Supplementary Information for

Genomic and metabolic analysis of fluoranthene degradation pathway in *Celeribacter indicus* P73^T

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Contents

Supplementary Text

Text S1 | COG analysis of the P73^T genome

Among the 4827 predicted protein-coding sequences (CDSs), 3908 (80.96%) were assigned to 22 different clusters of orthologous groups (COGs) (Data S1), including amino acid transport and metabolism (category E, 9.39%); inorganic ion transport and metabolism (P, 8.34%); carbohydrate transport and metabolism (G, 7.18%); transcription (K, 7.09%); energy production and conversion (C, 6.46%); replication, recombination and repair (L, 5.83%); and cell wall/membrane/envelope biogenesis (M, 5.27%).

Text S2 | Genomic islands

Genomic islands (GIs) were identified using IslandViewer[1]. Thirty-seven GIs (36 in the chromosome, one in plasmid pP73C) were predicted in the genome of strain P73^T by SIGI-HMM[1], comprising a total of 314,694-bp (6.33% of the genome) and 346 predicted CDSs (Figure S1, Data S2). Of the 346 CDSs, only 203 (58.67%) could be assigned to COGs, including replication, recombination and repair (L, up to 26.15%) and inorganic ion transport and metabolism (P, 11.93%), and both these categories were more abundant in the GIs than in the whole P73^T genome. Four of the GIs (GIs 9, 20, 35, 37) had a similar GC content as the average GC content of the chromosome (66 mol%) or plasmids (60 mol%), while the other 33 GIs all had a lower GC content (55 mol% to 63 mol%) compared with the average GC content of the chromosome. Fifteen of the 37 GIs contained mobile genetic elements, such as genes encoding transposase and integrase, that made the GIs self-mobilize. It has been suggested that the 3′ ends of the tRNAs are hot spots for the integration of foreign DNA into bacterial genomes[2]. In strain P73^T, GI 1 was located close to the 3′ end of tRNA-Met, GI 7 to tRNA-Ser, GI 9 to tRNA-Thr, GI 10 to tRNA-Ser, GI 18 to tRNA-Asn, GI 24 to tRNA-OTHER, and GI 27 to tRNA-Arg, supporting the identification of these seven regions as GIs.

Text S3 | Horizontal gene transfer

Horizontally transferred genes (HTG) in the P73^T genome were identified against the genomes of other bacteria in the IMG database (24 October 2013). Most of the predicted HTG in strain P73^T (56.6%, 424/749) had best hits to HTG from order *Rhizobiales* (Data S3). The COG analysis of these HTG showed that the genes assigned to inorganic ion transport and metabolism (12.12%), transcription (K, 11.36%), carbohydrate transport and metabolism (G, 9.72%), energy production and conversion (C, 7.95%), lipid transport and metabolism (I, 6.44%), and secondary metabolites biosynthesis transport and catabolism (Q, 6.44%) were more abundant in the *Rhizobiales* bacteria than in P73^T. Genes likely involved in PAH degradation were found among these HTG, such as ferredoxin (P73_0335, P73_1051, and P73_2118), ferredoxin:oxidoreductase FAD/NAD(P)-binding subunit (P73_1054 and P73_2874), ring-hydroxylating dioxygenases small subunit (P73_2150), ring-hydroxylating dioxygenases large subunit (P73_1053, P73_1958, P73_2151, P73_2875 and P73_4521), 4-hydroxylbenzoyl-CoA thioesterase (P73_0182) in benzoate degradation, dibenzothiophene desulfurization enzyme (P73_4012), naphthoate synthase (P73_4474), and cytochrome P450 (P73_0333 and P73_4763) (Data S3). Some tripartite ATP-independent periplasmic (TRAP) transporter genes (e.g. P73_0178 and P73_0179), which may be involved in aromatic compounds transport, were also among the HTG. These results suggested that strain P73^T may have used gene transfer to enhance its PAH degradation ability.

Text S4 | Transport systems

A total of 848 transport protein genes (Data S4) belonging to 102 transporter families were identified in the Transporter Classification (TC) Database (http://tcdb.org/)[3]. These transport protein genes made up about 17.57% of the total CDSs in the P73^T genome compared with 13.01% in the average bacterial genome in the IMG database. The encoded proteins of 371 of these genes were assigned to the ATP-binding cassette (ABC) superfamily (TC:3.A.1), members of which have been reported to translocate a wide variety of substrates including sugars, hydrocarbons, amino acids, ions, peptides, vitamins, toxins, lipids, proteins, and a large number of hydrophobic compounds and metabolites, including aromatic compounds, across extra- and intra-cellular membranes[4,5]. A further 96 transport protein genes were found to encode proteins belonging to the tripartite ATP-independent periplasmic transporter (TRAP-T) family (TC:2.A.56), members of which have been shown to be involved in the transport of widely divergent compounds, mostly carboxylate derivatives, including a variety of aromatic compounds[6]. For example, genes in the P73^T genome that encode TRAP transporters, namely P73_0171, P73_0172, P73_0173, P73_0178, and P73_0179 were located close to the gentisate 1,2-dioxygenase gene (P73_0175); P73_0342, P73_0343, and P73_0344 were adjacent to ring-hydroxylating dioxygenase genes (P73_0346 and P73_0347); and P73_2969 was close to the phthalate 4,5-dioxygenase gene (P73_2968). This arrangement suggests that these TRAP transporters may be involved in the transport of aromatic compounds with carboxylate groups. The other transporter genes in the P73^T genome were found to encode proteins belonging to the major facilitator superfamily (MFS, TC:2.A.1, 25 genes)[7], the tricarboxylate transporter (TTT) family (TC:2.A.80, 8 genes)[8], the outer membrane protein (FadL) family (TC:1.B.9, P73_0184 and P73_2224)[9], and the benzoate:H$^+$ symporter (BenE) family (TC:2.A.46, P73_3226)[7], all of which have been reported to be involved in the uptake of various aromatic compounds. Transporter genes for environmental adaption were also found in the P73^T genome: mercury ion transport protein genes (P73_4790–4792); arsenite efflux pump genes (P73_1256 and P73_3784); chromate transporter genes (P73_2501 and P73_4821); and a camphor resistance gene (P73_0682).

Text S5 | Regulation

The COG analysis identified 305 genes in the P73^T genome that were assigned to the transcription (K, 7.09%) category (Data S5). Fifty-three of these genes were predicted to encode the LysR-type transcriptional regulator (LTTR) family of proteins (COG0583), which represents the most abundant type of transcriptional regulator in prokaryotes[10]. LTTR family transcriptional regulators regulate a diverse set of genes, including genes involved in virulence, metabolism (including aromatic compounds degradation), quorum sensing, and motility[10,11]. For example, P73_0840, encoding the *pca* operon transcriptional activator PcaQ, was located in the *pca* gene cluster (P73_0836–0845) responsible for protocatechuate degradation; the LTTR family transcriptional activator *nahR* (P73_2028) was predicted previously to be salicylate-responsive[12]; and P73_0332, encoding a LTTR transcriptional regulator, was adjacent to the homogentisate 1,2-dioxygenase gene (P73_0329).

The multiple antibiotic resistance regulator (MarR) family (COG1846) were reported to regulate resistance to multiple antibiotics and degradation of aromatic compounds[11]. We identified 19 proteins in the P73^T genome that belonged to the MarR family transcriptional regulators, such as P73_0337, P73_0357, P73_1461, P73_2961, and P73_4393, which may regulate the degradation of aromatic compounds.

Ten genes were predicted to encode isocitrate lyase regulator (IclR) family transcriptional regulators, some members of which were reported to be involved in the degradation of aromatic compounds[13]; for example, P73_0836 encoded a β-ketoadipate pathway transcription regulator involved in protocatechuate degradation, and P73_0183 and P73_0327 encoded the IclR family transcriptional regulators that regulate the degradation of aromatic compounds.

In addition, other transcriptional regulators that belong to the AraC, GntR, TetR, and FNR families or to two component regulatory systems have been reported to be associated with the degradation pathways of aromatic compounds[11], and many genes in the P73^T genome were predicted to encode transcriptional regulators that belong these family (Data S5).

Text S6 | Plasmids

Together, the five plasmids in strain P73^T contained 438 CDSs, accounting for 9.07% of the total CDSs in the genome. The COG analysis showed that the genes in four COG functional groups (information storage and processing, cellular processes and signaling, metabolism, and poorly characterized) were distributed quite differently among the plasmids, indicating a specialized function for each plasmid (Figure S2). pP73A mainly contained genes involved in metabolism, such as carbohydrate transport and metabolism (G), energy production and conversion (C), and lipid transport and metabolism (I), while the other four plasmids had low abundances of genes involved in metabolism and high abundances of genes with no COG assignment. The genes involved in cellular processes and signaling were much fewer in pP73A, and much more abundant in pP73B. pP73C and pP73D had high abundances of genes in replication, recombination and repair (L), intracellular trafficking, secretion, and vesicular transport (U), and cell cycle control, cell division, and chromosome partitioning (D).

Phylogenetic analysis of the plasmid partition protein (*parA*) and plasmid replication protein (*rep*) genes has been used previously to gain insight into the origin and evolution of plasmids[14,15]. Neighbor-joining phylogenetic trees were constructed with the Rep (Figure 2A) and ParA (Figure 2B) protein sequences encoded by genes from the P73^T chromosome and plasmids. Plasmids pP73A, pP73B, and pP73C had putative replication systems including the *repABC* gene family, which are common in α-proteobacteria and essential for plasmid replication and stability[16]. Plasmid pP73D harbored a replication initiator protein A (RepA)-encoding gene (P73_4797), and a ParA-encoding gene (P73_4798), indicating that pP73D may be replicated by a theta replication mechanism[17]. Plasmid pP73E contained a replicase-encoding gene (P73_4817), which is annotated as *Firmicute* plasmid replication protein (RepL), and a PemK-like protein-encoding gene (P73_4819), which was reported to be responsible for plasmid stable inheritance[18]. No closely related homologue for the *parA* gene was detected in pP73E. Based on the HTG analysis, the replicative genes P73_4797 and P73_4817 were predicted to have originated from *Acetobacter aceti* ATCC 23746 (IMG Gene ID:2516943643) and the *Sphingobium yanoikuyae* ATCC 51230 (JCM 7371) plasmid pYAN-1, respectively (Data S3), in agreement with their predicted phylogenetic positions (Figure 2A). As shown in Figure 2, the ParA and Rep proteins encoded from the different plasmids belonged to different clades, suggesting that divergent evolution of the *parA* and *rep* genes had occurred, and confirming the important role of gene horizontal transfer, which has been reported previously[14].

Text S7 | Mutant generation

A gene deletion P73^T mutant was generated using of the *cre-lox* recombination method reported by Marx and Lidstrom[19]. *Escherichia coli* WM3064 was used as the conjugal donor strain, and pJK100 (allelic-exchange vector, Tc^R, Km^R) was used as the suicide vector[20]. The flanking regions of the P73_0346 gene targeted for deletion were amplified from genomic DNA with primer pairs: 0346UF, 5′-TAGATCTGAATTCAGACTGCCAGGGAGGAGTTTA-3′ and 0346UR, 5′-GTACCAATTGTACAGCGCATCGCCCAGATAGGT-3′; and 0346DF, 5′-CTACGTACGCGTGTTATTTCCGGGCCTGCCTAC-3′ and 0346DR,

5′-GTGAGCTCACCGGTTCCTCCCATGTTTGGTGTCTGT-3′. Then the flanking regions were inserted into the suicide vector pJK100 at the locations flanking a *loxP*-bounded kanamycin resistance cassette by ligation independent cloning[21]. The resultant plasmid pJK101 was transformed into the *E. coli* WM3064 conjugal donor strain, a strain that cannot grow without DAP. For conjugation, $P73^T$ was grown in 216L medium overnight, and then 1 mL of the culture was transferred to 10 mL fresh 216L. After 6–8 h of growth, 1 mL of the $P73^T$ culture was combined with the donor strain *E. coli* WM3064 at a ratio of 4:1; both strains were at an $OD_{600} = 0.6$. The mixture was washed twice in 216L medium, resuspended in 200 μL of 216L and spotted onto a 216L agar plate with DAP (50 μg/mL). After 24 h of incubation at 28 ℃, the cells were scraped off the plate, suspended in liquid 216L medium, washed twice in 216L, and spread onto a 216L agar plate with Km and no DAP. Positive double crossover integration of the suicide vector produced the mutant, ΔP73_0346::*kan*, that was Km resistant and Tc sensitive. The mutant was verified by DNA sequencing.

Text S8 | Analysis of intermediate metabolites in fluoranthene degradation

Strain $\mathbf{P73^T}$ was grown in artificial sea water (ASM) medium[73] supplemented with fluoranthene (20 mg/L) as the sole source of carbon and energy at 28 ℃ and 160 rpm. Metabolites were extracted and processed for analysis as described previously[4,5]. After 96 h of incubation, the culture was centrifuged at 12,000 g for 2 min. The cell-free supernatant was extracted with an equal volume of ethyl acetate under neutral and acidic (pH 2.5) conditions. The organic layer was dried over anhydrous sodium sulfate, evaporated to dryness on a rotary evaporator, and dissolved in 1 mL acetonitrile. Prior to GC-MS analysis, the dissolved sample was trimethylsilylated with *N*,*O*-bis(trimethylsilyl)-trifluoroacetamide with 1% trimethylchlorosilane. 200 μL of the concentrate and 100 μL of the silylation reagent were mixed in a sealed 1.5-ml sample vial (Shanghai Quandao Company, China) and heated in a water bath at 68 ℃ for 1 h. After silylation, the samples were analyzed by GC-MS (QP2010, Shimadzu, Kyoto, Japan) in the SCAN mode. Metabolites were determined based on the molecular and fragment ions in the mass spectra and the chromatographic retention time (R_t) of authentic compounds.

Supplementary Figures

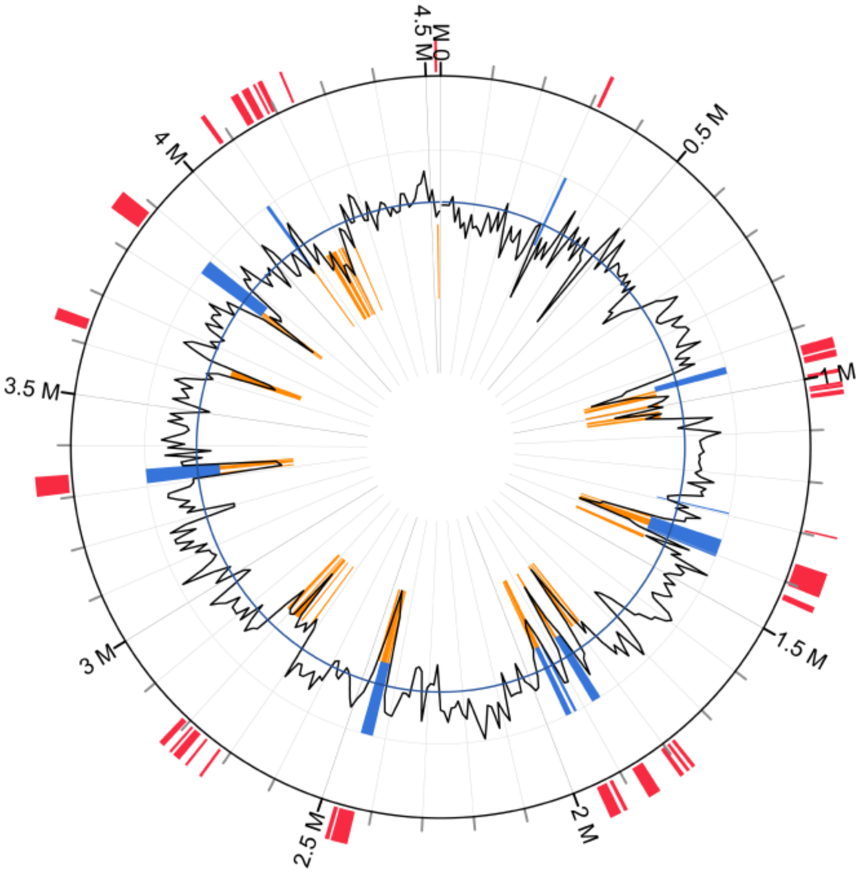

Figure S1 | Genomic islands (GIs) in the P73T chromosome predicted using different methods. Rings 1 (red), 2 (blue), and 3 (orange) represent the GIs predicted by multiple methods, IslandPath-DIMOB, and SIGI-HMM[1], respectively. The plot (black line) indicates the percentage of GC content.

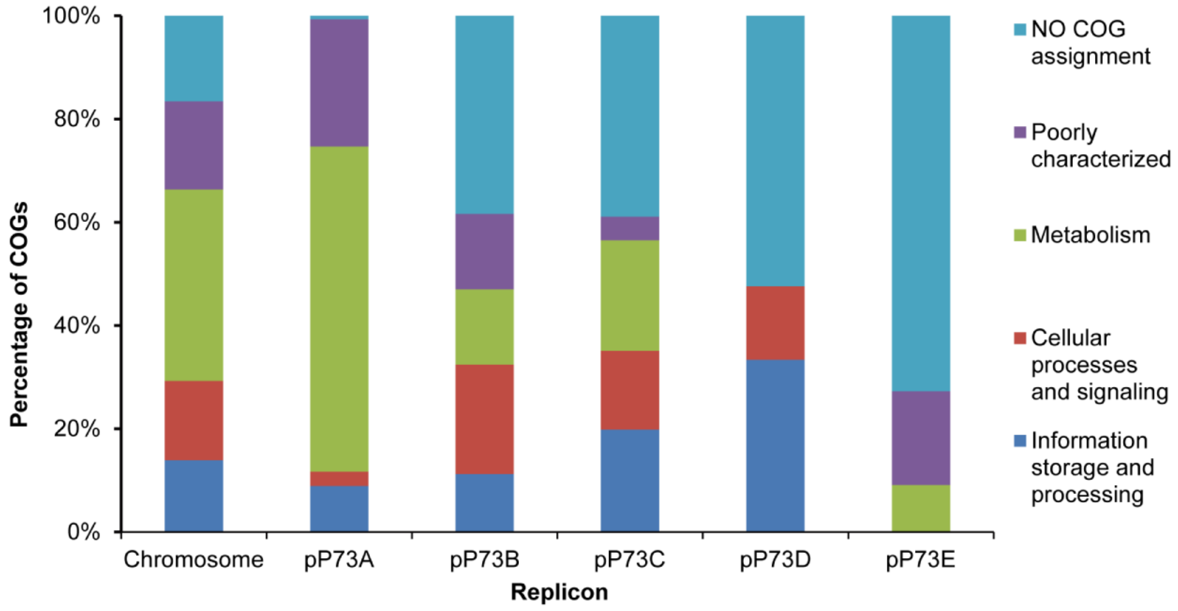

Figure S2 | COG distributions in the P73^T plasmids. The COG categories were grouped into four functional clusters: (i) information storage and processing (J, K, L, B); (ii) cellular processes and signaling (D, V, T, M, N, Z, U, O); (iii) metabolism (C, G, E, F, H, I, P, Q); (iv) poorly characterized (R, S).

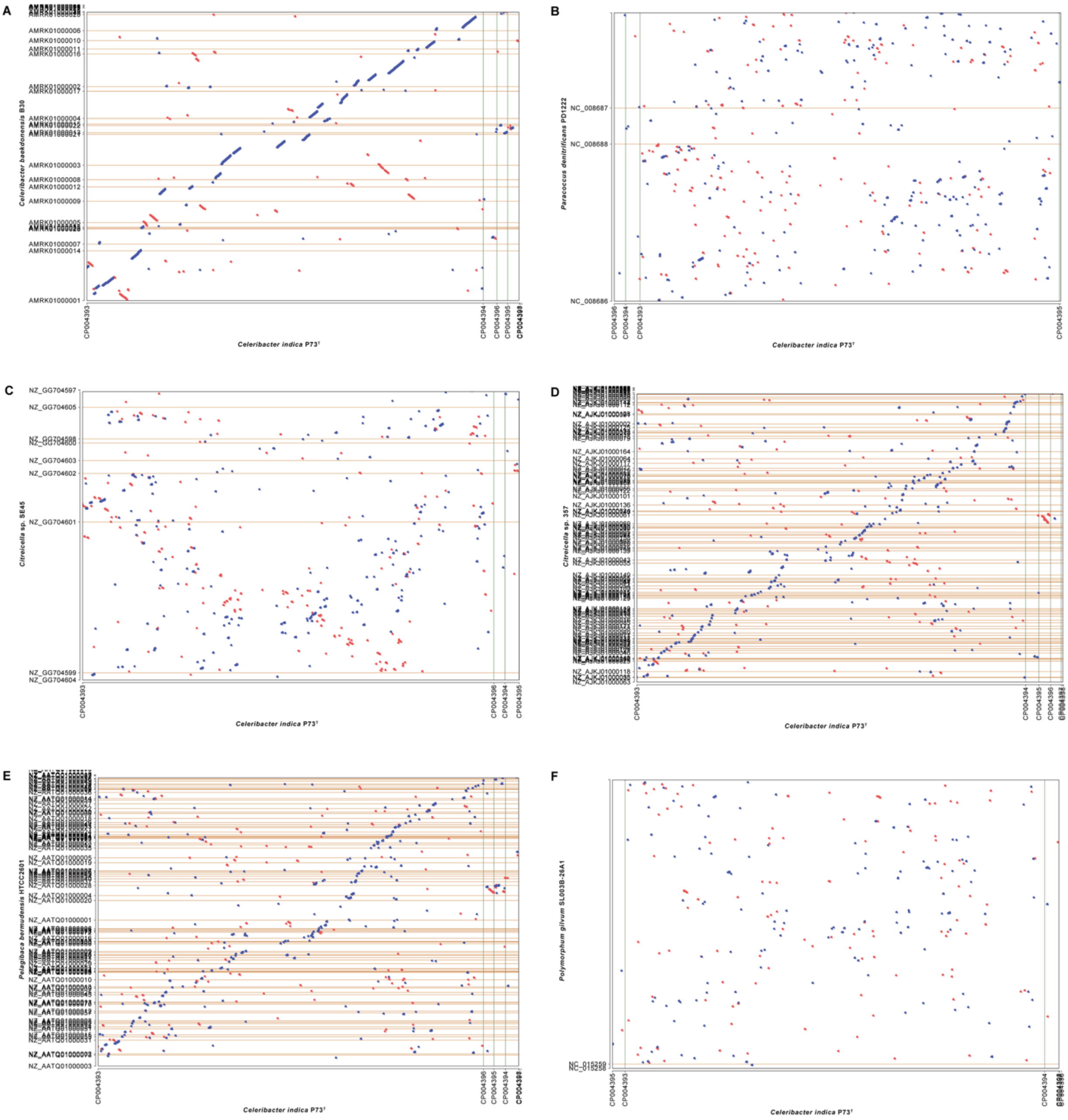

Figure S3 | Dot plots between the *Celeribacter indicus* P73^{T} genome and the genomes of six closely related bacteria. A, *Celeribacter baekdonensis* B30; **B**, *Paracoccus denitrificans* PD1222; **C**, *Citreicella* sp. SE45; **D**, *Citreicella* sp. 357; **E**, *Pelagibaca bermudensis* HTCC2601; **F**, *Polymorphum gilvum* SL003B-26A1. The MUMmer alignment program with the six frame amino acid translation of the DNA input sequences was used for the alignments. Red indicates the leading strand; blue indicates the lagging strand.

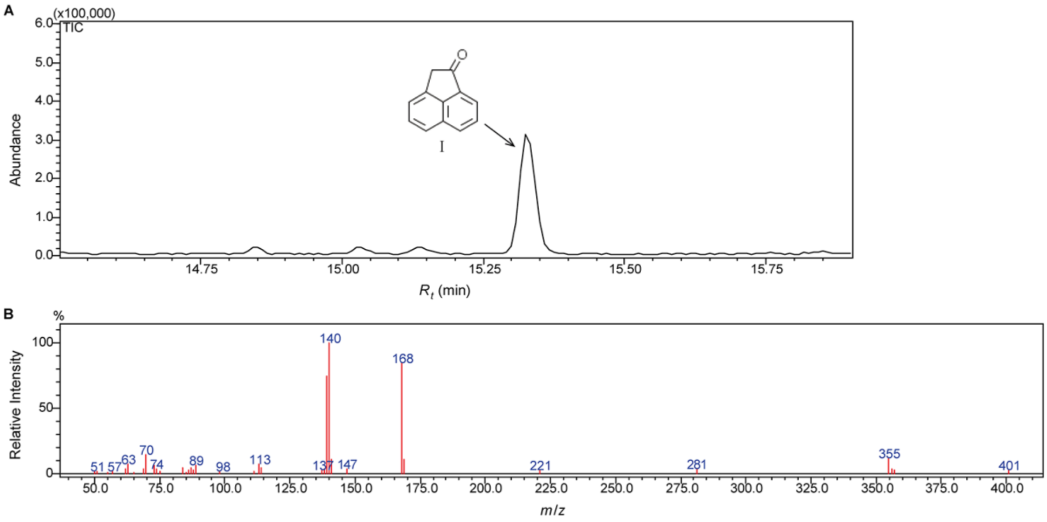

Figure S4. | GC-MS detection of metabolite I (acenaphthylene-1(*2H*)-one) obtained from fluoranthene degradation by strain P73^T. A, GC-MS profile; **B**, Mass spectrum. Metabolite I had a molecular ion at *m*/*z* (mass to charge ratio) 168 [M$^+$] and major fragment ions at *m*/*z* 140 ([M-28]), 139 ([M-29]), and 69 ([M-99]), and was proposed to be acenaphthylene-1(*2H*)-one (I).

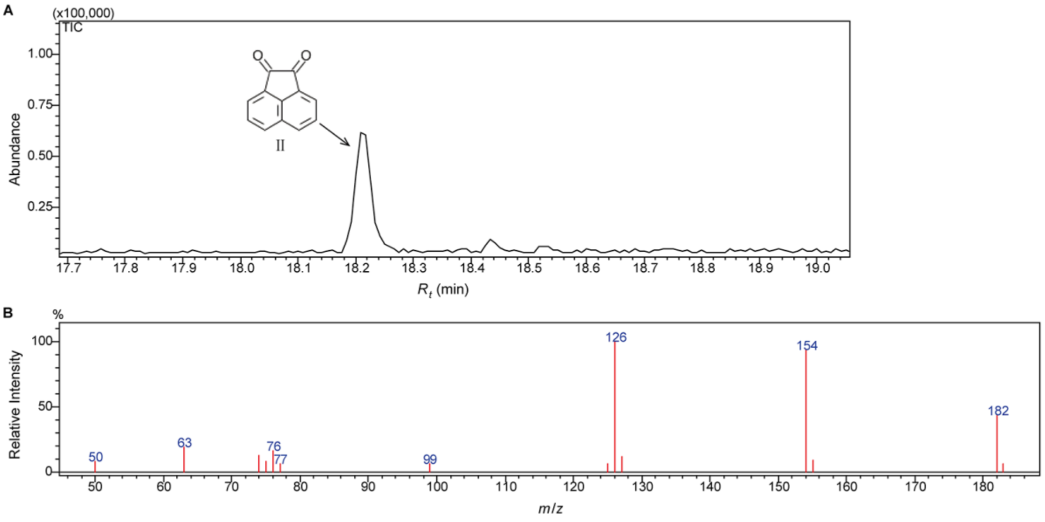

Figure S5 | GC-MS detection of metabolite II (acenaphthenequinone) obtained from fluoranthene degradation by strain P73^T. A, GC-MS profile; **B**, Mass spectrum. The metabolite peak had an R_t of 18.21 min, M$^+$ of 182, and major fragment ions at *m*/*z* 154 ([M-28]) and 126 ([M-56]), and this mass spectrum matched acenaphthenequinone (II) with a similarity of 90%.

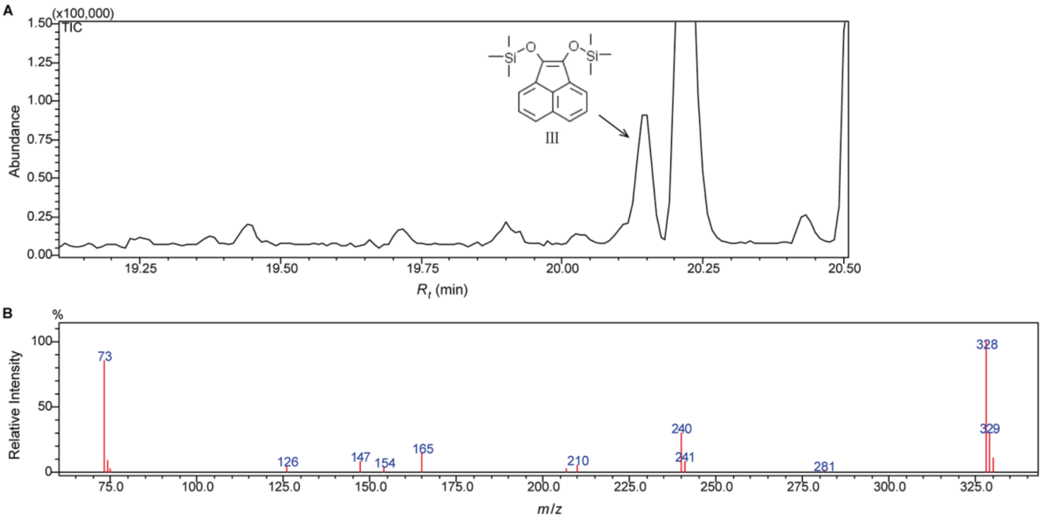

Figure S6 | GC-MS detection of metabolite III (1,2-dihydroxyacenaphthylene) obtained from fluoranthene degradation by strain P73^T. A, GC-MS profile**; B**, Mass spectrum. The peak had an R_t of 20.15 min, a molecular ion at *m*/*z* 328 [M$^+$], and major fragment ions at *m*/*z* 240 ([M-88]) and 73 ([M-255]), and this mass spectrum was comparable to that of acenaphthylene,1,2-bis(trimethylsilyloxy)-,trimethyl((2-[(trimethylsilyl)oxy]-1-acenaphthylenyl)oxy)silane. Therefore, this peak was predicted to correspond to a derivatized 1,2-dihydroxyacenaphthylene (III).

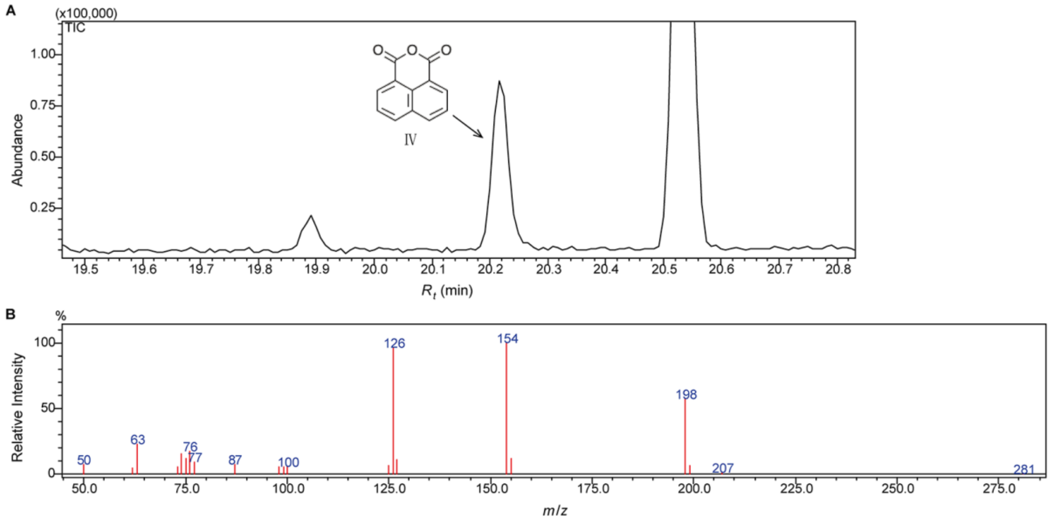

Figure S7 | GC-MS detection of metabolite IV (1,8-naphthalic anhydride) obtained from fluoranthene degradation by strain P73^T. A, GC-MS profile; **B**, Mass spectrum. The metabolite peak had an R_t of 20.22 min, a molecular ion at *m*/*z* 198 [M^+] and major fragment ions at *m*/*z* 154 ([M-44]), 126 ([M-72]), and 63 ([M-135]), and this mass spectrum matched 1,8-naphthalic anhydride (IV) with a similarity of 93%.

Supplementary Data

Data S1 | COG categories of the predicted *C. indicus* P73^T genes.

	COG categories	Gene count	% of total
R	General function prediction only	504	11.71
E	Amino acid transport and metabolism	404	9.39
S	Function unknown	376	8.74
P	Inorganic ion transport and metabolism	359	8.34
G	Carbohydrate transport and metabolism	309	7.18
K	Transcription	305	7.09
C	Energy production and conversion	278	6.46
L	Replication, recombination and repair	251	5.83
M	Cell wall/membrane/envelope biogenesis	227	5.27
J	Translation, ribosomal structure and biogenesis	168	3.9
H	Coenzyme transport and metabolism	165	3.83
O	Posttranslational modification, protein turnover, chaperones	162	3.76
I	Lipid transport and metabolism	154	3.58
Q	Secondary metabolites biosynthesis transport and catabolism	138	3.21
U	Intracellular trafficking, secretion, and vesicular transport	134	3.11
T	Signal transduction mechanisms	134	3.11
F	Nucleotide transport and metabolism	101	2.35
N	Cell motility	51	1.18
V	Defense mechanisms	43	1
D	Cell cycle control, cell division, chromosome partitioning	38	0.88
Z	Cytoskeleton	2	0.05
B	Chromatin structure and dynamics	1	0.02
Total		4304	

Data S2 | Predicted genomic islands (GIs), genes in the GIs, and COG categories of the genes in the P73^T genome. GIs predicted using different methods (Sheet 1); genes in the GIs predicted by the SIGI-HMM method (Sheet 2); and COG categories of the genes in the GIs (Sheet3).

Sheet 1 (Excel)

Start	End	Size	GI Prediction Program	CDS No.	GC (mol%)
pP73A					
134126	147776	13650	Predicted by multiple methods		
134126	147776	13650	IslandPath-DIMOB		
pP73B					

82019	90319	8300	Predicted by multiple methods		
82019	90319	8300	IslandPath-DIMOB		
pP73C					
10253	15689	5436	Predicted by multiple methods		
75687	83910	8223	Predicted by multiple methods		60
10253	15689	5436	SIGI-HMM	7	60.4
75687	83910	8223	IslandPath-DIMOB		
Chromosome					
311050	317763	6713	Predicted by multiple methods		
935216	954309	19093	Predicted by multiple methods		
957883	970007	12124	Predicted by multiple methods		
992143	999006	6863	Predicted by multiple methods		
1015653	1019934	4281	Predicted by multiple methods		
1020605	1025562	4957	Predicted by multiple methods		
1029934	1038139	8205	Predicted by multiple methods		
1293378	1296648	3270	Predicted by multiple methods		
1360376	1404710	44334	Predicted by multiple methods		
1423410	1434545	11135	Predicted by multiple methods		
1777105	1783670	6565	Predicted by multiple methods		
1789180	1795054	5874	Predicted by multiple methods		
1801935	1810082	8147	Predicted by multiple methods		
1853310	1876559	23249	Predicted by multiple methods		
1919787	1926624	6837	Predicted by multiple methods		
1932942	1953786	20844	Predicted by multiple methods		
2431801	2461964	30163	Predicted by multiple methods		
2465325	2473045	7720	Predicted by multiple methods		
2717933	2723051	5118	Predicted by multiple methods		
2750239	2754839	4600	Predicted by multiple methods		
2767673	2781976	14303	Predicted by multiple methods		
2786580	2791178	4598	Predicted by multiple methods		
2804186	2815040	10854	Predicted by multiple methods		
3308512	3343663	35151	Predicted by multiple methods		
3627053	3647869	20816	Predicted by multiple methods		
3848373	3883847	35474	Predicted by multiple methods		
4073801	4082491	8690	Predicted by multiple methods		
4137931	4152335	14404	Predicted by multiple methods		
4159890	4173781	13891	Predicted by multiple methods		
4182979	4187355	4376	Predicted by multiple methods		
4191742	4200902	9160	Predicted by multiple methods		
4234469	4238916	4447	Predicted by multiple methods		
4517554	4522207	4653	Predicted by multiple methods		66

948053	954309	6256	SIGI-HMM	11	60.9
957883	970007	12124	SIGI-HMM	11	62.6
992143	999006	6863	SIGI-HMM	12	60.9
1015653	1019934	4281	SIGI-HMM	5	58.1
1020605	1025562	4957	SIGI-HMM	7	61.3
1029934	1038139	8205	SIGI-HMM	8	61.9
1360376	1364871	4495	SIGI-HMM	3	56.4
1370830	1391441	20611	SIGI-HMM	15	57.3
1423410	1434545	11135	SIGI-HMM	12	65.7
1777105	1783670	6565	SIGI-HMM	8	61.6
1789180	1795054	5874	SIGI-HMM	7	58.7
1801935	1810082	8147	SIGI-HMM	8	55
1868412	1876559	8147	SIGI-HMM	8	55
1932942	1946181	13239	SIGI-HMM	16	59.8
1947933	1953786	5853	SIGI-HMM	9	63
2434811	2440717	5906	SIGI-HMM	9	58.5
2442386	2460796	18410	SIGI-HMM	22	55.7
2465325	2473045	7720	SIGI-HMM	12	62.3
2717933	2723051	5118	SIGI-HMM	7	61.4
2750239	2754839	4600	SIGI-HMM	8	65.4
2767673	2781976	14303	SIGI-HMM	16	58.9
2786580	2791178	4598	SIGI-HMM	6	62.5
2804186	2815040	10854	SIGI-HMM	12	60.3
3308855	3313845	4990	SIGI-HMM	5	58.3
3323033	3335848	12815	SIGI-HMM	10	56.3
3337843	3342531	4688	SIGI-HMM	9	59.3
3627053	3647869	20816	SIGI-HMM	13	58.9
3849567	3854060	4493	SIGI-HMM	5	55.4
3856466	3863807	7341	SIGI-HMM	10	59.1
4075898	4080821	4923	SIGI-HMM	6	60.1
4137931	4152335	14404	SIGI-HMM	12	62.9
4159890	4173781	13891	SIGI-HMM	11	60.1
4182979	4187355	4376	SIGI-HMM	7	58.8
4191742	4200902	9160	SIGI-HMM	10	60.8
4234469	4238916	4447	SIGI-HMM	5	65.1
4517554	4522207	4653	SIGI-HMM	4	62.9
311050	317763	6713	IslandPath-DIMOB		
935216	952356	17140	IslandPath-DIMOB		
1293378	1296648	3270	IslandPath-DIMOB		
1361089	1404710	43621	IslandPath-DIMOB		
1853310	1876158	22848	IslandPath-DIMOB		
1919787	1926624	6837	IslandPath-DIMOB		
1933972	1948634	14662	IslandPath-DIMOB		

2431801	2461964	30163	IslandPath-DIMOB		
3308512	3343663	35151	IslandPath-DIMOB		
3848373	3883847	35474	IslandPath-DIMOB		
4073801	4082491	8690	IslandPath-DIMOB		

Sheet 2 (Excel)

GI	Start	End	No. of CDSs	Locus_Tag	Product Name
Chromosome					
1	948053	954309	11	P73_0942	Antirestriction protein
1	948053	954309	11	P73_0943	ssDNA-specific exonuclease RecJ
1	948053	954309	11	P73_0944	DNA repair protein RadC
1	948053	954309	11	P73_0945	hypothetical protein
1	948053	954309	11	P73_0946	Uncharacterized conserved protein
1	948053	954309	11	P73_0947	transposase IS3/IS911 family protein
1	948053	954309	11	P73_0948	integrase catalytic subunit
1	948053	954309	11	P73_0949	HNS-type DNA binding protein
1	948053	954309	11	P73_0950	hypothetical protein
1	948053	954309	11	P73_0951	hypothetical protein
1	948053	954309	11	P73_0952	universal stress protein
2	957883	970007	11	P73_0956	hypothetical protein
2	957883	970007	11	P73_0957	hypothetical protein
2	957883	970007	11	P73_0958	hypothetical protein
2	957883	970007	11	P73_0959	integration host factor subunit beta
2	957883	970007	11	P73_0960	hypothetical protein
2	957883	970007	11	P73_0961	methylase/helicase
2	957883	970007	11	P73_0962	Toprim domain
2	957883	970007	11	P73_0963	Predicted protease with the C-terminal PDZ domain
2	957883	970007	11	P73_0964	replicative DNA helicase
2	957883	970007	11	P73_0965	transmembrane protein
2	957883	970007	11	P73_0966	hypothetical protein
3	992143	999006	12	P73_0994	Uncharacterized conserved small protein
3	992143	999006	12	P73_0995	LysR family transcriptional regulator
3	992143	999006	12	P73_0996	putative ErfK/YbiS/YcfS/YnhG protein
3	992143	999006	12	P73_0997	Allergen V5/Tpx-1 related protein
3	992143	999006	12	P73_0998	Uncharacterized protein SCO1/SenC/PrrC, involved in biogenesis of respiratory and photosynthetic systems
3	992143	999006	12	P73_0999	signal peptide protein
3	992143	999006	12	P73_1000	SCO-like protein
3	992143	999006	12	P73_1001	hypothetical protein
3	992143	999006	12	P73_1002	Protein-disulfide isomerase
3	992143	999006	12	P73_1003	disulfide bond formation-like protein

3	992143	999006	12	P73_1004	lipoprotein signal peptidase
3	992143	999006	12	P73_1005	S-isoprenylcysteine methyltransferase-like protein
4	1015653	1019934	5	P73_1019	integrase catalytic subunit
4	1015653	1019934	5	P73_1020	transposase IS3/IS911 family protein
4	1015653	1019934	5	P73_1021	Predicted kinase
4	1015653	1019934	5	P73_1022	transposase, mutator type
4	1015653	1019934	5	P73_1023	DNA methylase N-4/N-6 domain-containing protein
5	1020605	1025562	7	P73_1025	hypothetical protein
5	1020605	1025562	7	P73_1026	Uncharacterized conserved protein (DUF2285)
5	1020605	1025562	7	P73_1027	phage transcriptional regulator AlpA
5	1020605	1025562	7	P73_1028	replication initiator protein A
5	1020605	1025562	7	P73_1029	transposase
5	1020605	1025562	7	P73_1030	transposase, orfB
5	1020605	1025562	7	P73_1031	transposase IS3/IS911 family protein
6	1029934	1038139	8	P73_1037	transposase
6	1029934	1038139	8	P73_1038	transposase
6	1029934	1038139	8	P73_1039	binding-protein-dependent transporter inner membrane component
6	1029934	1038139	8	P73_1040	ABC transporter
6	1029934	1038139	8	P73_1041	NMT1/THI5-like domain-containing protein
6	1029934	1038139	8	P73_1042	methenyltetrahydrofolate synthetase
6	1029934	1038139	8	P73_1043	RpiR family transcriptional regulator
6	1029934	1038139	8	P73_1044	EmrB/QacA family drug resistance transporter
7	1360376	1364871	3	P73_1363	hypothetical protein
7	1360376	1364871	3	P73_1364	ribose ABC transporter periplasmic binding protein
7	1360376	1364871	3	P73_1365	ABC transporter
8	1370830	1391441	15	P73_1372	D-isomer specific 2-hydroxyacid dehydrogenase
8	1370830	1391441	15	P73_1373	autoinducer-2 (AI-2) kinase
8	1370830	1391441	15	P73_1374	Short chain dehydrogenase
8	1370830	1391441	15	P73_1375	transcriptional regulator
8	1370830	1391441	15	P73_1376	transcriptional regulator
8	1370830	1391441	15	P73_1377	D-lactate dehydrogenase (Cytochrome)
8	1370830	1391441	15	P73_1378	TRAP transporter solute receptor subunit DctP family protein 7
8	1370830	1391441	15	P73_1379	C4-dicarboxylate transport system (Permease small protein)
8	1370830	1391441	15	P73_1380	C4-dicarboxylate transport system (Permease large protein)
8	1370830	1391441	15	P73_1381	acetaldehyde dehydrogenase
8	1370830	1391441	15	P73_1382	4-hyroxy-2-oxovalerate/4-hydroxy-2-oxopentanoic acid aldolase
8	1370830	1391441	15	P73_1383	hypothetical protein
8	1370830	1391441	15	P73_1384	hypothetical protein
8	1370830	1391441	15	P73_1385	HipA domain-containing protein
8	1370830	1391441	15	P73_1386	LysR family transcriptional regulator

9	1423410	1434545	12	P73_1422	hypothetical protein
9	1423410	1434545	12	P73_1423	Reverse transcriptase (RNA-dependent DNA polymerase)
9	1423410	1434545	12	P73_1424	hypothetical protein
9	1423410	1434545	12	P73_1425	hypothetical protein
9	1423410	1434545	12	P73_1426	hypothetical protein
9	1423410	1434545	12	P73_1427	hypothetical protein
9	1423410	1434545	12	P73_1428	hypothetical protein
9	1423410	1434545	12	P73_1429	resolvase-like protein
9	1423410	1434545	12	P73_1430	Bifunctional DNA primase/polymerase, N-terminal
9	1423410	1434545	12	P73_1431	transcriptional regulator
9	1423410	1434545	12	P73_1432	hypothetical protein
9	1423410	1434545	12	P73_1433	phage integrase
10	1777105	1783670	8	P73_1767	LysR family transcriptional regulator
10	1777105	1783670	8	P73_1768	TetR family transcriptional regulator
10	1777105	1783670	8	P73_1769	multidrug resistance protein A
10	1777105	1783670	8	P73_1770	major facilitator transporter
10	1777105	1783670	8	P73_1771	TetR family transcriptional regulator
10	1777105	1783670	8	P73_1772	TetR family transcriptional regulator
10	1777105	1783670	8	P73_1773	Domain of Unknown Function with PDB structure (DUF3861)
10	1777105	1783670	8	P73_1774	dihydropteroic synthetase
11	1789180	1795054	7	P73_1782	replication initiator protein A
11	1789180	1795054	7	P73_1783	phage transcriptional regulator, AlpA
11	1789180	1795054	7	P73_1784	Uncharacterized conserved protein (DUF2285)
11	1789180	1795054	7	P73_1785	integrase catalytic subunit
11	1789180	1795054	7	P73_1786	transposase IS3/IS911 family protein
11	1789180	1795054	7	P73_1787	Uncharacterized conserved protein (DUF2285)
11	1789180	1795054	7	P73_1788	hypothetical protein
12	1801935	1810082	8	P73_1795	helix-turn-helix domain-containing protein
12	1801935	1810082	8	P73_1796	type I restriction-modification system M subunit
12	1801935	1810082	8	P73_1797	restriction modification system DNA specificity domain-containing protein
12	1801935	1810082	8	P73_1798	SMC protein, N-terminal domain-containing protein
12	1801935	1810082	8	P73_1799	hypothetical protein
12	1801935	1810082	8	P73_1800	Domain of unknown function (DUF3883)
12	1801935	1810082	8	P73_1801	hypothetical protein
12	1801935	1810082	8	P73_1802	hypothetical protein
13	1868412	1876559	8	P73_1868	helix-turn-helix domain-containing protein
13	1868412	1876559	8	P73_1869	type I restriction-modification system M subunit
13	1868412	1876559	8	P73_1870	restriction modification system DNA specificity domain-containing protein
13	1868412	1876559	8	P73_1871	SMC protein, N-terminal domain-containing protein
13	1868412	1876559	8	P73_1872	hypothetical protein

13	1868412	1876559	8	P73_1873	Domain of unknown function (DUF3883)
13	1868412	1876559	8	P73_1874	hypothetical protein
13	1868412	1876559	8	P73_1875	hypothetical protein
14	1932942	1946181	16	P73_1939	cytochrome c family protein
14	1932942	1946181	16	P73_1940	type 12 methyltransferase
14	1932942	1946181	16	P73_1941	hypothetical protein
14	1932942	1946181	16	P73_1942	Resolvase
14	1932942	1946181	16	P73_1943	Inosine/uridine-preferring nucleoside hydrolase
14	1932942	1946181	16	P73_1944	RpiR family transcriptional regulator
14	1932942	1946181	16	P73_1945	twin-arginine translocation pathway signal
14	1932942	1946181	16	P73_1946	twin-arginine translocation pathway signal
14	1932942	1946181	16	P73_1947	S-adenosylhomocysteine deaminase, methylthioadenosine deaminase
14	1932942	1946181	16	P73_1948	ABC transporter
14	1932942	1946181	16	P73_1949	nitrate/sulfonate/bicarbonate ABC transporter permease
14	1932942	1946181	16	P73_1950	ABC transporter-like protein permease
14	1932942	1946181	16	P73_1951	nucleoside 2-deoxyribosyltransferase
14	1932942	1946181	16	P73_1952	transposase, mutator type
14	1932942	1946181	16	P73_1953	integrase catalytic subunit
14	1932942	1946181	16	P73_1954	transposase IS3/IS911 family protein
15	1947933	1953786	9	P73_1956	transcriptional regulator
15	1947933	1953786	9	P73_1957	transposase IS4 family protein
15	1947933	1953786	9	P73_1958	(2Fe-2S)-binding domain-containing protein
15	1947933	1953786	9	P73_1959	SDR-family protein
15	1947933	1953786	9	P73_1960	hypothetical protein
15	1947933	1953786	9	P73_1961	hypothetical protein
15	1947933	1953786	9	P73_1962	hypothetical protein
15	1947933	1953786	9	P73_1963	hypothetical protein
15	1947933	1953786	9	P73_1964	hypothetical protein
16	2434811	2440717	9	P73_2428	dTDP-4-dehydrorhamnose 3,5-epimerase
16	2434811	2440717	9	P73_2429	dTDP-glucose 4,6-dehydratase
16	2434811	2440717	9	P73_2430	dTDP-4-dehydrorhamnose reductase
16	2434811	2440717	9	P73_2431	glucose-1-phosphate thymidylyltransferase
16	2434811	2440717	9	P73_2432	Transposase and inactivated derivatives
16	2434811	2440717	9	P73_2433	transposase
16	2434811	2440717	9	P73_2434	integrase catalytic region
16	2434811	2440717	9	P73_2435	transposase IS3/IS911 family protein
16	2434811	2440717	9	P73_2436	IS66 Orf2 family protein
17	2442386	2460796	22	P73_2438	transposase
17	2442386	2460796	22	P73_2439	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase
17	2442386	2460796	22	P73_2440	Transcription antiterminator

17	2442386	2460796	22	P73_2441	group 1 glycosyl transferase
17	2442386	2460796	22	P73_2442	group 1 glycosyl transferase
17	2442386	2460796	22	P73_2443	O-antigen ligase like membrane protein
17	2442386	2460796	22	P73_2444	glycosyl transferase family protein
17	2442386	2460796	22	P73_2445	hypothetical protein
17	2442386	2460796	22	P73_2446	Sulfotransferase family
17	2442386	2460796	22	P73_2447	polysaccharide biosynthesis protein
17	2442386	2460796	22	P73_2448	MarR family transcriptional regulator
17	2442386	2460796	22	P73_2449	transposase, mutator type
17	2442386	2460796	22	P73_2450	transposase
17	2442386	2460796	22	P73_2451	integrase catalytic subunit
17	2442386	2460796	22	P73_2452	transposase IS3/IS911 family protein
17	2442386	2460796	22	P73_2453	phage-related integrase
17	2442386	2460796	22	P73_2454	RelE/StbE family addiction module toxin
17	2442386	2460796	22	P73_2455	hypothetical protein
17	2442386	2460796	22	P73_2456	prophage CP4-57 regulatory
17	2442386	2460796	22	P73_2457	hypothetical protein
17	2442386	2460796	22	P73_2458	hypothetical protein
17	2442386	2460796	22	P73_2459	hypothetical protein
18	2465325	2473045	12	P73_2466	hypothetical protein
18	2465325	2473045	12	P73_2467	HNH endonuclease
18	2465325	2473045	12	P73_2468	hypothetical protein
18	2465325	2473045	12	P73_2469	phage protein
18	2465325	2473045	12	P73_2470	Phage protein, HK97, gp10
18	2465325	2473045	12	P73_2471	Protein of unknown function (DUF3168)
18	2465325	2473045	12	P73_2472	phage head-tail adaptor
18	2465325	2473045	12	P73_2473	P27 family phage terminase small subunit
18	2465325	2473045	12	P73_2474	Phage terminase-like protein
18	2465325	2473045	12	P73_2475	Phage-related minor tail protein
18	2465325	2473045	12	P73_2476	hypothetical protein
18	2465325	2473045	12	P73_2477	hypothetical protein
19	2717933	2723051	7	P73_2715	protease HtpX family protein
19	2717933	2723051	7	P73_2716	Heat shock protein Hsp20
19	2717933	2723051	7	P73_2717	heat shock protein Hsp20
19	2717933	2723051	7	P73_2718	heat shock protein Hsp20
19	2717933	2723051	7	P73_2719	LysR family transcriptional regulator
19	2717933	2723051	7	P73_2720	Uncharacterized conserved small protein
19	2717933	2723051	7	P73_2721	conjugation TrbI family protein
20	2750239	2754839	8	P73_2747	lytic transglycosylase, catalytic
20	2750239	2754839	8	P73_2748	Uncharacterized conserved protein
20	2750239	2754839	8	P73_2749	conjugal transfer protein precursor
20	2750239	2754839	8	P73_2750	Protein of unknown function (DUF2840)
20	2750239	2754839	8	P73_2751	plasmid segregation centromere-binding protein ParG

20	2750239	2754839	8	P73_2752	ATPase involved in chromosome partitioning,putative
20	2750239	2754839	8	P73_2753	replication protein A
20	2750239	2754839	8	P73_2754	Helix-turn-helix domain
21	2767673	2781976	16	P73_2766	hypothetical protein
21	2767673	2781976	16	P73_2767	hypothetical protein
21	2767673	2781976	16	P73_2768	hypothetical protein
21	2767673	2781976	16	P73_2769	hypothetical protein
21	2767673	2781976	16	P73_2770	hypothetical protein
21	2767673	2781976	16	P73_2771	putative ATPase
21	2767673	2781976	16	P73_2772	peptidase S8 family protein
21	2767673	2781976	16	P73_2773	Protein of unknown function (DUF982)
21	2767673	2781976	16	P73_2774	hypothetical protein
21	2767673	2781976	16	P73_2775	putative cystein protease, Transglutaminase-like domain protein
21	2767673	2781976	16	P73_2776	cold shock protein CspA
21	2767673	2781976	16	P73_2777	hypothetical protein
21	2767673	2781976	16	P73_2778	hypothetical protein
21	2767673	2781976	16	P73_2779	K+-dependent Na+/Ca+ exchanger related-protein
21	2767673	2781976	16	P73_2780	Uncharacterized conserved protein
21	2767673	2781976	16	P73_2781	hypothetical protein
22	2786580	2791178	6	P73_2786	Pyocin activator protein PrtN
22	2786580	2791178	6	P73_2787	Domain of unknown function (DUF4095)
22	2786580	2791178	6	P73_2788	hypothetical protein
22	2786580	2791178	6	P73_2789	putative cystein protease, Transglutaminase-like domain protein
22	2786580	2791178	6	P73_2790	hypothetical protein
22	2786580	2791178	6	P73_2791	hypothetical protein
23	2804186	2815040	12	P73_2797	transglutaminase
23	2804186	2815040	12	P73_2798	Di- and tricarboxylate transporters
23	2804186	2815040	12	P73_2799	CRP family transcriptional regulator
23	2804186	2815040	12	P73_2800	hypothetical protein
23	2804186	2815040	12	P73_2801	fatty acid desaturase
23	2804186	2815040	12	P73_2802	hypothetical protein
23	2804186	2815040	12	P73_2803	Transglutaminase-like enzymes, putative cysteine proteases
23	2804186	2815040	12	P73_2804	hypothetical protein
23	2804186	2815040	12	P73_2805	hypothetical protein
23	2804186	2815040	12	P73_2806	hypothetical protein
23	2804186	2815040	12	P73_2807	hypothetical protein
23	2804186	2815040	12	P73_2808	hypothetical protein
24	3308855	3313845	5	P73_3237	hypothetical protein
24	3308855	3313845	5	P73_3238	hypothetical protein
24	3308855	3313845	5	P73_3239	hypothetical protein
24	3308855	3313845	5	P73_3240	phage/plasmid primase, P4 family, C-terminal domain

24	3308855	3313845	5	P73_3241	hypothetical protein
25	3323033	3335848	10	P73_3252	hypothetical protein
25	3323033	3335848	10	P73_3253	hypothetical protein
25	3323033	3335848	10	P73_3254	bacteriophage DNA-invertase
25	3323033	3335848	10	P73_3255	histone-like nucleoid-structuring protein H-NS
25	3323033	3335848	10	P73_3256	hypothetical protein
25	3323033	3335848	10	P73_3257	DNA methyltransferase
25	3323033	3335848	10	P73_3258	restriction enzyme
25	3323033	3335848	10	P73_3259	McrBC 5-methylcytosine restriction system component
25	3323033	3335848	10	P73_3260	antirestriction protein
25	3323033	3335848	10	P73_3261	hypothetical protein
26	3337843	3342531	9	P73_3263	hypothetical protein
26	3337843	3342531	9	P73_3264	hypothetical protein
26	3337843	3342531	9	P73_3265	hypothetical protein
26	3337843	3342531	9	P73_3266	hypothetical protein
26	3337843	3342531	9	P73_3267	phosphoglycerate kinase
26	3337843	3342531	9	P73_3268	hypothetical protein
26	3337843	3342531	9	P73_3269	hypothetical protein
26	3337843	3342531	9	P73_3270	relaxase/mobilization nuclease domain-containing protein
26	3337843	3342531	9	P73_3271	hypothetical protein
27	3627053	3647869	13	P73_3555	EamA-like transporter family
27	3627053	3647869	13	P73_3556	AAA domain
27	3627053	3647869	13	P73_3557	hypothetical protein
27	3627053	3647869	13	P73_3558	hypothetical protein
27	3627053	3647869	13	P73_3559	ATPase central domain-containing protein
27	3627053	3647869	13	P73_3560	hypothetical protein
27	3627053	3647869	13	P73_3561	Molecular chaperone, HSP90 family
27	3627053	3647869	13	P73_3562	endonuclease
27	3627053	3647869	13	P73_3563	Domain of unknown function (DUF4420)
27	3627053	3647869	13	P73_3564	AIPR protein
27	3627053	3647869	13	P73_3565	DNA-cytosine methyltransferase
27	3627053	3647869	13	P73_3566	DNA mismatch endonuclease Vsr
27	3627053	3647869	13	P73_3567	TniQ
28	3849567	3854060	5	P73_3756	hypothetical protein
28	3849567	3854060	5	P73_3757	hypothetical protein
28	3849567	3854060	5	P73_3758	hypothetical protein
28	3849567	3854060	5	P73_3759	integrase catalytic subunit
28	3849567	3854060	5	P73_3760	transposase IS3/IS911 family protein
29	3856466	3863807	10	P73_3764	hypothetical protein
29	3856466	3863807	10	P73_3765	hypothetical protein
29	3856466	3863807	10	P73_3766	Thermostable 8-oxoguanine DNA glycosylase
29	3856466	3863807	10	P73_3767	hypothetical protein
29	3856466	3863807	10	P73_3768	nucleoside 2-deoxyribosyltransferase family protein

29	3856466	3863807	10	P73_3769	Predicted PP-loop superfamily ATPase
29	3856466	3863807	10	P73_3770	transposase, IS4 family protein
29	3856466	3863807	10	P73_3771	hypothetical protein
29	3856466	3863807	10	P73_3772	hypothetical protein
29	3856466	3863807	10	P73_3773	hypothetical protein
30	4075898	4080821	6	P73_3970	hypothetical protein
30	4075898	4080821	6	P73_3971	major facilitator family protein
30	4075898	4080821	6	P73_3972	transposase
30	4075898	4080821	6	P73_3973	transposase
30	4075898	4080821	6	P73_3974	aldo/keto reductase
30	4075898	4080821	6	P73_3975	transcriptional regulator
31	4137931	4152335	12	P73_4028	extracellular solute-binding protein family 1 protein
31	4137931	4152335	12	P73_4029	ribose-5-phosphate isomerase B
31	4137931	4152335	12	P73_4030	LysR family transcriptional regulator
31	4137931	4152335	12	P73_4031	peptide ABC transporter ATP-binding protein
31	4137931	4152335	12	P73_4032	ABC transporter permease
31	4137931	4152335	12	P73_4033	ABC transporter, membrane spanning protein (peptide)
31	4137931	4152335	12	P73_4034	ABC transporter substrate binding protein
31	4137931	4152335	12	P73_4035	oligopeptide ABC transporter substrate binding protein
31	4137931	4152335	12	P73_4036	aliphatic sulfonates family ABC transporter periplasmic ligand-binding protein
31	4137931	4152335	12	P73_4037	acyl-CoA dehydrogenase
31	4137931	4152335	12	P73_4038	monooxygenase
31	4137931	4152335	12	P73_4039	NAD-dependent epimerase/dehydratase
32	4159890	4173781	11	P73_4045	nodulation protein nolR
32	4159890	4173781	11	P73_4046	thiamine pyrophosphate protein TPP binding domain-containing protein
32	4159890	4173781	11	P73_4047	Predicted membrane protein
32	4159890	4173781	11	P73_4048	GntR family transcriptional regulator
32	4159890	4173781	11	P73_4049	family 5 extracellular solute-binding protein
32	4159890	4173781	11	P73_4050	binding-protein-dependent transporters inner membrane component
32	4159890	4173781	11	P73_4051	binding-protein-dependent transporters inner membrane component
32	4159890	4173781	11	P73_4052	ABC transporter
32	4159890	4173781	11	P73_4053	NAD-dependent epimerase/dehydratase
32	4159890	4173781	11	P73_4054	short-chain dehydrogenase/reductase SDR
32	4159890	4173781	11	P73_4055	phenylhydantoinase
33	4182979	4187355	7	P73_4063	hypothetical protein
33	4182979	4187355	7	P73_4064	MarR family transcriptional regulator
33	4182979	4187355	7	P73_4065	polysaccharide biosynthesis protein
33	4182979	4187355	7	P73_4066	transposase IS3/IS911 family protein
33	4182979	4187355	7	P73_4067	transposase, orfB

33	4182979	4187355	7	P73_4068	transposase IS3/IS911 family protein
33	4182979	4187355	7	P73_4069	integrase catalytic subunit
34	4191742	4200902	10	P73_4074	nitrate/sulfonate/bicarbonate ABC transporter ATPase
34	4191742	4200902	10	P73_4075	ABC transporter permease
34	4191742	4200902	10	P73_4076	LysR family transcriptional regulator
34	4191742	4200902	10	P73_4077	sulfonate/nitrate transporter
34	4191742	4200902	10	P73_4078	putative transposase
34	4191742	4200902	10	P73_4079	transposase
34	4191742	4200902	10	P73_4080	transposase
34	4191742	4200902	10	P73_4081	binding-protein-dependent transport system inner membrane protein
34	4191742	4200902	10	P73_4082	putative sulfonate ABC transporter ATP-binding protein
34	4191742	4200902	10	P73_4083	ABC transporter substrate-binding protein
35	4234469	4238916	5	P73_4113	Blr3415 protein
35	4234469	4238916	5	P73_4114	nitrilotriacetate monooxygenase
35	4234469	4238916	5	P73_4115	ABC transporter
35	4234469	4238916	5	P73_4116	binding-protein-dependent transport system inner membrane protein
35	4234469	4238916	5	P73_4117	NMT1/THI5 like domain-containing protein
36	4517554	4522207	4	P73_4379	transposase, IS4 family protein
36	4517554	4522207	4	P73_4380	transposase, IS4 family protein
36	4517554	4522207	4	P73_4381	transposase IS116/IS110/IS902 family protein
36	4517554	4522207	4	P73_4382	Flagellar hook-length control protein FliK
pP73C					
37	10253	15689	7	P73_4677	Prokaryotic E2 family E
37	10253	15689	7	P73_4678	Multiubiquitin
37	10253	15689	7	P73_4679	hypothetical protein
37	10253	15689	7	P73_4680	hypothetical protein
37	10253	15689	7	P73_4681	Predicted Zn peptidase
37	10253	15689	7	P73_4682	transposase, mutator type
37	10253	15689	7	P73_4683	single-stranded DNA-binding protein

Sheet 3 (Excel)

COG	Gene count	% of Total
L	57	26.15%
P	26	11.93%
K	20	9.17%
R	16	7.34%
E	15	6.88%
G	12	5.50%
M	12	5.50%
O	12	5.50%

S	11	5.05%
V	7	3.21%
C	6	2.75%
H	6	2.75%
F	5	2.29%
I	3	1.38%
U	3	1.38%
D	2	0.92%
Q	2	0.92%
T	2	0.92%
J	1	0.46%
Total	218	1

Data S3 | Horizontally transferred genes in the *Celeribacter indicus* P73^{T} genome. Horizontally transferred Genes (HTG) predicted in the IMG database (24 October 2013, Sheet 1); COG categories of HTG (Sheet 2).

Sheet 1 (Excel)

Locus Tag	Product Name	From Genome
P73_0008	transposase	Rhodopseudomonas palustris TIE-1
P73_0009	transposase	Bradyrhizobium sp. BTAi1
P73_0074	AraC family transcriptional regulator	Nitratireductor indicus C115
P73_0075	phospholipid-binding protein	Nitratireductor indicus C115
P73_0160	Transcriptional Regulator, LysR family protein	Pseudomonas psychrophila HA-4
P73_0161	CDP-6-deoxy-delta-3,4-glucoseen reductase	Bordetella petrii Se-1111R, DSM 12804
P73_0163	hydrolase	Pseudomonas resinovorans DSM 21078
P73_0164	carbon monoxide dehydrogenase subunit G	Azospirillum halopraeferens DSM 3675
P73_0165	molybdopterin dehydrogenase FAD-binding protein	Burkholderia graminis C4D1M
P73_0166	xanthine dehydrogenase	Burkholderia sp. UYPR1.413
P73_0167	(2Fe-2S)-binding domain-containing protein	Burkholderia sp. WSM3556
P73_0169	fumarylacetoacetate (FAA) hydrolase	Cupriavidus necator N-1, ATCC 43291
P73_0170	putative carboxymethylenebutenolidase	Bradyrhizobium sp. S23321
P73_0178	TRAP transporter, 4TM/12TM fusion protein	Nitratireductor pacificus pht-3B
P73_0179	TRAP transporter solute receptor, TAXI family protein	Nitratireductor pacificus pht-3B
P73_0181	long-chain-fatty-acid-CoA ligase	Nitratireductor pacificus pht-3B

P73_0182	4-hydroxylbenzoyl-CoA Thioesterase	Nitratireductor pacificus pht-3B
P73_0183	transcriptional repressor	Nitratireductor pacificus pht-3B
P73_0185	flavin reductase domain-containing FMN-binding protein	Frankia sp. EuI1c
P73_0186	TetR family transcriptional regulator	Amycolatopsis taiwanensis DSM 45107
P73_0187	acyl-CoA dehydrogenase-like protein	Mycobacterium sp. MOTT36Y
P73_0224	short-chain dehydrogenase/reductase sdr	Amycolatopsis thermoflava N1165, DSM 44574
P73_0226	Predicted xylanase/chitin deacetylase	Chromobacterium violaceum ATCC 12472
P73_0227	xylose isomerase domain-containing protein	Gamma proteobacterium sp. NOR51-B
P73_0228	short chain dehydrogenase	Streptomyces clavuligerus ATCC 27064
P73_0229	sugar ABC transporter	Rhizobium rhizogenes K84
P73_0231	ribose ABC transporter	Rhizobium rhizogenes K84
P73_0232	antibiotic biosynthesis monooxygenase	Cupriavidus necator N-1, ATCC 43291
P73_0233	MarR family transcriptional regulator	Cupriavidus necator N-1, ATCC 43291
P73_0310	Protein of unknown function DUF262	Rhodococcus sp. 114MFTsu3.1
P73_0329	homogentisate 1,2-dioxygenase	Bradyrhizobium sp. ORS285
P73_0330	fumarylacetoacetate hydrolase family protein	Burkholderia gladioli BSR3
P73_0332	LysR family transcriptional regulator	Burkholderia cenocepacia PC184
P73_0333	cytochrome P450	Parvibaculum lavamentivorans DS-1
P73_0335	ferredoxin	Asticcacaulis excentricus CB 48
P73_0337	MarR family transcriptional regulator	Nisaea denitrificans DSM 18348
P73_0338	long-chain-fatty-acid--CoA ligase	Rhodocista centenaria SW
P73_0339	enoyl-CoA hydratase	Azoarcus toluclasticus ATCC 700605
P73_0341	thiolase	Burkholderia sp. WSM4176
P73_0373	Domain of unknown function (DUF4145)	Bradyrhizobium sp. BTAi1
P73_0479	hypothetical protein	Rhizobium rhizogenes K84
P73_0480	phosphoglycerate mutase	Inquilinus limosus DSM 16000
P73_0497	ABC transporter substrate-binding protein	Nitratireductor indicus C115
P73_0498	ABC transporter	Nitratireductor indicus C115
P73_0499	hypothetical protein	Mesorhizobium opportunistum WSM2075 (final version from ORNL)
P73_0500	ribose ABC transporter ATP-binding protein	Bradyrhizobium sp. BTAi1
P73_0501	3-hydroxybutyryl-CoA dehydrogenase	Martelella mediterranea DSM 17316

P73_0502	alcohol dehydrogenase	Burkholderia sp. JPY251
P73_0503	putative periplasmic substrate binding protein	Martelella mediterranea DSM 17316
P73_0504	TRAP-type C4-dicarboxylate transport system small permease	Martelella mediterranea DSM 17316
P73_0505	TRAP dicarboxylate transporter	Martelella mediterranea DSM 17316
P73_0506	aldehyde dehydrogenase	Bradyrhizobium sp. ORS285
P73_0700	Polysaccharide pyruvyl transferase	Flavobacterium antarcticum DSM 19726
P73_0702	hypothetical protein	Truepera radiovictrix RQ-24, DSM 17093
P73_0703	polysaccharide export protein, translocase	Thioalkalivibrio sp. ALMg9
P73_0707	hypothetical protein	Pelagibacterium halotolerans B2
P73_0708	glycosyl transferase group 1	Chitinilyticum litopenaei DSM 21440
P73_0709	dTDP-glucose 4,6-dehydratase	Bacillus thuringiensis BMB171
P73_0710	family 2 glycosyl transferase	Methylocaldum szegediense O-12
P73_0711	putative Glycosyl transferase, group 1	Azospirillum sp. B510
P73_0712	acyltransferase 3	Bradyrhizobium sp. WSM2254
P73_0934	hypothetical protein	Xanthobacter autotrophicus Py2
P73_0935	DNA polymerase IV	Rhodospirillum photometricum DSM 122
P73_0937	ATPase AAA	Kaistia granuli DSM 23481
P73_0939	DEAD/DEAH box helicase	Rhodopseudomonas palustris DX-1
P73_0949	HNS-type DNA binding protein	Rhizobium mongolense USDA 1844
P73_0960	hypothetical protein	Desulfarculus baarsii 2st14, DSM 2075
P73_0964	replicative DNA helicase	Methylobacterium nodulans ORS 2060
P73_0966	hypothetical protein	Ochrobactrum anthropi ATCC 49188
P73_0967	single-stranded DNA-binding protein	Ochrobactrum anthropi ATCC 49188
P73_0968	XRE family transcriptional regulator	Bradyrhizobium japonicum in8p8
P73_0969	Uncharacterized conserved protein (DUF2285)	Ochrobactrum anthropi ATCC 49188
P73_0970	hypothetical protein	Ochrobactrum anthropi ATCC 49188
P73_0971	Uncharacterized conserved protein (DUF2285)	Ochrobactrum anthropi ATCC 49188

P73_0975	plasmid segregation centromere-binding protein ParG	Ochrobactrum anthropi ATCC 49188
P73_0977	conjugal transfer protein precursor	Ochrobactrum anthropi ATCC 49188
P73_0979	lytic transglycosylase	Ochrobactrum anthropi ATCC 49188
P73_0980	Type IV secretory pathway, VirD2 components (relaxase)	Ochrobactrum anthropi ATCC 49188
P73_0981	conjugal transfer coupling protein TraG	Ochrobactrum anthropi ATCC 49188
P73_0985	conjugal transfer protein TrbC	Nitratireductor indicus C115
P73_0988	conjugal transfer protein TrbJ	Ochrobactrum anthropi ATCC 49188
P73_0989	hypothetical protein	Ochrobactrum anthropi ATCC 49188
P73_0993	conjugation TrbI family protein	Kaistia adipata DSM 17808
P73_0994	Uncharacterized conserved small protein	Agrobacterium sp. 224MFTsu3.1
P73_0995	LysR family transcriptional regulator	Ochrobactrum anthropi ATCC 49188
P73_1007	Uncharacterized protein conserved in bacteria	Caulobacter crescentus OR37
P73_1008	cobalt-zinc-cadmium resistance protein CzcD	Nitratireductor indicus C115
P73_1018	60 kDa chaperonin	Ensifer fredii USDA 257
P73_1025	hypothetical protein	Chelativorans sp. BNC1
P73_1026	Uncharacterized conserved protein (DUF2285)	Hyphomicrobium zavarzinii ATCC 27496
P73_1028	replication initiator protein A	Hoeflea sp. 108
P73_1029	transposase	Hoeflea sp. 108
P73_1032	Ubiquinone/menaquinone biosynthesis methyltransferase	Agrobacterium sp. H13-3
P73_1039	binding-protein-dependent transporter inner membrane component	Thiothrix flexilis DSM 14609
P73_1040	ABC transporter	Thiothrix flexilis DSM 14609
P73_1041	NMT1/THI5-like domain-containing protein	Thiothrix flexilis DSM 14609
P73_1042	methenyltetrahydrofolate synthetase	Thiothrix flexilis DSM 14609
P73_1044	EmrB/QacA family drug resistance transporter	Inquilinus limosus DSM 16000
P73_1045	oligopeptide ABC transporter oligopeptide-binding protein	Rhizobium sp. CF142
P73_1046	ABC transporter ATP-binding protein	Rhizobium sp. CF142
P73_1047	peptide ABC transporter permease	Rhizobium sp. CF142
P73_1048	binding-protein-dependent transport systems inner membrane component	Rhizobium sp. CF142
P73_1051	aromatic-ring-hydroxylating dioxygenase, ferredoxin subunit	Rhizobium sp. CF142
P73_1052	LysR family transcriptional regulator	Rhizobium sp. CF142
P73_1053	Rieske (2Fe-2S) protein	Rhizobium sp. CF142

P73_1054	FAD-dependent pyridine nucleotide-disulfide oxidoreductase	Rhizobium sp. CF142
P73_1055	FabG	Rhizobium sp. CF142
P73_1064	LysR family transcriptional regulator	Bradyrhizobium elkanii WSM2783
P73_1065	oxidoreductase short-chain dehydrogenase/reductase family protein YdfG	Ensifer arboris LMG 14919
P73_1071	CinA domain-containing protein	Citromicrobium sp. JLT1363
P73_1088	alcohol dehydrogenase zinc-binding domain protein	Sphingomonas sp. LH128
P73_1089	TetR family transcriptional regulator	Rhizobium leguminosarum bv. trifolii WSM1325
P73_1090	NAD-dependent epimerase/dehydratase	Roseomonas cervicalis ATCC 49957
P73_1091	XRE family transcriptional regulator	Luteibacter sp. 22Crub2.1
P73_1098	protein fecR	Agrobacterium albertimagni AOL15
P73_1099	RNA polymerase sigma-70 family protein	Pseudomonas sp. M1
P73_1100	lipoprotein	Hoeflea sp. 108
P73_1101	ABC transporter	Nitratireductor aquibiodomus RA22 (Draft1)
P73_1102	ABC transporter	Hoeflea sp. 108
P73_1103	binding-protein-dependent transport system inner membrane protein	Nitratireductor aquibiodomus RA22 (Draft1)
P73_1104	binding-protein-dependent transport system inner membrane protein	Ochrobactrum intermedium J2
P73_1105	extracellular solute-binding protein	Aurantimonas ureilytica DSM 18598
P73_1108	short chain dehydrogenase	Burkholderia gladioli BSR3
P73_1109	LysR family transcriptional regulator	Thalassobaculum salexigens DSM 19539
P73_1110	HxlR family transcriptional regulator	Methylobacterium nodulans ORS 2060
P73_1111	NADP oxidoreductase coenzyme F420-dependent	Glaciibacter superstes DSM 21135
P73_1112	alcohol dehydrogenase zinc-binding domain-containing protein	delta proteobacterium NaphS2
P73_1116	TetR family transcriptional regulator	Bradyrhizobium sp. ARR65
P73_1117	short-chain dehydrogenase/reductase SDR	Terriglobus saanensis SP1PR4, DSM 23119
P73_1123	transporter	Yaniella halotolerans DSM 15476
P73_1133	Peroxiredoxin	Phyllobacterium sp. YR531
P73_1146	glutathione S-transferase	Nitratireductor indicus C115
P73_1288	hypothetical protein	Synechococcus elongatus PCC 7942
P73_1289	hypothetical protein	Desulfovibrio inopinatus DSM

		10711
P73_1296	major facilitator superfamily protein	Stenotrophomonas maltophilia K279a
P73_1297	transcriptional regulator	Amorphus coralli DSM 19760
P73_1332	BLUF domain-containing protein	Microbacterium paraoxydans 77MFTsu3.2
P73_1364	ribose ABC transporter periplasmic binding protein	Rhodospirillum rubrum S1, ATCC 11170
P73_1365	ABC transporter	Opitutaceae sp. TAV5
P73_1366	ribose ABC transporter permease	Pleomorphomonas oryzae DSM 16300
P73_1367	lactoylglutathione lyase-like protein	Haloterrigena turkmenica VKM B-1734, DSM 5511
P73_1369	binding-protein-dependent transport systems inner membrane component	Mesorhizobium ciceri CMG6
P73_1370	ABC transporter permease	Mesorhizobium ciceri CMG6
P73_1371	ABC transporter substrate binding protein	Inquilinus limosus DSM 16000
P73_1375	transcriptional regulator	Burkholderia thailandensis MSMB43
P73_1378	TRAP transporter solute receptor subunit DctP family protein 7	Acidovorax sp. JHL-9
P73_1381	acetaldehyde dehydrogenase	Marinobacter daepoensis DSM 16072
P73_1390	urocanate hydratase	Rhizobium leguminosarum bv. trifolii WSM1325
P73_1392	tripartite ATP-independent periplasmic transporter DctQ	Tistrella mobilis KA081020-065
P73_1394	CoA-transferase	Achromobacter xylosoxidans A8
P73_1395	acyl-CoA dehydrogenase	Achromobacter xylosoxidans A8
P73_1396	short-chain specific acyl-CoA dehydrogenase	Roseomonas cervicalis ATCC 49957
P73_1399	SNF2-related:helicase, C-terminal:type III restriction enzyme	Syntrophus aciditrophicus SB
P73_1400	glutathione S-transferase	Bradyrhizobium elkanii WSM1741
P73_1401	Uncharacterized protein conserved in bacteria	Tistrella mobilis KA081020-065
P73_1404	Uncharacterized conserved protein	Thiobacillus denitrificans DSM 12475
P73_1406	Transcriptional regulator	Tistrella mobilis KA081020-065
P73_1408	HlyD family secretion protein	Microvirga lupini Lut6
P73_1422	hypothetical protein	Azospirillum irakense DSM 11586
P73_1430	Bifunctional DNA primase/polymerase, N-terminal	Bradyrhizobium sp. CCGE-LA001
P73_1431	transcriptional regulator	Francisella sp. TX077308
P73_1434	alkanesulfonate monooxygenase	Pseudomonas sp. M1
P73_1435	Alkanesulfonate monooxygenase	Pseudomonas sp. M1

P73_1436	ABC-type Fe3+ transport system, substrate binding component	Pseudomonas sp. M1
P73_1437	spermidine/putrescine ABC transporter ATPase	Pseudomonas sp. M1
P73_1438	binding-protein-dependent transport system inner membrane protein	Pseudomonas sp. M1
P73_1440	ABC transporter-like protein	Azospirillum sp. B510
P73_1441	binding-protein-dependent transporter inner membrane component	Halobacillus kuroshimensis DSM 18393
P73_1442	aliphatic sulfonates family ABC transporter periplasmic ligand-binding protein	Inquilinus limosus DSM 16000
P73_1595	Predicted transcriptional regulators	Erythrobacter sp. NAP1
P73_1647	mannonate dehydratase	Actinopolymorpha alba DSM 45243
P73_1649	mannonate dehydratase	Ensifer fredii USDA 257
P73_1650	GntR family transcriptional regulator	Agrobacterium vitis S4
P73_1652	oligopeptide ABC transporter substrate binding protein	Agrobacterium sp. 224MFTsu3.1
P73_1653	dipeptide ABC transporter permease	Microvirga lotononidis WSM3557
P73_1654	dipeptide ABC transporter	Rhizobium rhizogenes K84
P73_1655	peptide ABC transporter ATP-binding protein	Rhizobium etli CIAT 652
P73_1656	ABC transporter	Rhizobium etli CIAT 894
P73_1667	L-lactate dehydrogenase (cytochrome) protein	Bradyrhizobium sp. EC3.3
P73_1753	hypothetical protein	Fodinicurvata sediminis DSM 21159
P73_1755	conjugation TrbI family protein	Kaistia adipata DSM 17808
P73_1762	conjugal transfer protein TrbB	Pleomorphomonas koreensis DSM 23070
P73_1764	P-type conjugative transfer ATPase TrbB	Kaistia adipata DSM 17808
P73_1766	conjugal transfer coupling protein TraG	Kaistia adipata DSM 17808
P73_1767	LysR family transcriptional regulator	Kaistia adipata DSM 17808
P73_1768	TetR family transcriptional regulator	Microvirga lotononidis WSM3557
P73_1769	multidrug resistance protein A	Ensifer fredii USDA 257
P73_1770	major facilitator transporter	Ensifer fredii USDA 257
P73_1774	dihydropteroic synthetase	Escherichia coli MS 124-1
P73_1775	Type IV secretory pathway, VirD2 components (relaxase)	Oligotropha carboxidovorans OM4
P73_1776	putative transglycosylase	Meganema perideroedes DSM 15528
P73_1777	Uncharacterized conserved protein	Bradyrhizobium japonicum in8p8
P73_1778	TraF peptidase. serine peptidase MEROPS family S26C	Kaistia adipata DSM 17808
P73_1782	replication initiator protein A	Rhodopseudomonas palustris DX-1
P73_1787	Uncharacterized conserved protein (DUF2285)	Kaistia adipata DSM 17808
P73_1788	hypothetical protein	Pleomorphomonas koreensis DSM 23070

P73_1789	hypothetical protein	Oligotropha carboxidovorans OM4
P73_1790	Uncharacterized conserved protein	Oligotropha carboxidovorans OM4
P73_1791	PilT domain-containing protein	Rhizobium tropici USDA 9039
P73_1792	Plasmid stability protein	Rhizobium tropici USDA 9039
P73_1793	hypothetical protein	Oligotropha carboxidovorans OM4
P73_1794	ParB-like domain protein	Oligotropha carboxidovorans OM4
P73_1796	type I restriction-modification system M subunit	Comamonas composti DSM 21721
P73_1797	restriction modification system DNA specificity domain-containing protein	Thiocapsa marina 5811, DSM 5653
P73_1798	SMC protein, N-terminal domain-containing protein	Rhizobium etli GR56
P73_1799	hypothetical protein	Rhizobium leguminosarum bv. trifolii WSM597
P73_1805	Predicted Zn peptidase	Sinobacter flavus DSM 18980
P73_1806	helix-hairpin-helix DNA-binding motif-containing protein	Aurantimonas manganoxydans SI85-9A1
P73_1807	Uncharacterized protein conserved in bacteria (DUF2188)	Nitrobacter sp. Nb-311A
P73_1808	hypothetical protein	Nitrobacter winogradskyi Nb-255
P73_1809	hypothetical protein	Nitrobacter winogradskyi Nb-255
P73_1811	Domain of unknown function (DUF4095)	Chamaesiphon minutus PCC 6605
P73_1853	serine/threonine protein kinase	Syntrophobacter fumaroxidans MPOB
P73_1860	Uncharacterized conserved protein (DUF2285)	Kaistia adipata DSM 17808
P73_1861	hypothetical protein	Pleomorphomonas koreensis DSM 23070
P73_1862	hypothetical protein	Oligotropha carboxidovorans OM4
P73_1863	Uncharacterized conserved protein	Oligotropha carboxidovorans OM4
P73_1864	PilT domain-containing protein	Rhizobium tropici USDA 9039
P73_1865	Plasmid stability protein	Rhizobium tropici USDA 9039
P73_1866	hypothetical protein	Oligotropha carboxidovorans OM4
P73_1867	ParB-like domain protein	Oligotropha carboxidovorans OM4
P73_1869	type I restriction-modification system M subunit	Comamonas composti DSM 21721
P73_1870	restriction modification system DNA specificity domain-containing protein	Thiocapsa marina 5811, DSM 5653
P73_1871	SMC protein, N-terminal domain-containing protein	Rhizobium etli GR56
P73_1872	hypothetical protein	Rhizobium leguminosarum bv. trifolii WSM597
P73_1878	Predicted Zn peptidase	Sinobacter flavus DSM 18980
P73_1879	helix-hairpin-helix DNA-binding motif-containing protein	Aurantimonas manganoxydans SI85-9A1
P73_1880	Uncharacterized protein conserved in bacteria (DUF2188)	Nitrobacter sp. Nb-311A
P73_1881	hypothetical protein	Nitrobacter winogradskyi Nb-255
P73_1882	hypothetical protein	Nitrobacter winogradskyi Nb-255
P73_1884	Domain of unknown function (DUF4095)	Chamaesiphon minutus PCC 6605

P73_1926	serine/threonine protein kinase	Syntrophobacter fumaroxidans MPOB
P73_1935	heavy metal translocating P-type ATPase	Chelativorans sp. BNC1
P73_1938	MerR family transcriptional regulator	Mesorhizobium alhagi CCNWXJ12-2
P73_1940	type 12 methyltransferase	Rhizobium sp. PDO1-076
P73_1941	hypothetical protein	Mesorhizobium alhagi CCNWXJ12-2
P73_1943	Inosine/uridine-preferring nucleoside hydrolase	Kaistia adipata DSM 17808
P73_1944	RpiR family transcriptional regulator	Rhizobium sp. CF142
P73_1945	twin-arginine translocation pathway signal	Rhizobium sp. CF142
P73_1946	twin-arginine translocation pathway signal	Rhizobium sp. CF142
P73_1947	S-adenosylhomocysteine deaminase, methylthioadenosine deaminase	Rhizobium sp. CF142
P73_1949	nitrate/sulfonate/bicarbonate ABC transporter permease	Rhizobium sp. CF142
P73_1950	ABC transporter-like protein permease	Rhizobium sp. CF142
P73_1951	nucleoside 2-deoxyribosyltransferase	Rhizobium leguminosarum bv. trifolii WSM1325
P73_1958	(2Fe-2S)-binding domain-containing protein	Burkholderia ubonensis Bu
P73_1963	hypothetical protein	Rhizobium sullae WSM1592
P73_1975	putative monooxygenase	Pseudomonas thermotolerans J53
P73_1976	N-carbamoylsarcosine amidase	Delftia sp. Cs1-4
P73_1977	polysaccharide deacetylase	Pseudonocardia asaccharolytica DSM 44247
P73_1978	helix-turn-helix domain-containing protein	Aneurinibacillus terranovensis DSM 18919
P73_1979	transposase	Rhodopseudomonas palustris TIE-1
P73_1980	transposase	Bradyrhizobium sp. BTAi1
P73_1981	Uncharacterized conserved protein	Caldimonas manganoxidans ATCC BAA-369
P73_1982	activator of Hsp90 ATPase 1 family protein	Inquilinus limosus DSM 16000
P73_1983	arsR family transcriptional regulator	Amycolatopsis nigrescens CSC17Ta-90, DSM 44992
P73_1991	cupin 2 barrel domain-containing protein	Nitratireductor pacificus pht-3B
P73_1993	GMC oxidoreductase	Novosphingobium sp. AP12
P73_1994	LysR family transcriptional regulator	Chelativorans sp. BNC1
P73_1995	putative luciferase-like monooxygenase	Sphingobium sp. AP49
P73_1996	monooxygenase	Sorangium cellulosum So ce 56
P73_1998	binding-protein-dependent transport system inner membrane protein	Chelativorans sp. BNC1
P73_1999	extracellular solute-binding protein	Chelativorans sp. BNC1
P73_2000	major facilitator superfamily transporter	Amorphus coralli DSM 19760

P73_2001	ABC transporter nucleotide binding/ATPase protein	Agrobacterium sp. ATCC 31749
P73_2002	Uncharacterized protein involved in propionate catabolism	Nitratireductor indicus C115
P73_2004	NADPH-dependent FMN reductase	Rhizobium sp. CF142
P73_2005	flavin-dependent reductase	Pseudomonas syringae CC1557 (CC1557)
P73_2006	XRE family transcriptional regulator	Beijerinckia indica indica ATCC 9039
P73_2007	biotin sulfoxide reductase	Nitratireductor indicus C115
P73_2008	LysR family transcriptional regulator	Burkholderia dolosa AUO158
P73_2011	CoA-binding protein	Jonquetella anthropi E3_33 E1
P73_2013	Uncharacterized protein conserved in bacteria	Variovorax paradoxus 4MFCol3.1
P73_2018	Uncharacterized protein conserved in bacteria	Cupriavidus necator N-1, ATCC 43291
P73_2019	transcriptional regulator	Rhizobium rhizogenes K84
P73_2020	6-phosphogluconate dehydrogenase	Rhizobium rhizogenes K84
P73_2021	2-hydroxyhepta-2,4-diene-1,7-dioate isomerase	Rhizobium rhizogenes K84
P73_2022	bleomycin resistance protein	Rhizobium rhizogenes K84
P73_2023	Alpha/beta hydrolase family	Acidothermus cellulolyticus 11B
P73_2024	alpha/beta hydrolase fold protein	Arthrobacter sp. 161MFSha2.1
P73_2025	ABC transporter	Agromyces subbeticus DSM 16689
P73_2026	binding-protein-dependent transport system inner membrane protein	Actinomadura flavalba DSM 45200
P73_2027	iron(III) ABC transporter iron (III)-binding protein	Actinomadura flavalba DSM 45200
P73_2028	HTH-type transcriptional activator nahR	Bradyrhizobium sp. WSM3983
P73_2029	LysR family transcriptional regulator	Magnetospirillum magnetotacticum MS-1
P73_2030	putative oxidoreductase protein	Streptomyces sp. CNY228
P73_2031	2OG-Fe(II) oxygenase	Bradyrhizobium elkanii WSM2783
P73_2032	cytosine deaminase-like protein	Methylobacterium chloromethanicum CM4
P73_2033	taurine catabolism dioxygenase TauD/TfdA	Caulobacter segnis ATCC 21756
P73_2034	NMT1/THI5-like domain-containing protein	Elioraea tepidiphila DSM 17972
P73_2035	aliphatic sulfonates transporter ATP-binding protein SsuB	Elioraea tepidiphila DSM 17972
P73_2036	ABC transporter permease	Alcaligenes faecalis phenolicus DSM 16503
P73_2040	replicative DNA helicase	Ensifer arboris LMG 14919
P73_2042	hypothetical protein	Cupriavidus sp. UYPR2.512
P73_2046	LysR family transcriptional regulator	Azospirillum halopraeferens DSM 3675
P73_2048	ABC transporter	Massilia niastensis DSM 21313
P73_2049	binding-protein-dependent transport system inner	Ottowia thiooxydans DSM 14619

	membrane protein	
P73_2050	TRAP dicarboxylate transporter subunit DctP	Halomonas halocynthiae DSM 14573
P73_2051	TRAP-type C4-dicarboxylate transport system, small permease component	Bordetella parapertussis 12822
P73_2052	TRAP dicarboxylate transporter subunit DctM	Polaromonas sp. JS666
P73_2053	aldo/keto reductase	Micromonospora carbonacea var. africana. ATCC 39149
P73_2054	3-oxoacyl-ACP reductase	Candidatus Poribacteria sp. WGA-A3 (final_clean_version)
P73_2055	polar amino acid ABC transporter inner membrane subunit	Inquilinus limosus DSM 16000
P73_2056	polar amino acid ABC transporter inner membrane subunit	Pantoea sp. GM01
P73_2057	ABC transporter	Methylobacterium sp. 4-46
P73_2058	extracellular solute-binding protein	Starkeya novella DSM 506
P73_2059	SMP-30/gluconolaconase/LRE domain-containing protein	Roseomonas cervicalis ATCC 49957
P73_2060	LysR family transcriptional regulator	Rhodovibrio salinarum DSM 9154
P73_2061	putative glyoxalase	Geopsychrobacter electrodiphilus DSM 16401
P73_2062	acetolactate synthase, large chain related protein	Streptomyces violaceoruber 3844-33C
P73_2063	amidohydrolase	Rubritepida flocculans DSM 14296
P73_2064	flavoprotein	Halalkalicoccus jeotgali B3, DSM 18796
P73_2066	polysaccharide deacetylase	Granulicella tundricola MP5ACTX9
P73_2067	thiamine pyrophosphate central domain-containing protein	Streptomyces violaceusniger Tu 4113
P73_2068	glucose-methanol-choline oxidoreductase	Methylobacterium nodulans ORS 2060
P73_2069	short-chain aldo-keto oxidoreductase	Pleomorphomonas koreensis DSM 23070
P73_2071	TRAP transport system, small permease protein	Bradyrhizobium canariense WSM4349
P73_2072	TRAP transporter, DctM subunit	Bradyrhizobium elkanii USDA 3254
P73_2073	transcription regulator MarR family protein	Cupriavidus necator N-1, ATCC 43291
P73_2079	aliphatic sulfonate ABC transporter permease	Phyllobacterium sp. YR531
P73_2082	taurine transport system permease	Mesorhizobium loti CJ3sym
P73_2083	taurine transporter ATP-binding subunit	Meganema perideroedes DSM 15528

P73_2084	taurine ABC transporter periplasmic binding protein	Meganema perideroedes DSM 15528
P73_2086	hypothetical protein	Streptomyces bingchenggensis BCW-1
P73_2087	Uncharacterized protein conserved in bacteria	Inquilinus limosus DSM 16000
P73_2089	TRAP dicarboxylate transporter subunit DctM	Verminephrobacter eiseniae EF01-2
P73_2091	AraC family transcriptional regulator	Bradyrhizobium elkanii WSM2783
P73_2092	regulatory protein LuxR	Inquilinus limosus DSM 16000
P73_2095	carbon monoxide dehydrogenase	Elioraea tepidiphila DSM 17972
P73_2096	TRAP dicarboxylate transporter subunit DctM	Martelella mediterranea DSM 17316
P73_2097	TRAP dicarboxylate transporter subunit DctQ	Martelella mediterranea DSM 17316
P73_2098	putative periplasmic substrate binding protein	Martelella mediterranea DSM 17316
P73_2100	UDP-glucose 4-epimerase	Pseudonocardia dioxanivorans CB1190
P73_2101	Predicted metal-dependent enzyme of the double-stranded beta helix superfamily	Bacillus panaciterrae DSM 19096
P73_2112	TRAP transporter-DctP subunit	Nitratireductor indicus C115
P73_2116	alkyl hydroperoxide reductase/ thiol specific antioxidant/ Mal allergen	Mesorhizobium ciceri bv biserrulae WSM1271
P73_2118	ferredoxin	Mesorhizobium australicum WSM2073
P73_2119	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	Rhizobium sp. 2MFCol3.1
P73_2120	ABC transporter permease	Ensifer meliloti Mlalz-1
P73_2121	aliphatic sulfonates ABC transporter substrate-binding protein	Ensifer meliloti SM11
P73_2122	drug resistance transporter, EmrB/QacA subfamily protein	Rhizobium sullae WSM1592
P73_2132	Glutathione S-transferase domain protein	Gluconacetobacter sp. SXCC-1
P73_2133	adenosine deaminase	Gluconacetobacter sp. SXCC-1
P73_2135	NitT/TauT family transport system ATP-binding protein	Gluconacetobacter sp. SXCC-1
P73_2136	NitT/TauT family transport system permease protein	Gluconacetobacter sp. SXCC-1
P73_2137	2OG-Fe(II) oxygenase	Gluconacetobacter sp. SXCC-1
P73_2138	transcriptional regulator, LacI family protein	Gluconacetobacter sp. SXCC-1
P73_2144	LysR family transcripitonal regulator	Martelella mediterranea DSM 17316
P73_2145	2OG-Fe(II) oxygenase	Methylobacterium populi BJ001
P73_2146	NMT1/THI5-like domain-containing protein	Pseudomonas azotifigens DSM 17556
P73_2150	aromatic hydrocarbon dioxygenase small subunit	Nocardioides sp. Iso805N

P73_2151	Rieske (2Fe-2S) domain-containing protein	Nocardioides sp. JS614
P73_2152	Predicted ester cyclase	Cryptosporangium arvum YU 629-21, DSM 44712
P73_2153	Phytanoyl-CoA dioxygenase (PhyH)	Conexibacter woesei Iso977N
P73_2213	Lysophospholipase	Laribacter hongkongensis HLHK9
P73_2260	transposase	Rhodopseudomonas palustris TIE-1
P73_2261	transposase	Bradyrhizobium sp. BTAi1
P73_2264	ParB-like domain protein	Oligotropha carboxidovorans OM4
P73_2265	hypothetical protein	Oligotropha carboxidovorans OM4
P73_2267	Acetyltransferase (GNAT) domain	Rhodopseudomonas palustris DX-1
P73_2268	Uncharacterized protein conserved in bacteria	Beijerinckia indica indica ATCC 9039
P73_2269	Uncharacterized conserved protein	Agrobacterium sp. 224MFTsu3.1
P73_2270	hypothetical protein	Oligotropha carboxidovorans OM4
P73_2271	hypothetical protein	Pleomorphomonas koreensis DSM 23070
P73_2272	Uncharacterized conserved protein (DUF2285)	Kaistia adipata DSM 17808
P73_2275	replication initiator protein A	Rhodopseudomonas palustris DX-1
P73_2279	TraF peptidase. serine peptidase MEROPS family S26C	Kaistia adipata DSM 17808
P73_2280	Uncharacterized conserved protein	Bradyrhizobium japonicum in8p8
P73_2281	putative transglycosylase	Meganema perideroedes DSM 15528
P73_2282	Type IV secretory pathway, VirD2 components (relaxase)	Oligotropha carboxidovorans OM4
P73_2283	TetR family transcriptional regulator	Rhizobium sp. CF142
P73_2284	Sterol-4-alpha-carboxylate 3-dehydrogenase,decarboxylating	Caulobacter sp. K31
P73_2285	LysR family transcriptional regulator	Brevundimonas naejangsanensis DSM 23858
P73_2286	conjugal transfer coupling protein TraG	Brevundimonas naejangsanensis DSM 23858
P73_2288	P-type conjugative transfer ATPase TrbB	Rhodopseudomonas palustris DX-1
P73_2291	conjugal transfer ATPase TrbE	Kaistia adipata DSM 17808
P73_2292	conjugal transfer protein TrbJ	Hoeflea sp. 108
P73_2297	conjugation TrbI family protein	Hoeflea sp. 108
P73_2298	Uncharacterized conserved small protein	Kaistia adipata DSM 17808
P73_2300	glucose/ribitol short chain dehydrogenase/reductase family protein	Alcanivorax dieselolei B5
P73_2322	Nitroreductase	Kaistia adipata DSM 17808
P73_2323	Asp/Glu racemase	Agrobacterium tumefaciens

		CCNWGS0286
P73_2324	ABC transporter permease	Rhizobium leguminosarum bv viciae WSM1455
P73_2325	ABC transporter permease	Rhizobium leguminosarum bv viciae WSM1455
P73_2327	ABC transporter ATP-binding protein	Agrobacterium tumefaciens CCNWGS0286
P73_2328	Hydantoinase	Agrobacterium tumefaciens CCNWGS0286
P73_2329	Uncharacterized conserved protein	Agrobacterium tumefaciens CCNWGS0286
P73_2330	Uncharacterized conserved protein	Kaistia adipata DSM 17808
P73_2331	transcriptional regulator, LuxR family protein	Kaistia adipata DSM 17808
P73_2332	xenobiotic compound monooxygenase A subunit	Chelativorans sp. BNC1
P73_2333	LuxR family transcriptional regulator	Chelativorans sp. BNC1
P73_2334	hydantoinase A	Bradyrhizobium sp. BTAi1
P73_2335	Uncharacterized conserved protein	Rhizobium leguminosarum bv. viciae Vh3
P73_2336	twin-arginine translocation pathway signal	Chelativorans sp. BNC1
P73_2337	binding-protein-dependent transport system inner membrane protein	Chelativorans sp. BNC1
P73_2338	binding-protein-dependent transport system inner membrane protein	Chelativorans sp. BNC1
P73_2339	oligopeptide/dipeptide ABC transporter ATPase	Chelativorans sp. BNC1
P73_2340	oligopeptide/dipeptide ABC transporter ATPase	Chelativorans sp. BNC1
P73_2360	ThiJ/PfpI family protein	Brucella sp. 83/13
P73_2361	MerR family regulatory protein	Phyllobacterium sp. YR531
P73_2362	NADH:flavin oxidoreductase	Brucella sp. BO2
P73_2363	Acetoacetate decarboxylase (ADC)	Acetobacter aceti ATCC 23746
P73_2364	alpha/beta hydrolase	Brevundimonas diminuta ATCC 11568
P73_2366	aldehyde dehydrogenase	Burkholderia cepacia UCB 717, ATCC 25416
P73_2367	D-3-phosphoglycerate dehydrogenase,NAD- binding protein	Ensifer medicae WSM1369
P73_2368	transcriptional regulator	Bradyrhizobium elkanii WSM2783
P73_2369	short chain dehydrogenase/reductase oxidoreductase	Novosphingobium aromaticivorans DSM 12444
P73_2370	2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase	Methanosarcina barkeri Fusaro, DSM 804
P73_2371	alcohol dehydrogenase zinc-binding domain-containing protein	delta proteobacterium NaphS2
P73_2378	TetR family transcriptional regulator	Xanthobacter sp. 126

P73_2379	putative sulfate ester transport system substrate-binding protein	Azospirillum brasilense Sp245
P73_2380	binding-protein-dependent transport system inner membrane protein	Beijerinckia indica indica ATCC 9039
P73_2381	putative alkanesulfonate transport protein, ABC superfamily, inner membrane component	Azospirillum brasilense Sp245
P73_2382	ABC transporter	Pseudomonas fluorescens A506
P73_2383	NADH-quinone oxidoreductase subunits H/I	Actinoplanes sp. SE50/110
P73_2401	phosphoribosyltransferase	Bradyrhizobium elkanii WSM1741
P73_2403	PEBP family protein	Tistrella mobilis KA081020-065
P73_2405	xanthine dehydrogenase molybdopterin binding subunit	Pelagibacterium halotolerans B2
P73_2406	sulfonate/nitrate transport system substrate-binding protein	Rhizobium sp. CF142
P73_2408	Transcriptional regulator	Pleomorphomonas koreensis DSM 23070
P73_2414	FMN-dependent oxidoreductase, nitrilotriacetate monooxygenase family	Agrobacterium sp. 224MFTsu3.1
P73_2420	ribose ABC transporter permease	Kaistia adipata DSM 17808
P73_2421	LacI family transcriptional regulator	Kaistia adipata DSM 17808
P73_2424	hypothetical protein	Candidatus Accumulibacter phosphatis Type IIA UW-1
P73_2426	gluconate 2-dehydrogenase (acceptor)	Nitratireductor indicus C115
P73_2427	Gluconate 2-dehydrogenase subunit 3	Nitratireductor indicus C115
P73_2439	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	Martelella mediterranea DSM 17316
P73_2444	glycosyl transferase family protein	Desulfovibrio alaskensis DSM 16109
P73_2447	polysaccharide biosynthesis protein	Bacillus chagannorensis DSM 18086
P73_2450	transposase	Asticcacaulis benevestitus DSM 16100
P73_2454	RelE/StbE family addiction module toxin	Acidithiobacillus ferrivorans SS3
P73_2510	Predicted phosphohydrolases	Methylobacterium extorquens AM1
P73_2646	exported xanthine dehydrogenase/CoxI family protein	Martelella mediterranea DSM 17316
P73_2742	heat shock protein HtpX	Aestuariibacter salexigens DSM 15300
P73_2743	TrkA-C domain protein	Salinimicrobium xinjiangense DSM 19287
P73_2771	putative ATPase	Sphingobium sp. SYK-6
P73_2772	peptidase S8 family protein	Sphingobium sp. SYK-6
P73_2809	Glycine/D-amino acid oxidases (deaminating)	Microvirga lupini Lut6

P73_2810	N-methylhydantoinase B/acetone carboxylase subunit alpha	Azorhizobium doebereinerae UFLA1-100
P73_2811	5-oxoprolinase	Azorhizobium doebereinerae UFLA1-100
P73_2812	LysR family transcription regulator protein	Burkholderia thailandensis Bt4
P73_2813	oligopeptide/dipeptide ABC transporter, ATPase subunit	Azorhizobium doebereinerae UFLA1-100
P73_2814	oligopeptide/dipeptide ABC transporter ATP-binding protein	Azorhizobium doebereinerae UFLA1-100
P73_2815	agropinic acid ABC transporter permease	Azorhizobium doebereinerae UFLA1-100
P73_2816	peptide ABC transporter	Azorhizobium doebereinerae UFLA1-100
P73_2817	LysR family transcriptional regulator	Azorhizobium doebereinerae UFLA1-100
P73_2818	D-isomer specific 2-hydroxyacid dehydrogenase	Azorhizobium doebereinerae UFLA1-100
P73_2819	mandelate racemase/muconate lactonizing protein	Elioraea tepidiphila DSM 17972
P73_2820	LecH	Polaromonas sp. JS666
P73_2822	putative sarcosine oxidase subunit alpha	Acidovorax delafieldii 2AN
P73_2829	N-carbamoylsarcosine amidase	Martelella mediterranea DSM 17316
P73_2830	transcriptional regulator	Martelella mediterranea DSM 17316
P73_2831	exported protein (TRAP-type transport system, periplasmic component)	Bordetella petrii Se-1111R, DSM 12804
P73_2834	arylmalonate decarboxylase	Tistrella mobilis KA081020-065
P73_2835	Domain of unknown function (DUF4392)	Fervidicoccus fontis Kam940
P73_2836	C4-dicarboxylate-binding periplasmic protein	Tistrella mobilis KA081020-065
P73_2837	putative DctQ (C4-dicarboxylate permease, small subunit)	Tistrella mobilis KA081020-065
P73_2838	Putative TRAP transporter large permease protein	Tistrella mobilis KA081020-065
P73_2840	hydantoinase B	Bordetella bronchiseptica RB50
P73_2842	LysR family transcriptional regulator	Rhodopseudomonas palustris CGA009
P73_2864	short-chain dehydrogenase/reductase sDR	Rhizobium sp. CF142
P73_2865	short-chain dehydrogenase	Rhizobium sp. CF142
P73_2868	GntR family transcriptional regulator	Rhizobium sp. CF142
P73_2869	putative amidohydrolase	Rhizobium sp. CF142
P73_2870	putative ABC transporter substrate binding protein	Rhizobium sp. CF142
P73_2871	short-chain dehydrogenase/reductase SDR	Rhizobium sp. CF142
P73_2872	ABC transporter	Rhizobium sp. CF142
P73_2873	binding-protein-dependent transporters inner membrane component	Rhizobium sp. CF142

P73_2874	ferredoxin:oxidoreductase FAD/NAD(P)-binding subunit	Rhizobium sp. CF142
P73_2875	Rieske (2Fe-2S) domain-containing protein	Rhizobium sp. CF142
P73_2876	putative amidohydrolase	Rhizobium sp. CF142
P73_2877	GntR family transcriptional regulator	Rhizobium sp. CF142
P73_2878	NIPSNAP family protein	Rhizobium sp. CF142
P73_2879	endoribonuclease L-PSP	Agrobacterium sp. ATCC 31749
P73_2884	Class I triheme cytochrome c	Aurantimonas manganoxydans SI85-9A1
P73_2946	Predicted Zn-dependent protease (DUF2268)	Rhizobium sp. CF142
P73_2973	arylmalonate decarboxylase	Azohydromonas australica DSM 1124
P73_2974	TRAP-type C4-dicarboxylate transport system, periplasmic component	Bordetella petrii Se-1111R, DSM 12804
P73_2977	hydantoinase B	Herbaspirillum sp. YR522
P73_2981	IclR family transcriptional regulator	Cupriavidus basilensis OR16
P73_2982	methanol/ethanol family PQQ-dependent dehydrogenase	Pseudomonas mendocina NK-01
P73_2983	Uncharacterized protein, possibly involved in utilization of glycolate and propanediol	Geodermatophilus obscurus G-20, DSM 43160
P73_2984	bacilysin biosynthesis oxidoreductase BacC	Hoeflea sp. 108
P73_3015	cyclopropane-fatty-acyl-phospholipid synthase	Ochrobactrum intermedium LMG 3301
P73_3091	flavonol synthase/dioxygenase	Agrobacterium vitis S4
P73_3100	D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding protein	Actinopolymorpha alba DSM 45243
P73_3101	2-hydroxy-3-oxopropionate reductase	Martelella mediterranea DSM 17316
P73_3102	hydroxypyruvate isomerase	Rhizobium sp. CF142
P73_3104	binding-protein-dependent transport system inner membrane protein	Rhizobium leguminosarum bv trifolii WSM2297
P73_3105	family 5 extracellular solute-binding protein	Truepera radiovictrix RQ-24, DSM 17093
P73_3106	Uncharacterized protein conserved in bacteria	Actinopolymorpha alba DSM 45243
P73_3107	oligopeptide/dipeptide ABC transporter ATPase	Truepera radiovictrix RQ-24, DSM 17093
P73_3108	oligopeptide/dipeptide ABC transporter ATPase	Truepera radiovictrix RQ-24, DSM 17093
P73_3109	binding-protein-dependent transport systems inner membrane component	Rhizobium leguminosarum bv viciae UPM1131
P73_3110	LacI family transcriptional regulator	Kaistia granuli DSM 23481
P73_3111	aldo-keto reductase	Rhizobium leguminosarum bv trifolii WSM2297
P73_3121	putative hydrolase phosphatase protein	Kaistia granuli DSM 23481

P73_3122	RpiR family transcriptional regulator	Advenella kashmirensis WT001
P73_3123	LacI family transcriptional regulator	Ensifer meliloti 4H41
P73_3125	binding-protein-dependent transport system inner membrane protein	Rhizobium leguminosarum bv. trifolii WSM2304
P73_3127	ABC transporter-like protein	Nitratireductor aquibiodomus RA22 (Draft1)
P73_3131	catalase	Methylobacterium populi BJ001
P73_3132	bacilysin biosynthesis oxidoreductase bacC	Marine gamma proteobacterium sp. HTCC2148
P73_3133	short-chain dehydrogenase/reductase SDR	Rhodopseudomonas palustris BisB5
P73_3134	ABC transporter substrate-binding protein	Oligotropha carboxidovorans OM4
P73_3135	3-oxoacyl-ACP reductase	Bradyrhizobium elkanii USDA 76
P73_3136	glutathione import ATP-binding protein GsiA	Oligotropha carboxidovorans OM4
P73_3137	peptide ABC transporter permease	Oligotropha carboxidovorans OM4
P73_3138	glutathione transport system permease GsiD	Oligotropha carboxidovorans OM4
P73_3139	SnoaL-like domain	Tolumonas auensis TA 4, DSM 9187
P73_3143	polysaccharide deacetylase family protein	Thalassobaculum salexigens DSM 19539
P73_3144	amidase	Aurantimonas manganoxydans SI85-9A1
P73_3145	Transcriptional regulator	Ensifer medicae WSM4191
P73_3147	ABC transporter-like protein	Bradyrhizobium sp. ARR65
P73_3148	binding-protein-dependent transporter inner membrane component	Bradyrhizobium elkanii WSM2783
P73_3149	Predicted flavoprotein involved in K+ transport	Plesiocystis pacifica SIR-1
P73_3150	ring-opening amidohydrolase	Azorhizobium doebereinerae UFLA1-100
P73_3152	Uncharacterized conserved protein	Halomonas anticariensis DSM 16096
P73_3161	acyl-CoA hydrolase	Agrobacterium sp. 224MFTsu3.1
P73_3170	transcriptional regulator	Brucella ovis ATCC 25840
P73_3219	transposase	Bradyrhizobium japonicum USDA 135
P73_3240	phage/plasmid primase, P4 family, C-terminal domain	Ensifer sp. TW10
P73_3242	Helix-turn-helix domain	Marinobacter sp. ELB17
P73_3244	integrase family protein	Methylocaldum szegediense O-12
P73_3257	DNA methyltransferase	Rhodococcus erythropolis PR4
P73_3258	restriction enzyme	Erwinia amylovora Ea273, ATCC 49946
P73_3259	McrBC 5-methylcytosine restriction system component	Streptomyces sp. 351MFTsu5.1
P73_3272	dienelactone hydrolase family protein	Pseudomonas sp. GM79

P73_3333	hypothetical protein	Pelagibacterium halotolerans B2
P73_3335	amine dehydrogenase	Azospirillum halopraeferens DSM 3675
P73_3336	methylamine utilization protein MauD	Pelagibacterium halotolerans B2
P73_3339	transcriptional regulator	Pelagibacterium halotolerans B2
P73_3380	Predicted periplasmic or secreted lipoprotein	Mesorhizobium alhagi CCNWXJ12-2
P73_3381	Uncharacterized conserved protein	Sphingomonas wittichii RW1
P73_3422	exopolysaccharide synthesis, exoD	Salinisphaera shabanensis E1L3A
P73_3461	Membrane proteins related to metalloendopeptidases	Pelagibacterium halotolerans B2
P73_3554	Uncharacterized protein conserved in bacteria, putative lipoprotein	Rhizobium mongolense USDA 1844
P73_3555	EamA-like transporter family	Nisaea denitrificans DSM 18348
P73_3561	Molecular chaperone, HSP90 family	Aromatoleum aromaticum EbN1
P73_3581	putative restriction endonuclease	Microvirga lupini Lut6
P73_3634	putative divalent heavy-metal cations transporter	Citromicrobium sp. JLT1363
P73_3662	extracellular nuclease	Ralstonia eutropha H16
P73_3676	Invasion associated locus B family protein	Bradyrhizobium sp. Cp5.3
P73_3677	serine protease/outer membrane autotransporter	Azohydromonas australica DSM 1124
P73_3679	DNA polymerase LigD polymerase domain-containing protein	Thalassobaculum salexigens DSM 19539
P73_3716	transcriptional regulator	Pseudomonas putida PC9
P73_3717	4-oxalomesaconate hydratase	Amorphus coralli DSM 19760
P73_3720	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases	Amorphus coralli DSM 19760
P73_3721	IclR family transcriptional regulator	Amorphus coralli DSM 19760
P73_3733	carbamate kinase	Martelella mediterranea DSM 17316
P73_3735	arginine deiminase	Arhodomonas aquaeolei DSM 8974
P73_3738	TRAP transporter DctQ-like subunit	Azospirillum brasilense Sp245
P73_3741	LysR family transcription regulator protein	Bradyrhizobium sp. WSM3983
P73_3742	thiamine pyrophosphate TPP-binding domain-containing protein	Streptomyces violaceoruber 3844-33C
P73_3745	TRAP dicarboxylate transporter subunit DctP	Neptuniibacter caesariensis MED92
P73_3746	class III aminotransferase	Roseomonas cervicalis ATCC 49957
P73_3747	Leucine-responsive regulatory protein	Inquilinus limosus DSM 16000
P73_3778	ABC transporter nucleotide binding/ATPase (glycerol-3-phosphate)	Ensifer meliloti 4H41
P73_3779	RpiR family transcriptional regulator	Rhizobium sp. CF142

P73_3780	Uncharacterized protein conserved in bacteria	Microvirga lupini Lut6
P73_3884	Salicylate hydroxylase	Pelagibacterium halotolerans B2
P73_3885	ABC transporter	Pelagibacterium halotolerans B2
P73_3886	ABC-transporter ATP-binding component	Pelagibacterium halotolerans B2
P73_3887	nitrate/sulfonate/bicarbonate ABC transporter permease	Pelagibacterium halotolerans B2
P73_3889	transcriptional regulator, TetR family protein	Pelagibacterium halotolerans B2
P73_3917	GntR family transcriptional regulator	Burkholderia xenovorans LB400
P73_3922	TonB-dependent outermembrane ferripyoverdine receptor FpvA	Pseudomonas chlororaphis chlororaphis GP72 (Draft1)
P73_3924	ECF subfamily RNA polymerase sigma-24 factor	Labrys methylaminiphilus JLW10
P73_3930	curli production assembly/transport component CsgG	Amorphus coralli DSM 19760
P73_3940	dihydroorotate dehydrogenase family protein	Nitratireductor aquibiodomus RA22 (Draft1)
P73_3944	RpiR family transcriptional regulator	Rhizobium sp. CF142
P73_3945	Asp/Glu racemase	Martelella mediterranea DSM 17316
P73_3947	ABC transporter, nucleotide binding/ATPase protein	Rhizobium sp. CF142
P73_3948	binding-protein-dependent transport system inner membrane protein	Rhizobium sp. CF142
P73_3949	ABC transporter, membrane spanning protein	Microvirga lupini Lut6
P73_3952	phosphoenolpyruvate carboxylase	Fulvimarina pelagi HTCC2506
P73_3956	nitrate/nitrite regulatory protein	Mesorhizobium loti USDA 3471
P73_3957	class V aminotransferase	Mesorhizobium loti R7A
P73_3958	citrate lyase beta subunit	Mesorhizobium australicum WSM2073
P73_3959	malate--CoA ligase subunit beta	Mesorhizobium sp. WSM3224
P73_3960	succinyl-CoA synthetase subunit alpha	Rhizobium sp. NGR234 (ANU265)
P73_3961	NAD-binding D-isomer specific 2-hydroxyacid dehydrogenase	Ensifer terangae WSM1721
P73_3962	TetR family transcriptional regulator	Hyphomicrobium sp. MC1
P73_3965	methyltransferase/corrinoid binding protein CmuA	Hyphomicrobium sp. MC1
P73_3967	electron transfer protein PaaE	Hyphomicrobium sp. MC1
P73_3968	imidazolonepropionase	Methylobacterium chloromethanicum CM4
P73_3969	5,10-methylenetetrahydrofolate reductase	Ensifer meliloti 1021
P73_3974	aldo/keto reductase	Rhizobium leguminosarum bv. trifolii WSM597
P73_3975	transcriptional regulator	Frateuria aurantia Kondo 67, DSM 6220
P73_3976	4'-phosphopantetheinyl transferase	Mesorhizobium ciceri WSM4083
P73_3987	ferric siderophore ABC transporter membrane protein	Nisaea denitrificans DSM 18348
P73_3991	Transposase and inactivated derivatives	Microvirga lupini Lut6

P73_4004	Domain of unknown function (DUF4091)	Beutenbergia cavernae HKI 0122, DSM 12333
P73_4005	Predicted membrane protein (DUF2207)	Martelella mediterranea DSM 17316
P73_4006	tripartite ATP-independent periplasmic transporter DctQ component	Achromobacter arsenitoxydans SY8
P73_4007	TRAP dicarboxylate transporter subunit DctP	Spirochaeta smaragdinae SEBR 4228, DSM 11293
P73_4009	FAD dependent oxidoreductase	Acetobacteraceae bacterium AT-5844
P73_4010	LysR family transcriptional regulator	Ensifer medicae WSM419
P73_4011	LysR family transcriptional regulator	Arthrobacter sp. 31Cvi3.1E
P73_4012	dibenzothiophene desulfurziation enzyme	Gordonia alkanivorans NBRC 16433
P73_4013	3-mercaptopyruvate sulfurtransferase	Gordonia paraffinivorans NBRC 108238
P73_4014	amidase	Gordonia alkanivorans NBRC 16433
P73_4015	haloacid dehalogenase domain-containing protein hydrolase	Gordonia paraffinivorans NBRC 108238
P73_4016	endoribonuclease L-PSP	Micromonospora sp. L5
P73_4017	hydroxyethylthiazole kinase	Burkholderia glumae BGR1
P73_4019	LysR family transcriptional regulator	Cupriavidus necator HPC(L)
P73_4021	NADH(P)-binding	Arhodomonas aquaeolei DSM 8974
P73_4023	GntR family transcriptional regulator	Ochrobactrum intermedium LMG 3301
P73_4024	Demethylmenaquinone methyltransferase	Arthrobacter phenanthrenivorans Sphe3
P73_4026	binding-protein-dependent transport systems inner membrane component	Kribbella flavida IFO 14399, DSM 17836
P73_4027	binding-protein-dependent transport systems inner membrane component	Kribbella flavida IFO 14399, DSM 17836
P73_4028	extracellular solute-binding protein family 1 protein	Kribbella flavida IFO 14399, DSM 17836
P73_4029	ribose-5-phosphate isomerase B	Elioraea tepidiphila DSM 17972
P73_4030	LysR family transcriptional regulator	Cupriavidus necator N-1, ATCC 43291
P73_4031	peptide ABC transporter ATP-binding protein	Rhizobium rhizogenes K84
P73_4032	ABC transporter permease	Ensifer meliloti 1021
P73_4033	ABC transporter, membrane spanning protein (peptide)	Agrobacterium tumefaciens C58-UWash
P73_4034	ABC transporter substrate binding protein	Rhizobium leguminosarum bv.

		trifolii CC283b
P73_4035	oligopeptide ABC transporter substrate binding protein	Rhizobium leguminosarum bv viciae UPM1131
P73_4036	aliphatic sulfonates family ABC transporter periplasmic ligand-binding protein	Amycolatopsis thermoflava N1165, DSM 44574
P73_4037	acyl-CoA dehydrogenase	Conexibacter woesei ID131577, DSM 14684
P73_4038	monooxygenase	Bradyrhizobium elkanii USDA 3254
P73_4039	NAD-dependent epimerase/dehydratase	Bordetella petrii Se-1111R, DSM 12804
P73_4040	Gamma-glutamyltranspeptidase protein	Acetobacter aceti ATCC 23746
P73_4041	ABC transporter substrate binding protein	Kaistia adipata DSM 17808
P73_4042	TRAP dicarboxylate transporter subunit DctM	Kaistia granuli DSM 23481
P73_4043	alkanesulfonate monooxygenase	Rhizobium sp. AP16
P73_4044	ABC transporter	Rhizobium sp. AP16
P73_4045	nodulation protein nolR	Agrobacterium sp. 10MFCol1.1
P73_4048	GntR family transcriptional regulator	Cupriavidus taiwanensis LMG 19424
P73_4049	family 5 extracellular solute-binding protein	Starkeya novella DSM 506
P73_4050	binding-protein-dependent transporters inner membrane component	Starkeya novella DSM 506
P73_4052	ABC transporter	Starkeya novella DSM 506
P73_4053	NAD-dependent epimerase/dehydratase	Starkeya novella DSM 506
P73_4059	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase	Martelella mediterranea DSM 17316
P73_4073	taurine catabolism dioxygenase TauD/TfdA	Cupriavidus taiwanensis STM6070
P73_4074	nitrate/sulfonate/bicarbonate ABC transporter ATPase	Variovorax paradoxus 110B
P73_4076	LysR family transcriptional regulator	Bradyrhizobium sp. ARR65
P73_4077	sulfonate/nitrate transporter	Comamonas testosteroni KF-1
P73_4081	binding-protein-dependent transport system inner membrane protein	Burkholderia sp. YI23
P73_4082	putative sulfonate ABC transporter ATP-binding protein	Burkholderia sp. YI23
P73_4083	ABC transporter substrate-binding protein	Mycobacterium smegmatis MC2 155
P73_4084	FMNH2-dependent monooxygenase	Xanthobacter sp. 126
P73_4085	FMN-dependent oxidoreductase, nitrilotriacetate monooxygenase	Streptomyces violaceusniger Tu 4113
P73_4086	putative acyl-CoA dehydrogenase	Burkholderia sp. YI23
P73_4087	putative oxidoreductase	Burkholderia cenocepacia MC0-3
P73_4088	TetR family transcriptional regulator	Pseudomonas sp. Ag1
P73_4090	putative cystine-binding periplasmic protein	Rhizobium etli CFN 42, DSM

		11541
P73_4092	ABC transporter ATPase	Meganema perideroedes DSM 15528
P73_4094	amidohydrolase	Meganema perideroedes DSM 15528
P73_4095	flavin-dependent oxidoreductase	Meganema perideroedes DSM 15528
P73_4096	luciferase-like monooxygenase superfamily protein	Meganema perideroedes DSM 15528
P73_4098	pyridoxamine 5'-phosphate oxidase	Agrobacterium sp. H13-3
P73_4099	twin-arginine translocation pathway signal	Chelativorans sp. BNC1
P73_4100	transcriptional regulator	Inquilinus limosus DSM 16000
P73_4102	transcriptional regulator, RpiR family	Hoeflea sp. 108
P73_4103	transport protein	Elioraea tepidiphila DSM 17972
P73_4104	TRAP-type transport system, small permease	Elioraea tepidiphila DSM 17972
P73_4107	hydantoin racemase	Cupriavidus basilensis OR16
P73_4108	short-chain dehydrogenase/reductase SDR	Mycobacterium chubuense NBB4
P73_4109	Tripartite tricarboxylate transporter TctB family	Burkholderia sp. WSM2232
P73_4111	Uncharacterized protein conserved in bacteria	Pelagibacterium halotolerans B2
P73_4113	Blr3415 protein	Cupriavidus necator N-1, ATCC 43291
P73_4117	NMT1/THI5 like domain-containing protein	Mesorhizobium opportunistum WSM2075 (final version from ORNL)
P73_4142	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase	Elioraea tepidiphila DSM 17972
P73_4143	hypothetical protein	Fischerella sp. PCC 9605
P73_4145	siderophore-interacting protein	Halomonas elongata DSM 2581
P73_4147	Fe3+ siderophore ABC transporter permease	Halomonas zhanjiangensis DSM 21076
P73_4148	transport system permease	Halomonas zhanjiangensis DSM 21076
P73_4314	glycosyl transferase family protein	Lysobacter defluvii DSM 18482
P73_4315	UDP-N-acetylenolpyruvoylglucosamine reductase	Martelella mediterranea DSM 17316
P73_4355	hypothetical protein	Halomonas lutea DSM 23508
P73_4376	alcohol dehydrogenase GroES domain-containing protein	Phyllobacterium sp. YR531
P73_4393	MarR family transcriptional regulator	Rhizobium leguminosarum bv viciae WSM1481
P73_4407	DNA-binding transcriptional activator MhpR	Pelagibacterium halotolerans B2
P73_4408	oxidoreductase	Duganella violaceinigra DSM 15887
P73_4409	ABC transporter permease	Mesorhizobium ciceri WSM4083

P73_4410	ABC transporter substrate-binding protein	Mesorhizobium ciceri CMG6
P73_4412	hypothetical protein	Martelella mediterranea DSM 17316
P73_4424	6-phosphogluconate dehydrogenase	Vulcanisaeta distributa DSM 14429
P73_4425	6-phosphogluconate dehydrogenase	Burkholderia sp. JPY347
P73_4427	6-phosphogluconate dehydrogenase	Burkholderia sp. JPY347
P73_4428	3-hydroxyisobutyrate dehydrogenase	Natranaerobius thermophilus JW/NM-WN-LF
P73_4429	enoyl-CoA hydratase/isomerase	Verminephrobacter eiseniae EF01-2
P73_4430	oxidoreductase, short-chain dehydrogenase/reductase	Bordetella petrii Se-1111R, DSM 12804
P73_4432	Predicted metal-dependent hydrolase of the TIM-barrel fold	Bradyrhizobium sp. th.b2
P73_4433	binding-protein-dependent transport system inner membrane protein	Chelativorans sp. BNC1
P73_4434	ABC transporter	Nitratireductor pacificus pht-3B
P73_4437	short chain dehydrogenase	Frankia sp. QA3
P73_4440	amino acid ABC transporter ATP-binding protein	Microvirga lupini Lut6
P73_4442	putative branched-chain amino acid ABC transporter, periplasmic component	Azospirillum lipoferum 4B
P73_4443	amidohydrolase 2	Delftia sp. Cs1-4
P73_4445	Uncharacterized conserved protein	Amycolatopsis taiwanensis DSM 45107
P73_4446	cupin	Methylobacterium nodulans ORS 2060
P73_4447	3-hydroxyacyl-CoA dehydrogenase	Chelativorans sp. BNC1
P73_4448	zinc-binding alcohol dehydrogenase	Chelativorans sp. BNC1
P73_4449	3-hydroxyacyl-CoA dehydrogenase	Chelativorans sp. BNC1
P73_4450	acyl-CoA dehydrogenase	Chelativorans sp. BNC1
P73_4451	short-chain dehydrogenase/reductase SDR	Chelativorans sp. BNC1
P73_4452	short chain enoyl-CoA hydratase	Chelativorans sp. BNC1
P73_4453	AMP-dependent synthetase and ligase	Chelativorans sp. BNC1
P73_4454	1,4-dihydroxy-2-naphthoate synthase	Chelativorans sp. BNC1
P73_4455	zinc-binding dehydrogenase family protein 6	Achromobacter arsenitoxydans SY8
P73_4458	carbon-monoxide dehydrogenase small subunit	Ensifer fredii HH103
P73_4460	acetyl coenzyme A synthetase	Amorphus coralli DSM 19760
P73_4462	6-phosphogluconate dehydrogenase	Azohydromonas australica DSM 1124
P73_4463	acyl-CoA dehydrogenase yngJ	Elioraea tepidiphila DSM 17972
P73_4465	2-methylcitrate dehydratase	Candidatus Nitrospira defluvii
P73_4469	TRAP-type C4-dicarboxylate transport system, small	Tistrella mobilis KA081020-065

	permease component	
P73_4470	TRAP-T family protein transporter, DctP (Periplasmic binding) subunit	Alcanivorax dieselolei B5
P73_4471	GMC oxidoreductase family protein 5	Achromobacter xylosoxidans A8
P73_4473	carbon monoxide dehydrogenase	Elioraea tepidiphila DSM 17972
P73_4474	naphthoate synthase	Acidovorax sp. JHL-9
P73_4477	3-hydroxyacyl-CoA dehydrogenase	Chelativorans sp. BNC1
P73_4478	acyl-CoA dehydrogenase	Chelativorans sp. BNC1
P73_4479	short-chain dehydrogenase/reductase SDR	Chelativorans sp. BNC1
P73_4480	short chain enoyl-CoA hydratase	Chelativorans sp. BNC1
P73_4481	AMP-dependent synthetase and ligase	Chelativorans sp. BNC1
P73_4482	1,4-dihydroxy-2-naphthoate synthase	Chelativorans sp. BNC1
P73_4483	L-carnitine dehydratase/bile acid-inducible protein F	Chelativorans sp. BNC1
P73_4484	amidohydrolase 2	Delftia sp. Cs1-4
P73_4485	acyl-CoA dehydrogenase yngJ	Salinisphaera shabanensis E1L3A
P73_4486	thiolase	Bordetella petrii Se-1111R, DSM 12804
P73_4488	enoyl-CoA hydratase	Chelativorans sp. BNC1
P73_4492	putative alcohol dehydrogenase	Rhizobium leguminosarum bv. viciae Vh3
P73_4493	aldehyde dehydrogenase	Variovorax paradoxus 4MFCol3.1
P73_4496	oxidoreductase, short-chain dehydrogenase/reductase	Bordetella petrii Se-1111R, DSM 12804
P73_4500	Predicted metal-dependent hydrolase of the TIM-barrel fold	Acidovorax delafieldii 2AN
P73_4502	putative aldehyde dehydrogenase	Rhizobium leguminosarum bv viciae 128C53
P73_4521	(2Fe-2S)-binding domain-containing protein	Novosphingobium sp. PP1Y
P73_4522	aldehyde oxidase and xanthine dehydrogenase molybdopterin binding protein	Rhizobium tropici CIAT899
P73_4560	TIR protein	Rhodopseudomonas palustris TIE-1
P73_4701	hypothetical protein	Desulfomonile tiedjei DCB-1, DSM 6799
P73_4750	salicylate esterase	Acinetobacter baylyi ADP1
P73_4756	transcriptional regulator	Methylobacterium sp. WSM2598
P73_4757	putative oxidoreductase	Bradyrhizobium sp. Ai1a-2
P73_4763	cytochrome P450	Novosphingobium aromaticivorans DSM 12444
P73_4764	AraC family transcriptional regulator	Azospirillum brasilense Sp245
P73_4765	TRAP dicarboxylate transporter subunit DctM	Pelagibacterium halotolerans B2
P73_4766	TRAP dicarboxylate transporter subunit DctQ	Pelagibacterium halotolerans B2
P73_4767	TRAP transporter solute receptor	Pelagibacterium halotolerans B2
P73_4768	alcohol dehydrogenase	Microvirga lupini Lut6

P73_4797	plasmid replication initiator	Acetobacter aceti ATCC 23746
P73_4800	T/G mismatch-specific endonuclease	Chlorobium phaeobacteroides DSM 266
P73_4801	hypothetical protein	Asticcacaulis excentricus CB 48
P73_4802	hypothetical protein	Methylobacterium populi BJ001
P73_4804	DNA-cytosine methyltransferase	Erythrobacter sp. NAP1
P73_4808	ATPase domain-containing protein	Escherichia coli LF82
P73_4817	replicase	Sphingobium yanoikuyae JCM 7371 plasmid pYAN-1
P73_4818	putative site-specific recombinase-resolvase	Salinarimonas rosea DSM 21201

Sheet 2 (Excel)

COG	Gene count	% of Total
R	105	13.3%
P	96	**12.1%**
K	90	**11.4%**
E	85	10.7%
G	77	**9.7%**
C	63	**8.0%**
I	51	**6.4%**
Q	51	**6.4%**
S	38	4.8%
L	26	3.3%
H	24	3.0%
M	19	2.4%
U	19	2.4%
O	15	1.9%
V	10	1.3%
F	7	0.9%
T	7	0.9%
J	5	0.6%
D	2	0.3%
N	2	0.3%
Total	792	

Data S4 | Transport protein genes in the *Celeribacter indicus* P73^T genome identified in the Transporter Classification (TC) Database. Transport protein genes predicted in the TC database (http://tcdb.org, 11 October 2013).

Locus Tag	Product Name	Func ID

P73_0004	amino acid transporter LysE	TC:2.A.76
P73_0014	ABC-2 type transporter	TC:3.A.1
P73_0015	Capsule polysaccharide export protein	TC:8.A.4
P73_0016	hypothetical protein	TC:3.A.1
P73_0018	ABC transporter related protein	TC:3.A.1
P73_0022	sulfate permease	TC:2.A.53
P73_0030	YGGT family	TC:9.A.4
P73_0037	Predicted permeases	TC:9.A.29
P73_0050	glutamine ABC transporter substrate-binding protein	TC:1.A.10
P73_0061	mechanosensitive ion channel MscS	TC:1.A.23
P73_0065	Uncharacterized conserved protein	TC:9.B.36
P73_0072	Permeases of the drug/metabolite transporter (DMT) superfamily	TC:2.A.7
P73_0081	Extracellular solute-binding protein, ABC transporter	TC:3.A.1
P73_0082	ABC-type spermidine/putrescine transport systems, ATPase component	TC:3.A.1
P73_0092	H+-transporting two-sector ATPase, alpha/beta subunit	TC:3.A.2
P73_0096	flagellar biosynthetic protein FliQ	TC:3.A.6
P73_0103	flagellar biosynthesis protein FlhB	TC:3.A.6
P73_0104	flagellar biosynthetic protein FliR	TC:3.A.6
P73_0105	flagellar biosynthesis protein FlhA	TC:3.A.6
P73_0107	flagellar motor protein MotA	TC:1.A.30
P73_0111	flagellar MS-ring protein	TC:3.A.6
P73_0113	flagellar motor switch protein FliN	TC:3.A.6
P73_0114	flagellar biosynthesis protein FliP	TC:3.A.6
P73_0119	chemotaxis MotB protein	TC:1.A.30
P73_0124	ammonium transporter	TC:1.A.11
P73_0138	ABC transporter substrate-binding protein	TC:3.A.1
P73_0154	Uncharacterized protein conserved in bacteria	TC:2.A.80
P73_0156	Uncharacterized protein conserved in bacteria	TC:2.A.80
P73_0158	FAD-binding dehydrogenase	TC:5.A.4
P73_0171	putative TRAP-type C4-dicarboxylate transport system large permease	TC:2.A.56
P73_0172	TRAP dicarboxylate transporter subunit DctQ	TC:2.A.56
P73_0173	TRAP dicarboxylate transporter subunit DctP	TC:2.A.56
P73_0178	TRAP transporter, 4TM/12TM fusion protein	TC:2.A.56
P73_0179	TRAP transporter solute receptor, TAXI family protein	TC:2.A.56
P73_0180	long-chain-fatty-acid-CoA ligase	TC:4.C.1
P73_0184	putative fatty acid/hydrocarbon transporter	TC:1.B.9
P73_0201	Uncharacterized protein conserved in bacteria	TC:3.A.8
P73_0209	transcription termination factor Rho	TC:3.A.2
P73_0229	sugar ABC transporter	TC:3.A.1
P73_0230	ribose ABC transporter substrate-binding protein	TC:3.A.1
P73_0231	ribose ABC transporter	TC:3.A.1
P73_0264	preprotein translocase subunit SecA	TC:3.A.5
P73_0269	molecular chaperone DnaK	TC:1.A.33

P73_0271	ABC transporter permease	TC:3.A.1
P73_0282	ABC transporter	TC:3.A.1
P73_0283	OstA family protein	TC:1.B.42
P73_0294	Permeases of the drug/metabolite transporter (DMT) superfamily	TC:2.A.7
P73_0303	Putative permease of the major facilitator superfamily MFS1	TC:2.A.1
P73_0321	ABC transporter	TC:3.A.1
P73_0322	thiamine transporter membrane protein	TC:3.A.1
P73_0323	thiamine-binding periplasmic protein	TC:3.A.1
P73_0324	sodium:dicarboxylate symporter	TC:2.A.23
P73_0338	long-chain-fatty-acid--CoA ligase	TC:4.C.1
P73_0342	family 7 extracellular solute-binding protein	TC:2.A.56
P73_0343	TRAP dicarboxylate transporter subunit DctQ	TC:2.A.56
P73_0344	TRAP C4-dicarboxylate transporter permease DctM	TC:2.A.56
P73_0355	OmpW family protein	TC:1.B.39
P73_0378	TRAP-type C4-dicarboxylate transport system, large permease component	TC:2.A.56
P73_0403	secreted periplasmic protein	TC:1.B.42
P73_0418	DNA transclocase FtsK	TC:3.A.12
P73_0419	outer membrane lipoprotein carrier protein LolA	TC:1.B.46
P73_0421	membrane transport-like protein	TC:2.A.69
P73_0429	Sodium/proline symporter	TC:2.A.21
P73_0453	Arabinose efflux permease	TC:2.A.1
P73_0457	SPFH domain, Band 7 family protein	TC:8.A.21
P73_0466	sulfite oxidase subunit YedZ	TC:5.B.1
P73_0466	sulfite oxidase subunit YedZ	TC:9.B.43
P73_0471	P-type ATPase, translocating	TC:3.A.3
P73_0496	inner-membrane translocator	TC:3.A.1
P73_0497	ABC transporter substrate-binding protein	TC:3.A.1
P73_0498	ABC transporter	TC:3.A.1
P73_0500	ribose ABC transporter ATP-binding protein	TC:3.A.1
P73_0503	putative periplasmic substrate binding protein	TC:2.A.56
P73_0504	TRAP-type C4-dicarboxylate transport system small permease	TC:2.A.56
P73_0505	TRAP dicarboxylate transporter	TC:2.A.56
P73_0510	MotA/TolQ/ExbB proton channel	TC:1.A.30
P73_0511	biopolymer transport protein ExbD/TolR	TC:1.A.30
P73_0512	biopolymer transport protein	TC:1.A.30
P73_0517	polysaccharide synthesis/modification protein	TC:9.A.41
P73_0533	Uncharacterized conserved protein	TC:2.A.89
P73_0536	transporter, MFS family protein	TC:2.A.1
P73_0556	Small-conductance mechanosensitive channel	TC:1.A.23
P73_0561	type I secretion membrane fusion protein	TC:8.A.1
P73_0562	type I secretion system ATPase	TC:3.A.1
P73_0567	ammonium transporter	TC:1.A.11
P73_0574	Permeases of the drug/metabolite transporter (DMT) superfamily	TC:2.A.7

P73_0579	LrgA family protein	TC:1.E.14
P73_0595	Predicted membrane protein	TC:1.A.62
P73_0597	lysine exporter protein LysE/YggA	TC:2.A.76
P73_0613	Predicted permeases	TC:9.A.29
P73_0619	PTS system mannose-specific EIIA component-like protein	TC:4.A.6
P73_0635	preprotein translocase subunit SecE	TC:3.A.5
P73_0656	voltage-gated sodium channel	TC:1.A.1
P73_0673	preprotein translocase subunit SecY	TC:3.A.5
P73_0682	camphor resistance protein CrcB	TC:9.B.71
P73_0686	glutamate/glutamine/aspartate/asparagine-binding protein BztA	TC:3.A.1
P73_0687	glutamate/glutamine/aspartate/asparagine ABC transporter permease	TC:3.A.1
P73_0688	amino acid ABC transporter permease	TC:3.A.1
P73_0689	ABC transporter	TC:3.A.1
P73_0693	membrane protein insertase	TC:3.A.5
P73_0703	polysaccharide export protein, translocase	TC:2.A.66
P73_0728	EmrB/QacA family drug resistance transporter	TC:2.A.1
P73_0729	multidrug resistance protein K	TC:8.A.1
P73_0747	signal recognition particle protein	TC:3.A.5
P73_0750	EamA-like transporter family	TC:2.A.7
P73_0753	F0F1 ATP synthase subunit A	TC:3.A.2
P73_0754	F0F1 ATP synthase subunit C	TC:3.A.2
P73_0755	F0F1 ATP synthase subunit B'	TC:3.A.2
P73_0756	F0F1 ATP synthase subunit B	TC:3.A.2
P73_0769	ABC transporter ATP-binding protein	TC:3.A.1
P73_0775	cation efflux system protein	TC:2.A.4
P73_0801	phosphonate ABC transporter ATP-binding protein	TC:3.A.1
P73_0802	phosphate uptake ABC transporter periplasmic solute-binding protein	TC:3.A.1
P73_0803	phosphonate ABC transporter permease	TC:3.A.1
P73_0804	phosphonate ABC transporter permease	TC:3.A.1
P73_0813	phosphonate C-P lyase system protein PhnK	TC:3.A.1
P73_0814	Fis family transcriptional regulator	TC:1.A.35
P73_0815	phosphonates transport ATP-binding protein PhnL	TC:3.A.1
P73_0826	ABC transporter-like protein	TC:3.A.1
P73_0827	Formate/nitrite family of transporters	TC:2.A.44
P73_0851	ABC transporter	TC:3.A.1
P73_0852	ABC transporter ATP-binding protein	TC:3.A.1
P73_0854	ABC transporter	TC:3.A.1
P73_0859	phosphate transporter	TC:2.A.20
P73_0862	cation transporter	TC:2.A.38
P73_0900	MATE efflux family protein	TC:2.A.66
P73_0925	AMP-binding domain protein	TC:4.C.1
P73_0929	ABC transporter ATP-binding protein/permease	TC:3.A.1
P73_0930	glycine betaine ABC transporter substrate-binding protein	TC:3.A.1

P73_0931	permease	TC:3.A.1
P73_0932	ABC transporter permease	TC:3.A.1
P73_0965	transmembrane protein	TC:9.A.29
P73_0981	conjugal transfer coupling protein TraG	TC:3.A.7
P73_0985	conjugal transfer protein TrbC	TC:3.A.7
P73_0986	conjugal transfer protein TrbB	TC:3.A.7
P73_0987	conjugal transfer ATPase TrbE	TC:3.A.7
P73_0990	conjugal transfer protein TrbL	TC:3.A.7
P73_0991	conjugal transfer protein TrbF	TC:3.A.7
P73_0992	P-type conjugative transfer protein TrbG	TC:3.A.7
P73_0993	conjugation TrbI family protein	TC:3.A.7
P73_1003	disulfide bond formation-like protein	TC:5.A.2
P73_1006	heavy metal translocating P-type ATPase	TC:3.A.3
P73_1008	cobalt-zinc-cadmium resistance protein CzcD	TC:2.A.4
P73_1013	cysteine ABC transporter ATP-binding protein/permease CydD	TC:3.A.1
P73_1014	manganese transport protein MntH	TC:2.A.55
P73_1034	iron siderophore/cobalamin ABC transporter ATP-binding protein	TC:3.A.1
P73_1035	iron siderophore/cobalamin ABC transporter permease	TC:3.A.1
P73_1036	iron siderophore/cobalamin ABC transporter periplasmic iron siderophore/cobalamin-binding protein	TC:3.A.1
P73_1039	binding-protein-dependent transporter inner membrane component	TC:3.A.1
P73_1040	ABC transporter	TC:3.A.1
P73_1044	EmrB/QacA family drug resistance transporter	TC:2.A.1
P73_1045	oligopeptide ABC transporter oligopeptide-binding protein	TC:3.A.1
P73_1046	ABC transporter ATP-binding protein	TC:3.A.1
P73_1047	peptide ABC transporter permease	TC:3.A.1
P73_1048	binding-protein-dependent transport systems inner membrane component	TC:3.A.1
P73_1057	TRAP-type C4-dicarboxylate transport system, periplasmic component	TC:2.A.56
P73_1059	ABC transporter	TC:3.A.1
P73_1062	extracellular solute-binding protein	TC:3.A.1
P73_1063	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_1067	ABC transporter ATPase	TC:3.A.1
P73_1068	ABC transporter	TC:3.A.1
P73_1070	ABC transporter substrate-binding protein	TC:3.A.1
P73_1078	ABC transporter-like protein	TC:3.A.1
P73_1079	phosphonate C-P lyase system protein, PhnL	TC:3.A.1
P73_1081	phosphonate/organophosphate ester transporter subunit	TC:3.A.1
P73_1082	ABC transporter, phosphonate, periplasmic substrate-binding protein phnD	TC:3.A.1
P73_1083	phosphonate ABC transporter inner membrane subunit	TC:3.A.1
P73_1084	phosphonate ABC transporter inner membrane subunit	TC:3.A.1
P73_1086	Predicted permeases	TC:9.B.28
P73_1092	Mn+2/Fe+2 ABC transporter substrate-binding protein SitA	TC:3.A.1
P73_1093	Mn+2/Fe+2 ABC transporter ATPase SitB	TC:3.A.1

P73_1094	ABC-3 protein	TC:3.A.1
P73_1095	Mn+2/Fe+2 ABC transporter inner membrane protein SitD	TC:3.A.1
P73_1097	heme receptor	TC:1.B.14
P73_1101	ABC transporter	TC:3.A.1
P73_1102	ABC transporter	TC:3.A.1
P73_1103	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_1104	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_1105	extracellular solute-binding protein	TC:3.A.1
P73_1114	protein secretion protein	TC:8.A.1
P73_1115	hydrophobe/amphiphile efflux-1 (HAE1) family transporter	TC:2.A.6
P73_1123	transporter	TC:2.A.47
P73_1124	ABC transporter	TC:3.A.1
P73_1126	aliphatic sulfonate ABC transporter permease	TC:3.A.1
P73_1132	sodium-dependent inorganic phosphate (Pi) transporter	TC:2.A.58
P73_1135	sulfate ABC transporter inner membrane subunit CysT	TC:3.A.1
P73_1137	sulfate ABC transporter ATPase	TC:3.A.1
P73_1140	sulfate ABC transporter ATPase	TC:3.A.1
P73_1143	sulfate ABC transporter, inner membrane subunit CysT	TC:3.A.1
P73_1144	sulfate adenylyltransferase	TC:3.A.1
P73_1150	ectoine/hydroxyectoine ABC transporter substrate-binding protein	TC:3.A.1
P73_1151	ectoine/hydroxyectoine ABC transporter permease EhuC	TC:3.A.1
P73_1152	amino acid ABC transporter permease	TC:3.A.1
P73_1153	ectoine/hydroxyectoine ABC transporter ATP- binding protein	TC:3.A.1
P73_1167	putative polysaccharide biosynthesis/export protein	TC:1.B.18
P73_1181	major facilitator superfamily protein	TC:2.A.1
P73_1192	MotA/TolQ/ExbB proton channel	TC:1.A.30
P73_1193	biopolymer transport protein ExbD/TolR	TC:1.A.30
P73_1215	Outer membrane general secretion pathway protein, secretin	TC:1.B.22
P73_1244	sulfate transporter	TC:2.A.53
P73_1256	ACR3 family arsenite efflux pump	TC:2.A.59
P73_1259	TolC family type I secretion outer membrane protein	TC:1.B.17
P73_1269	efflux ABC transporter transmembrane ATP-binding protein	TC:3.A.1
P73_1282	rhomboid family protein	TC:3.A.1
P73_1296	major facilitator superfamily protein	TC:2.A.1
P73_1303	major facilitator transporter	TC:2.A.1
P73_1322	hemolysin	TC:9.A.40
P73_1327	Uncharacterized protein conserved in bacteria	TC:2.A.7
P73_1343	major facilitator superfamily protein	TC:2.A.1
P73_1345	zinc (Zn2+)-iron permease family metal cation transporter	TC:2.A.5
P73_1352	phage head morphogenesis domain-containing protein	TC:9.B.78
P73_1364	ribose ABC transporter periplasmic binding protein	TC:3.A.1
P73_1365	ABC transporter	TC:3.A.1
P73_1366	ribose ABC transporter permease	TC:3.A.1

P73_1368	glycerol-3-phosphate transporter ATP-binding subunit	TC:3.A.1
P73_1369	binding-protein-dependent transport systems inner membrane component	TC:3.A.1
P73_1370	ABC transporter permease	TC:3.A.1
P73_1371	ABC transporter substrate binding protein	TC:3.A.1
P73_1378	TRAP transporter solute receptor subunit DctP family protein 7	TC:2.A.56
P73_1379	C4-dicarboxylate transport system (Permease small protein)	TC:2.A.56
P73_1380	C4-dicarboxylate transport system (Permease large protein)	TC:2.A.56
P73_1391	DctP	TC:2.A.56
P73_1392	tripartite ATP-independent periplasmic transporter DctQ	TC:2.A.56
P73_1393	TRAP dicarboxylate transporter subunit DctM	TC:2.A.56
P73_1408	HlyD family secretion protein	TC:8.A.1
P73_1436	ABC-type Fe3+ transport system, substrate binding component	TC:3.A.1
P73_1437	spermidine/putrescine ABC transporter ATPase	TC:3.A.1
P73_1438	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_1440	ABC transporter-like protein	TC:3.A.1
P73_1441	binding-protein-dependent transporter inner membrane component	TC:3.A.1
P73_1458	TRAP dicarboxylate transporter subunit DctM	TC:2.A.56
P73_1459	TRAP-type C4-dicarboxylate transport system, small permease component	TC:2.A.56
P73_1460	TRAP dicarboxylate transporter subunit DctP	TC:2.A.56
P73_1464	TRAP-type C4-dicarboxylate transporter periplasmic protein	TC:2.A.56
P73_1465	TRAP-type C4-dicarboxylate transport system, small permease component	TC:2.A.56
P73_1466	TRAP dicarboxylate transporter	TC:2.A.56
P73_1468	feruloyl-CoA synthase	TC:4.C.1
P73_1471	cobalt transport protein	TC:3.A.1
P73_1472	ABC transporter	TC:3.A.1
P73_1473	BioY protein	TC:2.A.88
P73_1506	OmpW family protein	TC:1.B.39
P73_1519	Predicted membrane protein	TC:2.A.7
P73_1520	Integral membrane protein, interacts with FtsH	TC:9.B.24
P73_1529	magnesium transporter	TC:9.A.19
P73_1532	Di- and tricarboxylate transporters	TC:2.A.47
P73_1535	L-lysine exporter	TC:2.A.75
P73_1536	Predicted permease, DMT superfamily	TC:2.A.7
P73_1539	citrate transporter	TC:2.A.47
P73_1546	formate dehydrogenase subunit alpha	TC:5.A.3
P73_1562	integral membrane protein, MarC family	TC:2.A.95
P73_1582	cytochrome c-type biogenesis protein CcmF	TC:9.B.14
P73_1597	C4-dicarboxylate-binding periplasmic protein DctP	TC:2.A.56
P73_1598	tripartite ATP-independent periplasmic transporter DctQ	TC:2.A.56
P73_1599	TRAP C4-dicarboxylate transport system permease DctM	TC:2.A.56
P73_1604	Predicted permeases	TC:2.A.7
P73_1610	Uncharacterized protein conserved in bacteria	TC:9.B.22
P73_1612	major facilitator superfamily protein	TC:2.A.1

P73_1623	protein translocase subunit yajC	TC:3.A.5
P73_1623	protein translocase subunit yajC	TC:9.B.18
P73_1624	preprotein translocase subunit SecD	TC:2.A.6
P73_1626	cytochrome c biogenesis protein CcmA	TC:3.A.1
P73_1627	heme exporter protein CcmB	TC:3.A.1
P73_1628	heme exporter protein CcmC	TC:9.B.14
P73_1636	Permeases of the drug/metabolite transporter (DMT) superfamily	TC:2.A.7
P73_1652	oligopeptide ABC transporter substrate binding protein	TC:3.A.1
P73_1653	dipeptide ABC transporter permease	TC:3.A.1
P73_1654	dipeptide ABC transporter	TC:3.A.1
P73_1655	peptide ABC transporter ATP-binding protein	TC:3.A.1
P73_1656	ABC transporter	TC:3.A.1
P73_1661	rhamnose ABC transporter periplasmic rhamnose-binding protein RhaS	TC:3.A.1
P73_1662	ribose import ATP-binding protein	TC:3.A.1
P73_1663	putative-binding-protein-dependent transport system permease	TC:3.A.1
P73_1664	sugar ABC transporter permease	TC:3.A.1
P73_1681	ion transport 2 family protein	TC:1.A.1
P73_1719	Permeases of the drug/metabolite transporter (DMT) superfamily	TC:2.A.7
P73_1722	sodium/proton antiporter, CPA1 family (TC 2.A.36)	TC:2.A.36
P73_1744	cytochrome c-type biogenesis protein CcdA	TC:5.A.1
P73_1748	mechanosensitive ion channel protein MscS	TC:1.A.23
P73_1755	conjugation TrbI family protein	TC:3.A.7
P73_1756	P-type conjugative transfer protein TrbG	TC:3.A.7
P73_1757	conjugal transfer protein TrbF	TC:3.A.7
P73_1758	conjugal transfer protein TrbL	TC:3.A.7
P73_1761	conjugal transfer ATPase TrbE	TC:3.A.7
P73_1762	conjugal transfer protein TrbB	TC:3.A.7
P73_1763	conjugal transfer protein TrbC	TC:3.A.7
P73_1766	conjugal transfer coupling protein TraG	TC:3.A.7
P73_1769	multidrug resistance protein A	TC:8.A.1
P73_1770	major facilitator transporter	TC:2.A.1
P73_1798	SMC protein, N-terminal domain-containing protein	TC:3.A.1
P73_1871	SMC protein, N-terminal domain-containing protein	TC:3.A.1
P73_1935	heavy metal translocating P-type ATPase	TC:3.A.3
P73_1948	ABC transporter	TC:3.A.1
P73_1949	nitrate/sulfonate/bicarbonate ABC transporter permease	TC:3.A.1
P73_1950	ABC transporter-like protein permease	TC:3.A.1
P73_1974	Predicted permease	TC:2.A.86
P73_1985	TRAP dicarboxylate transporter, DctP subunit	TC:2.A.56
P73_1986	tripartite ATP-independent periplasmic transporter DctQ	TC:2.A.56
P73_1987	TRAP dicarboxylate transporter, DctM subunit	TC:2.A.56
P73_1997	glutathione ABC transporter permease GsiC	TC:3.A.1
P73_1998	binding-protein-dependent transport system inner membrane protein	TC:3.A.1

P73_1999	extracellular solute-binding protein	TC:3.A.1
P73_2000	major facilitator superfamily transporter	TC:2.A.1
P73_2001	ABC transporter nucleotide binding/ATPase protein	TC:3.A.1
P73_2007	biotin sulfoxide reductase	TC:5.A.3
P73_2010	transmembrane protein	TC:2.A.80
P73_2013	Uncharacterized protein conserved in bacteria	TC:2.A.80
P73_2015	EmrB/QacA subfamily drug resistance transporter	TC:2.A.1
P73_2025	ABC transporter	TC:3.A.1
P73_2026	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_2027	iron(III) ABC transporter iron (III)-binding protein	TC:3.A.1
P73_2035	aliphatic sulfonates transporter ATP-binding protein SsuB	TC:3.A.1
P73_2036	ABC transporter permease	TC:3.A.1
P73_2039	ATPase, E1-E2 type	TC:3.A.3
P73_2043	ABC transporter substrate-binding protein	TC:3.A.1
P73_2044	ABC transporter substrate-binding protein	TC:3.A.1
P73_2047	ABC transporter substrate-binding protein	TC:3.A.1
P73_2048	ABC transporter	TC:3.A.1
P73_2049	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_2050	TRAP dicarboxylate transporter subunit DctP	TC:2.A.56
P73_2051	TRAP-type C4-dicarboxylate transport system, small permease component	TC:2.A.56
P73_2052	TRAP dicarboxylate transporter subunit DctM	TC:2.A.56
P73_2055	polar amino acid ABC transporter inner membrane subunit	TC:3.A.1
P73_2056	polar amino acid ABC transporter inner membrane subunit	TC:3.A.1
P73_2057	ABC transporter	TC:3.A.1
P73_2058	extracellular solute-binding protein	TC:3.A.1
P73_2070	ABC transporter substrate-binding protein	TC:2.A.56
P73_2071	TRAP transport system, small permease protein	TC:2.A.56
P73_2072	TRAP transporter, DctM subunit	TC:2.A.56
P73_2079	aliphatic sulfonate ABC transporter permease	TC:3.A.1
P73_2080	ABC transporter-like protein	TC:3.A.1
P73_2082	taurine transport system permease	TC:3.A.1
P73_2083	taurine transporter ATP-binding subunit	TC:3.A.1
P73_2084	taurine ABC transporter periplasmic binding protein	TC:3.A.1
P73_2088	TRAP-type mannitol/chloroaromatic compound transport system, small permease component	TC:2.A.56
P73_2089	TRAP dicarboxylate transporter subunit DctM	TC:2.A.56
P73_2090	TRAP dicarboxylate transporter- DctP subunit	TC:2.A.56
P73_2096	TRAP dicarboxylate transporter subunit DctM	TC:2.A.56
P73_2097	TRAP dicarboxylate transporter subunit DctQ	TC:2.A.56
P73_2098	putative periplasmic substrate binding protein	TC:2.A.56
P73_2103	ABC transporter	TC:3.A.1
P73_2104	transport system permease	TC:3.A.1
P73_2105	periplasmic binding protein	TC:3.A.1

P73_2110	TRAP dicarboxylate transporter subunit DctQ	TC:2.A.56
P73_2111	TRAP transporter, DctM subunit subfamily protein	TC:2.A.56
P73_2112	TRAP transporter-DctP subunit	TC:2.A.56
P73_2114	TonB-dependent receptor precursor	TC:1.B.14
P73_2117	FAD-dependent pyridine nucleotide-disulfide oxidoreductase	TC:5.A.4
P73_2119	ABC-type nitrate/sulfonate/bicarbonate transport system, ATPase component	TC:3.A.1
P73_2120	ABC transporter permease	TC:3.A.1
P73_2122	drug resistance transporter, EmrB/QacA subfamily protein	TC:2.A.1
P73_2124	C4-dicarboxylate transport system permease large protein	TC:2.A.56
P73_2125	Sialic acid TRAP transporter permease protein siaT	TC:2.A.56
P73_2126	C4-dicarboxylate transport system	TC:2.A.56
P73_2129	putative amino-acid ABC transporter, periplasmic solute-binding protein	TC:3.A.1
P73_2130	amino-acid ABC transporter, permease protein	TC:3.A.1
P73_2131	putative amino-acid ABC transporter, ATP-binding protein	TC:3.A.1
P73_2135	NitT/TauT family transport system ATP-binding protein	TC:3.A.1
P73_2136	NitT/TauT family transport system permease protein	TC:3.A.1
P73_2140	ABC transporter ATP-binding protein	TC:3.A.1
P73_2141	ABC transporter membrane subunit	TC:3.A.1
P73_2148	ABC transporter	TC:3.A.1
P73_2149	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_2158	membrane protein	TC:9.A.29
P73_2160	extracellular solute-binding protein	TC:3.A.1
P73_2161	ABC-type dipeptide/oligopeptide/nickel transport systems, permease component	TC:3.A.1
P73_2162	ABC transporter permease	TC:3.A.1
P73_2163	oligopeptide/dipeptide ABC transporter, ATPase subunit	TC:3.A.1
P73_2164	oligopeptide/dipeptide ABC transporter, ATPase subunit	TC:3.A.1
P73_2171	Sulfite exporter TauE/SafE	TC:9.A.29
P73_2190	extracellular solute-binding protein	TC:3.A.1
P73_2191	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_2192	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_2194	alpha-glucoside transport ATP-binding protein AglK	TC:3.A.1
P73_2195	tellurite resistance protein	TC:2.A.16
P73_2204	small multidrug resistance protein	TC:2.A.7
P73_2207	urease accessory protein	TC:2.A.99
P73_2210	Uncharacterized membrane protein	TC:2.A.89
P73_2216	spermidine/putrescine transport system permease	TC:3.A.1
P73_2217	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_2218	polyamine ABC transporter ATP-binding protein PotG	TC:3.A.1
P73_2223	EamA-like transporter family	TC:2.A.7
P73_2224	aromatic hydrocarbon degradation membrane protein	TC:1.B.9
P73_2225	Predicted permeases	TC:2.A.7
P73_2238	Predicted permeases	TC:9.A.29

P73_2239	ammonium transporter	TC:1.A.11
P73_2249	trk system potassium uptake protein TrkH	TC:2.A.38
P73_2253	small multidrug resistance protein	TC:2.A.7
P73_2286	conjugal transfer coupling protein TraG	TC:3.A.7
P73_2289	conjugal transfer protein TrbC	TC:3.A.7
P73_2290	conjugal transfer protein TrbB	TC:3.A.7
P73_2291	conjugal transfer ATPase TrbE	TC:3.A.7
P73_2294	conjugal transfer protein TrbL	TC:3.A.7
P73_2295	conjugal transfer protein TrbF	TC:3.A.7
P73_2296	P-type conjugative transfer protein TrbG	TC:3.A.7
P73_2297	conjugation TrbI family protein	TC:3.A.7
P73_2324	ABC transporter permease	TC:3.A.1
P73_2325	ABC transporter permease	TC:3.A.1
P73_2326	spermidine/putrescine-binding periplasmic protein	TC:3.A.1
P73_2327	ABC transporter ATP-binding protein	TC:3.A.1
P73_2336	twin-arginine translocation pathway signal	TC:3.A.1
P73_2337	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_2338	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_2339	oligopeptide/dipeptide ABC transporter ATPase	TC:3.A.1
P73_2340	oligopeptide/dipeptide ABC transporter ATPase	TC:3.A.1
P73_2375	ABC-2 type transporter	TC:3.A.1
P73_2376	ABC transporter related protein	TC:3.A.1
P73_2377	secretion protein HlyD family protein	TC:8.A.1
P73_2380	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_2381	putative alkanesulfonate transport protein, ABC superfamily, inner membrane component	TC:3.A.1
P73_2382	ABC transporter	TC:3.A.1
P73_2384	glucose-inhibited division protein A	TC:5.A.4
P73_2386	Binding-protein-dependent transport systems inner membrane component	TC:3.A.1
P73_2387	binding-protein-dependent transport systems inner membrane component	TC:3.A.1
P73_2388	Spermidine/putrescine-binding periplasmic protein	TC:3.A.1
P73_2389	spermidine/putrescine ABC transporter ATPase	TC:3.A.1
P73_2395	lysine exporter protein LysE/YggA	TC:2.A.76
P73_2397	Predicted permeases	TC:9.A.29
P73_2399	outer membrane receptor FepA	TC:1.B.14
P73_2411	ABC transporter permease	TC:3.A.1
P73_2412	ABC transporter related protein	TC:3.A.1
P73_2413	periplasmic binding protein/LacI transcriptional regulator	TC:3.A.1
P73_2415	transport system permease	TC:3.A.1
P73_2416	ferric vibriobactin receptor	TC:1.B.14
P73_2417	Bcr/CflA subfamily drug resistance transporter	TC:2.A.1
P73_2421	LacI family transcriptional regulator	TC:3.A.1
P73_2447	polysaccharide biosynthesis protein	TC:2.A.66

P73_2483	choline/carnitine/betaine transporter	TC:2.A.15
P73_2489	family 1 extracellular solute-binding protein	TC:3.A.1
P73_2501	chromate transporter	TC:2.A.51
P73_2503	polyamine ABC transporter substrate-binding protein	TC:3.A.1
P73_2504	membrane protein	TC:9.A.29
P73_2520	MFS transporter	TC:2.A.1
P73_2541	major facilitator superfamily protein	TC:2.A.1
P73_2545	ABC transporter substrate-binding protein	TC:3.A.1
P73_2561	phosphate transporter ATP-binding protein	TC:3.A.1
P73_2562	phosphate ABC transporter permease	TC:3.A.1
P73_2563	phosphate ABC transporter permease	TC:3.A.1
P73_2564	phosphate ABC transporter substrate-binding protein	TC:3.A.1
P73_2573	extracellular ligand-binding receptor	TC:3.A.1
P73_2574	ABC transporter	TC:3.A.1
P73_2575	branched-chain amino acid ABC transporter ATP-binding protein LivF	TC:3.A.1
P73_2576	branched-chain amino acid ABC transporter permease	TC:3.A.1
P73_2577	inner-membrane translocator	TC:3.A.1
P73_2590	Disulfide bond formation protein DsbB	TC:5.A.2
P73_2615	surface antigen (D15)	TC:1.B.33
P73_2632	Putative Mg2+ and Co2+ transporter CorB	TC:9.A.40
P73_2642	molybdate ABC transporter ATP-binding protein	TC:3.A.1
P73_2643	molybdate ABC transporter permease protein	TC:3.A.1
P73_2644	ABC molybdate transporter, periplasmic binding protein ModA	TC:3.A.1
P73_2650	Uncharacterized homolog of Blt101	TC:9.B.12
P73_2653	ABC transporter ATPase	TC:3.A.1
P73_2654	multiple antibiotic resistance (MarC)-like proteins	TC:2.A.95
P73_2658	YjgP/YjgQ family permease	TC:1.B.42
P73_2659	permease YjgP/YjgQ family protein	TC:1.B.42
P73_2660	organic solvent tolerance protein	TC:1.B.42
P73_2671	holdfast attachment protein C	TC:3.A.1
P73_2675	SmpA/OmlA domain-containing protein	TC:1.B.33
P73_2675	SmpA/OmlA domain-containing protein	TC:9.B.85
P73_2689	Na(+):H(+) antiporter	TC:2.A.36
P73_2700	acriflavin resistance protein	TC:2.A.6
P73_2711	sodium/hydrogen exchanger	TC:2.A.37
P73_2721	conjugation TrbI family protein	TC:3.A.7
P73_2722	conjugal transfer protein TrbG/VirB9/CagX	TC:3.A.7
P73_2723	conjugal transfer protein TrbF	TC:3.A.7
P73_2724	conjugal transfer protein TrbL	TC:3.A.7
P73_2727	conjugal transfer ATPase TrbE	TC:3.A.7
P73_2728	conjugal transfer protein TrbB	TC:3.A.7
P73_2729	conjugal transfer protein TrbC	TC:3.A.7
P73_2731	major facilitator superfamily protein	TC:2.A.1

P73_2737	Uncharacterized conserved protein	TC:9.B.36
P73_2745	conjugal transfer coupling protein TraG	TC:3.A.7
P73_2779	K+-dependent Na+/Ca+ exchanger related-protein	TC:2.A.19
P73_2798	Di- and tricarboxylate transporters	TC:2.A.47
P73_2813	oligopeptide/dipeptide ABC transporter, ATPase subunit	TC:3.A.1
P73_2814	oligopeptide/dipeptide ABC transporter ATP-binding protein	TC:3.A.1
P73_2815	agropinic acid ABC transporter permease	TC:3.A.1
P73_2816	peptide ABC transporter	TC:3.A.1
P73_2825	BioY protein	TC:2.A.88
P73_2831	exported protein (TRAP-type transport system, periplasmic component)	TC:2.A.56
P73_2832	TRAP C4-dicarboxylate transport system subunit DctQ	TC:2.A.56
P73_2833	TRAP transporter, DctM subunit	TC:2.A.56
P73_2836	C4-dicarboxylate-binding periplasmic protein	TC:2.A.56
P73_2837	putative DctQ (C4-dicarboxylate permease, small subunit)	TC:2.A.56
P73_2838	Putative TRAP transporter large permease protein	TC:2.A.56
P73_2843	Lipoprotein, YaeC family	TC:3.A.1
P73_2844	ABC-type metal ion transport system, permease component	TC:3.A.1
P73_2845	NLPA lipoprotein	TC:3.A.1
P73_2851	peptide ABC transporter ATPase	TC:3.A.1
P73_2852	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_2853	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_2854	extracellular solute-binding protein	TC:3.A.1
P73_2867	permease	TC:2.A.1
P73_2872	ABC transporter	TC:3.A.1
P73_2873	binding-protein-dependent transporters inner membrane component	TC:3.A.1
P73_2883	heavy metal translocating P-type ATPase	TC:3.A.3
P73_2890	xylose ABC transporter ATP-binding protein XylG	TC:3.A.1
P73_2891	Inner-membrane translocator	TC:3.A.1
P73_2892	D-xylose-binding periplasmic protein XylF	TC:3.A.1
P73_2898	sulfate permease	TC:2.A.53
P73_2948	TRAP C4-dicarboxylate transport system permease DctM	TC:2.A.56
P73_2949	TRAP-type mannitol/chloroaromatic compound transport system small permease-like protein	TC:2.A.56
P73_2950	twin-arginine translocation pathway signal	TC:2.A.56
P73_2962	EamA-like transporter family	TC:2.A.7
P73_2969	TRAP transporter, 4TM/12TM fusion protein	TC:2.A.56
P73_2974	TRAP-type C4-dicarboxylate transport system, periplasmic component	TC:2.A.56
P73_2975	TrapT family protein	TC:2.A.56
P73_2976	TRAP-T family transporter, DctQ (4 TMs) subunit	TC:2.A.56
P73_2986	putative periplasmic binding protein	TC:2.A.56
P73_3011	surface presentation of antigens (SPOA) protein	TC:3.A.6
P73_3021	binding-protein-dependent transport systems inner membrane component	TC:3.A.1
P73_3022	binding-protein-dependent transport systems inner membrane component	TC:3.A.1

P73_3023	ABC nitrate transporter, nucleotide binding/ATPase protein	TC:3.A.1
P73_3050	ABC transporter-like protein	TC:3.A.1
P73_3051	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_3060	RND family efflux transporter MFP subunit	TC:8.A.1
P73_3061	hydrophobe/amphiphile efflux-1 (HAE1) family protein	TC:2.A.6
P73_3071	polysaccharide biosynthesis protein	TC:2.A.66
P73_3078	putative exopolysaccharide production protein	TC:1.B.18
P73_3084	succinoglycan biosynthesis transport protein exoP	TC:8.A.3
P73_3086	TonB-dependent receptor	TC:1.B.14
P73_3087	periplasmic binding protein	TC:3.A.1
P73_3088	transport system permease	TC:3.A.1
P73_3089	ABC transporter	TC:3.A.1
P73_3104	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_3105	family 5 extracellular solute-binding protein	TC:3.A.1
P73_3107	oligopeptide/dipeptide ABC transporter ATPase	TC:3.A.1
P73_3108	oligopeptide/dipeptide ABC transporter ATPase	TC:3.A.1
P73_3109	binding-protein-dependent transport systems inner membrane component	TC:3.A.1
P73_3115	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_3116	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_3117	oligopeptide/dipeptide ABC transporter ATPase	TC:3.A.1
P73_3118	oligopeptide/dipeptide ABC transporter ATPase	TC:3.A.1
P73_3119	twin-arginine translocation pathway signal	TC:3.A.1
P73_3124	extracellular solute-binding protein	TC:3.A.1
P73_3125	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_3126	spermidine/putrescine ABC transporter permease	TC:3.A.1
P73_3127	ABC transporter-like protein	TC:3.A.1
P73_3134	ABC transporter substrate-binding protein	TC:3.A.1
P73_3136	glutathione import ATP-binding protein GsiA	TC:3.A.1
P73_3137	peptide ABC transporter permease	TC:3.A.1
P73_3138	glutathione transport system permease GsiD	TC:3.A.1
P73_3147	ABC transporter-like protein	TC:3.A.1
P73_3148	binding-protein-dependent transporter inner membrane component	TC:3.A.1
P73_3159	auxin efflux carrier	TC:2.A.69
P73_3192	voltage-gated CIC-type chloride channel	TC:2.A.49
P73_3206	cell division protein FtsW	TC:9.B.3
P73_3224	EmrB/QacA family drug resistance transporter	TC:2.A.1
P73_3226	inner membrane transport protein	TC:2.A.46
P73_3230	Outer membrane autotransporter barrel	TC:1.B.12
P73_3250	TraG/TraD family protein	TC:3.A.7
P73_3275	glutathione-regulated potassium-efflux system protein	TC:2.A.37
P73_3303	capsular polysaccharide export protein KpsS	TC:9.A.41
P73_3304	polysaccharide biosynthesis/export family protein	TC:1.B.18
P73_3305	capsular polysaccharide export protein KpsC	TC:9.A.41

P73_3355	ABC transporter ATP-binding protein	TC:3.A.1
P73_3356	lipoprotein releasing system transmembrane protein	TC:3.A.1
P73_3359	permease	TC:2.A.86
P73_3367	Na+/H+ antiporter NhaA	TC:2.A.33
P73_3378	multidrug resistance protein	TC:2.A.1
P73_3383	binding-protein-dependent transport systems inner membrane component	TC:3.A.1
P73_3403	ABC transporter	TC:3.A.1
P73_3414	Sec-independent protein translocase TatC	TC:2.A.64
P73_3415	twin-arginine translocation protein, TatB subunit	TC:2.A.64
P73_3416	Sec-independent translocation protein mttA/Hcf106	TC:2.A.64
P73_3418	ABC transporter	TC:3.A.1
P73_3429	NADH:ubiquinone oxidoreductase subunit N	TC:3.D.1
P73_3430	NADH:ubiquinone oxidoreductase subunit M	TC:3.D.1
P73_3431	NADH:ubiquinone oxidoreductase subunit L	TC:3.D.1
P73_3432	NADH:ubiquinone oxidoreductase subunit K	TC:3.D.1
P73_3433	NADH:ubiquinone oxidoreductase subunit J	TC:3.D.1
P73_3435	NADH dehydrogenase subunit I	TC:3.D.1
P73_3436	NADH:ubiquinone oxidoreductase subunit H	TC:3.D.1
P73_3438	NADH dehydrogenase subunit G	TC:5.A.3
P73_3441	NADH dehydrogenase I subunit F	TC:3.D.1
P73_3444	NADH dehydrogenase subunit E	TC:3.D.1
P73_3445	NADH dehydrogenase subunit D	TC:3.D.1
P73_3447	NADH dehydrogenase subunit C	TC:3.D.1
P73_3448	NADH dehydrogenase subunit B	TC:3.D.1
P73_3449	NADH:ubiquinone oxidoreductase subunit A	TC:3.D.1
P73_3459	NAD(P) transhydrogenase subunit beta	TC:3.D.2
P73_3483	cation transporter	TC:2.A.38
P73_3489	EamA-like transporter family	TC:2.A.7
P73_3490	MgtC/SapB transporter	TC:9.B.20
P73_3492	signal recognition particle-docking protein FtsY	TC:3.A.5
P73_3503	HflC protein	TC:8.A.21
P73_3504	Protein HflK	TC:8.A.21
P73_3514	preprotein translocase subunit SecG	TC:3.A.5
P73_3520	ABC transporter	TC:3.A.1
P73_3521	His/Glu/Gln/Arg/opine family ABC transporter substrate-binding protein	TC:3.A.1
P73_3522	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_3523	histidine transport system permease protein	TC:3.A.1
P73_3549	MATE efflux family protein	TC:2.A.66
P73_3555	EamA-like transporter family	TC:2.A.7
P73_3570	MscS mechanosensitive ion channel	TC:1.A.23
P73_3583	ABC transporter ATP-binding protein	TC:3.A.1
P73_3588	surface antigen (D15)	TC:1.B.33
P73_3589	Uncharacterized protein conserved in bacteria	TC:9.B.22

P73_3599	molecular chaperone DnaK	TC:1.A.33
P73_3646	F0F1 ATP synthase subunit epsilon	TC:3.A.2
P73_3647	F0F1 ATP synthase subunit beta	TC:3.A.2
P73_3648	F0F1 ATP synthase subunit gamma	TC:3.A.2
P73_3649	F0F1 ATP synthase subunit alpha	TC:3.A.2
P73_3650	ATP synthase subunit delta	TC:3.A.2
P73_3655	Flagellar motor protein	TC:1.A.30
P73_3666	TonB-dependent receptor plug	TC:1.B.14
P73_3668	periplasmic binding protein	TC:3.A.1
P73_3669	ABC transporter permease	TC:3.A.1
P73_3670	hemin importer ATP-binding subunit	TC:3.A.1
P73_3688	TonB-dependent receptor	TC:1.B.14
P73_3699	rod shape-determining protein RodA	TC:9.B.3
P73_3703	Na+/H+ antiporter NhaA	TC:2.A.33
P73_3704	capsule polysaccharide export ATP-binding protein KpsT	TC:3.A.1
P73_3705	capsule polysaccharide export	TC:8.A.4
P73_3706	Na/Pi-cotransporter II-like protein	TC:2.A.58
P73_3707	OmpA/MotB domain-containing protein	TC:1.A.30
P73_3712	Uncharacterized protein conserved in bacteria	TC:2.A.80
P73_3714	Uncharacterized protein conserved in bacteria	TC:2.A.80
P73_3718	TRAP transporter solute receptor, TAXI family protein	TC:2.A.56
P73_3719	TRAP transporter 4TM/12TM fusion protein	TC:2.A.56
P73_3724	ATP synthase F1 subunit gamma	TC:3.A.2
P73_3725	ATP synthase F1 subunit alpha	TC:3.A.2
P73_3726	ATP synthase F0 subunit B	TC:3.A.2
P73_3727	F0F1 ATP synthase subunit C	TC:3.A.2
P73_3728	F0F1 ATP synthase subunit A	TC:3.A.2
P73_3731	ATP synthase F1 subunit epsilon	TC:3.A.2
P73_3732	F0F1 ATP synthase subunit beta	TC:3.A.2
P73_3737	TRAP dicarboxylate transporter DctM subunit	TC:2.A.56
P73_3738	TRAP transporter DctQ-like subunit	TC:2.A.56
P73_3739	2,3-diketo-L-gulonate-binding periplasmic protein	TC:2.A.56
P73_3743	TRAP dicarboxylate transporter subunit DctM	TC:2.A.56
P73_3744	TRAP dicarboxylate transporter subunit DctQ	TC:2.A.56
P73_3745	TRAP dicarboxylate transporter subunit DctP	TC:2.A.56
P73_3750	Extracellular solute-binding protein, family 5 precursor	TC:3.A.1
P73_3751	oligopeptide/dipeptide ABC transporter ATPase	TC:3.A.1
P73_3752	peptide ABC transporter ATPase	TC:3.A.1
P73_3753	peptide/opine ABC transporter inner membrane protein	TC:3.A.1
P73_3754	peptide/opine ABC transporter inner membrane protein	TC:3.A.1
P73_3774	ABC transporter substrate binding protein (glycerol-3-phosphate)	TC:3.A.1
P73_3775	ABC transporter membrane spanning protein (glycerol-3-phosphate)	TC:3.A.1
P73_3776	ABC transporter membrane spanning protein (glycerol-3-phosphate)	TC:3.A.1

P73_3778	ABC transporter nucleotide binding/ATPase (glycerol-3-phosphate)	TC:3.A.1
P73_3784	ACR3 family arsenite efflux pump	TC:2.A.59
P73_3788	major facilitator transporter	TC:2.A.1
P73_3791	cation efflux protein	TC:2.A.4
P73_3808	ABC transporter	TC:3.A.1
P73_3809	putative ABC type branched chain amino acid transport system	TC:3.A.1
P73_3810	sugar ABC transporter permease	TC:3.A.1
P73_3811	bmp family protein	TC:3.A.1
P73_3819	ferrous-iron efflux pump FieF	TC:2.A.4
P73_3833	branched-chain amino acid ABC transporter periplasmic component-like protein	TC:3.A.1
P73_3835	integral membrane protein MviN	TC:2.A.66
P73_3836	Uncharacterized membrane protein (homolog of Drosophila rhomboid)	TC:3.A.1
P73_3843	sugar ABC transporter substrate-binding protein	TC:3.A.1
P73_3844	ribose import ATP-binding protein	TC:3.A.1
P73_3845	integral inner-membrane protein	TC:3.A.1
P73_3846	inner-membrane translocator	TC:3.A.1
P73_3847	Predicted permeases	TC:9.A.29
P73_3860	succinate dehydrogenase iron-sulfur subunit	TC:5.A.4
P73_3862	succinate dehydrogenase flavoprotein subunit	TC:5.A.4
P73_3864	succinate dehydrogenase subunit C	TC:5.A.4
P73_3869	Predicted permeases	TC:9.A.29
P73_3885	ABC transporter	TC:3.A.1
P73_3886	ABC-transporter ATP-binding component	TC:3.A.1
P73_3887	nitrate/sulfonate/bicarbonate ABC transporter permease	TC:3.A.1
P73_3899	sodium/solute symporter family protein	TC:2.A.21
P73_3905	copper-transporting P-type ATPase ActP	TC:3.A.3
P73_3910	transthyretin	TC:9.B.35
P73_3914	TRAP-type C4-dicarboxylate transport system periplasmic component-like protein	TC:3.A.1
P73_3915	ABC-type antimicrobial peptide transport system, ATPase component	TC:3.A.1
P73_3918	ABC-type Fe3+ transport system permease component	TC:3.A.1
P73_3930	curli production assembly/transport component CsgG	TC:1.B.48
P73_3932	major facilitator superfamily transporter	TC:2.A.1
P73_3936	TRAP dicarboxylate transporter subunit DctP	TC:2.A.56
P73_3937	tripartite AtP-independent periplasmic transporter subunit DctQ	TC:2.A.56
P73_3938	TRAP dicarboxylate transporter subunit DctM	TC:2.A.56
P73_3947	ABC transporter, nucleotide binding/ATPase protein	TC:3.A.1
P73_3948	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_3949	ABC transporter, membrane spanning protein	TC:3.A.1
P73_3950	extracellular solute-binding protein	TC:3.A.1
P73_3963	tetrahydromethanopterin S-methyltransferase subunit H	TC:3.C.1
P73_3971	major facilitator family protein	TC:2.A.1
P73_3982	efflux transporter inner membrane protein	TC:2.A.66

P73_3985	ABC-type cobalamin/Fe3+-siderophore transport system, ATPase component	TC:3.A.1
P73_3986	transport system permease	TC:3.A.1
P73_3987	ferric siderophore ABC transporter membrane protein	TC:3.A.1
P73_3988	periplasmic binding protein	TC:3.A.1
P73_3989	ferrichrome receptor precursor protein	TC:1.B.14
P73_3999	binding-protein-dependent transport systems inner membrane component	TC:3.A.1
P73_4001	maltose ABC transporter transmembrane protein	TC:3.A.1
P73_4002	extracellular solute-binding protein family 1	TC:3.A.1
P73_4003	putative sugar ABC transporter, ATP-binding protein	TC:3.A.1
P73_4006	tripartite ATP-independent periplasmic transporter DctQ component	TC:2.A.56
P73_4007	TRAP dicarboxylate transporter subunit DctP	TC:2.A.56
P73_4008	Sialic acid TRAP transporter permease protein siaT	TC:2.A.56
P73_4025	sugar ABC transporter	TC:3.A.1
P73_4026	binding-protein-dependent transport systems inner membrane component	TC:3.A.1
P73_4027	binding-protein-dependent transport systems inner membrane component	TC:3.A.1
P73_4028	extracellular solute-binding protein family 1 protein	TC:3.A.1
P73_4031	peptide ABC transporter ATP-binding protein	TC:3.A.1
P73_4032	ABC transporter permease	TC:3.A.1
P73_4033	ABC transporter, membrane spanning protein (peptide)	TC:3.A.1
P73_4034	ABC transporter substrate binding protein	TC:3.A.1
P73_4035	oligopeptide ABC transporter substrate binding protein	TC:3.A.1
P73_4041	ABC transporter substrate binding protein	TC:2.A.56
P73_4042	TRAP dicarboxylate transporter subunit DctM	TC:2.A.56
P73_4047	Predicted membrane protein	TC:2.A.7
P73_4049	family 5 extracellular solute-binding protein	TC:3.A.1
P73_4050	binding-protein-dependent transporters inner membrane component	TC:3.A.1
P73_4051	binding-protein-dependent transporters inner membrane component	TC:3.A.1
P73_4052	ABC transporter	TC:3.A.1
P73_4056	acetyltransferase	TC:8.A.3
P73_4058	Periplasmic protein involved in polysaccharide export	TC:1.B.18
P73_4065	polysaccharide biosynthesis protein	TC:2.A.66
P73_4074	nitrate/sulfonate/bicarbonate ABC transporter ATPase	TC:3.A.1
P73_4075	ABC transporter permease	TC:3.A.1
P73_4081	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_4082	putative sulfonate ABC transporter ATP-binding protein	TC:3.A.1
P73_4090	putative cystine-binding periplasmic protein	TC:3.A.1
P73_4091	ABC transporter substrate binding protein	TC:3.A.1
P73_4092	ABC transporter ATPase	TC:3.A.1
P73_4097	outer membrane receptor for ferrienterochelin and colicins	TC:1.B.14
P73_4103	transport protein	TC:2.A.56
P73_4104	TRAP-type transport system, small permease	TC:2.A.56
P73_4105	TRAP transporter, DctM subunit	TC:2.A.56
P73_4110	transmembrane protein	TC:2.A.80

P73_4111	Uncharacterized protein conserved in bacteria	TC:2.A.80
P73_4115	ABC transporter	TC:3.A.1
P73_4116	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_4120	type II and III secretion system protein	TC:1.B.22
P73_4137	outer membrane assembly factor	TC:1.B.33
P73_4138	Type I secretion membrane fusion protein, HlyD	TC:8.A.1
P73_4139	ABC transporter-like protein	TC:3.A.1
P73_4140	Outer membrane protein	TC:1.B.17
P73_4144	ABC transporter	TC:3.A.1
P73_4146	ABC transporter-like protein	TC:3.A.1
P73_4147	Fe3+ siderophore ABC transporter permease	TC:3.A.1
P73_4148	transport system permease	TC:3.A.1
P73_4149	ferric enterobactin-binding periplasmic protein FepB	TC:3.A.1
P73_4150	TonB-dependent siderophore receptor	TC:1.B.14
P73_4161	oligopeptide/dipeptide ABC transporter ATPase	TC:3.A.1
P73_4162	oligopeptide/dipeptide ABC transporter ATPase	TC:3.A.1
P73_4163	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_4164	peptide ABC transporter permease	TC:3.A.1
P73_4165	extracellular solute-binding protein	TC:3.A.1
P73_4166	ABC transporter-like protein	TC:3.A.1
P73_4167	binding-protein-dependent transport systems inner membrane component	TC:3.A.1
P73_4168	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_4169	family 1 extracellular solute-binding protein	TC:3.A.1
P73_4171	ABC transporter-like protein	TC:3.A.1
P73_4172	ABC transporter-like protein	TC:3.A.1
P73_4173	branched-chain amino acid ABC transporter permease	TC:3.A.1
P73_4174	branched-chain amino acid ABC transporter permease	TC:3.A.1
P73_4175	branched-chain amino acid ABC transporter substrate-binding protein	TC:3.A.1
P73_4177	ABC transporter ATP-binding protein	TC:3.A.1
P73_4180	copper-translocating P-type ATPase	TC:3.A.3
P73_4201	ABC peptide transporter	TC:3.A.1
P73_4204	oligopeptide/dipeptide uptake family ABC transporter, periplasmic substrate-binding protein	TC:3.A.1
P73_4211	ABC transporter-like protein	TC:3.A.1
P73_4212	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_4226	large-conductance mechanosensitive channel	TC:1.A.22
P73_4247	cell division protein FtsX	TC:3.A.1
P73_4248	cell division ATP-binding protein FtsE	TC:3.A.1
P73_4257	Predicted permeases	TC:2.A.7
P73_4267	AzlC family protein	TC:2.A.78
P73_4268	AzlD branched-chain amino acid transport	TC:2.A.78
P73_4276	AcrB/AcrD/AcrF family transporter	TC:2.A.6
P73_4297	Na+/Ca+ antiporter	TC:2.A.19

P73_4302	zinc import ATP-binding protein ZnuC	TC:3.A.1
P73_4303	zinc ABC transporter permease	TC:3.A.1
P73_4306	ABC transporter ATP-binding protein	TC:3.A.1
P73_4307	ABC transporter permease y4oR	TC:3.A.1
P73_4308	sorbitol/mannitol transport system permease protein	TC:3.A.1
P73_4309	extracellular solute-binding protein	TC:3.A.1
P73_4322	lipopolysaccharide biosynthesis family protein	TC:8.A.3
P73_4372	Oxidoreductase alpha (Molybdopterin) subunit	TC:5.A.3
P73_4377	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_4378	Binding-protein-dependent transport system inner membrane component	TC:3.A.1
P73_4401	transmembrane protein	TC:2.A.56
P73_4402	tripartite ATP-independent periplasmic transporter DctQ	TC:2.A.56
P73_4403	TRAP-type C4-dicarboxylate transport system, periplasmic component	TC:2.A.56
P73_4405	NAD(P) transhydrogenase subunit beta	TC:3.D.2
P73_4406	MFS permease	TC:2.A.1
P73_4409	ABC transporter permease	TC:3.A.1
P73_4410	ABC transporter substrate-binding protein	TC:3.A.1
P73_4411	ABC transporter	TC:3.A.1
P73_4413	ribose ABC transporter ATP-binding protein	TC:3.A.1
P73_4417	choline/carnitine/betaine transporter	TC:2.A.15
P73_4433	binding-protein-dependent transport system inner membrane protein	TC:3.A.1
P73_4434	ABC transporter	TC:3.A.1
P73_4438	branched-chain amino acid ABC transporter permease	TC:3.A.1
P73_4439	inner-membrane translocator	TC:3.A.1
P73_4440	amino acid ABC transporter ATP-binding protein	TC:3.A.1
P73_4441	branched chain amino acid ABC transporter ATPase	TC:3.A.1
P73_4442	putative branched-chain amino acid ABC transporter, periplasmic component	TC:3.A.1
P73_4444	TRAP-type C4-dicarboxylate transport system, periplasmic component	TC:2.A.56
P73_4453	AMP-dependent synthetase and ligase	TC:4.C.1
P73_4456	TRAP-T family protein transporter, DctP (Periplasmic binding) subunit	TC:2.A.56
P73_4461	putative permease, DMT superfamily protein	TC:2.A.7
P73_4468	TRAP-T family protein transporter, DctM (12 TMs) subunit	TC:2.A.56
P73_4469	TRAP-type C4-dicarboxylate transport system, small permease component	TC:2.A.56
P73_4470	TRAP-T family protein transporter, DctP (Periplasmic binding) subunit	TC:2.A.56
P73_4481	AMP-dependent synthetase and ligase	TC:4.C.1
P73_4503	TRAP dicarboxylate transporter- DctP subunit	TC:2.A.56
P73_4504	TRAP dicarboxylate transporter subunit DctM	TC:2.A.56
P73_4505	TRAP-type C4-dicarboxylate transport system, small permease component	TC:2.A.56
P73_4506	ABC ribose transporter, periplasmic solute-binding protein	TC:3.A.1
P73_4507	inner-membrane translocator	TC:3.A.1
P73_4508	ABC transporter-like protein	TC:3.A.1
P73_4532	oxidoreductase, flavocytochrome subunit	TC:5.B.1
P73_4532	oxidoreductase, flavocytochrome subunit	TC:9.B.43

P73_4537	ATPase P	TC:3.A.3
P73_4538	Uncharacterized membrane protein	TC:2.A.89
P73_4557	Uncharacterized membrane protein (homolog of Drosophila rhomboid)	TC:3.A.1
P73_4566	Type IV secretory pathway, VirD4 components	TC:3.A.7
P73_4571	TrbL/VirB6 plasmid conjugal transfer protein	TC:3.A.7
P73_4575	conjugation TrbI family protein	TC:3.A.7
P73_4576	conjugal transfer protein TrbG/VirB9/CagX	TC:3.A.7
P73_4577	VirB8 family protein	TC:3.A.7
P73_4578	Type IV secretion system proteins	TC:3.A.7
P73_4581	CagE TrbE VirB component of type IV transporter system	TC:3.A.7
P73_4582	type IV secretory pathway VirB3 family protein	TC:3.A.7
P73_4583	conjugal transfer protein TrbC	TC:3.A.7
P73_4590	cation diffusion facilitator family transporter	TC:2.A.4
P73_4592	cytochrome c biogenesis protein transmembrane region	TC:5.A.1
P73_4596	disulfide bond formation-like protein	TC:5.A.2
P73_4602	zinc/iron permease	TC:2.A.5
P73_4610	phosphonate ABC transporter phosphate-binding periplasmic component	TC:3.A.1
P73_4611	phosphonate/organophosphate ester transporter subunit	TC:3.A.1
P73_4612	phosphonate ABC transporter permease protein phnE	TC:3.A.1
P73_4614	heavy metal translocating P-type ATPase	TC:3.A.3
P73_4639	cytochrome c-type biogenesis protein CcmF	TC:9.B.14
P73_4645	copper-translocating P-type ATPase	TC:3.A.3
P73_4709	protein VirD4	TC:3.A.7
P73_4710	high-affinity nickel-transporter	TC:2.A.52
P73_4711	type IV secretion system protein VirB6	TC:3.A.7
P73_4714	type IV secretion system protein VirB10	TC:3.A.7
P73_4715	conjugal transfer protein TrbG/VirB9/CagX	TC:3.A.7
P73_4716	type IV secretion system protein VirB8	TC:3.A.7
P73_4717	Type IV secretion system proteins	TC:3.A.7
P73_4720	type IV secretion system protein VirB	TC:3.A.7
P73_4721	type IV secretory pathway virB3 protein	TC:3.A.7
P73_4722	type IV secretion system protein VirB2	TC:3.A.7
P73_4731	heavy metal translocating P-type ATPase	TC:3.A.3
P73_4745	thiol:disulfide interchange protein DsbD 1 precursor	TC:5.A.1
P73_4765	TRAP dicarboxylate transporter subunit DctM	TC:2.A.56
P73_4766	TRAP dicarboxylate transporter subunit DctQ	TC:2.A.56
P73_4767	TRAP transporter solute receptor	TC:2.A.56
P73_4780	TrbL/VirB6 plasmid conjugal transfer protein	TC:3.A.7
P73_4790	Membrane transport protein MerF	TC:9.A.2
P73_4790	Membrane transport protein MerF	TC:9.A.7
P73_4792	mercuric transporter MerT	TC:9.A.2
P73_4815	virD4 protein, putative	TC:3.A.7
P73_4821	chromate transporter	TC:2.A.51

Data S5 | Transcription genes in the P73^T genome related to transcription (COG category K).

Locus Tag	Gene Product Name	Function ID
P73_0641	DNA-directed RNA polymerase subunit beta (EC:2.7.7.6)	COG0085
P73_0642	DNA-directed RNA polymerase subunit beta' (EC:2.7.7.6)	COG0086
P73_0257	transcription elongation factor NusA	COG0195
P73_0677	DNA-directed RNA polymerase subunit alpha (EC:2.7.7.6)	COG0202
P73_0636	NusG antitermination factor	COG0250
P73_2440	Transcription antiterminator	COG0250
P73_4060	Transcription antiterminator	COG0250
P73_0602	(P)ppGpp synthetase I, SpoT/RelA (EC:2.7.6.5)	COG0317
P73_3389	urease accessory protein UreG	COG0378
P73_2792	putative ATP-dependent RNA helicase (EC:3.6.4.13)	COG0513
P73_3425	ATP-dependent RNA helicase (EC:3.6.4.13)	COG0513
P73_3610	putative ATP-dependent RNA helicase (EC:3.6.4.13)	COG0513
P73_4222	DEAD/DEAH box helicase (EC:3.6.4.13)	COG0513
P73_1853	serine/threonine protein kinase	COG0515
P73_1926	serine/threonine protein kinase	COG0515
P73_0053	ribonuclease R (EC:3.1.-)	COG0557
P73_3291	RNA polymerase factor sigma-32	COG0568
P73_3314	RNA polymerase sigma factor RpoD	COG0568
P73_3824	RNA polymerase factor sigma-32	COG0568
P73_0608	ribonuclease III (EC:3.1.26.3)	COG0571
P73_0079	protein GbuR	COG0583
P73_0157	LysR family transcriptional regulator	COG0583
P73_0160	Transcriptional Regulator, LysR family protein	COG0583
P73_0332	LysR family transcriptional regulator	COG0583
P73_0495	LysR family transcriptional regulator	COG0583
P73_0508	LysR family transcriptional regulator	COG0583
P73_0546	LysR family transcriptional regulator	COG0583
P73_0749	LysR family transcriptional regulator	COG0583
P73_0840	pca operon transcriptional activator PcaQ	COG0583
P73_0995	LysR family transcriptional regulator	COG0583
P73_1052	LysR family transcriptional regulator	COG0583
P73_1064	LysR family transcriptional regulator	COG0583
P73_1109	LysR family transcriptional regulator	COG0583
P73_1118	LysR family transcriptional regulator	COG0583
P73_1278	LysR family transcriptional regulator	COG0583
P73_1386	LysR family transcriptional regulator	COG0583
P73_1522	LysR family transcriptional regulator	COG0583
P73_1534	chromosome replication initiation inhibitor protein	COG0583

P73_1543	LysR family transcriptional regulator	COG0583
P73_1559	LysR family transcriptional regulator	COG0583
P73_1574	LysR family transcriptional regulator	COG0583
P73_1616	LysR family transcriptional regulator	COG0583
P73_1767	LysR family transcriptional regulator	COG0583
P73_1994	LysR family transcriptional regulator	COG0583
P73_2008	LysR family transcriptional regulator	COG0583
P73_2028	HTH-type transcriptional activator nahR	COG0583
P73_2029	LysR family transcriptional regulator	COG0583
P73_2046	LysR family transcriptional regulator	COG0583
P73_2060	LysR family transcriptional regulator	COG0583
P73_2127	LysR family transcriptional regulator	COG0583
P73_2144	LysR family transcripitonal regulator	COG0583
P73_2154	transcriptional regulator	COG0583
P73_2230	LysR family transcriptional regulator	COG0583
P73_2234	LysR family transcriptional regulator	COG0583
P73_2285	LysR family transcriptional regulator	COG0583
P73_2368	transcriptional regulator	COG0583
P73_2596	LysR family transcriptional regulator	COG0583
P73_2812	LysR family transcription regulator protein	COG0583
P73_2817	LysR family transcriptional regulator	COG0583
P73_2842	LysR family transcriptional regulator	COG0583
P73_3145	Transcriptional regulator	COG0583
P73_3528	putative transcriptional regulator	COG0583
P73_3716	transcriptional regulator	COG0583
P73_3741	LysR family transcription regulator protein	COG0583
P73_3931	LysR family transcriptional regulator	COG0583
P73_4010	LysR family transcriptional regulator	COG0583
P73_4011	LysR family transcriptional regulator	COG0583
P73_4018	LysR family transcriptional regulator	COG0583
P73_4019	LysR family transcriptional regulator	COG0583
P73_4030	LysR family transcriptional regulator	COG0583
P73_4076	LysR family transcriptional regulator	COG0583
P73_4517	transcriptional regulator	COG0583
P73_4756	transcriptional regulator	COG0583
P73_0751	ArsR family transcriptional regulator	COG0640
P73_1255	ArsR family transcriptional regulator	COG0640
P73_1552	transcriptional regulator SoxR	COG0640
P73_1983	arsR family transcriptional regulator	COG0640
P73_3787	ArsR family transcriptional regulator	COG0640
P73_3790	ArsR family transcriptional regulator	COG0640
P73_4045	nodulation protein nolR	COG0640
P73_0298	DNA-binding response regulator PetR	COG0745

P73_0381	hypothetical protein	COG0745
P73_0410	two component transcriptional regulator	COG0745
P73_0615	two component transcriptional regulator	COG0745
P73_2185	response regulator receiver protein, CheY like protein	COG0745
P73_2559	phosphate regulon transcriptional regulatory protein PhoB	COG0745
P73_2604	two component transcriptional regulator	COG0745
P73_3014	response regulator receiver protein	COG0745
P73_3902	response regulator receiver protein	COG0745
P73_4530	Two component transcriptional regulator, winged helix family protein	COG0745
P73_4636	two component transcriptional regulator	COG0745
P73_3298	N utilization substance family protein	COG0781
P73_4265	transcription elongation factor GreA	COG0782
P73_0896	MerR family transcriptional regulator	COG0789
P73_0897	MerR family transcriptional regulator	COG0789
P73_1938	MerR family transcriptional regulator	COG0789
P73_2361	MerR family regulatory protein	COG0789
P73_2681	Predicted transcriptional regulators	COG0789
P73_2882	MerR family transcriptional regulator	COG0789
P73_4594	MerR family transcriptional regulator	COG0789
P73_4730	MerR family transcriptional regulator	COG0789
P73_4793	putative heavy metal transcriptional regulator	COG0789
P73_0869	silent information regulator protein Sir2 (EC:3.5.1.-)	COG0846
P73_1818	superfamily II DNA/RNA helicase	COG1061
P73_1891	superfamily II DNA/RNA helicase	COG1061
P73_0209	transcription termination factor Rho	COG1158
P73_0785	class I and II aminotransferase	COG1167
P73_3917	GntR family transcriptional regulator	COG1167
P73_2540	transcription-repair coupling factor (EC:3.6.4.-)	COG1197
P73_2602	ATP-dependent DNA helicase RecG (EC:3.6.4.12)	COG1200
P73_2776	cold shock protein CspA	COG1278
P73_2793	cold-shock DNA-binding protein family protein	COG1278
P73_2990	cold-shock DNA-binding domain-containing protein	COG1278
P73_3537	cold-shock DNA-binding domain-containing protein	COG1278
P73_3586	cold shock protein CspA	COG1278
P73_0532	TetR family transcriptional regulator	COG1309
P73_0730	TetR family transcriptional regulator	COG1309
P73_0774	TetR family transcriptional regulator	COG1309
P73_0904	TetR family transcriptional regulator	COG1309
P73_1089	TetR family transcriptional regulator	COG1309
P73_1116	TetR family transcriptional regulator	COG1309
P73_1768	TetR family transcriptional regulator	COG1309
P73_2219	TetR family transcriptional regulator	COG1309
P73_2283	TetR family transcriptional regulator	COG1309

P73_2378	TetR family transcriptional regulator	COG1309
P73_3027	TetR family transcriptional regulator	COG1309
P73_3059	TetR family transcriptional regulator	COG1309
P73_3889	transcriptional regulator, TetR family protein	COG1309
P73_3895	TetR family transcriptional regulator	COG1309
P73_3962	TetR family transcriptional regulator	COG1309
P73_3975	transcriptional regulator	COG1309
P73_4088	TetR family transcriptional regulator	COG1309
P73_4100	transcriptional regulator	COG1309
P73_4608	DtxR family iron dependent repressor	COG1321
P73_3307	transcriptional regulator NrdR	COG1327
P73_3278	CarD family transcriptional regulator	COG1329
P73_1660	DeoR family transcriptional regulator	COG1349
P73_2856	DeoR family transcriptional regulator	COG1349
P73_3998	transcriptional repressor of aga operon	COG1349
P73_2684	condensin subunit ScpB	COG1386
P73_0137	DNA-binding protein	COG1396
P73_1091	XRE family transcriptional regulator	COG1396
P73_1524	XRE family transcriptional regulator	COG1396
P73_2544	DNA-binding protein	COG1396
P73_3227	puttative helix-turn-helix protein	COG1396
P73_0183	transcriptional repressor	COG1414
P73_0327	IclR family transcriptional regulator	COG1414
P73_0836	beta-ketoadipate pathway transcription regulator	COG1414
P73_1376	transcriptional regulator	COG1414
P73_1984	regulatory protein, IclR	COG1414
P73_2099	putative transcriptional regulator	COG1414
P73_2830	transcriptional regulator	COG1414
P73_2981	IclR family transcriptional regulator	COG1414
P73_3721	IclR family transcriptional regulator	COG1414
P73_4407	DNA-binding transcriptional activator MhpR	COG1414
P73_0219	heat-inducible transcription repressor	COG1420
P73_0214	chromosome-partitioning protein ParB	COG1475
P73_0953	ParB domain-containing protein nuclease	COG1475
P73_1794	ParB-like domain protein	COG1475
P73_1867	ParB-like domain protein	COG1475
P73_2264	ParB-like domain protein	COG1475
P73_2782	parB-like partition protein	COG1475
P73_4391	plasmid partitioning protein RepB-8	COG1475
P73_4526	parB-like partition protein	COG1475
P73_4528	ParB family protein	COG1475
P73_4545	parB-like partition protein	COG1475
P73_4669	plasmid partitioning protein RepB	COG1475

P73_4671	ParB family protein	COG1475
P73_1542	XRE family transcriptional regulator	COG1476
P73_1595	Predicted transcriptional regulators	COG1476
P73_4558	Predicted transcriptional regulators	COG1476
P73_4064	MarR family transcriptional regulator	COG1497
P73_4498	RNA polymerase factor sigma-54	COG1508
P73_3427	pantothenate kinase (EC:2.7.1.33)	COG1521
P73_1138	AsnC family transcriptional regulator	COG1522
P73_1156	AsnC family transcriptional regulator	COG1522
P73_1165	AsnC family transcriptional regulator	COG1522
P73_1274	AsnC/Lrp family transcriptional regulator	COG1522
P73_2393	AsnC family transcriptional regulator	COG1522
P73_2998	AsnC family transcriptional regulator	COG1522
P73_3468	AsnC family transcriptional regulator	COG1522
P73_3469	AsnC family transcriptional regulator	COG1522
P73_3621	putative leucine-responsive regulatory protein	COG1522
P73_3747	Leucine-responsive regulatory protein	COG1522
P73_4225	AsnC family transcriptional regulator	COG1522
P73_1099	RNA polymerase sigma-70 family protein	COG1595
P73_1495	RNA polymerase sigma factor	COG1595
P73_3348	RNA polymerase sigma factor	COG1595
P73_3924	ECF subfamily RNA polymerase sigma-24 factor	COG1595
P73_3977	extracytoplasmic-function sigma-70 factor	COG1595
P73_4354	ECF subfamily RNA polymerase sigma-24 factor	COG1595
P73_0372	LacI family transcriptional regulator	COG1609
P73_2138	transcriptional regulator, LacI family protein	COG1609
P73_2143	regulatory protein LacI:Periplasmic binding protein/LacI transcriptional regulator	COG1609
P73_2189	LacI family transcriptional regulator	COG1609
P73_2408	Transcriptional regulator	COG1609
P73_3110	LacI family transcriptional regulator	COG1609
P73_3123	LacI family transcriptional regulator	COG1609
P73_4170	LacI family transcriptional regulator	COG1609
P73_4511	LacI family transcriptional regulator	COG1609
P73_4274	Putative transcriptional regulator	COG1678
P73_2461	hypothetical protein	COG1725
P73_1110	HxlR family transcriptional regulator	COG1733
P73_1956	transcriptional regulator	COG1733
P73_3310	putative transcriptional regulator	COG1733
P73_1043	RpiR family transcriptional regulator	COG1737
P73_1944	RpiR family transcriptional regulator	COG1737
P73_3122	RpiR family transcriptional regulator	COG1737
P73_3779	RpiR family transcriptional regulator	COG1737

P73_3944	RpiR family transcriptional regulator	COG1737
P73_4102	transcriptional regulator, RpiR family	COG1737
P73_0601	DNA-directed RNA polymerase subunit omega (EC:2.7.7.6)	COG1758
P73_2705	DNA-directed RNA polymerase, omega subunit (EC:2.7.7.6)	COG1758
P73_1147	GntR family transcriptional regulator	COG1802
P73_2019	transcriptional regulator	COG1802
P73_2172	GntR-family transcription regulator	COG1802
P73_2390	transcriptional regulator, GntR family	COG1802
P73_2558	GntR family transcriptional regulator	COG1802
P73_2824	GntR family transcriptional regulator	COG1802
P73_2868	GntR family transcriptional regulator	COG1802
P73_2877	GntR family transcriptional regulator	COG1802
P73_3173	GntR family transcriptional regulator	COG1802
P73_3711	GntR family transcriptional regulator	COG1802
P73_3755	GntR family transcriptional regulator	COG1802
P73_3881	GntR family HTH-type transcriptional regulator	COG1802
P73_4048	GntR family transcriptional regulator	COG1802
P73_4587	XRE family transcriptional regulator	COG1813
P73_0233	MarR family transcriptional regulator	COG1846
P73_0253	MarR family transcriptional regulator	COG1846
P73_0297	transcriptional regulator	COG1846
P73_0307	MarR family transcriptional regulator	COG1846
P73_0337	MarR family transcriptional regulator	COG1846
P73_0357	MarR family transcriptional regulator	COG1846
P73_1406	Transcriptional regulator	COG1846
P73_1461	MarR family transcriptional regulator	COG1846
P73_1467	MarR family transcriptional regulator	COG1846
P73_2073	transcription regulator MarR family protein	COG1846
P73_2115	MarR family transcriptional regulator	COG1846
P73_2418	MarR family transcriptional regulator	COG1846
P73_2961	putative Transcriptional regulator, MarR family protein	COG1846
P73_2985	MarR family transcriptional regulator	COG1846
P73_3223	MarR family transcriptional regulator	COG1846
P73_3544	MarR family transcriptional regulator	COG1846
P73_3580	histone acetyltransferase HPA2-related acetyltransferase	COG1846
P73_4393	MarR family transcriptional regulator	COG1846
P73_4749	MarR family transcriptional regulator	COG1846
P73_2893	ROK family protein	COG1940
P73_3997	N-acetyl-D-glucosamine kinase (EC:2.7.1.59)	COG1940
P73_1145	BadM/Rrf2 family transcriptional regulator	COG1959
P73_2259	BadM/Rrf2 family transcriptional regulator	COG1959
P73_2344	iron-sulfur cluster assembly transcription factor IscR	COG1959
P73_1588	LexA repressor (EC:3.4.21.88)	COG1974

P73_4548	regulator PrlF	COG2002
P73_4524	S1 RNA-binding domain-containing protein	COG2183
P73_0125	GntR family transcriptional regulator	COG2186
P73_1650	GntR family transcriptional regulator	COG2186
P73_4023	GntR family transcriptional regulator	COG2186
P73_0807	GntR family transcriptional regulator	COG2188
P73_1073	transcriptional regulator, GntR family protein	COG2188
P73_2419	GntR family transcriptional regulator	COG2188
P73_0586	response regulator receiver-like protein	COG2197
P73_0679	transcriptional regulator	COG2197
P73_0758	LuxR family transcriptional regulator	COG2197
P73_2553	LuxR family autoinducer-binding transcriptional regulator	COG2197
P73_3851	LuxR family transcriptional regulator	COG2197
P73_3925	putative response regulator receiver protein	COG2197
P73_3956	nitrate/nitrite regulatory protein	COG2197
P73_4133	LuxR family two component transcriptional regulator	COG2197
P73_0074	AraC family transcriptional regulator	COG2207
P73_0847	transcriptional regulator	COG2207
P73_1106	AraC family transcriptional regulator	COG2207
P73_1297	transcriptional regulator	COG2207
P73_1978	helix-turn-helix domain-containing protein	COG2207
P73_2091	AraC family transcriptional regulator	COG2207
P73_2396	AraC family transcriptional regulator	COG2207
P73_2623	AraC family transcriptional regulator	COG2207
P73_3339	transcriptional regulator	COG2207
P73_4764	AraC family transcriptional regulator	COG2207
P73_0238	response regulator receiver domain/protein phosphatase 2C domain-containing protein	COG2208
P73_4316	putative transcriptional regulator	COG2345
P73_1970	Predicted transcriptional regulator	COG2378
P73_3417	Predicted transcriptional regulator	COG2378
P73_1375	transcriptional regulator	COG2390
P73_4310	DeoR family transcriptional regulator	COG2390
P73_0258	Predicted nucleic-acid-binding protein implicated in transcription termination	COG2740
P73_2092	regulatory protein LuxR	COG2771
P73_3517	transcriptional regulator	COG2808
P73_2331	transcriptional regulator, LuxR family protein	COG2909
P73_2861	Fis family GAF modulated sigma54 specific transcriptional regulator	COG3284
P73_4224	Fis family transcriptional regulator	COG3284
P73_1027	phage transcriptional regulator AlpA	COG3311
P73_1431	transcriptional regulator	COG3311
P73_2456	prophage CP4-57 regulatory	COG3311

P73_3605	response regulator	COG3437
P73_4628	transcriptional regulator	COG3609
P73_4811	transcriptional regulator	COG3620
P73_4475	sigma-54 dependent transcription regulator	COG3829
P73_4499	sigma-54 dependent transcription regulator	COG3829
P73_1752	Predicted transcriptional regulator	COG4190
P73_2302	Predicted transcriptional regulator	COG4190
P73_0188	photosynthetic apparatus regulatory protein	COG4567
P73_1402	RNA polymerase sigma factor protein (sigma-70)	COG4941
P73_0132	AraC family transcriptional regulator	COG4977
P73_4399	AraC family transcriptional regulator	COG4977
P73_4130	hypothetical protein	COG5137

Data S6 | Genes in the P73^T genome related to lipid transport and metabolism COG categories.

Locus Tag	Gene Product Name	COGs
P73_0066	3-oxoacid CoA-transferase, B subunit	COG2057
P73_0067	3-oxoacid CoA-transferase subunit A	COG1788
P73_0180	long-chain-fatty-acid-CoA ligase	COG0318
P73_0184	putative fatty acid/hydrocarbon transporter	COG2067
P73_0187	acyl-CoA dehydrogenase-like protein	COG1960
P73_0224	short-chain dehydrogenase/reductase sdr	COG1028
P73_0228	short chain dehydrogenase	COG1028
P73_0301	1-deoxy-D-xylulose-5-phosphate synthase	COG1154
P73_0338	long-chain-fatty-acid--CoA ligase	COG0318
P73_0339	enoyl-CoA hydratase	COG1024
P73_0341	thiolase	COG0183
P73_0349	2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase	COG1028
P73_0367	Putative lipid carrier protein	COG3154
P73_0399	enoyl-CoA hydratase/isomerase	COG1024
P73_0501	3-hydroxybutyryl-CoA dehydrogenase	COG1250
P73_0540	acetyl-CoA carboxylase, carboxyl transferase subunit beta	COG0777
P73_0598	4-hydroxy-3-methylbut-2-enyl diphosphate reductase	COG0761
P73_0606	4'-phosphopantetheinyl transferase	COG0736
P73_0612	isobutyryl-CoA dehydrogenase	COG1960
P73_0622	3-hydroxybutyryl-CoA dehydrogenase	COG1250
P73_0712	acyltransferase 3	COG1835
P73_0837	3-oxoacid CoA-transferase subunit A	COG1788
P73_0838	3-oxoacid CoA-transferase subunit B	COG2057
P73_0839	beta-ketoadipyl CoA thiolase	COG0183
P73_0882	AMP-dependent synthetase/ligase	COG0365
P73_0892	3-hydroxyacyl-CoA dehydrogenase	COG1250

P73_0893	acetyl-CoA acetyltransferase	COG0183
P73_0895	acyl-CoA dehydrogenase	COG1960
P73_0925	AMP-binding domain protein	COG0318
P73_0926	3-oxoacyl(acyl carrier protein) synthase III	COG0332
P73_1055	FabG	COG1028
P73_1108	short chain dehydrogenase	COG1028
P73_1111	NADP oxidoreductase coenzyme F420-dependent	COG1028
P73_1113	short-chain dehydrogenase/reductase SDR	COG1028
P73_1222	butyryl-CoA:acetate CoA transferase	COG2057
P73_1224	succinyl-CoA:3-ketoacid-CoA transferase subunit A	COG1788
P73_1308	enoyl-ACP reductase	COG0623
P73_1309	3-oxoacyl-ACP synthase	COG0304
P73_1310	3-hydroxydecanoyl(acyl carrier protein) dehydratase	COG0764
P73_1395	acyl-CoA dehydrogenase	COG1960
P73_1396	short-chain specific acyl-CoA dehydrogenase	COG1960
P73_1462	short-chain dehydrogenase/reductase SDR	COG1028
P73_1463	enoyl-CoA hydratase/isomerase	COG1024
P73_1468	feruloyl-CoA synthase	COG0318
P73_1470	Acyl-CoA dehydrogenase	COG1960
P73_1584	enoyl-CoA hydratase	COG1024
P73_1676	malonyl CoA-acyl carrier protein transacylase FabD	COG0331
P73_1677	3-oxoacyl-ACP reductase	COG1028
P73_1678	acyl carrier protein	COG0236
P73_1679	3-oxoacyl(acyl carrier protein) synthase II	COG0304
P73_2012	MaoC-like dehydratase	COG2030
P73_2020	6-phosphogluconate dehydrogenase	COG2084
P73_2030	putative oxidoreductase protein	COG1028
P73_2054	3-oxoacyl-ACP reductase	COG1028
P73_2159	short chain alcohol dehydrogenase-related dehydrogenase	COG1028
P73_2224	aromatic hydrocarbon degradation membrane protein	COG2067
P73_2237	cyclase/dehydrase	COG2867
P73_2241	phosphatidylglycerophosphatase	COG1267
P73_2242	2-C-methyl-D-erythritol 2,4-cyclodiphosphate synthase	COG0245
P73_2255	6-phosphogluconate dehydrogenase	COG2084
P73_2315	phospholipid/glycerol acyltransferase	COG0204
P73_2369	short chain dehydrogenase/reductase oxidoreductase	COG1028
P73_2370	2,5-dichloro-2,5-cyclohexadiene-1,4-diol dehydrogenase	COG1028
P73_2373	poly-beta-hydroxybutyrate polymerase domain protein	COG3243
P73_2494	Phytoene/squalene synthetase	COG1562
P73_2499	type 12 methyltransferase	COG3963
P73_2529	sterol carrier family protein	COG3255
P73_2546	3-hydroxybutyrate dehydrogenase	COG1028
P73_2613	(3R)-hydroxymyristoyl-ACP dehydratase	COG0764

P73_2617	1-deoxy-D-xylulose 5-phosphate reductoisomerase	COG0743
P73_2618	phosphatidate cytidylyltransferase	COG0575
P73_2619	undecaprenyl diphosphate synthase	COG0020
P73_2637	beta-ketoacyl synthase	COG0304
P73_2638	acyl carrier protein	COG0236
P73_2678	phosphate acyltransferase	COG0416
P73_2679	3-oxoacyl(acyl carrier protein) synthase III	COG0332
P73_2762	methylase/helicase	COG3963
P73_2794	fatty acid desaturase	COG3239
P73_2801	fatty acid desaturase	COG3239
P73_2864	short-chain dehydrogenase/reductase sDR	COG1028
P73_2871	short-chain dehydrogenase/reductase SDR	COG1028
P73_2909	4-hydroxy-3-methylbut-2-en-1-yl diphosphate synthase	COG0821
P73_2917	diacylglycerol kinase catalytic subunit	COG1597
P73_2984	bacilysin biosynthesis oxidoreductase BacC	COG1028
P73_2992	enoyl(acyl carrier protein) reductase	COG0623
P73_3004	PA-phosphatase-like phosphoesterase	COG0671
P73_3009	3-hydroxyacyl-CoA dehydrogenase	COG1250
P73_3017	acetate--CoA ligase	COG0365
P73_3031	biotin carboxyl carrier protein	COG0511
P73_3032	acetyl-CoA carboxylase biotin carboxylase subunit	COG4770
P73_3101	2-hydroxy-3-oxopropionate reductase	COG2084
P73_3132	bacilysin biosynthesis oxidoreductase bacC	COG1028
P73_3133	short-chain dehydrogenase/reductase SDR	COG1028
P73_3135	3-oxoacyl-ACP reductase	COG1028
P73_3161	acyl-CoA hydrolase	COG1607
P73_3283	sterol-binding domain-containing protein	COG3255
P73_3284	Lysophospholipase	COG2267
P73_3312	short-chain dehydrogenase/reductase SDR	COG1028
P73_3368	methylmalonyl-CoA mutase	COG1884
P73_3371	propionyl-CoA carboxylase subunit alpha	COG4770
P73_3377	propionyl-CoA carboxylase subunit beta	COG4799
P73_3494	alkane 1-monooxygenase	COG3239
P73_3531	poly(3-hydroxyalkanoate) polymerase	COG3243
P73_3532	polyhydroxyalkanoate depolymerase	COG4553
P73_3639	MaoC domain-containing protein dehydratase	COG2030
P73_3829	esterase	COG0657
P73_3853	methylmalonyl-CoA mutase large subunit	COG1884
P73_3865	MaoC domain-containing protein	COG2030
P73_3880	thioesterase superfamily protein	COG1607
P73_3897	acetate--CoA ligase	COG0365
P73_3919	Acyl-CoA dehydrogenase, C-terminal:Acyl-CoA dehydrogenase, central region:Acyl-CoA dehydrogenase, N-terminal:Acyl-CoA dehydrogenase, N-terminal	COG1960

P73_3993	short-chain alcohol dehydrogenase-like protein	COG0623
P73_4037	acyl-CoA dehydrogenase	COG1960
P73_4054	short-chain dehydrogenase/reductase SDR	COG1028
P73_4084	FMNH2-dependent monooxygenase	COG1960
P73_4086	putative acyl-CoA dehydrogenase	COG1960
P73_4108	short-chain dehydrogenase/reductase SDR	COG1028
P73_4196	7-alpha-hydroxysteroid dehydrogenase	COG1028
P73_4244	acetyl-CoA carboxylase carboxyltransferase subunit alpha	COG0825
P73_4246	phospholipid/glycerol acyltransferase	COG0204
P73_4255	acyltransferase	COG0183
P73_4256	acetoacetyl-CoA reductase	COG1028
P73_4262	4-diphosphocytidyl-2-C-methyl-D-erythritol kinase	COG1947
P73_4273	acyl-CoA dehydrogenase	COG1960
P73_4283	glycerol-3-phosphate acyltransferase PlsY	COG0344
P73_4294	CDP-diacylglycerol--glycerol-3-phosphate 3-phosphatidyltransferase	COG0558
P73_4296	short chain dehydrogenase	COG1028
P73_4305	sorbitol dehydrogenase	COG1028
P73_4368	short-chain dehydrogenase/reductase SDR	COG1028
P73_4369	3-oxoacyl-ACP reductase	COG1028
P73_4388	enoyl-CoA hydratase/isomerase	COG1024
P73_4424	6-phosphogluconate dehydrogenase	COG2084
P73_4425	6-phosphogluconate dehydrogenase	COG2084
P73_4427	6-phosphogluconate dehydrogenase	COG2084
P73_4428	3-hydroxyisobutyrate dehydrogenase	COG2084
P73_4429	enoyl-CoA hydratase/isomerase	COG1024
P73_4430	oxidoreductase, short-chain dehydrogenase/reductase	COG1028
P73_4447	3-hydroxyacyl-CoA dehydrogenase	COG1250
P73_4449	3-hydroxyacyl-CoA dehydrogenase	COG1250
P73_4450	acyl-CoA dehydrogenase	COG1960
P73_4452	short chain enoyl-CoA hydratase	COG1024
P73_4453	AMP-dependent synthetase and ligase	COG0318
P73_4462	6-phosphogluconate dehydrogenase	COG2084
P73_4463	acyl-CoA dehydrogenase yngJ	COG1960
P73_4477	3-hydroxyacyl-CoA dehydrogenase	COG1250
P73_4478	acyl-CoA dehydrogenase	COG1960
P73_4480	short chain enoyl-CoA hydratase	COG1024
P73_4481	AMP-dependent synthetase and ligase	COG0318
P73_4485	acyl-CoA dehydrogenase yngJ	COG1960
P73_4486	thiolase	COG0183
P73_4487	dehydratase	COG2030
P73_4488	enoyl-CoA hydratase	COG1024
P73_4491	beta-ketoadipyl-CoA thiolase PaaJ	COG0183
P73_4496	oxidoreductase, short-chain dehydrogenase/reductase	COG1028

P73_4696	putative methylase/helicase	COG3963

Data S7 | Genes in the P73^T genome related to cell motility and chemotaxis. Genes of cell motility, and chemotaxis predicted by 'KEGG Orthology (KO) terms' analyses (Sheet 1); Genes of COG category N (Sheet 2).

Sheet 1 (Excel)

Locus Tag	Gene Product Name	Func ID
P73_0088	flagellin-like protein	KO:K02406
P73_0092	H+-transporting two-sector ATPase, alpha/beta subunit (EC:3.6.3.14)	KO:K02412
P73_0093	flagellar basal body rod protein FlgB	KO:K02387
P73_0094	flagellar basal body rod protein FlgC	KO:K02388
P73_0095	flagellar hook-basal body protein FliE	KO:K02408
P73_0096	flagellar biosynthetic protein FliQ	KO:K02420
P73_0097	flagellar basal body rod protein FlgF	KO:K02391
P73_0098	flagellar basal body rod protein FlgG	KO:K02392
P73_0099	flagellar basal body P-ring biosynthesis protein FlgA	KO:K02386
P73_0100	flagellar basal body L-ring protein	KO:K02393
P73_0103	flagellar biosynthesis protein FlhB	KO:K02401
P73_0104	flagellar biosynthetic protein FliR	KO:K02421
P73_0105	flagellar biosynthesis protein FlhA	KO:K02400
P73_0107	flagellar motor protein MotA	KO:K02556
P73_0111	flagellar MS-ring protein	KO:K02409
P73_0112	hypothetical protein	KO:K02411
P73_0113	flagellar motor switch protein FliN	KO:K02417
P73_0114	flagellar biosynthesis protein FliP	KO:K02419
P73_0115	flagellar basal body P-ring protein	KO:K02394
P73_0116	flagellar hook-associated protein FlgL	KO:K02397
P73_0117	flagellar hook-associated protein FlgK	KO:K02396
P73_0118	flagellar hook protein FlgE	KO:K02390
P73_0119	chemotaxis MotB protein	KO:K02557
P73_1480	methyl-accepting chemotaxis protein McpH	KO:K03406
P73_1637	flagellar motor switch protein FliG	KO:K02410
P73_2176	methyl-accepting chemotaxis protein McpA	KO:K03406
P73_2177	chemotaxis-specific protein-glutamate methyltransferase (EC:3.1.1.61)	KO:K03412
P73_2178	chemoreceptor glutamine deamidase CheD (EC:3.5.1.44)	KO:K03411
P73_2181	chemotaxis protein CheY	KO:K03413
P73_2182	chemotaxis protein CheR (EC:2.1.1.80)	KO:K00575
P73_2183	chemotaxis protein CheW	KO:K03408
P73_2184	chemotaxis protein CheA (EC:2.7.13.3)	KO:K03407

P73_2185	response regulator receiver protein, CheY like protein	KO:K03413
P73_2186	Anti-anti-sigma regulatory factor (antagonist of anti-sigma factor)	KO:K03409
P73_2413	periplasmic binding protein/LacI transcriptional regulator	KO:K10439
P73_2421	LacI family transcriptional regulator	KO:K10439
P73_3011	surface presentation of antigens (SPOA) protein	KO:K02416
P73_3655	Flagellar motor protein	KO:K02557
P73_3896	methyl-accepting chemotaxis protein McpA	KO:K03406
P73_4153	two-component system, chemotaxis family,response regulator CheB (EC:2.1.1.80,EC:3.1.1.61)	KO:K13924
P73_4383	flagellar basal body rod modification protein	KO:K02389
P73_4506	ABC ribose transporter, periplasmic solute-binding protein	KO:K10439

Sheet 2 (Excel)

Locus Tag	Gene Product Name	COG
P73_0086	flagellar protein FlgJ	COG3951
P73_0088	flagellin-like protein	COG1344
P73_0089	flagellar biosynthesis regulatory protein FlaF	COG5442
P73_0090	flagellar biosynthesis repressor FlbT	COG5443
P73_0092	H+-transporting two-sector ATPase, alpha/beta subunit (EC:3.6.3.14)	COG1157
P73_0093	flagellar basal body rod protein FlgB	COG1815
P73_0094	flagellar basal body rod protein FlgC	COG1558
P73_0095	flagellar hook-basal body protein FliE	COG1677
P73_0096	flagellar biosynthetic protein FliQ	COG1987
P73_0097	flagellar basal body rod protein FlgF	COG4786
P73_0098	flagellar basal body rod protein FlgG	COG4786
P73_0099	flagellar basal body P-ring biosynthesis protein FlgA	COG1261
P73_0100	flagellar basal body L-ring protein	COG2063
P73_0103	flagellar biosynthesis protein FlhB	COG1377
P73_0104	flagellar biosynthetic protein FliR	COG1684
P73_0105	flagellar biosynthesis protein FlhA	COG1298
P73_0107	flagellar motor protein MotA	COG1291
P73_0110	flagellar basal body-associated protein FliL	COG1580
P73_0111	flagellar MS-ring protein	COG1766
P73_0112	hypothetical protein	COG1317
P73_0113	flagellar motor switch protein FliN	COG1886
P73_0114	flagellar biosynthesis protein FliP	COG1338
P73_0115	flagellar basal body P-ring protein	COG1706
P73_0116	flagellar hook-associated protein FlgL	COG1344
P73_0117	flagellar hook-associated protein FlgK	COG1256
P73_0118	flagellar hook protein FlgE	COG1749
P73_0119	chemotaxis MotB protein	COG1360
P73_0986	conjugal transfer protein TrbB	COG5268

P73_1210	type II secretion system protein	COG2064
P73_1480	methyl-accepting chemotaxis protein McpH	COG0840
P73_1637	flagellar motor switch protein FliG	COG1536
P73_1762	conjugal transfer protein TrbB	COG5268
P73_1849	Flagellin and related hook-associated proteins	COG1344
P73_1922	Flagellin and related hook-associated proteins	COG1344
P73_2176	methyl-accepting chemotaxis protein McpA	COG0840
P73_2177	chemotaxis-specific protein-glutamate methyltransferase (EC:3.1.1.61)	COG2201
P73_2178	chemoreceptor glutamine deamidase CheD (EC:3.5.1.44)	COG1871
P73_2182	chemotaxis protein CheR (EC:2.1.1.80)	COG1352
P73_2183	chemotaxis protein CheW	COG0835
P73_2184	chemotaxis protein CheA (EC:2.7.13.3)	COG0643
P73_2290	conjugal transfer protein TrbB	COG5268
P73_2512	Protein required for attachment to host cells	COG5622
P73_2728	conjugal transfer protein TrbB	COG5268
P73_3011	surface presentation of antigens (SPOA) protein	COG1868
P73_3380	Predicted periplasmic or secreted lipoprotein	COG1724
P73_3655	Flagellar motor protein	COG1360
P73_3707	OmpA/MotB domain-containing protein	COG1360
P73_3896	methyl-accepting chemotaxis protein McpA	COG0840
P73_4125	type II secretion system protein	COG2064
P73_4153	two-component system, chemotaxis family,response regulator CheB (EC:2.1.1.80,EC:3.1.1.61)	COG1352
P73_4383	flagellar basal body rod modification protein	COG1843

Data S8 | Genes in the P73^{T} genome involved in aromatic compounds degradation.

Locus Tag	Product Name
P73_0169	fumarylacetoacetate (FAA) hydrolase
P73_0170	putative carboxymethylenebutenolidase
P73_0171	putative TRAP-type C4-dicarboxylate transport system large permease
P73_0172	TRAP dicarboxylate transporter subunit DctQ
P73_0173	TRAP dicarboxylate transporter subunit DctP
P73_0174	Mycothiol maleylpyruvate isomerase N-terminal domain
P73_0175	gentisate 1,2-dioxygenase
P73_0176	maleylacetoacetate isomerase
P73_0177	fumarylpyruvate hydrolase
P73_0182	4-hydroxylbenzoyl-CoA Thioesterase
P73_0327	IclR family transcriptional regulator
P73_0328	monooxygenase
P73_0329	homogentisate 1,2-dioxygenase
P73_0330	fumarylacetoacetate hydrolase family protein

P73_0331	maleylacetoacetate isomerase MaiA
P73_0332	LysR family transcriptional regulator
P73_0333	cytochrome P450
P73_0334	aldehyde dehydrogenase
P73_0335	ferredoxin-NADPH reductase
P73_0336	choline dehydrogenase-like flavoprotein
P73_0337	MarR family transcriptional regulator
P73_0338	long-chain-fatty-acid--CoA ligase
P73_0339	enoyl-CoA hydratase
P73_0340	hypothetical protein
P73_0341	thiolase
P73_0342	family 7 extracellular solute-binding protein
P73_0343	TRAP dicarboxylate transporter subunit DctQ
P73_0344	TRAP C4-dicarboxylate transporter permease DctM
P73_0345	putative fatty acid-CoA racemase
P73_0346	IPB-dioxygenase, ISP large subunit
P73_0347	Biphenyl 2,3-dioxygenase subunit beta
P73_0348	phenylpropionate dioxygenase ferredoxin subunit
P73_0349	2,3-dihydroxy-2,3-dihydrophenylpropionate dehydrogenase
P73_0350	dehydrogenase PhnF
P73_0351	dihydrodipicolinate synthetase
P73_0352	2-hydroxychromene-2-carboxylate isomerase
P73_0353	catechol 2,3-dioxygenase
P73_0354	pyridine nucleotide-disulfide oxidoreductase
P73_0355	OmpW family protein
P73_0356	glutathione S-transferase domain-containing protein
P73_0357	MarR family transcriptional regulator
P73_0363	cytochrome P450 family protein
P73_0364	alkane 1-monooxygenase
P73_0470	zinc-binding alcohol dehydrogenase family protein
P73_0501	3-hydroxybutyryl-CoA dehydrogenase
P73_0506	aldehyde dehydrogenase
P73_0507	extradiol ring-cleavage dioxygenase III subunit B
P73_0554	pyridine nucleotide-disulfide oxidoreductase
P73_0622	3-hydroxybutyryl-CoA dehydrogenase
P73_0805	hexapeptide repeat-containing transferase
P73_0835	putative two-component response regulator
P73_0836	beta-ketoadipate pathway transcription regulator
P73_0837	3-oxoacid CoA-transferase subunit A
P73_0838	3-oxoacid CoA-transferase subunit B
P73_0839	beta-ketoadipyl CoA thiolase
P73_0840	pca operon transcriptional activator PcaQ
P73_0841	3-oxoadipate enol-lactonase

P73_0842	4-carboxymuconolactone decarboxylase
P73_0843	Protocatechuate 3,4-dioxygenase, beta subunit
P73_0844	protocatechuate 3,4-dioxygenase subunit alpha
P73_0845	3-carboxy-cis,cis-muconate cycloisomerase
P73_0846	4-hydroxybenzoate 3-monooxygenase
P73_0893	acetyl-CoA acetyltransferase
P73_0895	acyl-CoA dehydrogenase
P73_0898	phenylacetic acid degradation-related protein
P73_0899	Uncharacterized protein, possibly involved in aromatic compounds catabolism
P73_0908	aromatic compounds catabolism protein
P73_1051	aromatic-ring-hydroxylating dioxygenase, ferredoxin subunit
P73_1052	LysR family transcriptional regulator
P73_1053	Rieske (2Fe-2S) protein
P73_1054	FAD-dependent pyridine nucleotide-disulfide oxidoreductase
P73_1085	phosphonate metabolism protein
P73_1121	muconate and chloromuconate cycloisomerase
P73_1122	benzenetriol dioxygenase
P73_1245	Conserved protein/domain typically associated with flavoprotein oxygenases, DIM6/NTAB family
P73_1304	3-oxoadipate enol-lactonase
P73_1381	acetaldehyde dehydrogenase
P73_1382	4-hyroxy-2-oxovalerate/4-hydroxy-2-oxopentanoic acid aldolase
P73_1453	Mycothiol maleylpyruvate isomerase N-terminal domain
P73_1454	gentisate 1,2-dioxygenase
P73_1455	maleylacetoacetate isomerase
P73_1456	fumarylpyruvate hydrolase
P73_1457	salicylate hydroxylase
P73_1550	S-(hydroxymethyl)glutathione dehydrogenase
P73_1592	cytochrome P450
P73_1746	cytochrome P450 family protein
P73_2150	aromatic hydrocarbon dioxygenase small subunit
P73_2151	Rieske (2Fe-2S) domain-containing protein
P73_2167	ferredoxin
P73_2169	ferredoxin
P73_2223	EamA-like transporter family
P73_2224	aromatic hydrocarbon degradation membrane protein
P73_2225	Predicted permeases
P73_2321	putative thioesterase superfamily protein
P73_2874	ferredoxin:oxidoreductase FAD/NAD(P)-binding subunit
P73_2875	Rieske (2Fe-2S) domain-containing protein
P73_2927	FAD-binding monooxygenase
P73_2960	Rieske (2Fe-2S) iron-sulfur domain-containing protein
P73_2961	putative Transcriptional regulator, MarR family protein

P73_2962	EamA-like transporter family
P73_2963	hypothetical protein
P73_2964	4,5-dihydroxyphthalate decarboxylase
P73_2965	oxidoreductase domain-containing protein
P73_2966	ferredoxin-NADPH reductase
P73_2967	S-mandelate dehydrogenase (MdlB)
P73_2968	Phthalate 4,5-dioxygenase
P73_3226	inner membrane transport protein
P73_3227	puttative helix-turn-helix protein
P73_3434	carboxymuconolactone decarboxylase
P73_3499	ferredoxin
P73_3884	Salicylate hydroxylase
P73_4038	monooxygenase
P73_4255	acyltransferase
P73_4376	alcohol dehydrogenase GroES domain-containing protein
P73_4415	ring hydroxylating dioxygenase, alpha-subunit
P73_4416	iron-sulfur cluster-binding protein
P73_4426	carboxymuconolactone decarboxylase
P73_4446	cupin
P73_4447	3-hydroxyacyl-CoA dehydrogenase
P73_4474	naphthoate synthase
P73_4485	acyl-CoA dehydrogenase yngJ
P73_4491	beta-ketoadipyl-CoA thiolase PaaJ
P73_4501	4-oxalocrotonate tautomerase
P73_4516	cupin
P73_4517	transcriptional regulator
P73_4518	putative carboxymuconolactone decarboxylase
P73_4519	oxidoreductase
P73_4520	cupin
P73_4521	(2Fe-2S)-binding domain-containing protein
P73_4522	aldehyde oxidase and xanthine dehydrogenase molybdopterin binding protein
P73_4757	putative oxidoreductase
P73_4758	ferredoxin reductase
P73_4762	ferredoxin
P73_4763	cytochrome P450
P73_4764	AraC family transcriptional regulator
P73_4773	fumarylpyruvate hydrolase
P73_4774	maleylacetoacetate isomerase
P73_4775	gentisate 1,2-dioxygenase

Data S9 | Genes in the P73^T genome without homologs in the B30 genome. The IMG 'Phylogenetic Profiler for Single Genes' was used. Maximum e-value = 0.00001; minimum identity = 30%.

Locus Tag	Gene Name
P73_0008	transposase
P73_0009	transposase
P73_0017	transposase, mutator type
P73_0045	transposase
P73_0046	transposase
P73_0074	AraC family transcriptional regulator
P73_0075	phospholipid-binding protein
P73_0076	hypothetical protein
P73_0077	hypothetical protein
P73_0079	protein GbuR
P73_0081	Extracellular solute-binding protein, ABC transporter
P73_0083	transposase IS116/IS110/IS902 family protein
P73_0085	transposase, IS4 family protein
P73_0102	hypothetical protein
P73_0148	extensin-like protein
P73_0160	Transcriptional Regulator, LysR family protein
P73_0162	Predicted lactoylglutathione lyase
P73_0163	hydrolase
P73_0164	carbon monoxide dehydrogenase subunit G
P73_0165	molybdopterin dehydrogenase FAD-binding protein
P73_0168	SnoaL-like domain
P73_0170	putative carboxymethylenebutenolidase
P73_0171	putative TRAP-type C4-dicarboxylate transport system large permease
P73_0172	TRAP dicarboxylate transporter subunit DctQ
P73_0173	TRAP dicarboxylate transporter subunit DctP
P73_0179	TRAP transporter solute receptor, TAXI family protein
P73_0182	4-hydroxylbenzoyl-CoA Thioesterase
P73_0183	transcriptional repressor
P73_0184	putative fatty acid/hydrocarbon transporter
P73_0186	TetR family transcriptional regulator
P73_0187	acyl-CoA dehydrogenase-like protein
P73_0225	membrane DoxD-like family protein
P73_0226	Predicted xylanase/chitin deacetylase
P73_0227	xylose isomerase domain-containing protein
P73_0230	ribose ABC transporter substrate-binding protein

P73_0232	antibiotic biosynthesis monooxygenase
P73_0233	MarR family transcriptional regulator
P73_0302	molybdate ABC transporter permease
P73_0307	MarR family transcriptional regulator
P73_0310	Protein of unknown function DUF262
P73_0311	transposase IS66
P73_0312	IS66 Orf2 family protein
P73_0313	transposase IS3/IS911 family protein
P73_0314	HsdR family type I site-specific deoxyribonuclease
P73_0315	Protein of unknown function (DUF2384)
P73_0324	sodium:dicarboxylate symporter
P73_0325	putative transposase for insertion sequence element
P73_0327	IclR family transcriptional regulator
P73_0329	homogentisate 1,2-dioxygenase
P73_0330	fumarylacetoacetate hydrolase family protein
P73_0331	maleylacetoacetate isomerase MaiA
P73_0332	LysR family transcriptional regulator
P73_0333	cytochrome P450
P73_0337	MarR family transcriptional regulator
P73_0338	long-chain-fatty-acid--CoA ligase
P73_0340	hypothetical protein
P73_0341	thiolase
P73_0342	family 7 extracellular solute-binding protein
P73_0343	TRAP dicarboxylate transporter subunit DctQ
P73_0346	IPB-dioxygenase, ISP large subunit
P73_0347	Biphenyl 2,3-dioxygenase subunit beta
P73_0348	phenylpropionate dioxygenase ferredoxin subunit
P73_0350	dehydrogenase PhnF
P73_0351	dihydrodipicolinate synthetase
P73_0352	2-hydroxychromene-2-carboxylate isomerase
P73_0353	catechol 2,3-dioxygenase
P73_0355	OmpW family protein
P73_0356	glutathione S-transferase domain-containing protein
P73_0357	MarR family transcriptional regulator
P73_0358	L-2,4-diaminobutyric acid acetyltransferase
P73_0360	L-ectoine synthase
P73_0361	aspartate kinase
P73_0362	Crp/Fnr family transcriptional regulator
P73_0368	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
P73_0369	3-octaprenyl-4-hydroxybenzoate carboxy-lyase
P73_0373	Domain of unknown function (DUF4145)
P73_0374	hypothetical protein
P73_0429	Sodium/proline symporter

P73_0431	hypothetical protein
P73_0432	cyclic nucleotide-binding protein
P73_0438	Putative amidoligase enzyme
P73_0453	Arabinose efflux permease
P73_0460	hypothetical protein
P73_0462	hypothetical protein
P73_0467	putative transposase
P73_0469	universal stress protein
P73_0473	Uncharacterized iron-regulated membrane protein
P73_0472	transposase
P73_0474	transposase
P73_0475	Uncharacterized iron-regulated membrane protein
P73_0476	hypothetical protein
P73_0479	hypothetical protein
P73_0480	phosphoglycerate mutase
P73_0481	precorrin 6A synthase
P73_0485	precorrin methylase
P73_0491	precorrin-3B synthase
P73_0494	Predicted metal-binding protein
P73_0495	LysR family transcriptional regulator
P73_0496	inner-membrane translocator
P73_0497	ABC transporter substrate-binding protein
P73_0498	ABC transporter
P73_0499	hypothetical protein
P73_0501	3-hydroxybutyryl-CoA dehydrogenase
P73_0502	alcohol dehydrogenase
P73_0503	putative periplasmic substrate binding protein
P73_0504	TRAP-type C4-dicarboxylate transport system small permease
P73_0505	TRAP dicarboxylate transporter
P73_0520	transposase
P73_0519	hypothetical protein
P73_0521	transposase
P73_0522	transposase
P73_0530	cytochrome c'
P73_0531	Peptidase inhibitor I78 family
P73_0658	bacterioferritin
P73_0659	hypothetical protein
P73_0700	Polysaccharide pyruvyl transferase
P73_0701	group 1 glycosyl transferase
P73_0702	hypothetical protein
P73_0703	polysaccharide export protein, translocase
P73_0704	O-antigen ligase like membrane protein
P73_0705	hypothetical protein

P73_0706	hypothetical protein
P73_0707	hypothetical protein
P73_0708	glycosyl transferase group 1
P73_0710	family 2 glycosyl transferase
P73_0711	putative Glycosyl transferase, group 1
P73_0712	acyltransferase 3
P73_0719	group 1 glycosyl transferase
P73_0720	conserved hypothetical protein
P73_0723	Thiamine biosynthesis protein ThiS
P73_0728	EmrB/QacA family drug resistance transporter
P73_0729	multidrug resistance protein K
P73_0730	TetR family transcriptional regulator
P73_0738	OmpA/MotB domain-containing protein
P73_0757	hypothetical protein
P73_0759	transposase
P73_0760	transposase
P73_0766	Lipid A 3-O-deacylase (PagL)
P73_0820	hypothetical protein
P73_0822	Uncharacterized protein conserved in bacteria
P73_0827	Formate/nitrite family of transporters
P73_0828	PRC-barrel domain
P73_0829	Uncharacterized protein conserved in bacteria
P73_0830	Uncharacterized stress protein (general stress protein 26)
P73_0832	radical SAM family protein
P73_0834	hypothetical protein
P73_0835	putative two-component response regulator
P73_0874	hypothetical protein
P73_0918	hybrid cluster protein-associated redox disulfide domain
P73_0923	hypothetical protein
P73_0924	hypothetical protein
P73_0927	hypothetical protein
P73_0934	hypothetical protein
P73_0936	McrBC 5-methylcytosine restriction system component
P73_0937	ATPase AAA
P73_0938	Filamentation induced by cAMP protein Fic
P73_0939	DEAD/DEAH box helicase
P73_0940	ORF-3 family protein
P73_0941	histone family protein nucleoid-structuring protein H-NS
P73_0945	hypothetical protein
P73_0946	Uncharacterized conserved protein
P73_0949	HNS-type DNA binding protein
P73_0950	hypothetical protein
P73_0951	hypothetical protein

P73_0952	universal stress protein
P73_0960	hypothetical protein
P73_0964	replicative DNA helicase
P73_0965	transmembrane protein
P73_0966	hypothetical protein
P73_0970	hypothetical protein
P73_0983	hypothetical protein
P73_1001	hypothetical protein
P73_1005	S-isoprenylcysteine methyltransferase-like protein
P73_1007	Uncharacterized protein conserved in bacteria
P73_1017	hypothetical protein
P73_1021	Predicted kinase
P73_1022	transposase, mutator type
P73_1024	hypothetical protein
P73_1025	hypothetical protein
P73_1026	Uncharacterized conserved protein (DUF2285)
P73_1029	transposase
P73_1030	transposase, orfB
P73_1031	transposase IS3/IS911 family protein
P73_1032	Ubiquinone/menaquinone biosynthesis methyltransferase
P73_1037	transposase
P73_1038	transposase
P73_1039	binding-protein-dependent transporter inner membrane component
P73_1041	NMT1/THI5-like domain-containing protein
P73_1042	methenyltetrahydrofolate synthetase
P73_1043	RpiR family transcriptional regulator
P73_1044	EmrB/QacA family drug resistance transporter
P73_1045	oligopeptide ABC transporter oligopeptide-binding protein
P73_1049	ammonia monooxygenase
P73_1050	MmgE/PrpD family protein
P73_1051	aromatic-ring-hydroxylating dioxygenase, ferredoxin subunit
P73_1053	Rieske (2Fe-2S) protein
P73_1055	FabG
P73_1056	hypothetical protein
P73_1057	TRAP-type C4-dicarboxylate transport system, periplasmic component
P73_1058	Transposase DDE domain group 1
P73_1072	NAD synthetase
P73_1086	Predicted permeases
P73_1087	hypothetical protein
P73_1089	TetR family transcriptional regulator
P73_1090	NAD-dependent epimerase/dehydratase
P73_1091	XRE family transcriptional regulator
P73_1092	Mn+2/Fe+2 ABC transporter substrate-binding protein SitA

P73_1093	Mn+2/Fe+2 ABC transporter ATPase SitB
P73_1094	ABC-3 protein
P73_1095	Mn+2/Fe+2 ABC transporter inner membrane protein SitD
P73_1096	heme oxygenase-like protein
P73_1097	heme receptor
P73_1098	protein fecR
P73_1100	lipoprotein
P73_1103	binding-protein-dependent transport system inner membrane protein
P73_1104	binding-protein-dependent transport system inner membrane protein
P73_1105	extracellular solute-binding protein
P73_1106	AraC family transcriptional regulator
P73_1107	Protein of unknown function (DUF2000)
P73_1111	NADP oxidoreductase coenzyme F420-dependent
P73_1112	alcohol dehydrogenase zinc-binding domain-containing protein
P73_1116	TetR family transcriptional regulator
P73_1123	transporter
P73_1125	aliphatic sulfonate ABC transporter substrate-binding protein
P73_1126	aliphatic sulfonate ABC transporter permease
P73_1127	coenzyme F420-dependent N5 N10-methylene tetrahydromethanopterin reductase-like protein
P73_1128	taurine dioxygenase
P73_1129	NADPH-dependent FMN reductase
P73_1130	FAD dependent oxidoreductase
P73_1131	Predicted esterase of the alpha/beta hydrolase fold
P73_1132	sodium-dependent inorganic phosphate (Pi) transporter
P73_1134	sulfate ABC transporter permease
P73_1135	sulfate ABC transporter inner membrane subunit CysT
P73_1136	sulfate ABC transporter substrate-binding protein
P73_1138	AsnC family transcriptional regulator
P73_1139	hypothetical protein
P73_1142	hypothetical protein
P73_1143	sulfate ABC transporter, inner membrane subunit CysT
P73_1144	sulfate adenylyltransferase
P73_1145	BadM/Rrf2 family transcriptional regulator
P73_1158	ribonucleoside-diphosphate reductase class Ib glutaredoxin subunit
P73_1159	ribonucleotide reductase stimulatory protein
P73_1160	ribonucleotide-diphosphate reductase subunit alpha
P73_1161	ribonucleotide-diphosphate reductase subunit beta
P73_1174	hypothetical protein
P73_1200	trans-aconitate 2-methyltransferase
P73_1203	putative phosphoesterase
P73_1204	DEAD/DEAH box helicase
P73_1223	GSCFA family

P73_1238	Predicted Zn-dependent hydrolases of the beta-lactamase fold
P73_1243	Branched-chain amino acid aminotransferase/4-amino-4-deoxychorismate lyase
P73_1254	hypothetical protein
P73_1255	ArsR family transcriptional regulator
P73_1256	ACR3 family arsenite efflux pump
P73_1257	arsenate reductase
P73_1265	fructosamine/ketosamine-3-kinase
P73_1283	phage integrase
P73_1284	tail tape measure protein, TP901 family
P73_1285	putative transposase for insertion sequence element
P73_1286	hypothetical protein
P73_1287	carbohydrate-binding family V/XII
P73_1288	hypothetical protein
P73_1289	hypothetical protein
P73_1290	hypothetical protein
P73_1291	glycoside hydrolase family protein
P73_1292	hypothetical protein
P73_1293	hypothetical protein
P73_1296	major facilitator superfamily protein
P73_1297	transcriptional regulator
P73_1299	isochorismatase family protein
P73_1302	hypothetical protein
P73_1313	oxidoreductase FAD/NAD(P)-binding subunit
P73_1325	Appr-1-p processing protein
P73_1327	Uncharacterized protein conserved in bacteria
P73_1331	hypothetical protein
P73_1332	BLUF domain-containing protein
P73_1339	Uncharacterized protein conserved in bacteria
P73_1341	Uncharacterized enzyme involved in biosynthesis of extracellular polysaccharides
P73_1350	Uncharacterized protein conserved in bacteria
P73_1352	phage head morphogenesis domain-containing protein
P73_1353	transposase IS116/IS110/IS902 family protein
P73_1355	transposase, IS4 family protein
P73_1356	Protein of unknown function (DUF1436)
P73_1357	Protein of unknown function (DUF1436)
P73_1358	Protein of unknown function (DUF1436)
P73_1363	hypothetical protein
P73_1364	ribose ABC transporter periplasmic binding protein
P73_1366	ribose ABC transporter permease
P73_1367	lactoylglutathione lyase-like protein
P73_1369	binding-protein-dependent transport systems inner membrane component
P73_1370	ABC transporter permease
P73_1371	ABC transporter substrate binding protein

P73_1374	Short chain dehydrogenase
P73_1375	transcriptional regulator
P73_1376	transcriptional regulator
P73_1379	C4-dicarboxylate transport system (Permease small protein)
P73_1381	acetaldehyde dehydrogenase
P73_1382	4-hyroxy-2-oxovalerate/4-hydroxy-2-oxopentanoic acid aldolase
P73_1383	hypothetical protein
P73_1384	hypothetical protein
P73_1385	HipA domain-containing protein
P73_1386	LysR family transcriptional regulator
P73_1387	allantoinase
P73_1389	OsrF
P73_1390	urocanate hydratase
P73_1391	DctP
P73_1392	tripartite ATP-independent periplasmic transporter DctQ
P73_1395	acyl-CoA dehydrogenase
P73_1396	short-chain specific acyl-CoA dehydrogenase
P73_1399	SNF2-related:helicase, C-terminal:type III restriction enzyme
P73_1402	RNA polymerase sigma factor protein (sigma-70)
P73_1403	Uncharacterized protein conserved in bacteria
P73_1405	Uncharacterized conserved protein
P73_1406	Transcriptional regulator
P73_1407	major facilitator superfamily transporter
P73_1408	HlyD family secretion protein
P73_1418	Domain of unknown function (DUF4272)
P73_1422	hypothetical protein
P73_1423	Reverse transcriptase (RNA-dependent DNA polymerase)
P73_1424	hypothetical protein
P73_1425	hypothetical protein
P73_1426	hypothetical protein
P73_1427	hypothetical protein
P73_1428	hypothetical protein
P73_1430	Bifunctional DNA primase/polymerase, N-terminal
P73_1431	transcriptional regulator
P73_1432	hypothetical protein
P73_1433	phage integrase
P73_1434	alkanesulfonate monooxygenase
P73_1435	Alkanesulfonate monooxygenase
P73_1436	ABC-type Fe3+ transport system, substrate binding component
P73_1438	binding-protein-dependent transport system inner membrane protein
P73_1439	ABC-type nitrate/sulfonate/bicarbonate transport systems, periplasmic components
P73_1441	binding-protein-dependent transporter inner membrane component
P73_1442	aliphatic sulfonates family ABC transporter periplasmic ligand-binding protein

P73_1490	hypothetical protein
P73_1491	Uncharacterized conserved protein
P73_1492	Small integral membrane protein
P73_1493	two-component response regulator
P73_1494	hypothetical protein
P73_1496	sensor signal transduction histidine kinase
P73_1516	transposase
P73_1519	Predicted membrane protein
P73_1538	glycosyl transferase
P73_1539	citrate transporter
P73_1553	hypothetical protein
P73_1564	hypothetical protein
P73_1595	Predicted transcriptional regulators
P73_1596	hypothetical protein
P73_1605	hypothetical protein
P73_1615	hypothetical protein
P73_1619	phospholipase, patatin family protein
P73_1620	hypothetical protein
P73_1645	putative IS256 family transposase
P73_1647	mannonate dehydratase
P73_1649	mannonate dehydratase
P73_1650	GntR family transcriptional regulator
P73_1651	5-dehydro-4-deoxyglucarate dehydratase
P73_1652	oligopeptide ABC transporter substrate binding protein
P73_1657	N-acylglucosamine 2-epimerase
P73_1658	putative sugar isomerase
P73_1659	short chain dehydrogenase
P73_1660	DeoR family transcriptional regulator
P73_1661	rhamnose ABC transporter periplasmic rhamnose-binding protein RhaS
P73_1663	putative-binding-protein-dependent transport system permease
P73_1664	sugar ABC transporter permease
P73_1665	Uncharacterized conserved protein
P73_1666	carbohydrate kinase
P73_1681	ion transport 2 family protein
P73_1682	hypothetical protein
P73_1700	Glycosyltransferases, probably involved in cell wall biogenesis
P73_1701	Domain of unknown function (DUF4174)
P73_1717	putative arylesterase
P73_1737	hypothetical protein
P73_1738	monooxygenase
P73_1750	hypothetical protein
P73_1751	hypothetical protein
P73_1752	Predicted transcriptional regulator

P73_1753	hypothetical protein
P73_1765	CopG family transcriptional regulator
P73_1767	LysR family transcriptional regulator
P73_1768	TetR family transcriptional regulator
P73_1769	multidrug resistance protein A
P73_1770	major facilitator transporter
P73_1771	TetR family transcriptional regulator
P73_1772	TetR family transcriptional regulator
P73_1773	Domain of Unknown Function with PDB structure (DUF3861)
P73_1774	dihydropteroic synthetase
P73_1787	Uncharacterized conserved protein (DUF2285)
P73_1788	hypothetical protein
P73_1792	Plasmid stability protein
P73_1793	hypothetical protein
P73_1795	helix-turn-helix domain-containing protein
P73_1796	type I restriction-modification system M subunit
P73_1797	restriction modification system DNA specificity domain-containing protein
P73_1798	SMC protein, N-terminal domain-containing protein
P73_1799	hypothetical protein
P73_1801	hypothetical protein
P73_1802	hypothetical protein
P73_1803	recombinase
P73_1804	Protein of unknown function (DUF2924)
P73_1805	Predicted Zn peptidase
P73_1806	helix-hairpin-helix DNA-binding motif-containing protein
P73_1807	Uncharacterized protein conserved in bacteria (DUF2188)
P73_1808	hypothetical protein
P73_1809	hypothetical protein
P73_1810	Nucleotidyl transferase of unknown function (DUF1814)
P73_1811	Domain of unknown function (DUF4095)
P73_1813	hypothetical protein
P73_1814	AAA domain
P73_1815	Protein of unknown function (DUF669)
P73_1816	hypothetical protein
P73_1817	hypothetical protein
P73_1818	superfamily II DNA/RNA helicase
P73_1819	hypothetical protein
P73_1820	hypothetical protein
P73_1821	hypothetical protein
P73_1822	hypothetical protein
P73_1823	modification methylase DpnIIB
P73_1824	putative site-specific DNA methylase
P73_1825	hypothetical protein

P73_1826	Protein of unknown function (DUF3489)
P73_1827	hypothetical protein
P73_1828	hypothetical protein
P73_1829	terminase small subunit, Nu1
P73_1830	phage terminase large subunit (GpA)
P73_1831	hypothetical protein
P73_1832	phage portal protein, lambda family
P73_1833	peptidase U35 phage prohead HK97
P73_1834	Uncharacterized conserved protein
P73_1835	hypothetical protein
P73_1836	hypothetical protein
P73_1837	hypothetical protein
P73_1838	hypothetical protein
P73_1839	hypothetical protein
P73_1840	Lambda phage tail tape-measure protein (Tape_meas_lam_C)
P73_1842	hypothetical protein
P73_1843	hypothetical protein
P73_1844	lysozyme
P73_1845	hypothetical protein
P73_1852	Type I site-specific deoxyribonuclease, HsdR family protein
P73_1853	serine/threonine protein kinase
P73_1854	hypothetical protein
P73_1855	hypothetical protein
P73_1856	peptidase M15A
P73_1857	hypothetical protein
P73_1858	transposase IS116/IS110/IS902 family protein
P73_1859	hypothetical protein
P73_1860	Uncharacterized conserved protein (DUF2285)
P73_1861	hypothetical protein
P73_1865	Plasmid stability protein
P73_1866	hypothetical protein
P73_1868	helix-turn-helix domain-containing protein
P73_1869	type I restriction-modification system M subunit
P73_1870	restriction modification system DNA specificity domain-containing protein
P73_1871	SMC protein, N-terminal domain-containing protein
P73_1872	hypothetical protein
P73_1874	hypothetical protein
P73_1875	hypothetical protein
P73_1876	recombinase
P73_1877	Protein of unknown function (DUF2924)
P73_1878	Predicted Zn peptidase
P73_1879	helix-hairpin-helix DNA-binding motif-containing protein
P73_1880	Uncharacterized protein conserved in bacteria (DUF2188)

P73_1881	hypothetical protein
P73_1882	hypothetical protein
P73_1883	Nucleotidyl transferase of unknown function (DUF1814)
P73_1884	Domain of unknown function (DUF4095)
P73_1886	hypothetical protein
P73_1887	AAA domain
P73_1888	Protein of unknown function (DUF669)
P73_1889	hypothetical protein
P73_1890	hypothetical protein
P73_1891	superfamily II DNA/RNA helicase
P73_1892	hypothetical protein
P73_1893	hypothetical protein
P73_1894	hypothetical protein
P73_1895	hypothetical protein
P73_1896	modification methylase DpnIIB
P73_1897	putative site-specific DNA methylase
P73_1898	hypothetical protein
P73_1899	Protein of unknown function (DUF3489)
P73_1900	hypothetical protein
P73_1901	hypothetical protein
P73_1902	terminase small subunit, Nu1
P73_1903	phage terminase large subunit (GpA)
P73_1904	hypothetical protein
P73_1905	phage portal protein, lambda family
P73_1906	peptidase U35 phage prohead HK97
P73_1907	Uncharacterized conserved protein
P73_1908	hypothetical protein
P73_1909	hypothetical protein
P73_1910	hypothetical protein
P73_1911	hypothetical protein
P73_1912	hypothetical protein
P73_1913	Lambda phage tail tape-measure protein (Tape_meas_lam_C)
P73_1915	hypothetical protein
P73_1916	hypothetical protein
P73_1917	lysozyme
P73_1918	hypothetical protein
P73_1925	Type I site-specific deoxyribonuclease, HsdR family protein
P73_1926	serine/threonine protein kinase
P73_1927	hypothetical protein
P73_1928	hypothetical protein
P73_1929	peptidase M15A
P73_1930	hypothetical protein
P73_1932	transposase, IS4 family protein

P73_1933	hypothetical protein
P73_1936	heavy metal transport/detoxification protein
P73_1937	Uncharacterized protein conserved in bacteria
P73_1940	type 12 methyltransferase
P73_1941	hypothetical protein
P73_1942	Resolvase
P73_1943	Inosine/uridine-preferring nucleoside hydrolase
P73_1944	RpiR family transcriptional regulator
P73_1945	twin-arginine translocation pathway signal
P73_1946	twin-arginine translocation pathway signal
P73_1947	S-adenosylhomocysteine deaminase, methylthioadenosine deaminase
P73_1949	nitrate/sulfonate/bicarbonate ABC transporter permease
P73_1950	ABC transporter-like protein permease
P73_1951	nucleoside 2-deoxyribosyltransferase
P73_1952	transposase, mutator type
P73_1955	cytosine deaminase-like protein metal-dependent hydrolase
P73_1960	hypothetical protein
P73_1961	hypothetical protein
P73_1962	hypothetical protein
P73_1963	hypothetical protein
P73_1964	hypothetical protein
P73_1965	hypothetical protein
P73_1966	hypothetical protein
P73_1967	hypothetical protein
P73_1968	PIN domain-containing protein
P73_1969	AbrB family transcriptional regulator
P73_1970	Predicted transcriptional regulator
P73_1974	Predicted permease
P73_1977	polysaccharide deacetylase
P73_1978	helix-turn-helix domain-containing protein
P73_1979	transposase
P73_1980	transposase
P73_1981	Uncharacterized conserved protein
P73_1982	activator of Hsp90 ATPase 1 family protein
P73_1984	regulatory protein, IclR
P73_1985	TRAP dicarboxylate transporter, DctP subunit
P73_1986	tripartite ATP-independent periplasmic transporter DctQ
P73_1988	dihydroorotate dehydrogenase
P73_1989	hypothetical protein
P73_1990	HpcH/HpaI aldolase
P73_1991	cupin 2 barrel domain-containing protein
P73_1994	LysR family transcriptional regulator
P73_1995	putative luciferase-like monooxygenase

P73_1996	monooxygenase
P73_1999	extracellular solute-binding protein
P73_2000	major facilitator superfamily transporter
P73_2002	Uncharacterized protein involved in propionate catabolism
P73_2004	NADPH-dependent FMN reductase
P73_2005	flavin-dependent reductase
P73_2007	biotin sulfoxide reductase
P73_2009	Tripartite tricarboxylate transporter TctB family
P73_2012	MaoC-like dehydratase
P73_2013	Uncharacterized protein conserved in bacteria
P73_2014	putative sensor histidine kinase
P73_2016	hypothetical protein
P73_2017	hypothetical protein
P73_2018	Uncharacterized protein conserved in bacteria
P73_2019	transcriptional regulator
P73_2020	6-phosphogluconate dehydrogenase
P73_2022	bleomycin resistance protein
P73_2023	Alpha/beta hydrolase family
P73_2024	alpha/beta hydrolase fold protein
P73_2026	binding-protein-dependent transport system inner membrane protein
P73_2027	iron(III) ABC transporter iron (III)-binding protein
P73_2029	LysR family transcriptional regulator
P73_2030	putative oxidoreductase protein
P73_2033	taurine catabolism dioxygenase TauD/TfdA
P73_2034	NMT1/THI5-like domain-containing protein
P73_2038	isoleucine patch superfamily carbonic anhydrase/acetyltransferase
P73_2040	replicative DNA helicase
P73_2041	HNH endonuclease domain-containing protein
P73_2042	hypothetical protein
P73_2043	ABC transporter substrate-binding protein
P73_2044	ABC transporter substrate-binding protein
P73_2045	putative ribulose-5-phosphate 4-epimerase-like epimerase
P73_2046	LysR family transcriptional regulator
P73_2047	ABC transporter substrate-binding protein
P73_2049	binding-protein-dependent transport system inner membrane protein
P73_2050	TRAP dicarboxylate transporter subunit DctP
P73_2051	TRAP-type C4-dicarboxylate transport system, small permease component
P73_2053	aldo/keto reductase
P73_2055	polar amino acid ABC transporter inner membrane subunit
P73_2058	extracellular solute-binding protein
P73_2059	SMP-30/gluconolaconase/LRE domain-containing protein
P73_2061	putative glyoxalase
P73_2062	acetolactate synthase, large chain related protein

P73_2063	amidohydrolase
P73_2064	flavoprotein
P73_2065	hypothetical protein
P73_2066	polysaccharide deacetylase
P73_2069	short-chain aldo-keto oxidoreductase
P73_2070	ABC transporter substrate-binding protein
P73_2071	TRAP transport system, small permease protein
P73_2074	aliphatic sulfonate ABC transporter periplasmic ligand-binding protein
P73_2075	transposase, IS4 family protein
P73_2077	transposase IS116/IS110/IS902 family protein
P73_2078	aliphatic sulfonate ABC transporter periplasmic ligand-binding protein
P73_2081	alkanesulfonate monooxygenase
P73_2082	taurine transport system permease
P73_2084	taurine ABC transporter periplasmic binding protein
P73_2086	hypothetical protein
P73_2087	Uncharacterized protein conserved in bacteria
P73_2088	TRAP-type mannitol/chloroaromatic compound transport system, small permease component
P73_2090	TRAP dicarboxylate transporter- DctP subunit
P73_2091	AraC family transcriptional regulator
P73_2092	regulatory protein LuxR
P73_2093	putative cyclase
P73_2096	TRAP dicarboxylate transporter subunit DctM
P73_2098	putative periplasmic substrate binding protein
P73_2099	putative transcriptional regulator
P73_2100	UDP-glucose 4-epimerase
P73_2101	Predicted metal-dependent enzyme of the double-stranded beta helix superfamily
P73_2102	Uncharacterized conserved protein
P73_2105	periplasmic binding protein
P73_2106	esterase
P73_2107	enterobactin synthase subunit F
P73_2108	phosphopantetheine-binding protein
P73_2109	AMP-dependent synthetase and ligase
P73_2110	TRAP dicarboxylate transporter subunit DctQ
P73_2112	TRAP transporter-DctP subunit
P73_2114	TonB-dependent receptor precursor
P73_2115	MarR family transcriptional regulator
P73_2116	alkyl hydroperoxide reductase/ thiol specific antioxidant/ Mal allergen
P73_2117	FAD-dependent pyridine nucleotide-disulfide oxidoreductase
P73_2118	ferredoxin
P73_2120	ABC transporter permease
P73_2121	aliphatic sulfonates ABC transporter substrate-binding protein
P73_2122	drug resistance transporter, EmrB/QacA subfamily protein

P73_2123	dehydrogenase
P73_2128	acetyltransferase
P73_2129	putative amino-acid ABC transporter, periplasmic solute-binding protein
P73_2132	Glutathione S-transferase domain protein
P73_2134	NMT1/THI5-like domain-containing protein
P73_2139	ABC transporter periplasmic protein
P73_2141	ABC transporter membrane subunit
P73_2142	Arylsulfotransferase (ASST)
P73_2143	regulatory protein LacI:Periplasmic binding protein/LacI transcriptional regulator
P73_2144	LysR family transcripitonal regulator
P73_2147	thiamine biosynthesis protein
P73_2149	binding-protein-dependent transport system inner membrane protein
P73_2150	aromatic hydrocarbon dioxygenase small subunit
P73_2151	Rieske (2Fe-2S) domain-containing protein
P73_2152	Predicted ester cyclase
P73_2153	Phytanoyl-CoA dioxygenase (PhyH)
P73_2179	transposase
P73_2202	hypothetical protein
P73_2208	hypothetical protein
P73_2210	Uncharacterized membrane protein
P73_2213	Lysophospholipase
P73_2214	GSCFA family
P73_2215	hypothetical protein
P73_2238	Predicted permeases
P73_2252	hypothetical protein
P73_2260	transposase
P73_2261	transposase
P73_2263	hypothetical protein
P73_2265	hypothetical protein
P73_2266	hypothetical protein
P73_2267	Acetyltransferase (GNAT) domain
P73_2268	Uncharacterized protein conserved in bacteria
P73_2271	hypothetical protein
P73_2272	Uncharacterized conserved protein (DUF2285)
P73_2283	TetR family transcriptional regulator
P73_2284	Sterol-4-alpha-carboxylate 3-dehydrogenase,decarboxylating
P73_2285	LysR family transcriptional regulator
P73_2287	CopG family transcriptional regulator
P73_2299	transcription regulator, TetR family protein
P73_2300	glucose/ribitol short chain dehydrogenase/reductase family protein
P73_2301	hypothetical protein
P73_2302	Predicted transcriptional regulator
P73_2303	Site-specific recombinase

P73_2308	hypothetical protein
P73_2322	Nitroreductase
P73_2323	Asp/Glu racemase
P73_2325	ABC transporter permease
P73_2326	spermidine/putrescine-binding periplasmic protein
P73_2328	Hydantoinase
P73_2329	Uncharacterized conserved protein
P73_2330	Uncharacterized conserved protein
P73_2331	transcriptional regulator, LuxR family protein
P73_2332	xenobiotic compound monooxygenase A subunit
P73_2334	hydantoinase A
P73_2335	Uncharacterized conserved protein
P73_2336	twin-arginine translocation pathway signal
P73_2348	hypothetical protein
P73_2349	hypothetical protein
P73_2350	methyltransferase FkbM
P73_2351	Uncharacterized conserved protein
P73_2355	hypothetical protein
P73_2362	NADH:flavin oxidoreductase
P73_2363	Acetoacetate decarboxylase (ADC)
P73_2364	alpha/beta hydrolase
P73_2365	putative non-heme chloroperoxidase
P73_2368	transcriptional regulator
P73_2378	TetR family transcriptional regulator
P73_2379	putative sulfate ester transport system substrate-binding protein
P73_2380	binding-protein-dependent transport system inner membrane protein
P73_2381	putative alkanesulfonate transport protein, ABC superfamily, inner membrane component
P73_2383	NADH-quinone oxidoreductase subunits H/I
P73_2384	glucose-inhibited division protein A
P73_2392	ketosteroid isomerase-like protein
P73_2394	Predicted esterase of the alpha/beta hydrolase fold
P73_2396	AraC family transcriptional regulator
P73_2397	Predicted permeases
P73_2398	Predicted ATPase
P73_2399	outer membrane receptor FepA
P73_2400	nitroreductase
P73_2401	phosphoribosyltransferase
P73_2403	PEBP family protein
P73_2406	sulfonate/nitrate transport system substrate-binding protein
P73_2407	Protein of unknown function (DUF3016)
P73_2408	Transcriptional regulator
P73_2413	periplasmic binding protein/LacI transcriptional regulator
P73_2414	FMN-dependent oxidoreductase, nitrilotriacetate monooxygenase family

P73_2416	ferric vibriobactin receptor
P73_2418	MarR family transcriptional regulator
P73_2419	GntR family transcriptional regulator
P73_2422	hypothetical protein
P73_2424	hypothetical protein
P73_2426	gluconate 2-dehydrogenase (acceptor)
P73_2427	Gluconate 2-dehydrogenase subunit 3
P73_2434	integrase catalytic region
P73_2435	transposase IS3/IS911 family protein
P73_2436	IS66 Orf2 family protein
P73_2437	transposase IS66
P73_2438	transposase
P73_2439	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase
P73_2440	Transcription antiterminator
P73_2441	group 1 glycosyl transferase
P73_2442	group 1 glycosyl transferase
P73_2443	O-antigen ligase like membrane protein
P73_2444	glycosyl transferase family protein
P73_2445	hypothetical protein
P73_2446	Sulfotransferase family
P73_2447	polysaccharide biosynthesis protein
P73_2448	MarR family transcriptional regulator
P73_2449	transposase, mutator type
P73_2450	transposase
P73_2453	phage-related integrase
P73_2454	RelE/StbE family addiction module toxin
P73_2455	hypothetical protein
P73_2456	prophage CP4-57 regulatory
P73_2457	hypothetical protein
P73_2458	hypothetical protein
P73_2459	hypothetical protein
P73_2460	hypothetical protein
P73_2461	hypothetical protein
P73_2462	hypothetical protein
P73_2463	HK97 family phage portal protein
P73_2464	hypothetical protein
P73_2465	HK97 family phage major capsid protein
P73_2466	hypothetical protein
P73_2467	HNH endonuclease
P73_2468	hypothetical protein
P73_2469	phage protein
P73_2470	Phage protein, HK97, gp10

P73_2471	Protein of unknown function (DUF3168)
P73_2472	phage head-tail adaptor
P73_2473	P27 family phage terminase small subunit
P73_2474	Phage terminase-like protein
P73_2475	Phage-related minor tail protein
P73_2476	hypothetical protein
P73_2477	hypothetical protein
P73_2480	Crp/FNR family transcriptional regulator
P73_2481	signal transduction histidine kinase
P73_2486	Predicted peroxiredoxins
P73_2491	Uncharacterized protein conserved in bacteria
P73_2497	beta-lactamase
P73_2508	hypothetical protein
P73_2510	Predicted phosphohydrolases
P73_2511	hypothetical protein
P73_2512	Protein required for attachment to host cells
P73_2528	hypothetical protein
P73_2572	soluble aldose sugar dehydrogenase YliI
P73_2581	Polyketide cyclase / dehydrase and lipid transport
P73_2583	short chain oxidoreductase
P73_2584	Protein of unknown function (DUF2934)
P73_2585	Protein of unknown function (DUF1451)
P73_2586	hypothetical protein
P73_2587	hypothetical protein
P73_2591	hypothetical protein
P73_2595	hypothetical protein
P73_2596	LysR family transcriptional regulator
P73_2609	hypothetical protein
P73_2608	Uncharacterized protein conserved in bacteria
P73_2624	hypothetical protein
P73_2634	heat shock protein HtpX
P73_2649	hypothetical protein
P73_2650	Uncharacterized homolog of Blt101
P73_2652	hypothetical protein
P73_2698	CBS-domain-containing membrane protein
P73_2701	alkylphosphonate utilization protein PhnA
P73_2703	integrase family protein
P73_2704	SPW repeat
P73_2705	DNA-directed RNA polymerase, omega subunit
P73_2706	ETC complex I subunit region
P73_2708	hypothetical protein
P73_2709	amylo-alpha-1,6-glucosidase
P73_2710	group 1 glycosyl transferase

P73_2711	sodium/hydrogen exchanger
P73_2715	protease HtpX family protein
P73_2716	Heat shock protein Hsp20
P73_2717	heat shock protein Hsp20
P73_2733	small heat-shock protein molecular chaperone
P73_2734	heat shock protein Hsp20
P73_2737	Uncharacterized conserved protein
P73_2739	YfdX protein
P73_2742	heat shock protein HtpX
P73_2743	TrkA-C domain protein
P73_2759	hypothetical protein
P73_2763	Fic family protein
P73_2767	hypothetical protein
P73_2768	hypothetical protein
P73_2770	hypothetical protein
P73_2771	putative ATPase
P73_2772	peptidase S8 family protein
P73_2773	Protein of unknown function (DUF982)
P73_2775	putative cystein protease, Transglutaminase-like domain protein
P73_2777	hypothetical protein
P73_2778	hypothetical protein
P73_2786	Pyocin activator protein PrtN
P73_2787	Domain of unknown function (DUF4095)
P73_2788	hypothetical protein
P73_2790	hypothetical protein
P73_2791	hypothetical protein
P73_2794	fatty acid desaturase
P73_2795	hypothetical protein
P73_2799	CRP family transcriptional regulator
P73_2800	hypothetical protein
P73_2801	fatty acid desaturase
P73_2802	hypothetical protein
P73_2804	hypothetical protein
P73_2805	hypothetical protein
P73_2806	hypothetical protein
P73_2807	hypothetical protein
P73_2808	hypothetical protein
P73_2817	LysR family transcriptional regulator
P73_2819	mandelate racemase/muconate lactonizing protein
P73_2822	putative sarcosine oxidase subunit alpha
P73_2825	BioY protein
P73_2826	biotin synthase
P73_2828	pyridoxal kinase

P73_2830	transcriptional regulator
P73_2831	exported protein (TRAP-type transport system, periplasmic component)
P73_2832	TRAP C4-dicarboxylate transport system subunit DctQ
P73_2834	arylmalonate decarboxylase
P73_2835	Domain of unknown function (DUF4392)
P73_2836	C4-dicarboxylate-binding periplasmic protein
P73_2837	putative DctQ (C4-dicarboxylate permease, small subunit)
P73_2839	decarboxylase
P73_2840	hydantoinase B
P73_2848	choline/ethanolamine kinase
P73_2849	aminoglycoside phosphotransferase
P73_2850	allantoate amidohydrolase
P73_2854	extracellular solute-binding protein
P73_2858	acetone carboxylase subunit gamma
P73_2860	acetone carboxylase subunit beta
P73_2864	short-chain dehydrogenase/reductase sDR
P73_2865	short-chain dehydrogenase
P73_2866	dihydrodipicolinate synthetase
P73_2867	permease
P73_2869	putative amidohydrolase
P73_2870	putative ABC transporter substrate binding protein
P73_2873	binding-protein-dependent transporters inner membrane component
P73_2875	Rieske (2Fe-2S) domain-containing protein
P73_2876	putative amidohydrolase
P73_2879	endoribonuclease L-PSP
P73_2884	Class I triheme cytochrome c
P73_2885	Uncharacterized protein conserved in bacteria
P73_2917	diacylglycerol kinase catalytic subunit
P73_2918	metallophosphoesterase
P73_2946	Predicted Zn-dependent protease (DUF2268)
P73_2958	amidohydrolase 2
P73_2959	hypothetical protein
P73_2960	Rieske (2Fe-2S) iron-sulfur domain-containing protein
P73_2961	putative Transcriptional regulator, MarR family protein
P73_2962	EamA-like transporter family
P73_2963	hypothetical protein
P73_2964	4,5-dihydroxyphthalate decarboxylase
P73_2965	oxidoreductase domain-containing protein
P73_2970	hypothetical protein
P73_2972	acetolactate synthase II
P73_2973	arylmalonate decarboxylase
P73_2974	TRAP-type C4-dicarboxylate transport system, periplasmic component
P73_2976	TRAP-T family transporter, DctQ (4 TMs) subunit

P73_2977	hydantoinase B
P73_2978	N-methylhydantoinase A/acetone carboxylase, beta subunit
P73_2981	IclR family transcriptional regulator
P73_2985	MarR family transcriptional regulator
P73_2986	putative periplasmic binding protein
P73_2988	streptomycin 3"-adenylyltransferase
P73_2994	hypothetical protein
P73_3004	PA-phosphatase-like phosphoesterase
P73_3019	PRC-barrel domain
P73_3024	glyoxalase/bleomycin resistance protein/dioxygenase
P73_3042	bacterioferritin
P73_3043	bacterioferritin-associated ferredoxin
P73_3058	hypothetical protein
P73_3070	hypothetical protein
P73_3071	polysaccharide biosynthesis protein
P73_3072	putative glycosyltransferase
P73_3073	Glycosyltransferase
P73_3074	succinoglycan biosynthesis protein ExoM
P73_3076	putative licheninase
P73_3077	succinoglycan biosynthesis protein ExoO
P73_3078	putative exopolysaccharide production protein
P73_3079	family 2 glycosyl transferase
P73_3080	succinoglycan biosynthesis protein ExoA
P73_3081	putative glycosyl transferase
P73_3082	oxidoreductase domain-containing protein
P73_3083	O-antigen polymerase
P73_3084	succinoglycan biosynthesis transport protein exoP
P73_3085	glucose sorbosone dehydrogenase
P73_3099	allophanate hydrolase subunit 1
P73_3100	D-isomer specific 2-hydroxyacid dehydrogenase NAD-binding protein
P73_3105	family 5 extracellular solute-binding protein
P73_3106	Uncharacterized protein conserved in bacteria
P73_3110	LacI family transcriptional regulator
P73_3112	Uncharacterized protein conserved in bacteria
P73_3113	hypothetical protein
P73_3114	glycerophosphoryl diester phosphodiesterase
P73_3119	twin-arginine translocation pathway signal
P73_3122	RpiR family transcriptional regulator
P73_3123	LacI family transcriptional regulator
P73_3124	extracellular solute-binding protein
P73_3126	spermidine/putrescine ABC transporter permease
P73_3130	flavin reductase domain-containing protein
P73_3131	catalase

P73_3134	ABC transporter substrate-binding protein
P73_3139	SnoaL-like domain
P73_3140	cyclododecanone monooxygenase
P73_3141	sodium/bile acid symporter family (MazG-like protein)
P73_3142	polysaccharide deacetylase
P73_3143	polysaccharide deacetylase family protein
P73_3145	Transcriptional regulator
P73_3146	ABC transporter substrate binding protein
P73_3148	binding-protein-dependent transporter inner membrane component
P73_3149	Predicted flavoprotein involved in K+ transport
P73_3150	ring-opening amidohydrolase
P73_3151	peptidylglycine alpha-amidating monooxygenase
P73_3152	Uncharacterized conserved protein
P73_3167	Protein of unknwon function (DUF3008)
P73_3170	transcriptional regulator
P73_3171	hypothetical protein
P73_3179	lytic transglycosylase
P73_3181	(3S)-malyl-CoA thioesterase
P73_3208	DNA topoisomerase
P73_3219	transposase
P73_3220	transposase
P73_3237	hypothetical protein
P73_3238	hypothetical protein
P73_3239	hypothetical protein
P73_3240	phage/plasmid primase, P4 family, C-terminal domain
P73_3241	hypothetical protein
P73_3242	Helix-turn-helix domain
P73_3243	hypothetical protein
P73_3244	integrase family protein
P73_3245	resolvase-like protein
P73_3246	hypothetical protein
P73_3247	hypothetical protein
P73_3248	hypothetical protein
P73_3249	hypothetical protein
P73_3250	TraG/TraD family protein
P73_3251	Uncharacterized protein containing a von Willebrand factor type A (vWA) domain
P73_3252	hypothetical protein
P73_3253	hypothetical protein
P73_3255	histone-like nucleoid-structuring protein H-NS
P73_3256	hypothetical protein
P73_3257	DNA methyltransferase
P73_3258	restriction enzyme
P73_3259	McrBC 5-methylcytosine restriction system component

P73_3261	hypothetical protein
P73_3262	Filamentation induced by cAMP protein Fic
P73_3263	hypothetical protein
P73_3264	hypothetical protein
P73_3265	hypothetical protein
P73_3266	hypothetical protein
P73_3267	phosphoglycerate kinase
P73_3268	hypothetical protein
P73_3269	hypothetical protein
P73_3270	relaxase/mobilization nuclease domain-containing protein
P73_3271	hypothetical protein
P73_3272	dienelactone hydrolase family protein
P73_3286	N-acetyltransferase GCN5
P73_3287	transcriptional regulator, TraR/DksA family
P73_3328	cytochrome o ubiquinol oxidase subunit II
P73_3330	cytochrome o ubiquinol oxidase subunit III (Ubiquinol oxidase chain C)
P73_3331	cytochrome C oxidase subunit IV
P73_3332	putative SURF1 family protein
P73_3339	transcriptional regulator
P73_3340	peptidase T
P73_3351	exsB protein
P73_3354	Putative homoserine kinase type II (protein kinase fold)
P73_3370	hypothetical protein
P73_3380	Predicted periplasmic or secreted lipoprotein
P73_3381	Uncharacterized conserved protein
P73_3422	exopolysaccharide synthesis, exoD
P73_3423	hypothetical protein
P73_3462	Adenylate kinase and related kinases
P73_3472	hypothetical protein
P73_3490	MgtC/SapB transporter
P73_3502	Uncharacterized protein conserved in bacteria (DUF2065)
P73_3512	DNA-O6-methylguanine--protein-cysteine S-methyltransferase/transcriptional regulator Ada
P73_3539	hypothetical protein
P73_3547	bleMBL
P73_3554	Uncharacterized protein conserved in bacteria, putative lipoprotein
P73_3555	EamA-like transporter family
P73_3556	AAA domain
P73_3558	hypothetical protein
P73_3560	hypothetical protein
P73_3561	Molecular chaperone, HSP90 family
P73_3562	endonuclease
P73_3563	Domain of unknown function (DUF4420)

P73_3564	AIPR protein
P73_3565	DNA-cytosine methyltransferase
P73_3566	DNA mismatch endonuclease Vsr
P73_3567	TniQ
P73_3570	MscS mechanosensitive ion channel
P73_3574	CHAD domain-containing protein
P73_3581	putative restriction endonuclease
P73_3582	hypothetical protein
P73_3584	hypothetical protein
P73_3585	hypothetical protein
P73_3587	type 12 methyltransferase
P73_3606	Hemerythrin HHE cation binding domain
P73_3624	hypothetical protein
P73_3634	putative divalent heavy-metal cations transporter
P73_3635	hypothetical protein
P73_3662	extracellular nuclease
P73_3665	ybaK/ebsC protein
P73_3673	Hpt domain
P73_3676	Invasion associated locus B family protein
P73_3677	serine protease/outer membrane autotransporter
P73_3678	Ku protein, prokaryotic
P73_3679	DNA polymerase LigD polymerase domain-containing protein
P73_3680	Predicted membrane protein
P73_3683	diacylglycerol kinase
P73_3684	hypothetical protein
P73_3688	TonB-dependent receptor
P73_3691	Transposase DDE domain group 1
P73_3706	Na/Pi-cotransporter II-like protein
P73_3708	hemolysin-type calcium-binding region
P73_3709	2,3-dimethylmalate lyase
P73_3710	PrpF family protein
P73_3711	GntR family transcriptional regulator
P73_3712	Uncharacterized protein conserved in bacteria
P73_3713	Tripartite tricarboxylate transporter TctB family
P73_3717	4-oxalomesaconate hydratase
P73_3718	TRAP transporter solute receptor, TAXI family protein
P73_3720	2-polyprenyl-6-methoxyphenol hydroxylase and related FAD-dependent oxidoreductases
P73_3721	IclR family transcriptional regulator
P73_3722	aldo/keto reductase
P73_3723	transcriptional regulator
P73_3733	carbamate kinase
P73_3735	arginine deiminase
P73_3736	arginine repressor

P73_3738	TRAP transporter DctQ-like subunit
P73_3739	2,3-diketo-L-gulonate-binding periplasmic protein
P73_3740	hypothetical protein
P73_3742	thiamine pyrophosphate TPP-binding domain-containing protein
P73_3744	TRAP dicarboxylate transporter subunit DctQ
P73_3745	TRAP dicarboxylate transporter subunit DctP
P73_3748	Peptidase S15
P73_3749	Major facilitator superfamily MFS_1
P73_3750	Extracellular solute-binding protein, family 5 precursor
P73_3755	GntR family transcriptional regulator
P73_3756	hypothetical protein
P73_3757	hypothetical protein
P73_3758	hypothetical protein
P73_3761	hypothetical protein
P73_3762	hypothetical protein
P73_3763	hypothetical protein
P73_3764	hypothetical protein
P73_3765	hypothetical protein
P73_3766	Thermostable 8-oxoguanine DNA glycosylase
P73_3767	hypothetical protein
P73_3768	nucleoside 2-deoxyribosyltransferase family protein
P73_3769	Predicted PP-loop superfamily ATPase
P73_3770	transposase, IS4 family protein
P73_3771	hypothetical protein
P73_3772	hypothetical protein
P73_3774	ABC transporter substrate binding protein (glycerol-3-phosphate)
P73_3775	ABC transporter membrane spanning protein (glycerol-3-phosphate)
P73_3776	ABC transporter membrane spanning protein (glycerol-3-phosphate)
P73_3777	glycerophosphoryl diester phosphodiesterase
P73_3779	RpiR family transcriptional regulator
P73_3780	Uncharacterized protein conserved in bacteria
P73_3784	ACR3 family arsenite efflux pump
P73_3785	arsenate reductase
P73_3786	arsenical resistance protein arsh
P73_3788	major facilitator transporter
P73_3789	hypothetical protein
P73_3790	ArsR family transcriptional regulator
P73_3793	putative transposase
P73_3794	transposase mutator type
P73_3816	protein YjbJ
P73_3854	acylphosphatase
P73_3856	hypothetical protein
P73_3859	Inner membrane protein involved in colicin E2 resistance

P73_3861	exoV domain-containing protein
P73_3876	hypothetical protein
P73_3885	ABC transporter
P73_3887	nitrate/sulfonate/bicarbonate ABC transporter permease
P73_3888	ABC-type nitrate/sulfonate/bicarbonate transport system, substrate binding protein
P73_3917	GntR family transcriptional regulator
P73_3918	ABC-type Fe3+ transport system permease component
P73_3919	Acyl-CoA dehydrogenase, C-terminal:Acyl-CoA dehydrogenase, central region:Acyl-CoA dehydrogenase, N-terminal:Acyl-CoA dehydrogenase, N-terminal
P73_3920	transposase, orfB
P73_3921	transposase IS3/IS911 family protein
P73_3922	TonB-dependent outermembrane ferripyoverdine receptor FpvA
P73_3923	putative transmembrane sensor protein
P73_3924	ECF subfamily RNA polymerase sigma-24 factor
P73_3928	hypothetical protein
P73_3929	hypothetical protein
P73_3930	curli production assembly/transport component CsgG
P73_3932	major facilitator superfamily transporter
P73_3935	Transcriptional regulator, XRE family protein
P73_3936	TRAP dicarboxylate transporter subunit DctP
P73_3937	tripartite AtP-independent periplasmic transporter subunit DctQ
P73_3939	oxidoreductase FAD-binding subunit
P73_3940	dihydroorotate dehydrogenase family protein
P73_3941	amidase
P73_3943	hypothetical protein
P73_3944	RpiR family transcriptional regulator
P73_3946	nitrate/sulfonate/bicarbonate ABC transporter periplasmic protein
P73_3948	binding-protein-dependent transport system inner membrane protein
P73_3949	ABC transporter, membrane spanning protein
P73_3950	extracellular solute-binding protein
P73_3951	peptidase M24
P73_3952	phosphoenolpyruvate carboxylase
P73_3956	nitrate/nitrite regulatory protein
P73_3962	TetR family transcriptional regulator
P73_3963	tetrahydromethanopterin S-methyltransferase subunit H
P73_3964	methyltransferase CmuC
P73_3966	regulatory protein FmdB
P73_3967	electron transfer protein PaaE
P73_3968	imidazolonepropionase
P73_3969	5,10-methylenetetrahydrofolate reductase
P73_3970	hypothetical protein
P73_3971	major facilitator family protein
P73_3972	transposase

P73_3973	transposase
P73_3975	transcriptional regulator
P73_3976	4'-phosphopantetheinyl transferase
P73_3977	extracytoplasmic-function sigma-70 factor
P73_3978	L-ornithine 5-monooxygenase
P73_3979	putative siderophore biosynthesis protein
P73_3980	esterase
P73_3982	efflux transporter inner membrane protein
P73_3983	mbtH-like protein
P73_3984	amino acid adenylation domain-containing protein
P73_3986	transport system permease
P73_3988	periplasmic binding protein
P73_3989	ferrichrome receptor precursor protein
P73_3990	HipA-like C-terminal domain/HipA-like N-terminal domain
P73_3991	Transposase and inactivated derivatives
P73_3992	HipA-like protein
P73_3993	short-chain alcohol dehydrogenase-like protein
P73_3994	tagatose-6-phosphate ketose/aldose isomerase
P73_3996	N-acetylglucosamine-6-phosphate deacetylase
P73_3997	N-acetyl-D-glucosamine kinase
P73_3998	transcriptional repressor of aga operon
P73_4000	hypothetical protein
P73_3999	binding-protein-dependent transport systems inner membrane component
P73_4001	maltose ABC transporter transmembrane protein
P73_4002	extracellular solute-binding protein family 1
P73_4004	Domain of unknown function (DUF4091)
P73_4005	Predicted membrane protein (DUF2207)
P73_4006	tripartite ATP-independent periplasmic transporter DctQ component
P73_4007	TRAP dicarboxylate transporter subunit DctP
P73_4009	FAD dependent oxidoreductase
P73_4010	LysR family transcriptional regulator
P73_4011	LysR family transcriptional regulator
P73_4012	dibenzothiophene desulfurziation enzyme
P73_4013	3-mercaptopyruvate sulfurtransferase
P73_4015	haloacid dehalogenase domain-containing protein hydrolase
P73_4016	endoribonuclease L-PSP
P73_4017	hydroxyethylthiazole kinase
P73_4018	LysR family transcriptional regulator
P73_4019	LysR family transcriptional regulator
P73_4020	Hydrolases of the alpha/beta superfamily
P73_4021	NADH(P)-binding
P73_4022	riboflavin synthase subunit beta
P73_4023	GntR family transcriptional regulator

P73_4024	Demethylmenaquinone methyltransferase
P73_4026	binding-protein-dependent transport systems inner membrane component
P73_4028	extracellular solute-binding protein family 1 protein
P73_4029	ribose-5-phosphate isomerase B
P73_4030	LysR family transcriptional regulator
P73_4034	ABC transporter substrate binding protein
P73_4035	oligopeptide ABC transporter substrate binding protein
P73_4036	aliphatic sulfonates family ABC transporter periplasmic ligand-binding protein
P73_4037	acyl-CoA dehydrogenase
P73_4038	monooxygenase
P73_4039	NAD-dependent epimerase/dehydratase
P73_4040	Gamma-glutamyltranspeptidase protein
P73_4041	ABC transporter substrate binding protein
P73_4043	alkanesulfonate monooxygenase
P73_4044	ABC transporter
P73_4045	nodulation protein nolR
P73_4046	thiamine pyrophosphate protein TPP binding domain-containing protein
P73_4047	Predicted membrane protein
P73_4048	GntR family transcriptional regulator
P73_4049	family 5 extracellular solute-binding protein
P73_4053	NAD-dependent epimerase/dehydratase
P73_4054	short-chain dehydrogenase/reductase SDR
P73_4056	acetyltransferase
P73_4057	Protein-tyrosine-phosphatase
P73_4058	Periplasmic protein involved in polysaccharide export
P73_4059	UDP-N-acetylmuramyl pentapeptide phosphotransferase/UDP-N-acetylglucosamine-1-phosphate transferase
P73_4060	Transcription antiterminator
P73_4063	hypothetical protein
P73_4064	MarR family transcriptional regulator
P73_4065	polysaccharide biosynthesis protein
P73_4066	transposase IS3/IS911 family protein
P73_4067	transposase, orfB
P73_4073	taurine catabolism dioxygenase TauD/TfdA
P73_4077	sulfonate/nitrate transporter
P73_4078	putative transposase
P73_4079	transposase
P73_4080	transposase
P73_4081	binding-protein-dependent transport system inner membrane protein
P73_4083	ABC transporter substrate-binding protein
P73_4084	FMNH2-dependent monooxygenase
P73_4085	FMN-dependent oxidoreductase, nitrilotriacetate monooxygenase
P73_4086	putative acyl-CoA dehydrogenase

P73_4087	putative oxidoreductase
P73_4088	TetR family transcriptional regulator
P73_4089	asparaginase
P73_4090	putative cystine-binding periplasmic protein
P73_4091	ABC transporter substrate binding protein
P73_4093	acetyltransferase
P73_4095	flavin-dependent oxidoreductase
P73_4096	luciferase-like monooxygenase superfamily protein
P73_4097	outer membrane receptor for ferrienterochelin and colicins
P73_4098	pyridoxamine 5'-phosphate oxidase
P73_4100	transcriptional regulator
P73_4101	hypothetical protein
P73_4104	TRAP-type transport system, small permease
P73_4106	Amidohydrolase
P73_4109	Tripartite tricarboxylate transporter TctB family
P73_4111	Uncharacterized protein conserved in bacteria
P73_4112	PRC-barrel domain
P73_4113	Blr3415 protein
P73_4114	nitrilotriacetate monooxygenase
P73_4117	NMT1/THI5 like domain-containing protein
P73_4129	hypothetical protein
P73_4135	hypothetical protein
P73_4136	hypothetical protein
P73_4142	UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D- alanine ligase
P73_4143	hypothetical protein
P73_4149	ferric enterobactin-binding periplasmic protein FepB
P73_4150	TonB-dependent siderophore receptor
P73_4151	ATP dependent DNA ligase
P73_4152	putative exonuclease, DNA ligase-associated
P73_4153	two-component system, chemotaxis family,response regulator CheB
P73_4154	Crp/Fnr-family transcriptional regulator
P73_4156	oxidoreductase subunit
P73_4157	xanthine dehydrogenase YagR molybdenum-binding subunit
P73_4158	short-chain dehydrogenase/reductase SDR
P73_4159	hypothetical protein
P73_4165	extracellular solute-binding protein
P73_4193	hypothetical protein
P73_4271	hypothetical protein
P73_4291	Predicted ester cyclase
P73_4313	hypothetical protein
P73_4314	glycosyl transferase family protein
P73_4315	UDP-N-acetylenolpyruvoylglucosamine reductase
P73_4316	putative transcriptional regulator

P73_4319	resorcinol 4-hydroxylase reductase subunit
P73_4320	DoxX family protein
P73_4324	phosphoketolase
P73_4326	hypothetical protein
P73_4328	hypothetical protein
P73_4329	hypothetical protein
P73_4330	superoxide dismutase, copper/zinc binding protein
P73_4331	hypothetical protein
P73_4332	hypothetical protein
P73_4334	transport-associated protein
P73_4335	Uncharacterized protein conserved in bacteria
P73_4336	Protein of unknwon function (DUF3008)
P73_4337	broad-specificity glycerol dehydrogenase, subunit SldA
P73_4338	exopolysaccharide synthesis, ExoD
P73_4339	cytochrome c, class I
P73_4340	Cytochrome c oxidase caa3-type, assembly factor CtaG-related protein
P73_4341	hypothetical protein
P73_4343	cytochrome c, monoheme
P73_4344	fatty acid alpha hydroxylase
P73_4345	methyltransferase
P73_4346	NAD-dependent epimerase/dehydratase
P73_4347	Uncharacterized protein conserved in bacteria
P73_4348	Uncharacterized protein conserved in bacteria
P73_4349	Uncharacterized protein conserved in bacteria
P73_4350	group 1 glycosyl transferase
P73_4351	nucleoside diphosphate epimerase
P73_4352	nucleoside-diphosphate-sugar epimerase
P73_4353	threonine dehydrogenase
P73_4354	ECF subfamily RNA polymerase sigma-24 factor
P73_4355	hypothetical protein
P73_4356	Predicted periplasmic or secreted lipoprotein
P73_4357	hypothetical protein
P73_4358	hypothetical protein
P73_4359	hypothetical protein
P73_4362	ribonuclease BN
P73_4363	Protein of unknown function (DUF3618)
P73_4364	Protein of unknown function (DUF1469)
P73_4365	hypothetical protein
P73_4366	trehalose-phosphatase
P73_4371	Quinol oxidase subunit II QxtB
P73_4372	Oxidoreductase alpha (Molybdopterin) subunit
P73_4374	cytochrome c oxidase subunit III
P73_4375	cytochrome C oxidase subunit IV

P73_4377	binding-protein-dependent transport system inner membrane protein
P73_4378	Binding-protein-dependent transport system inner membrane component
P73_4379	transposase, IS4 family protein
P73_4381	transposase IS116/IS110/IS902 family protein
P73_4392	replication initiation protein RepC
P73_4393	MarR family transcriptional regulator
P73_4402	tripartite ATP-independent periplasmic transporter DctQ
P73_4403	TRAP-type C4-dicarboxylate transport system, periplasmic component
P73_4407	DNA-binding transcriptional activator MhpR
P73_4409	ABC transporter permease
P73_4410	ABC transporter substrate-binding protein
P73_4412	hypothetical protein
P73_4424	6-phosphogluconate dehydrogenase
P73_4426	carboxymuconolactone decarboxylase
P73_4428	3-hydroxyisobutyrate dehydrogenase
P73_4429	enoyl-CoA hydratase/isomerase
P73_4432	Predicted metal-dependent hydrolase of the TIM-barrel fold
P73_4433	binding-protein-dependent transport system inner membrane protein
P73_4435	nitrate/sulfonate/bicarbonate ABC transporter periplasmic protein-like protein
P73_4443	amidohydrolase 2
P73_4444	TRAP-type C4-dicarboxylate transport system, periplasmic component
P73_4445	Uncharacterized conserved protein
P73_4446	cupin
P73_4454	1,4-dihydroxy-2-naphthoate synthase
P73_4456	TRAP-T family protein transporter, DctP (Periplasmic binding) subunit
P73_4457	carbon monoxide dehydrogenase medium subunit
P73_4459	carbon monoxide dehydrogenase subunit G (CoxG) family protein
P73_4461	putative permease, DMT superfamily protein
P73_4463	acyl-CoA dehydrogenase yngJ
P73_4465	2-methylcitrate dehydratase
P73_4469	TRAP-type C4-dicarboxylate transport system, small permease component
P73_4470	TRAP-T family protein transporter, DctP (Periplasmic binding) subunit
P73_4472	Zn-dependent hydrolases, including glyoxylases
P73_4473	carbon monoxide dehydrogenase
P73_4482	1,4-dihydroxy-2-naphthoate synthase
P73_4484	amidohydrolase 2
P73_4487	dehydratase
P73_4488	enoyl-CoA hydratase
P73_4492	putative alcohol dehydrogenase
P73_4494	thioesterase-like protein
P73_4495	Predicted thioesterase
P73_4497	Predicted nucleic-acid-binding protein containing a Zn-ribbon
P73_4500	Predicted metal-dependent hydrolase of the TIM-barrel fold

P73_4501	4-oxalocrotonate tautomerase
P73_4502	putative aldehyde dehydrogenase
P73_4503	TRAP dicarboxylate transporter- DctP subunit
P73_4512	Uncharacterized conserved protein
P73_4513	transposase, IS4 family protein
P73_4515	transposase IS116/IS110/IS902 family protein
P73_4516	cupin
P73_4517	transcriptional regulator
P73_4518	putative carboxymuconolactone decarboxylase
P73_4519	oxidoreductase
P73_4520	cupin
P73_4522	aldehyde oxidase and xanthine dehydrogenase molybdopterin binding protein
P73_4527	replication initiation protein RepC
P73_4532	oxidoreductase, flavocytochrome subunit
P73_4539	hypothetical protein
P73_4541	hypothetical protein
P73_4543	hypothetical protein
P73_4545	parB-like partition protein
P73_4546	hypothetical protein
P73_4547	hypothetical protein
P73_4548	regulator PrlF
P73_4549	Toxin with endonuclease activity YhaV
P73_4550	StaA
P73_4554	hypothetical protein
P73_4555	ParB-like nuclease
P73_4556	hypothetical protein
P73_4557	Uncharacterized membrane protein (homolog of Drosophila rhomboid)
P73_4558	Predicted transcriptional regulators
P73_4559	Reverse transcriptase (RNA-dependent DNA polymerase)
P73_4560	TIR protein
P73_4562	Micrococcal nuclease (thermonuclease) homologs
P73_4563	hypothetical protein
P73_4564	Helix-turn-helix domain
P73_4567	hypothetical protein
P73_4568	Prokaryotic homologs of the JAB domain
P73_4569	Dinucleotide-utilizing enzymes involved in molybdopterin and thiamine biosynthesis family 2
P73_4570	hypothetical protein
P73_4572	hypothetical protein
P73_4573	Domain of unknown function (DUF4177)
P73_4580	hypothetical protein
P73_4587	XRE family transcriptional regulator
P73_4588	hypothetical protein

P73_4605	hypothetical protein
P73_4607	putative inner membrane protein
P73_4609	Cytochrome c peroxidase
P73_4610	phosphonate ABC transporter phosphate-binding periplasmic component
P73_4617	integrase, catalytic region (modular protein)
P73_4618	transposase
P73_4622	hypothetical protein
P73_4623	putative Zn peptidase
P73_4624	Uncharacterized protein conserved in bacteria (DUF2188)
P73_4625	hypothetical protein
P73_4649	hypothetical protein
P73_4655	hypothetical protein
P73_4656	hypothetical protein
P73_4663	excisionase
P73_4666	Predicted nucleic-acid-binding protein, contains PIN domain
P73_4667	SpoVT/AbrB-like cell growth regulatory protein
P73_4676	putative transposase for insertion sequence element
P73_4679	hypothetical protein
P73_4680	hypothetical protein
P73_4682	transposase, mutator type
P73_4687	putative transposase for insertion sequence element
P73_4693	Protein of unknown function (DUF2384)
P73_4694	RES domain
P73_4701	hypothetical protein
P73_4700	hypothetical protein
P73_4702	putative type II DNA modification enzyme
P73_4737	hypothetical protein
P73_4749	MarR family transcriptional regulator
P73_4750	salicylate esterase
P73_4751	Predicted hydrolases or acyltransferases (alpha/beta hydrolase superfamily)
P73_4752	transposase
P73_4753	transposase
P73_4754	integrase, catalytic region (modular protein)
P73_4755	transposase
P73_4759	IS66 family insertion sequence transposase
P73_4760	IS66 Orf2 family protein
P73_4761	integrase catalytic region
P73_4763	cytochrome P450
P73_4764	AraC family transcriptional regulator
P73_4766	TRAP dicarboxylate transporter subunit DctQ
P73_4767	TRAP transporter solute receptor
P73_4768	alcohol dehydrogenase
P73_4770	IS5 family transposase OrfA

P73_4772	transposase IS116/IS110/IS902 family protein
P73_4776	hypothetical protein
P73_4777	IS5 family transposase OrfA
P73_4779	transposase IS116/IS110/IS902 family protein
P73_4782	hypothetical protein
P73_4783	ISBmu7b transposase
P73_4784	DNA replication protein
P73_4788	hypothetical protein
P73_4790	Membrane transport protein MerF
P73_4792	mercuric transporter MerT
P73_4796	hypothetical protein
P73_4797	plasmid replication initiator
P73_4799	C-5 cytosine-specific DNA methylase
P73_4800	T/G mismatch-specific endonuclease
P73_4801	hypothetical protein
P73_4802	hypothetical protein
P73_4804	DNA-cytosine methyltransferase
P73_4805	ATP-binding region ATPase domain protein
P73_4806	Transposase DDE domain group 1
P73_4807	ATP-binding region ATPase domain protein
P73_4808	ATPase domain-containing protein
P73_4809	hypothetical protein
P73_4811	transcriptional regulator
P73_4813	mobilization protein
P73_4814	mobilization protein
P73_4815	virD4 protein, putative
P73_4816	hypothetical protein
P73_4817	replicase
P73_4818	putative site-specific recombinase-resolvase
P73_4819	Uncharacterized protein conserved in bacteria
P73_4820	chromate resistance exported protein
P73_4822	hypothetical protein
P73_4824	putative MobA
P73_4823	hypothetical protein
P73_4825	hypothetical protein
P73_4826	MobC
P73_4827	hypothetical protein

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