Fig.S1 The dispersion and parallelity of transcriptome sequencing. (A) The overall expression level of genes in four groups. (B) The scatter diagrams of all genes' levels among four groups. (C) The scatter diagrams of gene expression in groups between JZ6_10 and JZ6_28, TZ19_10 and TZ19_28, JZ6_10 and TZ19_10.

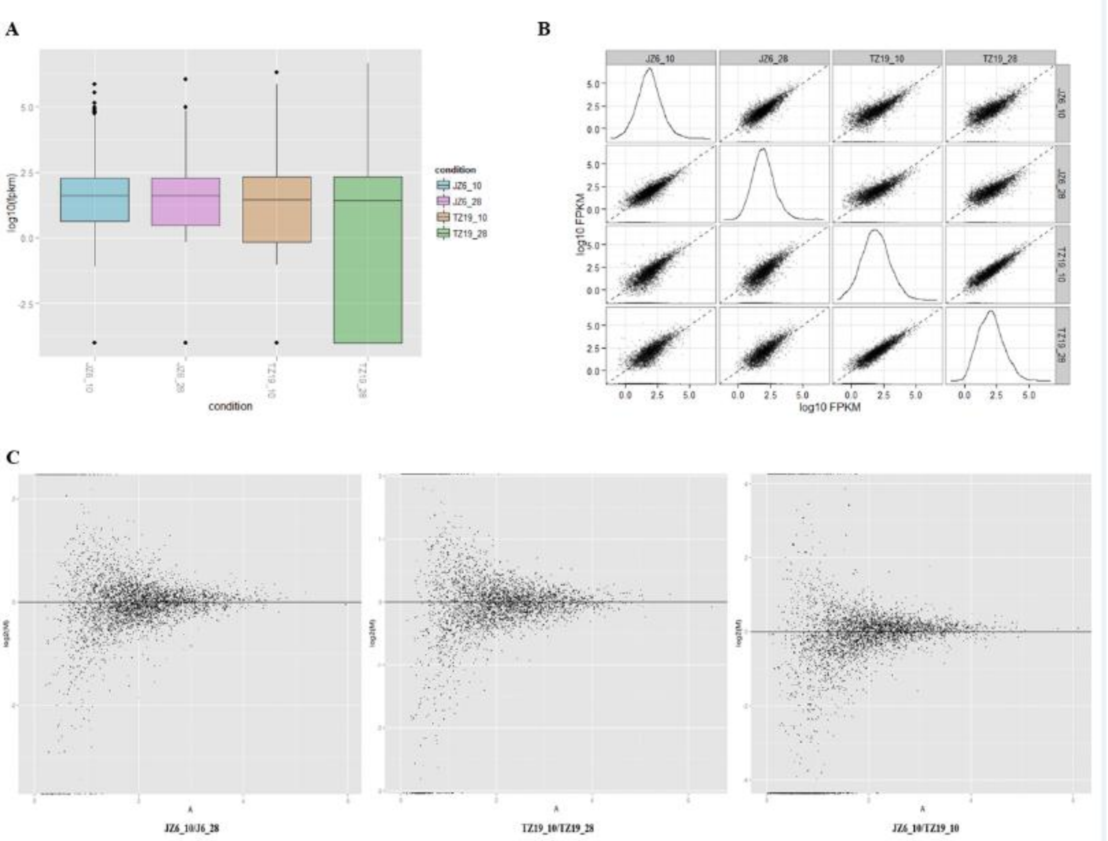

Fig.S2 The KEGG analysis of up-regulated genes of JZ6_10 group in “Two-component system” pathway. (The genes participated in this pathway of *V. splendidus* were labled with orange and green. And the red genes were up-regulated in JZ6 at 10 ℃).

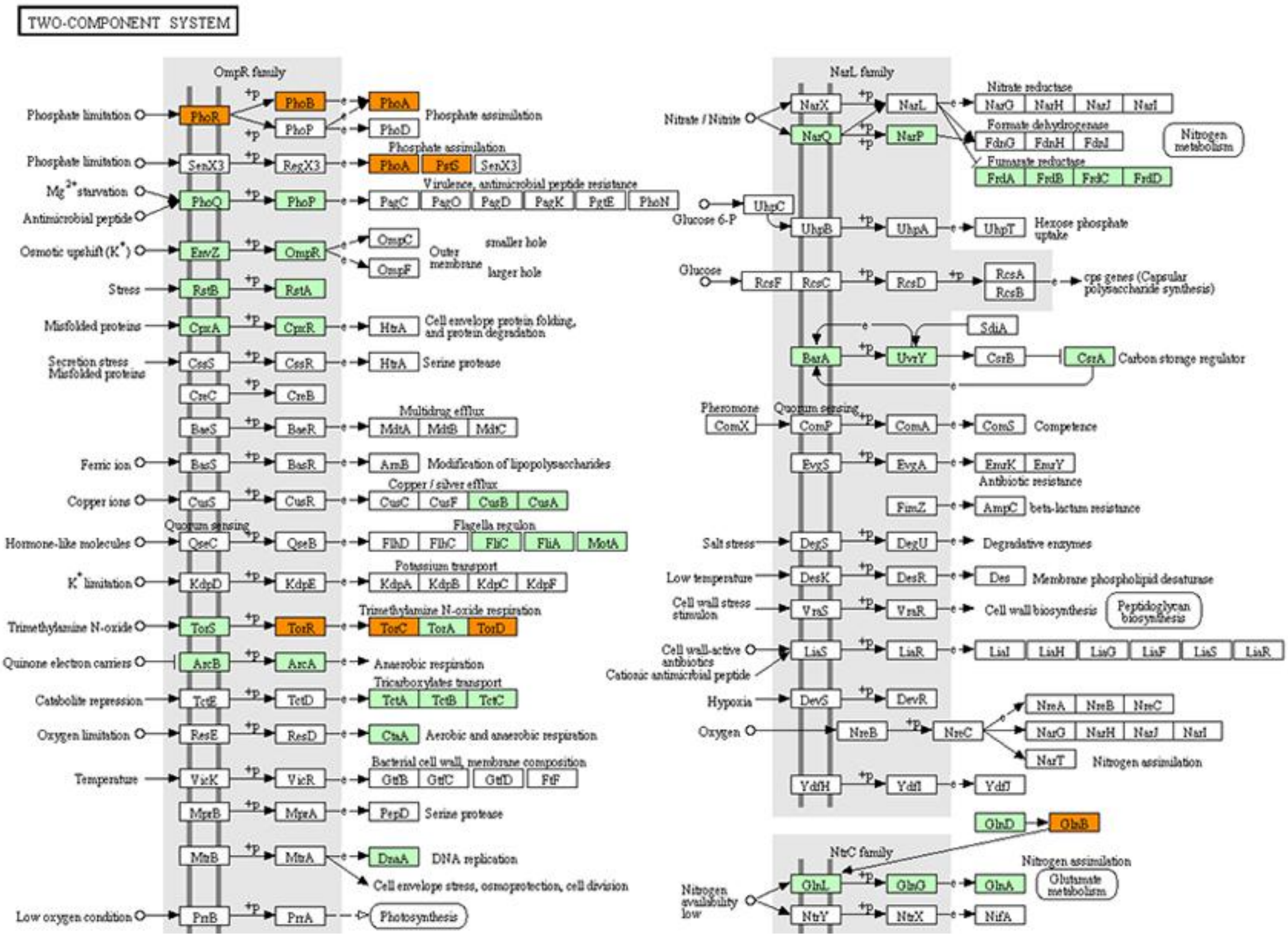

Fig.S3 The KEGG analysis of up-regulated genes of JZ6_10 group in “Prokaryotic-type ABC transporters” pathway. (The genes participated in this pathway of *V. splendidus* were labled with orange and green. And the red genes were up-regulated in JZ6 at 10 ℃).

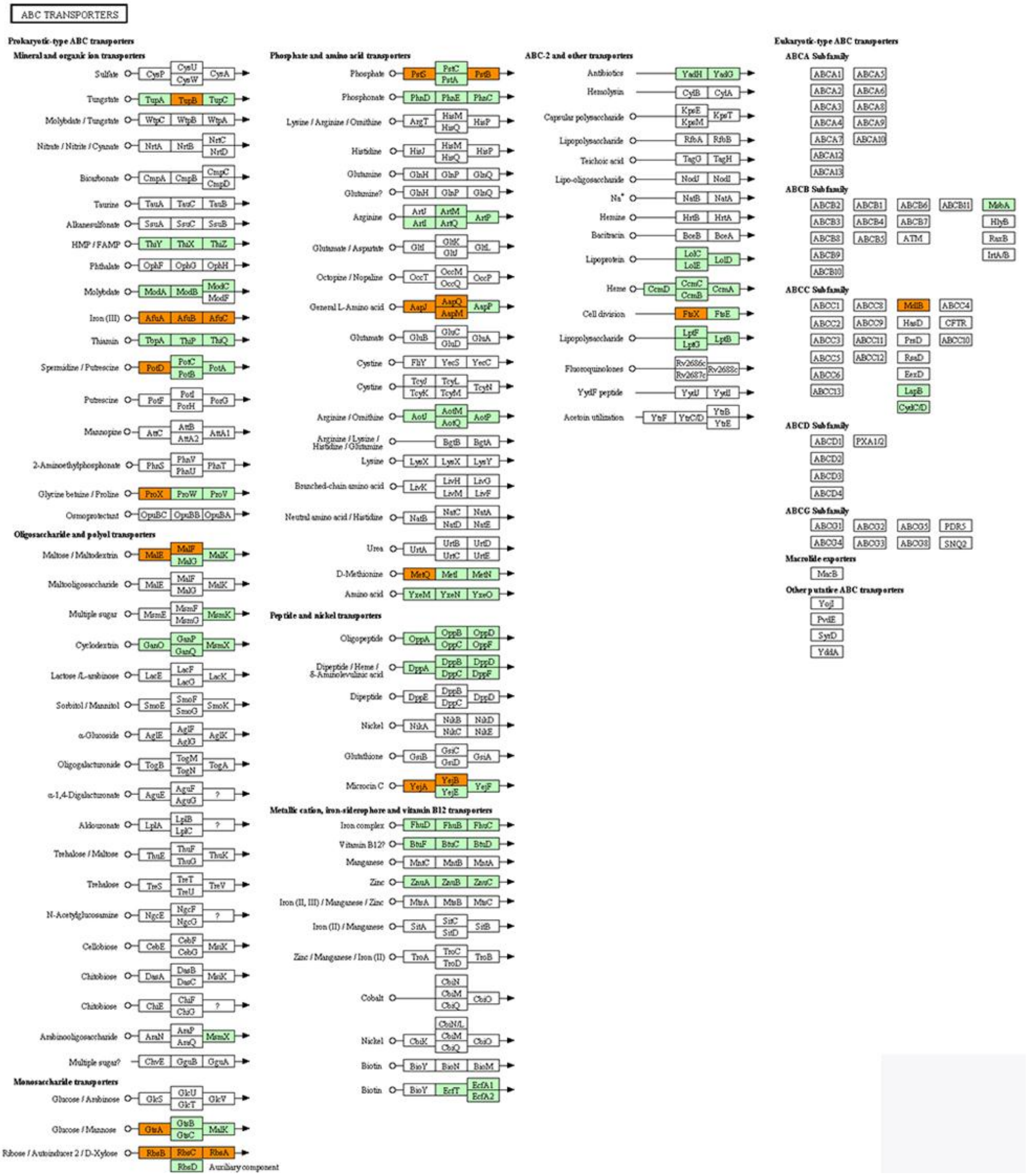

Fig.S4 The KEGG analysis of up-regulated genes of JZ6_10 group in “Vibrio Cholerae pathogenic cycle” pathway. (The genes participated in this pathway of *V. splendidus* were labled with orange and green. And the red genes were up-regulated in JZ6 at 10 ℃).

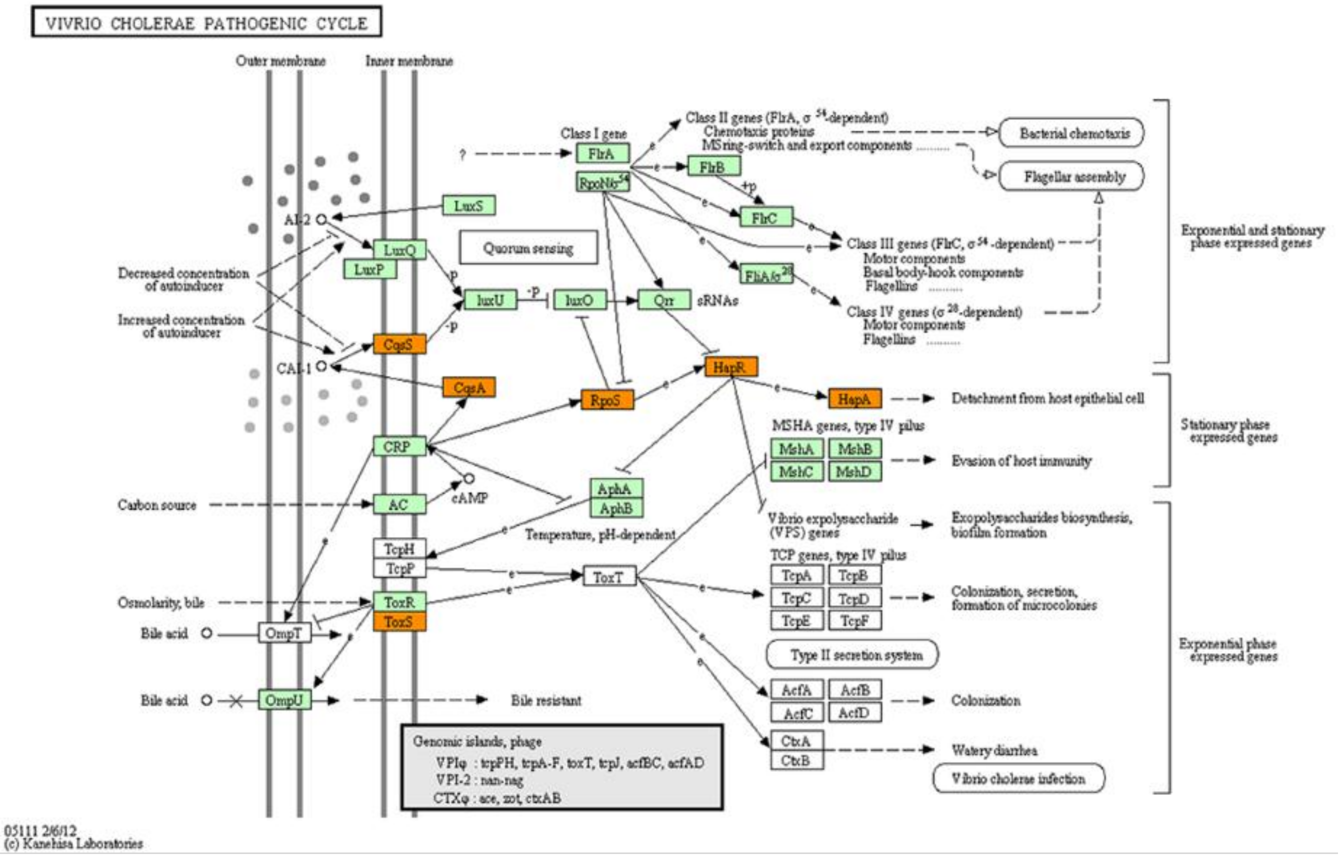

Fig.S5 The Go distribution and gene enrichment analysis of down-regulated genes of strain JZ6 at 10 ℃ (JZ6_10).

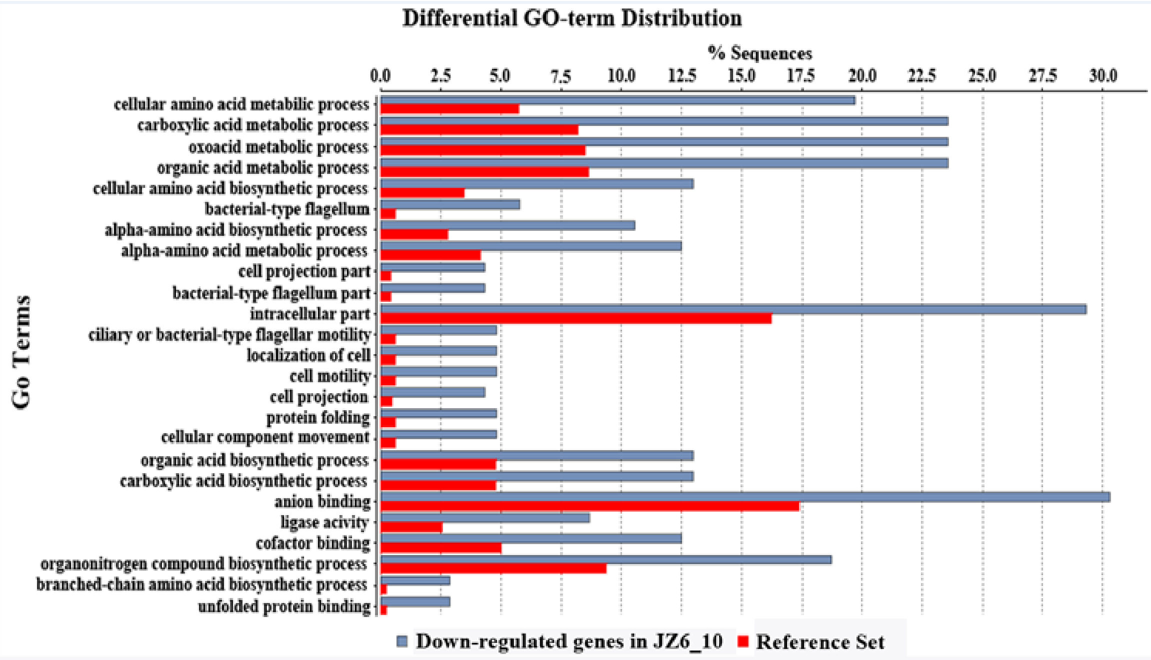

Table S1 List of differentially expressed genes in strain JZ6 at 10 ℃ (JZ6_10) versus at 28 ℃ (JZ6_28).

Gene name	Group1	Group2	States	FPKM1	FPKM2	E-value1	E-value2	Significant
putative transport protein	JZ6_10	JZ6_28	OK	6.29448	1303.28	0	0	yes
PTS system, IIB component	JZ6_10	JZ6_28	OK	13.8336	2669.43	4.90E-07	1.37E-06	yes
ABC transporter: substrate binding protein precursor	JZ6_10	JZ6_28	OK	26.2372	2321.19	0	0	yes
ABC transporter: transmembrane protein; Arginine uptake	JZ6_10	JZ6_28	OK	6.73578	550.432	4.44E-15	2.16E-14	yes
putative glycosyltransferase	JZ6_10	JZ6_28	OK	22.6609	1690.4	0	0	yes
PTS system, 3-keto-L-gulonate specific IIA component	JZ6_10	JZ6_28	OK	39.6289	2810.94	0	0	yes
putative transporter	JZ6_10	JZ6_28	OK	1.1261	65.0182	5.08E-08	1.55E-07	yes
hypothetical protein	JZ6_10	JZ6_28	OK	96.2575	5402.93	2.73E-06	7.07E-06	yes
Small heat shock protein ibpA (16 kDa heat shock protein A)	JZ6_10	JZ6_28	OK	139.761	7145.19	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	8.49346	419.298	0	0	yes
Transcriptional regulator	JZ6_10	JZ6_28	OK	3.73512	164.399	3.99E-07	1.12E-06	yes
Choline dehydrogenase	JZ6_10	JZ6_28	OK	1.25336	53.6046	4.92E-07	1.37E-06	yes
ABC transporter: transmembrane protein; Arginine uptake	JZ6_10	JZ6_28	OK	22.8406	935.016	0	0	yes
NAD-dependent aldehyde dehydrogenase	JZ6_10	JZ6_28	OK	1.50403	49.9922	2.94E-06	7.57E-06	yes
ABC transporter: ATP-binding protein	JZ6_10	JZ6_28	OK	22.9317	594.951	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	3.8441	88.5471	3.29E-06	8.44E-06	yes
putative transporter, BCCT family	JZ6_10	JZ6_28	OK	4.34448	85.8436	1.28E-12	5.40E-12	yes
Histidinol-phosphate aminotransferase	JZ6_10	JZ6_28	OK	32.0353	605.631	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	65.6758	1231.95	0	0	yes
argininosuccinate synthase	JZ6_10	JZ6_28	OK	176.545	2921	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	56.0905	865.372	0	0	yes
Transcriptional regulator, TetR family	JZ6_10	JZ6_28	OK	57.1252	826.165	0	0	yes
Lysine-arginine-ornithine-binding periplasmic protein	JZ6_10	JZ6_28	OK	106.503	1516.25	0	0	yes
L-lactate permease	JZ6_10	JZ6_28	OK	4.44025	62.1566	1.07E-10	4.02E-10	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	8.73954	119.452	0	0	yes
N-acetyl-gamma-glutamyl-phosphate reductase	JZ6_10	JZ6_28	OK	103.488	1366.32	0	0	yes
conserved hypothetical protein	JZ6_10	JZ6_28	OK	377.671	4980.41	0	0	yes
L-lactate dehydrogenase	JZ6_10	JZ6_28	OK	7.28756	95.9656	1.88E-11	7.42E-11	yes
flagellar hook-associated protein FlgK	JZ6_10	JZ6_28	OK	4.57262	58.9758	2.45E-11	9.57E-11	yes

Glycyl-tRNA synthetase beta chain	JZ6_10	JZ6_28	OK	15.21	186.976	0	0	yes
Acetylglutamate kinase	JZ6_10	JZ6_28	OK	77.8444	954.321	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	59.3809	715.545	2.42E-11	9.44E-11	yes
hypothetical protein	JZ6_10	JZ6_28	OK	9.39791	113.117	0	0	yes
Carbamoyl-phosphate synthase large chain	JZ6_10	JZ6_28	OK	43.1336	497.917	0	0	yes
Fe-S oxidoreductase	JZ6_10	JZ6_28	OK	6.11561	70.1894	0	0	yes
cytochrome c oxidase, subunit CcoO	JZ6_10	JZ6_28	OK	126.44	1425.66	0	0	yes
Glycyl-tRNA synthetase alpha chain	JZ6_10	JZ6_28	OK	36.7181	397.757	0	0	yes
L-serine dehydratase 1	JZ6_10	JZ6_28	OK	30.9238	304.364	0	0	yes
Acyl-CoA dehydrogenase	JZ6_10	JZ6_28	OK	68.8662	670.898	0	0	yes
Permease of the drug-metabolite transporter (DMT) superfamily	JZ6_10	JZ6_28	OK	21.8879	212.075	8.88E-16	4.47E-15	yes
outer membrane protein N	JZ6_10	JZ6_28	OK	13.089	124.039	3.98E-12	1.63E-11	yes
cytochrome c oxidase, subunit CcoP	JZ6_10	JZ6_28	OK	14.1405	133.814	1.18E-11	4.73E-11	yes
Hypothetical membrane protein	JZ6_10	JZ6_28	OK	35.323	331.425	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	45.7886	421.694	0	0	yes
Bifunctional protein argH	JZ6_10	JZ6_28	OK	91.2848	816.266	0	0	yes
putative nitrogen regulatory protein P-II family protein	JZ6_10	JZ6_28	OK	72.6985	640.838	9.50E-12	3.82E-11	yes
sensor protein LuxN	JZ6_10	JZ6_28	OK	2.66893	22.8647	2.51E-07	7.17E-07	yes
Flagellar basal-body rod protein flgF	JZ6_10	JZ6_28	OK	20.6809	175.219	3.13E-12	1.29E-11	yes
Conserved hypothetical protein; putative exported	JZ6_10	JZ6_28	OK	8.14155	68.2498	8.41E-09	2.74E-08	yes
hypothetical protein	JZ6_10	JZ6_28	OK	16.4876	138.071	1.50E-07	4.39E-07	yes
Aldehyde dehydrogenase	JZ6_10	JZ6_28	OK	25.32	206.171	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	6.30138	49.5391	6.40E-08	1.94E-07	yes
Permease of the drug metabolite transporter (DMT) superfamily	JZ6_10	JZ6_28	OK	15.0415	117.157	1.73E-10	6.38E-10	yes
sodium/solute symporter	JZ6_10	JZ6_28	OK	8.11371	63.181	5.72E-12	2.32E-11	yes
hypothetical protein	JZ6_10	JZ6_28	OK	37.1602	288.632	1.10E-08	3.53E-08	yes
putative endoribonuclease	JZ6_10	JZ6_28	OK	61.7596	478.678	5.20E-11	1.98E-10	yes
conserved hypothetical protein	JZ6_10	JZ6_28	OK	1219.77	9344.31	2.22E-16	1.15E-15	yes
hypothetical protein	JZ6_10	JZ6_28	OK	79.8809	593.696	0	0	yes
Adenylosuccinate synthetase	JZ6_10	JZ6_28	OK	13.9595	101.16	2.71E-12	1.13E-11	yes
Histone acetyltransferase HPA2 and related acetyltransferases	JZ6_10	JZ6_28	OK	55.3548	400.594	0	0	yes
putative permease	JZ6_10	JZ6_28	OK	12.3691	87.4376	3.27E-07	9.26E-07	yes

ubiquinol-cytochrome c reductase,cytochrome c1	JZ6_10	JZ6_28	OK	90.2499	637.267	0	0	yes
succinate dehydrogenase	JZ6_10	JZ6_28	OK	182.263	1282.81	0	0	yes
Carbamoyl-phosphate synthase, small subunit	JZ6_10	JZ6_28	OK	63.5744	445.287	0	0	yes
putative chaperone protein dnaK (Heat shock protein 70)	JZ6_10	JZ6_28	OK	5.56352	38.8005	3.53E-10	1.27E-09	yes
putative permease	JZ6_10	JZ6_28	OK	175.766	1217.8	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	1187.02	8194.28	0	0	yes
60 kDa chaperonin (Protein Cpn60) (groEL protein)	JZ6_10	JZ6_28	OK	178.571	1226.63	0	0	yes
DNA-binding response regulator	JZ6_10	JZ6_28	OK	145.382	978.573	0	0	yes
Chaperone protein dnaK	JZ6_10	JZ6_28	OK	733.564	4902.79	0	0	yes
putative lipoprotein	JZ6_10	JZ6_28	OK	46.5239	306.032	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	9.38637	61.5224	4.57E-12	1.87E-11	yes
Flagellar P-ring protein precursor	JZ6_10	JZ6_28	OK	14.0166	91.216	3.42E-09	1.14E-08	yes
Amino acid transporter	JZ6_10	JZ6_28	OK	44.8753	289.868	4.01E-13	1.74E-12	yes
ATP-dependent protease hslV	JZ6_10	JZ6_28	OK	71.2614	444.71	0	0	yes
2-oxoglutarate dehydrogenase E1 component	JZ6_10	JZ6_28	OK	154.675	961.49	0	0	yes
Isocitrate lyase	JZ6_10	JZ6_28	OK	30.7935	188.621	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	25.6317	156.364	7.11E-15	3.41E-14	yes
hypothetical protein	JZ6_10	JZ6_28	OK	27.3301	165.859	7.77E-07	2.13E-06	yes
putative acetoin utilization protein	JZ6_10	JZ6_28	OK	303.152	1837.5	0	0	yes
Acetolactate synthase isozyme II large subunit	JZ6_10	JZ6_28	OK	13.1651	79.0869	2.40E-13	1.05E-12	yes
putative Co-chaperonin GroES	JZ6_10	JZ6_28	OK	208.262	1250.75	1.52E-12	6.39E-12	yes
Urocanate hydratase	JZ6_10	JZ6_28	OK	6.62024	39.4756	3.05E-07	8.67E-07	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	88.9207	528.152	3.89E-06	9.90E-06	yes
conserved hypothetical protein	JZ6_10	JZ6_28	OK	82.2961	484.286	0	0	yes
ATP phosphoribosyltransferase	JZ6_10	JZ6_28	OK	220.641	1296.48	0	0	yes
MutT/nudix family protein	JZ6_10	JZ6_28	OK	24.5238	139.36	3.70E-06	9.45E-06	yes
Tripartite ATP-independent periplasmic transporters, DctQ	JZ6_10	JZ6_28	OK	41.1812	230.987	4.17E-14	1.91E-13	yes
putative hydrolase	JZ6_10	JZ6_28	OK	110.034	614.013	0	0	yes
Transcriptional regulator	JZ6_10	JZ6_28	OK	32.5615	181.218	4.49E-11	1.72E-10	yes
Ribonuclease P protein component	JZ6_10	JZ6_28	OK	77.0445	427.667	7.97E-08	2.39E-07	yes
Iron-regulated membrane protein	JZ6_10	JZ6_28	OK	7.0595	39.0313	1.90E-06	5.02E-06	yes
tetraacyldisaccharide 4'-kinase	JZ6_10	JZ6_28	OK	24.3241	134.459	7.84E-12	3.16E-11	yes

NifU-related domain containing protein	JZ6_10	JZ6_28	OK	75.4602	414.399	0	0	yes
Flagellin core protein A	JZ6_10	JZ6_28	OK	36.8291	201.716	0	0	yes
conserved hypothetical protein	JZ6_10	JZ6_28	OK	231.31	1265.9	0	0	yes
Hypothetical membrane protein	JZ6_10	JZ6_28	OK	16.1258	87.5234	2.55E-10	9.30E-10	yes
Chaperone protein htpG	JZ6_10	JZ6_28	OK	79.6572	428.341	0	0	yes
putative cation transport ATPase	JZ6_10	JZ6_28	OK	8.36461	44.4171	5.33E-10	1.89E-09	yes
Ubiquinol-cytochrome c reductase, cytochrome B	JZ6_10	JZ6_28	OK	130.049	682.909	0	0	yes
Polar flagellar FlgC	JZ6_10	JZ6_28	OK	149.409	780.493	2.66E-15	1.31E-14	yes
hypothetical protein	JZ6_10	JZ6_28	OK	1088.46	5621.49	3.76E-07	1.06E-06	yes
Phosphoglycerate dehydrogenase	JZ6_10	JZ6_28	OK	14.3924	74.3184	1.68E-06	4.46E-06	yes
putative lactoylglutathione lyase	JZ6_10	JZ6_28	OK	57.9042	298.534	3.70E-08	1.14E-07	yes
ATP-dependent hsl protease ATP-binding subunit hslU	JZ6_10	JZ6_28	OK	97.2388	496.917	0	0	yes
Polar flagellin B	JZ6_10	JZ6_28	OK	123.178	629.386	0	0	yes
putative succinate dehydrogenase, flavoprotein subunit	JZ6_10	JZ6_28	OK	325.864	1664.98	0	0	yes
Serine transporter	JZ6_10	JZ6_28	OK	75.0097	381.09	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	137.524	681.485	4.44E-14	2.03E-13	yes
Adenylosuccinate lyase	JZ6_10	JZ6_28	OK	142.699	688.806	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	17.4352	83.9872	7.62E-07	2.09E-06	yes
Phenylalanyl-tRNA synthetase beta chain	JZ6_10	JZ6_28	OK	67.2875	321.09	0	0	yes
Dihydrolipoyllysine-residue succinyltransferase	JZ6_10	JZ6_28	OK	242.93	1147.16	0	0	yes
putative tyrosine-protein kinase (wzc)	JZ6_10	JZ6_28	OK	18.6752	87.2546	0	0	yes
Phosphoenolpyruvate carboxykinase	JZ6_10	JZ6_28	OK	2390.69	11132.9	0	0	yes
Mg(2+) transport ATPase protein C	JZ6_10	JZ6_28	OK	120.532	558.945	4.66E-15	2.26E-14	yes
Glutathione reductase	JZ6_10	JZ6_28	OK	111.934	512.091	0	0	yes
AraC-type DNA-binding domain-containing protein	JZ6_10	JZ6_28	OK	22.387	101.776	2.42E-07	6.95E-07	yes
hypothetical protein	JZ6_10	JZ6_28	OK	115.467	519.455	3.48E-06	8.91E-06	yes
NAD-dependent malic enzyme	JZ6_10	JZ6_28	OK	61.0781	273.921	0	0	yes
Aconitate hydratase 2 (Citrate hydro-lyase 2)	JZ6_10	JZ6_28	OK	306.731	1373.44	0	0	yes
Flagellar biosynthesis protein flhF	JZ6_10	JZ6_28	OK	52.5143	233.508	0	0	yes
putative cytochrome b561	JZ6_10	JZ6_28	OK	424.132	1885.14	0	0	yes
Phospho-2-dehydro-3-deoxyheptonate aldolase, Phe-sensitive	JZ6_10	JZ6_28	OK	129.731	574.809	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	35.1931	155.651	7.65E-09	2.49E-08	yes

transport ATP-binding protein MsbA	JZ6_10	JZ6_28	OK	18.18	79.9544	5.57E-12	2.27E-11	yes
dipeptide/tripeptide permease	JZ6_10	JZ6_28	OK	26.9772	117.095	9.61E-14	4.31E-13	yes
putative cation efflux system component	JZ6_10	JZ6_28	OK	781.121	3374.77	0	0	yes
Hypothetical transcriptional regulator	JZ6_10	JZ6_28	OK	62.7805	270.197	2.46E-08	7.73E-08	yes
Histidinol dehydrogenase	JZ6_10	JZ6_28	OK	67.8488	289.682	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	22937.3	97145.9	7.93E-11	2.99E-10	yes
UDP-N-acetylmuramoylalanyl-D-glutamate--2,6-diaminopimelate ligase	JZ6_10	JZ6_28	OK	11.7132	49.5152	1.11E-06	2.99E-06	yes
NnrS protein	JZ6_10	JZ6_28	OK	31.392	131.87	3.75E-12	1.54E-11	yes
Cystathionine beta-lyase	JZ6_10	JZ6_28	OK	27.9498	116.43	7.40E-11	2.79E-10	yes
Chaperone protein DnaJ	JZ6_10	JZ6_28	OK	143.471	596.301	0	0	yes
Leucyl-tRNA synthetase	JZ6_10	JZ6_28	OK	81.749	337.67	0	0	yes
Trigger factor	JZ6_10	JZ6_28	OK	535.73	2202.03	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	175.098	716.751	2.44E-15	1.20E-14	yes
Cysteine desulfurase	JZ6_10	JZ6_28	OK	308.143	1255.89	0	0	yes
polar flagellin	JZ6_10	JZ6_28	OK	34.4578	139.5	1.07E-13	4.80E-13	yes
Na(+)-translocating NADH-quinone reductase subunit C	JZ6_10	JZ6_28	OK	333.607	1348.98	0	0	yes
Imidazole glycerol phosphate synthase subunit hisH	JZ6_10	JZ6_28	OK	86.079	347.626	1.44E-12	6.06E-12	yes
hypothetical transcriptional regulator, TetR family	JZ6_10	JZ6_28	OK	43.5786	175.885	1.13E-07	3.33E-07	yes
NifU-related protein	JZ6_10	JZ6_28	OK	455.92	1833.01	0	0	yes
chemotaxis protein CheB	JZ6_10	JZ6_28	OK	30.0581	120.767	3.17E-10	1.14E-09	yes
Hypothetical oxidoreductase	JZ6_10	JZ6_28	OK	52.2316	209.801	9.83E-11	3.68E-10	yes
Glutamate synthase	JZ6_10	JZ6_28	OK	20.3558	81.7287	0	0	yes
Redox-sensitive transcriptional activator soxR	JZ6_10	JZ6_28	OK	90.0105	358.858	4.55E-08	1.40E-07	yes
Histidine biosynthesis bifunctional protein hisB	JZ6_10	JZ6_28	OK	59.1905	235.861	0	0	yes
3-ketoacyl-CoA thiolase (Fatty acid oxidation complexbeta subunit)	JZ6_10	JZ6_28	OK	81.5861	324.436	0	0	yes
putative cytochrome b561	JZ6_10	JZ6_28	OK	615.121	2428.42	2.22E-16	1.15E-15	yes
DctQ, TRAP-type C4-dicarboxylate transport system, large permease componer	JZ6_10	JZ6_28	OK	69.0494	270.653	0	0	yes
Glyceraldehyde-3-phosphate dehydrogenase	JZ6_10	JZ6_28	OK	49.3713	192.269	0	0	yes
DnaK-related protein	JZ6_10	JZ6_28	OK	33.6419	130.729	0	0	yes
Glycerol kinase	JZ6_10	JZ6_28	OK	38.5067	149.26	0	0	yes
Inositol monophosphate family protein	JZ6_10	JZ6_28	OK	132.299	512.728	0	0	yes
magnesium transporter	JZ6_10	JZ6_28	OK	36.9785	143.196	1.33E-14	6.29E-14	yes

Cytochrome c-type biogenesis protein ccmF	JZ6_10	JZ6_28	OK	50.8073	196.71	0	0	yes
Oxaloacetate decarboxylase beta chain	JZ6_10	JZ6_28	OK	39.0471	150.891	1.17E-12	4.95E-12	yes
Succinate dehydrogenase hydrophobic membrane anchor protein	JZ6_10	JZ6_28	OK	599.571	2311.38	0	0	yes
Histidine transport ATP-binding protein hisP	JZ6_10	JZ6_28	OK	87.6273	336.363	8.88E-16	4.47E-15	yes
Histidinol-phosphate aminotransferase	JZ6_10	JZ6_28	OK	35.7737	136.676	1.32E-10	4.91E-10	yes
Flagellar basal body protein FlgB	JZ6_10	JZ6_28	OK	1981.57	7570.65	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	89.689	341.685	1.49E-06	3.99E-06	yes
hypothetical protein	JZ6_10	JZ6_28	OK	75.6618	288.152	5.55E-15	2.68E-14	yes
Ferrous iron transport protein B	JZ6_10	JZ6_28	OK	22.7773	86.3712	1.82E-14	8.54E-14	yes
penicillin-binding protein 1B	JZ6_10	JZ6_28	OK	14.6879	55.6137	1.04E-10	3.90E-10	yes
Serine acetyltransferase	JZ6_10	JZ6_28	OK	119.161	450.925	0	0	yes
putative transcriptional regulator	JZ6_10	JZ6_28	OK	25.3763	95.1978	6.60E-07	1.82E-06	yes
Fumarate reductase subunit C	JZ6_10	JZ6_28	OK	1058.09	3966.87	0	0	yes
Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	JZ6_10	JZ6_28	OK	30.4152	113.679	0	0	yes
Na(+)-translocating NADH-quinone reductase subunit B	JZ6_10	JZ6_28	OK	252.146	939.61	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	38.4453	142.948	3.51E-06	8.97E-06	yes
3-isopropylmalate dehydratase large subunit	JZ6_10	JZ6_28	OK	45.111	166.744	0	0	yes
Tryptophan synthase beta chain	JZ6_10	JZ6_28	OK	49.8532	184.165	2.00E-15	9.88E-15	yes
2-isopropylmalate synthase	JZ6_10	JZ6_28	OK	244.067	894.344	0	0	yes
Flagellar biosynthesis protein flhA	JZ6_10	JZ6_28	OK	17.8814	65.4049	1.09E-10	4.07E-10	yes
Fumarate reductase iron-sulfur protein	JZ6_10	JZ6_28	OK	588.152	2143.47	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	331.837	1204.86	2.68E-07	7.66E-07	yes
prolyl-tRNA synthetase	JZ6_10	JZ6_28	OK	87.68	316.266	0	0	yes
acetylornithine deacetylase	JZ6_10	JZ6_28	OK	76.11	274.325	0	0	yes
Homoserine dehydrogenase	JZ6_10	JZ6_28	OK	66.5993	238.677	0	0	yes
Flagellar M-ring protein	JZ6_10	JZ6_28	OK	13.4481	47.861	8.20E-07	2.24E-06	yes
Thioredoxin reductase	JZ6_10	JZ6_28	OK	82.2432	292.311	0	0	yes
Anaerobic nitric oxide reductase transcription regulator	JZ6_10	JZ6_28	OK	75.1635	265.671	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	21.1497	73.4254	1.44E-06	3.85E-06	yes
Flagellar hook-basal body complex protein fliE	JZ6_10	JZ6_28	OK	937.703	3234.74	0	0	yes
Glutamate decarboxylase	JZ6_10	JZ6_28	OK	13.6464	47.0654	2.05E-06	5.38E-06	yes
hypothetical protein	JZ6_10	JZ6_28	OK	26.5226	89.4811	2.08E-09	7.04E-09	yes

Glycine dehydrogenase (Glycine cleavage system P-protein)	JZ6_10	JZ6_28	OK	123.87	414.437	0	0	yes
Phosphoserine aminotransferase	JZ6_10	JZ6_28	OK	80.7651	269.755	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	455.339	1520.02	0	0	yes
Electron transport complex protein RnfC (fragment)	JZ6_10	JZ6_28	OK	20.7682	69.2058	2.88E-10	1.04E-09	yes
glutamate synthase, large subunit	JZ6_10	JZ6_28	OK	8.5615	28.5028	2.54E-09	8.55E-09	yes
Transcriptional regulator	JZ6_10	JZ6_28	OK	225.883	751.888	0	0	yes
Bifunctional purine biosynthesis protein purH	JZ6_10	JZ6_28	OK	63.4492	208.81	0	0	yes
Methylisocitrate lyase	JZ6_10	JZ6_28	OK	32.8685	106.817	1.19E-06	3.21E-06	yes
chloride channel protein EriC	JZ6_10	JZ6_28	OK	28.9434	93.8792	9.62E-10	3.34E-09	yes
Na+-driven multidrug efflux pump	JZ6_10	JZ6_28	OK	102.58	331.023	0	0	yes
Anaerobic C4-dicarboxylate transporter	JZ6_10	JZ6_28	OK	37.0669	119.296	4.85E-10	1.73E-09	yes
Hypothetical ABC transporter ATP-binding protein	JZ6_10	JZ6_28	OK	59.5473	191.37	0	0	yes
3-isopropylmalate dehydratase small subunit	JZ6_10	JZ6_28	OK	61.5129	197.62	4.00E-07	1.12E-06	yes
Flagellar motor switch protein fliG	JZ6_10	JZ6_28	OK	26.5225	85.1288	2.42E-06	6.31E-06	yes
putative HTH-type transcriptional regulator	JZ6_10	JZ6_28	OK	47.9183	153.283	9.13E-08	2.73E-07	yes
Transcriptional regulator	JZ6_10	JZ6_28	OK	33.3396	106.31	5.12E-07	1.43E-06	yes
Fumarate reductase subunit D	JZ6_10	JZ6_28	OK	1186.67	3760.94	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	55.9939	175.242	8.75E-14	3.93E-13	yes
conserved hypothetical protein	JZ6_10	JZ6_28	OK	16.826	52.5579	7.88E-09	2.57E-08	yes
Transketolase	JZ6_10	JZ6_28	OK	193.734	604.476	0	0	yes
Predicted transcriptional regulator	JZ6_10	JZ6_28	OK	432.239	1348.09	0	0	yes
Biosynthetic arginine decarboxylase	JZ6_10	JZ6_28	OK	543.431	1689.26	0	0	yes
Cytochrome c-type biogenesis protein	JZ6_10	JZ6_28	OK	94.1438	292	9.50E-07	2.58E-06	yes
Transcriptional regulator, LysR family	JZ6_10	JZ6_28	OK	54.2077	167.988	4.14E-09	1.37E-08	yes
Cytochrome c oxidase polypeptide I homolog	JZ6_10	JZ6_28	OK	208.193	640.619	0	0	yes
Shikimate kinase	JZ6_10	JZ6_28	OK	659.285	2026.43	0	0	yes
Replicative DNA helicase	JZ6_10	JZ6_28	OK	31.0224	95.2743	1.27E-08	4.07E-08	yes
Na(+)-translocating NADH-quinone reductase subunit F	JZ6_10	JZ6_28	OK	222.75	683.934	0	0	yes
ribonuclease E	JZ6_10	JZ6_28	OK	156.879	481.063	0	0	yes
Chemotaxis protein CheZ	JZ6_10	JZ6_28	OK	321.166	977.867	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	4350.51	13220.6	3.63E-10	1.30E-09	yes
Ribosomal protein L2	JZ6_10	JZ6_28	OK	644.857	1954.06	0	0	yes

DNA helicase II	JZ6_10	JZ6_28	OK	47.3064	143.061	0	0	yes
tyrosyl-tRNA synthetase	JZ6_10	JZ6_28	OK	123.906	374.084	0	0	yes
transcriptional regulator	JZ6_10	JZ6_28	OK	101.616	304.832	1.11E-10	4.15E-10	yes
Fatty oxidation complex, alpha subunit	JZ6_10	JZ6_28	OK	118.744	355.057	0	0	yes
Nuclease sbcCD subunit C	JZ6_10	JZ6_28	OK	26.5802	79.4531	0	0	yes
DNA polymerase I	JZ6_10	JZ6_28	OK	28.8312	86.1723	6.66E-16	3.37E-15	yes
1-(5-phosphoribosyl)-5-	JZ6_10	JZ6_28	OK	91.31	270.928	1.56E-10	5.78E-10	yes
putative peptidase	JZ6_10	JZ6_28	OK	45.6841	135.229	1.11E-15	5.56E-15	yes
hypothetical permease	JZ6_10	JZ6_28	OK	22.3304	65.8286	8.06E-11	3.03E-10	yes
Proline dehydrogenase	JZ6_10	JZ6_28	OK	96.9406	284.986	0	0	yes
Extracellular solute-binding protein, family 7	JZ6_10	JZ6_28	OK	257.664	752.891	0	0	yes
Na(+)-translocating NADH-quinone reductase subunit D	JZ6_10	JZ6_28	OK	722.038	2052.21	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	677.555	1917.27	0	0	yes
Aspartate aminotransferase	JZ6_10	JZ6_28	OK	215.007	607.385	0	0	yes
Methyl-accepting chemotaxis protein	JZ6_10	JZ6_28	OK	28.4657	80.4041	2.01E-09	6.85E-09	yes
Phosphoribosylaminoimidazole-succinocarboxamide synthase	JZ6_10	JZ6_28	OK	64.1184	180.645	1.69E-11	6.66E-11	yes
conserved hypothetical protein	JZ6_10	JZ6_28	OK	43.5119	122.244	3.20E-08	9.93E-08	yes
ATP synthase delta chain	JZ6_10	JZ6_28	OK	757.763	2124.96	0	0	yes
Hypothetical M22 peptidase homolog yeaZ	JZ6_10	JZ6_28	OK	81.4083	227.989	2.93E-08	9.14E-08	yes
Na(+)-translocating NADH-quinone reductase subunit E	JZ6_10	JZ6_28	OK	351.615	981.641	0	0	yes
Flagellar hook capping protein FlgD	JZ6_10	JZ6_28	OK	804.725	2245.31	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	27.9496	77.958	8.31E-07	2.27E-06	yes
1;4-alpha-glucan branching enzyme	JZ6_10	JZ6_28	OK	78.1724	217.19	0	0	yes
putative Penicillin-binding protein	JZ6_10	JZ6_28	OK	223.309	619.753	0	0	yes
ABC-type sugar transport system, ATP-binding protein	JZ6_10	JZ6_28	OK	42.5264	117.752	2.24E-07	6.45E-07	yes
GMP synthase	JZ6_10	JZ6_28	OK	81.7146	225.789	0	0	yes
phosphoenolpyruvate carboxylase	JZ6_10	JZ6_28	OK	26.8689	74.1732	2.94E-12	1.21E-11	yes
isopenicillin N synthase	JZ6_10	JZ6_28	OK	85.8604	235.906	1.21E-10	4.50E-10	yes
conserved hypothetical protein	JZ6_10	JZ6_28	OK	101.418	278.487	3.84E-06	9.79E-06	yes
Glutamate synthase	JZ6_10	JZ6_28	OK	54.7663	150.038	3.66E-12	1.50E-11	yes
Sodium/proline symporter	JZ6_10	JZ6_28	OK	144.449	395.349	0	0	yes
Preprotein translocase subunit SecF	JZ6_10	JZ6_28	OK	188.15	510.947	0	0	yes

Exodeoxyribonuclease V gamma chain	JZ6_10	JZ6_28	OK	24.422	66.1851	4.64E-14	2.12E-13	yes
Guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase	JZ6_10	JZ6_28	OK	74.8926	202.178	2.22E-16	1.15E-15	yes
Chromosome partition protein mukB	JZ6_10	JZ6_28	OK	18.0082	48.5996	2.53E-13	1.11E-12	yes
Flagellar hook protein flgE	JZ6_10	JZ6_28	OK	315.942	844.807	0	0	yes
Succinyl-CoA synthetase beta chain	JZ6_10	JZ6_28	OK	204.742	546.835	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	34.8466	92.7927	2.89E-15	1.41E-14	yes
Shikimate dehydrogenase	JZ6_10	JZ6_28	OK	95.2912	251.036	3.45E-10	1.24E-09	yes
HesB family protein	JZ6_10	JZ6_28	OK	786.306	2056.15	1.78E-15	8.80E-15	yes
Phosphoglucomutase	JZ6_10	JZ6_28	OK	109.503	285.981	0	0	yes
Ribosomal protein S19	JZ6_10	JZ6_28	OK	1218.8	3179.05	1.55E-15	7.72E-15	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	95.815	249.019	3.22E-14	1.49E-13	yes
Co-chaperone protein hscB homolog	JZ6_10	JZ6_28	OK	120.045	311.592	3.77E-07	1.06E-06	yes
Serine hydroxymethyltransferase 1	JZ6_10	JZ6_28	OK	146.748	380.898	0	0	yes
Malate synthase	JZ6_10	JZ6_28	OK	106.776	274.276	1.89E-07	5.49E-07	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	735.592	1889.44	1.43E-06	3.82E-06	yes
ATP synthase alpha chain	JZ6_10	JZ6_28	OK	528.714	1357.65	0	0	yes
Chemotaxis protein cheA	JZ6_10	JZ6_28	OK	31.7122	81.3412	5.85E-10	2.07E-09	yes
HSP70 molecular chaperone HscA	JZ6_10	JZ6_28	OK	29.272	74.2315	7.29E-08	2.20E-07	yes
FolC bifunctional protein	JZ6_10	JZ6_28	OK	38.9177	98.6779	4.74E-07	1.32E-06	yes
Probable aminotransferase yfbQ	JZ6_10	JZ6_28	OK	50.4131	126.818	4.44E-08	1.36E-07	yes
hypothetical protein	JZ6_10	JZ6_28	OK	79.0357	198.11	4.15E-07	1.16E-06	yes
Na+/H+-exchanging protein	JZ6_10	JZ6_28	OK	60.6168	151.906	4.03E-12	1.65E-11	yes
Ribosomal protein S6 modification protein	JZ6_10	JZ6_28	OK	2779.66	6958.11	0	0	yes
anthranilate synthase alpha subunit	JZ6_10	JZ6_28	OK	31.9754	79.6679	3.77E-07	1.06E-06	yes
Prolyl 4-hydroxylase alpha subunit homologue	JZ6_10	JZ6_28	OK	218.039	542.227	2.79E-13	1.22E-12	yes
A/G-specific adenine glycosylase	JZ6_10	JZ6_28	OK	57.0357	141.676	9.12E-08	2.73E-07	yes
HemY protein	JZ6_10	JZ6_28	OK	108.336	267.833	7.33E-15	3.51E-14	yes
Protein export chaperon	JZ6_10	JZ6_28	OK	933.821	2291.48	0	0	yes
Imidazole glycerol phosphate synthase subunit hisF1	JZ6_10	JZ6_28	OK	122.025	298.931	1.72E-09	5.89E-09	yes
Citrate synthase	JZ6_10	JZ6_28	OK	650.67	1585.45	0	0	yes
Asparagine synthetase B, glutamine-hydrolyzing	JZ6_10	JZ6_28	OK	73.9122	179.789	1.87E-14	8.74E-14	yes
Alanyl-tRNA synthetase	JZ6_10	JZ6_28	OK	95.6207	232.34	0	0	yes

Ribosomal protein L23	JZ6_10	JZ6_28	OK	1928.79	4634.92	0	0	yes
Recombination protein recR	JZ6_10	JZ6_28	OK	185.239	444.326	3.87E-10	1.39E-09	yes
3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogen	JZ6_10	JZ6_28	OK	70.9051	169.923	4.56E-07	1.28E-06	yes
Protein grpE (HSP-70 cofactor)	JZ6_10	JZ6_28	OK	309.826	738.444	5.00E-14	2.28E-13	yes
Membrane protein	JZ6_10	JZ6_28	OK	1060.73	2527.46	0	0	yes
Pyrroline-5-carboxylate reductase	JZ6_10	JZ6_28	OK	67.823	161.284	3.75E-06	9.56E-06	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	85.2496	200.786	1.49E-06	3.96E-06	yes
Transketolase 1	JZ6_10	JZ6_28	OK	221.257	519.535	0	0	yes
3;4-dihydroxy-2-butanone 4-phosphate synthase	JZ6_10	JZ6_28	OK	108.587	254.859	5.05E-07	1.41E-06	yes
Exodeoxyribonuclease V beta chain	JZ6_10	JZ6_28	OK	15.8344	37.1421	2.30E-07	6.62E-07	yes
Phosphoribosylaminoimidazole carboxylase ATPase subunit	JZ6_10	JZ6_28	OK	48.3067	113.238	2.08E-06	5.45E-06	yes
Malate synthase domain protein	JZ6_10	JZ6_28	OK	514.648	1197.54	0	0	yes
Aspartate-semialdehyde dehydrogenase	JZ6_10	JZ6_28	OK	211.837	491.811	0	0	yes
Isoleucyl-tRNA synthetase	JZ6_10	JZ6_28	OK	140.827	326.322	0	0	yes
Octaprenyl-diphosphate synthase	JZ6_10	JZ6_28	OK	144.565	332.856	7.35E-14	3.32E-13	yes
Transcriptional regulator, AraC family	JZ6_10	JZ6_28	OK	99.8424	229.135	1.69E-08	5.37E-08	yes
Hemolysin III	JZ6_10	JZ6_28	OK	337.17	767.72	2.22E-16	1.15E-15	yes
ribosomal protein L6	JZ6_10	JZ6_28	OK	1121.27	2542.87	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	1217.05	2749.56	2.44E-06	6.35E-06	yes
putative methyltransferase	JZ6_10	JZ6_28	OK	301.383	680.272	4.45E-13	1.93E-12	yes
sodium-dependent transporter	JZ6_10	JZ6_28	OK	85.2107	192.265	5.43E-11	2.07E-10	yes
2-octaprenyl-6-methoxyphenol hydroxylase	JZ6_10	JZ6_28	OK	63.9101	144.111	2.58E-07	7.37E-07	yes
glycine cleavage system T protein	JZ6_10	JZ6_28	OK	112.522	253.6	5.34E-12	2.18E-11	yes
Anaerobic C4-dicarboxylate transporter dcuA	JZ6_10	JZ6_28	OK	487.789	1098.27	0	0	yes
putative ATPase	JZ6_10	JZ6_28	OK	57.6931	129.843	3.35E-09	1.12E-08	yes
hypothetical protein	JZ6_10	JZ6_28	OK	2109.27	4740.84	3.51E-14	1.62E-13	yes
putative cold shock protein	JZ6_10	JZ6_28	OK	15978.2	35904.1	0	0	yes
Succinyl-CoA synthetase alpha chain	JZ6_10	JZ6_28	OK	407.019	914.538	0	0	yes
Hypothetical acetyltransferase	JZ6_10	JZ6_28	OK	237.883	533.911	5.03E-08	1.54E-07	yes
Transcriptional regulator, LysR family	JZ6_10	JZ6_28	OK	261.829	584.282	0	0	yes
Oxaloacetate decarboxylase alpha chain	JZ6_10	JZ6_28	OK	124.86	277.582	0	0	yes
Ribosomal protein L30	JZ6_10	JZ6_28	OK	2957.12	6573.71	2.28E-10	8.32E-10	yes

Permease family protein	JZ6_10	JZ6_28	OK	67.922	150.838	1.99E-08	6.27E-08	yes
ParA family protein	JZ6_10	JZ6_28	OK	112.34	249.156	1.98E-12	8.28E-12	yes
Flagellin C	JZ6_10	JZ6_28	OK	99.3729	220.243	4.42E-10	1.58E-09	yes
Phosphoenolpyruvate-protein phosphotransferase ptsP	JZ6_10	JZ6_28	OK	111.478	246.649	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	5710.2	12608.4	0	0	yes
cytidine deaminase	JZ6_10	JZ6_28	OK	129.082	284.943	5.40E-10	1.91E-09	yes
hypothetical protein	JZ6_10	JZ6_28	OK	45.6285	100.658	2.89E-10	1.05E-09	yes
chemotaxis protein CheY	JZ6_10	JZ6_28	OK	427.11	940.384	5.43E-08	1.65E-07	yes
Phosphoribosylformylglycinamidine synthase	JZ6_10	JZ6_28	OK	72.7189	159.17	0	0	yes
ATP synthase B chain	JZ6_10	JZ6_28	OK	1586.28	3468.04	0	0	yes
Threonine dehydratase	JZ6_10	JZ6_28	OK	75.4577	164.926	1.71E-10	6.30E-10	yes
putative ribosomal RNA small subunit methyltransferase D	JZ6_10	JZ6_28	OK	70.7785	154.671	4.64E-07	1.30E-06	yes
Gamma-glutamyl phosphate reductase	JZ6_10	JZ6_28	OK	57.3746	125.283	8.99E-07	2.45E-06	yes
Glutaminyl-tRNA synthetase	JZ6_10	JZ6_28	OK	442.711	965.655	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	7389.66	16114.4	0	0	yes
NADP-dependent malic enzyme	JZ6_10	JZ6_28	OK	107.609	234.302	1.63E-11	6.44E-11	yes
Topoisomerase IV subunit A	JZ6_10	JZ6_28	OK	72.1869	156.485	3.75E-14	1.73E-13	yes
DNA gyrase, subunit A	JZ6_10	JZ6_28	OK	340.822	738.651	0	0	yes
Threonine synthase	JZ6_10	JZ6_28	OK	83.8424	181.513	1.59E-09	5.46E-09	yes
3-deoxy-manno-octulosonate cytidylyltransferase	JZ6_10	JZ6_28	OK	108.628	235.116	1.19E-06	3.21E-06	yes
Glycerol-3-phosphate dehydrogenase (NAD+)	JZ6_10	JZ6_28	OK	64.081	137.686	2.07E-06	5.43E-06	yes
PhoH-like protein	JZ6_10	JZ6_28	OK	142.284	305.395	9.87E-13	4.19E-12	yes
Probable exodeoxyribonuclease VII small subunit	JZ6_10	JZ6_28	OK	1406.9	2992.13	1.80E-07	5.23E-07	yes
Aminopeptidase P	JZ6_10	JZ6_28	OK	61.1196	129.436	1.20E-09	4.13E-09	yes
glyoxylase II family protein	JZ6_10	JZ6_28	OK	192.245	406.308	3.74E-08	1.15E-07	yes
ATP synthase beta chain	JZ6_10	JZ6_28	OK	1414.36	2986.94	0	0	yes
tryptophanyl-tRNA synthetase	JZ6_10	JZ6_28	OK	437.679	924.198	0	0	yes
Chromosomal replication initiator protein dnaA	JZ6_10	JZ6_28	OK	163.934	345.795	2.22E-16	1.15E-15	yes
Ribosomal protein L4	JZ6_10	JZ6_28	OK	787.296	1642.33	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	172.207	358.754	2.18E-09	7.38E-09	yes
signal transduction histidine kinase	JZ6_10	JZ6_28	OK	76.8082	157.556	2.57E-08	8.05E-08	yes
ATP-dependent Lon protease	JZ6_10	JZ6_28	OK	171.182	350.652	0	0	yes

RctB protein	JZ6_10	JZ6_28	OK	68.0998	138.401	3.12E-10	1.13E-09	yes
Inosine-5'-monophosphate dehydrogenase	JZ6_10	JZ6_28	OK	215.868	434.241	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	36.3711	67.207	9.66E-08	2.88E-07	yes
Pyridoxal phosphate biosynthetic protein pdxJ	JZ6_10	JZ6_28	OK	546.846	272.824	2.46E-11	9.61E-11	yes
ABC transporter: Substrate-binding protein precursor; Maltooligosaccharides u	JZ6_10	JZ6_28	OK	266.587	132.424	1.21E-10	4.51E-10	yes
putative ribosomal protein L7/L12	JZ6_10	JZ6_28	OK	6530.62	3237.58	0	0	yes
DNA-binding protein HU-beta	JZ6_10	JZ6_28	OK	9129.82	4524.68	0	0	yes
Acetyl-coenzyme A carboxylase carboxyl transferase subunit alpha	JZ6_10	JZ6_28	OK	1057.4	523.117	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	3794.9	1873.71	0	0	yes
3-oxoacyl-	JZ6_10	JZ6_28	OK	417.602	206.033	2.22E-16	1.15E-15	yes
Antioxidant, AhpC/Tsa family	JZ6_10	JZ6_28	OK	5258	2588.51	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	20069	9845.12	4.10E-08	1.26E-07	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	7122.06	3472.04	3.92E-13	1.70E-12	yes
aminotransferase, class II/CqsA	JZ6_10	JZ6_28	OK	22.805	#DIV/0!	1.69E-06	4.48E-06	yes
putative GTP cyclohydrolase II	JZ6_10	JZ6_28	OK	438.15	213.518	8.75E-07	2.38E-06	yes
Peptidyl-prolyl cis-trans isomerase B	JZ6_10	JZ6_28	OK	2058.96	1002.24	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	69.0543	33.5869	0	0	yes
putative factor-for-inversion stimulation protein	JZ6_10	JZ6_28	OK	1637.13	795.165	1.04E-07	3.09E-07	yes
DNA topoisomerase I	JZ6_10	JZ6_28	OK	492.603	238.715	0	0	yes
Transcriptional regulator	JZ6_10	JZ6_28	OK	693.87	333.612	3.35E-06	8.59E-06	yes
ABC transporter: Substrate binding protein precursor	JZ6_10	JZ6_28	OK	460.395	220.856	5.18E-11	1.97E-10	yes
RNA polymerase sigma factor rpoD (Sigma-70)	JZ6_10	JZ6_28	OK	2816.38	1345.16	0	0	yes
Inner membrane protein	JZ6_10	JZ6_28	OK	2186.89	1038.13	0	0	yes
Aspartate carbamoyltransferase, catalytic chain	JZ6_10	JZ6_28	OK	310.139	146.774	1.26E-10	4.68E-10	yes
conserved hypothetical protein	JZ6_10	JZ6_28	OK	2716.36	1283.46	0	0	yes
putative anti-sigma B factor antagonist	JZ6_10	JZ6_28	OK	1233.53	581.573	1.39E-06	3.71E-06	yes
hypothetical protein	JZ6_10	JZ6_28	OK	8637.95	4071.31	0	0	yes
DNA-directed RNA polymerase beta' chain	JZ6_10	JZ6_28	OK	937.593	440.802	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	4565.85	2144.08	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	1229.62	576.7	0	0	yes
Phosphoenolpyruvate-protein phosphotransferase	JZ6_10	JZ6_28	OK	770.707	359.023	0	0	yes
Flavodoxin	JZ6_10	JZ6_28	OK	2461.58	1141.69	0	0	yes

Transcriptional regulatory protein	JZ6_10	JZ6_28	OK	157.778	72.8779	1.50E-07	4.39E-07	yes
Endonuclease III	JZ6_10	JZ6_28	OK	298.496	137.8	1.05E-06	2.84E-06	yes
AsmA protein	JZ6_10	JZ6_28	OK	292.82	135.026	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	1715.25	787.599	6.49E-09	2.13E-08	yes
hypothetical protein	JZ6_10	JZ6_28	OK	758.215	348.047	2.11E-06	5.54E-06	yes
Protein flaG	JZ6_10	JZ6_28	OK	1213.05	555.667	3.57E-12	1.47E-11	yes
hypothetical protein	JZ6_10	JZ6_28	OK	762.706	347.534	5.56E-13	2.40E-12	yes
ABC transporter: Transmembrane and ATP-binding protein	JZ6_10	JZ6_28	OK	136.434	62.1462	9.82E-13	4.17E-12	yes
7-cyano-7-deazaguanine reductase	JZ6_10	JZ6_28	OK	297.862	135.404	1.56E-09	5.35E-09	yes
50S ribosomal protein L29	JZ6_10	JZ6_28	OK	32934.6	14939.7	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	19176.9	8674.29	0	0	yes
Thioredoxin	JZ6_10	JZ6_28	OK	7303.67	3292.32	0	0	yes
CTP synthase (UTP--ammonia ligase)	JZ6_10	JZ6_28	OK	2580.64	1159.54	0	0	yes
purine nucleoside phosphorylase	JZ6_10	JZ6_28	OK	1074.99	482.591	0	0	yes
UDP-N-acetylglucosamine 1-carboxyvinyltransferase	JZ6_10	JZ6_28	OK	835.671	375.028	0	0	yes
putative regulatory protein	JZ6_10	JZ6_28	OK	877.894	393.881	1.43E-06	3.83E-06	yes
ABC transporter: Substrate binding protein precursor	JZ6_10	JZ6_28	OK	301.035	134.863	6.16E-10	2.17E-09	yes
Alanine dehydrogenase	JZ6_10	JZ6_28	OK	5806.39	2598.19	0	0	yes
Peptidase B	JZ6_10	JZ6_28	OK	478.422	213.966	0	0	yes
2-dehydro-3-deoxyphosphooctonate aldolase	JZ6_10	JZ6_28	OK	292.245	130.396	1.60E-09	5.48E-09	yes
Spermidine/putrescine-binding periplasmic protein precursor	JZ6_10	JZ6_28	OK	346.531	154.267	5.55E-15	2.68E-14	yes
Glutaredoxin	JZ6_10	JZ6_28	OK	489.549	217.591	4.00E-10	1.43E-09	yes
Nitrogen regulatory protein P-II	JZ6_10	JZ6_28	OK	4301.29	1906.74	0	0	yes
3-hydroxydecanoyl-	JZ6_10	JZ6_28	OK	692.704	306.658	4.81E-11	1.84E-10	yes
putative peptidase	JZ6_10	JZ6_28	OK	229.479	101.536	2.58E-13	1.13E-12	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	197.634	87.0429	8.17E-08	2.45E-07	yes
CreA protein	JZ6_10	JZ6_28	OK	812.393	357.606	2.83E-11	1.10E-10	yes
Biotin carboxylase	JZ6_10	JZ6_28	OK	220.261	96.6051	4.04E-12	1.66E-11	yes
UDP-N-acetylmuramate-alanine ligase	JZ6_10	JZ6_28	OK	283.009	124.107	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	513.003	223.769	0	0	yes
Protease degQ precursor	JZ6_10	JZ6_28	OK	275.793	120.282	1.11E-15	5.56E-15	yes
6-phosphogluconate dehydrogenase	JZ6_10	JZ6_28	OK	598.654	261.023	0	0	yes

PTS system, glucose-specific IIBC component	JZ6_10	JZ6_28	OK	2731.61	1189.92	0	0	yes
Sugar fermentation stimulation protein homolog	JZ6_10	JZ6_28	OK	481.492	209.74	8.97E-14	4.03E-13	yes
Ribonuclease D	JZ6_10	JZ6_28	OK	472.136	205.215	0	0	yes
50S ribosomal subunit protein L36	JZ6_10	JZ6_28	OK	44760.5	19380.3	5.21E-08	1.59E-07	yes
Ferric uptake regulation protein	JZ6_10	JZ6_28	OK	4951.12	2137.8	0	0	yes
hypothetical arginine repressor	JZ6_10	JZ6_28	OK	594.904	256.803	4.57E-10	1.63E-09	yes
hypothetical translation factor	JZ6_10	JZ6_28	OK	598.245	258.229	1.57E-12	6.60E-12	yes
Elongation factor P	JZ6_10	JZ6_28	OK	2701.38	1162.91	0	0	yes
FkpA protein	JZ6_10	JZ6_28	OK	2366.07	1016.74	0	0	yes
sigma-E factor negative regulatory protein RseA	JZ6_10	JZ6_28	OK	3548.13	1515.54	0	0	yes
GTP cyclohydrolase-2	JZ6_10	JZ6_28	OK	624.045	266.33	1.81E-13	7.98E-13	yes
Oxidoreductase, aldo/keto reductase 2 family	JZ6_10	JZ6_28	OK	319.925	136.416	1.82E-12	7.62E-12	yes
serine hydroxymethyltransferase	JZ6_10	JZ6_28	OK	1049.68	447.394	0	0	yes
Peptide methionine sulfoxide reductase msrB	JZ6_10	JZ6_28	OK	3993.64	1701.95	0	0	yes
DNA repair protein recO	JZ6_10	JZ6_28	OK	209.902	89.2639	2.91E-06	7.50E-06	yes
ribosomal protein L34	JZ6_10	JZ6_28	OK	28074.3	11935.2	2.17E-11	8.50E-11	yes
transcription antitermination protein NusG	JZ6_10	JZ6_28	OK	3981.53	1678.69	0	0	yes
Multidrug resistance protein	JZ6_10	JZ6_28	OK	225.85	95.0967	2.22E-11	8.70E-11	yes
putative outer membrane protein	JZ6_10	JZ6_28	OK	417.581	175.471	3.87E-06	9.86E-06	yes
RNA-binding protein Hfq	JZ6_10	JZ6_28	OK	2690.22	1126.4	1.56E-11	6.18E-11	yes
sensor histidine kinase/response regulator	JZ6_10	JZ6_28	OK	60.0667	25.0677	1.80E-06	4.77E-06	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	148.502	61.8944	1.11E-14	5.27E-14	yes
5-carboxymethyl-2-hydroxymuconate isomerase	JZ6_10	JZ6_28	OK	1092.79	453.529	1.35E-08	4.31E-08	yes
ATP-dependent RNA helicase	JZ6_10	JZ6_28	OK	513.101	212.869	0	0	yes
Glycine cleavage system regulatory protein	JZ6_10	JZ6_28	OK	1337.39	554.211	0	0	yes
Electron transport complex protein rnfE	JZ6_10	JZ6_28	OK	227.518	94.2622	2.33E-06	6.07E-06	yes
sodium/dicarboxylate symporter	JZ6_10	JZ6_28	OK	115.309	47.0835	8.35E-08	2.50E-07	yes
hypothetical protein	JZ6_10	JZ6_28	OK	221.251	90.295	5.14E-08	1.56E-07	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	393.804	159.723	7.35E-11	2.77E-10	yes
33 kDa chaperonin (Heat shock protein 33 homolog)	JZ6_10	JZ6_28	OK	531.486	215.106	0	0	yes
Thiol:disulfide interchange protein dsbA precursor	JZ6_10	JZ6_28	OK	969.386	392.1	0	0	yes
ribosomal subunit interface protein	JZ6_10	JZ6_28	OK	13015.2	5244.69	0	0	yes

L-threonine 3-dehydrogenase	JZ6_10	JZ6_28	OK	236.55	95.04	4.63E-11	1.77E-10	yes
Peptidase	JZ6_10	JZ6_28	OK	154.888	62.1086	1.21E-08	3.90E-08	yes
Aspartate carbamoyltransferase regulatory chain	JZ6_10	JZ6_28	OK	553.9	221.543	2.38E-09	8.04E-09	yes
HTH-type transcriptional regulator luxR	JZ6_10	JZ6_28	OK	860.788	343.366	0	0	yes
peptide chain release factor 3	JZ6_10	JZ6_28	OK	288	114.75	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	12049.6	4800.5	2.22E-16	1.15E-15	yes
Arginine deiminase	JZ6_10	JZ6_28	OK	108.164	43.0111	7.33E-07	2.02E-06	yes
SAM-dependent methyltransferase	JZ6_10	JZ6_28	OK	375.821	149.022	9.03E-13	3.84E-12	yes
Phosphocarrier protein HPr	JZ6_10	JZ6_28	OK	7150.98	2832.27	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	549.07	216.732	1.05E-08	3.39E-08	yes
sigma-E factor regulatory protein RseC	JZ6_10	JZ6_28	OK	694.519	273.973	1.92E-11	7.55E-11	yes
Aminotransferase, CqsA	JZ6_10	JZ6_28	OK	1141.75	446.578	0	0	yes
putative LuxO repressor protein	JZ6_10	JZ6_28	OK	146.557	56.8924	2.35E-11	9.18E-11	yes
conserved hypothetical protein	JZ6_10	JZ6_28	OK	29173.3	11277.3	0	0	yes
Ribosomal-protein-serine acetyltransferase	JZ6_10	JZ6_28	OK	251.112	96.8347	3.74E-06	9.54E-06	yes
Dihydrolipoyllysine-residue acetyltransferase component of pyruvatedehydroge	JZ6_10	JZ6_28	OK	195.531	75.3145	0	0	yes
Protein proQ homolog	JZ6_10	JZ6_28	OK	2851.01	1093.95	0	0	yes
preprotein translocase, SecE subunit	JZ6_10	JZ6_28	OK	11835.6	4540.29	0	0	yes
Response regulator	JZ6_10	JZ6_28	OK	235.736	90.3196	1.05E-13	4.71E-13	yes
Tail-specific protease precursor	JZ6_10	JZ6_28	OK	949.648	363.524	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	6351.87	2427.71	4.86E-07	1.36E-06	yes
Universal stress protein A	JZ6_10	JZ6_28	OK	4801.84	1830.43	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	110.622	42.1528	1.11E-07	3.27E-07	yes
Chitinase	JZ6_10	JZ6_28	OK	49.124	18.7176	8.15E-08	2.44E-07	yes
Ribonucleoside-diphosphate reductase 1 alpha subunit	JZ6_10	JZ6_28	OK	663.101	252.065	0	0	yes
Formamidopyrimidine-DNA glycosylase	JZ6_10	JZ6_28	OK	318.808	120.455	1.21E-11	4.82E-11	yes
hypothetical regulatory components of sensory transduction	JZ6_10	JZ6_28	OK	523.639	197.448	0	0	yes
Ferritin-like protein	JZ6_10	JZ6_28	OK	3524.8	1325.63	0	0	yes
putative peptidase T	JZ6_10	JZ6_28	OK	118.318	44.2023	4.07E-08	1.25E-07	yes
ribosome modulation factor	JZ6_10	JZ6_28	OK	6266.19	2339	1.10E-07	3.26E-07	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	425.256	157.979	4.73E-11	1.81E-10	yes
hypothetical protein	JZ6_10	JZ6_28	OK	214.169	79.0949	1.33E-15	6.64E-15	yes

FxsA protein	JZ6_10	JZ6_28	OK	1567.06	578.61	0	0	yes
Molybdenum cofactor biosynthesis protein A	JZ6_10	JZ6_28	OK	747.635	274.613	0	0	yes
Amino-acid ABC transporter permease protein	JZ6_10	JZ6_28	OK	124.547	45.6778	1.28E-08	4.12E-08	yes
thymidine phosphorylase	JZ6_10	JZ6_28	OK	716.323	262.695	0	0	yes
Probable ubiquinone biosynthesis protein ubiB	JZ6_10	JZ6_28	OK	214.7	78.5638	0	0	yes
Chaperone protein torD	JZ6_10	JZ6_28	OK	1094.38	400.163	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	1383.08	504.35	4.55E-13	1.97E-12	yes
hypothetical protein	JZ6_10	JZ6_28	OK	815.769	296.855	2.69E-14	1.25E-13	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	394.007	142.745	0	0	yes
ABC transporter: Transmembrane protein	JZ6_10	JZ6_28	OK	131.833	47.6521	1.15E-07	3.40E-07	yes
Outer membrane protein	JZ6_10	JZ6_28	OK	254.592	92.0196	4.47E-11	1.71E-10	yes
D-erythrose-4-phosphate dehydrogenase	JZ6_10	JZ6_28	OK	1072	387.11	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	152.752	54.7604	0	0	yes
ABC transporter: substrate-binding protein precursor (BP)	JZ6_10	JZ6_28	OK	224.307	80.1043	3.89E-12	1.59E-11	yes
Adenosine deaminase	JZ6_10	JZ6_28	OK	285.002	101.763	2.46E-14	1.15E-13	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	2877.6	1025.5	0	0	yes
Malonyl CoA-acyl carrier protein transacylase	JZ6_10	JZ6_28	OK	524.887	186.913	0	0	yes
Formate dehydrogenase alpha chain	JZ6_10	JZ6_28	OK	71.8488	25.3511	9.74E-13	4.13E-12	yes
Deoxyribodipyrimidine photolyase	JZ6_10	JZ6_28	OK	159.149	56.1242	1.23E-13	5.47E-13	yes
GMP reductase	JZ6_10	JZ6_28	OK	370.694	130.337	0	0	yes
ATP-dependent protease LA-related	JZ6_10	JZ6_28	OK	94.6934	33.1161	2.32E-13	1.02E-12	yes
NapD protein	JZ6_10	JZ6_28	OK	1286.68	449.911	1.05E-09	3.64E-09	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	125.84	43.9515	5.00E-08	1.53E-07	yes
PrkA serine protein kinase	JZ6_10	JZ6_28	OK	1061.98	368.887	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	10175.5	3527.18	0	0	yes
UDP-N-acetylmuramoylalanine--D-glutamate ligase	JZ6_10	JZ6_28	OK	174.616	60.4884	7.34E-13	3.14E-12	yes
Hypoxanthine phosphoribosyltransferase	JZ6_10	JZ6_28	OK	923.938	319.646	0	0	yes
ABC transporter: substrate binding protein precursor	JZ6_10	JZ6_28	OK	120.826	41.7848	2.95E-14	1.37E-13	yes
long-chain acyl-CoA synthetase	JZ6_10	JZ6_28	OK	150.581	51.7878	2.00E-15	9.88E-15	yes
Cytochrome c-type protein TorC	JZ6_10	JZ6_28	OK	664.605	228.382	0	0	yes
putative protease	JZ6_10	JZ6_28	OK	59.2982	20.251	5.55E-11	2.11E-10	yes
DNA recombination protein rmuC homolog	JZ6_10	JZ6_28	OK	93.3021	31.8546	1.51E-09	5.19E-09	yes

Long-chain-fatty-acid--CoA ligase	JZ6_10	JZ6_28	OK	329.022	112.329	0	0	yes
Glucose-6-phosphate isomerase	JZ6_10	JZ6_28	OK	739.604	252.373	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	293.33	99.9228	6.40E-07	1.77E-06	yes
PfaA, omega-3 polyunsaturated fatty acid synthase	JZ6_10	JZ6_28	OK	13.4226	4.54648	3.62E-08	1.12E-07	yes
Sigma-E factor regulatory protein rseB homolog precursor	JZ6_10	JZ6_28	OK	342.916	115.871	0	0	yes
methyltransferase-related protein	JZ6_10	JZ6_28	OK	2034.5	684.827	0	0	yes
anaerobic ribonucleoside-triphosphate reductase	JZ6_10	JZ6_28	OK	1177.24	394.473	0	0	yes
Hypothetical UPF0325 protein	JZ6_10	JZ6_28	OK	5915.81	1957.22	0	0	yes
putative amino acid ABC transporter, periplasmic amino acid-binding portion	JZ6_10	JZ6_28	OK	871.099	287.11	0	0	yes
2-amino-3-ketobutyrate coenzyme A ligase	JZ6_10	JZ6_28	OK	98.6127	32.4893	9.02E-08	2.70E-07	yes
ABC transporter: transmembrane protein	JZ6_10	JZ6_28	OK	99.4673	32.5936	1.15E-06	3.10E-06	yes
transcriptional regulator	JZ6_10	JZ6_28	OK	1066.35	348.643	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	3807.44	1243.8	0	0	yes
Oxygen-independent coproporphyrinogen III oxidase	JZ6_10	JZ6_28	OK	253.681	82.7788	0	0	yes
Glyceraldehyde-3-phosphate dehydrogenase A	JZ6_10	JZ6_28	OK	7799.03	2542.84	0	0	yes
Similar to putative lipid carrier protein	JZ6_10	JZ6_28	OK	588.439	191.67	2.44E-15	1.20E-14	yes
TRAP-type uncharacterized transport system,fused permease component	JZ6_10	JZ6_28	OK	381.841	124.315	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	416.057	133.444	8.75E-07	2.38E-06	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	110.949	35.5463	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	6079.47	1940.93	1.80E-14	8.44E-14	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	590.721	188.568	0	0	yes
Uridine kinase	JZ6_10	JZ6_28	OK	1164.02	371.012	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	227.027	72.2825	2.53E-11	9.86E-11	yes
ATP-dependent Clp protease ATP-binding subunit clpX	JZ6_10	JZ6_28	OK	3494.64	1106.99	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	1725.52	546.546	1.55E-15	7.72E-15	yes
hypothetical protein	JZ6_10	JZ6_28	OK	2052.68	647.986	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	472.846	149.205	1.08E-08	3.47E-08	yes
putative sodium/substrate symport	JZ6_10	JZ6_28	OK	294.888	92.9762	0	0	yes
Ribosomal RNA large subunit methyltransferase	JZ6_10	JZ6_28	OK	357.713	111.5	2.22E-16	1.15E-15	yes
hypothetical protein	JZ6_10	JZ6_28	OK	47093.7	14601	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	51.3773	15.8918	4.51E-09	1.49E-08	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	30203.1	9322.67	0	0	yes

putative tyrosine-phosphatase	JZ6_10	JZ6_28	OK	293.597	90.2255	1.97E-06	5.19E-06	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	118.087	36.2687	1.09E-08	3.51E-08	yes
deoxyribose-phosphate aldolase	JZ6_10	JZ6_28	OK	1634.09	499.907	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	989.936	302.052	3.79E-12	1.56E-11	yes
TorCAD operon transcriptional regulatory protein torR	JZ6_10	JZ6_28	OK	1278.88	389.225	0	0	yes
ATP-dependent Clp protease, ATP-binding subunit ClpA	JZ6_10	JZ6_28	OK	1428.58	434.399	0	0	yes
Thiamine biosynthesis protein thiI	JZ6_10	JZ6_28	OK	644.15	192.637	0	0	yes
ABC transporter, permease protein	JZ6_10	JZ6_28	OK	188.82	56.4247	1.07E-07	3.18E-07	yes
Membrane-fusion protein AcrA	JZ6_10	JZ6_28	OK	78.5131	23.3501	2.78E-06	7.18E-06	yes
immunogenic protein precursor	JZ6_10	JZ6_28	OK	3216.61	953.171	0	0	yes
ABC transporter: Transmembrane protein	JZ6_10	JZ6_28	OK	199.363	58.8266	0	0	yes
Cyclopropane-fatty-acyl-phospholipid synthase	JZ6_10	JZ6_28	OK	69.139	20.2602	6.82E-07	1.88E-06	yes
hypothetical protein	JZ6_10	JZ6_28	OK	1952.82	571.607	0	0	yes
Transmembrane regulatory protein toxS	JZ6_10	JZ6_28	OK	358.616	104.648	7.19E-10	2.52E-09	yes
putative Cys/Met metabolism pyridoxal-phosphate-dependent enzyme	JZ6_10	JZ6_28	OK	671.967	196.065	0	0	yes
putative transporter fused subunits of ABC superfamily: ATP-binding compone	JZ6_10	JZ6_28	OK	524.138	152.716	0	0	yes
ABC transporter: Transmembrane protein	JZ6_10	JZ6_28	OK	139.94	40.7586	1.65E-09	5.65E-09	yes
hypothetical protein	JZ6_10	JZ6_28	OK	1268.12	368.806	1.87E-09	6.36E-09	yes
hypothetical protein	JZ6_10	JZ6_28	OK	3471.12	1007.98	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	116.864	33.923	1.66E-06	4.40E-06	yes
Cell division protein ftsY	JZ6_10	JZ6_28	OK	817.819	232.308	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	459.454	130.048	0	0	yes
3-oxoacyl-	JZ6_10	JZ6_28	OK	351.339	98.6439	0	0	yes
3-oxoacyl-	JZ6_10	JZ6_28	OK	3144.62	876.643	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	324.728	90.4436	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	308.13	85.4748	1.91E-13	8.40E-13	yes
Biotin synthesis protein bioC	JZ6_10	JZ6_28	OK	107.612	29.7354	2.12E-06	5.57E-06	yes
D-methionine-binding lipoprotein metQ precursor	JZ6_10	JZ6_28	OK	720.52	197.331	0	0	yes
RNA polymerase associated protein rapA	JZ6_10	JZ6_28	OK	197.983	53.9347	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	98733.5	26446.7	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	390.21	104.402	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	330.262	88.0712	0	0	yes

universal stress protein A	JZ6_10	JZ6_28	OK	413.508	109.687	1.53E-08	4.87E-08	yes
Membrane protein	JZ6_10	JZ6_28	OK	138.973	36.8167	2.04E-10	7.50E-10	yes
hypothetical protein	JZ6_10	JZ6_28	OK	33172.8	8750.45	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	64.9941	17.1348	4.83E-08	1.47E-07	yes
putative muconate cycloisomerase	JZ6_10	JZ6_28	OK	141.453	37.1	5.27E-10	1.87E-09	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	51.0579	13.3704	7.13E-07	1.97E-06	yes
RNA-binding protein	JZ6_10	JZ6_28	OK	995.052	260.245	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	171.101	44.2315	5.20E-12	2.12E-11	yes
ABC transporter: ATP-binding protein	JZ6_10	JZ6_28	OK	385.945	99.2986	0	0	yes
Lipid A biosynthesis lauroyl acyltransferase	JZ6_10	JZ6_28	OK	180.719	46.129	2.23E-12	9.28E-12	yes
putative response regulator receiver:Metal-dependent phosphohydrolase	JZ6_10	JZ6_28	OK	111.6	28.4473	5.00E-09	1.65E-08	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	15401.1	3920.08	0	0	yes
putative dimethylmenaquinone methyltransferase	JZ6_10	JZ6_28	OK	435.083	110.74	2.00E-15	9.88E-15	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	95.0602	24.1904	6.07E-11	2.30E-10	yes
putative ATPase involved in DNA repair	JZ6_10	JZ6_28	OK	1362.3	346.236	0	0	yes
ABC transporter: Substrate-binding protein precursor	JZ6_10	JZ6_28	OK	107.275	27.0638	1.71E-10	6.29E-10	yes
hypothetical protein	JZ6_10	JZ6_28	OK	1611.33	405.005	0	0	yes
4-hydroxyphenylpyruvate dioxygenase (4HPPD) (hemolysin)	JZ6_10	JZ6_28	OK	127.179	31.6067	3.65E-10	1.31E-09	yes
hypothetical protein	JZ6_10	JZ6_28	OK	2809.8	685.9	0	0	yes
Long-chain fatty acid transport protein precursor	JZ6_10	JZ6_28	OK	371.154	90.5681	0	0	yes
Phosphoserine aminotransferase	JZ6_10	JZ6_28	OK	244.863	59.5574	0	0	yes
putative deoxycytidylate deaminase	JZ6_10	JZ6_28	OK	5561.38	1348.4	0	0	yes
Universal stress protein B homolog	JZ6_10	JZ6_28	OK	4982.59	1206.42	0	0	yes
transporter, BCCT family	JZ6_10	JZ6_28	OK	396.012	95.4314	0	0	yes
putative KHG/KDPG aldolase	JZ6_10	JZ6_28	OK	229.611	55.0885	9.59E-10	3.33E-09	yes
Phosphoserine phosphatase	JZ6_10	JZ6_28	OK	422.333	101.144	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	466.119	111.233	0	0	yes
3-oxoacyl-	JZ6_10	JZ6_28	OK	1738.42	405.203	0	0	yes
putative hemolysin	JZ6_10	JZ6_28	OK	148.632	34.5432	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	784.322	182.192	8.05E-09	2.62E-08	yes
5'-nucleotidase/2',3'-cyclic phosphodiesterase	JZ6_10	JZ6_28	OK	181.213	41.9977	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	722.393	167.387	2.55E-07	7.28E-07	yes

Conserved hypothetical protein	JZ6_10	JZ6_28	OK	2193.12	504.744	0	0	yes
Predicted periplasmic protein	JZ6_10	JZ6_28	OK	175.599	40.1859	4.01E-08	1.23E-07	yes
glycine cleavage system H protein	JZ6_10	JZ6_28	OK	15896.9	3634.12	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	1301.17	295.094	3.38E-08	1.05E-07	yes
PTS family enzyme IIA	JZ6_10	JZ6_28	OK	142.352	32.1112	0	0	yes
S-adenosylmethionine:2-demethylmenaquinone methyltransferase	JZ6_10	JZ6_28	OK	3328.63	741.023	0	0	yes
ABC transporter: two domain ATP-binding protein	JZ6_10	JZ6_28	OK	55.0251	12.2207	8.63E-08	2.58E-07	yes
putative glycine betaine transporter	JZ6_10	JZ6_28	OK	40.2209	8.90533	3.28E-06	8.42E-06	yes
GTP-binding protein era homolog	JZ6_10	JZ6_28	OK	2160.47	473.301	0	0	yes
S-adenosylmethionine synthetase	JZ6_10	JZ6_28	OK	456.887	100.082	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	6967.27	1523.63	0	0	yes
putative phosphate permease	JZ6_10	JZ6_28	OK	249.471	53.7666	0	0	yes
Pyruvate kinase I	JZ6_10	JZ6_28	OK	4800.74	1027.19	0	0	yes
putative sensor protein	JZ6_10	JZ6_28	OK	103.528	22.0067	3.82E-14	1.76E-13	yes
Sensor histidine kinase, CqsS	JZ6_10	JZ6_28	OK	67.1794	14.0415	5.32E-10	1.89E-09	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	341648	71207.1	0	0	yes
hypothetical lipoprotein-related protein	JZ6_10	JZ6_28	OK	1166.05	241.217	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	514.808	106.391	0	0	yes
Acyl carrier protein	JZ6_10	JZ6_28	OK	48634.1	10022.4	0	0	yes
Na+/H+ antiporter NhaD and related arsenite permeases	JZ6_10	JZ6_28	OK	114.069	23.2905	5.44E-14	2.48E-13	yes
Alkaline phosphatase III precursor	JZ6_10	JZ6_28	OK	259.999	52.2893	0	0	yes
putative capsular polysaccharide biosynthesis protein	JZ6_10	JZ6_28	OK	120.284	24.1452	7.23E-07	1.99E-06	yes
Sulfite reductase	JZ6_10	JZ6_28	OK	81.0717	16.0728	1.46E-13	6.49E-13	yes
chemotactic transducer-related protein	JZ6_10	JZ6_28	OK	30.9865	6.07763	6.49E-10	2.29E-09	yes
ABC transporter: ATP-binding protein	JZ6_10	JZ6_28	OK	142.216	27.7888	9.19E-14	4.12E-13	yes
Soluble lytic murein transglycosylase	JZ6_10	JZ6_28	OK	42.2215	8.24326	4.01E-07	1.12E-06	yes
Glyceraldehyde-3-phosphate dehydrogenase 3	JZ6_10	JZ6_28	OK	68.2867	13.303	3.20E-06	8.22E-06	yes
hypothetical protein	JZ6_10	JZ6_28	OK	727.274	141.181	0	0	yes
Probable sigma(54) modulation protein	JZ6_10	JZ6_28	OK	2787.92	540.309	0	0	yes
ABC transporter: Transmembrane protein	JZ6_10	JZ6_28	OK	52.2864	10.0918	4.45E-13	1.93E-12	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	1143.66	220.6	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	27120.8	5208.81	0	0	yes

putative cytochrome c, class I	JZ6_10	JZ6_28	OK	54.6764	10.4887	2.55E-07	7.28E-07	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	867.567	164.362	2.32E-07	6.66E-07	yes
Methionine sulfoxide reductase	JZ6_10	JZ6_28	OK	182.837	34.5041	0	0	yes
putative alcohol dehydrogenase	JZ6_10	JZ6_28	OK	693.791	130.629	0	0	yes
Multi antimicrobial extrusion protein MatE	JZ6_10	JZ6_28	OK	65.321	12.2694	1.45E-08	4.64E-08	yes
Protoheme IX farnesyltransferase	JZ6_10	JZ6_28	OK	88.6007	16.6323	1.72E-07	4.98E-07	yes
ABC transporter: Transmembrane and ATP-binding protein	JZ6_10	JZ6_28	OK	316.893	59.2151	0	0	yes
ABC transporter: Substrate binding protein precursor	JZ6_10	JZ6_28	OK	91.3874	16.7836	8.28E-12	3.33E-11	yes
putative esterase	JZ6_10	JZ6_28	OK	348.017	63.5831	0	0	yes
putative Holliday junction resolvase	JZ6_10	JZ6_28	OK	648.155	116.728	2.22E-16	1.15E-15	yes
AcrB/AcrD/AcrF family	JZ6_10	JZ6_28	OK	35.8746	6.4545	4.42E-11	1.69E-10	yes
putative two-component sensor	JZ6_10	JZ6_28	OK	226.494	40.7308	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	157.261	28.2662	8.61E-07	2.35E-06	yes
hypothetical protein	JZ6_10	JZ6_28	OK	4456.43	799.709	0	0	yes
transcriptional regulator, LuxR family	JZ6_10	JZ6_28	OK	248.882	43.9328	2.82E-11	1.09E-10	yes
hypothetical protein	JZ6_10	JZ6_28	OK	7618.37	1336.13	0	0	yes
putative membrane protein	JZ6_10	JZ6_28	OK	62.4287	10.9441	6.23E-07	1.73E-06	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	370.042	64.6109	0	0	yes
putative glutamate synthetase	JZ6_10	JZ6_28	OK	68.0379	11.6983	1.64E-10	6.05E-10	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	552.749	94.0914	0	0	yes
Heat shock protein	JZ6_10	JZ6_28	OK	1946.43	329.249	0	0	yes
Sigma-54 dependent transcriptional regulator	JZ6_10	JZ6_28	OK	53.2288	8.95144	3.19E-07	9.02E-07	yes
Oxidoreductase, short-chain dehydrogenase/reductase family	JZ6_10	JZ6_28	OK	229.546	38.2687	3.63E-13	1.58E-12	yes
hypothetical protein	JZ6_10	JZ6_28	OK	3623.34	602.246	2.22E-16	1.15E-15	yes
ABC transporter: Transmembrane protein	JZ6_10	JZ6_28	OK	79.2216	12.8987	2.21E-12	9.23E-12	yes
Conserved hypothetical receptor	JZ6_10	JZ6_28	OK	206.546	33.1432	0	0	yes
putative transduction protein	JZ6_10	JZ6_28	OK	28.9903	4.62264	1.45E-07	4.25E-07	yes
Predicted phosphatase/phosphohexomutase	JZ6_10	JZ6_28	OK	418.384	66.7	0	0	yes
5'-nucleotidase/2',3'-cyclic phosphodiesterase	JZ6_10	JZ6_28	OK	500.154	79.5041	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	380.532	60.4047	0	0	yes
Diaminobutyrate--2-oxoglutarate aminotransferase	JZ6_10	JZ6_28	OK	49.5599	7.81403	2.89E-15	1.41E-14	yes
putative alkaline phosphatase	JZ6_10	JZ6_28	OK	736.695	114.418	0	0	yes

hypothetical protein	JZ6_10	JZ6_28	OK	1431.68	219.852	8.27E-12	3.33E-11	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	101.296	15.4267	1.12E-06	3.02E-06	yes
Cell division protein ftsX	JZ6_10	JZ6_28	OK	181.613	27.4652	8.66E-15	4.13E-14	yes
Integration host factor beta-subunit (IHF-beta)	JZ6_10	JZ6_28	OK	46177.6	6971.21	0	0	yes
Molybdenum cofactor biosynthesis protein E	JZ6_10	JZ6_28	OK	394.252	59.1935	3.69E-12	1.52E-11	yes
hypothetical protein	JZ6_10	JZ6_28	OK	301.489	44.5403	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	14713.1	2158.34	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	318.758	46.3875	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	62632.7	8985.06	0	0	yes
putative threonine efflux protein	JZ6_10	JZ6_28	OK	148.571	21.2466	4.38E-07	1.23E-06	yes
Phenylalanine-4-hydroxylase	JZ6_10	JZ6_28	OK	190.852	27.1723	8.16E-13	3.48E-12	yes
hypothetical protein	JZ6_10	JZ6_28	OK	1174.01	165.961	0	0	yes
Universal stress protein E	JZ6_10	JZ6_28	OK	1712.46	241.176	0	0	yes
Amino acid ABC transporter	JZ6_10	JZ6_28	OK	5584.43	785.752	0	0	yes
Purine nucleoside phosphorylase	JZ6_10	JZ6_28	OK	1943.41	271.117	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	180.372	24.8241	2.66E-10	9.69E-10	yes
Outer membrane protein	JZ6_10	JZ6_28	OK	211.413	29.079	0	0	yes
Phosphotransferase system, fructose-specific IIC component	JZ6_10	JZ6_28	OK	54.3763	7.43673	2.25E-10	8.22E-10	yes
hypothetical protein	JZ6_10	JZ6_28	OK	363.175	49.089	4.70E-09	1.55E-08	yes
Transmembrane water channel Aquaporin Z	JZ6_10	JZ6_28	OK	106.649	14.0227	3.89E-06	9.89E-06	yes
Protein mazG homolog	JZ6_10	JZ6_28	OK	921.818	121.032	0	0	yes
putative membrane protein	JZ6_10	JZ6_28	OK	58.896	7.6071	9.36E-08	2.79E-07	yes
Cell division protein BolA	JZ6_10	JZ6_28	OK	2343.39	299.445	0	0	yes
Acyl-coenzyme A synthetases	JZ6_10	JZ6_28	OK	274.148	35.026	0	0	yes
putative metal-dependent hydrolase	JZ6_10	JZ6_28	OK	90.9285	11.6071	7.90E-08	2.37E-07	yes
hypothetical protein	JZ6_10	JZ6_28	OK	170.654	21.7126	6.66E-16	3.37E-15	yes
hypothetical protein	JZ6_10	JZ6_28	OK	109.99	13.9868	2.91E-14	1.35E-13	yes
Transcriptional regulator	JZ6_10	JZ6_28	OK	313.956	39.421	4.44E-16	2.26E-15	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	3772.68	473.192	0	0	yes
ABC transporter: transmembrane protein	JZ6_10	JZ6_28	OK	75.3259	9.42918	2.33E-06	6.07E-06	yes
Integration host factor, alpha subunit	JZ6_10	JZ6_28	OK	15066.2	1825.77	0	0	yes
Flp pilus assembly protein	JZ6_10	JZ6_28	OK	154.652	18.4313	0	0	yes

NAD-dependent aldehyde dehydrogenase	JZ6_10	JZ6_28	OK	39.4764	4.66708	1.18E-06	3.18E-06	yes
Short-chain dehydrogenase/reductase	JZ6_10	JZ6_28	OK	90.5037	10.6855	1.17E-06	3.16E-06	yes
putative ornithine carbamoyltransferase	JZ6_10	JZ6_28	OK	1282.16	147.425	0	0	yes
Penicillin-insensitive murein endopeptidase precursor	JZ6_10	JZ6_28	OK	83.8356	9.52576	7.61E-07	2.09E-06	yes
putative outer membrane protein	JZ6_10	JZ6_28	OK	476.223	53.271	0	0	yes
Probable lactoylglutathione lyase	JZ6_10	JZ6_28	OK	8564.53	923.157	0	0	yes
ABC-type Fe3+ transport system, periplasmic component	JZ6_10	JZ6_28	OK	814.177	86.9659	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	37.4217	3.97827	3.33E-07	9.42E-07	yes
hypothetical protein	JZ6_10	JZ6_28	OK	118.987	12.5049	2.66E-15	1.31E-14	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	474.278	49.1594	2.48E-09	8.35E-09	yes
Zinc-binding dehydrogenase	JZ6_10	JZ6_28	OK	278.749	28.3091	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	100.719	10.2152	1.33E-15	6.64E-15	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	207.09	20.9982	1.33E-15	6.64E-15	yes
hypothetical protein	JZ6_10	JZ6_28	OK	1203.46	121.911	2.04E-07	5.89E-07	yes
inosine monophosphate dehydrogenase-related protein	JZ6_10	JZ6_28	OK	1497.42	149.181	0	0	yes
ABC-type sugar transport system, periplasmic component	JZ6_10	JZ6_28	OK	557.635	54.1971	0	0	yes
Arylsulfatase	JZ6_10	JZ6_28	OK	1077	102.594	0	0	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	21431.8	2015.62	0	0	yes
Predicted phosphatase/phosphohexomutase	JZ6_10	JZ6_28	OK	378.193	35.3445	0	0	yes
Transcriptional regulator, LysR family	JZ6_10	JZ6_28	OK	1922.21	179.64	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	237.029	21.9304	1.02E-14	4.85E-14	yes
Periplasmic protein involved in polysaccharide export	JZ6_10	JZ6_28	OK	69.5887	6.4357	1.04E-14	4.96E-14	yes
hypothetical protein	JZ6_10	JZ6_28	OK	765.519	69.6474	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	209.483	18.901	0	0	yes
Protein cyaY	JZ6_10	JZ6_28	OK	15017.7	1346.11	0	0	yes
Polyphosphate kinase	JZ6_10	JZ6_28	OK	91.9833	8.22039	0	0	yes
TPR-repeat-containing protein	JZ6_10	JZ6_28	OK	116.446	10.2597	1.14E-10	4.26E-10	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	181.639	15.9612	2.44E-15	1.20E-14	yes
putative periplasmic protein	JZ6_10	JZ6_28	OK	1433.04	124.647	0	0	yes
Conserved hypothetical protein	JZ6_10	JZ6_28	OK	79849.2	6802.57	0	0	yes
hypothetical membrane protein	JZ6_10	JZ6_28	OK	45.1535	3.54721	1.53E-06	4.07E-06	yes
Dethiobiotin synthetase	JZ6_10	JZ6_28	OK	331.371	25.9491	0	0	yes

Hypothetical protein	JZ6_10	JZ6_28	OK	66.6789	5.19767	1.50E-06	4.01E-06	yes
NADH oxidase	JZ6_10	JZ6_28	OK	59.6919	4.63607	1.34E-06	3.59E-06	yes
putative cytochrome c oxidase, subunit I	JZ6_10	JZ6_28	OK	408.789	31.0357	0	0	yes
putative outer membrane lipoprotein	JZ6_10	JZ6_28	OK	143874	10833.6	0	0	yes
Predicted membrane-associated, metal-dependent hydrolase	JZ6_10	JZ6_28	OK	95.9241	7.14014	8.44E-15	4.03E-14	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	371.66	27.0453	1.13E-09	3.90E-09	yes
DNA-binding response regulator PhoB	JZ6_10	JZ6_28	OK	583.169	41.2896	0	0	yes
NADH dehydrogenase subunit II-related protein	JZ6_10	JZ6_28	OK	41246.1	2859.84	0	0	yes
ABC transporter: Substrate-binding protein precursor; phosphate uptake	JZ6_10	JZ6_28	OK	1621.36	111.03	0	0	yes
conserved hypothetical protein	JZ6_10	JZ6_28	OK	653.134	44.3665	0	0	yes
Hypothetical protein containg GGDEF domain	JZ6_10	JZ6_28	OK	329.016	22.2399	0	0	yes
putative membrane protein	JZ6_10	JZ6_28	OK	750.814	48.6522	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	234.757	13.7821	6.90E-08	2.08E-07	yes
ABC transporter: Substrate binding protein precursor	JZ6_10	JZ6_28	OK	768.094	44.4511	0	0	yes
putative transcriptional activator	JZ6_10	JZ6_28	OK	148.759	8.45522	4.42E-08	1.36E-07	yes
RpoS-like sigma factor	JZ6_10	JZ6_28	OK	728.066	40.7599	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	30579.9	1701.48	0	0	yes
Flp pilus assembly protein	JZ6_10	JZ6_28	OK	189.81	10.3781	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	413.054	21.9095	1.96E-08	6.18E-08	yes
Molybdenum cofactor biosynthesis protein B	JZ6_10	JZ6_28	OK	580.674	30.1627	0	0	yes
Carbamate kinase	JZ6_10	JZ6_28	OK	404.58	20.2517	0	0	yes
putative stomatin-like protein	JZ6_10	JZ6_28	OK	138.951	6.93989	9.70E-09	3.14E-08	yes
putative carbamate kinase	JZ6_10	JZ6_28	OK	1074.56	51.1161	0	0	yes
Arginine deiminase	JZ6_10	JZ6_28	OK	2406.34	111.768	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	175.335	7.95422	3.15E-09	1.05E-08	yes
hypothetical protein	JZ6_10	JZ6_28	OK	977.069	42.6144	0	0	yes
hypothetical protein	JZ6_10	JZ6_28	OK	1211.98	52.1524	1.58E-09	5.42E-09	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	518.241	21.0617	0	0	yes
ABC transporter: substrate binding protein precursor	JZ6_10	JZ6_28	OK	151.885	5.60258	7.33E-15	3.51E-14	yes
hypothetical protein	JZ6_10	JZ6_28	OK	30498	1088.7	0	0	yes
Dihydrolipoyl dehydrogenase	JZ6_10	JZ6_28	OK	292.517	9.63112	0	0	yes
Tryptophanase (L-tryptophan indole-lyase)	JZ6_10	JZ6_28	OK	354.204	11.1271	0	0	yes

ABC-type multidrug transport system, ATPase and permease component	JZ6_10	JZ6_28	OK	821.774	24.1945	0	0	yes
putative endoribonuclease	JZ6_10	JZ6_28	OK	142.857	3.87374	2.98E-12	1.23E-11	yes
putative Glycosyl transferase	JZ6_10	JZ6_28	OK	355.131	9.29366	0	0	yes
Exopolyphosphatase	JZ6_10	JZ6_28	OK	64.7712	1.49115	2.35E-07	6.75E-07	yes
Outer membrane protein	JZ6_10	JZ6_28	OK	1596.33	36.6176	0	0	yes
putative Acid phosphatase homologue	JZ6_10	JZ6_28	OK	868.126	14.3472	1.33E-15	6.64E-15	yes
Extracellular zinc metalloprotease	JZ6_10	JZ6_28	OK	2521.28	37.0821	0	0	yes
putative orphan protein	JZ6_10	JZ6_28	OK	469.715	6.78235	5.41E-09	1.78E-08	yes
Hypothetical protein	JZ6_10	JZ6_28	OK	706.627	8.03175	6.80E-10	2.39E-09	yes
Predicted integral membrane protein	JZ6_10	JZ6_28	OK	4926.04	30.7236	2.28E-12	9.49E-12	yes

Table S2 List of differentially expressed genes in strain TZ19 at 10 ℃ (TZ19_10) versus at 28 ℃ (TZ19_28).

Gene name	Group1	Group2	States	FPKM1	FPKM2	E-value1	E-value2	Significant
hypothetical protein	TZ19_10	TZ19_28	OK	49.4012	1475.96	0	0	yes
Sulfate adenylate transferase subunit 1	TZ19_10	TZ19_28	OK	8.79409	233.466	0	0	yes
long-chain fatty acid transport protein	TZ19_10	TZ19_28	OK	2.78423	59.7365	6.74E-08	2.04E-07	yes
Urocanate hydratase	TZ19_10	TZ19_28	OK	8.0525	125.827	0	0	yes
Histidine ammonia-lyase	TZ19_10	TZ19_28	OK	3.23397	49.7067	5.24E-09	1.73E-08	yes
Malate synthase	TZ19_10	TZ19_28	OK	313.307	4362.97	0	0	yes
putative integral membrane protein	TZ19_10	TZ19_28	OK	17.1623	232.567	0	0	yes
Conserved hypothetical protein; putative exported	TZ19_10	TZ19_28	OK	35.2708	470.119	0	0	yes
ABC transporter: Substrate binding protein precursor	TZ19_10	TZ19_28	OK	15.7751	174.244	0	0	yes
ABC-type sugar transport system, ATP-binding protein	TZ19_10	TZ19_28	OK	23.8259	241.65	0	0	yes
Phenylalanine-4-hydroxylase	TZ19_10	TZ19_28	OK	102.306	1027.52	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	210.34	2022.54	4.91E-10	1.75E-09	yes
Aconitase A	TZ19_10	TZ19_28	OK	2.03286	19.5286	2.08E-06	5.47E-06	yes
Acetyl-CoA acetyltransferase	TZ19_10	TZ19_28	OK	123.822	1091.64	0	0	yes
Glycerophosphoryl diester phosphodiesterase family protein	TZ19_10	TZ19_28	OK	20.8565	182.933	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	212.83	1687.53	0	0	yes
Succinyl-CoA synthetase alpha chain	TZ19_10	TZ19_28	OK	973.903	7684.16	0	0	yes
NAD(P) transhydrogenase, beta subunit	TZ19_10	TZ19_28	OK	74.9464	587.659	0	0	yes
Oxaloacetate decarboxylase beta chain	TZ19_10	TZ19_28	OK	19.1997	149.086	8.44E-15	4.03E-14	yes
2-oxoglutarate dehydrogenase E1 component	TZ19_10	TZ19_28	OK	421.557	3236.8	0	0	yes
succinate dehydrogenase	TZ19_10	TZ19_28	OK	317.372	2422.3	0	0	yes
Dihydrolipoyllysine-residue succinyltransferase	TZ19_10	TZ19_28	OK	414.693	3054.46	0	0	yes
putative Sodium/sulfate symporter	TZ19_10	TZ19_28	OK	4.65236	34.0545	1.98E-06	5.21E-06	yes
cytochrome c oxidase, subunit CcoQ	TZ19_10	TZ19_28	OK	3451.77	24344.6	0	0	yes
ABC transporter: Substrate binding protein precursor	TZ19_10	TZ19_28	OK	75.3839	517.541	0	0	yes
ABC-type multidrug transport system, ATPase and permease component	TZ19_10	TZ19_28	OK	802.614	5487.05	0	0	yes
cytochrome c oxidase, subunit CcoO	TZ19_10	TZ19_28	OK	472.649	3213.36	0	0	yes
Succinylglutamic semialdehyde dehydrogenase	TZ19_10	TZ19_28	OK	124.142	843.76	0	0	yes
putative outer membrane lipoprotein	TZ19_10	TZ19_28	OK	49098.4	333017	0	0	yes

hypothetical protein	TZ19_10	TZ19_28	OK	289.911	1960.84	0	0	yes
DNA-3-methyladenine glycosylase	TZ19_10	TZ19_28	OK	15.39	102.882	1.37E-07	4.03E-07	yes
putative endoribonuclease	TZ19_10	TZ19_28	OK	212.59	1376.59	0	0	yes
Outer membrane protein	TZ19_10	TZ19_28	OK	595.93	3832.53	0	0	yes
putative response regulator	TZ19_10	TZ19_28	OK	273.367	1757.85	0	0	yes
Glycerophosphoryl diester phosphodiesterase	TZ19_10	TZ19_28	OK	16.8588	104.067	4.17E-07	1.17E-06	yes
Nuclease sbcCD subunit C	TZ19_10	TZ19_28	OK	3.62164	21.7123	4.20E-09	1.39E-08	yes
Long-chain fatty acid transport protein precursor	TZ19_10	TZ19_28	OK	15.1493	90.5611	8.32E-13	3.55E-12	yes
Nucleoside diphosphate kinase	TZ19_10	TZ19_28	OK	1211.14	7179	0	0	yes
3-deoxy-manno-octulosonate cytidylyltransferase	TZ19_10	TZ19_28	OK	17.5477	103.544	8.53E-07	2.33E-06	yes
Aspartate carbamoyltransferase regulatory chain	TZ19_10	TZ19_28	OK	367.127	2141.3	0	0	yes
tetraacyldisaccharide 4'-kinase	TZ19_10	TZ19_28	OK	60.9534	346.339	0	0	yes
Malate synthase domain protein	TZ19_10	TZ19_28	OK	1533.58	8697.73	0	0	yes
Acetyltransferase	TZ19_10	TZ19_28	OK	37.3256	211.354	4.45E-09	1.47E-08	yes
D-alanyl-D-alanine carboxypeptidase	TZ19_10	TZ19_28	OK	74.6302	421.851	0	0	yes
ABC transporter: transmembrane protein	TZ19_10	TZ19_28	OK	38.6648	217.665	4.40E-14	2.01E-13	yes
cytochrome c oxidase, subunit CcoP	TZ19_10	TZ19_28	OK	403.897	2242.77	0	0	yes
Cytochrome c-type protein TorC	TZ19_10	TZ19_28	OK	203.258	1121.26	0	0	yes
potassium uptake protein TrkH	TZ19_10	TZ19_28	OK	8.55392	47.1611	3.45E-07	9.75E-07	yes
putative tyrosine-protein kinase (wzc)	TZ19_10	TZ19_28	OK	11.6208	63.9901	4.37E-14	2.00E-13	yes
DctQ, TRAP-type C4-dicarboxylate transport system, large permease compone	TZ19_10	TZ19_28	OK	10.9206	59.88	5.78E-08	1.75E-07	yes
Catalase	TZ19_10	TZ19_28	OK	88.4654	483.342	0	0	yes
Extracellular solute-binding protein, family 7	TZ19_10	TZ19_28	OK	45.6275	248.629	0	0	yes
Succinyl-CoA synthetase beta chain	TZ19_10	TZ19_28	OK	420.875	2289.52	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	17.5237	95.1976	0	0	yes
ATP-dependent protease LA-related	TZ19_10	TZ19_28	OK	83.8634	445.555	0	0	yes
Methyl-accepting chemotaxis protein	TZ19_10	TZ19_28	OK	15.1123	80.1932	2.22E-15	1.09E-14	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	8.7332	46.1872	1.27E-06	3.41E-06	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	201.331	1047.32	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	34.8008	179.144	0	0	yes
Psp operon transcriptional activator	TZ19_10	TZ19_28	OK	21.1131	107.475	9.69E-09	3.14E-08	yes
napE protein	TZ19_10	TZ19_28	OK	851.891	4278.57	1.45E-07	4.24E-07	yes

ATP synthase beta chain	TZ19_10	TZ19_28	OK	1347.35	6763.37	0	0	yes
putative hemolysin	TZ19_10	TZ19_28	OK	38.3938	190.521	0	0	yes
Agmatinase (Agmatine ureohydrolase)	TZ19_10	TZ19_28	OK	100.634	492.789	0	0	yes
ATP-dependent Clp protease adaptor protein clpS	TZ19_10	TZ19_28	OK	8341.63	40810.8	0	0	yes
putative trimethylamine-N-oxide reductase	TZ19_10	TZ19_28	OK	308.584	1474.37	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	141.084	669.568	0	0	yes
Malate dehydrogenase	TZ19_10	TZ19_28	OK	1230.74	5771.4	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	802.149	3730.68	0	0	yes
conserved hypothetical protein	TZ19_10	TZ19_28	OK	72.365	336.428	1.32E-10	4.91E-10	yes
Imidazole glycerol phosphate synthase subunit hisH	TZ19_10	TZ19_28	OK	37.5516	174.484	7.22E-08	2.18E-07	yes
Phosphoribosylamine--glycine ligase	TZ19_10	TZ19_28	OK	36.2395	168.314	0	0	yes
putative sodium/hydrogen exchanger family protein	TZ19_10	TZ19_28	OK	11.3143	51.4512	3.01E-09	1.01E-08	yes
decarboxylase family protein	TZ19_10	TZ19_28	OK	30.9518	140.718	4.44E-16	2.26E-15	yes
Acyl-coenzyme A synthetases	TZ19_10	TZ19_28	OK	23.8115	107.885	2.22E-16	1.15E-15	yes
hypothetical protein	TZ19_10	TZ19_28	OK	2353.38	10646.7	0	0	yes
ABC transporter IM-ABC: Transmembrane and ATP binding protein	TZ19_10	TZ19_28	OK	10.9742	49.6044	1.10E-09	3.79E-09	yes
Na(+)-translocating NADH-quinone reductase subunit C	TZ19_10	TZ19_28	OK	523.529	2350.21	0	0	yes
Polyhydroxyalkanoic acid synthase	TZ19_10	TZ19_28	OK	772.991	3447.26	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	123.16	547.294	1.44E-12	6.07E-12	yes
periplasmic nitrate reductase, cytochrome c-type protein	TZ19_10	TZ19_28	OK	747.576	3298	0	0	yes
histidine ammonia-lyase protein	TZ19_10	TZ19_28	OK	14.6753	64.4556	1.34E-09	4.60E-09	yes
Periplasmic dipeptide transport protein precursor	TZ19_10	TZ19_28	OK	394.833	1709.34	0	0	yes
Carbamoyl-phosphate synthase large chain	TZ19_10	TZ19_28	OK	113.868	486.036	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	1263.9	5317.39	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	17.6182	74.1188	7.98E-08	2.40E-07	yes
putative succinate dehydrogenase, flavoprotein subunit	TZ19_10	TZ19_28	OK	335.897	1401.91	0	0	yes
Carboxypeptidase	TZ19_10	TZ19_28	OK	36.8773	153.398	0	0	yes
Aspartate carbamoyltransferase	TZ19_10	TZ19_28	OK	570.433	2366.28	0	0	yes
6-phosphogluconate dehydrogenase	TZ19_10	TZ19_28	OK	352.128	1456.41	0	0	yes
Flagellar hook-basal body complex protein fliE	TZ19_10	TZ19_28	OK	949.598	3897.46	0	0	yes
Ketol-acid reductoisomerase	TZ19_10	TZ19_28	OK	265.671	1089.87	0	0	yes
Flagellin C	TZ19_10	TZ19_28	OK	189.418	774.695	0	0	yes

hypothetical protein	TZ19_10	TZ19_28	OK	89.1776	363.656	0	0	yes
Glycyl-tRNA synthetase beta chain	TZ19_10	TZ19_28	OK	72.6302	292.778	0	0	yes
Oligopeptide transport ATP-binding protein oppF	TZ19_10	TZ19_28	OK	107.865	433.475	0	0	yes
Transcriptional regulator, LysR family	TZ19_10	TZ19_28	OK	55.2889	222.023	1.82E-14	8.54E-14	yes
Protein flaG	TZ19_10	TZ19_28	OK	378.517	1512.14	0	0	yes
ATP phosphoribosyltransferase	TZ19_10	TZ19_28	OK	311.324	1225.23	0	0	yes
Arginine N-succinyltransferase, beta chain	TZ19_10	TZ19_28	OK	165.7	649.541	0	0	yes
putative nitrogen regulatory protein P-II family protein	TZ19_10	TZ19_28	OK	123.916	484.881	1.31E-06	3.52E-06	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	66.7928	261.299	8.66E-07	2.36E-06	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	52.4126	203.493	2.34E-11	9.16E-11	yes
Formate dehydrogenase	TZ19_10	TZ19_28	OK	86.1658	333.881	0	0	yes
putative ABC transporter, ATP-binding protein	TZ19_10	TZ19_28	OK	65.5725	253.673	0	0	yes
sodium/solute symporter	TZ19_10	TZ19_28	OK	33.4502	129.275	0	0	yes
Peptide transport system permease protein sapC	TZ19_10	TZ19_28	OK	26.3082	101.197	1.17E-07	3.46E-07	yes
Formate dehydrogenase iron-sulfur subunit	TZ19_10	TZ19_28	OK	156.756	599.859	0	0	yes
methyl-accepting chemotaxis protein	TZ19_10	TZ19_28	OK	18.6071	71.1817	1.25E-08	4.03E-08	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	1784.15	6813.38	0	0	yes
Endonuclease III	TZ19_10	TZ19_28	OK	78.5013	299.457	3.64E-12	1.50E-11	yes
Topoisomerase IV subunit A	TZ19_10	TZ19_28	OK	32.5265	123.021	0	0	yes
ATP synthase epsilon chain	TZ19_10	TZ19_28	OK	2112.53	7987.95	0	0	yes
Aconitate hydratase 2 (Citrate hydro-lyase 2)	TZ19_10	TZ19_28	OK	309.791	1165.11	0	0	yes
Cysteine synthase A	TZ19_10	TZ19_28	OK	1207.59	4535.84	0	0	yes
Electron transport complex protein rnfG	TZ19_10	TZ19_28	OK	96.6544	362.986	9.51E-13	4.04E-12	yes
Electron transport complex protein rnfD	TZ19_10	TZ19_28	OK	19.261	71.4321	7.35E-07	2.02E-06	yes
TPR-repeat-containing protein	TZ19_10	TZ19_28	OK	8.00057	29.6651	3.66E-06	9.34E-06	yes
hypothetical protein	TZ19_10	TZ19_28	OK	53.1138	195.685	1.27E-07	3.75E-07	yes
Predicted ferredoxin	TZ19_10	TZ19_28	OK	299.133	1097.32	2.74E-09	9.21E-09	yes
Electron transport complex protein rnfE	TZ19_10	TZ19_28	OK	42.252	154.667	1.35E-06	3.62E-06	yes
Formate dehydrogenase alpha chain	TZ19_10	TZ19_28	OK	122.999	449.247	0	0	yes
Electron transport complex protein RnfC (fragment)	TZ19_10	TZ19_28	OK	10.712	39.0705	3.57E-07	1.01E-06	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	13.0924	47.4599	0	0	yes
ABC transporter: ATP-binding protein	TZ19_10	TZ19_28	OK	36.6606	132.838	2.74E-06	7.09E-06	yes

Beta-glucosidase	TZ19_10	TZ19_28	OK	17.9789	65.077	1.58E-07	4.60E-07	yes
Oligoribonuclease	TZ19_10	TZ19_28	OK	342.943	1234.84	0	0	yes
Citrate synthase	TZ19_10	TZ19_28	OK	1026.35	3693.72	0	0	yes
ATPase	TZ19_10	TZ19_28	OK	32.1731	114.793	0	0	yes
Phosphoenolpyruvate carboxykinase	TZ19_10	TZ19_28	OK	7506.93	26708.8	0	0	yes
Secreted/periplasmic Zn-dependent peptidases,insulinase-like	TZ19_10	TZ19_28	OK	15.75	55.8283	1.42E-13	6.30E-13	yes
Glutathione reductase	TZ19_10	TZ19_28	OK	238.968	846.232	0	0	yes
aerobic respiration control sensor protein ArcB	TZ19_10	TZ19_28	OK	50.0147	175.016	0	0	yes
ABC transporter: Transmembrane and ATP-binding protein	TZ19_10	TZ19_28	OK	13.7617	48.0503	2.52E-06	6.55E-06	yes
Conserved acetyl CoA synthase	TZ19_10	TZ19_28	OK	16.1052	56.1557	1.05E-09	3.64E-09	yes
ubiquinol-cytochrome c reductase,cytochrome c1	TZ19_10	TZ19_28	OK	246.244	855.306	0	0	yes
conserved hypothetical protein	TZ19_10	TZ19_28	OK	543.213	1861.85	0	0	yes
Leucyl/phenylalanyl-tRNA--protein transferase	TZ19_10	TZ19_28	OK	67.0364	229.635	5.45E-10	1.93E-09	yes
MoxR-like ATPase	TZ19_10	TZ19_28	OK	44.5754	152.283	2.27E-11	8.86E-11	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	279.944	955.247	0	0	yes
Type II secretory pathway, ATPase EpsE	TZ19_10	TZ19_28	OK	31.5213	106.454	1.43E-10	5.30E-10	yes
putative chaperone protein dnaK (Heat shock protein 70)	TZ19_10	TZ19_28	OK	9.04719	30.475	1.35E-06	3.62E-06	yes
Na(+)-translocating NADH-quinone reductase subunit D	TZ19_10	TZ19_28	OK	1582.95	5311.88	0	0	yes
Tfp pilus assembly protein	TZ19_10	TZ19_28	OK	36.2516	121.467	8.56E-09	2.78E-08	yes
ATP-dependent helicase	TZ19_10	TZ19_28	OK	29.0348	97.1344	0	0	yes
ABC transporter: Transmembrane protein; Maltooligosaccharide uptake	TZ19_10	TZ19_28	OK	172.954	578.175	0	0	yes
putative two-component response regulator	TZ19_10	TZ19_28	OK	18.4884	61.3004	7.01E-07	1.93E-06	yes
ATP synthase alpha chain	TZ19_10	TZ19_28	OK	1260.26	4170.39	0	0	yes
sulfate adenylate transferase, subunit 2	TZ19_10	TZ19_28	OK	54.7455	180.664	1.41E-09	4.85E-09	yes
DNA mismatch repair protein mutL	TZ19_10	TZ19_28	OK	35.2543	116.085	0	0	yes
Oligopeptide transport ATP-binding protein oppD	TZ19_10	TZ19_28	OK	221.927	730.517	0	0	yes
cytochrome c-type protein	TZ19_10	TZ19_28	OK	191.004	625.032	4.84E-14	2.21E-13	yes
Glutamate synthase	TZ19_10	TZ19_28	OK	49.2248	160.691	1.55E-15	7.72E-15	yes
Proline dehydrogenase	TZ19_10	TZ19_28	OK	135.877	442.337	0	0	yes
Tryptophanase (L-tryptophan indole-lyase)	TZ19_10	TZ19_28	OK	49.0342	158.856	8.88E-16	4.47E-15	yes
Chromosome partition protein mukB	TZ19_10	TZ19_28	OK	41.8096	135.258	0	0	yes
Acetoacetyl-CoA reductase	TZ19_10	TZ19_28	OK	892.724	2886.4	0	0	yes

Hypothetical protein	TZ19_10	TZ19_28	OK	225.938	730.283	0	0	yes
polar flagellin	TZ19_10	TZ19_28	OK	86.6043	277.545	0	0	yes
Sodium/proline symporter	TZ19_10	TZ19_28	OK	211.414	676.852	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	69.1124	219.85	0	0	yes
sigma-E factor negative regulatory protein RseA	TZ19_10	TZ19_28	OK	2314.77	7362.94	0	0	yes
Pyruvate kinase II	TZ19_10	TZ19_28	OK	113.815	361.421	0	0	yes
Na(+)-translocating NADH-quinone reductase subunit B	TZ19_10	TZ19_28	OK	543.656	1723.8	0	0	yes
Acyl-CoA dehydrogenase	TZ19_10	TZ19_28	OK	70.6426	222.951	0	0	yes
Probable amino-acid ABC transporter ATP-binding protein	TZ19_10	TZ19_28	OK	39.4476	124.342	1.64E-06	4.35E-06	yes
phosphoserine phosphatase	TZ19_10	TZ19_28	OK	53.4991	168.116	1.18E-10	4.40E-10	yes
Phosphoenolpyruvate synthase/pyruvate phosphate dikinase	TZ19_10	TZ19_28	OK	51.8429	162.145	0	0	yes
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)pyrophosphoryl-u	TZ19_10	TZ19_28	OK	64.0017	200.033	3.28E-13	1.43E-12	yes
Aldehyde dehydrogenase	TZ19_10	TZ19_28	OK	34.9754	109.092	8.46E-11	3.18E-10	yes
Acetylglutamate kinase	TZ19_10	TZ19_28	OK	79.0098	246.004	1.31E-10	4.86E-10	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	22.4807	69.5506	2.80E-14	1.30E-13	yes
Na(+)-translocating NADH-quinone reductase subunit F	TZ19_10	TZ19_28	OK	515.445	1579.1	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	424.261	1294.1	2.33E-09	7.86E-09	yes
hypothetical protein	TZ19_10	TZ19_28	OK	2958.97	8990.43	9.31E-07	2.53E-06	yes
hypothetical protein	TZ19_10	TZ19_28	OK	905.626	2746.16	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	31.8227	95.7057	9.33E-08	2.79E-07	yes
ABC transporter: Membrane fusion protein	TZ19_10	TZ19_28	OK	25.6206	76.6191	9.64E-07	2.62E-06	yes
Ubiquinol-cytochrome c reductase, cytochrome B	TZ19_10	TZ19_28	OK	671.335	2002.5	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	31.0745	92.6667	4.66E-15	2.26E-14	yes
Transcriptional regulator	TZ19_10	TZ19_28	OK	6421.44	19065.2	0	0	yes
Cytochrome c oxidase polypeptide I homolog	TZ19_10	TZ19_28	OK	416.078	1235.1	0	0	yes
Mg(2+) transport ATPase protein C	TZ19_10	TZ19_28	OK	167.038	495.608	6.62E-11	2.50E-10	yes
Glutathione-regulated potassium-efflux system protein kefC (K(+)/H(+)antipor	TZ19_10	TZ19_28	OK	27.353	80.7957	1.40E-09	4.80E-09	yes
ABC transporter: substrate binding protein precursor	TZ19_10	TZ19_28	OK	50.2213	148.293	0	0	yes
Chemotaxis protein cheA	TZ19_10	TZ19_28	OK	38.6924	114.068	0	0	yes
Sulfite reductase	TZ19_10	TZ19_28	OK	58.2846	171.756	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	46.4946	135.865	0	0	yes
ATP synthase delta chain	TZ19_10	TZ19_28	OK	1324.48	3859.96	0	0	yes

Cyclopropane-fatty-acyl-phospholipid synthase	TZ19_10	TZ19_28	OK	123.51	359.73	0	0	yes
Oligopeptide transport system permease protein oppB	TZ19_10	TZ19_28	OK	239.261	692.674	0	0	yes
Uroporphyrin-III C-methyltransferase	TZ19_10	TZ19_28	OK	100.8	291.197	3.81E-13	1.65E-12	yes
D-3-phosphoglycerate dehydrogenase	TZ19_10	TZ19_28	OK	117.163	336.237	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	409.041	1169.97	1.64E-06	4.36E-06	yes
Histidinol dehydrogenase	TZ19_10	TZ19_28	OK	47.6116	135.162	1.53E-10	5.66E-10	yes
ATP synthase gamma chain	TZ19_10	TZ19_28	OK	1976.66	5610.82	0	0	yes
putative multidrug resistance efflux pump	TZ19_10	TZ19_28	OK	111.13	315.246	0	0	yes
Tryptophan synthase beta chain	TZ19_10	TZ19_28	OK	131.968	373.387	0	0	yes
Permease of the drug-metabolite transporter (DMT) superfamily	TZ19_10	TZ19_28	OK	116.808	330.397	1.78E-15	8.80E-15	yes
ABC transporter: Substrate-binding protein precursor	TZ19_10	TZ19_28	OK	49.5232	139.978	3.52E-11	1.36E-10	yes
Glyceraldehyde-3-phosphate dehydrogenase	TZ19_10	TZ19_28	OK	96.9735	274.034	0	0	yes
6-phosphogluconolactonase	TZ19_10	TZ19_28	OK	131.322	371.047	1.01E-13	4.54E-13	yes
glutamate synthase, large subunit	TZ19_10	TZ19_28	OK	7.20772	20.3552	1.72E-06	4.56E-06	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	1992.6	5608.49	0	0	yes
Nitrogen regulatory protein	TZ19_10	TZ19_28	OK	234.706	659.383	4.82E-12	1.97E-11	yes
Tryptophan synthase alpha chain	TZ19_10	TZ19_28	OK	189.618	532.052	0	0	yes
DNA-directed RNA polymerase beta chain	TZ19_10	TZ19_28	OK	522.191	1452.6	0	0	yes
putative M6 secreted metalloprotease precursor	TZ19_10	TZ19_28	OK	12.24	34.0043	1.08E-06	2.92E-06	yes
Ribosomal protein L22	TZ19_10	TZ19_28	OK	16888.9	46880.8	0	0	yes
chemotaxis protein CheB	TZ19_10	TZ19_28	OK	35.9378	99.4577	4.01E-07	1.13E-06	yes
Penicillin-binding protein 1A	TZ19_10	TZ19_28	OK	53.3716	147.641	0	0	yes
23S rRNA (guanosine-2'-O-)-methyltransferase rlmB	TZ19_10	TZ19_28	OK	60.5379	166.534	5.65E-07	1.57E-06	yes
hypothetical protein	TZ19_10	TZ19_28	OK	718.064	1975.04	1.65E-08	5.26E-08	yes
tolA protein	TZ19_10	TZ19_28	OK	36.3922	99.727	2.63E-06	6.81E-06	yes
hypothetical protein	TZ19_10	TZ19_28	OK	1978.83	5420.63	0	0	yes
Exodeoxyribonuclease V gamma chain	TZ19_10	TZ19_28	OK	29.1119	79.7252	2.22E-16	1.15E-15	yes
putative transporter	TZ19_10	TZ19_28	OK	53.1991	145.442	1.59E-12	6.66E-12	yes
transcriptional regulator, LuxR family	TZ19_10	TZ19_28	OK	79.8585	218.267	5.87E-07	1.63E-06	yes
Cellodextrin-phosphorylase	TZ19_10	TZ19_28	OK	15.6896	42.8411	8.18E-07	2.24E-06	yes
hypothetical protein	TZ19_10	TZ19_28	OK	416.265	1134.66	2.77E-08	8.66E-08	yes
Phosphoribosylformylglycinamidine synthase	TZ19_10	TZ19_28	OK	102.199	278.466	0	0	yes

4-hydroxythreonine-4-phosphate dehydrogenase	TZ19_10	TZ19_28	OK	146.952	399.156	0	0	yes
SOJ-like and chromosome partitioning protein	TZ19_10	TZ19_28	OK	58.025	157.538	1.83E-06	4.82E-06	yes
Sensor protein barA	TZ19_10	TZ19_28	OK	12.4197	33.7155	9.46E-07	2.57E-06	yes
UDP-N-acetylmuramoyl-tripeptide--D-alanyl-D-alanine ligase	TZ19_10	TZ19_28	OK	80.6976	216.062	4.66E-15	2.26E-14	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	2100.72	5618.75	0	0	yes
ABC transporter: type A secreted protein (SSA)	TZ19_10	TZ19_28	OK	255.507	683.37	2.02E-11	7.93E-11	yes
Na(+)-translocating NADH-quinone reductase subunit E	TZ19_10	TZ19_28	OK	851.909	2275.54	0	0	yes
putative protease	TZ19_10	TZ19_28	OK	30.5632	81.3041	3.13E-13	1.36E-12	yes
Phenylalanyl-tRNA synthetase beta chain	TZ19_10	TZ19_28	OK	210.633	558.439	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	198.951	527.166	1.98E-08	6.26E-08	yes
Pyruvate dehydrogenase E1 component	TZ19_10	TZ19_28	OK	432.713	1143.01	0	0	yes
conserved hypothetical protein	TZ19_10	TZ19_28	OK	3882.81	10218.5	0	0	yes
Fatty oxidation complex, alpha subunit	TZ19_10	TZ19_28	OK	243.803	640.42	0	0	yes
Flagellar biosynthesis protein flhF	TZ19_10	TZ19_28	OK	45.6301	119.75	1.36E-11	5.43E-11	yes
Ribosomal RNA small subunit methyltransferase B	TZ19_10	TZ19_28	OK	85.7836	224.089	0	0	yes
type II secretory pathway, pseudopilin EpsG	TZ19_10	TZ19_28	OK	657.554	1711.24	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	112.935	293.244	4.09E-07	1.15E-06	yes
Phosphoserine aminotransferase	TZ19_10	TZ19_28	OK	171.735	444.524	0	0	yes
Ribosomal protein S19	TZ19_10	TZ19_28	OK	2730.4	7067.31	0	0	yes
Dihydrolipoyllysine-residue acetyltransferase component of pyruvatedehydroge	TZ19_10	TZ19_28	OK	242.527	626.611	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	54.7271	141.243	4.56E-07	1.28E-06	yes
hypothetical protein	TZ19_10	TZ19_28	OK	184.395	475.796	0	0	yes
putative multidrug resistance protein	TZ19_10	TZ19_28	OK	15.4381	39.3904	2.77E-07	7.89E-07	yes
2-amino-4-hydroxy-6-hydroxymethyldihydropteridinepyrophosphokinase	TZ19_10	TZ19_28	OK	336.24	856.88	1.80E-14	8.44E-14	yes
ABC transporter: Substrate-binding protein precursor; phosphate uptake	TZ19_10	TZ19_28	OK	1588.98	4047.61	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	1623.01	4131.11	0	0	yes
3-hydroxyisobutyrate dehydrogenase and related beta-hydroxyacid dehydrogen	TZ19_10	TZ19_28	OK	93.7701	238.03	1.58E-10	5.85E-10	yes
Potassium uptake protein TrkA	TZ19_10	TZ19_28	OK	47.6532	120.847	3.24E-09	1.08E-08	yes
hypothetical protein	TZ19_10	TZ19_28	OK	229.271	580.175	1.76E-06	4.66E-06	yes
ABC-type transport system	TZ19_10	TZ19_28	OK	111.346	281.594	1.62E-10	6.00E-10	yes
Iron-containing alcohol dehydrogenase	TZ19_10	TZ19_28	OK	204.994	517.722	0	0	yes
Disulfide bond formation protein B	TZ19_10	TZ19_28	OK	127.253	321.018	8.32E-07	2.27E-06	yes

putative homocysteine synthase	TZ19_10	TZ19_28	OK	71.3789	179.615	1.09E-11	4.37E-11	yes
Anaerobic C4-dicarboxylate transporter	TZ19_10	TZ19_28	OK	77.5749	194.512	2.91E-12	1.20E-11	yes
Acyl-coenzyme A dehydrogenase	TZ19_10	TZ19_28	OK	16.4215	41.0582	1.62E-06	4.31E-06	yes
hypothetical protein	TZ19_10	TZ19_28	OK	525.995	1314.99	0	0	yes
Homoserine kinase	TZ19_10	TZ19_28	OK	85.2799	213.094	7.42E-10	2.60E-09	yes
putative Mg2+ and Co2+ transporter CorB	TZ19_10	TZ19_28	OK	129.484	323.235	0	0	yes
ABC transporter: Transmembrane protein	TZ19_10	TZ19_28	OK	37.8191	94.3525	4.61E-08	1.41E-07	yes
Periplasmic oligopeptide-binding protein	TZ19_10	TZ19_28	OK	1950.92	4862.98	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	98.3934	245.074	0	0	yes
Glutamate synthase	TZ19_10	TZ19_28	OK	80.7837	200.227	0	0	yes
3,4-dihydroxy-2-butanone 4-phosphate synthase	TZ19_10	TZ19_28	OK	260.59	645.865	0	0	yes
Phospho-N-acetylmuramoyl-pentapeptide-transferase	TZ19_10	TZ19_28	OK	79.0474	195.485	5.97E-09	1.96E-08	yes
putative glutamate synthase precursor	TZ19_10	TZ19_28	OK	74.606	184.341	4.52E-07	1.27E-06	yes
L-threonine 3-dehydrogenase	TZ19_10	TZ19_28	OK	146.22	360.994	4.44E-16	2.26E-15	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	2288.37	5640.92	0	0	yes
Imidazole glycerol phosphate synthase subunit hisF1	TZ19_10	TZ19_28	OK	98.0342	241.208	4.40E-08	1.35E-07	yes
Hypothetical ABC transporter ATP-binding protein	TZ19_10	TZ19_28	OK	78.9422	192.217	4.44E-16	2.26E-15	yes
Peptidase B	TZ19_10	TZ19_28	OK	233.923	568.598	0	0	yes
Arginine deiminase	TZ19_10	TZ19_28	OK	111.601	270.943	3.06E-14	1.42E-13	yes
Pyrroline-5-carboxylate reductase	TZ19_10	TZ19_28	OK	134.218	325.248	1.76E-11	6.93E-11	yes
Oligopeptide transport system permease protein oppC	TZ19_10	TZ19_28	OK	277.583	669.316	0	0	yes
Exodeoxyribonuclease V beta chain	TZ19_10	TZ19_28	OK	58.5626	141.096	0	0	yes
1-(5-phosphoribosyl)-5-	TZ19_10	TZ19_28	OK	91.5412	220.066	1.16E-06	3.14E-06	yes
Gamma-glutamyl phosphate reductase	TZ19_10	TZ19_28	OK	37.7682	90.5887	2.33E-06	6.08E-06	yes
Aminopeptidase P	TZ19_10	TZ19_28	OK	26.8272	64.2119	1.22E-06	3.28E-06	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	459.923	1097.37	0	0	yes
Oligopeptidase A	TZ19_10	TZ19_28	OK	99.4156	237.012	0	0	yes
AsmA protein	TZ19_10	TZ19_28	OK	290.528	690.499	0	0	yes
putative two-component sensor	TZ19_10	TZ19_28	OK	33.6627	79.9971	1.98E-09	6.75E-09	yes
Anaerobic dehydrogenase	TZ19_10	TZ19_28	OK	428.779	1012.41	0	0	yes
putative cytochrome b561	TZ19_10	TZ19_28	OK	636.742	1501.89	8.68E-07	2.37E-06	yes
Dihydrolipoyl dehydrogenase	TZ19_10	TZ19_28	OK	1329.96	3130.54	0	0	yes

Osmolarity sensor protein envZ	TZ19_10	TZ19_28	OK	55.7199	131.06	3.12E-08	9.68E-08	yes
ABC-type Fe3+ transport system, periplasmic component	TZ19_10	TZ19_28	OK	2627.74	6165.03	0	0	yes
ABC transporter: substrate-binding protein precursor (BP)	TZ19_10	TZ19_28	OK	167.541	392.158	2.22E-16	1.15E-15	yes
chemotaxis protein CheY	TZ19_10	TZ19_28	OK	680.212	1590.43	5.74E-13	2.47E-12	yes
phosphopentomutase	TZ19_10	TZ19_28	OK	675.52	1574.08	0	0	yes
Pterin-4a-carbinolamine dehydratase	TZ19_10	TZ19_28	OK	889.904	2062.11	0	0	yes
Hypothetical protein ybbK	TZ19_10	TZ19_28	OK	175.825	407.321	2.22E-15	1.09E-14	yes
Probable aminotransferase yfbQ	TZ19_10	TZ19_28	OK	108.536	250.495	1.28E-13	5.69E-13	yes
N,N'-diacetylchitobiase precursor	TZ19_10	TZ19_28	OK	25.4834	58.7808	9.71E-08	2.89E-07	yes
Tryptophan biosynthesis protein trpCF	TZ19_10	TZ19_28	OK	48.4604	111.623	7.71E-08	2.32E-07	yes
FKBP-type 16 kDa peptidyl-prolyl cis-trans isomerase	TZ19_10	TZ19_28	OK	330.068	755.965	2.89E-09	9.69E-09	yes
Transketolase	TZ19_10	TZ19_28	OK	475.994	1086.47	0	0	yes
Cold shock-like protein cspD	TZ19_10	TZ19_28	OK	23772.1	54158.2	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	873.537	1989.71	2.22E-13	9.77E-13	yes
Guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase	TZ19_10	TZ19_28	OK	160.755	364.598	0	0	yes
Glucose-1-phosphate adenylyltransferase 1	TZ19_10	TZ19_28	OK	576.256	1302.55	0	0	yes
Topoisomerase IV subunit B	TZ19_10	TZ19_28	OK	113.613	256.497	0	0	yes
PhoH-like protein	TZ19_10	TZ19_28	OK	53.723	120.871	1.96E-06	5.18E-06	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	304.791	683.47	2.80E-10	1.02E-09	yes
Ribosomal protein L2	TZ19_10	TZ19_28	OK	1119.77	2507.68	0	0	yes
Ribosomal protein L23	TZ19_10	TZ19_28	OK	2509.57	5611.28	0	0	yes
Fumarate reductase iron-sulfur protein	TZ19_10	TZ19_28	OK	508.236	1128.5	0	0	yes
putative Exodeoxyribonuclease V alpha chain	TZ19_10	TZ19_28	OK	29.3707	64.9556	7.36E-07	2.03E-06	yes
Small-conductance mechanosensitive channel	TZ19_10	TZ19_28	OK	568.676	1251.26	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	800.78	1761.5	0	0	yes
NifU-related protein	TZ19_10	TZ19_28	OK	980.489	2154.22	7.33E-15	3.51E-14	yes
hypothetical protein	TZ19_10	TZ19_28	OK	2.10E+06	4.60E+06	0	0	yes
Acetylornithine aminotransferase	TZ19_10	TZ19_28	OK	1198.68	2610.41	0	0	yes
Isocitrate lyase	TZ19_10	TZ19_28	OK	55.1633	119.715	5.66E-08	1.72E-07	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	24064.3	51733.8	0	0	yes
similar to onserved hypothetical protein	TZ19_10	TZ19_28	OK	180.575	388.088	1.53E-06	4.07E-06	yes
Hypothetical acetyltransferase	TZ19_10	TZ19_28	OK	578.743	1237.05	2.22E-15	1.09E-14	yes

aminoacyl-histidine dipeptidase	TZ19_10	TZ19_28	OK	306.801	652.803	0	0	yes
Glutamine synthetase	TZ19_10	TZ19_28	OK	1779.42	3782.42	0	0	yes
conserved hypothetical protein	TZ19_10	TZ19_28	OK	10271.5	21814.1	4.12E-11	1.58E-10	yes
ATP synthase C chain	TZ19_10	TZ19_28	OK	7495.33	15903.5	0	0	yes
glycine cleavage system T protein	TZ19_10	TZ19_28	OK	151.545	321.309	3.87E-13	1.68E-12	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	522.128	1102.94	3.18E-08	9.88E-08	yes
2-dehydro-3-deoxyphosphooctonate aldolase	TZ19_10	TZ19_28	OK	224.96	474.996	1.78E-15	8.80E-15	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	305.826	644.922	3.53E-06	9.03E-06	yes
cold shock DNA-binding domain protein	TZ19_10	TZ19_28	OK	15167.6	31749.3	0	0	yes
Fumarate hydratase class I	TZ19_10	TZ19_28	OK	398.43	833.603	0	0	yes
Arginine deiminase	TZ19_10	TZ19_28	OK	3908.73	8151.73	0	0	yes
flagellar hook-associated protein FlaH	TZ19_10	TZ19_28	OK	112.563	234.752	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	884.679	1820.91	0	0	yes
ATP synthase B chain	TZ19_10	TZ19_28	OK	2257.29	4590.51	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	549.215	1116.26	6.44E-15	3.09E-14	yes
Peptidoglycan-associated lipoprotein precursor	TZ19_10	TZ19_28	OK	3280.36	6664.58	0	0	yes
ParA family protein	TZ19_10	TZ19_28	OK	1902.21	3860.97	0	0	yes
Maltodextrin phosphorylase	TZ19_10	TZ19_28	OK	93.2359	189.008	0	0	yes
Sodium/alanine symporter	TZ19_10	TZ19_28	OK	248.725	501.751	0	0	yes
Cytochrome c-type biogenesis protein ccmF	TZ19_10	TZ19_28	OK	108.711	218.573	1.12E-13	4.99E-13	yes
Cation-efflux pump fieF	TZ19_10	TZ19_28	OK	106.158	212.594	1.29E-06	3.46E-06	yes
Fructose-1,6-bisphosphatase	TZ19_10	TZ19_28	OK	286.239	572.733	0	0	yes
Riboflavin biosynthesis protein ribF	TZ19_10	TZ19_28	OK	892.355	445.804	0	0	yes
transcriptional regulator	TZ19_10	TZ19_28	OK	657.471	327.11	5.55E-15	2.68E-14	yes
SspB	TZ19_10	TZ19_28	OK	788.433	389.917	2.62E-09	8.80E-09	yes
50S ribosomal protein L14	TZ19_10	TZ19_28	OK	36267.2	17922.9	0	0	yes
NAD-dependent deacetylase	TZ19_10	TZ19_28	OK	1016.02	501.747	0	0	yes
Phosphoribosylaminoimidazole carboxylase ATPase subunit	TZ19_10	TZ19_28	OK	169.177	83.4749	1.55E-06	4.12E-06	yes
putative ATPase involved in DNA repair	TZ19_10	TZ19_28	OK	1000.64	493.584	1.73E-11	6.83E-11	yes
Ribosomal protein S16	TZ19_10	TZ19_28	OK	16442.2	8105.09	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	1346.62	663.764	0	0	yes
CTP synthase (UTP--ammonia ligase)	TZ19_10	TZ19_28	OK	5187.52	2552.88	0	0	yes

ribosomal protein S6	TZ19_10	TZ19_28	OK	3272.78	1609.71	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	129.784	63.5415	1.43E-11	5.69E-11	yes
Ribonuclease T (RNase T)	TZ19_10	TZ19_28	OK	502.291	245.773	1.25E-10	4.67E-10	yes
SAM-dependent methyltransferase	TZ19_10	TZ19_28	OK	250.584	122.348	2.13E-06	5.58E-06	yes
hypothetical protein	TZ19_10	TZ19_28	OK	6103.92	2963.52	0	0	yes
putative acyl-CoA synthetase	TZ19_10	TZ19_28	OK	3693.68	1766.87	0	0	yes
ribosomal protein L1	TZ19_10	TZ19_28	OK	1776.59	848.336	0	0	yes
Cysteinyl-tRNA synthetase	TZ19_10	TZ19_28	OK	366.808	174.378	0	0	yes
Hypoxanthine phosphoribosyltransferase	TZ19_10	TZ19_28	OK	2419.81	1148.93	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	334.701	158.742	9.17E-08	2.74E-07	yes
hypothetical protein	TZ19_10	TZ19_28	OK	335.082	157.599	2.39E-08	7.52E-08	yes
hypothetical protein	TZ19_10	TZ19_28	OK	497.502	233.988	6.62E-09	2.17E-08	yes
Porphobilinogen deaminase	TZ19_10	TZ19_28	OK	772.022	361.492	0	0	yes
DNA repair protein RecN	TZ19_10	TZ19_28	OK	146.47	68.3221	5.08E-10	1.81E-09	yes
ABC transporters: Transmembrane and ATP-binding protein	TZ19_10	TZ19_28	OK	82.6457	38.4471	9.88E-07	2.68E-06	yes
Aspartate ammonia-lyase	TZ19_10	TZ19_28	OK	4972.49	2294.67	0	0	yes
Glucose-6-phosphate 1-dehydrogenase	TZ19_10	TZ19_28	OK	363.38	167.682	0	0	yes
3-hydroxydecanoyl-	TZ19_10	TZ19_28	OK	936.565	428.964	5.62E-13	2.42E-12	yes
putative hydrolase	TZ19_10	TZ19_28	OK	555.441	254.245	1.58E-07	4.59E-07	yes
ribosome modulation factor	TZ19_10	TZ19_28	OK	142626	65020.3	0	0	yes
ParA family protein	TZ19_10	TZ19_28	OK	225.688	102.569	4.26E-11	1.63E-10	yes
Probable monothiol glutaredoxin	TZ19_10	TZ19_28	OK	7388.06	3351.53	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	523.372	236.778	1.34E-06	3.59E-06	yes
Transcription termination factor Rho	TZ19_10	TZ19_28	OK	1963.35	886.839	0	0	yes
6,7-dimethyl-8-ribityllumazine synthase	TZ19_10	TZ19_28	OK	2979.22	1337.69	0	0	yes
Glycerol kinase	TZ19_10	TZ19_28	OK	240.219	107.731	1.67E-14	7.83E-14	yes
3-phosphoglycerate kinase part 2	TZ19_10	TZ19_28	OK	2984.93	1337.22	0	0	yes
putative alkaline phosphatase	TZ19_10	TZ19_28	OK	94.6132	42.3043	1.99E-07	5.77E-07	yes
Glutamyl-tRNA synthetase	TZ19_10	TZ19_28	OK	1782.52	795.969	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	34993.8	15604.7	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	10209.7	4535.49	2.64E-13	1.16E-12	yes
phage shock protein B	TZ19_10	TZ19_28	OK	6455.25	2861.07	0	0	yes

N utilization substance protein B homolog	TZ19_10	TZ19_28	OK	2641.52	1169.72	0	0	yes
Peptidyl-tRNA hydrolase	TZ19_10	TZ19_28	OK	1414.98	625.007	0	0	yes
putative ribosomal RNA small subunit methyltransferase D	TZ19_10	TZ19_28	OK	429.137	189.276	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	530.244	233.219	9.57E-07	2.60E-06	yes
NADP-dependent malic enzyme	TZ19_10	TZ19_28	OK	216.902	94.8647	1.38E-11	5.49E-11	yes
5;10-methylenetetrahydrofolate reductase	TZ19_10	TZ19_28	OK	245.857	107.334	1.65E-09	5.63E-09	yes
Phosphoenolpyruvate-protein phosphotransferase	TZ19_10	TZ19_28	OK	1902.97	823.855	0	0	yes
tyrosyl-tRNA synthetase	TZ19_10	TZ19_28	OK	946.869	407.964	0	0	yes
SspA	TZ19_10	TZ19_28	OK	3898.47	1675.06	0	0	yes
D-erythrose-4-phosphate dehydrogenase	TZ19_10	TZ19_28	OK	1318.15	565.374	0	0	yes
50S ribosomal protein L21	TZ19_10	TZ19_28	OK	32588.9	13908.8	0	0	yes
peptide chain release factor 3	TZ19_10	TZ19_28	OK	558.579	237.464	0	0	yes
ribosomal large subunit pseudouridine synthase D	TZ19_10	TZ19_28	OK	928.454	390.27	0	0	yes
Peptidyl-prolyl cis-trans isomerase B	TZ19_10	TZ19_28	OK	5078.9	2134.23	0	0	yes
Aerobic respiration control protein arcA	TZ19_10	TZ19_28	OK	7883.59	3312.1	0	0	yes
Pyruvate formate-lyase 1-activating enzyme	TZ19_10	TZ19_28	OK	600.984	251.154	4.44E-16	2.26E-15	yes
50S ribosomal protein L27	TZ19_10	TZ19_28	OK	167082	69741.9	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	71.5089	29.746	2.15E-06	5.62E-06	yes
Transcriptional regulator	TZ19_10	TZ19_28	OK	3046.51	1260.73	0	0	yes
Aspartate carbamoyltransferase regulatory chain	TZ19_10	TZ19_28	OK	776.349	321.121	1.39E-11	5.53E-11	yes
ABC transporter: Substrate binding protein precursor	TZ19_10	TZ19_28	OK	166.745	68.6479	4.42E-07	1.24E-06	yes
conserved hypothetical protein	TZ19_10	TZ19_28	OK	504.781	207.479	1.07E-13	4.79E-13	yes
Hypothetical tRNA/rRNA methyltransferase	TZ19_10	TZ19_28	OK	399.389	162.914	1.55E-06	4.13E-06	yes
Superfamily II DNA and RNA helicase	TZ19_10	TZ19_28	OK	386.71	157.1	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	13773.7	5595.44	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	3926.26	1589	5.68E-14	2.58E-13	yes
inosine guanosine kinase	TZ19_10	TZ19_28	OK	146.852	59.0937	5.82E-09	1.92E-08	yes
manganese-dependent inorganic pyrophosphatase	TZ19_10	TZ19_28	OK	3197.23	1283.1	0	0	yes
ribosomal protein L5	TZ19_10	TZ19_28	OK	8553.5	3420.56	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	32544.3	12935.5	0	0	yes
TorCAD operon transcriptional regulatory protein torR	TZ19_10	TZ19_28	OK	917.48	364.602	0	0	yes
putative peroxiredoxin bcp	TZ19_10	TZ19_28	OK	522.076	206.622	1.71E-08	5.42E-08	yes

LuxT regulator	TZ19_10	TZ19_28	OK	1377.68	543.97	0	0	yes
Long-chain fatty acid transport protein precursor	TZ19_10	TZ19_28	OK	770.267	304.086	0	0	yes
Phosphoribosylaminoimidazole carboxylase catalytic subunit	TZ19_10	TZ19_28	OK	439.464	172.964	1.51E-08	4.80E-08	yes
Phospho-2-dehydro-3-deoxyheptonate aldolase,Trp-sensitive	TZ19_10	TZ19_28	OK	857.076	336.124	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	401.66	157.339	0	0	yes
transcription elongation factor GreA	TZ19_10	TZ19_28	OK	2540.19	991.822	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	969.966	373.426	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	296.82	113.741	0	0	yes
Alcohol dehydrogenase/acetaldehyde dehydrogenase	TZ19_10	TZ19_28	OK	6290.93	2404.76	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	311.965	118.788	2.22E-16	1.15E-15	yes
putative N-acetyl-D-glucosamine kinase	TZ19_10	TZ19_28	OK	202.078	75.9033	1.39E-08	4.44E-08	yes
SlyX protein	TZ19_10	TZ19_28	OK	1794.93	672.921	2.80E-06	7.23E-06	yes
GMP reductase	TZ19_10	TZ19_28	OK	1003.07	373.453	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	8539.55	3174.1	0	0	yes
2-hydroxy-3-oxopropionate reductase	TZ19_10	TZ19_28	OK	2295.41	850.828	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	29315	10808.7	0	0	yes
Ribosomal protein S18	TZ19_10	TZ19_28	OK	11224.7	4138.03	0	0	yes
Uridine kinase	TZ19_10	TZ19_28	OK	1549.07	565.165	0	0	yes
Glucosamine-6-phosphate isomerase	TZ19_10	TZ19_28	OK	354.653	129.351	3.13E-14	1.45E-13	yes
Aspartokinase	TZ19_10	TZ19_28	OK	871.344	317.64	0	0	yes
Transcriptional regulator	TZ19_10	TZ19_28	OK	277.028	100.939	1.23E-12	5.21E-12	yes
Ribosomal protein L33	TZ19_10	TZ19_28	OK	101870	36946.3	0	0	yes
nitrate/nitrite sensor protein NarQ	TZ19_10	TZ19_28	OK	1075.56	389.872	0	0	yes
putative SAM-dependent methyltransferase	TZ19_10	TZ19_28	OK	161.456	58.2687	3.59E-10	1.29E-09	yes
ribosomal protein L34	TZ19_10	TZ19_28	OK	75421.5	27176.6	0	0	yes
Cell division protein BolA	TZ19_10	TZ19_28	OK	1595.85	573.84	5.22E-11	1.99E-10	yes
putative alkylphosphonate uptake protein	TZ19_10	TZ19_28	OK	1451.38	521.21	0	0	yes
Predicted integral membrane protein	TZ19_10	TZ19_28	OK	4982.43	1779.16	0	0	yes
Glycine cleavage system transcriptional	TZ19_10	TZ19_28	OK	794.186	283.136	0	0	yes
uridine phosphorylase	TZ19_10	TZ19_28	OK	4668.88	1661.23	0	0	yes
Ribonuclease D	TZ19_10	TZ19_28	OK	273.812	97.3765	0	0	yes
Similar to ribosomal protein S15	TZ19_10	TZ19_28	OK	6868.55	2439.98	0	0	yes

ribosomal protein S21	TZ19_10	TZ19_28	OK	65056.3	23016.6	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	271.362	95.6686	2.95E-11	1.15E-10	yes
hypothetical protein	TZ19_10	TZ19_28	OK	1610.85	566.792	7.10E-08	2.14E-07	yes
putative transporter fused subunits of ABC superfamily: ATP-binding compone	TZ19_10	TZ19_28	OK	513.729	180.488	5.64E-13	2.43E-12	yes
(3R)-hydroxymyristoyl-	TZ19_10	TZ19_28	OK	286.79	100.753	6.16E-07	1.71E-06	yes
Acetate kinase	TZ19_10	TZ19_28	OK	357.066	125.42	0	0	yes
cytosine deaminase	TZ19_10	TZ19_28	OK	261.165	91.4353	0	0	yes
Lipoprotein-releasing system transmembrane protein lolC	TZ19_10	TZ19_28	OK	93.3225	32.5646	1.43E-07	4.20E-07	yes
hypothetical protein	TZ19_10	TZ19_28	OK	839.266	292.659	7.93E-11	2.99E-10	yes
Dihydroorotate dehydrogenase	TZ19_10	TZ19_28	OK	359.16	124.576	0	0	yes
putative ribonuclease	TZ19_10	TZ19_28	OK	280.265	96.8809	1.84E-11	7.23E-11	yes
Phospho-2-dehydro-3-deoxyheptonate aldolase,Tyr-sensitive	TZ19_10	TZ19_28	OK	188.324	65.0864	1.52E-11	6.01E-11	yes
hypothetical protein	TZ19_10	TZ19_28	OK	128.481	44.2018	2.74E-08	8.56E-08	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	85.9279	29.5608	6.02E-09	1.98E-08	yes
putative zinc uptake regulation protein	TZ19_10	TZ19_28	OK	2213.11	760.964	0	0	yes
Phosphoribosylaminoimidazole-succinocarboxamide synthase	TZ19_10	TZ19_28	OK	128.341	43.9204	7.98E-09	2.60E-08	yes
Glutamyl-tRNA reductase	TZ19_10	TZ19_28	OK	235.931	80.2705	2.22E-16	1.15E-15	yes
ATP-dependent RNA helicase	TZ19_10	TZ19_28	OK	201.713	68.1027	1.84E-14	8.64E-14	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	37266.2	12459.7	0	0	yes
ribosomal protein L11 methyltransferase	TZ19_10	TZ19_28	OK	421.319	140.383	0	0	yes
putative multiple antibiotic transporter	TZ19_10	TZ19_28	OK	2127.4	704.582	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	8070.43	2671.05	0	0	yes
Flavodoxin	TZ19_10	TZ19_28	OK	7344.73	2426.46	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	844.405	278.942	1.92E-13	8.45E-13	yes
Chromosomal replication initiator protein dnaA	TZ19_10	TZ19_28	OK	152.335	50.2086	6.36E-13	2.73E-12	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	733195	241346	0	0	yes
Predicted phosphatase/phosphohexomutase	TZ19_10	TZ19_28	OK	171.768	56.3224	1.20E-06	3.23E-06	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	209.123	68.1326	1.58E-14	7.42E-14	yes
Guanylate kinase	TZ19_10	TZ19_28	OK	618.35	201.358	0	0	yes
Elongation factor P	TZ19_10	TZ19_28	OK	3461.62	1126.64	0	0	yes
conserved hypothetical protein	TZ19_10	TZ19_28	OK	204.085	66.2911	3.52E-07	9.94E-07	yes
putative factor-for-inversion stimulation protein	TZ19_10	TZ19_28	OK	3592.03	1163.22	0	0	yes

Dihydrolipoyl dehydrogenase	TZ19_10	TZ19_28	OK	99.6635	32.2661	4.84E-10	1.72E-09	yes
Spermidine/putrescine-binding periplasmic protein precursor	TZ19_10	TZ19_28	OK	507.973	164.347	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	92746	30000.4	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	782.27	251.186	1.48E-07	4.33E-07	yes
Phenylalanyl-tRNA synthetase alpha chain	TZ19_10	TZ19_28	OK	792.35	252.568	0	0	yes
Conserved hypothetical protein; putative membrane protein	TZ19_10	TZ19_28	OK	540.8	171.675	2.22E-16	1.15E-15	yes
hypothetical protein	TZ19_10	TZ19_28	OK	10211	3233.5	0	0	yes
NAD-dependent aldehyde dehydrogenase	TZ19_10	TZ19_28	OK	198.778	62.1134	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	2855.86	870.55	0	0	yes
nptA protein	TZ19_10	TZ19_28	OK	1373.86	417.687	0	0	yes
putative methyl-accepting chemotaxis protein	TZ19_10	TZ19_28	OK	156.539	47.3926	5.08E-07	1.42E-06	yes
ATP-dependent RNA helicase, DEAD box family	TZ19_10	TZ19_28	OK	355.181	107.112	0	0	yes
putative ABC transporter periplasmic solute binding protein	TZ19_10	TZ19_28	OK	463.885	139.791	0	0	yes
Organic radical activating enzyme	TZ19_10	TZ19_28	OK	184.029	55.1301	4.09E-07	1.15E-06	yes
Protein ybbN	TZ19_10	TZ19_28	OK	118.715	35.545	3.24E-07	9.17E-07	yes
predicted N6-adenine-specific DNA methylase	TZ19_10	TZ19_28	OK	108.871	32.4556	2.44E-15	1.20E-14	yes
hypothetical protein	TZ19_10	TZ19_28	OK	768.34	227.174	2.51E-12	1.04E-11	yes
lipoprotein NlpI	TZ19_10	TZ19_28	OK	279.874	82.4816	1.33E-15	6.64E-15	yes
hypothetical protein	TZ19_10	TZ19_28	OK	828.761	241.674	2.93E-08	9.14E-08	yes
putative sulfate transporter	TZ19_10	TZ19_28	OK	78.9804	22.8005	6.72E-10	2.37E-09	yes
S-adenosylmethionine:2-demethylmenaquinone methyltransferase	TZ19_10	TZ19_28	OK	3186.67	919.402	0	0	yes
Aspartate carbamoyltransferase, catalytic chain	TZ19_10	TZ19_28	OK	374.509	107.6	0	0	yes
Pectin degradation protein	TZ19_10	TZ19_28	OK	1424.47	408.873	1.33E-13	5.91E-13	yes
Preprotein translocase subunit SecG	TZ19_10	TZ19_28	OK	23999.2	6783.51	0	0	yes
Peptidase	TZ19_10	TZ19_28	OK	435.643	123.02	0	0	yes
Hypothetical adenine-specific methylase	TZ19_10	TZ19_28	OK	752.671	212.226	0	0	yes
Fructose-1,6-bisphosphatase class II glpX	TZ19_10	TZ19_28	OK	350.572	97.9131	0	0	yes
3-dehydroquinate synthase	TZ19_10	TZ19_28	OK	2264.62	632.161	0	0	yes
Lysine-sensitive aspartokinase III	TZ19_10	TZ19_28	OK	225.979	62.7274	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	1435.44	396.311	0	0	yes
conserved hypothetical protein	TZ19_10	TZ19_28	OK	884.251	243.842	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	2977.39	811.016	0	0	yes

Translation initiation factor IF-1	TZ19_10	TZ19_28	OK	27314.2	7435.76	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	7205.53	1951.25	0	0	yes
Biotin synthase	TZ19_10	TZ19_28	OK	92.6047	25.0447	1.15E-07	3.39E-07	yes
hypothetical protein	TZ19_10	TZ19_28	OK	692.329	186.636	8.28E-14	3.73E-13	yes
tRNA-dihydrouridine synthase B	TZ19_10	TZ19_28	OK	414.768	111.533	0	0	yes
MutT/nudix family protein	TZ19_10	TZ19_28	OK	561.71	150.12	0	0	yes
NupC family protein	TZ19_10	TZ19_28	OK	2934.67	774.386	0	0	yes
Cytochrome c biogenesis ATP-binding export protein ccmA (heme exporter pr	TZ19_10	TZ19_28	OK	498.632	131.404	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	423.845	111.123	1.57E-08	5.01E-08	yes
50S ribosomal protein L24	TZ19_10	TZ19_28	OK	25239	6606.14	0	0	yes
3-hydroxy-3-methylglutaryl-coenzyme A reductase	TZ19_10	TZ19_28	OK	80.013	20.9105	9.82E-09	3.18E-08	yes
Transcriptional activator	TZ19_10	TZ19_28	OK	16507.2	4250.05	0	0	yes
ATP-dependent RNA helicase srmB	TZ19_10	TZ19_28	OK	1094.22	279.207	0	0	yes
putative protease	TZ19_10	TZ19_28	OK	389.061	98.311	0	0	yes
Chaperone protein torD	TZ19_10	TZ19_28	OK	2352.79	591.822	0	0	yes
Inosine-5'-monophosphate dehydrogenase	TZ19_10	TZ19_28	OK	1208.44	302.452	0	0	yes
Transposase (orfA) of insertion sequence ISVisp4 ; IS3 family subgroup IS3	TZ19_10	TZ19_28	OK	367.534	90.6699	1.16E-08	3.72E-08	yes
Ribosomal large subunit pseudouridine synthase F	TZ19_10	TZ19_28	OK	529.418	130.484	0	0	yes
putative Na+/H+ antiporter	TZ19_10	TZ19_28	OK	245.355	59.9065	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	34.9394	8.52917	2.32E-07	6.66E-07	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	177.319	42.8305	6.62E-09	2.17E-08	yes
hypothetical regulatory components of sensory transduction	TZ19_10	TZ19_28	OK	233.857	56.4372	1.33E-15	6.64E-15	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	217.891	52.2324	1.68E-10	6.19E-10	yes
HTH-type transcriptional repressor purR	TZ19_10	TZ19_28	OK	686.979	164.554	0	0	yes
30S ribosomal protein S20	TZ19_10	TZ19_28	OK	136629	32550.5	0	0	yes
Holliday junction DNA helicase ruvA	TZ19_10	TZ19_28	OK	203.145	47.9076	1.26E-07	3.72E-07	yes
Predicted N-acetylglucosaminyl transferase	TZ19_10	TZ19_28	OK	263.691	62.1802	0	0	yes
Serine--pyruvate aminotransferase	TZ19_10	TZ19_28	OK	70.5475	16.6309	6.53E-07	1.80E-06	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	4739.18	1110.56	4.48E-10	1.60E-09	yes
putative Na+/H+ antiporter	TZ19_10	TZ19_28	OK	116.502	27.2067	2.75E-13	1.20E-12	yes
ATP-dependent RNA helicase	TZ19_10	TZ19_28	OK	726.967	169.076	0	0	yes
Isochorismate synthase	TZ19_10	TZ19_28	OK	287.516	66.7023	0	0	yes

conserved hypothetical protein	TZ19_10	TZ19_28	OK	5951.36	1374.76	0	0	yes
Fatty acid metabolism regulator protein	TZ19_10	TZ19_28	OK	3281	757.597	0	0	yes
ribosomal protein S2	TZ19_10	TZ19_28	OK	7257.49	1673.94	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	4774.62	1091.05	0	0	yes
formate transporter 1	TZ19_10	TZ19_28	OK	725.405	164.09	0	0	yes
fumarate and nitrate reduction regulatory protein	TZ19_10	TZ19_28	OK	5325.26	1202.31	0	0	yes
S-adenosylmethionine synthetase	TZ19_10	TZ19_28	OK	1082.93	241.214	0	0	yes
Ribosomal protein L28	TZ19_10	TZ19_28	OK	38480.6	8560.91	0	0	yes
Similar to putative lipid carrier protein	TZ19_10	TZ19_28	OK	448.491	99.6776	1.04E-14	4.96E-14	yes
Ribonuclease P protein component	TZ19_10	TZ19_28	OK	645.399	142.884	1.17E-11	4.67E-11	yes
cold shock protein	TZ19_10	TZ19_28	OK	215904	47770.2	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	1498.03	329.56	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	186.169	40.541	3.93E-10	1.41E-09	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	5665.61	1220.93	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	661.778	141.906	9.25E-07	2.52E-06	yes
conserved hypothetical protein	TZ19_10	TZ19_28	OK	2369.42	496.448	0	0	yes
Response regulator	TZ19_10	TZ19_28	OK	201.883	41.3778	0	0	yes
Adenosine deaminase	TZ19_10	TZ19_28	OK	1004.16	200.476	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	7373.6	1460.91	2.32E-11	9.06E-11	yes
inosine-guanosine kinase	TZ19_10	TZ19_28	OK	75.1592	14.7987	1.29E-08	4.14E-08	yes
Inner membrane sodium/carboxyalte symporter	TZ19_10	TZ19_28	OK	137.897	26.9454	6.22E-15	2.99E-14	yes
Outer membrane protein	TZ19_10	TZ19_28	OK	2426.43	473.666	0	0	yes
Conserved DnaJ related protein	TZ19_10	TZ19_28	OK	142.615	27.6222	7.14E-10	2.51E-09	yes
ATP-dependent RNA helicase	TZ19_10	TZ19_28	OK	85.8781	16.3962	5.56E-10	1.97E-09	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	512.821	96.9337	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	554.73	104.703	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	968.066	181.894	0	0	yes
7-cyano-7-deazaguanine reductase	TZ19_10	TZ19_28	OK	562.965	104.518	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	1803.3	332.228	2.46E-10	8.97E-10	yes
hypothetical protein	TZ19_10	TZ19_28	OK	7186.93	1291.43	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	391.967	69.9442	0	0	yes
Predicted acetyltransferase	TZ19_10	TZ19_28	OK	1564.27	278.971	0	0	yes

Predicted Fe-S-cluster redox enzyme	TZ19_10	TZ19_28	OK	455.545	81.0237	0	0	yes
putative peptidase T	TZ19_10	TZ19_28	OK	477.197	84.6376	0	0	yes
Probable tRNA(5-methylaminomethyl-2-thiouridylate)-methyltransferase	TZ19_10	TZ19_28	OK	314.436	54.9463	0	0	yes
TyrA, Chorismate mutase T-prephenate dehydrogenase	TZ19_10	TZ19_28	OK	178.438	31.0741	8.88E-16	4.47E-15	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	49435.9	8584.7	0	0	yes
Deoxyribodipyrimidine photolyase-related protein	TZ19_10	TZ19_28	OK	81.1472	13.9184	1.66E-12	6.95E-12	yes
Para-aminobenzoate synthase component I	TZ19_10	TZ19_28	OK	60.2227	10.1744	6.44E-09	2.11E-08	yes
Peroxiredoxin	TZ19_10	TZ19_28	OK	428.867	71.0819	2.42E-14	1.13E-13	yes
16S rRNA uridine-516 pseudouridylate synthase	TZ19_10	TZ19_28	OK	491.465	80.5341	0	0	yes
Long-chain-fatty-acid--CoA ligase	TZ19_10	TZ19_28	OK	187.265	30.1347	0	0	yes
tRNA-dihydrouridine synthase A	TZ19_10	TZ19_28	OK	111.11	17.6006	1.45E-09	4.98E-09	yes
UDP-N-acetylenolpyruvoylglucosamine reductase	TZ19_10	TZ19_28	OK	156.565	24.5251	1.22E-13	5.44E-13	yes
Ribonuclease PH	TZ19_10	TZ19_28	OK	2184.6	339.599	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	56.3078	8.66225	5.33E-07	1.48E-06	yes
Dethiobiotin synthetase	TZ19_10	TZ19_28	OK	602.452	91.184	0	0	yes
putative HTH-type transcriptional regulator	TZ19_10	TZ19_28	OK	156.703	23.627	1.33E-08	4.26E-08	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	36476.3	5437.45	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	76879.8	10245.2	0	0	yes
Anthranilate synthase component II	TZ19_10	TZ19_28	OK	124.114	15.8169	1.36E-06	3.64E-06	yes
ATP-dependent RNA helicase	TZ19_10	TZ19_28	OK	1900.05	240.402	0	0	yes
putative endoribonuclease	TZ19_10	TZ19_28	OK	335.869	41.2486	0	0	yes
Inositol monophosphate family protein	TZ19_10	TZ19_28	OK	1909.82	230.767	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	98.2476	11.5191	4.24E-07	1.19E-06	yes
3-dehydroquinate dehydratase	TZ19_10	TZ19_28	OK	4039.07	471.559	0	0	yes
Hemolysin III	TZ19_10	TZ19_28	OK	820.455	95.6703	0	0	yes
hypothetical protein	TZ19_10	TZ19_28	OK	168.145	19.5382	5.56E-13	2.39E-12	yes
Permease of the major facilitator superfamily	TZ19_10	TZ19_28	OK	131.377	14.828	2.89E-15	1.41E-14	yes
D-methionine transport ATP-binding protein metN	TZ19_10	TZ19_28	OK	161.082	17.6192	1.33E-15	6.64E-15	yes
Probable anaerobic C4-dicarboxylate transporter dcuC	TZ19_10	TZ19_28	OK	181.747	18.8289	0	0	yes
Conserved hypothetical protein	TZ19_10	TZ19_28	OK	525.989	53.2283	3.45E-10	1.24E-09	yes
Orotate phosphoribosyltransferase	TZ19_10	TZ19_28	OK	199.25	19.4954	1.61E-10	5.94E-10	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	99.2717	6.6716	1.06E-07	3.13E-07	yes

putative tricarboxylic transport TctC	TZ19_10	TZ19_28	OK	321.285	21.1481	0	0	yes
Hypothetical protein	TZ19_10	TZ19_28	OK	9171.61	538.927	0	0	yes
Glycerol uptake facilitator	TZ19_10	TZ19_28	OK	163.548	9.51572	4.30E-12	1.76E-11	yes
hypothetical protein	TZ19_10	TZ19_28	OK	16074.1	847.572	0	0	yes
acyl-CoA desaturase	TZ19_10	TZ19_28	OK	365.646	18.5974	0	0	yes
Glycerol-3-phosphate dehydrogenase	TZ19_10	TZ19_28	OK	311.221	14.8722	0	0	yes
ATPase involved in DNA repair	TZ19_10	TZ19_28	OK	3374.76	148.02	0	0	yes

Table S3 List of differentially expressed genes in strain JZ6 at 10 ℃ (JZ6_10) versus strain TZ19 at 10 ℃ (TZ19_10).

Gene name	Group1	Group2	States	FPKM1	FPKM2	E-value1	E-value2	Significant
hypothetical protein	JZ6_10	TZ19_10	OK	26.5531	83062.6	0	0	yes
Polyhydroxyalkanoic acid synthase	JZ6_10	TZ19_10	OK	0.57432	772.991	5.10E-12	2.08E-11	yes
Acetoacetyl-CoA reductase	JZ6_10	TZ19_10	OK	0.88513	892.724	2.80E-06	7.24E-06	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	14.0388	4159.24	1.38E-14	6.50E-14	yes
putative tricarboxylic transport TctC	JZ6_10	TZ19_10	OK	2.47798	321.285	5.04E-11	1.92E-10	yes
hypothetical protein	JZ6_10	TZ19_10	OK	96.2575	7373.6	4.26E-07	1.19E-06	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	5.7217	432.045	4.72E-07	1.32E-06	yes
putative ABC transporter periplasmic solute binding protein	JZ6_10	TZ19_10	OK	6.4733	463.885	0	0	yes
Glucosamine-6-phosphate isomerase	JZ6_10	TZ19_10	OK	6.25754	354.653	1.67E-14	7.83E-14	yes
putative acyl-CoA synthetase	JZ6_10	TZ19_10	OK	74.2214	3693.68	0	0	yes
putative transporter	JZ6_10	TZ19_10	OK	1.1261	54.2618	2.00E-07	5.79E-07	yes
ABC transporter: ATP-binding protein	JZ6_10	TZ19_10	OK	14.6714	597.51	0	0	yes
regulator of sigma D	JZ6_10	TZ19_10	OK	262.818	10671.2	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	207.475	8392.93	2.92E-08	9.12E-08	yes
hypothetical protein	JZ6_10	TZ19_10	OK	667.048	23020.9	4.44E-15	2.16E-14	yes
cytochrome c oxidase, subunit CcoP	JZ6_10	TZ19_10	OK	14.1405	403.897	0	0	yes
Transcriptional regulator	JZ6_10	TZ19_10	OK	32.5615	872.831	0	0	yes
2-hydroxy-3-oxopropionate reductase	JZ6_10	TZ19_10	OK	87.2358	2295.41	0	0	yes
Transposase (orfA) of insertion sequence ISVisp4 ; IS3 family subgroup IS3	JZ6_10	TZ19_10	OK	14.8799	367.534	1.67E-08	5.31E-08	yes
cytochrome c oxidase, subunit CcoQ	JZ6_10	TZ19_10	OK	140.985	3451.77	2.17E-06	5.68E-06	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	377.332	9171.61	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	8286.15	193324	0	0	yes
MutT/nudix family protein	JZ6_10	TZ19_10	OK	24.5238	561.71	0	0	yes
ribosome modulation factor	JZ6_10	TZ19_10	OK	6266.19	142626	0	0	yes
sulfite reductase, gamma subunit-related protein	JZ6_10	TZ19_10	OK	73.2245	1609.2	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	2288.65	49435.9	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	241.228	4774.62	0	0	yes
Transposase (orfA) of insertion sequence ISVisp4 ; IS3 family subgroup IS3	JZ6_10	TZ19_10	OK	21.257	367.534	2.72E-09	9.13E-09	yes
melanin biosynthesis protein TyrA	JZ6_10	TZ19_10	OK	25.7813	444.699	0	0	yes

Enoyl-CoA hydratase/isomerase	JZ6_10	TZ19_10	OK	17.702	298.206	0	0	yes
Chitinase	JZ6_10	TZ19_10	OK	5.51621	89.5651	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	350.629	5665.61	0	0	yes
Sec-independent protein secretion pathway component TatC	JZ6_10	TZ19_10	OK	27.6126	443.664	0	0	yes
Methylated-DNA-protein-cysteine methyltransferase	JZ6_10	TZ19_10	OK	96.9988	1458.46	4.44E-16	2.26E-15	yes
mutT domain protein-like	JZ6_10	TZ19_10	OK	9.1779	137.716	3.40E-09	1.13E-08	yes
Inositol monophosphate family protein	JZ6_10	TZ19_10	OK	132.299	1909.82	0	0	yes
similar to conserved hypothetical protein	JZ6_10	TZ19_10	OK	98.1887	1402.59	3.14E-10	1.13E-09	yes
Chromosome partition protein mukE	JZ6_10	TZ19_10	OK	7.39181	104.825	2.05E-07	5.93E-07	yes
putative ribonuclease	JZ6_10	TZ19_10	OK	20.4432	280.265	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	4.29716	57.8259	3.47E-09	1.16E-08	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1102.59	14096.7	0	0	yes
Phosphoribosylaminoimidazole carboxylase catalytic subunit	JZ6_10	TZ19_10	OK	34.5005	439.464	5.55E-15	2.68E-14	yes
Shikimate dehydrogenase	JZ6_10	TZ19_10	OK	95.2912	1186.77	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	22.3746	275.653	1.84E-08	5.82E-08	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	37.7114	452.956	0	0	yes
Hypothetical oxidoreductase	JZ6_10	TZ19_10	OK	52.2316	583.872	0	0	yes
Predicted phosphatase/phosphohexomutase	JZ6_10	TZ19_10	OK	15.708	171.768	5.46E-10	1.93E-09	yes
Cysteine synthase	JZ6_10	TZ19_10	OK	82.6176	874.312	0	0	yes
Acetyl-CoA synthase	JZ6_10	TZ19_10	OK	128.971	1362.66	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	649.105	6836.9	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	17.0825	178.159	1.46E-08	4.67E-08	yes
Histidine transport ATP-binding protein hisP	JZ6_10	TZ19_10	OK	87.6273	885.702	0	0	yes
Uridylate kinase	JZ6_10	TZ19_10	OK	135.902	1347.05	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1023.25	10083.3	4.44E-16	2.26E-15	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	8.73954	85.9279	4.86E-14	2.22E-13	yes
Prolyl endopeptidase	JZ6_10	TZ19_10	OK	19.2166	187.436	0	0	yes
Phosphoheptose isomerase	JZ6_10	TZ19_10	OK	37.4397	360.061	2.22E-16	1.15E-15	yes
Outer membrane protein	JZ6_10	TZ19_10	OK	254.592	2426.43	0	0	yes
Glycerol uptake facilitator	JZ6_10	TZ19_10	OK	17.4079	163.548	2.53E-12	1.05E-11	yes
Transcriptional regulator	JZ6_10	TZ19_10	OK	693.87	6421.44	0	0	yes
5'-nucleotidase (Nucleoside 5'-monophosphatephosphohydrolase)	JZ6_10	TZ19_10	OK	13.4195	123.824	4.93E-09	1.63E-08	yes

hypothetical protein	JZ6_10	TZ19_10	OK	21.0872	193.044	7.58E-07	2.08E-06	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	198.154	1803.3	1.28E-13	5.68E-13	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	218.541	1977.15	3.41E-06	8.74E-06	yes
Outer membrane protein OmpW	JZ6_10	TZ19_10	OK	241.905	2180.56	0	0	yes
putative amino-acid ABC transporter-binding protein patH precursor	JZ6_10	TZ19_10	OK	62.5657	558.785	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	43.6456	389.325	3.09E-10	1.12E-09	yes
Peroxiredoxin	JZ6_10	TZ19_10	OK	48.4815	428.867	1.22E-14	5.79E-14	yes
Preprotein translocase subunit SecF	JZ6_10	TZ19_10	OK	188.15	1644.17	0	0	yes
nitrate/nitrite sensor protein NarQ	JZ6_10	TZ19_10	OK	123.303	1075.56	0	0	yes
Organic solvent tolerance protein	JZ6_10	TZ19_10	OK	10.2077	88.7016	0	0	yes
cytosine deaminase	JZ6_10	TZ19_10	OK	30.1297	261.165	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	1168.47	10118.4	0	0	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	23.0834	198.372	6.64E-10	2.34E-09	yes
Cob(I)yrinic acid a,c-diamide adenosyltransferase	JZ6_10	TZ19_10	OK	16.5588	140.39	4.58E-08	1.40E-07	yes
hypothetical protein	JZ6_10	TZ19_10	OK	25.0945	211.625	2.29E-14	1.07E-13	yes
Alcohol dehydrogenase/acetaldehyde dehydrogenase	JZ6_10	TZ19_10	OK	748.562	6290.93	0	0	yes
Ribonuclease P protein component	JZ6_10	TZ19_10	OK	77.0445	645.399	7.37E-12	2.98E-11	yes
Small heat shock protein ibpA (16 kDa heat shock protein A)	JZ6_10	TZ19_10	OK	139.761	1170.54	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	30.6223	254.463	6.72E-08	2.03E-07	yes
Membrane protein	JZ6_10	TZ19_10	OK	1060.73	8798.87	0	0	yes
Pectin degradation protein	JZ6_10	TZ19_10	OK	175.658	1424.47	0	0	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	685.931	5432.36	0	0	yes
Oligoribonuclease	JZ6_10	TZ19_10	OK	43.3578	342.943	5.02E-14	2.29E-13	yes
Ribosome recycling factor	JZ6_10	TZ19_10	OK	164.059	1293.07	0	0	yes
Lysine-sensitive aspartokinase III	JZ6_10	TZ19_10	OK	28.8969	225.979	0	0	yes
putative ornithine carbamoyltransferase	JZ6_10	TZ19_10	OK	1282.16	9992.93	0	0	yes
tyrosyl-tRNA synthetase	JZ6_10	TZ19_10	OK	123.906	946.869	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	88.6992	677.146	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	21.0683	159.354	5.55E-15	2.68E-14	yes
Fructose/tagatose bisphosphate aldolase	JZ6_10	TZ19_10	OK	1513.22	11429.3	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	993.231	7434.25	0	0	yes
Glycine dehydrogenase (Glycine cleavage system P-protein)	JZ6_10	TZ19_10	OK	123.87	926.851	0	0	yes

Tellurite resistance protein	JZ6_10	TZ19_10	OK	10.1279	75.1666	5.71E-08	1.73E-07	yes
Exoribonuclease II	JZ6_10	TZ19_10	OK	126.087	935.719	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	291.751	2139.51	0	0	yes
elongation factor Tu	JZ6_10	TZ19_10	OK	183.999	1347.98	0	0	yes
cold shock protein	JZ6_10	TZ19_10	OK	29800.2	215904	0	0	yes
Pantoate--beta-alanine ligase	JZ6_10	TZ19_10	OK	57.0263	411.221	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	119.345	844.405	0	0	yes
Response regulator	JZ6_10	TZ19_10	OK	28.5952	201.883	0	0	yes
Porphobilinogen deaminase	JZ6_10	TZ19_10	OK	109.641	772.022	0	0	yes
Aromatic-amino-acid aminotransferase	JZ6_10	TZ19_10	OK	105.744	738.014	0	0	yes
Conserved hypothetical protein; putative membrane protein	JZ6_10	TZ19_10	OK	78.9329	540.8	0	0	yes
Dihydroorotate dehydrogenase	JZ6_10	TZ19_10	OK	52.9231	359.16	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	354.245	2399.23	9.86E-07	2.67E-06	yes
Glycerophosphoryl diester phosphodiesterase precursor	JZ6_10	TZ19_10	OK	34.9346	236.5	0	0	yes
fumarate and nitrate reduction regulatory protein	JZ6_10	TZ19_10	OK	787.252	5325.26	0	0	yes
Thiosulfate sulfurtransferase	JZ6_10	TZ19_10	OK	13.8934	93.7214	2.69E-08	8.42E-08	yes
50S ribosomal protein L27	JZ6_10	TZ19_10	OK	24971.7	167082	0	0	yes
putative response regulator	JZ6_10	TZ19_10	OK	40.9401	273.367	2.35E-09	7.93E-09	yes
putative sigma-54 modulation protein	JZ6_10	TZ19_10	OK	11498	76729.2	0	0	yes
Uncharacterized protein	JZ6_10	TZ19_10	OK	2098.57	13979.1	0	0	yes
GMP synthase	JZ6_10	TZ19_10	OK	81.7146	536.193	0	0	yes
ribosomal protein S2	JZ6_10	TZ19_10	OK	1108.51	7257.49	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	78.6222	512.105	0	0	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	136.434	884.251	0	0	yes
Cysteine synthase A	JZ6_10	TZ19_10	OK	186.618	1207.59	0	0	yes
putative multiple antibiotic transporter	JZ6_10	TZ19_10	OK	329.184	2127.4	0	0	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	926.23	5951.36	0	0	yes
PrkA serine protein kinase	JZ6_10	TZ19_10	OK	1061.98	6822.81	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	77.5033	497.502	0	0	yes
6-phospho-beta-glucosidase	JZ6_10	TZ19_10	OK	21.5043	136.255	0	0	yes
Universal stress protein F	JZ6_10	TZ19_10	OK	250.887	1589.14	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	16.0457	100.267	0	0	yes

Glycerol kinase	JZ6_10	TZ19_10	OK	38.5067	240.219	0	0	yes
Cystathionine beta-lyase	JZ6_10	TZ19_10	OK	27.9498	174.111	0	0	yes
Transcriptional regulator, LysR family	JZ6_10	TZ19_10	OK	22.1053	137.045	4.69E-11	1.79E-10	yes
putative excinuclease ABC subunit C	JZ6_10	TZ19_10	OK	19.556	119.96	6.10E-08	1.85E-07	yes
Phosphoglycolate phosphatase	JZ6_10	TZ19_10	OK	33.4288	204.873	5.72E-11	2.17E-10	yes
hypothetical protein	JZ6_10	TZ19_10	OK	5710.2	34993.8	0	0	yes
Oligopeptide transport system permease protein oppC	JZ6_10	TZ19_10	OK	45.6123	277.583	0	0	yes
magnesium transporter	JZ6_10	TZ19_10	OK	36.9785	224.943	0	0	yes
putative ribosomal RNA small subunit methyltransferase D	JZ6_10	TZ19_10	OK	70.7785	429.137	0	0	yes
putative lactoylglutathione lyase	JZ6_10	TZ19_10	OK	57.9042	346.857	2.26E-09	7.64E-09	yes
sodium-dependent transporter	JZ6_10	TZ19_10	OK	85.2107	509.243	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	93.0104	554.73	0	0	yes
Para-aminobenzoate synthase component I	JZ6_10	TZ19_10	OK	10.1187	60.2227	1.05E-08	3.38E-08	yes
hypothetical protein	JZ6_10	TZ19_10	OK	3038.92	17979.1	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	31.0257	183.17	1.72E-08	5.44E-08	yes
2-dehydro-3-deoxygluconokinase	JZ6_10	TZ19_10	OK	81.8015	481.896	0	0	yes
Septum site-determining protein minC	JZ6_10	TZ19_10	OK	48.2176	279.526	7.04E-14	3.18E-13	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1088.46	6288.03	2.98E-08	9.27E-08	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	60.5725	349.679	6.66E-16	3.37E-15	yes
3-dehydroquinate dehydratase	JZ6_10	TZ19_10	OK	700.151	4039.07	0	0	yes
Adenylate kinase	JZ6_10	TZ19_10	OK	398.277	2295.51	0	0	yes
Glycyl-tRNA synthetase alpha chain	JZ6_10	TZ19_10	OK	36.7181	210.635	1.11E-15	5.56E-15	yes
Aldehyde dehydrogenase	JZ6_10	TZ19_10	OK	25.32	144.766	0	0	yes
Zinc-binding dehydrogenase	JZ6_10	TZ19_10	OK	278.749	1577.35	0	0	yes
Flagellar basal-body rod protein flgF	JZ6_10	TZ19_10	OK	20.6809	116.452	3.51E-08	1.09E-07	yes
hypothetical protein	JZ6_10	TZ19_10	OK	190.851	1074.13	0	0	yes
Transcriptional activator	JZ6_10	TZ19_10	OK	2942.99	16507.2	0	0	yes
Inosine-5'-monophosphate dehydrogenase	JZ6_10	TZ19_10	OK	215.868	1208.44	0	0	yes
Protein grpE (HSP-70 cofactor)	JZ6_10	TZ19_10	OK	309.826	1728.13	0	0	yes
Fumarate reductase subunit C	JZ6_10	TZ19_10	OK	1058.09	5888.2	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	157.956	873.537	1.27E-12	5.34E-12	yes
6-phosphofructokinase	JZ6_10	TZ19_10	OK	1365.87	7516.92	0	0	yes

Acetolactate synthase isozyme II large subunit	JZ6_10	TZ19_10	OK	13.1651	72.4363	2.76E-12	1.14E-11	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	272.448	1498.03	0	0	yes
Bifunctional purine biosynthesis protein purH	JZ6_10	TZ19_10	OK	63.4492	346.199	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	50.0731	271.362	1.55E-15	7.72E-15	yes
HTH-type transcriptional regulator cysB	JZ6_10	TZ19_10	OK	15.5989	84.5177	1.44E-07	4.23E-07	yes
Serine hydroxymethyltransferase 1	JZ6_10	TZ19_10	OK	146.748	792.791	0	0	yes
3-dehydroquinate synthase	JZ6_10	TZ19_10	OK	422.369	2264.62	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	331.837	1773.58	3.77E-12	1.55E-11	yes
Permease of the drug-metabolite transporter (DMT) superfamily	JZ6_10	TZ19_10	OK	21.8879	116.808	9.29E-09	3.02E-08	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	21.3375	113.289	2.86E-10	1.04E-09	yes
hypothetical protein	JZ6_10	TZ19_10	OK	63.3386	334.701	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1301.17	6870.14	0	0	yes
Pterin-4a-carbinolamine dehydratase	JZ6_10	TZ19_10	OK	169.297	889.904	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	186.715	973.518	2.22E-16	1.15E-15	yes
NAD-dependent malic enzyme	JZ6_10	TZ19_10	OK	61.0781	315.721	0	0	yes
Ubiquinol-cytochrome c reductase, cytochrome B	JZ6_10	TZ19_10	OK	130.049	671.335	0	0	yes
Transcriptional regulator, TetR family	JZ6_10	TZ19_10	OK	57.1252	292.405	4.02E-13	1.74E-12	yes
FKBP-type peptidyl-prolyl cis-trans isomerases 1	JZ6_10	TZ19_10	OK	940.122	4758.67	0	0	yes
Shikimate kinase	JZ6_10	TZ19_10	OK	659.285	3335.67	0	0	yes
NAD-dependent deacetylase	JZ6_10	TZ19_10	OK	201.06	1016.02	0	0	yes
putative hydrolase	JZ6_10	TZ19_10	OK	110.034	555.441	4.44E-16	2.26E-15	yes
NAD-dependent aldehyde dehydrogenase	JZ6_10	TZ19_10	OK	39.4764	198.778	0	0	yes
cation transport ATPase	JZ6_10	TZ19_10	OK	4.95241	24.8636	2.42E-06	6.31E-06	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	84.5167	423.845	2.79E-10	1.01E-09	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	6.98058	34.9394	4.42E-08	1.36E-07	yes
Transcriptional regulator	JZ6_10	TZ19_10	OK	92.2079	460.545	0	0	yes
Protein seqA	JZ6_10	TZ19_10	OK	2566.76	12644.1	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	62.1656	305.826	8.14E-07	2.23E-06	yes
hypothetical protein	JZ6_10	TZ19_10	OK	78.6722	386.401	2.76E-06	7.14E-06	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	146.678	719.111	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	152.528	744.84	9.78E-08	2.91E-07	yes
hypothetical protein	JZ6_10	TZ19_10	OK	20.1261	98.2476	1.65E-06	4.37E-06	yes

hypothetical protein	JZ6_10	TZ19_10	OK	80.5721	392.941	2.01E-10	7.37E-10	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	308.352	1496.22	2.22E-16	1.15E-15	yes
Glycyl-tRNA synthetase beta chain	JZ6_10	TZ19_10	OK	15.21	72.6302	2.02E-14	9.46E-14	yes
Probable ATP-dependent helicase dinG	JZ6_10	TZ19_10	OK	14.4116	68.4492	2.89E-13	1.26E-12	yes
Oligopeptide transport system permease protein oppB	JZ6_10	TZ19_10	OK	50.3975	239.261	4.44E-16	2.26E-15	yes
hypothetical protein	JZ6_10	TZ19_10	OK	187.079	884.383	0	0	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	43.2305	204.085	2.29E-09	7.73E-09	yes
ADP compounds hydrolase nudE	JZ6_10	TZ19_10	OK	67.077	314.732	2.02E-11	7.91E-11	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	23.3298	109.34	3.31E-06	8.50E-06	yes
Lipoyl synthase	JZ6_10	TZ19_10	OK	91.6574	429.302	0	0	yes
dipeptide/tripeptide permease	JZ6_10	TZ19_10	OK	26.9772	126.308	3.33E-15	1.62E-14	yes
peptide ABC transporter, periplasmic peptide-binding protein	JZ6_10	TZ19_10	OK	88.9511	413.258	0	0	yes
L-serine dehydratase 1	JZ6_10	TZ19_10	OK	30.9238	143.275	1.33E-15	6.64E-15	yes
Methionine Repressor metJ	JZ6_10	TZ19_10	OK	397.419	1834.01	0	0	yes
ATP-dependent DNA helicase recG	JZ6_10	TZ19_10	OK	15.3697	70.7837	1.38E-13	6.14E-13	yes
uridine phosphorylase	JZ6_10	TZ19_10	OK	1013.81	4668.88	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	7122.06	32544.3	0	0	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	162.937	741.855	0	0	yes
Sec-independent protein translocase protein tatB homolog	JZ6_10	TZ19_10	OK	1826.73	8305.29	0	0	yes
ATPase involved in DNA repair	JZ6_10	TZ19_10	OK	743.246	3374.76	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	37.0487	167.48	1.27E-13	5.65E-13	yes
5;10-methylenetetrahydrofolate reductase	JZ6_10	TZ19_10	OK	54.3923	245.857	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	58.9133	266.199	2.59E-10	9.44E-10	yes
Uracil phosphoribosyltransferase	JZ6_10	TZ19_10	OK	594.99	2688.15	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	177.953	801.214	0	0	yes
Phenylalanyl-tRNA synthetase alpha chain	JZ6_10	TZ19_10	OK	176.588	792.35	0	0	yes
Methionine aminopeptidase	JZ6_10	TZ19_10	OK	317.713	1415.13	0	0	yes
Hypothetical Iron-sulfur protein	JZ6_10	TZ19_10	OK	461.995	2054.34	1.78E-15	8.80E-15	yes
Ribosomal protein L22	JZ6_10	TZ19_10	OK	3809.32	16888.9	0	0	yes
Glutamine synthetase	JZ6_10	TZ19_10	OK	403.686	1779.42	0	0	yes
carbonic anhydrase, family 3	JZ6_10	TZ19_10	OK	207.025	911.013	0	0	yes
Signal transduction histidine kinase	JZ6_10	TZ19_10	OK	8.62858	37.7747	3.06E-06	7.87E-06	yes

Adenylosuccinate lyase	JZ6_10	TZ19_10	OK	142.699	621.631	0	0	yes
Probable (di)nucleoside polyphosphate hydrolase	JZ6_10	TZ19_10	OK	1857.55	8083.8	0	0	yes
Alpha/beta hydrolase fold	JZ6_10	TZ19_10	OK	90.1819	391.785	0	0	yes
Transcriptional regulator	JZ6_10	TZ19_10	OK	30.2222	131.072	2.91E-06	7.51E-06	yes
Serine transporter	JZ6_10	TZ19_10	OK	75.0097	323.792	0	0	yes
putative acetoin utilization protein	JZ6_10	TZ19_10	OK	303.152	1296.68	0	0	yes
Sua5/YciO/YrdC family protein	JZ6_10	TZ19_10	OK	46.2658	196.706	7.48E-08	2.25E-07	yes
Succinate dehydrogenase cytochrome	JZ6_10	TZ19_10	OK	1310.71	5552.86	0	0	yes
Hypothetical UPF0274 protein	JZ6_10	TZ19_10	OK	139.963	592.631	0	0	yes
Phospho-2-dehydro-3-deoxyheptonate aldolase,Tyr-sensitive	JZ6_10	TZ19_10	OK	44.9173	188.324	2.44E-15	1.20E-14	yes
hypothetical protein	JZ6_10	TZ19_10	OK	183.473	768.34	1.71E-14	8.04E-14	yes
general secretion pathway protein N	JZ6_10	TZ19_10	OK	22.7358	94.87	3.63E-06	9.28E-06	yes
Probable monothiol glutaredoxin	JZ6_10	TZ19_10	OK	1775.81	7388.06	0	0	yes
3-isopropylmalate dehydratase small subunit	JZ6_10	TZ19_10	OK	61.5129	255.688	2.69E-10	9.78E-10	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	689.958	2855.86	0	0	yes
putative O-methyltransferase	JZ6_10	TZ19_10	OK	31.4989	130.068	3.68E-11	1.42E-10	yes
sodium/solute symporter	JZ6_10	TZ19_10	OK	8.11371	33.4502	3.74E-06	9.54E-06	yes
Thioredoxin reductase	JZ6_10	TZ19_10	OK	82.2432	338.785	0	0	yes
Ferredoxin	JZ6_10	TZ19_10	OK	294.377	1212.33	1.45E-07	4.23E-07	yes
Aspartokinase	JZ6_10	TZ19_10	OK	211.735	871.344	0	0	yes
Threonine aldolase	JZ6_10	TZ19_10	OK	18.2453	74.8262	1.69E-06	4.49E-06	yes
peroxiredoxin family protein/glutaredoxin	JZ6_10	TZ19_10	OK	492.977	2018.76	0	0	yes
formate transporter 1	JZ6_10	TZ19_10	OK	177.88	725.405	0	0	yes
ribosomal protein L5	JZ6_10	TZ19_10	OK	2101.88	8553.5	0	0	yes
nptA protein	JZ6_10	TZ19_10	OK	338.563	1373.86	0	0	yes
Soluble lytic murein transglycosylase precursor	JZ6_10	TZ19_10	OK	54.1842	218.864	0	0	yes
Transcriptional regulator	JZ6_10	TZ19_10	OK	755.299	3046.51	0	0	yes
putative peptidase T	JZ6_10	TZ19_10	OK	118.318	477.197	0	0	yes
Translation initiation inhibitor, yjgF family	JZ6_10	TZ19_10	OK	160.919	645.974	1.19E-09	4.10E-09	yes
putative multidrug resistance efflux pump	JZ6_10	TZ19_10	OK	27.872	111.13	4.31E-10	1.54E-09	yes
putative sulfurtransferase	JZ6_10	TZ19_10	OK	22.4515	89.3618	9.06E-07	2.47E-06	yes
Glutamate synthase	JZ6_10	TZ19_10	OK	20.3558	80.7837	0	0	yes

Transcriptional regulator, MarR family	JZ6_10	TZ19_10	OK	138.27	544.533	3.38E-13	1.47E-12	yes
hypothetical protein	JZ6_10	TZ19_10	OK	72.8522	286.045	8.88E-16	4.47E-15	yes
putative Penicillin-binding protein	JZ6_10	TZ19_10	OK	223.309	875.542	0	0	yes
putative Co-chaperonin GroES	JZ6_10	TZ19_10	OK	208.262	813.285	1.95E-07	5.65E-07	yes
ribosomal protein S6	JZ6_10	TZ19_10	OK	853.794	3272.78	0	0	yes
Ribosomal protein S6 modification protein	JZ6_10	TZ19_10	OK	2779.66	10576.8	0	0	yes
Bifunctional protein argH	JZ6_10	TZ19_10	OK	91.2848	344.873	0	0	yes
Dihydroxy-acid dehydratase	JZ6_10	TZ19_10	OK	34.0708	128.248	0	0	yes
Ca2+/Na+ antiporter	JZ6_10	TZ19_10	OK	28.7265	107.606	6.93E-08	2.09E-07	yes
Glycerol-3-phosphate dehydrogenase	JZ6_10	TZ19_10	OK	83.1794	311.221	0	0	yes
cytochrome c oxidase, subunit CcoO	JZ6_10	TZ19_10	OK	126.44	472.649	4.44E-16	2.26E-15	yes
Phosphoserine aminotransferase	JZ6_10	TZ19_10	OK	80.7651	301.269	0	0	yes
Acyl carrier protein	JZ6_10	TZ19_10	OK	540.336	2010.33	9.57E-12	3.84E-11	yes
ABC transporter, ATP-binding protein	JZ6_10	TZ19_10	OK	114.242	423.391	0	0	yes
Exodeoxyribonuclease V beta chain	JZ6_10	TZ19_10	OK	15.8344	58.5626	0	0	yes
Heat shock protein	JZ6_10	TZ19_10	OK	1946.43	7196.8	0	0	yes
Aminopeptidase N	JZ6_10	TZ19_10	OK	91.2741	336.875	0	0	yes
sensor histidine kinase	JZ6_10	TZ19_10	OK	58.7188	216.672	0	0	yes
Arylsulfatase A	JZ6_10	TZ19_10	OK	32.4753	119.037	4.11E-14	1.89E-13	yes
transcription-repair coupling factor	JZ6_10	TZ19_10	OK	50.6188	184.773	0	0	yes
HTH-type protein slmA	JZ6_10	TZ19_10	OK	50.5596	183.29	6.36E-07	1.76E-06	yes
DnaK-related protein	JZ6_10	TZ19_10	OK	33.6419	121.673	0	0	yes
RNA methyltransferase, TrmH family	JZ6_10	TZ19_10	OK	38.3753	138.521	2.10E-07	6.06E-07	yes
Serine--pyruvate aminotransferase	JZ6_10	TZ19_10	OK	19.5675	70.5475	1.55E-06	4.13E-06	yes
50S ribosomal protein L24	JZ6_10	TZ19_10	OK	7041.9	25239	0	0	yes
DNA-binding protein HU-alpha	JZ6_10	TZ19_10	OK	7774.67	27782.4	0	0	yes
3-phosphoglycerate kinase part 2	JZ6_10	TZ19_10	OK	835.34	2984.93	0	0	yes
Cold shock-like protein cspD	JZ6_10	TZ19_10	OK	6708.52	23772.1	0	0	yes
Acetylornithine aminotransferase	JZ6_10	TZ19_10	OK	339.545	1198.68	0	0	yes
Adenosine deaminase	JZ6_10	TZ19_10	OK	285.002	1004.16	0	0	yes
Polar flagellar protein FlaK	JZ6_10	TZ19_10	OK	47.9994	168.763	0	0	yes
Phospho-2-dehydro-3-deoxyheptonate aldolase,Trp-sensitive	JZ6_10	TZ19_10	OK	244.193	857.076	0	0	yes

Phosphoribosylaminoimidazole carboxylase ATPase subunit	JZ6_10	TZ19_10	OK	48.3067	169.177	2.22E-13	9.78E-13	yes
Ribosomal large subunit pseudouridine synthase C	JZ6_10	TZ19_10	OK	465.615	1621.94	0	0	yes
Periplasmic oligopeptide-binding protein	JZ6_10	TZ19_10	OK	561.051	1950.92	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	85.4788	296.82	0	0	yes
Single-strand binding protein (SSB) (Helix-destabilizing protein)	JZ6_10	TZ19_10	OK	272.409	943.963	0	0	yes
Hypothetical UPF0265 protein	JZ6_10	TZ19_10	OK	2727.53	9445.38	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	35.4184	122.344	5.13E-10	1.82E-09	yes
ADP-L-glycero-D-manno-heptose-6-epimerase	JZ6_10	TZ19_10	OK	68.0981	234.46	1.75E-14	8.24E-14	yes
Acetyl-coenzyme A carboxylase carboxyl transferase subunit beta	JZ6_10	TZ19_10	OK	534.04	1830.03	0	0	yes
type II secretory pathway, pseudopilin EpsG	JZ6_10	TZ19_10	OK	192.222	657.554	5.50E-13	2.37E-12	yes
2,3-bisphosphoglycerate-independent phosphoglycerate mutase	JZ6_10	TZ19_10	OK	301.66	1031.88	0	0	yes
GTP-binding protein HflX	JZ6_10	TZ19_10	OK	492.642	1676.23	0	0	yes
Smf protein	JZ6_10	TZ19_10	OK	89.1378	302.794	0	0	yes
cAMP-binding proteins	JZ6_10	TZ19_10	OK	4191.1	14191.6	0	0	yes
PTS system N-acetylglucosamine-specific EIICBA component	JZ6_10	TZ19_10	OK	471.365	1589.61	0	0	yes
Predicted ATP-dependent serine protease	JZ6_10	TZ19_10	OK	34.6526	116.682	1.19E-11	4.75E-11	yes
cell division protein FtsH	JZ6_10	TZ19_10	OK	854.877	2871.92	0	0	yes
ATP-dependent Clp protease proteolytic subunit	JZ6_10	TZ19_10	OK	1689.29	5662.97	0	0	yes
putative cell division protein FtsN	JZ6_10	TZ19_10	OK	151.027	505.782	4.66E-15	2.26E-14	yes
ribosomal protein L6	JZ6_10	TZ19_10	OK	1121.27	3727.05	0	0	yes
Histidine transport system permease protein hisQ	JZ6_10	TZ19_10	OK	45.1648	149.558	5.13E-07	1.43E-06	yes
Homoserine kinase	JZ6_10	TZ19_10	OK	25.9212	85.2799	3.59E-06	9.19E-06	yes
putative transmembrane transport protein	JZ6_10	TZ19_10	OK	57.4769	188.994	4.81E-12	1.96E-11	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	436.647	1435.44	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	204.067	670.624	2.52E-06	6.55E-06	yes
ABC transporter: Substrate-binding protein precursor; Maltooligosaccharides uptake	JZ6_10	TZ19_10	OK	266.587	875.552	0	0	yes
SlyX protein	JZ6_10	TZ19_10	OK	546.634	1794.93	6.88E-08	2.08E-07	yes
Protease II (Oligopeptidase B)	JZ6_10	TZ19_10	OK	11.2001	36.5564	1.51E-06	4.04E-06	yes
Biosynthetic arginine decarboxylase	JZ6_10	TZ19_10	OK	543.431	1773.48	0	0	yes
ABC transporter: substrate-binding protein precursor	JZ6_10	TZ19_10	OK	29.6102	96.5324	5.65E-11	2.15E-10	yes
glyoxylase II family protein	JZ6_10	TZ19_10	OK	192.245	624.692	0	0	yes
Formate acetyltransferase	JZ6_10	TZ19_10	OK	2223.8	7219.26	0	0	yes

hypothetical protein	JZ6_10	TZ19_10	OK	1849.13	6002.05	0	0	yes
Hypothetical lipoprotein	JZ6_10	TZ19_10	OK	70.9117	229.737	9.41E-10	3.27E-09	yes
ABC-type Fe3+ transport system, periplasmic component	JZ6_10	TZ19_10	OK	814.177	2627.74	0	0	yes
Guanosine-3',5'-bis(diphosphate) 3'-pyrophosphohydrolase	JZ6_10	TZ19_10	OK	57.9591	186.75	0	0	yes
Transketolase 1	JZ6_10	TZ19_10	OK	221.257	711.334	0	0	yes
NadC	JZ6_10	TZ19_10	OK	86.9728	278.768	4.00E-15	1.95E-14	yes
putative N-acetyl-D-glucosamine kinase	JZ6_10	TZ19_10	OK	63.3982	202.078	4.57E-11	1.75E-10	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	22.5945	71.9495	3.94E-08	1.21E-07	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1798.01	5711.02	0	0	yes
Asparagine synthetase B, glutamine-hydrolyzing	JZ6_10	TZ19_10	OK	73.9122	232.823	0	0	yes
Prolyl 4-hydroxylase alpha subunit homologue	JZ6_10	TZ19_10	OK	218.039	686.593	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	509.48	1601.74	4.44E-16	2.26E-15	yes
Leucyl-tRNA synthetase	JZ6_10	TZ19_10	OK	81.749	257.005	0	0	yes
Deoxyribodipyrimidine photolyase-related protein	JZ6_10	TZ19_10	OK	25.8165	81.1472	3.77E-09	1.26E-08	yes
Transcription activator ToxR	JZ6_10	TZ19_10	OK	31.4852	98.9258	3.91E-06	9.94E-06	yes
Phosphoenolpyruvate carboxykinase	JZ6_10	TZ19_10	OK	2390.69	7506.93	0	0	yes
Antioxidant, AhpC/Tsa family	JZ6_10	TZ19_10	OK	5258	16474.6	0	0	yes
Phenylalanyl-tRNA synthetase beta chain	JZ6_10	TZ19_10	OK	67.2875	210.633	0	0	yes
putative excinuclease ABC subunit C	JZ6_10	TZ19_10	OK	38.7805	121.378	3.69E-08	1.14E-07	yes
Ribosomal protein L30	JZ6_10	TZ19_10	OK	2957.12	9247.93	0	0	yes
50S ribosomal protein L21	JZ6_10	TZ19_10	OK	10434.2	32588.9	0	0	yes
Transcriptional regulator	JZ6_10	TZ19_10	OK	88.7006	277.028	7.99E-15	3.82E-14	yes
Orotate phosphoribosyltransferase	JZ6_10	TZ19_10	OK	63.8318	199.25	2.71E-07	7.74E-07	yes
Carbamoyl-phosphate synthase, small subunit	JZ6_10	TZ19_10	OK	63.5744	198.137	7.19E-14	3.25E-13	yes
SspA	JZ6_10	TZ19_10	OK	1254.6	3898.47	0	0	yes
ATP-dependent RNA helicase, DEAD box family	JZ6_10	TZ19_10	OK	115.125	355.181	0	0	yes
Orotidine 5'-phosphate decarboxylase	JZ6_10	TZ19_10	OK	145.361	448.042	2.89E-15	1.41E-14	yes
50S ribosomal subunit protein L36	JZ6_10	TZ19_10	OK	44760.5	137590	0	0	yes
Adenylate cyclase	JZ6_10	TZ19_10	OK	126.685	389.374	0	0	yes
Glutaredoxin	JZ6_10	TZ19_10	OK	2531.97	7751.07	0	0	yes
Hypothetical M22 peptidase homolog yeaZ	JZ6_10	TZ19_10	OK	81.4083	248.922	6.91E-10	2.43E-09	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	613.802	1867.47	0	0	yes

Cell division protein ftsZ	JZ6_10	TZ19_10	OK	935.508	2843.44	0	0	yes
Pyruvate dehydrogenase E1 component	JZ6_10	TZ19_10	OK	142.377	432.713	0	0	yes
putative aromatic ring-cleaving dioxygenase	JZ6_10	TZ19_10	OK	208.215	632.685	1.33E-06	3.57E-06	yes
Homoserine dehydrogenase	JZ6_10	TZ19_10	OK	66.5993	202.329	0	0	yes
Methylase of chemotaxis methyl-accepting protein CheR	JZ6_10	TZ19_10	OK	124.932	378.828	2.22E-16	1.15E-15	yes
Alanyl-tRNA synthetase	JZ6_10	TZ19_10	OK	95.6207	289.913	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	220.479	666.354	1.36E-06	3.65E-06	yes
hypothetical protein	JZ6_10	TZ19_10	OK	788.638	2382.51	0	0	yes
UDP-N-acetylmuramate:L-alanyl-gamma-D-glutamyl-meso-diaminopimelateligase	JZ6_10	TZ19_10	OK	57.8923	174.447	6.42E-14	2.91E-13	yes
Cytochrome c553	JZ6_10	TZ19_10	OK	444.195	1336.67	8.49E-11	3.19E-10	yes
Ribonuclease T (RNase T)	JZ6_10	TZ19_10	OK	166.946	502.291	0	0	yes
DNA transformation protein	JZ6_10	TZ19_10	OK	667.569	2006.53	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	301.489	905.626	0	0	yes
Autonomous glycyl radical cofactor	JZ6_10	TZ19_10	OK	6155.46	18447.8	0	0	yes
ATP-dependent RNA helicase	JZ6_10	TZ19_10	OK	635.787	1900.05	0	0	yes
Flavodoxin	JZ6_10	TZ19_10	OK	2461.58	7344.73	0	0	yes
putative protease	JZ6_10	TZ19_10	OK	130.429	389.061	0	0	yes
Malate synthase domain protein	JZ6_10	TZ19_10	OK	514.648	1533.58	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	1365.87	4067.62	0	0	yes
Glutaminase	JZ6_10	TZ19_10	OK	66.3445	196.424	1.50E-10	5.57E-10	yes
Cytochrome c-type biogenesis protein ccmE	JZ6_10	TZ19_10	OK	131.743	389.775	2.65E-08	8.29E-08	yes
DNA-directed RNA polymerase omega chain	JZ6_10	TZ19_10	OK	3902.91	11462.6	0	0	yes
Malate synthase	JZ6_10	TZ19_10	OK	106.776	313.307	2.30E-09	7.76E-09	yes
hypothetical protein	JZ6_10	TZ19_10	OK	345.764	1011.38	0	0	yes
Superoxide dismutase	JZ6_10	TZ19_10	OK	2248.75	6548.19	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	364.479	1055.86	0	0	yes
NifU-related domain containing protein	JZ6_10	TZ19_10	OK	75.4602	217.945	3.67E-09	1.22E-08	yes
Outer membrane protein	JZ6_10	TZ19_10	OK	34.6048	99.5152	7.35E-10	2.58E-09	yes
outer membrane protein TolC	JZ6_10	TZ19_10	OK	673.014	1928.39	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	737890	2.10E+06	0	0	yes
Seryl-tRNA synthetase	JZ6_10	TZ19_10	OK	939.949	2679.8	0	0	yes
Chaperone protein dnaK	JZ6_10	TZ19_10	OK	733.564	2089.47	0	0	yes

Naphthoate synthase	JZ6_10	TZ19_10	OK	487.458	1387.35	0	0	yes
Aspartyl-tRNA synthetase	JZ6_10	TZ19_10	OK	268.738	764.249	0	0	yes
FolD bifunctional protein	JZ6_10	TZ19_10	OK	117.164	332.298	2.66E-14	1.24E-13	yes
ATP-dependent RNA helicase RhlB	JZ6_10	TZ19_10	OK	219.454	620.968	0	0	yes
ribosomal protein S4	JZ6_10	TZ19_10	OK	1831.56	5161.18	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	344.996	970.642	3.64E-13	1.58E-12	yes
Peptidase	JZ6_10	TZ19_10	OK	154.888	435.643	0	0	yes
50S ribosomal protein L35	JZ6_10	TZ19_10	OK	22011.9	61881.4	0	0	yes
UTP--glucose-1-phosphate uridylyltransferase	JZ6_10	TZ19_10	OK	225.633	632.474	0	0	yes
Cytochrome d ubiquinol oxidase subunit I	JZ6_10	TZ19_10	OK	352.972	989.337	0	0	yes
ATP synthase subunit I	JZ6_10	TZ19_10	OK	3244.23	9090.4	0	0	yes
transcription elongation factor GreA	JZ6_10	TZ19_10	OK	907.605	2540.19	0	0	yes
Transcriptional regulator	JZ6_10	TZ19_10	OK	120.009	335.234	1.91E-06	5.05E-06	yes
hypothetical protein	JZ6_10	TZ19_10	OK	910.527	2543.24	4.14E-13	1.79E-12	yes
Glutamyl-tRNA synthetase	JZ6_10	TZ19_10	OK	638.552	1782.52	0	0	yes
putative protein involved in catabolism of external DNA	JZ6_10	TZ19_10	OK	47.6905	132.482	1.70E-06	4.51E-06	yes
putative carbamate kinase	JZ6_10	TZ19_10	OK	1074.56	2982.43	0	0	yes
Permease family protein	JZ6_10	TZ19_10	OK	67.922	188.091	4.86E-14	2.22E-13	yes
Carbon storage regulator homolog	JZ6_10	TZ19_10	OK	11702	32370.8	0	0	yes
DNA polymerase I	JZ6_10	TZ19_10	OK	28.8312	79.6982	1.74E-13	7.68E-13	yes
hypothetical protein	JZ6_10	TZ19_10	OK	177.567	490.202	6.66E-14	3.02E-13	yes
Chaperone protein htpG	JZ6_10	TZ19_10	OK	79.6572	219.784	0	0	yes
phosphoenolpyruvate carboxylase	JZ6_10	TZ19_10	OK	26.8689	73.8753	3.62E-12	1.49E-11	yes
Na+/H+-dicarboxylate symporter	JZ6_10	TZ19_10	OK	50.8306	139.205	2.01E-10	7.39E-10	yes
Ribonuclease PH	JZ6_10	TZ19_10	OK	798.064	2184.6	0	0	yes
Transcription elongation factor greB	JZ6_10	TZ19_10	OK	258.989	708.011	5.11E-13	2.20E-12	yes
ubiquinol-cytochrome c reductase,cytochrome c1	JZ6_10	TZ19_10	OK	90.2499	246.244	6.55E-09	2.15E-08	yes
2-oxoglutarate dehydrogenase E1 component	JZ6_10	TZ19_10	OK	154.675	421.557	0	0	yes
Transcription elongation protein nusA	JZ6_10	TZ19_10	OK	380.839	1032.59	0	0	yes
Nucleoside diphosphate kinase	JZ6_10	TZ19_10	OK	447.28	1211.14	0	0	yes
GMP reductase	JZ6_10	TZ19_10	OK	370.694	1003.07	0	0	yes
putative zinc uptake regulation protein	JZ6_10	TZ19_10	OK	818.555	2213.11	0	0	yes

flagellar motor protein	JZ6_10	TZ19_10	OK	69.3232	186.987	1.98E-07	5.74E-07	yes
iron-sulfur cluster-binding protein NapF	JZ6_10	TZ19_10	OK	144.337	389.01	6.96E-08	2.10E-07	yes
putative general secretion pathway protein A	JZ6_10	TZ19_10	OK	20.9963	56.4464	2.52E-06	6.56E-06	yes
ribosomal protein L34	JZ6_10	TZ19_10	OK	28074.3	75421.5	0	0	yes
HTH-type transcriptional regulator luxR	JZ6_10	TZ19_10	OK	860.788	2312.14	0	0	yes
ribosomal protein L1	JZ6_10	TZ19_10	OK	661.886	1776.59	0	0	yes
Flavodoxin-2	JZ6_10	TZ19_10	OK	267.031	716.303	3.22E-14	1.49E-13	yes
Hypothetical tRNA/rRNA methyltransferase	JZ6_10	TZ19_10	OK	150.326	399.389	1.41E-07	4.13E-07	yes
Tryptophan synthase beta chain	JZ6_10	TZ19_10	OK	49.8532	131.968	1.36E-08	4.36E-08	yes
Carbamoyl-phosphate synthase large chain	JZ6_10	TZ19_10	OK	43.1336	113.868	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	612.947	1609.65	2.43E-06	6.33E-06	yes
hypothetical protein	JZ6_10	TZ19_10	OK	4350.51	11410.8	1.32E-07	3.86E-07	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	482.265	1263.9	3.06E-06	7.89E-06	yes
Hypoxanthine phosphoribosyltransferase	JZ6_10	TZ19_10	OK	923.938	2419.81	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	195.27	511.216	2.22E-16	1.15E-15	yes
3-methyl-2-oxobutanoate hydroxymethyltransferase	JZ6_10	TZ19_10	OK	87.1892	227.742	6.41E-09	2.10E-08	yes
Tyrosine recombinase xerD	JZ6_10	TZ19_10	OK	93.5508	244.033	2.03E-11	7.95E-11	yes
Protein smtA	JZ6_10	TZ19_10	OK	104.353	270.363	5.13E-10	1.82E-09	yes
Transcriptional regulatory protein ompR	JZ6_10	TZ19_10	OK	824.039	2127.09	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	356.762	914.787	0	0	yes
Oxaloacetate decarboxylase alpha chain	JZ6_10	TZ19_10	OK	124.86	320.103	0	0	yes
Flagellin core protein A	JZ6_10	TZ19_10	OK	36.8291	94.1571	1.55E-06	4.13E-06	yes
Protein smg homolog	JZ6_10	TZ19_10	OK	600.938	1534.42	0	0	yes
DNA-directed RNA polymerase, alpha subunit	JZ6_10	TZ19_10	OK	2589.59	6610.92	0	0	yes
Isoleucyl-tRNA synthetase	JZ6_10	TZ19_10	OK	140.827	358.247	0	0	yes
Adenylosuccinate synthetase	JZ6_10	TZ19_10	OK	1106.16	2812.82	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	216.714	549.215	1.45E-11	5.75E-11	yes
2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase	JZ6_10	TZ19_10	OK	180.797	457.22	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	51.3773	129.784	4.44E-16	2.26E-15	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	172.207	434.487	3.11E-15	1.52E-14	yes
50S ribosomal protein L32	JZ6_10	TZ19_10	OK	18275.8	46051.1	0	0	yes
methionyl-tRNA synthetase	JZ6_10	TZ19_10	OK	181.056	455.459	0	0	yes

Glycerol-3-phosphate dehydrogenase (NAD+)	JZ6_10	TZ19_10	OK	64.081	161.198	3.56E-09	1.19E-08	yes
polar flagellin	JZ6_10	TZ19_10	OK	34.4578	86.6043	3.89E-06	9.90E-06	yes
ribosomal protein S13	JZ6_10	TZ19_10	OK	3203.52	8003.01	0	0	yes
L-aspartate oxidase	JZ6_10	TZ19_10	OK	228.172	569.848	0	0	yes
ribosomal subunit interface protein	JZ6_10	TZ19_10	OK	13015.2	32471.2	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	3246.41	8070.43	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	542.865	1346.62	0	0	yes
Polar flagellin B	JZ6_10	TZ19_10	OK	123.178	305.356	0	0	yes
Aspartate carbamoyltransferase	JZ6_10	TZ19_10	OK	230.479	570.433	0	0	yes
Trigger factor	JZ6_10	TZ19_10	OK	535.73	1324.33	0	0	yes
Phosphoenolpyruvate-protein phosphotransferase	JZ6_10	TZ19_10	OK	770.707	1902.97	0	0	yes
Peptidyl-prolyl cis-trans isomerase B	JZ6_10	TZ19_10	OK	2058.96	5078.9	0	0	yes
ribosomal protein S8	JZ6_10	TZ19_10	OK	1280.67	3158.9	0	0	yes
N-acetylglucosamine repressor	JZ6_10	TZ19_10	OK	286.721	706.279	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	758.215	1867.56	0	0	yes
A/G-specific adenine glycosylase	JZ6_10	TZ19_10	OK	57.0357	140.339	7.37E-08	2.22E-07	yes
Transketolase	JZ6_10	TZ19_10	OK	193.734	475.994	0	0	yes
Hypothetical adenine-specific methylase	JZ6_10	TZ19_10	OK	306.372	752.671	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	5533.14	13573.9	0	0	yes
Queuine tRNA-ribosyltransferase	JZ6_10	TZ19_10	OK	167.539	410.383	0	0	yes
Dipeptide/tripeptide permease	JZ6_10	TZ19_10	OK	339.445	829.112	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	85.2496	207.804	5.25E-07	1.46E-06	yes
Guanylate kinase	JZ6_10	TZ19_10	OK	253.74	618.35	8.44E-14	3.80E-13	yes
Hemolysin III	JZ6_10	TZ19_10	OK	337.17	820.455	0	0	yes
Hypothetical acetyltransferase	JZ6_10	TZ19_10	OK	237.883	578.743	1.40E-09	4.81E-09	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	12049.6	29315	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	108.111	262.551	1.55E-09	5.33E-09	yes
Na(+)-translocating NADH-quinone reductase subunit E	JZ6_10	TZ19_10	OK	351.615	851.909	4.66E-15	2.26E-14	yes
Aerobic respiration control protein arcA	JZ6_10	TZ19_10	OK	3253.91	7883.59	0	0	yes
Multidrug resistance protein	JZ6_10	TZ19_10	OK	114.307	276.679	4.44E-16	2.26E-15	yes
Cytochrome c biogenesisprotein ccmG (Thiol:disulfide interchange protein dsbE)	JZ6_10	TZ19_10	OK	165.286	399.981	1.27E-07	3.75E-07	yes
Xanthine phosphoribosyltransferase	JZ6_10	TZ19_10	OK	546.71	1320.65	0	0	yes

ABC transporter: ATP-binding protein	JZ6_10	TZ19_10	OK	83.1419	200.585	2.22E-07	6.40E-07	yes
Methyl-accepting chemotaxis protein	JZ6_10	TZ19_10	OK	48.1509	116.16	2.15E-10	7.86E-10	yes
ATP synthase C chain	JZ6_10	TZ19_10	OK	3114.26	7495.33	0	0	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	987.829	2369.42	0	0	yes
RctB protein	JZ6_10	TZ19_10	OK	68.0998	163.147	2.44E-15	1.20E-14	yes
Succinyl-CoA synthetase alpha chain	JZ6_10	TZ19_10	OK	407.019	973.903	0	0	yes
ATP synthase alpha chain	JZ6_10	TZ19_10	OK	528.714	1260.26	0	0	yes
DNA-binding response regulator PhoB	JZ6_10	TZ19_10	OK	583.169	1385.98	0	0	yes
S-adenosylmethionine synthetase	JZ6_10	TZ19_10	OK	456.887	1082.93	0	0	yes
ATP-dependent RNA helicase srmB	JZ6_10	TZ19_10	OK	462.827	1094.22	0	0	yes
anthranilate synthase alpha subunit	JZ6_10	TZ19_10	OK	31.9754	75.5598	2.12E-06	5.56E-06	yes
lipoprotein NlpI	JZ6_10	TZ19_10	OK	118.921	279.874	9.64E-11	3.61E-10	yes
Bacteriocin production protein	JZ6_10	TZ19_10	OK	197.072	463.639	1.05E-07	3.13E-07	yes
putative endoribonuclease	JZ6_10	TZ19_10	OK	142.857	335.869	0	0	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	231.31	543.213	0	0	yes
UDP-3-O-acyl-N-acetylglucosamine deacetylase	JZ6_10	TZ19_10	OK	947.167	2220.34	0	0	yes
30S ribosomal protein S10	JZ6_10	TZ19_10	OK	5444.56	12747.9	0	0	yes
6,7-dimethyl-8-ribityllumazine synthase	JZ6_10	TZ19_10	OK	1274.66	2979.22	0	0	yes
Protein pmbA	JZ6_10	TZ19_10	OK	158.042	368.848	0	0	yes
50S ribosomal protein L3	JZ6_10	TZ19_10	OK	2241.22	5221.05	0	0	yes
Aspartate aminotransferase	JZ6_10	TZ19_10	OK	215.007	500.75	0	0	yes
Chromosome partition protein mukB	JZ6_10	TZ19_10	OK	18.0082	41.8096	1.63E-09	5.56E-09	yes
Ribose-phosphate pyrophosphokinase	JZ6_10	TZ19_10	OK	992.43	2303.76	0	0	yes
Ribosomal large subunit pseudouridine synthase F	JZ6_10	TZ19_10	OK	228.075	529.418	0	0	yes
Na(+)-translocating NADH-quinone reductase subunit F	JZ6_10	TZ19_10	OK	222.75	515.445	0	0	yes
ribosome-binding factor A	JZ6_10	TZ19_10	OK	212.196	490.681	2.75E-06	7.12E-06	yes
Octaprenyl-diphosphate synthase	JZ6_10	TZ19_10	OK	144.565	332.591	3.93E-14	1.81E-13	yes
ribosomal large subunit pseudouridine synthase D	JZ6_10	TZ19_10	OK	404.358	928.454	0	0	yes
Polar flagellar FlgM homolog	JZ6_10	TZ19_10	OK	390.851	895.509	4.27E-10	1.52E-09	yes
putative transcriptional regulator (BolA family)	JZ6_10	TZ19_10	OK	3226.93	7378.76	0	0	yes
Phosphocarrier protein HPr	JZ6_10	TZ19_10	OK	7150.98	16293	0	0	yes
Spermidine/putrescine-binding periplasmic protein precursor	JZ6_10	TZ19_10	OK	81.5425	185.572	3.79E-08	1.17E-07	yes

ABC transporter: Transmembrane protein; Maltooligosaccharide uptake	JZ6_10	TZ19_10	OK	76.0564	172.954	1.29E-06	3.47E-06	yes
tryptophanyl-tRNA synthetase	JZ6_10	TZ19_10	OK	437.679	994.8	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	6079.47	13773.7	0	0	yes
Methionine synthase	JZ6_10	TZ19_10	OK	26.3652	59.7118	6.22E-10	2.19E-09	yes
Acetate kinase	JZ6_10	TZ19_10	OK	636.872	1433.68	0	0	yes
Hypothetical protein ybbK	JZ6_10	TZ19_10	OK	78.1323	175.825	5.30E-07	1.47E-06	yes
ribosomal protein L11 methyltransferase	JZ6_10	TZ19_10	OK	187.785	421.319	8.33E-14	3.75E-13	yes
Ribosomal protein S19	JZ6_10	TZ19_10	OK	1218.8	2730.4	1.51E-10	5.58E-10	yes
putative esterase	JZ6_10	TZ19_10	OK	73.552	164.393	1.13E-07	3.33E-07	yes
oxaloacetate decarboxylase gamma chain	JZ6_10	TZ19_10	OK	1141.23	2550.51	1.24E-14	5.88E-14	yes
cystathionine gamma-synthase	JZ6_10	TZ19_10	OK	53.0213	118.478	1.32E-06	3.55E-06	yes
Phosphoglucomutase	JZ6_10	TZ19_10	OK	109.503	243.309	0	0	yes
Ribonuclease III	JZ6_10	TZ19_10	OK	348.397	770.723	2.22E-16	1.15E-15	yes
Ribosomal protein L28	JZ6_10	TZ19_10	OK	17438.2	38480.6	0	0	yes
Alanine dehydrogenase	JZ6_10	TZ19_10	OK	5806.39	12768.8	0	0	yes
Superfamily II DNA and RNA helicase	JZ6_10	TZ19_10	OK	176.026	386.71	0	0	yes
putative factor-for-inversion stimulation protein	JZ6_10	TZ19_10	OK	1637.13	3592.03	0	0	yes
Na(+)-translocating NADH-quinone reductase subunit D	JZ6_10	TZ19_10	OK	722.038	1582.95	0	0	yes
thiol:disulfide interchange protein	JZ6_10	TZ19_10	OK	138.747	303.754	8.62E-09	2.80E-08	yes
Ubiquinol-cytochrome c reductase,iron-sulfur subunit	JZ6_10	TZ19_10	OK	997.291	2178.86	0	0	yes
DNA primase	JZ6_10	TZ19_10	OK	271.239	592.001	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	95.815	209.123	1.87E-09	6.36E-09	yes
gonadoliberin III-related protein	JZ6_10	TZ19_10	OK	88.3174	192.45	2.95E-12	1.22E-11	yes
Glutamate-1-semialdehyde aminotransferase	JZ6_10	TZ19_10	OK	142.624	310.589	6.66E-16	3.37E-15	yes
HTH-type transcriptional repressor cytR	JZ6_10	TZ19_10	OK	75.8651	165.091	8.38E-07	2.29E-06	yes
SH3 domain protein	JZ6_10	TZ19_10	OK	144.755	313.634	2.09E-06	5.48E-06	yes
N-acetylglucosamine-6-phosphate deacetylase	JZ6_10	TZ19_10	OK	152.089	329.091	1.21E-13	5.40E-13	yes
Ribosomal protein S11	JZ6_10	TZ19_10	OK	1747.31	3772.15	0	0	yes
Na(+)-translocating NADH-quinone reductase subunit B	JZ6_10	TZ19_10	OK	252.146	543.656	0	0	yes
ParA family protein	JZ6_10	TZ19_10	OK	883.396	1902.21	0	0	yes
NifU-related protein	JZ6_10	TZ19_10	OK	455.92	980.489	1.73E-07	5.02E-07	yes
Chaperone protein torD	JZ6_10	TZ19_10	OK	1094.38	2352.79	0	0	yes

Guanosine-5'-triphosphate,3'-diphosphate pyrophosphatase	JZ6_10	TZ19_10	OK	74.8926	160.755	5.06E-10	1.80E-09	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	341648	733195	0	0	yes
ATP-dependent Lon protease	JZ6_10	TZ19_10	OK	171.182	367.324	0	0	yes
Cytochrome c-type biogenesis protein ccmF	JZ6_10	TZ19_10	OK	50.8073	108.711	1.47E-08	4.69E-08	yes
Cytochrome c4 precursor	JZ6_10	TZ19_10	OK	1028.98	2197.99	0	0	yes
Glutathione reductase	JZ6_10	TZ19_10	OK	111.934	238.968	6.92E-12	2.80E-11	yes
Protein recA (Recombinase A)	JZ6_10	TZ19_10	OK	969.042	2066.48	0	0	yes
60 kDa chaperonin (Protein Cpn60) (groEL protein)	JZ6_10	TZ19_10	OK	178.571	379.467	0	0	yes
Probable sigma(54) modulation protein	JZ6_10	TZ19_10	OK	2787.92	5914.93	0	0	yes
Diaminopimelate decarboxylase	JZ6_10	TZ19_10	OK	138.884	294.503	6.02E-13	2.59E-12	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	168.122	356.326	0	0	yes
putative lipoprotein	JZ6_10	TZ19_10	OK	338.483	715.978	8.34E-12	3.36E-11	yes
Sugar fermentation stimulation protein homolog	JZ6_10	TZ19_10	OK	481.492	1018.1	0	0	yes
Fatty acid metabolism regulator protein	JZ6_10	TZ19_10	OK	1556.1	3281	0	0	yes
Dihydroorotase	JZ6_10	TZ19_10	OK	172.723	364.034	8.22E-15	3.93E-14	yes
putative Na+/H+ antiporter	JZ6_10	TZ19_10	OK	55.4222	116.502	1.09E-06	2.95E-06	yes
Oligopeptide transport ATP-binding protein oppD	JZ6_10	TZ19_10	OK	105.695	221.927	9.38E-08	2.80E-07	yes
LuxT regulator	JZ6_10	TZ19_10	OK	657.55	1377.68	2.82E-14	1.31E-13	yes
SspB	JZ6_10	TZ19_10	OK	376.917	788.433	2.95E-10	1.07E-09	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	192.351	402.076	4.82E-07	1.34E-06	yes
Predicted N-acetylglucosaminyl transferase	JZ6_10	TZ19_10	OK	126.513	263.691	1.97E-11	7.73E-11	yes
predicted N6-adenine-specific DNA methylase	JZ6_10	TZ19_10	OK	52.2497	108.871	1.18E-08	3.80E-08	yes
hypothetical protein	JZ6_10	TZ19_10	OK	221.284	460.961	1.59E-07	4.63E-07	yes
Erythronate-4-phosphate dehydrogenase	JZ6_10	TZ19_10	OK	133.535	277.218	4.76E-11	1.82E-10	yes
Long-chain fatty acid transport protein precursor	JZ6_10	TZ19_10	OK	371.154	770.267	0	0	yes
Preprotein translocase subunit SecG	JZ6_10	TZ19_10	OK	11612.9	23999.2	0	0	yes
Phosphate acetyltransferase	JZ6_10	TZ19_10	OK	94.3627	194.748	1.11E-15	5.56E-15	yes
manganese-dependent inorganic pyrophosphatase	JZ6_10	TZ19_10	OK	1551.39	3197.23	0	0	yes
putative permease	JZ6_10	TZ19_10	OK	175.766	362.096	6.59E-14	2.99E-13	yes
Succinyl-CoA synthetase beta chain	JZ6_10	TZ19_10	OK	204.742	420.875	0	0	yes
Fatty oxidation complex, alpha subunit	JZ6_10	TZ19_10	OK	118.744	243.803	0	0	yes
Transcriptional regulator of succinylCoA synthetase operon	JZ6_10	TZ19_10	OK	260.444	534.735	6.87E-11	2.60E-10	yes

N utilization substance protein B homolog	JZ6_10	TZ19_10	OK	1287.48	2641.52	0	0	yes
Succinylglutamic semialdehyde dehydrogenase	JZ6_10	TZ19_10	OK	60.5602	124.142	3.52E-07	9.92E-07	yes
DNA-binding protein HU-beta	JZ6_10	TZ19_10	OK	9129.82	18700	0	0	yes
Peptidoglycan-associated lipoprotein precursor	JZ6_10	TZ19_10	OK	1604.2	3280.36	0	0	yes
Hypothetical UPF0325 protein	JZ6_10	TZ19_10	OK	5915.81	12082.3	0	0	yes
NADH dehydrogenase	JZ6_10	TZ19_10	OK	98.6263	199.918	2.20E-09	7.44E-09	yes
Probable tRNA(5-methylaminomethyl-2-thiouridylate)-methyltransferase	JZ6_10	TZ19_10	OK	155.475	314.436	9.71E-12	3.89E-11	yes
Ubiquinone/menaquinone biosynthesis methyltransferase ubiE	JZ6_10	TZ19_10	OK	327.179	659.975	2.89E-15	1.41E-14	yes
NADP-dependent malic enzyme	JZ6_10	TZ19_10	OK	107.609	216.902	1.91E-09	6.49E-09	yes
CTP synthase (UTP--ammonia ligase)	JZ6_10	TZ19_10	OK	2580.64	5187.52	0	0	yes
ParA family protein	JZ6_10	TZ19_10	OK	112.34	225.688	1.39E-09	4.76E-09	yes
1,4-dihydroxy-2-naphthoate octaprenyltransferase	JZ6_10	TZ19_10	OK	162.491	326.379	1.75E-09	5.97E-09	yes
50S ribosomal subunit protein L20	JZ6_10	TZ19_10	OK	7077.76	14162.6	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	455.339	225.938	7.88E-08	2.37E-07	yes
tRNA modification GTPase trmE	JZ6_10	TZ19_10	OK	131.94	65.3867	2.15E-07	6.21E-07	yes
Periplasmic dipeptide transport protein precursor	JZ6_10	TZ19_10	OK	801.343	394.833	0	0	yes
Peptidase B	JZ6_10	TZ19_10	OK	478.422	233.923	0	0	yes
ATP-dependent helicase	JZ6_10	TZ19_10	OK	59.524	29.0348	9.21E-10	3.21E-09	yes
Uroporphyrinogen-III synthase	JZ6_10	TZ19_10	OK	358.083	174.438	4.01E-08	1.23E-07	yes
Ribosomal RNA large subunit methyltransferase	JZ6_10	TZ19_10	OK	357.713	173.963	2.39E-10	8.72E-10	yes
methyl-accepting chemotaxis protein	JZ6_10	TZ19_10	OK	112.759	54.7186	2.30E-06	5.99E-06	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	409.672	198.467	3.54E-06	9.04E-06	yes
preprotein translocase, SecE subunit	JZ6_10	TZ19_10	OK	11835.6	5704.14	0	0	yes
ATP synthase epsilon chain	JZ6_10	TZ19_10	OK	4383.41	2112.53	0	0	yes
chlorohydrolase/deaminase family protein	JZ6_10	TZ19_10	OK	125.097	59.1091	2.20E-07	6.35E-07	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	594.9	280.924	4.44E-16	2.26E-15	yes
UDP-N-acetylglucosamine 1-carboxyvinyltransferase	JZ6_10	TZ19_10	OK	835.671	393.444	0	0	yes
GTP-binding protein era homolog	JZ6_10	TZ19_10	OK	2160.47	1014.86	0	0	yes
Phosphoserine phosphatase	JZ6_10	TZ19_10	OK	422.333	197.08	2.44E-09	8.21E-09	yes
long-chain acyl-CoA synthetase	JZ6_10	TZ19_10	OK	150.581	69.7091	2.25E-10	8.23E-10	yes
ABC transporter: Substrate-binding protein precursor	JZ6_10	TZ19_10	OK	107.275	49.5232	2.40E-06	6.25E-06	yes
Membrane protein	JZ6_10	TZ19_10	OK	554.128	254.702	0	0	yes

Transcriptional regulator, LysR family	JZ6_10	TZ19_10	OK	1922.21	876.903	0	0	yes
putative nucleoprotein/polynucleotide-associated enzyme	JZ6_10	TZ19_10	OK	540.053	246.023	1.47E-07	4.30E-07	yes
hypothetical protein	JZ6_10	TZ19_10	OK	351.659	160.074	3.44E-06	8.81E-06	yes
Formyltetrahydrofolate deformylase	JZ6_10	TZ19_10	OK	208.944	94.1848	3.13E-07	8.86E-07	yes
Topoisomerase IV subunit A	JZ6_10	TZ19_10	OK	72.1869	32.5265	1.15E-07	3.39E-07	yes
FKBP-type 16 kDa peptidyl-prolyl cis-trans isomerase	JZ6_10	TZ19_10	OK	734.414	330.068	1.06E-08	3.41E-08	yes
Protein hflC	JZ6_10	TZ19_10	OK	1465.46	655.42	0	0	yes
hypothetical regulatory components of sensory transduction	JZ6_10	TZ19_10	OK	523.639	233.857	0	0	yes
Catalase	JZ6_10	TZ19_10	OK	199.548	88.4654	7.91E-13	3.38E-12	yes
Conserved hypothetical protein; putative hemolysin-type calcium-binding region	JZ6_10	TZ19_10	OK	17.6101	7.77094	3.50E-12	1.44E-11	yes
Iron-containing alcohol dehydrogenase	JZ6_10	TZ19_10	OK	467.209	204.994	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	266.288	116.129	1.92E-08	6.08E-08	yes
phosphoglucomutase/phosphomannomutase family protein MrsA	JZ6_10	TZ19_10	OK	99.3337	43.2225	1.62E-06	4.31E-06	yes
tRNA pseudouridine 55 synthase	JZ6_10	TZ19_10	OK	203.748	88.6223	2.99E-08	9.30E-08	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	549.07	238.098	9.04E-07	2.46E-06	yes
GTP cyclohydrolase I	JZ6_10	TZ19_10	OK	453.159	196.047	8.48E-11	3.19E-10	yes
5'-nucleotidase/2',3'-cyclic phosphodiesterase	JZ6_10	TZ19_10	OK	500.154	215.876	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	390.21	168.145	4.82E-14	2.20E-13	yes
Arylsulfatase regulator	JZ6_10	TZ19_10	OK	140.012	60.2451	1.90E-08	6.00E-08	yes
putative acetyltransferase	JZ6_10	TZ19_10	OK	1176.25	500.207	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	171.478	72.2933	2.85E-08	8.89E-08	yes
GTP-binding protein lepA	JZ6_10	TZ19_10	OK	438.861	184.933	0	0	yes
Uroporphyrin-III C-methyltransferase	JZ6_10	TZ19_10	OK	151.966	63.8911	3.44E-06	8.81E-06	yes
Similar to ressure-regulated ORF-like protein	JZ6_10	TZ19_10	OK	2594.25	1086.38	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	762.706	318.599	0	0	yes
ABC transporter: substrate binding protein precursor	JZ6_10	TZ19_10	OK	120.826	50.2213	5.36E-12	2.18E-11	yes
putative oligopeptidase F	JZ6_10	TZ19_10	OK	76.5681	31.7865	1.41E-07	4.14E-07	yes
Acyl dehydratase	JZ6_10	TZ19_10	OK	1020.46	421.678	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	3695.17	1524.15	4.38E-09	1.45E-08	yes
Valine-pyruvate aminotransferase	JZ6_10	TZ19_10	OK	113.288	46.6541	1.71E-08	5.43E-08	yes
PTS system trehalose-specific EIIBC component	JZ6_10	TZ19_10	OK	158.106	65.0175	3.64E-10	1.31E-09	yes
Translation elongation factor P	JZ6_10	TZ19_10	OK	2325.58	955.385	0	0	yes

hypothetical protein	JZ6_10	TZ19_10	OK	815.945	335.082	0	0	yes
Arginine repressor	JZ6_10	TZ19_10	OK	528.494	217.008	3.24E-07	9.17E-07	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	171.101	70.2339	6.48E-08	1.96E-07	yes
5'-nucleotidase/2',3'-cyclic phosphodiesterase	JZ6_10	TZ19_10	OK	181.213	73.4538	2.55E-13	1.12E-12	yes
Transcriptional regulator, LysR family	JZ6_10	TZ19_10	OK	445.356	179.978	8.88E-16	4.47E-15	yes
Protease IV (Endopeptidase IV)	JZ6_10	TZ19_10	OK	137.056	55.2028	1.07E-12	4.54E-12	yes
Sodium/glutamate symporter	JZ6_10	TZ19_10	OK	117.206	46.9768	1.29E-07	3.81E-07	yes
Ribulose-phosphate 3-epimerase	JZ6_10	TZ19_10	OK	1299.71	520.921	0	0	yes
Oligopeptidase A	JZ6_10	TZ19_10	OK	248.126	99.4156	0	0	yes
putative biotin carboxyl carrier protein	JZ6_10	TZ19_10	OK	380.989	151.329	2.85E-07	8.12E-07	yes
hypothetical protein	JZ6_10	TZ19_10	OK	8637.95	3425.58	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	15401.1	6089.38	0	0	yes
putative outer membrane protein	JZ6_10	TZ19_10	OK	417.581	164.289	1.72E-06	4.55E-06	yes
ATP-dependent RNA helicase	JZ6_10	TZ19_10	OK	513.101	201.713	0	0	yes
outer membrane protein OmpA	JZ6_10	TZ19_10	OK	365.388	143.563	0	0	yes
2,4-dienoyl-CoA reductase	JZ6_10	TZ19_10	OK	127.447	49.9466	9.28E-14	4.16E-13	yes
HemY protein	JZ6_10	TZ19_10	OK	108.336	42.4237	2.90E-07	8.22E-07	yes
Ribonuclease G	JZ6_10	TZ19_10	OK	145.545	56.0288	1.40E-10	5.19E-10	yes
hypothetical protein	JZ6_10	TZ19_10	OK	45.6285	17.5237	8.65E-07	2.36E-06	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1141.75	438.198	0	0	yes
Na+/H+ antiporter NhaD and related arsenite permeases	JZ6_10	TZ19_10	OK	114.069	43.3299	1.62E-09	5.56E-09	yes
Dihydrofolate reductase	JZ6_10	TZ19_10	OK	636.017	241.524	5.01E-11	1.91E-10	yes
Exodeoxyribonuclease III	JZ6_10	TZ19_10	OK	223.74	84.7499	6.65E-09	2.18E-08	yes
PhoH-like protein	JZ6_10	TZ19_10	OK	142.284	53.723	4.49E-09	1.49E-08	yes
GTP-binding protein typA/bipA	JZ6_10	TZ19_10	OK	2512	946.347	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	4208.34	1578.87	0	0	yes
Thiamine biosynthesis protein thiI	JZ6_10	TZ19_10	OK	644.15	240.908	0	0	yes
Outer membrane protein	JZ6_10	TZ19_10	OK	1596.33	595.93	0	0	yes
Carbon starvation protein CstA	JZ6_10	TZ19_10	OK	80.9335	30.1206	1.10E-07	3.25E-07	yes
pyridine nucleotide-disulfide oxidoreductase,class I	JZ6_10	TZ19_10	OK	81.9096	30.0893	2.38E-07	6.83E-07	yes
Acyl carrier protein	JZ6_10	TZ19_10	OK	48634.1	17821	0	0	yes
Pyridoxamine-phosphate oxidase	JZ6_10	TZ19_10	OK	357.175	130.694	1.33E-11	5.30E-11	yes

Hypothetical protein	JZ6_10	TZ19_10	OK	1817.14	662.575	4.44E-16	2.26E-15	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1201.54	437.685	1.22E-11	4.85E-11	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	99.7572	36.2532	2.09E-06	5.49E-06	yes
D-alanine--D-alanine ligase	JZ6_10	TZ19_10	OK	129.799	47.0365	7.46E-07	2.05E-06	yes
succinylglutamate desuccinylase	JZ6_10	TZ19_10	OK	611.331	221.176	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	518.241	186.169	0	0	yes
Transcriptional regulator	JZ6_10	TZ19_10	OK	199.79	71.3485	4.44E-16	2.26E-15	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	100.719	35.6468	2.26E-09	7.64E-09	yes
Nitrogen regulatory protein	JZ6_10	TZ19_10	OK	668.283	234.706	4.15E-12	1.70E-11	yes
ABC transporter, ATP-binding protein	JZ6_10	TZ19_10	OK	131.331	45.6468	3.61E-06	9.23E-06	yes
membrane protein HemX	JZ6_10	TZ19_10	OK	177.986	61.3198	1.21E-13	5.41E-13	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	513.003	176.18	0	0	yes
putative outer membrane lipoprotein	JZ6_10	TZ19_10	OK	143874	49098.4	0	0	yes
Dihydrolipoyl dehydrogenase	JZ6_10	TZ19_10	OK	292.517	99.6635	0	0	yes
Pyridoxal phosphate biosynthetic protein pdxJ	JZ6_10	TZ19_10	OK	546.846	185.513	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1211.98	409.041	4.71E-07	1.32E-06	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	240.449	80.5954	2.35E-07	6.74E-07	yes
Protease degQ precursor	JZ6_10	TZ19_10	OK	275.793	92.3697	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1247.19	416.265	5.34E-10	1.89E-09	yes
Methylglyoxal synthase	JZ6_10	TZ19_10	OK	359.293	119.521	3.47E-07	9.79E-07	yes
putative amino acid ABC transporter, periplasmic amino acid-binding portion	JZ6_10	TZ19_10	OK	871.099	289.471	0	0	yes
DNA polymerase III, epsilon subunit	JZ6_10	TZ19_10	OK	318.34	105.555	1.58E-12	6.63E-12	yes
Probable amino-acid ABC transporter ATP-binding protein	JZ6_10	TZ19_10	OK	120.215	39.4476	3.11E-06	7.99E-06	yes
hypothetical protein	JZ6_10	TZ19_10	OK	459.454	150.312	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	318.758	103.913	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	191.521	61.6565	2.62E-06	6.80E-06	yes
ATPase	JZ6_10	TZ19_10	OK	100.135	32.1731	0	0	yes
transcriptional regulator, LuxR family	JZ6_10	TZ19_10	OK	248.882	79.8585	1.13E-08	3.63E-08	yes
hypothetical translation factor	JZ6_10	TZ19_10	OK	598.245	189.145	2.22E-16	1.15E-15	yes
hypothetical protein	JZ6_10	TZ19_10	OK	14932.8	4696.11	0	0	yes
Protein flaG	JZ6_10	TZ19_10	OK	1213.05	378.517	0	0	yes
GTP1/Obg family protein	JZ6_10	TZ19_10	OK	1055.26	327.075	0	0	yes

hypothetical protein	JZ6_10	TZ19_10	OK	76.7347	23.727	1.51E-07	4.40E-07	yes
Deoxyribodipyrimidine photolyase	JZ6_10	TZ19_10	OK	159.149	49.1525	4.44E-16	2.26E-15	yes
ABC transporter: Transmembrane protein	JZ6_10	TZ19_10	OK	199.363	61.5719	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	308.13	95.1015	1.03E-11	4.15E-11	yes
23S rRNA (guanosine-2'-O-)-methyltransferase rlmB	JZ6_10	TZ19_10	OK	196.203	60.5379	1.61E-09	5.53E-09	yes
hypothetical protein	JZ6_10	TZ19_10	OK	33172.8	10211	0	0	yes
Deoxyguanosinetriphosphate triphosphohydrolase-like protein	JZ6_10	TZ19_10	OK	89.0812	27.3201	4.18E-09	1.39E-08	yes
Cytochrome c-type protein TorC	JZ6_10	TZ19_10	OK	664.605	203.258	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	237.029	71.8993	2.03E-10	7.44E-10	yes
tRNA pseudouridine synthase D	JZ6_10	TZ19_10	OK	159.306	48.1422	8.61E-11	3.23E-10	yes
Prolipoprotein diacylglyceryltransferase	JZ6_10	TZ19_10	OK	326.611	98.652	1.11E-15	5.56E-15	yes
cytochrome c-type protein	JZ6_10	TZ19_10	OK	638.593	191.004	1.38E-14	6.50E-14	yes
Ribosomal-protein-serine acetyltransferase	JZ6_10	TZ19_10	OK	251.112	75.0913	2.11E-07	6.09E-07	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	257.129	76.5392	1.67E-06	4.43E-06	yes
Similar to ribosomal protein S15	JZ6_10	TZ19_10	OK	23253.5	6868.55	0	0	yes
Protein nrfC homolog precursor	JZ6_10	TZ19_10	OK	326.669	96.391	2.75E-12	1.14E-11	yes
Maf-like protein	JZ6_10	TZ19_10	OK	306.403	90.2799	3.53E-11	1.36E-10	yes
UDP-N-acetylglucosamine--N-acetylmuramyl-(pentapeptide)pyrophosphoryl-undecaprenol N-acetylglucosamine transferase	JZ6_10	TZ19_10	OK	217.734	64.0017	1.55E-15	7.72E-15	yes
hypothetical protein	JZ6_10	TZ19_10	OK	3623.34	1054.62	8.27E-11	3.11E-10	yes
putative D-alanyl-D-alanine carboxypeptidase	JZ6_10	TZ19_10	OK	94.7772	27.4466	5.54E-08	1.69E-07	yes
hypothetical protein	JZ6_10	TZ19_10	OK	2481.41	718.064	1.08E-12	4.57E-12	yes
putative transcriptional activator	JZ6_10	TZ19_10	OK	148.759	43.0009	3.81E-07	1.07E-06	yes
putative ATPase	JZ6_10	TZ19_10	OK	57.6931	16.57	5.53E-07	1.54E-06	yes
phosphoenolpyruvate synthase	JZ6_10	TZ19_10	OK	180.566	51.7145	2.98E-10	1.08E-09	yes
predicted ATP-dependent endonuclease	JZ6_10	TZ19_10	OK	50.0356	14.1756	4.60E-07	1.29E-06	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	110.949	31.0745	0	0	yes
Probable cysteine desulfurase	JZ6_10	TZ19_10	OK	107.12	29.9904	7.90E-10	2.76E-09	yes
Transcriptional regulator	JZ6_10	TZ19_10	OK	136.091	38.0098	1.69E-06	4.48E-06	yes
Alkaline phosphatase III precursor	JZ6_10	TZ19_10	OK	259.999	72.2684	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	197.634	54.7271	9.73E-13	4.13E-12	yes
hypothetical protein	JZ6_10	TZ19_10	OK	322.123	89.1776	2.66E-15	1.31E-14	yes

Conserved hypothetical protein	JZ6_10	TZ19_10	OK	207.09	57.1953	1.66E-13	7.35E-13	yes
ABC transporter IM-ABC: Transmembrane and ATP binding protein	JZ6_10	TZ19_10	OK	40.3879	10.9742	2.55E-07	7.29E-07	yes
Methionine sulfoxide reductase	JZ6_10	TZ19_10	OK	182.837	49.346	4.62E-14	2.11E-13	yes
hypothetical protein	JZ6_10	TZ19_10	OK	30579.9	8214.01	0	0	yes
nitrite reductase periplasmic cytochrome c552	JZ6_10	TZ19_10	OK	1033.34	277.401	0	0	yes
DNA mismatch repair protein mutS	JZ6_10	TZ19_10	OK	52.5986	13.9131	7.87E-12	3.17E-11	yes
Endonuclease III	JZ6_10	TZ19_10	OK	298.496	78.5013	3.60E-12	1.48E-11	yes
Chemotaxis protein	JZ6_10	TZ19_10	OK	116.084	30.4472	1.74E-07	5.06E-07	yes
universal stress protein A	JZ6_10	TZ19_10	OK	413.508	108.376	6.99E-08	2.11E-07	yes
chemotactic transducer-related protein	JZ6_10	TZ19_10	OK	30.9865	8.10245	6.17E-09	2.03E-08	yes
sensor histidine kinase/response regulator	JZ6_10	TZ19_10	OK	60.0667	15.6597	3.05E-09	1.02E-08	yes
Hypothetical ABC transporter ATP-binding protein	JZ6_10	TZ19_10	OK	156.8	40.5471	0	0	yes
putative hemolysin	JZ6_10	TZ19_10	OK	148.632	38.3938	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	832.402	213.886	2.22E-16	1.15E-15	yes
RNA polymerase associated protein rapA	JZ6_10	TZ19_10	OK	197.983	50.7266	0	0	yes
transcriptional regulator, LuxR family	JZ6_10	TZ19_10	OK	299.768	76.7928	3.52E-12	1.45E-11	yes
putative permease perM	JZ6_10	TZ19_10	OK	71.5544	18.2418	2.10E-06	5.51E-06	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	414.682	104.455	7.51E-07	2.06E-06	yes
hypothetical protein	JZ6_10	TZ19_10	OK	109.99	27.6095	2.12E-11	8.32E-11	yes
putative Holliday junction resolvase	JZ6_10	TZ19_10	OK	648.155	162.651	3.18E-14	1.47E-13	yes
hypothetical protein	JZ6_10	TZ19_10	OK	79.8809	19.8479	2.18E-07	6.28E-07	yes
Glutamine amidotransferases class-II	JZ6_10	TZ19_10	OK	231.376	57.3442	1.02E-12	4.31E-12	yes
Arabinose 5-phosphate isomerase	JZ6_10	TZ19_10	OK	114.937	28.3082	9.63E-10	3.35E-09	yes
3-deoxy-D-manno-octulosonate 8-phosphate phosphatase	JZ6_10	TZ19_10	OK	604.594	148.442	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	47.3092	11.4423	5.44E-13	2.34E-12	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	6351.87	1524.7	2.35E-10	8.59E-10	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	893.647	212.83	2.22E-16	1.15E-15	yes
Phosphoadenosine phosphosulfate reductase	JZ6_10	TZ19_10	OK	109.946	26.1248	1.76E-06	4.66E-06	yes
Probable GTP-binding protein	JZ6_10	TZ19_10	OK	666.949	158.4	0	0	yes
hypothetical arginine repressor	JZ6_10	TZ19_10	OK	594.904	140.548	0	0	yes
ABC transporter: substrate binding protein precursor	JZ6_10	TZ19_10	OK	151.885	35.8751	2.22E-16	1.15E-15	yes
DNA polymerase III subunit tau	JZ6_10	TZ19_10	OK	193.909	45.4014	0	0	yes

ABC transporter: Transmembrane protein	JZ6_10	TZ19_10	OK	139.94	32.536	5.04E-13	2.18E-12	yes
Acyl-coenzyme A dehydrogenase	JZ6_10	TZ19_10	OK	71.039	16.4215	2.22E-16	1.15E-15	yes
hypothetical protein	JZ6_10	TZ19_10	OK	363.175	83.6518	4.92E-08	1.50E-07	yes
tRNA pseudouridine synthase C	JZ6_10	TZ19_10	OK	107.307	24.7148	1.46E-06	3.89E-06	yes
Cation/multidrug efflux pump	JZ6_10	TZ19_10	OK	73.3043	16.8718	0	0	yes
Molybdenum cofactor biosynthesis protein E	JZ6_10	TZ19_10	OK	394.252	90.1725	1.60E-10	5.92E-10	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	229.313	52.4126	1.35E-13	6.01E-13	yes
NADH dehydrogenase subunit II-related protein	JZ6_10	TZ19_10	OK	41246.1	9425.57	0	0	yes
O-succinylbenzoate synthase	JZ6_10	TZ19_10	OK	107.59	24.5508	4.04E-08	1.24E-07	yes
Protein cyaY	JZ6_10	TZ19_10	OK	15017.7	3390.11	0	0	yes
Riboflavin synthase alpha chain	JZ6_10	TZ19_10	OK	197.004	43.9731	1.69E-08	5.38E-08	yes
hypothetical protein	JZ6_10	TZ19_10	OK	191.404	42.2606	8.75E-13	3.73E-12	yes
Protoheme IX farnesyltransferase	JZ6_10	TZ19_10	OK	88.6007	19.3094	2.72E-07	7.75E-07	yes
AcrB/AcrD/AcrF family	JZ6_10	TZ19_10	OK	35.8746	7.78481	1.16E-10	4.33E-10	yes
Cell division protein ftsW	JZ6_10	TZ19_10	OK	65.5057	13.99	4.53E-07	1.27E-06	yes
UDP-3-O-	JZ6_10	TZ19_10	OK	665.557	138.966	0	0	yes
quinolone resistance determinant (experimentally demonstrated)	JZ6_10	TZ19_10	OK	183.469	38.1859	9.75E-09	3.16E-08	yes
Cell division protein ftsY	JZ6_10	TZ19_10	OK	817.819	169.845	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	72.8111	15.0278	1.81E-11	7.12E-11	yes
Collagenase and related protease	JZ6_10	TZ19_10	OK	60.1132	12.2435	1.89E-12	7.92E-12	yes
Flp pilus assembly protein	JZ6_10	TZ19_10	OK	154.652	31.4032	0	0	yes
Signal transduction histidine kinase	JZ6_10	TZ19_10	OK	30.0595	6.10091	1.47E-08	4.68E-08	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1174.01	237.782	0	0	yes
sodium/dicarboxylate symporter	JZ6_10	TZ19_10	OK	115.309	23.2777	1.15E-14	5.47E-14	yes
Ferrochelatase (Protoheme ferro-lyase)	JZ6_10	TZ19_10	OK	172.825	33.8775	1.11E-15	5.56E-15	yes
putative membrane protein	JZ6_10	TZ19_10	OK	62.4287	12.2205	7.65E-07	2.10E-06	yes
Diaminobutyrate--2-oxoglutarate aminotransferase	JZ6_10	TZ19_10	OK	49.5599	9.57785	2.20E-14	1.03E-13	yes
DNA recombination protein rmuC homolog	JZ6_10	TZ19_10	OK	93.3021	17.8179	1.52E-13	6.72E-13	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	69.0543	13.0924	0	0	yes
5-carboxymethyl-2-hydroxymuconate isomerase	JZ6_10	TZ19_10	OK	1092.79	205.944	8.12E-13	3.46E-12	yes
hypothetical protein	JZ6_10	TZ19_10	OK	4456.43	839.266	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	370.042	69.1124	0	0	yes

Riboflavin biosynthesis protein ribD	JZ6_10	TZ19_10	OK	94.0702	17.5422	5.48E-10	1.94E-09	yes
Electron transport complex protein rnfE	JZ6_10	TZ19_10	OK	227.518	42.252	7.96E-11	3.00E-10	yes
Protein mazG homolog	JZ6_10	TZ19_10	OK	921.818	167.527	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	6295.7	1128.82	5.34E-10	1.89E-09	yes
Periplasmic protein involved in polysaccharide export	JZ6_10	TZ19_10	OK	69.5887	12.4552	4.17E-14	1.91E-13	yes
ABC transporter: Membrane fusion protein	JZ6_10	TZ19_10	OK	144.171	25.6206	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	867.567	153.774	1.35E-06	3.62E-06	yes
Nitroreductase family protein	JZ6_10	TZ19_10	OK	216.006	38.281	4.37E-12	1.79E-11	yes
Extracellular solute-binding protein, family 7	JZ6_10	TZ19_10	OK	257.664	45.6275	0	0	yes
Malate synthase G	JZ6_10	TZ19_10	OK	118.485	20.9104	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	4565.85	802.149	0	0	yes
Glycogen synthase	JZ6_10	TZ19_10	OK	171.205	29.9372	0	0	yes
1-acyl-sn-glycerol-3-phosphate acyltransferase	JZ6_10	TZ19_10	OK	437.353	75.8291	0	0	yes
ABC transporter: Substrate binding protein precursor	JZ6_10	TZ19_10	OK	91.3874	15.7751	3.75E-12	1.54E-11	yes
Hypothetical ABC transporter ATP-binding protein	JZ6_10	TZ19_10	OK	124.364	21.39	3.78E-09	1.26E-08	yes
Predicted flavodoxin oxidoreductases	JZ6_10	TZ19_10	OK	577.138	99.0939	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	722.393	123.69	3.83E-08	1.18E-07	yes
Membrane protein	JZ6_10	TZ19_10	OK	138.973	23.5845	1.77E-13	7.83E-13	yes
Glutathione-regulated potassium-efflux system protein kefC (K(+)/H(+)antiporter)	JZ6_10	TZ19_10	OK	162.129	27.353	0	0	yes
Glycerophosphoryl diester phosphodiesterase	JZ6_10	TZ19_10	OK	100.394	16.8588	9.06E-07	2.47E-06	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	330.262	55.4475	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1254.65	210.34	3.00E-06	7.73E-06	yes
CreA protein	JZ6_10	TZ19_10	OK	812.393	135.676	0	0	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	345.125	57.1706	0	0	yes
Membrane-fusion protein AcrA	JZ6_10	TZ19_10	OK	78.5131	12.9229	2.88E-08	8.97E-08	yes
ABC transporter: Substrate binding protein precursor	JZ6_10	TZ19_10	OK	460.395	75.3839	0	0	yes
3-deoxy-manno-octulosonate cytidylyltransferase	JZ6_10	TZ19_10	OK	108.628	17.5477	3.60E-07	1.02E-06	yes
hypothetical protein	JZ6_10	TZ19_10	OK	989.936	159.866	2.22E-16	1.15E-15	yes
LuxO repressor protein	JZ6_10	TZ19_10	OK	143.505	23.1239	0	0	yes
DctQ, TRAP-type C4-dicarboxylate transport system, large permease component	JZ6_10	TZ19_10	OK	69.0494	10.9206	2.30E-09	7.77E-09	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	2695.55	424.261	0	0	yes
Lipid A biosynthesis lauroyl acyltransferase	JZ6_10	TZ19_10	OK	180.719	28.4258	4.44E-16	2.26E-15	yes

Transcriptional regulatory protein tyrR	JZ6_10	TZ19_10	OK	111.998	17.6028	3.33E-15	1.62E-14	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	30203.1	4739.18	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	557.233	87.0333	3.02E-12	1.25E-11	yes
hypothetical protein	JZ6_10	TZ19_10	OK	62.9414	9.82752	2.41E-07	6.93E-07	yes
Autoinducer 2-binding periplasmic protein luxP precursor	JZ6_10	TZ19_10	OK	63.0129	9.67216	6.51E-07	1.80E-06	yes
ABC transporter, permease protein	JZ6_10	TZ19_10	OK	188.82	28.378	3.35E-11	1.30E-10	yes
UDP-N-acetylmuramoylalanine--D-glutamate ligase	JZ6_10	TZ19_10	OK	174.616	25.9835	0	0	yes
putative two-component sensor	JZ6_10	TZ19_10	OK	226.494	33.6627	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	67.1794	9.84403	1.01E-11	4.03E-11	yes
putative LuxO repressor protein	JZ6_10	TZ19_10	OK	146.557	20.6578	0	0	yes
Cytochrome c-type biogenesis protein ccmB (heme exporter protein B)	JZ6_10	TZ19_10	OK	197.023	27.727	1.30E-10	4.82E-10	yes
putative GTP cyclohydrolase II	JZ6_10	TZ19_10	OK	438.15	61.2868	0	0	yes
Acetolactate synthase isozyme III small subunit	JZ6_10	TZ19_10	OK	529.029	73.8605	1.11E-15	5.56E-15	yes
Tryptophanase (L-tryptophan indole-lyase)	JZ6_10	TZ19_10	OK	354.204	49.0342	0	0	yes
putative periplasmic protein	JZ6_10	TZ19_10	OK	1433.04	198.177	0	0	yes
Hypothetical competence damage protein CinA	JZ6_10	TZ19_10	OK	164.674	22.6364	0	0	yes
Nuclease sbcCD subunit C	JZ6_10	TZ19_10	OK	26.5802	3.62164	3.04E-11	1.18E-10	yes
putative Cys/Met metabolism pyridoxal-phosphate-dependent enzyme	JZ6_10	TZ19_10	OK	671.967	91.3247	0	0	yes
putative muconate cycloisomerase	JZ6_10	TZ19_10	OK	141.453	19.1408	9.55E-14	4.28E-13	yes
Hypothetical ABC transporter ATP-binding protein	JZ6_10	TZ19_10	OK	39.6166	5.30083	2.84E-07	8.09E-07	yes
Lysine-arginine-ornithine-binding periplasmic protein	JZ6_10	TZ19_10	OK	106.503	14.2029	2.71E-07	7.75E-07	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1963.55	259.431	6.44E-15	3.09E-14	yes
hypothetical protein	JZ6_10	TZ19_10	OK	727.274	95.7562	0	0	yes
Oxygen-independent coproporphyrinogen III oxidase-like protein	JZ6_10	TZ19_10	OK	86.21	11.3097	9.17E-12	3.69E-11	yes
Osmotically inducible protein C	JZ6_10	TZ19_10	OK	206.53	27.0113	1.28E-06	3.44E-06	yes
putative alkaline phosphatase	JZ6_10	TZ19_10	OK	736.695	94.6132	0	0	yes
TPR-repeat-containing protein	JZ6_10	TZ19_10	OK	116.446	14.7697	2.00E-09	6.79E-09	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	273.799	34.526	2.89E-14	1.34E-13	yes
putative RNA-binding proteins	JZ6_10	TZ19_10	OK	8737.27	1081.52	0	0	yes
Predicted periplasmic solute-binding protein	JZ6_10	TZ19_10	OK	120.433	14.9074	1.35E-11	5.39E-11	yes
putative secretion protein	JZ6_10	TZ19_10	OK	80.6554	9.97066	1.65E-09	5.63E-09	yes
Transmembrane regulatory protein toxS	JZ6_10	TZ19_10	OK	358.616	43.9677	1.70E-12	7.12E-12	yes

ABC transporter: Membrane fusion protein	JZ6_10	TZ19_10	OK	139.711	17.093	2.40E-14	1.12E-13	yes
hypothetical protein	JZ6_10	TZ19_10	OK	10798.2	1295.75	8.88E-16	4.47E-15	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	234.11	28.0078	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	1383.08	164.525	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	514.808	60.6812	0	0	yes
Peptide methionine sulfoxide reductase msrB	JZ6_10	TZ19_10	OK	3993.64	469.548	0	0	yes
putative membrane protein	JZ6_10	TZ19_10	OK	58.896	6.69755	1.29E-09	4.44E-09	yes
Hypothetical response regulatory protein	JZ6_10	TZ19_10	OK	289.209	32.2133	0	0	yes
Lipase precursor	JZ6_10	TZ19_10	OK	73.3608	8.05794	1.26E-06	3.39E-06	yes
putative permease	JZ6_10	TZ19_10	OK	94.9159	10.4152	1.63E-10	6.03E-10	yes
putative smp protein	JZ6_10	TZ19_10	OK	106.993	11.6878	3.41E-06	8.73E-06	yes
ABC transporter: Transmembrane protein	JZ6_10	TZ19_10	OK	131.833	14.3481	1.08E-12	4.57E-12	yes
Transcriptional regulator, AraC family	JZ6_10	TZ19_10	OK	99.8424	10.6753	5.03E-08	1.54E-07	yes
ABC transporter (IM-ABC)	JZ6_10	TZ19_10	OK	26.697	2.8468	9.98E-07	2.70E-06	yes
conserved protein	JZ6_10	TZ19_10	OK	344.161	36.6498	8.95E-14	4.02E-13	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	2877.6	304.791	0	0	yes
RNA polymerase sigma factor, sigma-70 family	JZ6_10	TZ19_10	OK	199.106	20.9888	1.32E-10	4.90E-10	yes
Penicillin-insensitive murein endopeptidase precursor	JZ6_10	TZ19_10	OK	83.8356	8.79193	7.92E-07	2.17E-06	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	181.639	18.7871	5.55E-15	2.68E-14	yes
MSHA biogenesis protein MshL	JZ6_10	TZ19_10	OK	86.5548	8.80702	6.31E-14	2.86E-13	yes
hypothetical membrane protein	JZ6_10	TZ19_10	OK	45.1535	4.58483	5.43E-07	1.51E-06	yes
Succinate dehydrogenase hydrophobic membrane anchor protein	JZ6_10	TZ19_10	OK	599.571	60.2822	3.52E-10	1.27E-09	yes
hypothetical protein	JZ6_10	TZ19_10	OK	278.535	28.0018	1.37E-06	3.68E-06	yes
putative transcriptional regulator	JZ6_10	TZ19_10	OK	282.097	28.1288	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	32.377	3.22517	4.75E-07	1.33E-06	yes
hypothetical protein	JZ6_10	TZ19_10	OK	977.069	96.9659	0	0	yes
putative biofilm-associated surface protein	JZ6_10	TZ19_10	OK	46.2166	4.48258	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	3471.12	334.594	0	0	yes
Lipase chaperone	JZ6_10	TZ19_10	OK	92.2027	8.84725	8.60E-08	2.57E-07	yes
RpoS-like sigma factor	JZ6_10	TZ19_10	OK	728.066	67.8966	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	453.287	41.8736	9.15E-14	4.11E-13	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	1143.66	105.512	0	0	yes

Transglycosylase, Slt family	JZ6_10	TZ19_10	OK	286.314	25.9171	0	0	yes
Flp pilus assembly protein	JZ6_10	TZ19_10	OK	189.81	17.0638	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	75.6618	6.64645	2.67E-06	6.91E-06	yes
Acyl-coenzyme A synthetases	JZ6_10	TZ19_10	OK	274.148	23.8115	0	0	yes
Ribonuclease HI	JZ6_10	TZ19_10	OK	190.361	16.3647	1.60E-11	6.32E-11	yes
hypothetical protein	JZ6_10	TZ19_10	OK	237.441	20.347	6.23E-09	2.05E-08	yes
ABC transport system, Transmembrane and ATP-binding site (ABC-IM)	JZ6_10	TZ19_10	OK	48.9982	4.04581	1.03E-09	3.59E-09	yes
putative cytochrome c, class I	JZ6_10	TZ19_10	OK	54.6764	4.47899	1.04E-08	3.35E-08	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	243.034	19.7548	3.57E-06	9.12E-06	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	4278.66	342.257	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	2670.02	211.476	0	0	yes
ABC transporter: Membrane fusion protein (MFP)	JZ6_10	TZ19_10	OK	68.3034	5.31042	4.09E-09	1.36E-08	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1725.52	133.172	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1715.25	131.305	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	14713.1	1100.79	0	0	yes
ABC transporter: Transmembrane and ATP-binding protein	JZ6_10	TZ19_10	OK	136.434	9.32064	0	0	yes
putative LysR-type regulator	JZ6_10	TZ19_10	OK	86.7438	5.90496	6.04E-07	1.67E-06	yes
hypothetical protein	JZ6_10	TZ19_10	OK	380.532	25.7315	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	138.586	9.24439	1.59E-09	5.45E-09	yes
hypothetical protein	JZ6_10	TZ19_10	OK	234.863	15.4031	2.40E-08	7.54E-08	yes
ABC transporter: transmembrane protein	JZ6_10	TZ19_10	OK	64.1633	4.2032	2.76E-10	1.00E-09	yes
hypothetical protein; putative exported protein	JZ6_10	TZ19_10	OK	1241.53	78.8393	1.59E-06	4.23E-06	yes
putative deoxycytidylate deaminase	JZ6_10	TZ19_10	OK	5561.38	352.269	0	0	yes
Transcriptional regulator	JZ6_10	TZ19_10	OK	313.956	19.3382	1.07E-14	5.06E-14	yes
Multi antimicrobial extrusion protein MatE	JZ6_10	TZ19_10	OK	65.321	3.98626	1.95E-09	6.63E-09	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	79849.2	4845.6	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	6967.27	419.098	0	0	yes
putative sensor protein	JZ6_10	TZ19_10	OK	103.528	6.12771	8.33E-14	3.75E-13	yes
hypothetical protein	JZ6_10	TZ19_10	OK	131.543	7.77519	1.31E-07	3.85E-07	yes
AcrR, Transcriptional regulator	JZ6_10	TZ19_10	OK	597.618	35.1261	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	154.161	8.7332	0	0	yes
NOL1/NOP2/sun family protein	JZ6_10	TZ19_10	OK	172.009	9.70975	0	0	yes

Glyoxalase family protein	JZ6_10	TZ19_10	OK	223.756	12.367	3.49E-07	9.86E-07	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	51.0579	2.74326	1.01E-08	3.26E-08	yes
putative Glycosyl transferase	JZ6_10	TZ19_10	OK	355.131	18.7712	0	0	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	377.671	19.8161	4.77E-11	1.82E-10	yes
Hypothetical UPF0105 protein yfcH	JZ6_10	TZ19_10	OK	276.004	14.3451	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	1952.82	98.459	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	180.372	9.0261	6.36E-10	2.24E-09	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	393.804	19.5894	0	0	yes
Protein nrfD	JZ6_10	TZ19_10	OK	816.907	38.6441	0	0	yes
Aconitase A	JZ6_10	TZ19_10	OK	43.1637	2.03286	4.11E-11	1.58E-10	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	125.84	5.81356	3.06E-11	1.19E-10	yes
putative periplasmic protein	JZ6_10	TZ19_10	OK	79.6162	3.62439	3.44E-07	9.71E-07	yes
putative cold shock protein	JZ6_10	TZ19_10	OK	15978.2	722.279	0	0	yes
ABC transporter: Transmembrane and ATP-binding protein	JZ6_10	TZ19_10	OK	316.893	13.7617	0	0	yes
KtrA	JZ6_10	TZ19_10	OK	152.466	6.59835	1.48E-06	3.94E-06	yes
Polyphosphate kinase	JZ6_10	TZ19_10	OK	91.9833	3.80229	2.22E-16	1.15E-15	yes
hypothetical protein	JZ6_10	TZ19_10	OK	214.169	8.65593	0	0	yes
Membrane-associated phospholipid phosphatase	JZ6_10	TZ19_10	OK	122.402	4.72198	1.46E-12	6.14E-12	yes
Conserved hypothetical protein; putative GTP binding protein	JZ6_10	TZ19_10	OK	62.7996	2.4189	7.34E-09	2.40E-08	yes
hypothetical protein	JZ6_10	TZ19_10	OK	8489.92	326.007	0	0	yes
Zn-dependent protease	JZ6_10	TZ19_10	OK	142.575	4.91568	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	29.1137	0.95007	1.43E-07	4.20E-07	yes
transcriptional regulator, TetR family	JZ6_10	TZ19_10	OK	308.379	9.9505	7.77E-13	3.32E-12	yes
putative Cytochrome c biogenesis factor	JZ6_10	TZ19_10	OK	352.818	11.0608	5.18E-13	2.23E-12	yes
RecA regulator RecX	JZ6_10	TZ19_10	OK	169.149	5.09073	5.43E-09	1.79E-08	yes
hypothetical protein	JZ6_10	TZ19_10	OK	765.519	22.9592	0	0	yes
ABC transporter: Transmembrane protein	JZ6_10	TZ19_10	OK	52.2864	1.56546	3.19E-12	1.32E-11	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	371.66	10.6626	4.32E-08	1.33E-07	yes
putative transporter	JZ6_10	TZ19_10	OK	94.7966	2.64168	4.62E-07	1.29E-06	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	653.134	17.6818	0	0	yes
RIO1 family protein	JZ6_10	TZ19_10	OK	182.921	4.73325	1.06E-09	3.68E-09	yes
Conserved hypothetical receptor	JZ6_10	TZ19_10	OK	206.546	5.17063	0	0	yes

Flp pilus assembly protein CpaB	JZ6_10	TZ19_10	OK	195.647	4.28769	3.25E-09	1.09E-08	yes
Transcriptional regulators, LysR family	JZ6_10	TZ19_10	OK	137.914	2.53737	4.22E-07	1.18E-06	yes
Chitinase	JZ6_10	TZ19_10	OK	49.124	0.82736	7.45E-09	2.43E-08	yes
predicted ATPase with chaperone activity	JZ6_10	TZ19_10	OK	437.38	6.79591	0	0	yes
hypothetical protein	JZ6_10	TZ19_10	OK	175.335	2.52305	3.23E-06	8.29E-06	yes
Formamidopyrimidine-DNA glycosylase	JZ6_10	TZ19_10	OK	318.808	4.14978	1.54E-11	6.10E-11	yes
Extracellular zinc metalloprotease	JZ6_10	TZ19_10	OK	2521.28	31.8837	0	0	yes
Transcriptional regulator, LysR family	JZ6_10	TZ19_10	OK	261.829	3.30519	5.47E-10	1.94E-09	yes
Response regulator	JZ6_10	TZ19_10	OK	235.736	2.78394	5.10E-12	2.08E-11	yes
conserved hypothetical protein	JZ6_10	TZ19_10	OK	29173.3	307.291	0	0	yes
Conserved hypothetical protein	JZ6_10	TZ19_10	OK	209.483	2.03379	4.54E-11	1.74E-10	yes
hypothetical protein	JZ6_10	TZ19_10	OK	118.987	1.09512	2.42E-07	6.95E-07	yes
putative regulatory protein	JZ6_10	TZ19_10	OK	877.894	7.93025	2.22E-07	6.40E-07	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	3772.68	29.1846	6.14E-10	2.17E-09	yes
Hypothetical protein containg GGDEF domain	JZ6_10	TZ19_10	OK	329.016	2.34301	3.10E-10	1.12E-09	yes
Transcriptional regulator	JZ6_10	TZ19_10	OK	196.838	1.12526	3.31E-06	8.50E-06	yes
ABC-type sugar transport system, periplasmic component	JZ6_10	TZ19_10	OK	557.635	2.72008	0	0	yes
Hypothetical protein	JZ6_10	TZ19_10	OK	27120.8	28.7404	0	0	yes