.3862,peg.3863,peg.3668,peg.3669,peg.2870,peg.2758,peg.2808,peg.3999,peg.3880,peg.3712,peg.2544,peg.3471,peg.2603,peg.3083,peg.3473,peg.3842,peg.2946,peg.3503,peg.3668,peg.3154,peg.3502,peg.3979,peg.2610,peg.2755,peg.3879,peg.3880,peg.4015,peg.3653,peg.3668,peg.2870,peg.3653,peg.3860,peg.3861,peg.3862,peg.3863,peg.2870,peg.3710,peg.3709,peg.2603,peg.4137,peg.3713,peg.3710,peg.3709,peg.3714,peg.3715,peg.4137,peg.3142,peg.4042,peg.4184

369

peg.1347,peg.1348,peg.1345,peg.1346,peg.895,peg.1854,peg.1855,peg.1857,peg.1858,peg.1859,peg.1860,peg.1861,peg.1862,peg.1863,peg.1864,peg.1865,peg.1866,peg.1357,peg.1355,peg.1356,peg.1667,peg.1155,peg.1159,peg.1158,peg.1157,peg.1156,peg.2104,peg.1856,peg.2293,peg.620,peg.852,peg.842,peg.192,peg.848,peg.844,peg.620,peg.1347,peg.1348,peg.1345,peg.1346,peg.895,peg.1846,peg.2134,peg.1687,peg.192,peg.887,peg.2226,peg.789,peg.1353,peg.1352,peg.275,peg.1073,peg.1828,peg.276,peg.804,peg.1845,peg.1494,peg.620,peg.1906,peg.1846,peg.2134,peg.524,peg.192,peg.1372,peg.789,peg.1845,peg.1494,peg.42,peg.331,peg.330,peg.1895,peg.2328,peg.2329,peg.609,peg.2331,peg.481,peg.268,peg.19,peg.2179,peg.2176,peg.2327,peg.2159,peg.1892,peg.1893,peg.1894,peg.183,peg.421,peg.877,peg.866,peg.867,peg.865,peg.1518,peg.1519,peg.1516,peg.1514,peg.1515,peg.3860,peg.3861,peg.3862,peg.3863,peg.3526,peg.4400,peg.4398,peg.4399,peg.4396,peg.4394,peg.4397,peg.4393,peg.4395,peg.3020,peg.2621,peg.3806,peg.3951,peg.3804,peg.3999,peg.3803,peg.3980,peg.4184,peg.3796,peg.4180,peg.3818,peg.2721,peg.3860,peg.3861,peg.3862,peg.3863,peg.4153,peg.2544,peg.3653,peg.2946,peg.3794,peg.2938,peg.3154,peg.2866,peg.2631,peg.2939,peg.3803,peg.3495,peg.4180,peg.3818,peg.3786,peg.3970,peg.3971,peg.3232,peg.2894,peg.3477,peg.3476,peg.3475,peg.3881,peg.3467,peg.3468,peg.3469,peg.3129,peg.3534,peg.4163,peg.3201,peg.3203,peg.3202,peg.4043,peg.4331,peg.4195,peg.4191,peg.4190,peg.3204

Energy metabolism

172

Lipid metabolism

peg.2086,peg.2258,peg.2085,peg.1820,peg.110,peg.2036,peg.275,peg.1073,peg.1828,peg.276,peg.1068,peg.2088,peg.213,peg.1805,peg.214,peg.573,peg.361,peg.574,peg.2083,peg.1608,peg.700,peg.182,peg.573,peg.361,peg.574,peg.1063,peg.1955,peg.1145,peg.2230,peg.1553,peg.1608,peg.1478,peg.700,peg.2123,peg.117,peg.213,peg.1240,peg.1179,peg.1804,peg.2653,peg.2938,peg.2603,peg.3576,peg.3399,peg.3473,peg.4179,peg.3502,peg.3523,peg.3842,peg.4045,peg.4061,peg.4060,peg.3445,peg.4066,peg.4070,peg.2709,peg.3857,peg.3576,peg.2595,peg.3523,peg.3166,peg.4070,peg.4064,peg.4062,peg.3711,peg.2590,peg.4219

67

Nucleotide metabolism

104

peg.1220,peg.1219,peg.251,peg.1193,peg.1833,peg.1199,peg.30,peg.2481,peg.44,peg.28,peg.1541,peg.348,peg.1666,peg.1681,peg.1680,peg.1326,peg.670,peg.1259,peg.1248,peg.250,peg.1879,peg.350,peg.671,peg.1045,peg.1851,peg.1112,peg.1247,peg.1204,peg.757,peg.758,peg.409,peg.1220,peg.1219,peg.1011,peg.412,peg.411,peg.190,peg.669,peg.1250,peg.145,peg.1402,peg.2091,peg.44,peg.2075,peg.1617,peg.1403,peg.147,peg.2243,peg.671,peg.285,peg.1045,peg.1851,peg.2454,peg.1059,peg.1112,peg.409,peg.3110,peg.3683,peg.3243,peg.3244,peg.3233,peg.3388,peg.3416,peg.3467,peg.3125,peg.3499,peg.3468,peg.3469,peg.3535,peg.3207,peg.4338,peg.2548,peg.4120,peg.3744,peg.3787,peg.2726,peg.3820,peg.3109,peg.3163,peg.3415,peg.3568,peg.4156,peg.3497,peg.4084,peg.3048,peg.2754,peg.3993,peg.3996,peg.3424,peg.3422,peg.2801,peg.3243,peg.3244,peg.2604,peg.3125,peg.2863,peg.3535,peg.3496,peg.3754,peg.3755,peg.3497,peg.3608,peg.2532,peg.3996

		peg.293,peg.42,peg.331,peg.330,peg.412,peg.411,peg.1833,peg.924,peg.2351,peg.1110,peg.466,peg.199,peg.1488,peg.19,peg.103,peg.1313,peg.136,peg.1852,peg.190 6,peg.177,peg.74,peg.2034,peg.2033,peg.690,peg.688,peg.176,peg.524,peg.1676,peg.1573,peg.1910,peg.1372,peg.689,peg.1281,peg.620,peg.1906,peg.186,peg.183,pe g.421,peg.924,peg.1921,peg.877,peg.800,peg.1676,peg.1910,peg.370,peg.1900,peg.868,peg.1521,peg.104,peg.1281,peg.1444,peg.213,peg.1921,peg.1805,peg.214,peg. 1921,peg.685,peg.1573,peg.1852,peg.1054,peg.2343,peg.1279,peg.1027,peg.293,peg.1532,peg.1350,peg.1741,peg.1805,peg.214,peg.1533,peg.1281,peg.197,peg.42,pe g.415,peg.924,peg.2343,peg.198,peg.196,peg.2435,peg.199,peg.19,peg.103,peg.2201,peg.1852,peg.1023,peg.1532,peg.1243,peg.924,peg.1741,peg.975,peg.1533,peg.2 93,peg.924,peg.1517,peg.924,peg.1741,peg.2191,peg.1517,peg.1350,peg.1805,peg.214,peg.1234,peg.2191,peg.924,peg.1111,peg.1371,peg.1814,peg.277,peg.1436,peg. .3190,peg.2807,peg.4390,peg.2617,peg.2726,peg.4406,peg.3820,peg.3754,peg.3755,peg.3414,peg.4123,peg.2946,peg.3794,peg.4054,peg.3668,peg.3154,peg.2866,peg. 2522,peg.3502,peg.3777,peg.3871,peg.3445,peg.2584,peg.2583,peg.4006,peg.3776,peg.2662,peg.4134,peg.3778,peg.4162,peg.2523,peg.3786,peg.2532,peg.3794,peg. 4054,peg.3050,peg.3876,peg.3881,peg.3811,peg.3239,peg.2807,peg.4136,peg.2866,peg.3607,peg.3401,peg.3871,peg.3129,peg.3208,peg.3240,peg.4006,peg.4163,peg. 2662,peg.3317,peg.3815,peg.3316,peg.3402,peg.3412,peg.3410,peg.2739,peg.3411,peg.3778,peg.4162,peg.3668,peg.4136,peg.3713,peg.4125,peg.4136,peg.4285,peg. 3712,peg.3710,peg.3709,peg.4135,peg.3714,peg.3715,peg.4134,peg.4137,peg.4054,peg.3757,peg.3955,peg.3871,peg.3586,peg.3642,peg.4080,peg.3702,peg.3701,peg. 3778,peg.4162,peg.3668,peg.2807,peg.3955,peg.3383,peg.3565,peg.3239,peg.2807,peg.3384,peg.3809,peg.3240,peg.4187,peg.4188,peg.4123,peg.2854,peg.2853,peg. 2531,peg.2856,peg.2858,peg.2859,peg.2857,peg.2860,peg.2938,peg.2807,peg.2531,peg.3607,peg.3386,peg.2603,peg.2745,peg.3473,peg.2630,peg.2807,peg.2531,peg. 3607,peg.2745,peg.3668,peg.3539,peg.3884,peg.2581,peg.2865,peg.2807,peg.2531,peg.3607,peg.3984,peg.3258,peg.2579,peg.2580,peg.2584,peg.2583,peg.3983,peg. 2582,peg.3256,peg.3257
Amino acid metabolism	315	peg.241,peg.1199,peg.1146,peg.242,peg.240,peg.238,peg.237,peg.1150,peg.2101,peg.2204,peg.1142,peg.2228,peg.348,peg.882,peg.1834,peg.212,peg.1141,peg.367,p eg.2218,peg.2221,peg.1824,peg.2492,peg.822,peg.1295,peg.244,peg.1368,peg.671,peg.522,peg.1204,peg.2117,peg.1921,peg.221,peg.154,peg.685,peg.1133,peg.148,p eg.2086,peg.2258,peg.1820,peg.1623,peg.1621,peg.1622,peg.1625,peg.1624,peg.1068,peg.220,peg.1035,peg.2088,peg.1285,peg.2126,peg.1286,peg.634,peg.2228,peg. 2089,peg.1640,peg.1638,peg.1637,peg.1636,peg.1611,peg.3,peg.1046,peg.1171,peg.1840,peg.1829,peg.2314,peg.1011,peg.251,peg.688,peg.1687,peg.521,peg.1247,pe g.2314,peg.856,peg.218,peg.245,peg.209,peg.1201,peg.1155,peg.1897,peg.2485,peg.947,peg.1231,peg.1233,peg.536,peg.1229,peg.572,peg.571,peg.211,peg.202,peg.1 311,peg.517,peg.1834,peg.1230,peg.516,peg.2139, peg.3082,peg.3081,peg.4032,peg.3139,peg.3856,peg.3082,peg.4042,peg.3762,peg.2723,peg.4077,peg.3741,peg.2866,peg.3776,peg.3805,peg.3180,peg.3190,peg.4151, peg.2804,peg.3679,peg.4338,peg.2693,peg.3497,peg.2618,peg.3996,peg.4125,peg.3227,peg.4136,peg.3684,peg.3179,peg.3229,peg.3710,peg.3709,peg.4135,peg.3228, peg.3497,peg.4137,peg.2539,peg.4035,peg.3748,peg.3226,peg.4032,peg.3522,peg.3956,peg.2660,peg.3484,peg.3771,peg.2772,peg.3485,peg.3748,peg.4153,peg.3876, peg.3154,peg.3890,peg.2610,peg.2938,peg.3473,peg.4086,peg.4085,peg.3212,peg.3196,peg.3470,peg.4087,peg.3924,peg.2575,peg.4175,peg.3537,peg.4364 peg.213,peg.1805,peg.825,peg.214,peg.1605,peg.2049,peg.1834,peg.189,peg.189,peg.189,peg.825,peg.1471,peg.213,peg.2435,peg.2201,peg.1805,peg.214,peg.825,pe g.1085,peg.1085,peg.190,peg.669,peg.1085,peg.1402,peg.1617,peg.147,peg.1879,peg.2191,peg.2524,peg.2938,peg.3850,peg.2603,peg.3473,peg.3850,peg.2524,peg.29 17,peg.2524,peg.2938,peg.2603,peg.3473,peg.2938,peg.2928,peg.3473,peg.2938,peg.2928,peg.3473,peg.3110,peg.3233,peg.2928,peg.2604,peg.3125,peg.3109 peg.1447,peg.620,peg.852,peg.1430,peg.687,peg.1906,peg.74,peg.1798,peg.293,peg.1532,peg.93,peg.1349,peg.1347,peg.1348,peg.1345,peg.1346,peg.895,peg.42,peg. 331,peg.330,peg.2218,peg.1895,peg.2328,peg.2329,peg.609,peg.2331,peg.842,peg.843,peg.213,peg.183,peg.1350,peg.1054,peg.2343,peg.2351,peg.1391,peg.489,peg. 2150,peg.1846,peg.2481,peg.2134,peg.189,peg.524,peg.1279,peg.2435,peg.1687,peg.2049,peg.192,peg.487,peg.1344,peg.887,peg.2226,peg.1932,peg.209,peg.1027,pe g.2045,peg.877,peg.1805,peg.1378,peg.848,peg.844,peg.488,peg.825,peg.214,peg.1372,peg.1326,peg.1605,peg.789,peg.1353,peg.1352,peg.19,peg.275,peg.1073,peg.1 828,peg.276,peg.1897,peg.2485,peg.2179,peg.2176,peg.2246,peg.1834,peg.1453,peg.1446,peg.1454,peg.1452,peg.2159,peg.804,peg.2295,peg.119,peg.1393,peg.1533, peg.1471,peg.1845,peg.757,peg.758,peg.21,peg.1494, peg.2946,peg.2721,peg.2756,peg.3794,peg.2938,peg.4054,peg.2621,peg.3670,peg.3757,peg.3860,peg.3861,peg.3862,peg.3863,peg.4153,peg.3970,peg.3971,peg.3477, peg.3476,peg.3668,peg.3475,peg.3154,peg.3806,peg.3774,peg.3669,peg.2870,peg.3955,peg.2866,peg.2522,peg.2631,peg.4057,peg.3951,peg.3467,peg.3502,peg.3777, peg.2758,peg.4265,peg.3804,peg.3871,peg.3468,peg.3469,peg.3129,peg.2939,peg.3534,peg.3850,peg.3586,peg.3999,peg.3803,peg.2755,peg.3879,peg.3880,peg.4015, peg.2544,peg.3653,peg.3495,peg.3642,peg.4086,peg.3776,peg.4085,peg.4080,peg.3980,peg.2622,peg.4184,peg.3796,peg.3870,peg.2524,peg.3386,peg.3212,peg.3196, peg.3415,peg.3470,peg.4043,peg.4180,peg.4087,peg.2952,peg.2635,peg.2632,peg.2633,peg.3818,peg.3471,peg.2603,peg.3431,peg.2917,peg.3778,peg.4162,peg.3083, peg.2523,peg.3473,peg.3842,peg.3786,peg.3424,peg.3422
Metabolism of cofactors and vitamins	162	peg.232,peg.233,peg.29,peg.3896
Xenobiotics biodegradation and metabolism	52	peg.229,peg.230,peg.228,peg.319,peg.625,peg.626,peg.150,peg.1186,peg.2082,peg.151,peg.1185,peg.231,peg.655,peg.1057,peg.616,peg.320,peg.1590,peg.1298,peg.4 24,peg.1400,peg.79,peg.80,peg.1685,peg.1318,peg.718,peg.3911,peg.3902,peg.3914,peg.3895,peg.3905,peg.3309,peg.3918,peg.2700,peg.3916,peg.3919,peg.3910,peg. .2971,peg.3913,peg.3921,peg.3903,peg.4168,peg.4356,peg.2701,peg.3900,peg.3920,peg.3909,peg.3906,peg.3545,peg.2862,peg.3922,peg.3898,peg.3930,peg.3899,peg. 3908,peg.3312,peg.3912,peg.3546,peg.3917,peg.3763,peg.3915,peg.3897,peg.3904,peg.3548,peg.3929,peg.3907,peg.3890,peg.3978,peg.2703,peg.3761,peg.3322,peg. 2877,peg.2773,peg.3453,peg.3196,peg.2781,peg.2699,peg.2698,peg.3120,peg.2805,peg.3183,peg.3855
Microbial metabolism in diverse environments	187	peg.181,peg.1137,peg.226,peg.1138,peg.636,peg.205,peg.206,peg.207,peg.1136,peg.1284,peg.3688,peg.3901,peg.3184,peg.3760,peg.3313,peg.4253,peg.4359,peg.368 9,peg.2724
Genetic Information pr	4	
Transcription		
Translation		
Folding, sorting and degradation	19	

		peg.31,peg.615,peg.7,peg.1072,peg.425,peg.1296,peg.2092,peg.1194,peg.678,peg.1071,peg.77,peg.891,peg.31,peg.7,peg.986,peg.613,peg.1342,peg.716,peg.152,peg.31,peg.7,peg.1633,peg.1954,peg.2112,peg.31,peg.1072,peg.425,peg.1296,peg.2092,peg.1194,peg.678,peg.1080,peg.1006,peg.1148,peg.716,peg.7,peg.1072,peg.425,peg.1296,peg.2092,peg.1194,peg.678,peg.1019,peg.1018,peg.1016,peg.26,peg.1191,peg.1196,peg.716,peg.3515,peg.3601,peg.4354,peg.3245,peg.2751,peg.3620,peg.3246,peg.2612,peg.2951,peg.3515,peg.3194,peg.2566,peg.3515,peg.4076,peg.3619,peg.2835,peg.3515,peg.4354,peg.3245,peg.2751,peg.3620,peg.3827,peg.3111,peg.4076,peg.3981,peg.2770,peg.4354,peg.3245,peg.2751,peg.3547,peg.3620,peg.2769,peg.2768,peg.3324,peg.3181,peg.4353,peg.4169
Replication and repair	86	peg.1456,peg.1457,peg.1458,peg.1385,peg.1384,peg.1383,peg.1670,peg.1668,peg.1669,peg.1126,peg.999,peg.1001,peg.1000,peg.866,peg.867,peg.865,peg.308,peg.309,peg.310,peg.2365,peg.2366,peg.1486,peg.2166,peg.2167,peg.2168,peg.2169,peg.258,peg.672,peg.869,peg.1380,peg.698,peg.694,peg.695,peg.697,peg.2122,peg.2124,peg.1109,peg.302,peg.427,peg.312,peg.311,peg.2113,peg.2114,peg.256,peg.255,peg.254,peg.253,peg.1304,peg.1302,peg.1303,peg.1301,peg.257,peg.809,peg.1835,peg.1837,peg.1836,peg.1838,peg.828,peg.829,peg.830,peg.831,peg.2499,peg.1904,peg.1902,peg.97,peg.99,peg.98,peg.428,peg.2438,peg.2439,peg.2440,peg.2441,peg.2442,peg.1526,peg.1104,peg.141,peg.140,peg.139,peg.142,peg.1558,peg.1559,peg.1518,peg.1519,peg.1516,peg.1514,peg.1515,peg.1892,peg.1893,peg.1894,peg.2227,peg.2232,peg.2235,peg.2234,peg.1448,peg.1450,peg.1449,peg.1174,peg.1175,peg.2263,peg.2262,peg.2261,peg.2260,peg.2259,peg.1116,peg.2464,peg.603,peg.1700,peg.2278,peg.2279,peg.873,peg.2094,peg.875,peg.85,peg.1317,peg.299,peg.379,peg.1869,peg.874,peg.1009,peg.297,peg.1748,peg.1749,peg.1750,peg.1751,peg.1752,peg.1753,peg.1754,peg.1755,peg.1756,peg.1757,peg.1758,peg.1760,peg.1744,peg.181,peg.1137,peg.226,peg.1138,peg.636,peg.205,peg.206,peg.207,peg.1136,peg.2397,peg.2392,peg.2394,peg.2380,peg.2377,peg.2376,peg.2375,peg.2374,peg.2373,peg.2382,peg.1284,peg.2383,peg.2402,peg.347,peg.4243,peg.4242,peg.4245,peg.4244,peg.4246,peg.3428,peg.2828,peg.3430,peg.3235,peg.3236,peg.4384,peg.4386,peg.4385,peg.4387,peg.3201,peg.3203,peg.3202,peg.3729,peg.3728,peg.3727,peg.2926,peg.2925,peg.2927,peg.3837,peg.2710,peg.4222,peg.4221,peg.4220,peg.4413,peg.3209,peg.3838,peg.4251,peg.4252,peg.2761,peg.2763,peg.2762,peg.4093,peg.4094,peg.4095,peg.4096,peg.2904,peg.2901,peg.2903,peg.2902,peg.2900,peg.3976,peg.3974,peg.3973,peg.3975,peg.2999,peg.3000,peg.3001,peg.3058,peg.2687,peg.2684,peg.2685,peg.2686,peg.4416,peg.4415,peg.4414,peg.2555,peg.2553,peg.2554,peg.4144,peg.2597,peg.3218,peg.2734,peg.2733,peg.2732,peg.2731,peg.2912,peg.2909,peg.2910,peg.2911,peg.2822,peg.2672,peg.2674,peg.2675,peg.2673,peg.3054,peg.4307,peg.4306,peg.4305,peg.4304,peg.3033,peg.3174,peg.2962,peg.2963,peg.2964,peg.2965,peg.4195,peg.4191,peg.4190,peg.2601,peg.2600,peg.2599,peg.2598,peg.3059,peg.3060,peg.3061,peg.2884,peg.2883,peg.4100,peg.4099,peg.4098,peg.3629,peg.3625,peg.3624,peg.3204,peg.3217,peg.3216,peg.4145,peg.4142,peg.2953,peg.2766,peg.3579,peg.2765,peg.2952,peg.3127,peg.2664,peg.2665,peg.2666,peg.2635,peg.2632,peg.2633,peg.2954,peg.3688,peg.3901,peg.3313,peg.4253,peg.4467,peg.4475,peg.4468,peg.4476,peg.4359,peg.3360,peg.3365,peg.3356,peg.3355,peg.3367,peg.3364,peg.3689
Environmental informa		
	298	peg.1616,peg.895,peg.2328,peg.2329,peg.2330,peg.2331,peg.1357,peg.1355,peg.1356,peg.1977,peg.1055,peg.106,peg.2265,peg.1332,peg.1331,peg.1330,peg.19,peg.1412,peg.1126,peg.1986,peg.1970,peg.1969,peg.2027,peg.1959,peg.1971,peg.301,peg.1708,peg.187,peg.1973,peg.1974,peg.1978,peg.1979,peg.1567,peg.1707,peg.170,peg.2296,peg.422,peg.75,peg.1966,peg.49,peg.1125,peg.2308,peg.1920,peg.1329,peg.333,peg.1124,peg.2309,peg.1328,peg.2325,peg.2182,peg.1225,peg.1223,peg.2324,peg.2183,peg.1224,peg.1953,peg.17,peg.16,peg.1919,peg.1483,peg.1373,peg.1523,peg.1374,peg.34,peg.159,peg.1376,peg.1399,peg.1398,peg.1397,peg.1304,peg.1302,peg.1303,peg.1301,peg.347,peg.1709,peg.1414,peg.1484,peg.1485,peg.48,peg.1413,peg.91,peg.1214,peg.1234
Membrane transport		peg.1886,peg.91,peg.574,peg.1063,peg.574,peg.1197,peg.3860,peg.3861,peg.3862,peg.3863,peg.3157,peg.4032,peg.2842,peg.2843,peg.2844,peg.4113,peg.2845,peg.4387,peg.4355,peg.4421,peg.4112,peg.2515,peg.3320,peg.3511,peg.3158,peg.3206,peg.2593,peg.2850,peg.3719,peg.2841,peg.2840,peg.3451,peg.2728,peg.4000,peg.4213,peg.3072,peg.3937,peg.4410,peg.4001,peg.2727,peg.4212,peg.3073,peg.4411,peg.3501,peg.2848,peg.4316,peg.2849,peg.4315,peg.3161,peg.3159,peg.3936,peg.3783,peg.3069,peg.3070,peg.3068,peg.2806,peg.3954,peg.4267,peg.4310,peg.4034,peg.3071,peg.3657,peg.3125,peg.2621,peg.2631,peg.3804,peg.3495,peg.3142,peg.2631,peg.3818
Signal transduction	153	peg.244,peg.1234,peg.91,peg.2500,peg.2721,peg.2653
	6	peg.1166,peg.1164,peg.767,peg.1165,peg.1064,peg.1132,peg.1243,peg.19,peg.1197,peg.4355,peg.3601,peg.3697,peg.3692,peg.3698,peg.3694,peg.3693,peg.2653,peg.4039,peg.3962
Cellular process		
Transport and catabolism	19	peg.2228,peg.1371,peg.1746,peg.69,peg.69,peg.71,peg.70,peg.72,peg.2349,peg.2356,peg.2355,peg.2354,peg.1970,peg.1969,peg.181,peg.226,peg.636,peg.1136,peg.1920,peg.1328,peg.577,peg.1141,peg.2227,peg.105,peg.1484,peg.1485,peg.2257,peg.544,peg.104,peg.3258,peg.2579,peg.2580,peg.3957,peg.2653,peg.4243,peg.4242,peg.4245,peg.4244,peg.4246,peg.3964,peg.3963,peg.3966,peg.3965,peg.3967,peg.4158,peg.3688,peg.3901,peg.3313,peg.4253,peg.4359,peg.3825,peg.3316,peg.4410,peg.4411,peg.3161,peg.3159,peg.3746,peg.2597,peg.3954,peg.2601,peg.2600,peg.2599,peg.2598,peg.4025,peg.4027,peg.4026,peg.4024,peg.4023,peg.4028
Cell growth and death	69	peg.183,peg.2027,peg.1748,peg.1749,peg.1750,peg.1751,peg.1752,peg.1753,peg.1754,peg.1755,peg.1756,peg.1757,peg.1758,peg.1759,peg.873,peg.2094,peg.301,peg.266,peg.1953,peg.1986,peg.2027,peg.350,peg.1953,peg.1412,peg.1986,peg.1970,peg.1969,peg.2027,peg.2028,peg.873,peg.1041,peg.1256,peg.333,peg.1225,peg.1223,peg.1224,peg.1953,peg.1440,peg.4113,peg.4112,peg.3454,peg.3320,peg.3825,peg.4084,peg.3316,peg.3501,peg.3954,peg.2579,peg.2580,peg.3320,peg.4156,peg.3501,peg.3954,peg.3360,peg.3366,peg.3369,peg.3372,peg.3373,peg.3356,peg.3364,peg.4039,peg.4274,peg.4047,peg.4048,peg.3454,peg.3320,peg.2826,peg.4152,peg.4084,peg.3223,peg.3316,peg.4000,peg.4001,peg.3501,peg.3783,peg.3954,peg.3177,peg.2838
Quorum sensing	78	
Biofilm formation		

	Cell motility		peg.1977,peg.2011,peg.2005,peg.2004,peg.1971,peg.1972,peg.187,peg.1973,peg.1974,peg.1978,peg.1979,peg.1980,peg.1567,peg.2296,peg.422,peg.75,peg.1966,peg.1987,peg.1988,peg.1989,peg.1990,peg.1991,peg.1992,peg.1993,peg.1994,peg.1995,peg.1996,peg.1997,peg.1998,peg.1986,peg.1985,peg.1983,peg.1982,peg.1970,peg.1969,peg.2027,peg.1959,peg.2017,peg.2014,peg.2012,peg.2011,peg.2010,peg.2009,peg.2008,peg.2007,peg.2006,peg.2005,peg.2004,peg.2003,peg.2002,peg.2001,peg.2000,peg.2016,peg.2015,peg.258,peg.2028,peg.1971,peg.1972,peg.614,peg.301,peg.1984,peg.2515,peg.3511,peg.2593,peg.2850,peg.3719,peg.4416,peg.3054,peg.4421
Organismal systems	Immune system	69	peg.1959,peg.1263,peg.1197,peg.2019,peg.4423,peg.2020,peg.4421,peg.4118
	Endocrine system	8	peg.2150,peg.1372,peg.852,peg.4046,peg.1197,peg.1656,peg.58,peg.2123,peg.4039,peg.3818,peg.4201,peg.2631,peg.2758,peg.2653,peg.4179,peg.3711
	Environmental adaptation	16	peg.1155,peg.223,peg.1959,peg.1197,peg.347,peg.2653,peg.4179,peg.3927,peg.4421
		9	

Supplementary Table 5. Comparison of the genomic features of *Pectobacterium carotovorum* subsp. *carotovorum* (*Pcc*) ICMP 5702 and other *Pectobacterium* spp.

Feature	ICMP 5702	PCC 21	WPP 14	PCCS1	SX309	BC S7
Size (bp)	4,774,457	4,842,771	4,892,225	4,899,898	4,966,299	4,933,575
No. of contigs	46	1	1	1	1	1
Shape of DNA	Linear	Circular	Linear	Linear	Circular	Circular
G+C content	51.9	52.18	52.1	51.6	52.2	51.8
No. of CDS	4520	4479	4545	4602	4584	4869
Transfer RNAs	72	76	79	83	76	78
Ribosomal RNAs	12	22	22	22	22	22
Plasmid	0	0	0	0	0	0
CRISPR repeats	8	4	7	6	9	5
Cluster gene No.	4188	4115	4305	3994	4197	4067
Total family	4153	4087	4215	3947	4144	3968
Unique gene family	7	1	12	11	7	36
Tandem repeats	232	183	187	164	181	132
CDS, protein coding sequence.						